

FACTORS PATOGÈNICS
CONVERGENTS EN TAUPATIES

TESI DOCTORAL
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Al meu avi Josep

Als meus pares, la meva germana i l'abuelita

A la Bego

Als meus avis Gabriel i Maribel,
i al meu tiet Josep M^a

L'oblit és desmemòria, desarrel, despreocupació, formes que semblen les d'una absència o buit. Però val pensar-ho d'una altra manera: l'oblit allibera el present de tot allò que li és aliè. Brinda un present que ens repta a comprovar què som capaços de fer amb ell. I amb tot, a vegades es precisa l'oblit d'un mateix: no prendre's massa seriosament, alleujar-se de la càrrega de ser un mateix i deixar de ser-ne esclau. Permetre la irrupció d'allò que no havíem ni sospitat.

Mariela Saez, sobre la
Farmacia del Olvido, de Rogelio Moreno

AGRAÏMENTS

Durant quatre anys de tesi se m'han acumulat una gran quantitat de coses a agrair i una gran quantitat de persones a qui fer-ho. Aquesta pàgina no donarà per tant.

A l'Isidre. Gràcies per obrir-me la porta i deixar-me entrar. I, per una vegada dins, guiar-me, orientar-me, aconsellar-me i confiar en mi. També per escoltar-me i donar-me un camí en tots els moments que ho he necessitat de debò. Ah! I per recomanar-me bons llibres.

A la Berta. Per ensenyar-me incontables coses. Per convertir-te en una amiga des del primer dia. Perquè cada discussió que semblava que ens anàvem a matar acabava amb rialles (no sempre immediatament) i sobretot, amb idees noves sobre com fer o no fer un experiment. Espero poder continuar discutint amb tu molt de temps.

A la gent del laboratori, estimada família nombrosa. L'Ester Pérez, l'Anna Martínez, la Sandra, el Gerard (que caminem junts des de fa tants anys), l'Agustí, la Marga i la Rossi (que amb tot l'amor del món sempre han estat allà per recordar-me la diferència entre el caliu i el desordre), l'Anna Gómez, la Janu, l'Ester Dalfó, la Marta Barrachina (qui, juntament amb la Sandra m'ha ensenyat pacientment moltes coses que necessiten paciència, com cuidar cèl·lules obsessionades en fer castells). La Laia, hereva de la tau i amb qui m'agradaria haver treballat més temps. També la Judith, el Guido, la Loli, la Meri, la Laura, la Maria, el Salva i el Jesús, la Beatrice, la Marta Martínez, l'Ester Aso, la Gemma i l'Anton.

A la gent del 4145. La Mireia, el Joan, el Jonathan, la Imma, la Laura, la Xènia, el Marc, l'Àlex, la Laia, l'Artur i l'Adriana. I no únicament per tot l'ajuda que m'han prestat en la infinitat de problemes amb què he irrumpit al seu laboratori tot hiperventil·lant i atabalat (centrífugues que fan coses rares, gradients de sacarosa, cèl·lules i una llarg etcètera).

Als meus amics, i en especial al Guillem i en Joan, amb qui he compartit en profunditat molts dels problemes que han anat sorgint durant aquest quatre anys. He dit quatre anys? Volia dir vint-i-cinc.

A la Bego, que m'ha escoltat i tranquil·litzat com un bàlsam durant les meves incursions al món de la neurosi. Gràcies per això i per moltíssim més.

Als meus pares, Gabriel i Mercè, i a la meva germana Elisabet, per escoltar amb una cella aixecada, però escoltar al cap i a la fi, les particularitats de la proteïna tau i per recolzar-me des de sempre.

Als meus avis. La Mari Carmen, cada diumenge preguntat-me "Cómo va la tesis?" "Ya casi está abuelita, ya casi". M'ha esperonat positivament més del què es pensa. I al meu avi Josep. Si hagués de demanar un desig ara mateix, no seria altre que pogués estar el dia de la lectura i sentir-se feliç com sé que ho faria. I també comprendre la importància que ha tingut per mi la seva presència des de sempre, en veure que li dedico aquesta tesi. La malaltia d'Alzheimer també ens ha jugat a nosaltres una mala passada.

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ABREVIATURES

MA: Malaltia d'Alzheimer
PSP: Paràlisi supranuclear progressiva
DCB: Degeneració cortico-basal
MP: Malaltia de Parkinson
DFTP-17: Demència frontotemporal amb parquinsonisme lligada al cromosoma 17
MPI: Malaltia de Pick
MGA: Malaltia dels grans argiròfils
DCL: Demència amb cossos de Lewy
MAP: Microtubule associated protein (proteïna associada a microtúbuls)
APP: Proteïna precursora del pèptid amiloide
AAC: Angiopatia amiloidea cerebral
PSEN1 i PSEN 2: Presinilina 1 i 2
NGF: Nerve growth factor (factor de creixement neuronal)
EGF: Epidermal growth factor (factor de creixement de l'epidermis)
LTP: Long term potential (Potenciació a llarg termini)
LDL: Low density lipoprotein (lipoproteïna de baixa densitat)
ROS: Radical oxygen species (radicals lliures d'oxigen)
PET: Positron emission tomography (tomografia per emissió de positrons)
DFT: Demència fronto-temporal
CA: Cornu Ammonis
UHL-1: Ubiquitin carboxi-terminal hydrolase L1 (hidrolasa carboxi-terminal de la ubiquitina)
PINK-1: PTEN-induced putative kinase (cinasa putativa induïda per PTEN)
LRRK2: Leucine rich repeat kinase (cinasa amb repeticions riques en leucina)
PHF: Paired helical filaments (filaments aparellats hel·licoidalment)
GSK3-beta: Glycogen sintase kinase (cinasa de la glicogen sintasa)
Cdk5: Cyclin dependent kinase (cinasa dependent de ciclina)
PKA: Protein kinase A (cinasa de proteïna A)
CaMKII: Calcium/Calmodulin-dependent protein kinase (cinasa dependent de calci/calmodulina)
ERK: Extracellular signal-regulated kinase (cinase regulada per senyals extracel·lulars)
SAPK/JNK: Stress-activated protein kinase/c-Jun NH2-terminal kinase (cinasa de proteïna activada per estrès/ cinasa de l'amino-terminal de c-Jun)
PP: Protein phosphatase (fosfatasa de proteïna)
NFT: Neurofibrillary tangles (cabdells neurofibril·lars)
ATF-2: Activating transcription factor (factor de transcripció d'activació)
AP-1: Activating protein (proteïna d'activació)
CREB : cAMP response element binding protein (proteïna d'unió a l'element de resposta a AMPc)
CBP: CREB binding protein (proteïna d'unió a CREB)
MAPK: Mitogen-activated protein kinase (cinasa de proteïna activada per mitògen)
AEC: Atàxia espino-cerebel·losa
TGF: Transforming growth factor (factor de creixement transformant)
SOD: Superòxid dismutasa
HSP: Heat shock protein (proteïna de xoc tèrmic)
UBB: ubiquitina
CEL: Carboxi-etil-lisina
HNE: 4-hidroxinonenal
MDAL: Malondialdehid-lisina
CML: Carboxi-metil-lisina

PUFA: Polyunsaturated fatty acid (àcid gras poli insaturat)
AGE: Advanced glycation end product (producte final de glicació avançada)
RAGE: Receptor d'AGEs
8OHG: 8-hidroxiguanosina
DIGE: Differential in gel electrophoresis (diferencial en electroforesis de gel)
NGFR: Nerve growth factor receptor (receptor del factor de creixement neuronal)
IL-1: Interleucina 1
MCI: Mild cognitive impairment (dèficit cognitiu lleu)
GFAP: Glial fibrillary acidic protein (proteïna fibril·lar àcida de la glia)
TNF: Tumor necrosis factor (factor de necrosi tumoral)

Introducció

1- LES MALALTIES NEURODEGENERATIVES

Demència

La demència senil és una síndrome que té com a principal factor de risc l'edat. Que el principal factor de risc sigui l'edat no vol dir que aquesta sigui la causa de la demència. Fins els anys 70, es considerava la demència com una conseqüència dels problemes associats a la senilitat, i els efectes d'aquesta senilitat eren prou amplis com per respondre a qualsevol problema que patís algú de més de 60 anys. La demència es defineix com la pèrdua o davallada de facultats cognitives sempre i quan aquestes afectin a diferents dominis de la cognició; si la pèrdua afecta una funció cognitiva concreta es considera un desordre específic. A més, normalment el terme demència s'aplica quan la pèrdua cognitiva afecta significativament la capacitat d'independència de l'individu. Aquesta síndrome sovint s'expressa amb pèrdua de memòria, dificultats en el llenguatge, problemes de visió de l'espai, problemes de raonament i alteracions de l'estat d'ànim i de la personalitat. La senilitat no comporta automàticament la demència, però si que comporta un cert grau de dèficit cognitiu. Aquest dèficit no està en relació amb pèrdua del volum cerebral, com sovint ocorre amb la demència, sino que es tracta de canvis com per exemple una pèrdua gradual de memòria, un augment de l'estabilitat emocional o una pèrdua d'assimetria hemisfèrica.

Fa dècades que sabem que la demència, tal com l'hem definit, és causada per malalties neurològiques. I en la majoria dels casos, per malalties neurodegeneratives com la malaltia d'Alzheimer.

Malalties neurodegeneratives

Les malalties neurodegeneratives són malalties molt complexes que poden involucrar diferents susceptibilitats genètiques o factors ambientals. En general presenten pèrdua neuronal, estrés oxidatiu i la presència d'unes inclusions anòmales de naturalesa proteica tant intracel·lulars (més freqüentment) com extracel·lulars (és el cas del pèptid amiloide) en el cervell. Les malalties neurodegeneratives més importants es poden classificar en funció de la proteïna majoritària dins d'aquestes inclusions: taupaties i

sinucleïnopaties. Les primeres presenten agregats de proteïna tau i les segones presenten agregats d'alfa-sinucleïna.

1.1 Taupaties

Les taupaties es caracteritzen per presentar acúmuls intracel·lulars (en neurones i cèl·lules glials) de proteïna tau anormalment hiperfosforil·lada. Aquests agregats poden ser de diferents tipus i es poden trobar en regions diferents del cervell depenent de la taupatia. En el grup de les taupaties trobem: la malaltia d'Alzheimer (MA), la paràlisi supranuclear progressiva (PSP), la malaltia de Pick (MPi), la malaltia dels grans argiròfils (MGA), la degeneració cortico-basal (DCB) i un conjunt de malalties causades per diferents mutacions al gen de la tau anomenades demències frontotemporals amb parkinsonisme lligades al cromosoma 17 (FTDP-17-TAU).

1.1.1 Malaltia d'Alzheimer

La malaltia d'Alzheimer és la causa més freqüent de demència. La prevalència, amb dades d'Europa i Nord-Amèrica, entre la població de 65 a 69 anys és d'1 de cada 100 individus. Aquesta prevalència es dobla cada 5 anys per sobre de 69, fins arribar a ser d'entre un 20% i un 50% al voltant dels 85 anys (Hy and Keller, 2000). Clínicament comporta un seguit de dèficits cognitius que inclouen una pèrdua de memòria a curt termini, de capacitat d'orientació, dificultats del llenguatge, pèrdua d'atenció i funció visuo-espacial, així com de capacitat intel·lectual per resoldre problemes, fer judicis i l'agilitat mental en el raonament (Green et al., 1990, Welsh et al., 1991).

Macroscòpicament la MA presenta atròfia cerebral que afecta principalment al lòbul temporal. Això inclou estructures com l'escorça entorrinal, l'hipocamp i l'amígdala (Najlerahim and Bowen, 1988). Microscòpicament la MA presenta mort neuronal i pèrdua de sinapsis entre les neurones supervivents. La pèrdua neuronal és progressiva i afecta predominantment a l'escorça entorrinal, temporal i parietal, l'hipocamp, amígdala, nucli basal de Meynert, locus ceruleus i nuclis del rafe (Whitehouse et al., 1981, Whitehouse et al., 1982, Kremer et al., 1991). La pèrdua de sinapsis es tradueix en una reducció d'espines dendrítiques i dendrites a les neurones piramidals de l'escorça i de l'hipocamp. A més també

s'ha descrit una reducció de l'expressió de proteïnes sinàptiques en aquestes regions (Clinton et al., 1994).

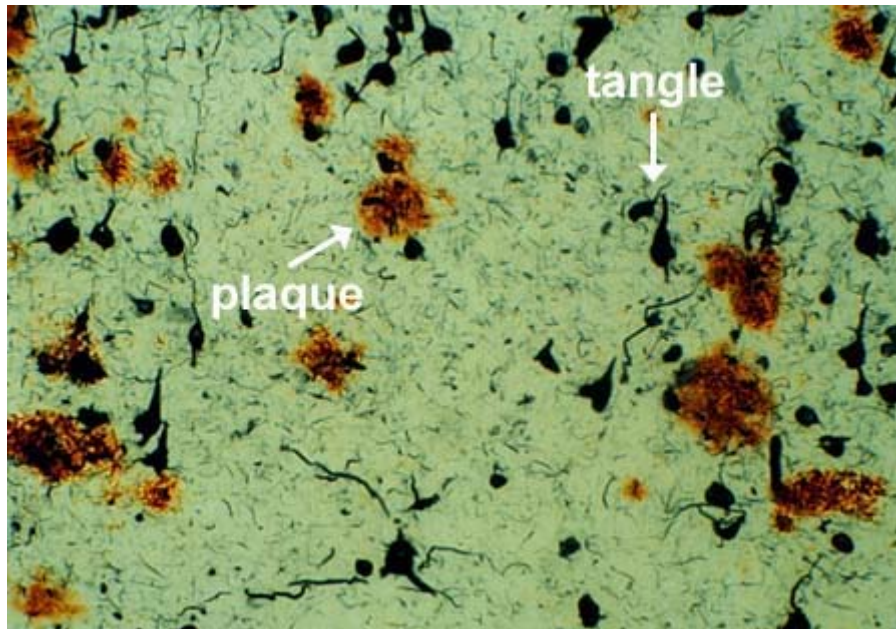
TAUPATIA	CLÍNICA	ZONES PRINCIPALMENT AFECTADES	TIPUS D'INCLUSIONS
<i>Malaltia d'Alzheimer</i>	Dèficit cognitiu amb pèrdua de memòria, d'orientació, atenció, llenguatge, funció visual-espacial i disminució de la capacitat intel·lectual. Canvis de la personalitat.	Còrtex entorrinal, hipocamp, amígdala i progressió cap a la major part del còrtex.	Cabdells neurofibril·lars Neurites distròfiques amb filaments de tau Plaques senils
<i>Paràlisi Supranuclear Progressiva</i>	Parquinsonisme, inestabilitat postural, oftalmoplègia supranuclear (dificultat dels pacients per moure els ulls) i demència.	Algunes zones dels ganglis basals, el cerebel i el còrtex cerebral.	Cabdells neurofibril·lars Neurites distròfiques amb filaments de tau Filaments de tau a astròcits
<i>Malaltia dels Grans Argiròfils (o argirofílics)</i>	Canvis de personalitat, agressivitat, conducta social inapropiada, dèficit cognitiu i demència.	Àrees transentorrinal i entorrinal. Còrtex temporal.	Grans argiròfils Inclusions de tau a oligodendròcits
<i>Malaltia de Pick</i>	Canvis de comportament i en la funció del llenguatge, que pot evolucionar fins al mutisme. Problemes en distingir expressions facials. Afectacions visuals.	Còrtex frontal-temporal	Cossos de Pick Alguns cabdells neurofibril·lars
<i>Demència corticobasal</i>	Rigidesa, distònia i moviments mioclònics, membre fantasma. Demència amb canvis de personalitat, desordre de la conducta i problemes d'atenció.	Còrtex cerebral i mesencèfal.	Cossos corticobasals Neurites distròfiques amb filaments de tau Plaques de tau en astròcits Inclusions de tau a oligodendròcits
<i>Demència frontotemporal amb parkinsonisme associada al cromosoma 17</i>	Canvis en el comportament i la personalitat (desinhibició, apatia, comportament compulsiu, hiperreligiositat, pèrdua d'higiene personal i altres). Dèficit cognitiu. Afectacions motores (parquinsonisme).	Còrtex, alguns nuclis subcorticals, substància blanca i medulla espinal	<i>Depèn de la mutació que presenti el gen de la tau es poden trobar:</i> Cabdells neurofibril·lars Cossos de Pick Inclusions de tau en oligodendròcits Plaques de tau en astròcits

Taula 1. Les principals taupaties i les seves característiques.

(La demència. Omnis Cellula 13. Març 2007. Santpere G)

Microscòpicament, aquesta malaltia es defineix per la presència de dos tipus d'agregats proteïcs: els agregats de proteïna tau en cabdells neurofibril·lars, pre-cabdells neurofibril·lars, filaments del neuròpil i neurites distròfiques (sobretot en neurones, les cèl·lules glials es troben molt poc

afectades a la MA); i els agregats de pèptid amiloide extracel·lulars que s'anomenen plaques d'amiloide.



Plaques amiloides (plaque) i cabdells neurofibril·lars (tangle)

1.1.1.1 Inclusions de tau

La proteïna tau és una MAP o proteïna associada als microtúbuls. La seva funció fisiològica més ben caracteritzada és la d'ajudar a estabilitzar i polimeritzar els microtúbuls de tubulina. De la proteïna tau se'n parla més detalladament a l'apartat 3.

Els cabdells neurofibril·lars (tangles) són una estructura formada majoritàriament per tau hiperfosforil·lada que té forma de llàgrima i ocupa un gran espai dins de la cèl·lula. En aquestes estructures la proteïna tau es troba formant fibril·les. De vegades es poden observar cabdells neurofibril·lars que no es troben dins de cèl·lules. Això és degut a que la cèl·lula ha mort i el cabdell "orfe" s'anomena cabdell fantasma (o ghost tangle) (Uchihara et al., 2001).

Els pre-cabdells neurofibril·lars (pre-tangles) on hi ha depòsits de tau però no forma fibril·les i correspon a un estadi primerenc en l'evolució del tangle (Uchihara et al., 2001).

Els filaments del neuropil són acúmuls de tau en forma de fibril·les que es dipositen en feixos que es poden trobar a la dendrita apical de les neurones piramidals (Braak et al., 1986).

Les neurites distròfiques es formen per l'acumulació de tau hiperfosforil·lada als processos neuronals que es troben al voltant de les plaques senils. Aquests agregats formen uns engruiximents anòmals de les neurites (Dickson et al., 1999).

1.1.1.2 Les plaques d'amiloide

Les plaques d'amiloide estan formades per l'acumulació extracel·lular d'amiloide cerebral. En general les estructures amiloidees estan formades per dos components comuns a tots els amiloides que són els component AP (part proteica) i els mucopolisacàrids; i per un tercer component que és específic de cada amiloide. En aquest cas el component específic és el pèptid amiloide derivat de la proteòlisi de la proteïna precursora del pèptid amiloide (APP). Aquesta proteïna es troba a la membrana, conté més de 700 aminoàcids i té una funció poc coneguda. La proteòlisi de l'APP es pot produir per l'acció de tres enzims (o conjunt de proteïnes) anomenats α , β i γ -secretases. Si tallen l' α i el γ , es produeix un pèptid no amiloidogènic; per contra, si tallen la combinació β i γ -secretases s'allibera el pèptid amiloide. Els pèptids amiloides alliberats que es troben a les plaques són l'1-40 i l'1-42, en relació al nombre d'aminoàcids que presenten.

Existeixen dos tipus de plaques amiloides en funció del seu grau de compactació que a la vegada depèn del grau en què el pèptid amiloide està formant fibril·les (Ikeda et al., 1989). Les plaques senils són les més compactes i tenen una mida d'unes 100 a 200 micres de diàmetre. Estan formades per una part central enriquida en pèptid 1-40 envoltada d'una capa més difosa de pèptid 1-42. Aquestes plaques són les que es troben envoltades de neurites distròfiques i de cèl·lules glials. Les plaques difoses en canvi no presenten neurites distròfiques ni cèl·lules glials al seu voltant i són molt més variables en forma i tamany (de 20 a 1000 micres de diàmetre) i també apareixen de forma més desdibuixada. No tenen un nucli central amb acumulació de pèptid 1-40 sino que estan constituïdes bàsicament de pèptid 1-42 (Wisniewski et al., 1989).

També es pot identificar un altre tipus de placa, anomenada placa de tipus A, que no presenta neurites distròfiques però sí cèl·lules glials associades i tenen un tamany de 100 a 200 micres. S'ha proposat que la formació de les plaques es produeix passant per aquests estadis (Ikeda et al., 1989).

1.1.1.3 Altres aspectes microscòpics

Els cossos d'Hirano

Són uns agregats proteics que tenen forma d'espina de peix que es troben en el citoplasma de neurones piramidals de l'hipocamp. Estan constituïts per filaments de 10nm de diàmetre i contenen sobretot actina i proteïnes associades a l'actina; però també s'hi pot trobar tau, neurofilaments i fragments C-terminal de l'APP.

Angiopatia amiloidea cerebral (AAC)

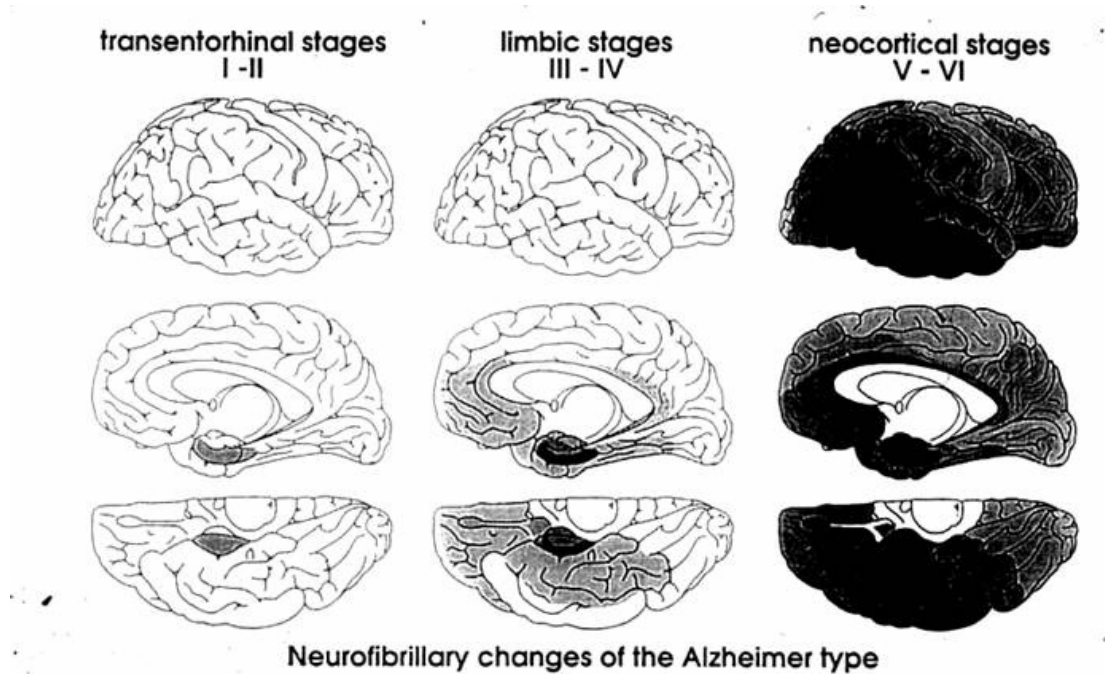
L'angiopatia amiloidea és una malaltia que es pot trobar per si sola però la considerarem en aquest subapartat de la malaltia d'Alzheimer perquè és molt freqüent trobar-la en associació amb aquesta (en un 80% dels casos de MA).

L'angiopatia amiloidea afecta als vasos sanguinis que irriguen tant les meninges com l'escorça cerebral i el cerebel. El pèptid amiloide (sobretot l'1-40) s'acumula a les parets dels vasos i pot estendre's pel parènquima formant plaques. Aquesta darrera forma amb plaques s'anomena angiopatia dishòrica i pot afectar la funció de la barrera hemato-encefàlica (Vinters, 1987).

1.1.1.4 Estadis de la malaltia d'Alzheimer

Està acceptat que la malaltia d'Alzheimer progressa de forma previsible pel que fa al nombre creixent de zones per on s'extén la patologia relacionada amb els agregats de tau. La càrrega de tau és el caràcter més útil per establir un estadiatge neuropatològic que tingui una correspondència amb l'estadiatge clínic. L'amiloide no serveix en aquest sentit, perquè es distribueix de manera més caòtica essent possible trobar plaques a l'escorça quan el pacient encara no presenta cap aspecte clínic de la malaltia. El criteri utilitzat (de Braak i Braak)

correspon a la distribució dels agregats de tau i diferencia 6 estadis de la malaltia (Braak and Braak, 1991).



Estadiatge de la MA de Braak i Braak

Classificació de Braak i Braak:

- I- Escorça entorrinal
- II- Escorça entorrinal més afectada
- III- Hipocamp, zones límbiques i major afectació escorça entorrinal
- IV- Augmenta el nombre de lesions a les regions anteriors
- V- Neoescorça
- VI- Neoescorça més afectada

Els estadis I i II són pre-clínic, asimptomàtics, i la clínica es comença a veure en l'estadi III amb un discret deteriorament cognitiu. La demència apareix a partir de l'estadi V (Braak and Braak, 1991).

1.1.1.5 Hipòtesis proposades per explicar la MA

1) La cascada amiloide

Segons aquesta hipòtesi, l'amiloide es situa al principi de la seqüència d'esdeveniments patològics i causa en tots els casos de MA la subsegüent aparició de degeneració neurofibril·lar, mort neuronal i al final, i a conseqüència dels processos anteriors, la demència.

Existeix un petit percentatge de malalts d'Alzheimer que ho són per causes hereditàries. Aquests casos d'Alzheimer familiar estan al voltant d'un 5% dels casos de MA. S'han trobat diverses i nombroses mutacions a tres gens: el gen que codifica l'APP, la presinilina-1 (PSEN1) i la presinilina-2 (PSEN2) (Goate et al., 1991, Sherrington et al., 1995). Les tres proteïnes estan involucrades en la producció de pèptid amiloide; les PSEN col·laboren en la funció gamma-secretasa. Les mutacions a les presinilines són les més nombroses (més de 160 mutacions identificades). L'efecte d'aquestes mutacions és una alteració de la funció de tall de la presinilina que dona lloc a un augment dels nivells d'amiloide 42 respecte de l'amiloide 40, afavorint la formació de plaques (Bertram and Tanzi, 2005).

Les mutacions en el gen de l'APP afavoreixen l'aparició de les plaques. Un augment de la dosi gènica d'APP també pot comportar la malaltia, i s'associa amb les duplicacions gèniques o amb la Síndrome de Down. La trisomia del cromosoma 21, on està localitzat el gen de l'APP, comporta als malalts l'aparició de plaques amiloides i cabdells neurofibril·lars en els seus cervells després dels 40 o 50 anys (Selkoe, 1991).

Les formes familiars d'Alzheimer únicament es poden diferenciar de la forma esporàdica per l'edat d'aparició. Les formes familiars poden manifestar-se abans dels 60 anys. La resta d'aspectes clínics i neuropatològics són indistingibles. I aquest fet és l'argument clau de la hipòtesi de la cascada amiloide (Selkoe, 1991).

Es proposa que la placa en si mateixa no està implicada en la funció tòxica, però que és font de substàncies amb aquesta capacitat, per exemple és font de radicals lliures (McLellan et al., 2003) i d'amiloide sol·luble (Selkoe, 1991). Cada vegada es tenen més dades que apunten a la major capacitat patogènica de l'amiloide oligomèric o lliure per sobre de les plaques ja formades. Les formes solubles lliures de l'amiloide són les que exercien la toxicitat mitjançant mecanismes encara desconeguts (Selkoe, 1991). Entre els mecanismes de toxicitat de l'amiloide soluble proposats hi ha l'estrés oxidatiu (que s'analitza en l'apartat 5) o les interaccions anòmales del pèptid amb lípids de membrana que poden afectar la seva integritat o estabilitat. Recolzant la aquesta hipòtesi, existeix el fet que la immunització passiva contra l'amiloide en ratolins transgènics és capaç de millorar el seu comportament abans de l'aparició de les primeres plaques (Kotilinek et al., 2002). El pèptid amiloide es produeix de manera normal en els individus sans i és possible detectar-lo en el líquid cefaloraquídi. El què es proposa és que un increment cronificat de la seva producció (com en el cas de la síndrome de Down o per determinades mutacions) o una reducció de la seva eliminació és el què acaba precipitant i formant les plaques a més d'exercir la seva funció tòxica (Selkoe, 1991, Seubert et al., 1992). La forma en què es troba en els cervells de MA és majoritàriament la de fragments N-terminal de l'amiloide 42, en concret la 3-42 en comparació a la predominant 1-42 del cervell de la gent gran sense clínica de MA (Piccini et al., 2005).

Les plaques senils, però, no són inoqües. A nivell morfològic s'observa que les plaques poden modificar l'entorn. Al voltant de les plaques s'hi troben les neurites distròfiques, que a més de tau hiperfosforil·lada contenen també una gran quantitat de mitocondris i de vacuoles autofàgiques (Perez-Gracia et al., 2008). Es produeix també un fenomen d'atracció de dendrites, espines i cons de creixement que donen lloc a neurites de formes i engruximents aberrants (Knafo et al., 2009). Aquest fet pot tenir relació amb l'acúmulo de factors de creixement (com el Nerve Growth Factor (NGF) o l'Epidermal Growth Factor (EGF)) a l'interior de les plaques. Aquestes malformacions en les projeccions neuronals poden perjudicar directament les projeccions cortico-corticals (D'Amore et al., 2003, Delatour et al., 2004).

2) Canvis en la proteïna tau

Una segona postura resitua la proteïna tau a l'origen de la malaltia. Principalment els arguments més forts són dos: la forta correlació entre dipòsits de tau i clínica en la MA (Gomez-Isla et al., 1997), i l'existència d'un gran nombre de mutacions al gen de la tau que comporten l'aparició del grup de malalties anomenades Demències Frontotemporals amb Parkinsonismes lligades al cromosoma 17 (DFTP17) (Lynch et al., 1994). A més, recentment s'ha vist que mutacions a la PSEN1 en pacients diagnosticats de demència fronto-temporal mostren inclusions de tau i absència d'acúmul d'amiloide. Mutacions de PSEN1 també poden accelerar la formació de cabdells neurofibril·lars sense afectar el ritme de deposició de l'amiloide (Tanemura et al., 2006).

A la MA s'observa que la tau hiperfosforil·lada es transloca de l'axó, on ha de realitzar la seva funció fisiològica normal, al compartiment somatodendrític (Konzack et al., 2007). Aquesta pèrdua de funció comporta una deficiència en el transport axonal i conseqüentment, a la degeneració neuronal. Per altra banda es discuteix també sobre el poder patogènic d'un possible guany de funció tòxica o bé del propi agregat de tau, o bé de la tau lliure o oligomèrica dins de la cèl·lula. Es parla amb més detall d'aquests aspectes a l'apartat 3.

Altres perspectives per explicar la MA

1) Vulnerabilitat selectiva de diferents tipus neuronals

La degeneració neurofibril·lar afecta a les neurones de projecció (d'axons llargs) en primera instància i no afecta fins cap a etapes finals les neurones d'axons curts, com les piramidals de les capes II i IV de la neo-escorça (Hyman and Gomez-Isla, 1994). La manera en què progressa la distribució de la patologia, com hem vist en els criteris de Braak i Braak, sembla anar a la inversa del gradient de mielinització que es dona en el cervell (Braak et al., 2000). És a dir, les primeres zones que es veuen afectades estan molt poc mielinitzades i les darreres ho estan més. Les zones més noves evolutivament parlant són més immadures pel què fa a la seva mielinització i són les primeres zones de la neo-escorça en veure's afectades: àrees d'associació d'ordre superior i àrea pre-

frontal, entre d'altres. Les àrees motores o sensorials primàries, més antigues, presenten un grau de mielinització major i queden afectades molt al final de la malaltia. La idea proposada és que les neurones no mielinitzades són més sensibles i estan més desprotegides a efectes de la malaltia com l'estrés oxidatiu (Braak et al., 2000).

2) Increment de la càrrega de neuro-plasticitat

S'ha observat que els factors de risc i les mutacions causatives de la MA afecten d'alguna manera la capacitat plàstica del cervell. La primera resposta del cervell a aquesta sobrecàrrega de les necessitats plàstiques inclouria un augment de fosforil·lació de tau i un augment del recanvi de l'APP, produint al final, després d'una perturbació prolongada de la plasticitat, els dos tipus d'agregats que defineixen la malaltia (Mesulam, 2000).

La plasticitat neuronal inclou processos com la ramificació de dendrites, la formació d'espines, el remodelament sinàptic, les potenciacions a llarg termini (LTP), l'extensió dendrítica i axonal, la sinaptogènesi i la neurogènesi. Tots aquests processos són més presents a les estructures límbiques que inclouen l'hipocamp, l'amígdala i l'escorça entorrinal, regions on comença a aparèixer la degeneració neurofibril·lar (Mesulam, 1999).

Trobem doncs que L'alfa-APP soluble, el fragment gran de l'APP que es desprèn del tall de la alfa-secretasa, té propietats que promouen la neuroplasticitat (sinaptogènesi i LTPs), mentre que el pèptid amiloide inhibeix l'extensió axonal i els LTPs (Roch et al., 1994, Ishida et al., 1997). Així mateix, les mutacions a les presinilines també poden tenir un efecte sobre la plasticitat interferint en la funció normal d'aquestes o augmentant el tall de l'APP (Furukawa et al., 1998, Mesulam, 2000).

Entre els factors de risc que poden afectar la capacitat plàstica del cervell trobem: La deficiència d'estrògens, donats el efectes protectors que confereixen, ja que promouen la plasticitat dendrítica en les neurones límbiques (Ferreira and Caceres, 1991). L'edat, el principal factor de risc de la MA, també està relacionada amb una pèrdua de neuroplasticitat (Mori, 1993). I finalment la presència de l'al·lel E4, de la proteïna ApoE, el més ben establert factor de risc

genètic de la MA (Strittmatter et al., 1993). La proteïna ApoE té una funció de transport i recaptació de colesterol també involucrada en creixement axonal i sinaptogènesi,. La presència de l'al·lel E4 redueix l'edat d'aparició de la malaltia i aquest efecte depèn de la dosi gènica (més efecte en homozigosi i menys en heterozigosi). Contràriament a altres al·lells com l'E3, l'E4 inhibeix el creixement de neurites i la plasticitat dendrítica (Nathan et al., 1994).

2) Cascada d'activació de proteases

Es centra en l'activació primerenca i progressiva de sistemes proteolítics com l'endosomal-lisosomal o el calpaïna-calpastatina. La idea es basa en la proposta que tots els factors genètics i ambiental de la MA acaben activant o alterant aquests sistemes proteolítics. S'ha observat que cathepsines i calpaïnes poden directament o indirecta promoure l'acumulació del beta-amiloide, la degeneració neurofibril·lar i la neurodegeneració (Nixon, 2000).

3) Desregulació de la homeostasi del colesterol. Hipòtesis metabòlica/transducció de senyal.

Aquesta teoria proposa que una reducció de la fluïdesa de les membranes amb l'edat les podria fer més susceptibles als insults metabòlics o ambientals. Molts receptors importants es troben concentrats en els microdominis de membrana (rafts lipídics). Aquests microdominis estan molt enriquits en esfingomièlina i colesterol i s'han proposat com a plataformes de transducció de senyal. Alteracions en la recaptació i/o metabolisme del colesterol podria afectar el tràfic de proteïnes de membrana causant pèrdues funcionals a la neurona i problemes de plasticitat sinàptica. La idea es sustenta bàsicament en la funció de l'APP i l'ApoE en relació al moviment de LDLs i la recaptació de colesterol (Lynch and Mobley, 2000). L'al·lel E4 de l'ApoE sembla menys apte que els altres al·lells (E3 i E2) en l'obtenció de colesterol lliure. Per altra banda, el pèptid amiloide es podria unir a l'ApoE i disminuir la recaptació de colesterol (Nathan et al., 1994, Lynch and Mobley, 2000). Aquesta teoria no dóna a la tau un paper rellevant, tot i que com es parlarà més endavant, s'ha proposat que la tau també pugui interactuar amb la membrana i tenir un paper en la transducció de senyal.

4) Defectes mitocondrials

Aquesta hipòtesis situa els mitocondris al centre d'un espiral que es retroalimenta com a causa de la neurodegeneració. Els aspectes que es veuen alterats quan es malmeten els mitocondris són el metabolisme energètic, l'estrés oxidatiu (producció de ROS) i l'homeostasi del Ca⁺⁺ (Blass, 2000).

Altres taupaties:

1.1.2 La paràlisi supranuclear progressiva (PSP)

La PSP és una taupatia infreqüent (amb una prevalència d'entre 3 i 6 casos per cada 100.000 habitants amb edat de tenir la malaltia). Les manifestacions clíniques inclouen desordres del moviment com bradiquinèsia, inestabilitat postural amb freqüents caigudes cap enrera, parkinsonisme i paràlisi supranuclear de la vista. Aquests desordres motors poden anar seguits, en estadis més avançats, de demència.

Macroscòpicament, els cervells de malalts de PSP presenten cert nivell d'atròfia en algunes regions com el tàlam i nuclis subtalàmics, i una decoloració de la substància negra, però no són canvis específics de la malaltia (Verny et al., 1996). A nivell microscòpic la PSP presenta pèrdua neuronal sobretot en nuclis del tronc de l'encèfal i diencèfal (com el globus pallidus, estriat o els nuclis subtalàmics); però també pot afectar l'escorça cerebral (Dickson, 1999). En aquestes regions, a més de pèrdua neuronal, s'observen incusions de tau hiperfosforil·lada tant en neurones com en cèl·lules glials (Dickson, 1999). A les neurones s'hi troben cabdells neurofibril·lars, pre-cabdells o filaments del neuropil com a la MA. Els oligodendròcits poden presentar unes incusions de tau anomenades *coiled bodies*. I als astrocits s'hi poden observar unes incusions al citoplasma que donen lloc a diferents morfologies (Dickson, 1999).

Probablement per la seva raresa no es coneix gaire bé la manera en què la PSP es desenvolupa i no s'han definit estadiatges com els de Braak i Braak per la MA. La major evidència de la regió del cervell on s'origina la malaltia prové de l'estudi dels únics pacients que han desenvolupat una forma familiar de PSP, dels quals encara no se n'ha trobat el gen causant. Tal com s'observa per

tècniques de neuroimatge com el PET, sembla que aquesta forma autosòmica dominant de la malaltia provoca primer de tot alteracions a l'estriat (caudat/putamen) seguides d'alteracions al globus pallidus i als nuclis subtalàmics (de Yebenes et al., 1995, Piccini et al., 2001, Ros et al., 2005).

1.1.3 Malaltia dels grans argiròfils (MGA)

La MGA és una malaltia esporàdica que està darrera d'aproximadament un 5% dels casos de demència. La malaltia a més pot donar lloc a alteracions del comportament, canvis de la personalitat, desestabilització de l'estat d'ànim, així com certa amnèsia, irritabilitat i agitació. El diagnòstic precís de la MGA ha de realitzar-se postmortem, pel fet que la clínica és força indistingible de la dels malats de MA.

Macroscòpicament, els cervells de malalts de MGA no presenten canvis gaire vistosos, només una lleugera atrofia fronto-temporal (Braak and Braak, 1998, Tolnay et al., 2001). Neuropatològicament la MGA es defineix per la presència d'acúmul·ls de tau hiperfosforil·lada a les dendrites de les neurones que tenen forma de grans i s'anomenen grans argiròfils (perquè es poden tenyir amb tècniques de plata). A més dels grans també es poden trobar pre-cabdells neurofibril·lars en neurones, *coiled bodies* en oligodendròcits, i dipòsits de tau granulars en astròcits (menys compactes que a la PSP) (Tolnay et al., 2001).

Les zones que es veuen més afectades són aproximadament les mateixes que en els primers estadis de la MA: escorça entorrinal, hipocamp, amígdala i l'escorça temporal propera. Per això la clínica de la MGA pot confondre's amb la dels primers estadis de la MA.

La MGA es troba molt sovint en associació amb altres taupaties, com la MA, PSP o DCB; i també amb sinucleïnopaties com la MP i la DCL (Seno et al., 2000, Togo and Dickson, 2002). L'elevada co-ocurrència ha fet que alguns autors proposin que la MGA no és una malaltia independent (Martinez-Lage and Munoz, 1997). La presència de grans argiròfils al cervell sembla força freqüent en edats avançades (fins un 43%, en una de les sèries descrites) (Saito et al., 2002). Sovint la co-presència de MGA i MA s'ha vist infraestimada pel fet que amb determinades tècniques de tinció d'inclusions de tau, la major presència

d'estructures en la MA emmascara la presència dels grans argiròfils, molt més petits. Amb l'ajuda d'anticossos específics contra el tipus de tau que s'acumula en els grans (veure apartat de tau), o amb anticossos que detecten proteïnes associades als grans (com la p62 o la ubiquitina) s'ha vist que la freqüència de MGA en AD és major (Fujino et al., 2005, Scott and Lowe, 2007).

Molt recentment s'ha identificat una mutació en el gen de la tau, la S305I, que és capaç desenvolupar una neuropatologia semblant a la de MGA, amb presència de grans argiròfils (Kovacs et al., 2008). Aquest és l'únic cas que es podria comparar a una forma familiar de la malaltia, encara que es considera dins el grup de les DFTP-17.

La progressió de la malaltia ha estat estudiada i s'han fet algunes propostes d'estadiatge. Aquests descriuen la progressió de les zones afectades des de la part anterior de l'hipocamp cap a la posterior (Saito et al., 2004).

1.1.4 La malaltia de Pick (MPi)

La MPi és una taupatia rara que es classifica clínicament dins del gran grup de demències fronto-temporals (DFT). La prevalència d'aquesta malaltia no es coneix amb seguretat degut al solapament clínic amb altres tipus de demència fronto-temporal (Neary et al., 1998). Aquesta malaltia comporta un deteriorament progressiu de la personalitat, del comportament, i també del llenguatge. Entre els problemes comportamentals més evidents es troba la desinhibició social (Neary et al., 1998).

Macroscopicament, el cervell dels malalts de MPi pot presentar un elevat grau d'atròfia dels lòbuls frontals i temporals, que es pot estendre pels lòbuls parietals. Mentre que l'atròfia i mort neuronal pot afectar estructures límbiques, l'hipocamp es troba ben preservat (Dickson, 1998).

A nivell microscòpic s'observen els anomenats cossos de Pick, dipòsits esfèrics a l'interior de les neurones de proteïna tau hiperfosforil·lada. Aquestes inclusions s'observen majoritàriament a l'hipocamp (gir dentat, CA1) i en capes superiors de l'escorça entorrinal i la neocorça. Un aspecte particularment

interessant de la malaltia és que al gir dentat no s'observa mort neuronal, mentre que gairebé totes les neurones presenten cossos de Pick a l'interior (Dickson, 1998).

A la MPi també es poden trobar alguns cabdells neurofibril·lars en àrees límbiques o a la neocorça, però en capes diferents de les que es troben a la MA. Els oligodendròcits presenten un variable nombre de *coiled bodies* a la substància blanca i els astròcits també presenten inclusions, que són diferents de les que s'observen a la PSP. Un caràcter important a assenyalar, és un elevat grau de gliosi per l'escorça i a la substància blanca de sota, així com en altres zones afectades com el nucli caudat (Komori, 1999).

1.2 Alfa-sinucleïnopaties

Les alfa-sinucleïnopaties són malalties neurodegeneratives que comparteixen la presència d'inclusions de la proteïna alpha-sinucleïna. Aquesta proteïna és un membre de la família de les sinucleïnes i presenta 140 aminoàcids (Jakes et al., 1994). S'expressa per totes les regions del cervell i es troba particularment enriquida en terminals sinàptics. La seva funció dins la cèl·lula no es coneix, però se la relaciona amb el transport de vesícules sinàptiques i amb la funció de xaperona (Clayton and George, 1999).

La malaltia de Parkinson, la demència amb cossos de Lewy i l'atròfia multisistèmica són alpha-sinucleïnopaties. Les dues primeres fa temps que es proposen per diversos autors com estadis diferents d'una mateixa malaltia (Jellinger, 2008). De manera que la malaltia de Parkinson, que afecta sobretot el mesencèfal, en progressar i estendre's per l'escorça cerebral esdevindria la demència amb cossos de Lewy (Braak et al., 2002, Braak et al., 2003). Els agregats de sinucleïna que presenten les neurones tant la MP com la DCL són iguals, mentre que de l'atròfia multisistèmica presenta un altre tipus d'agregats al citoplasma de cèl·lules oligodendroglials (Papp et al., 1989).

1.2.1 La malaltia de Parkinson (MP)

La MP és la malaltia neurodegenerativa més prevalent entre la gent gran després de la MA. Clínicament es pot diagnosticar de manera força específica però pel fet que hi ha altres malalties que poden donar parkinsonisme el diagnòstic definitiu s'ha de donar postmortem. La clínica de la malaltia cursa amb tremolors, inestabilitat de la postura, acinèsia i rigidesa (Forno, 1996).

A nivell macroscòpic s'observa poc més que una depigmentació de la substantia nigra i del locus ceruleus. Microscòpicament, hi ha una elevada mortalitat de neurones dopaminèrgiques a la substantia nigra pars compacta, i es defineix la malaltia com a Parkinson quan la mortalitat en aquesta zona arriba al 60%. A més de la pèrdua neuronal en aquestes regions es troba una elveda gliosi i les inclusions d'alfa-sinucleïna al citoplasma d'algunes neurones que s'anomenen cossos de Lewy; i també a les neurites, que reben el nom de neurites de Lewy (Forno, 1996, Goedert, 2001, Shults, 2006).

Diferents mutacions a un nombre considerable de gens poden donar lloc a formes familiars de MP. Trobem mutacions a la pròpia alfa-sinucleïna, però també al gens de UCHL-1 (ubiquitin carboxi-terminal hydrolase L1), Parkin, DJ-1, PINK-1 (PTEN-induced putative kinase), ATP13A2 (p-type ATPase), HTRA2 (Htra serine peptidase 2) i LRRK2. També s'han identificat mutacions en altres loci (PARK3, 10, 11, i 12) tot i que el gen concret encara no es coneix (Tan and Skipper, 2007).

1.2.2 La demència amb cossos de Lewy (DCL)

És una malaltia que comporta una demència progressiva (la forma més comuna de demència després de la MA) a més dels fenòmens neurològics associats a la MP. Les manifestacions clíniques més comunes impliquen els dèficits d'atenció, alucinacions visuals i parquinsonisme (Weisman and McKeith, 2007). Macroscòpicament, la malaltia no presenta atròfia cerebral significativa, però si pot presentar de forma variable una pal·lidesa de la substància negra i del locus ceruleus (Weisman and McKeith, 2007) Els aspectes microscòpics són els mateixos que a la MP però extesos per l'escorça cerebral: cossos de Lewy i

neurites de Lewy. Sovint es troba associada a la MA donant lloc a la DCL forma comuna (un 80% dels casos). Quan no hi ha caràcters de tipus MA s'anomena DCL forma pura (el 20% restant dels casos) (Weisman and McKeith, 2007).

Mutacions en el gen de la sinucleïna poden donar com a resultat la DCL (Bonifati, 2008). És un argument més per considerar aquestes dues malalties (DCL i MP) com a parts d'un mateix espectre.

2- L'ESTUDI DE PROTEÏNES, I MODIFICACIONS POST-TRADUCCIONALS ASSOCIADES, EN TEIXIT CEREBRAL HUMÀ CONGELAT

Els estudis bioquímics que es fan sobre malalties neurodegeneratives tenen major valor si es fan sobre el substrat real, el cervell humà, que sobre models experimentals. Però existeixen una sèrie de factors que fan que treballar amb mostres humanes pugui ser complicat pel fet que la mostra pot no estar òptimament conservada. És prioritari establir les condicions de preservació òptimes de les mostres per tal d'evitar la degradació o la modificació de les proteïnes, dels lípids i dels àcids nucleics. Treballar amb mostres subòptimament preservades pot portar a resultats alterats i a conclusions errònies. També és necessari establir quins efectes reals tenen els diferents factors que poden convertir una mostra en subòptima sobre els diferents elements d'aquesta.

Els factors més rellevants que poden influir en la preservació del teixit cerebral humà, tant abans de la mort com després, són:

Premortem. L'estat metabòlic, drogues i substàncies tòxiques, infeccions i hipòxies (un estat d'hipòxia prolongat o l'acidosi metabòlica poden alterar el pH del teixit). La duració prolongada del període agònic incrementa l'efecte d'aquests factors.

Postmortem. Els dos factors principals que intervenen després de la mort són la rapidesa en què s'extreu el cervell, es processa i es congela, per una banda, i la

temperatura a què ha estat el cervell fins la congelació, per l'altra (Buesa et al., 2004).

D'especial interès per la feina que aquí es presenta és el que fa referència a la preservació de les proteïnes i de les seves modificacions post-traduccionals, en especial la fosforil·lació. Els estudis que s'han fet en aquest sentit fins ara permeten arribar a una conclusió: les proteïnes són sensibles al postmortem, però ho són de manera diferent. Algunes són més sensibles a la temperatura, altres ho són més al temps entre la mort i la congelació, i altres resisteixen els dos factors i són estables.

La majoria d'estudis s'han realitzat en proteïnes concretes i de manera secundària, i molts d'aquests s'han portat a terme sobre teixit animal, de rata o ratolí (Schwab et al., 1994, Li et al., 1996, Siew et al., 2004). Són necessaris estudis metodològics generals en cervell humà que puguin servir de referència per la manipulació d'aquestes mostres per tal de què s'optimitzin al màxim per la recerca i que siguin aplicables als diferents bancs de teixits.

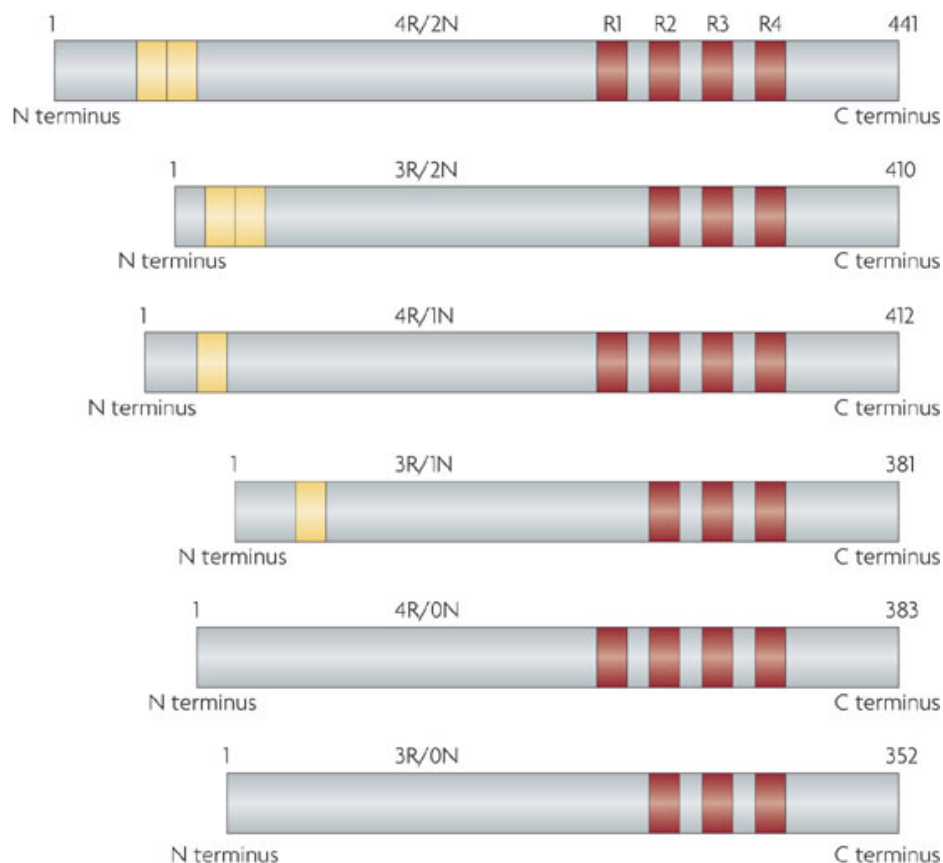
3- LA PROTEÏNA TAU

Als anys 80 es va identificar la proteïna tau com el principal component dels filaments aparellats hel·licoidalment (paired helical filaments, PHF), que formen els cabdells neurofibril·lars i les neurites distròfiques en la malaltia d'Alzheimer (Weingarten et al. 1975), així com les inclusions pròpies de les altres taupaties.

La tau és una de les MAP o proteïnes associades a microtúbuls (Microtubule associated protein). La seva funció és la d'ajudar a estabilitzar i polimeritzar el microtúbuls (Weingarten et al., 1975), per la qual cosa està dotada de tres o quatre dominis repetits d'unió a la tubulina.

En el cervell adult s'expressen sis isoformes de tau generades a partir de l'empalmament alternatiu d'un gen situat al cromosoma 17q21. Les sis isoformes

es diferencien per la presència o absència dels exons 2, 3 i 10. La nomenclatura pels exons N-terminal és 0N, 1N i 2N en funció del nombre d'exons presents. L'exó 10 és funcionalment important perquè conté un dels quatre dominis d'unió a la tubulina. Les tres isoformes amb l'exó 10 s'anomenen 4R i les altres tres, sense l'exó 10, 3R. En etapes fetals, només s'expressa la isoforma més petita (0N3R) (Lee et al., 1988).



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Les sis isoformes de tau que s'expressen al cervell adult (Ballatore et al., 2007)

A més dels dominis d'unió a la tubulina, situats a la part mitja de l'extrem C-terminal, la tau presenta una regió N-terminal anomenada domini de projecció. S'ha proposat que aquest domini pot interactuar amb la membrana i conferir a la tau altres funcions més enllà de la que se li atribueix actualment (Lee et al., 2004).

La unió de la tau al microtúbul està controlada per un balanç de fosforil·lació i desfosforil·lació de múltiples epítops (Serines i Treonines) en els dominis d'unió. Quan els dominis estan fosforil·lats la tau es desenganxa del microtúbul (Drechsel et al., 1992).

3.1 Modificacions post-traduccionals

3.1.1 Hiperfosforil·lació

3.1.1.1 Diferents isoformes per diferents taupaties

En les taupaties, la tau es troba hiperfosforil·lada i forma agregats anòmals en forma de filaments. Les isoformes que s'hiperfosforilen i s'agreguen no sempre són les mateixes en totes les taupaties. En la MA ho fan totes sis, en la PSP, DCB i MGA ho fan només les 4R i en la MPi, ho fan només les 3R. En els cas de les DFTP-17, depèn de la mutació de tau que presentin; per exemple, les mutacions que dificulten l'empalmament alternatiu de l'exó 10 presenten només les isoformes 4R (Lee et al., 2001). Aquestes diferències queden ben reflectides quan s'estudia la tau hiperfosforil·lada per Western Blot: la MA presenta un patró de tres bandes a 68, 64 i 62 KDa, les taupaties amb 4R presenten només les de 68 i 64 KDa, i les 3R presenten les de 64 i 62 KDa. Sovint es pot observar també una banda a 72KDa corresponent a la isoforma més gran (Lee et al., 2001).

3.1.1.2 Cinases involucrades en la hiperfosforil·lació

La hiperfosforil·lació de tau afecta a més de 30 serines i treonines, i s'han identificat moltes cinases amb la capacitat de fosforil·lar la tau. Les més importants són la GSK3-beta, la Cdk5, la PKA, la CaMKII, la ERK1/2, p38 i SAPK/JNK (Ferrer et al., 2005). A més de serines i treonines, la tau és substrat de tirosina-cinases com la Fyn (Lee et al., 2004) o c-Abl (Derkinderen et al., 2005). A la taula apareixen els epítops de tau específics d'algunes d'aquestes i altres cinases.

Residue ^a	Foetal rat tau ^b	Adult rat tau ^b	PHF-tau ^c	Protein kinase ^d
Thr 175			*	MAPK
Thr 181	+	+	+	MAPK
Ser 184/185			*	
Ser 198	+		+	
Ser 199	+		+	MAPK, GSK-3
Ser 202	+	+	+	MAPK, CDK5
Ser 208			+	
Ser 210			+	
Thr 212			+	MAPK, GSK-3
Ser 214			+	PKA, PKC
Thr 217	+		+	GSK-3
Thr 231	+	+	+	GSK-3, CDK5
Ser 235	+		+	MAPK, GSK-3, CDK5
Ser 237			*	PK
Ser 238			*	
Ser 262		+	+	GSK-3, PKA, PKC, p110K, PK
Ser 356			*	GSK-3, PKA, p110K
Ser 396	+		+	MAPK, GSK-3
Ser 400	+		+	GSK-3
Thr 403			+	
Ser 404	+	+	+	MAPK, GSK-3, CDK5
Ser 409	+		+	PKA
Ser 412			+	
Ser 413	+		+	GSK-3
Ser 422			+	MAPK

3.1.1.3 Fosfatases que desfosforil·len la tau

La desfosforil·lació de tau va a càrrec de la família de les PP (protein phosphatase). *In vitro*, s'ha observat que algunes de les PP que s'expressen en el cervell poden desfosforil·lar la tau: PP1, PP2A, PP2B i PP5 (Liu et al., 2005). *In vivo*, PP1, PP2A i PP5 són les més importants. La PP2A sembla ser la més activa desfosforil·lant tau i en la MA presenta una disminució del seu mRNA (Vogelsberg-Ragaglia et al., 2001) i, junt amb la PP1 i PP5, una disminució de la seva activitat (Sontag et al., 2004b, Liu et al., 2005). La metil·lació de la subunitat catalítica de la PP2A sembla que juga un paper important alhora de reclutar les altres dues subunitats reguladores de l'holoenzim funcional. En models tractats amb pèptid amiloide on s'observa un increment de fosforil·lació de tau, també s'observa una disminució de la metil·lació de PP2A (Sontag et al., 2004a, Zhou et al., 2008).

3.1.2 Glicosil·lació

La tau també es troba anormalment glicosil·lada en la MA, i aquest canvi sembla precedir la hiperfosforil·lació. Sembla que un tipus concret de O-glicosil·lació està inversament relacionada amb la fosforil·lació de tau. Alguns autors consideren aquesta modificació un bon objectiu sobre el qual desenvolpar fàrmacs protectors de la desglicosil·lació (Robertson et al., 2004, Fischer, 2008).

3.1.3 Proteòlisi

3.1.3.1 *Fragments de tau i formació d'agregats*

El truncatge de la tau està resultant ser un fenomen de gran importància en la seqüència d'esdeveniments que porta a la formació dels agregats patològics. Els PHF estan formats per un nucli resistent a proteases i una coberta sensible. S'ha vist mitjançant l'ús d'anticossos depenents de conformació que el nucli està format principalment per fragments de tau (Novak et al., 1991, Novak et al., 1993). Aquests anticossos també posen de manifest la destrucció i creació d'epítops deguts a fosforil·lacions i talls. Així doncs, s'ha proposat un model per explicar la seqüència de modificacions que pateix la tau per arribar al trosset de proteïna que vertebrava els PHF, en relació a la formació de cabdells neurofibril·lars (Guillozet-Bongaarts et al., 2005). El fragment final, després de tot el procés, correspon a una regió de la tau que conté només els dominis d'interacció amb la tubulina i l'extrem C-terminal tallat a l'àcid glutàmic 391 (Skrabana et al., 2004). Aquest model sobre observacions en MA, sembla adaptar-se bé també a la MPi (Mondragon-Rodriguez et al., 2008).

3.1.3.2 *Efectes nocius de l'expressió dels fragments*

Estudis *in vitro* demostren que determinats fragments poden desencadenar apoptosi (Fasulo et al., 2000), promoure la polimerització de tau (Abraha et al., 2000), així com provocar un mal ensamblatge dels microtúbuls. Estudis en ratolins transgènics que sobreexpressen alguns d'aquests fragments han aportat informació rellevant (Zilka et al., 2006). Per una banda, l'expressió del fragment tau151-391, que *in vitro* és capaç d'afavorir un mal ensamblatge dels microtúbuls, és suficient per generar degeneració neurofibril·lar del tipus MA. A més, els complexos de tau estan formats per la tau humana del transgen i la tau endògena de la rata en una proporció 1:1, és a dir, la tau truncada és capaç d'agregar la tau murina endògena (Zilka et al., 2006). I per altra banda, l'expressió de fragments truncats comporta en la rata un augment de radicals lliures i una distribució anòmala dels mitocondris (Cente et al., 2006).

3.1.3.3 Proteases responsables de la fragmentació

Diverses proteases poden tallar la tau *in vitro*: caspases, calpaïnes, trombina, catepsina D, tripsina i quimiotripsina. El paper que juguen cada una d'elles *in vivo* encara no està ben clar, però algunes d'elles s'han trobat colocalitzant amb les inclusions de tau en algunes taupaties. En els experiments *in vitro*, així com en el model de truncatge d'abans, s'observa una relació entre fosforil·lació i truncatge. La primera va abans que la segona i a vegades protegeix de l'acció de la proteasa, com passa amb la trombina i amb la caspasa-3. La trombina pot tallar la tau a diferents dianes *in vitro*, i això es pot prevenir mitjançant la fosforil·lació de tau per GSK3-beta (Arai et al., 2005). La trombina i el seu precursor, la protrombina, estan predominantment expressades al fetge però en MA també s'expressen a les neurones i a les cèl·lules glials i s'acumulen als NFT (Arai et al., 2006).

Caspases i calpaïnes comparteixen molts dels seus substrats i la seva activació *in vitro* està relacionada amb fenòmens apoptòtics (Raynaud and Marcilhac, 2006). La calpaïna-1 s'ha vist activada en algunes malalties neurodegeneratives com la MA (Saito et al., 1993) i, *in vitro*, pot tallar la tau a diferents dianes (Canu et al., 1998). La calpaïna-2 s'ha trobat activada i colocalitzant amb la tau en els NFT a la MA, la síndrome de Down, la PSP, la DCB i en alguns cossos de Pick (un 10%) a la MPi (Adamec et al., 2002). A més a més, la calpaïna està involucrada en la fosforil·lació de tau pel fet que és la responsable del tall de p35 a p25 que, unit a la Cdk5, promou la fosforil·lació de tau per part d'aquesta cinasa (Patrick et al., 1999).

La tau es pot tallar per múltiples caspases al residu Asp421 (caspasa-1, -3, -6 i -7) i la tau resultant s'agrega formant filaments més ràpidament que la tau sencera (Gamblin et al., 2003). La caspasa-3 es troba en els NFT en la MA. La caspasa-6 també es troba en les inclusions de tau i s'ha observat que *in vitro* és responsable del tall al residu N-terminal D13. Aquest tall, conjuntament amb el de la caspasa-3 a Asp421, sembla que es produeixen a la mateixa etapa primerenca de formació dels NFT (Horowitz et al., 2004).

3.2 Poder patogènic de la tau

Com s'ha comentat al primer apartat, pel fet que les formes familiars de la MA estan causades per mutacions que afecten directament a la formació de pèptid amiloide i presenten també degeneració neurofibril·lar, és lògic conferir un paper a la tau que estigui subjecte als efectes de la “cascada amiloide”. Els dèficits cognitius i la mort neuronal, però, presenten una més forta correlació amb els dipòsits de tau que amb les plaques d'amiloide (Ballatore et al., 2007).

La resta de taupaties no presenta dipòsits d'amiloide i les mutacions al gen de la tau no tenen cap efecte sobre l'acumulació d'amiloide, però si són la causa d'una subgrup de taupaties anomenades demències frontotemporal amb parkinsonisme associades a mutacions al gen de la tau (FTDP-17).

Aquestes dades posen de manifest la importància patogènica de la tau. Però no està clar de quina manera la tau exerceix aquest efecte nociu. La patogenicitat s'ha atribuït tant al cos d'inclusió com a la tau soluble, però tot i que el cos d'inclusió de cada taupatia ocupa un espai molt gran dins de la cèl·lula i pot dificultar funcions de transport en el seu interior, sembla més probable que la funció tòxica la desenvolupi en el seu estat soluble. De fet la cèl·lula és capaç de resistir molts anys en convivència amb el cos d'inclusió (Morsch et al., 1999); i existeix un argument molt citat que es basa en l'observació d'un ratolí transgènic, que expressa la tau mutada d'una FTDP-17, a qui se li suprimeix de sobte l'expressió d'aquesta tau patogènica (Santacruz et al., 2005). Aquesta supressió millora el dèficit de memòria i estabilitza la supervivència neuronal però no atura la formació de cabdells neurofibril·lars, encara que l'única tau que s'expressa a partir de llavors és la del propi ratolí.

Els models animals, majoritàriament ratolins transgènics, són de gran ajuda per l'estudi de la funció patogènica de tau. Se n'han produït de molts tipus donant resultats molt diversos, depenent del nombre i el tipus d'isoformes de tau que sobreexpressen, si es silencia o no l'expressió de tau endògena del ratolí (que només expressa les isoformes 4R) així com del promotor que utilitzen (Duyckaerts et al., 2008, Frank et al., 2008).

4- PROTEÏNES ASSOCIADES ALS DIPÒSITS DE TAU EN TAUPATIES

La tau no està sola en les inclusions, tant siguin cabdells neurofibril·lars, cossos de Pick com grans argiròfils, etc. Mitjançant tècniques de microscopia òptica, confocal o electrònica es pot observar que els filaments de tau i, a major escala, les inclusions, estan poblades d'un notable nombre d'altres proteïnes. És de gran importància identificar quines són aquestes proteïnes, si encara són actives, si estan deixant de fer la seva funció normal pel fet de trobar-se segregades a la inclusió, si estan col·laborant per formar o estabilitzar la inclusió o si, per contra, proven de desfer-la.

Un altre aspecte important en l'estudi de les proteïnes associades a les inclusions és la recerca de similituds i diferències entre taupaties i altres malalties neurodegeneratives amb agregats proteïcs. Trobar elements diferencials o comuns pel què fa a la composició proteïca de les inclusions pot donar pistes sobre els mecanismes generals o específics que donen lloc a aquestes.

En aquest apartat es descriuen algunes proteïnes que, per diferents motius de rellevància, s'han estudiat en relació als agregats de tau. Afegim aquí la presència en inclusions del factor de transcripció Sp1, descrita per primera vegada en un dels treballs que conforma aquesta tesi.

4.1 Cinases

Existeixen moltes cinases que tenen la capacitat de fosforil·lar la tau. Aquestes cinases col·localitzen amb la tau a l'interior de les inclusions en totes les taupaties estudiades i algunes d'elles, com la GSK3-beta, la p38 i la SAPK/JNK, s'han aïllat i comprovat que encara són actives quan es posen en contacte amb un substrat genèric com és la proteïna bàsica de la mielina o amb la tau recombinant (Puig et al., 2004, Ferrer et al., 2005). Encara que un dels substrats d'aquestes múltiples cinases de tau és la pròpia tau, en tenen més. I com veurem, pot ocórrer que algun d'aquests substrats (factors de transcripció, cinases i altres) puguin estar també atrapats dins de les inclusions, de manera

que es perpetuin o s'alimentin estats conformacionals o sublocalitzacions cel·lulars (sobretot en factors de transcripció) determinades amb conseqüències funcionals importants.

La regulació de l'activitat de les cinases es produeix per fosforil·lacions en llocs específics. És important determinar en quin estat es troben aquestes cinases en les inclusions. El cas de la GSK3-beta és un cas curiós en el sentit que la forma que es troba en més abundància dins de les inclusions de tau és la forma teòricament inactiva (aquella que està fosforil·lada a la Ser9 per una altra cinasa anomenada Akt (Stambolic and Woodgett, 1994)), mentre que la forma activa (la fosforil·lada a la ser21) hi està pràcticament absent (Ferrer et al., 2005). Tot i així, com s'ha comentat, una vegada aïllada demostra que continua activa; l'explicació podria venir de l'estudi d'una xaperona de la que es parlarà més endavant a l'apartat 4.1.3.

4.2 Factors de transcripció

4.2.1 Factors de transcripció induïbles: c-fos i c-jun

Un dels primers factors de transcripció que es va descriure en mamífers és l'AP-1 (activador de proteïna-1). Es va veure que aquest factor podia estar involucrat en una gran varietat de respostes que inclouen supervivència, proliferació, diferenciació i mort (Shaulian and Karin, 2002). Aquest ampli ventall de funcions es deu a la seva naturalesa heterogènia. L'AP-1 és un dímer que pot formar-se per homo o heterodímers de diferents proteïnes pertanyents a diferents famílies: Fos (c-Fos, Fos B, Fra-1 i Fra-2), Jun (c-Jun, Jun B, Jun D), ATF (ATF-2, LRF1/ATF3, B-ATF, JDP1 i JDP2) i la família Maf (Karin et al., 1997), i unir-se a l'ADN a la seqüència consens TGAC/GTCA. Fos i Jun són els principals components d'AP-1. Fos i Jun són gens de resposta immediata que s'activen en resposta a l'estrés quan es veuen fosforil·lats per cinases d'estrés com la JNK (c-jun N-terminal kinase)/SAPK (stress-activated protein kinase) (Gupta et al., 1996) o de manera indirecta (via activació d'ATF2 i Elk-1), per la p38 (Hazzalin et al., 1996). La relació entre l'activació de c-Fos i c-Jun i la mort neuronal va quedar clara fa anys mitjançant dues observacions. La primera és que l'eliminació de l'expressió d'aquests factors *in vitro* o *in vivo* incrementa la supervivència de les neurones quan s'enfronten a diferents estímuls nocius (Martin et al., 1988, Eilers et al., 1998, Ham et al., 2000). La segona és que si

s'evita la fosforil·lació de c-Jun mitjançant mutacions als epítops fosforil·lables per JNK s'evita també l'apoptosi induïda per privació de factors tròfics i també la sensibilitat a l'excitotoxicitat induïda per àcid kaínic (Behrens et al., 1999, Le-Niculescu et al., 1999).

L'estudi de l'expressió d'aquests factors induïbles ha estat realitzada sobre algunes malalties neurodegeneratives com la MA i sobre alguns models animals d'aquestes malalties. Fins al moment no s'ha pogut demostrar una relació entre l'expressió anòmala d'aquests factors i els seus activadors amb un augment de mort neuronal per apoptosi en les taupaties. Probablement les conseqüències de la desregulació d'aquests factors de resposta immediata es produeixen tan ràpidament que se'n fa molt difícil la mesura en el teixit postmortem.

L'expressió de c-jun i c-fos ha estat particularment estudiada en la MA. En aquesta malaltia la rellevància d'AP-1 (en especial l'homodímer jun:jun) és notable pel fet que és un dels factors de transcripció que podrien regular l'expressió de la proteïna APP, i tenir per tant un efecte sobre la producció d'amiloide (King and Scott Turner, 2004). S'ha descrit que la immunoreactivitat de c-jun es veu incrementada a la MA (Anderson et al., 1996), en especial en neurones amb cabdells neurofibril·lars. L'augment d'expressió de c-jun a l'hipocamp de malalts de MA coincideix amb l'observació d'un increment de mRNA en aquesta zona. L'expressió de c-Jun en cèl·lules glials al voltant de plaques també s'ha vist incrementada. Cal mencionar que les observacions sobre el factor de transcripció c-Jun mitjançant tècniques d'immunohistoquímica poden haver-se de reinterpretar a la llum d'anticossos més específics que els utilitzats en alguns d'aquests estudis, que poden estar reconeixent epítops similars d'altres proteïnes (Ferrer, 2006).

El paper i localització de c-Fos en la MA també és controvertit sobretot pel què fa a la seva presència en cabdells neurofibril·lars i plaques senils. Però sembla que els seus nivells d'expressió estan augmentats en l'hipocamp de malalts de MA (Anderson et al., 1994, Marcus et al., 1998).

4.2.2 CREB i ATF-2

CREB (cAMP response element binding protein) i ATF-2 (activating transcription factor 2) són factors de transcripció relacionats amb gran quantitat de processos cel·lulars. CREB, una vegada fosforil·lat esdevé actiu i es pot unir a la CBP (CREB binding protein) i activar la transcripció gènica; també es pot activar per altres vies que inclouen les MAPK com p38 i ERK (Yamamoto et al., 1988). CREB es troba relacionat sobretot amb fenòmens de supervivència i proliferació, així com de creixement de neurites i diferenciació neuronal en determinades poblacions de neurones. Com hem dit, aquests factors de transcripció poden estar regulats per la forma activa (fosforil·lada) de la cinasa d'estrés p38. ATF-2, a més, també pot ser fosforil·lat per JNK. Com s'ha dit, les dues cinases d'estrés (p38 i JNK) es troben a les inclusions en totes les taupaties (Ferrer et al., 2005); els nivells d'expressió i la localització d'aquests dos factors de transcripció han estat parcialment estudiats en la MA. De moment els resultats assenyalen diferències subtils, si n'hi ha, en els nivells d'expressió pel que fa a ATF-2. En el cas de CREB, els nivells totals no varien però si sembla que els nivells de la forma fosforil·lada de CREB disminueixen en la MA (Yamamoto-Sasaki et al., 1999).

4.2.3 Sp1

La família Sp es compon d'una colla de factors de transcripció de tipus « zinc finger » (dits de zinc) que es poden unir a regions dels promotors amb caixes GC de gran quantitat de gens (Philipsen and Suske, 1999). Aquest factors poden reprimir o promoure l'expressió dels gens en funció de seu estat de fosforil·lació i dels co-activadors o co-repressors que intervinguin en el procés (Chu and Ferro, 2005).

El factor de transcripció Sp1 és particularment interessant perquè s'ha vist que es troba atrapat a les inclusions intranuclears de huntingtina mutada a la malaltia de Huntington. Aquesta associació té una explicació clara i es pot preveure pel fet que Sp1 posseeix uns dominis d'activació rics en glutamina. L'alteració que pateix la huntingtina en la malaltia de Huntington consisteix precisament en extensions de poli-Glutamina (DiFiglia et al., 1997). Aquestes extensions atrapen l'Sp1 enganxant-se als seus propis dominis rics en

glutamina i també, i pel mateix motiu, a un dels co-activadors de Sp1, (TAF)II130 (Freiman and Tjian, 2002).

Hi ha altres malalties neurodegeneratives que estan causades per extensions de poli-glutamina. Són el grup de les atàxies espino-cerebel·loso (AECs). En alguna AEC, causada per extensions de poli-glutamina en una proteïna anomenada ataxina (Ross, 1997) que també s'agrega formant inclusions, també s'ha trobat la presència d'Sp1 en aquestes inclusions (Shimohata et al., 2000).

El possible segrest d'Sp1 en inclusions en la MA i en altres taupaties és interessant per més d'un motiu. El primer és que Sp1 està directament involucrat en el control de l'expressió de l'APP dependent de TGF-beta (Docagne et al., 2004); i també de l'expressió de BACE1 i BACE2 (Christensen et al., 2004, Sun et al., 2005), que estan involucrades en la funció beta-secretasa, que com hem vist és responsable del tall de l'APP i la producció de pèptid amiloide. A més, Sp1 està també involucrat en la regulació de l'expressió de tau (Heicklen-Klein and Ginzburg, 2000). Essent un factor de transcripció amb poder regulador de les principals proteïnes de la neuropatologia de la MA i altres taupaties, queda pendent l'estudi de l'expressió d'Sp1 en aquestes malalties.

Un segon motiu per estudiar l'Sp1 en les malalties neurodegeneratives és el fet que la seva expressió pugui estar en relació a una resposta compensatòria davant de l'estrés oxidatiu. Això és el que sembla indicar el fet que es detecta un fort increment d'expressió d'aquest factor en resposta a l'estrés oxidatiu sobre neurones corticals embrionàries. L'estrés oxidatiu incrementat sembla que és un fenomen comú en moltes malalties i en especial en malalties neurodegeneratives. El següent apartat està exclusivament dedicat a parlar d'aquest aspecte. El rol d'Sp1 en relació a l'estrés oxidatiu queda reforçat per la seva capacitat d'induir l'expressió de la superoxid dismutasa 2 (SOD-2) (Xu et al., 2002). Aquest enzim s'encarrega en els mitocondris de protegir contra els excessos de les espècies radicals d'oxigen (ROS) (Melov, 2002).

4.3 14-3-3

Als agregats proteics s'hi troben xaperones com algunes de la família de les "heat shock proteins" (HSP) o la família de les 14-3-3. La 14-3-3 és una família de proteïnes composta de 7 isoformes diferents (beta, epsilon, eta, gamma, tau, sigma, zeta) que representen aproximadament un 1% del total de proteïnes solubles del cervell. Exerceixen la seva funció unint-se a proteïnes que presentin un motiu fosfo-serina determinat. Entre les múltiples funcions que duen a terme hi ha la de xaperona, però poden veure's involucrades en funcions reguladores de diferents vies de senyalització (d'apoptosi, control del cicle cel·lular i transport vesicular, entre d'altres) (Ferl, 1996, Darling et al., 2005, Muslin and Lau, 2005, Aitken, 2006, Hermeking and Benzinger, 2006). Tota cèl·lula eucariota expressa una isoforma o altra de 14-3-3 i s'han identificat més de 100 proteïnes que hi poden interaccionar (Dougherty and Morrison, 2004). En el cervell humà adult estan molt expressades i dins les neurones d'un cervell normal es poden detectar en el citoplasma i a les sinapsis (Fu et al., 2000).

Alguns estudis han indicat que algunes proteïnes 14-3-3, i en especial la isoforma zeta, es troben localitzades en els cabdells neurofibril·lars en la MA (Layfield et al., 1996, Umahara et al., 2004b). A més de trobar-se en les incusions, altres estudis assenyalen que algunes isoformes (zeta, gamma i epsilon) es troben sobre-expressades en MA i dues d'elles també en la síndrome de Down (Fountoulakis et al., 1999, Soulie et al., 2004).

La localització d'isoformes de 14-3-3 en les incusions de tau té sentit per dos motius. El primer és que la tau pot interactuar almenys amb dues isoformes de 14-3-3 (zeta i beta) en extractes de cervell; però no amb dues altres (gamma i epsilon) (Hashiguchi et al., 2000). El segon motiu és que aquestes proteïnes tenen entre les seves funcions la de regular algunes cinases com la GSK3-beta i la CAMK (Hashiguchi et al., 2000), les dues amb l'habilitat de fosforil·lar tau i presents en les incusions. S'ha descrit que dímers de la isoforma zeta poden unir-se al mateix temps amb la tau i la GSK3-beta de manera que es promou la fosforil·lació de la primera per part de la segona (Agarwal-Mawal et al., 2003). I a més, la 14-3-3 és capaç, mitjançant la seva unió a la GSK3-beta fosforil·lada a la serina 9, la forma inactiva, de mantenir aquesta cinasa activa (Yuan et al., 2004). Aquesta és una possible explicació, com s'avançava a l'apartat 4.1.1, de perquè

la forma inactiva de la GSK3-beta sembla mantenir la seva activitat tan a jutjar pels epítops de tau que es troben fosforil·lats en les inclusions, com pels assajos d'activitat cinasa.

4.4 UBB+1 i p62

A més de les xaperones, fins a cert punt és esperable que en els agregats proteics tant de tau com d'altres proteïnes que s'observen a les malalties neurodegeneratives s'hi involucrin proteïnes relacionades amb la degradació proteosomal. Així doncs, la totalitat d'inclusions proteïques que s'han identificat en malalties neurodegeneratives es poden detectar amb anticossos que reconeguin la ubiquïtina. Un cert tipus de complex proteosomal (26S) és capaç d'eliminar proteïnes mal plegades un cop aquestes s'associen a la ubiquïtina. L'objectiu d'aquest marcatge és la degradació d'aquestes proteïnes mal plegades, i el motiu de què la inclusió no desaparegui una vegada les seves proteïnes són poli-ubiquïtinitzades s no es coneix amb exactitud però poden tenir-hi a veure dues observacions. La primera és que el sistema de degradació proteosomal pot estar alterat i la seva activitat, disminuïda. I això s'ha pogut observar en MA i altres taupaties, així com en sinucleïnopaties (Layfield et al., 2003).

La segona observació és la presència en les inclusions d'una forma mutada de la ubiquïtina, la UBB+1 (van Leeuwen et al., 1998). Aquesta, no es tracta d'una mutació hereditària sinó somàtica, que es produeix a nivell d'ARNm i dona lloc a una ubiquïtina modificada en el seu extrem C-terminal. Aquesta forma mutada no serveix per ubiquïtinitzar proteïnes però en canvi pot ser ubiquïtinitzada per la ubiquïtina normal i degradada al proteasoma. El problema apareix quan els nivells de UBB+1 són alts; llavors el proteasoma queda saturat i inutil·litzat (Lindsten et al., 2002). La UBB+1 es troba en les inclusions de tau en MA i en altres taupaties, la qual cosa suggereix un motiu adicional de mal funcionament del proteasoma en aquestes cèl·lules.

La proteïna p62 o Sequestosome 1 s'ha vist involucrada en processos d'agregació proteica i en la funció de llançadora de proteïnes poli-ubiquïtinitzades cap al proteasoma (Nakaso et al., 2004, Seibenhener et al., 2004). A la seva regió C-terminal, la p62 conté un domini d'unió a la ubiquïtina i

s'ha vist que és capaç de facilitar la degradació proteosomal de la proteïna tau. La regulació de la seva expressió corre a càrrec majoritàriament de factors de transcripció com l'Sp1, AP-1 i NFKbeta; i determinats insults, com són la inhibició dels proteasoma o l'augment de radicals lliures, poden induir-ne l'expressió. Una sobreexpressió de p62 comporta en cèl·lules la formació de grans inclusions. Aquestes dues últimes observacions suggereixen un paper per la p62 com a promotora de la formació d'inclusions. La interpretació d'aquest fenomen està en la línia de considerar les inclusions un mecanisme protector per empaquetar proteïnes anòmales o mal plegades. La p62 es troba present en inclusions de tau en diferents taupaties i també en inclusions d'alfa-sinucleïna en sinucleïnopaties (Zatloukal et al., 2002, Scott and Lowe, 2007); així com en agregats d'altres malalties com són les atàxies espinocerebelars (observacions pròpies).

4.5 LRRK2

La LRRK2 (Leucine Rich Repeat Kinase-2) és una proteïna enorme (de 2527 aminoàcids) el gen de la qual fa pocs anys es va trobar mutat en diverses famílies amb Parkinson familiar. Des de llavors s'han identificat al voltant de 30 mutacions en el seu gen (Mata et al., 2005). Aquestes mutacions en conjunt però en especial una d'elles (G2019S, la més freqüent) poden explicar fins un 13% dels casos totals de Parkinson familiar, i fins un 2% dels esporàdics (Di Fonzo et al., 2005, Farrer et al., 2005, Mata et al., 2005, Clark et al., 2006, Ishihara et al., 2006).

La funció d'aquesta proteïna no es coneix del cert però s'ha descrit que:

- 1) S'uneix a moltes proteïnes com xaperones (HSP90) (Hurtado-Lorenzo and Anand, 2008), proteïnes del citoesquelet (Jaleel et al., 2007, Gandhi et al., 2008) i de transport de vesícules entre d'altres (Shin et al., 2008).
- 2) Té capacitat d'hidrolitzar l'ATP amb el seu domini GTPasa (Guo et al., 2007).
- 3) Té activitat cinasa (Guo et al., 2007); amb el domini cinasa s'ha vist que és capaç de fosforil·lar el residu regulador de proteïnes d'unió a l'actina i la membrana com són l'eZRina, la radixina i la moesina (Jaleel et al., 2007).
- 4) Regular l'endocitosi regulada per clatrina mitjançant la interacció amb la pròpia clatrina, i amb la Rab5a (Shin et al., 2008).

S'hipotetitzava que aquesta proteïna pot tenir d'alguna manera relació amb les taupaties, bàsicament per dos motius. El primer és que algunes mutacions en el gen de la LRRK2 poden donar patologies pleiomòrfiques, és a dir que la mateixa mutació pot donar lloc a un Parkinson típic, o pot donar lloc a mort neuronal sense inclusions, o amb inclusions només reactives per ubiquitina i d'altres fenotips (Mata et al., 2006). És d'especial interès que un dels fenotips que pot donar és l'acúmul de tau en forma de cabdells neurofibril·lars distribuïts de manera que recorda una PSP (Zimprich et al., 2004, Rajput et al., 2006). Per tant, la mateixa mutació pot causar agregats de sinucleïna, de tau, d'ubiquitina o cap inclusió (Zimprich et al., 2004). S'ha proposat que els efectes patogènics d'aquesta proteïna mutada es troben al capdamunt de les vies de neurodegeneració que porten a la formació d'inclusions, tant de tau com d'alpha-sinucleïna (Mata et al., 2006).

El segon motiu és que alguns autors han assenyalat que la LRRK2 es troba present tant en agregats d'alpha-sinucleïna (cossos de Lewy) (Miklossy et al., 2006, Higashi et al., 2007, Melrose et al., 2007, Perry et al., 2008) com en inclusions de tau en diferents taupaties (Miklossy et al., 2006, Miklossy et al., 2007), tot i que aquest fet és motiu de controvèrsia. Mentre que alguns anticossos detecten LRRK2 a les inclusions, altres no ho fan (Giasson et al., 2006). Una possible explicació és que depèn de l'epítip. En general sembla que quan l'anticòs està fabricat per reconèixer extrems de la proteïna (en especial el C-terminal) és capaç de tenir les inclusions tant de tau com de sinucleïna. Per contra, quan l'epítip contra el qual ha estat dirigit es troba a regions internes de LRRK2 no es detecta la proteïna en cap inclusió. És per aquest motiu que alguns autors han proposat que el que realment es troba dins de les inclusions són fragments de LRRK2, i que la forma sencera o no hi és, o té els epítips emmascarats (Higashi et al., 2007).

La qüestió no està encara gens clara perquè un altre aspecte a tenir en compte és l'especificitat d'aquests anticossos, de la qual cosa en pot servir de reflexe el patró de bandes que detecten per Western blot. Algunes conclusions s'han tret d'estudis on s'utilitzen només determinats anticossos que generen molts dubtes respecte la seva especificitat quan s'analitzen per Western blot, pel fet que reconeixen moltes altres bandes apart de la corresponent a LRRK2, i en alguns casos aquesta no apareix (Miklossy et al., 2006, Melrose et al., 2007,

Alegre-Abarrategui et al., 2008). Abans de continuar especulant sobre el paper de LRRK2 en les inclusions tant en taupaties com en sinucleïnopaties, cal revisar de manera conjunta els resultats obtinguts fins ara i els anticossos utilitzats per obtenir-los.

5- ESTRÉS OXIDATIU EN TAUPATIES

L'estrés oxidatiu és un fenomen que generalment es defineix com un excés de radicals lliures d'oxigen (ROS) que sobrepassa, o com a mínim obliga a contra-actuar, els sistemes antioxidants de defensa de l'organisme. Existeix un gran nombre d'evidències que vinculen l'estrés oxidatiu amb moltes malalties neurodegeneratives.

Els radicals lliures d'oxigen són produïts pel fet de dur a terme un metabolisme aeròbic. Aquest es produeix als mitocondris, que esdevenen així el principal lloc de producció de radicals lliures, com el superòxid (O₂⁻). Els radicals lliures es caracteritzen per ser formes molt reactives, propietat que s'explica pel fet de posseir un o més electrons desaparellats. També entren en aquest grup les molècules òxid nítric (NO), el radical hidroxil (OH⁻) i el peròxid d'hidrogen (H₂O₂). L'organisme compta amb una sèrie d'enzims que permeten l'eliminació d'aquests ROS. La superòxid dismutasa (SOD), que és capaç de transformar el superòxid en peròxid d'hidrogen (H₂O₂). També col·laboren a l'eliminació de ROS la catalasa, la glutatió reductasa i la glutatió peroxidasa. Es proposa que la glia, en concret els astròcits, tenen un paper molt important en la protecció de la neurones de l'acció dels ROS. A més, els astròcits posseeixen una major concentració de glutatió reduït així com d'enzims del metabolisme del glutatió.

Quan els sistemes anti estrés oxidatiu fallen i l'estrés supera les defenses, sembla que les cèl·lules moren per apoptosi en poques hores (Perry et al., 1998a, Perry et al., 1998b). Per tant, i tenint en compte que les cèl·lules dels malalts de diferents malalties neurodegeneratives no moren de cop, el què sembla és que en aquest tipus de malalties les defenses en realitat no estan sobrepassades,

sinó, com es demostra en molts casos, estan augmentades per compensar l'amenaça (Perry, 2003)..

Els ROS poden actuar sobre proteïnes, lípids i àcids nucleics i alterar el funcionament d'aquestes molècules. Els estudis que aquí es presenten es centren en la identificació de proteïnes modificades per l'efecte de l'estrés oxidatiu. Els ROS poden actuar directament sobre les proteïnes, o bé indirectament modificant àcids grassos i glúcids, i creant adductes reactius amb la capacitat d'unir-se a les proteïnes.

Els adductes que provenen de la glicoxidació o bé de la lipoxidació es poden reconèixer amb anticossos específics que permeten la identificació de les proteïnes modificades. El carboxi-etil-lisina (CEL) prové de la glicoxidació, el 4-hidroxinonenal (HNE) i el malondialdehid-lisina (MDAL) de la lipoxidació dels àcids grassos poli-insaturats (PUFAs) i el carboxi-metil-lisina (CML) prové tant d'un com de l'altre procés. Un altre marcador és l'increment d'AGEs (advanced glycation end products), així com del seu receptor, RAGE, que és un membre de la superfamília de les immunoglobulines a través dels quals els AGEs realitzen els seus efectes sobre les cèl·lules com pot ser l'activació de cinases (Schmidt et al., 2000). Els AGEs són grups carbonils producte de la glicoxidació que reaccionen amb les lisines de les proteïnes (Dalle-Donne et al., 2006). Altres adductes en proteïnes poden venir del peroxinitrit que prové de radicals lliures d'oxigen i nitrogen; aquests poden unir-se a les tirosines de les proteïnes donant lloc a les nitrotirosines, que també es poden usar de marcador amb anticossos específics.

S'ha descrit que el dany oxidatiu en proteïnes, lípids i àcids nucleics es veu incrementat amb l'edat (Stadtman, 2006), i alguns d'aquests danys també es detecten en models murins de senilitat accelerada (SAMP8) (Nabeshi et al., 2006). Però aquest augment del dany oxidatiu és major en malalts de diferents malalties neurodegeneratives (Perry, 2003).

En el cas de la MA s'han trobat nivells més elevats de diferents marcadors d'estrés: AGEs (Smith et al., 1994), nitració (Smith et al., 1997b), lipoxidació i glicoxidació (Smith et al., 1996, Sayre et al., 1997). L'origen d'aquesta major concentració de dany oxidatiu es relaciona amb diverses possibles fonts: el

pèptid amiloide soluble, el pèptid amiloide fibril·lar, els cabdells neurofibril·lars, problemes mitocondrials i l'edat. Els metalls que es concentren a les plaques amiloides, com el coure, el ferro o l'alumini (Good et al., 1992, Smith et al., 1997a), són també fonts d'estrés oxidatiu. Per últim, la microglia també contribueix amb l'alliberació de NO i O₂⁻ que poden combinar-se i formar el peroxinitrit. S'ha proposat també, a partir de certes observacions, que entre els efectes dels radicals lliures hi ha un increment de la producció d'amiloide i de tau fosforil·lada. Per exemple, un estudi indica que l'estrés oxidatiu induït per H₂O₂ augmenta l'activitat del promotor de BACE1 i, per tant, l'activitat Beta-secretasa i la producció de pèptid amiloide (Tong et al., 2005). Així mateix, el tractament en cultius primaris corticals de rata amb Fe i H₂O₂ augmenta notablement la fosforil·lació de tau (Lovell et al., 2004). La relació causa efecte entre el pèptid amiloide i l'increment d'estrés oxidatiu s'ha pogut observar en diferents models. En cèl·lules, per exemple, l'adició de vitamina E, un conegut antioxidant, fa disminuir la toxicitat provocada pel pèptid amiloide (Yatin et al., 2000, Munoz et al., 2005).

Mentre que determinats autors proposen, en base a diferents treballs *in vitro* o en models animals, que l'amiloide o la tau són una font capital de producció de radicals lliures, altres paren atenció a una paradoxa evident quan s'estudia aquesta associació d'una manera diferent. Observar les modificacions de les proteïnes per dany oxidatiu pot ser enganyós pel fet que una vegada modificades poden formar agregats i enlentir el seu recanvi. Això pot portar a situar en el present d'una cèl·lula un dany oxidatiu que va ocórrer en el passat, mentre que en la realitat present la cèl·lula no es troba estressada (Perry, 2003). L'estrés oxidatiu immediat es mesura millor observant les modificacions oxidatives dels àcids nuclèics mitjançant la detecció de la 8-hidroxiuanosina (8OHG), resultant de l'atac de grups hidroxils a les guanidines. El que s'ha vist és que neurones amb cabdells neurofibril·lars, encara que mostraven un augment de marcadors de lipo o glicoxidació, tenien uns nivells molt baixos de 8OHG. També és paradoxal que els malalts de MA amb més dipòsits d'amiloide presenten els nivells més baixos de 8OHG (Hensley et al., 1994). Aquestes observacions han portat a alguns autors a proposar un paper per les inclusions de tau i d'amiloide com a un mecanisme, de la cèl·lula, antioxidant compensador. Tanmateix, cal mencionar el fet que estudis sobre l'activitat del proteasoma 20S, particularment avesat en la degradació de les proteïnes oxidades, han mostrat

que les proteïnes malmeses pel dany oxidatiu són ràpidament degradades i proteïnes noves es comencen a sintetitzar, de manera que el recanvi es produeix més ràpidament (Davies, 2001). Però si no es degraden al ritme necessari, aquestes proteïnes modificades poden formar agregats degut a unions covalents i un augment de la seva hidrofobicitat (Grant et al., 1993), la qual cosa si és capaç de retardar el seu recanvi.

Diversos marcadors d'estrès oxidatiu s'han trobat augmentats en altres taupaties menys estudiades com la PSP (Albers et al., 1999, Albers et al., 2000), MPi (Montine et al., 1997, Zarkovic, 2003) o DFTP-17 (Martinez et al., 2008a), però no hi ha tanta feina feta com a la MA; això és especialment cert pel què fa a la MGA, on no s'han realitzat encara molts d'aquests anàlisis. Molt més ben descrit està l'increment de marcadors d'estrès oxidatiu en sinucleïnopaties, com el PD o la DCL (Dexter et al., 1989, Castellani et al., 1996, Floor and Wetzel, 1998, Jenner, 2003).

Les modificacions causades per l'estrès oxidatiu sobre els aminoàcids de les proteïnes sovint pot comportar una pèrdua de funció o d'activitat enzimàtica (Uchida et al., 1997). És per això que un dels principals interessos consisteix en identificar quines són exactament les proteïnes diana del dany oxidatiu en les malalties neurodegeneratives. És d'especial interès conèixer si existeixen proteïnes diana en zones del cervell encara no afectades per la malaltia quan aquesta es troba en una fase més primerenca. Conèixer les proteïnes que comencen a fer fallida previament a la clínica i/o a l'aparició d'inclusions podria tenir un valor diagnòstic o terapèutic.

Objectius

Objectiu general:

- **Estudiar els components proteïcs i les seves possibles modificacions post-traduccionals en les inclusions anòmales de diferents taupaties i sinucleïnopaties.**

Objectius concrets:

1.- Establir la sensibilitat de les mostres de teixit cerebral humà en relació a la possible degradació de les proteïnes i de les seves modificacions post-traduccionals (en especial la fosforil·lació) com a conseqüència del inevitable retard en el processament postmortem del sistema nerviós humà. Establir les condicions bàsiques per treballar amb condicions òptimes de no degradació de proteïnes.

2.- Estudiar els patrons de possibles fragments de tau en diferents taupaties així com l'expressió de diferents proteases de tau.

3.- Estudiar l'expressió de diferents factors de transcripció relacionats amb estrès (c-fos, c-jun, ATF2, CREB) i amb la regulació de proteïnes clau (Sp1) en taupaties i sinucleïnopaties i la seva associació amb les inclusions proteïques.

4.- Estudiar mecanismes patogènics en la poc coneguda taupatia malaltia de grans argiròfils (MGA).

5.- Revisar i tractar d'establir la presència o absència de la proteïna LRRK2 en els agregats de tau i de sinucleïna en taupaties i sinucleïnopaties, respectivament.

6.- Identificar proteïnes modificades per l'estrès oxidatiu en fraccions enriquides en filaments de tau hiperfosforil·lada en la malaltia d'Alzheimer.

7.- Caracteritzar neuropatològica i bioquímicament els estadiatges primerencs i pre-clínics de la taupatia paràlisi supranuclear progressiva. Estudiar els patrons de tau hiperfosforil·lada i possibles fragments en aquesta malaltia així com dianes d'estrès oxidatiu.

Resultats

1

Brain protein preservation largely depends on the postmortem storage temperature: implications for study of proteins in human neurologic diseases and management of brain banks: a BrainNet Europe Study

ORIGINAL ARTICLE

Brain Protein Preservation Largely Depends on the Postmortem Storage Temperature: Implications for Study of Proteins in Human Neurologic Diseases and Management of Brain Banks: A BrainNet Europe Study

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Abstract

The present study was designed to reveal protein modifications in control cases related with postmortem delay and temperature of storage in 3 paradigms in which the same postmortem tissue sample (frontal cortex) was frozen a short time after death or stored at 1°C, 4°C, or room temperature and then frozen at –80°C at different intervals. No evidence of protein degradation as revealed with monodimensional gel electrophoresis and Western blotting was observed in samples artificially stored at 1°C and then frozen at different intervals up to 50 hours after death. However, the levels of several proteins were modified in samples stored at 4°C and this effect was more marked in samples stored at room temperature. Two-dimensional gel electrophoresis and mass spectrometry further corroborated these observations and permitted the identification of other proteins vulnerable or resistant to postmortem delay. Finally, gel electrophoresis and Western blotting of sarkosyl-insoluble fractions in Alzheimer disease showed reduced intensity of phospho-tau-specific bands with postmortem delay with the effects being more dramatic when the brain samples were stored at room temperature for long periods. These results emphasize the necessity of reducing the body temperature after death to minimize protein degradation.

Key Words: Brain banks, Human brain tissue, Postmortem delay, Protein preservation.

INTRODUCTION

Although several experimental approaches and animal models have been used to mimic situations occurring in human degenerative diseases of the nervous system, the direct study of human brain tissue is crucial to increasing our understanding of real human neurodegenerative disorders. Optimal material quality is, however, a determining condition to avoid pitfalls related to tissue obtained at postmortem under suboptimal conditions. Many factors can affect the preservation of brain tissue before and after death. Premortem, the most relevant factors are the metabolic state, the use of toxic substances and drugs, infections, seizures, and hypoxia. Moreover, their detrimental effects can be augmented by a prolonged agonal state. At postmortem, delay among brain extraction, storage and tissue processing, as well as environmental temperature, are the most critical factors (1). Because the 2 last factors are the easiest to control, we have focused our study on postmortem delay and temperature to determine their relevance in the degree of preservation and degradation of brain proteins. This is an important issue because protein expression levels, as revealed by gel electrophoresis and Western blotting, are currently used in studies of human diseases of the nervous system.

One-time studies with human brain tissue have shown the importance of assessing the effects of postmortem delay on the preservation of target proteins. According to these observations, it has been shown that some proteins are very resistant to postmortem delay, whereas others are not. For example, Li et al studied the effects of postmortem delay (between 5 and 21 hours) in the expression levels of G-proteins in human prefrontal cortex (2). Under the same conditions, G α -i1, G α -i2, G α -S, and G β were stable, whereas G α -q and G α -o were vulnerable to postmortem delay. Similarly, Siew et al, focusing on the expression of pre- and postsynaptic proteins in the rat cerebral cortex at

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This study was supported by the European Commission under the Sixth Framework Programme (BrainNet Europe II, LSHM-CT-2004-503039).

different intervals postmortem, showed that synaptophysin and PSD-95 remained stable throughout the period studied, whereas the expression levels of syntaxin decreased at 48 hours when the brain was stored at room temperature and at 72 hours when the brain was maintained at 4°C (3). Similar results were obtained when examining the effects of postmortem delay and temperature on selected synaptic proteins by immunohistochemistry (4). Delayed tissue processing after death results in variable modifications in the expression levels of the microtubule-associated proteins tau, MAP2, MAP1B, and MAP5 (5, 6). Nucleosides in the brain are also subject to postmortem degradation (7).

Effects of postmortem delay are also important when studying posttranslational modifications in certain human degenerative diseases as hyperphosphorylated tau band profiles in sarkosyl-insoluble fractions in Alzheimer disease (AD) and other tauopathies (8, 9). Modifications in the expression levels of phosphorylated proteins may be related to the presence of still active proteases and phosphatases in the postmortem brain (10, 11).

The present BrainNet Europe study concerning preservation trials was designed to reveal protein modifications in human postmortem brains in several paradigms. For this purpose, the same tissue sample was frozen shortly after death or stored at 1°C, 4°C, or at room temperature for varying time periods and then frozen at -80°C until use. The samples were analyzed by gel electrophoresis and Western blotting with a battery of antibodies including synapsin-related proteins, kinases, proteins of the cytoskeleton, trophic factor receptors, membrane protein, protein related with oxidative stress, protein associated with apoptotic pathway, and members of the ubiquitin proteasome system. The selection of these proteins was made at random to represent a varied range of proteins that can be possible targets for study in human diseases of the nervous system. Other samples were analyzed by bidimensional (2D) gel electrophoresis, in-gel digestion, and mass spectrometry. This permitted the identification of other proteins vulnerable to postmortem delay. Finally, the effects of postmortem delay on posttranslational modifications related to tau hyperphosphorylation in tauopathies were examined by gel electrophoresis and Western blotting of sarkosyl-insoluble fractions in cases with Alzheimer disease. Because it has been reported that another source of variation in the postmortem vulnerability of certain proteins is as a result of their regional location in the brain (3), the present study focused on human brain frontal cortex to eliminate possible regional bias.

MATERIALS AND METHODS

Human Brain Tissue

Protein preservation was examined in several paradigms that try to mimic postmortem delay degradation in the human brain. Review of clinical records and general autopsy reports revealed that all patients showed minimal evidence of prolonged agonal state. No evidence of neurologic disease, drug intake, or metabolic disease was noticed. The patients studied included 3 men and one woman. The age at

death was 68, 66, 65, and 63 years, and the cause of death was heart failure in 3 cases and pneumonia in the fourth. The brains were obtained for research after written consent from the relatives following the guidelines of the local ethics committee of the IDIBELL-Hospital Universitari de Bellvitge. In all cases, half of the brain was stored in 4% paraformaldehyde in phosphate buffer for 3 weeks and then processed for the current neuropathologic study. The other half of the brain, except the frontal lobe, was immediately cut in coronal sections, frozen, and stored at -80°C. Part of the left frontal lobe, including Brodmann areas 8, 9, 45, and 46, was used for the present study. The basal pH of the brain tissue was 6.8, 7.2, and 6.9 in the 4 cases.

Finally, the frontal cortex (areas 8) of 4 cases with AD stage VI/C according to Braak and Braak was used in the study of phospho-tau degradation in relation to postmortem delay (12). AD cases were 2 men and 2 women aged 72, 68, 78, and 81 years. The neuropathologic diagnosis was carried out using the same regions and methods as described previously.

Paradigms Mimicking Delayed Postmortem Delay; Modifications of Storage Time and Ambient Temperature

In case 1, samples were obtained and frozen 2 hours after death or stored for 3, 6, 21, and 48 hours (i.e. 5, 8, 23, and 50 hours of postmortem delay) at 4°C and then frozen at -80°C. In case 2, samples were obtained and frozen 2 hours and 15 minutes after death or stored for 2 hours 45 minutes, 5 hours 45 minutes, 13 hours 45 minutes, 22 hours 45 minutes, and 48 hours (i.e. 5, 8, 16, 23, and 50 hours of postmortem delay) at 1°C and then frozen at -80°C. In case 3, samples were obtained and frozen 2 hours after death or stored for 3, 6, 21, and 48 hours (i.e. 5, 8, 23, and 50 hours of postmortem delay) at room temperature (23°C) and then frozen at -80°C. In case 4, samples were obtained and frozen 2 hours after death or stored for 3, 6, 22, and 46 hours (i.e. 5, 8, 24, and 48 hours of postmortem delay) at room temperature (22°C) and then frozen at -80°C.

Regarding AD cases, the brains were obtained 2 hours after death in 2 cases (cases AD1 and AD2) and the samples of the left frontal cortex were rapidly frozen at -80°C or stored at room temperature for different time periods and then frozen at 5, 8, 26, and 50 hours after death. Another case (case AD3) was obtained at 6 hours after death and then frozen or stored at room temperature for different time periods and then frozen at 8, 12, 18, 24, and 48 hours after death. The fourth case (case AD4) was obtained 8 hours after death and then frozen. Later, part of the sample was thawed and pieces were maintained at room temperature until 12, 18, 24, and 48 hours after death and then frozen until use. In every case, the blocks were wrapped in normal kitchen aluminum foil and maintained at room temperature in a plastic box with appropriate humidity conditions until frozen.

Biochemical Studies

Frontal cortex homogenates at the different time points in the first 3 paradigms were subjected to monodimensional gel electrophoresis and Western blotting. Twenty-three

antibodies recognizing specific proteins were analyzed. These antibodies included proteins involved in the cytoskeleton and synapses, membrane proteins, trophic factors and their receptors, proteins involved in cell survival and cell death, and transcription factors (Table 1). Every sample was processed per triplicate on different days.

In addition, the same tissue samples were examined in several human brain banks: Milan, Vienna, Munich, Edinburgh, and Bologna. Western blotting was restricted to 4 proteins (AKT-P, CaM kinase II, β -actin, and α -tubulin) in these laboratories. The antibodies were provided by the laboratory of reference so that the same aliquots were used by the different partners.

Bidimensional gel electrophoresis of the first, second, and fourth case was carried out in Barcelona. Finally, monodimensional gel electrophoresis and Western blotting of sarkosyl-insoluble fractions was carried out in the 4 cases with AD in Barcelona.

Monodimensional Gel Electrophoresis and Western Blotting

Brain samples (0.2 g) were homogenized separately in a glass homogenizer in 1 mL of homogenizer Buffer (10 mM

Tris-HCl pH 7.4, 100 mM NaCl, 10 mM EDTA, 0.5% sodium deoxycholate, and 0.5% NP40) and complete protease inhibitor cocktail (Roche Molecular Systems, Madrid, Spain). After a brief centrifugation at 15,000 rpm (4°C for 5 minutes), the pellet was discarded and the concentration of the resulting supernatant was determined by the bicinchoninic acid (BCA) method with bovine serum albumin as a standard.

For Western blot studies, 30 μ g was mixed with reducing sample buffer and processed for 10% SDS-PAGE electrophoresis and then transferred to nitrocellulose membranes (400 mA, 90 minutes). Immediately afterward, the membranes were incubated with 5% skimmed milk in TBS-T buffer (100 mM Tris-buffered saline, 140 mM NaCl, and 0.1% Tween 20, pH 7.4) for 30 minutes at room temperature and then incubated with the primary antibody in TBS-T containing 3% BSA (Sigma, Madrid, Spain) at 4°C overnight. The characteristics of the primary antibodies are given in Table 1.

Subsequently, the membranes were incubated for 45 minutes at room temperature with the corresponding secondary antibody labeled with horseradish peroxidase (Dako, Madrid, Spain) at a dilution of 1:1000 and washed

TABLE 1. Characteristics of the Antibodies Used

Antibody	Origin	Supplier	Location	Dilution
Synaptic proteins				
Rabphilin	Mouse	Transduction	BD Biosciences, Madrid	1/350
Syntaxin	Rabbit	Calbiochem	Bionova	1/500
Rab3a	Rabbit	Santa Cruz	Quimigranel, Barcelona	1/200
α -synuclein	Rabbit	Chemicon	Pacisa Giralt, Madrid	
Kinases				
Mek 1	Mouse	Transduction	BD Biosciences	1/500
P38-P	Rabbit	Calbiochem	Bionova, Madrid	1/100
SAPK-JNK-P	Rabbit	Cell Signaling	Servicios Hospitalarios, Barcelona	1/50
Erk 42-44	Mouse	Transduction	BD Biosciences	1/500
AKT-P	Rabbit	Cell Signaling	Servicios Hospitalarios	1/500
Camk II α	Mouse	Zymed	Servicios Hospitalarios	1/200
Cdk 5	Rabbit	Calbiochem	Bionova	1/500
Fyn k	Mouse	Transduction	BD Biosciences	1/500
GSK-P Ser 9	Rabbit	Oncogene	Bionova	1/500
Cytoskeletal proteins				
α -tubulin	Mouse	Sigma	Sigma, Madrid	1/4,000
β -tubulin	Mouse	Sigma	Sigma	1/4,000
β -actin	Mouse	Sigma	Sigma	1/5,000
Trophic factor receptors				
EGF-R	Mouse	Chemicon	Pacisa Giralt, Madrid	1/200
TrkB	Rabbit	Santa Cruz	Quimigranel	1/200
Membrane protein				
PLC β 1	Rabbit	Santa Cruz	Quimigranel	1/200
Oxidative stress				
iNOS	Rabbit	Santa Cruz	Quimigranel	1/1,000
Apoptosis				
Bcl-2	Mouse	Novocastra	Servicios Hospitalarios	1/50
Proteasome				
Proteasome 11	Rabbit	Affinity	Bionova	1/500
Proteasome 20	Mouse	Biomol Intl.	Quimigranel	1/500

with TBS-T for 30 minutes. Protein bands were visualized with the chemiluminescence ECL method (Amersham, Barcelona, Spain).

The protocols used for gel electrophoresis and Western blotting differed slightly from one center to another. Methodological differences can be found on the BrainNet web site (http://www.brainnet-europe.org/activities/frameset_activities.htm).

Densitometry and Processing of Data

Protein expression levels were determined by densitometry of the specific bands using Total Lab v2.01 software (Pharmacia, Orsay, France). The results were normalized for β -actin. The numeric data obtained per triplicate for every protein at a given time period were expressed as a percentage of decrease compared with the corresponding basal (2-hour) values.

Two-Dimensional Gel Electrophoresis

Samples of the frontal cortex (0.1 g) were homogenized in homogenizer buffer (50 mM Tris pH 7.4 containing 150 mM NaCl, 1 mM EDTA, 1 mM EGTA, 1% Triton X-100, and a cocktail of protease and phosphatase inhibitors) and centrifuged at 15,000 rpm for 5 minutes. The pellet was discarded and the concentration of protein from the resulting supernatant was determined by BCA method. Equal amounts of protein were mixed with a buffer containing, at final concentrations, 40 mM Tris pH 7.5, 7 M urea, 2 M thiourea 0.2% Biolite (v/v), 4% CHAPS (Bio-Rad, Barcelona, Spain), 2 mM Tributylphosphine solution, and bromophenol blue in a total volume of 350 μ L.

In the first dimension electrophoresis, 350 μ L of sample solution was applied on an immobilized 17-cm pH 3–10 nonlinear gradient ReadyStrip IPG strip (Bio-Rad, Barcelona, Spain) at both the basic and acidic ends of the strip. The strips were actively rehydrated for 16 hours at 50 V and the proteins were focused at 300 V for 2 hours after which time the voltage was gradually increased over 4 hours to 1,000 V. Focusing was continued at 1,000 V for 2 hours and gradually increased to 8,000 V over 8 hours; it then continued at 8,000 V for 10 hours. For the second dimension separation, IPG strips were equilibrated for 15 minutes in 50 mM Tris-HCl (pH 6.8) containing 6 M urea, 2% (wt/v) SDS, 30% (v/v) glycerol, and 2% dithiothreitol and then reequilibrated for 15 minutes in the same buffer containing 2.5% iodoacetamide. The strips were placed on 10% polyacrylamide gels and electrophoresed at 50 V overnight. For gel staining, an MS-modified silver staining method (Amersham) was used as described by the manufacturer.

In-Gel Digestion

Proteins were in-gel-digested with trypsin (Sequencing grade modified; Promega, Barcelona, Spain) in the automatic Investigator ProGest robot of Genomic Solutions. Briefly, excised gels spots were washed sequentially with ammonium bicarbonate buffer and acetonitrile. Proteins were reduced and alkylated for 30 minutes with 10 mM DTT solution and 100 mM solution of iodine acetamide, respectively. After sequential washings with buffer and acetonitrile, proteins were digested overnight at 37°C with trypsin 0.27 nM. Tryptic peptides were extracted from the gel

matrix with 10% formic acid and acetonitrile. The extracts were pooled and dried in a vacuum centrifuge.

Acquisition of MS and MS/MS Spectra

Proteins manually excised from the 2D gels were digested and analyzed by CapLC-nano-ESI-MS-MS mass spectrometry. The tryptic digested peptide samples were analyzed using on-line liquid chromatography (CapLC; Micromass-Waters, Beverly, MA) coupled to tandem mass spectrometry (Q-TOF Global; Micromass-Waters). Samples were resuspended in 12 μ L of 10% formic acid solution, and 4 μ L was injected for chromatographic separation into a reverse-phase capillary C_{18} column (75 μ m of internal diameter and 15 cm in length, PepMap column; LC Packings, Sunnyvale, CA). The eluted peptides were ionized through coated nano-ES needles (PicoTip; New Objective, Woburn, MA). A capillary voltage of 1,800 to 2,200 V was applied together with a cone voltage of 80 V. The collision in the collision-induced dissociation was 25 to 35 eV, and argon was used as the collision gas. Data were generated in PKL file format and submitted for database searching in MASCOT server (Matrix Science, Boston, MA) using the NCBI database with the following parameters: trypsin enzyme, one missed cleavage, carbamidomethyl C as fixed modification and oxidized (M) as variable modification, and mass tolerance of 150 to 250 ppm. Probability-based MOWSE score was used to determine the level of confidence in the identification of specific isoforms from the mass spectra. This probability equals $10^{(-\text{MOWSE score}/10)}$. MOWSE scores greater than 48 were considered to offer high confidence of identification.

Gel Electrophoresis and Western Blotting of Sarkosyl-Insoluble Fractions in Alzheimer Disease

Frozen samples of approximately 2 g from the frontal cortex (area 8) were gently homogenized in a glass tissue grinder in 10 vol (w/v) with cold suspension buffer (10 mM TRIS-HCl, pH 7.4, 0.8 M NaCl, 1 mM EGTA, 10% sucrose). The homogenates were first centrifuged at 20,000 rpm and the supernatant (S1) was retained. The pellet was rehomogenized in 5 vol of homogenization buffer and recentrifuged. The 2 supernatants (S1 and S2) were then mixed and incubated with 0.1% N-lauroylsarcosinate (sarkosyl) for 1 hour at room temperature while being shaken. Samples were then centrifuged at 100,000 rpm in a Ti70 Beckman rotor. Sarkosyl-insoluble pellets (P3) were resuspended (0.2 mL/g starting material) in 50 mM TRIS-HCl (pH 7.4). Protein concentrations were determined with the BCA method. Equal amounts of protein (75 μ g) were loaded on to 10% sodium dodecylsulfate polyacrylamide gel electrophoresis and then electrophoretically transferred to nitrocellulose membranes (Hybond-C Extra; Amersham) at 400 mA/gel at 4°C. The membranes were blocked for 1 hour at room temperature with 5% nonfat dry milk in Tris-buffered saline containing 0.1% Tween 20 (TTBS) and were then incubated with rabbit polyclonal phosphospecific antibodies to tauSer422 (Calbiochem, La Jolla, CA). After washing with TTBS, blots were incubated with anti-rabbit IgG conjugated with horseradish peroxidase 1:1000 (Dako)

for 45 minutes at room temperature. Immunoreactive bands were visualized by chemiluminescence using the ECL method (Amersham).

RESULTS

Monodimensional Gel Electrophoresis and Western Blotting

Samples Stored at 4°C and Then Frozen

Monodimensional gel electrophoresis and Western blotting in case 1 (samples obtained and frozen at 2 hours (basal values) or stored at 4°C and then frozen at 5, 8, 16, 23, and 50 hours after death showed variable patterns of protein preservation with time (Fig. 1). Some proteins were vulnerable, particularly after 23 hours, whereas others remained practically unaffected at 50 hours. The most resistant proteins were β-actin, p38-P, proteasome 20, and proteasome 11. These proteins were considered suitable for the control of protein loading, and β-actin in particular was used for densitometric studies. Therefore, densitometric

values for a given protein were normalized for the corresponding values of β-actin. Examples of the diagrams and densitometric values are shown in Figure 2.

For comparative purposes, proteins were categorized according to the percentage of reduction of the densitometric intensity normalized for β-actin through time of postmortem. Data are summarized as follows: 1) proteins with no reduction at 23 and 50 hours when compared with basal values: p38-P, proteasome 11, β-actin, and proteasome 20S; 2) proteins with a percentage of reduction between 30% and 50% of basal values at 50 hours: SAPK/JNK-P, syntaxin, α-tubulin, and Fyn K; 3) proteins with a percentage of reduction between 60% and 90% from control values at 50 hours: Mek 1, rabphilin, α-synuclein, P-MAPK-ERK44/ERK42, rab3a, AKT-P, β-tubulin, CamK II, Cdk5, EGF-R, TrkB, Bcl-2, GSK Ser9, iNOS, and PLC β1; and 4) percentage of reduction between 40% and 60% at 23 hours: Mek 1, P-MAPK/ERK 44, AKT-P, CamK II, Cdk5, TrkB, Bcl-2, and iNOS.

Interestingly, the expression levels of all the proteins examined were preserved at 5 and 8 hours when compared

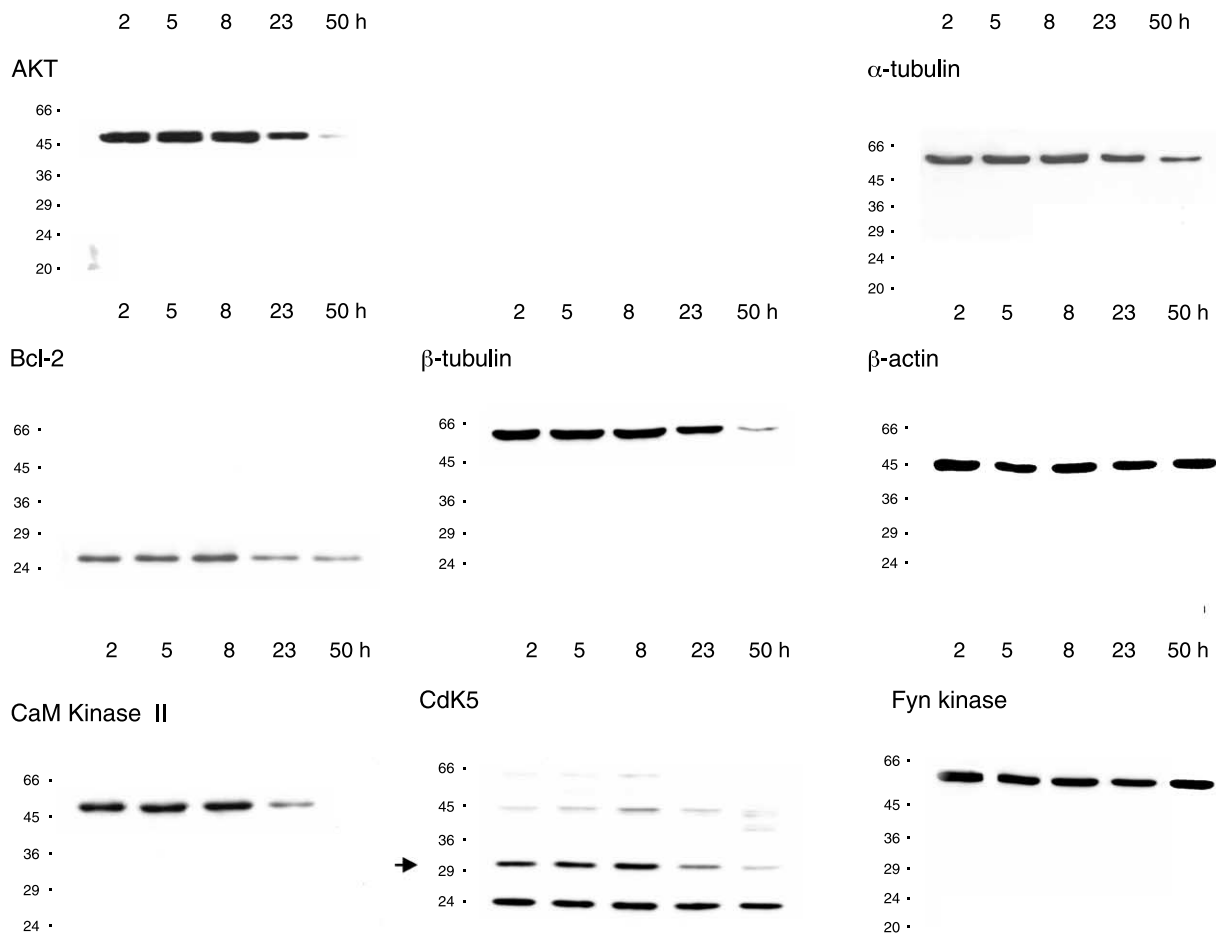


FIGURE 1. Western blots to several proteins in frontal cortex homogenates obtained and frozen 2 hours after death or stored for 3, 6, 21, and 48 hours (i.e. 5, 8, 23, and 50 hours of postmortem delay) at 4°C and then frozen at -80°C (case 1). Note that the decrease in the intensity of the bands with time postmortem is variable from one protein to another. Degradation of the majority of proteins occurs at 50 hours.

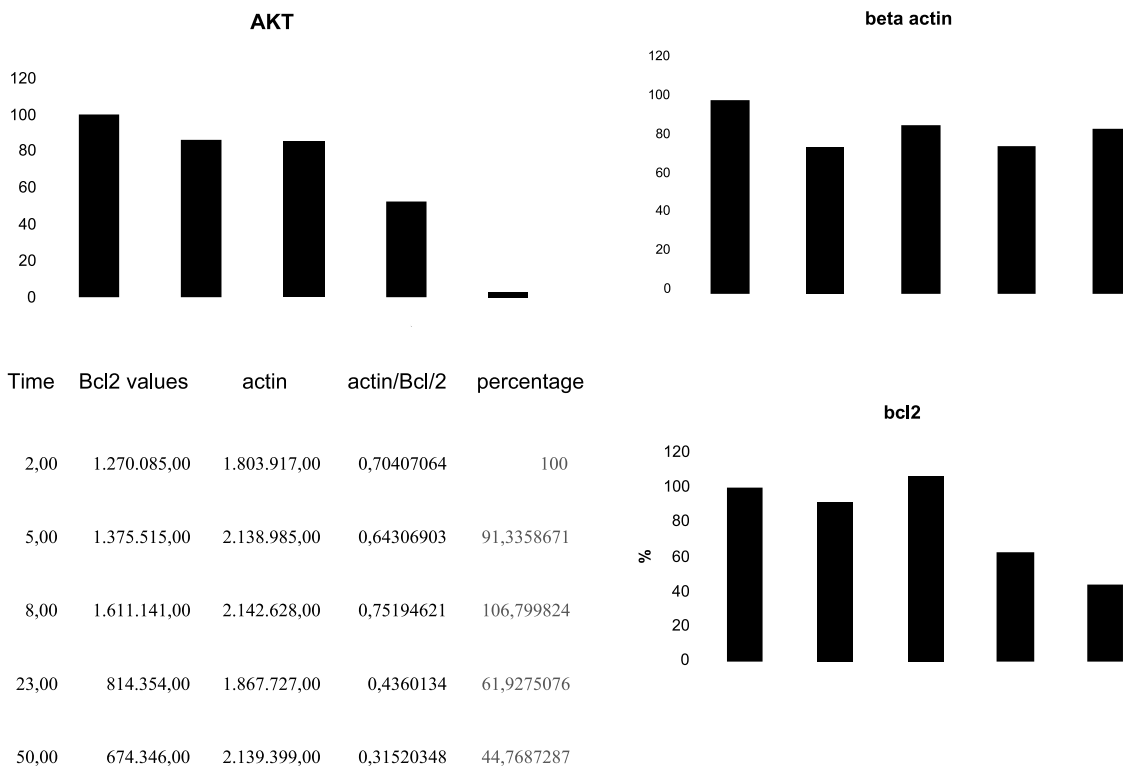


FIGURE 2. Examples of protein expression levels as determined by densitometry using Total Lab v2.01 software (Pharmacia, Orsay, France). The results are normalized for β-actin. The numeric data obtained for every protein at a given time period were finally expressed as a percentage of decrease compared with the corresponding basal values. Note variable vulnerability to postmortem delay in samples stored at 4°C and then frozen. The levels of AKT-P are markedly decreased with time, whereas the expression levels of β-actin remain stable. Graphics and numeric data of Bcl-2 have been used as an example.

with basal values. Day-to-day variations were ruled out by carrying out the experiments per triplicate in different days. The same results were obtained in the 3 different days, thus indicating high reproducibility.

Samples Stored at 1°C and Then Frozen

No modifications in staining were observed in the frontal samples of case 2 obtained and frozen 2 hours and 15 minutes after death (basal values) or stored for 2 hours 45 minutes, 5 hours 45 minutes, 22 hours 45 minutes, and 48 hours (i.e. 5, 8, 23, and 50 hours of postmortem delay) at 1°C, and then frozen at -80°C. Like in the previous paradigm, densitometric studies for every protein were normalized for β-actin.

Samples Stored at Room Temperature (23°C) and Then Frozen

Monodimensional Gel Electrophoresis and Western Blotting in Cases 3 and 4

Samples were obtained and frozen at 2 hours (basal values) or stored at 23°C and then frozen at 5, 8, 23, and 50 hours after death showed more severe patterns of protein degradation with time. All proteins examined except proteasome components were reduced at 50 hours. Data are summarized as follows: 1) proteins with no reduction at 23 hours when compared with basal values: p38-P, proteasome 11, β-actin, and proteasome 20S; 2) proteins with a

percentage of reduction between 30% and 50% of basal values at 23 hours: SAPK/JNK-P, syntaxin, α-tubulin, Fyn K, and α-synuclein; 3) proteins with a percentage of reduction between 60% and 90% from control values at 23 hours: Mek 1, rabphilin, α-synuclein, P-MAPK-ERK44/ERK42, rab3a, AKT-P, β-tubulin, CamK II, Cdk5, EGF-R, TrkB, Bcl-2, GSK Ser9, iNOS, and PLCβ1; and 4) percentage of reduction between 40% and 60% at 8 hours: Mek 1, P-MAPK/ERK 44, AKT-P, TrkB, and PLCβ1.

Interlaboratory Variations

Some experiments were carried out in parallel in other laboratories using similar protocols although with individual variations. Four proteins were validated in these studies: β-actin, AKT-P, Cam kinase II, and α-tubulin. Similar results were obtained for the various paradigms in the different laboratories.

Two-Dimensional Gel Electrophoresis, Silver Staining Detection, In-Gel Digestion, and Mass Spectrometry Analysis

Two-dimensional gels of frontal homogenates of case 2 stored at 1°C for different time periods up to 50 hours postmortem and then frozen at -80°C were stained with silver. Under these specific conditions, no differences were seen in the number and quality of the silver spots at 2 hours 15 minutes, 5, 8, 23, and 50 hours (data not shown).

TABLE 2. Identification of Proteins Vulnerable to Postmortem Delay in Samples Stored at 4°C for 50 Hours and Then Frozen at -80°C (case 1)

Spot	Calculated pI	KDa Nominal mass	Protein	Score Coverage	Number of Peptides Matched	G1 Accession Number
1	4.59	14.5	α -synuclein	69 sequence: 11%	1	gi 1230575
2	4.41	14.3	β -synuclein	78 sequence: 16%	2	gi 48255903
3	5.54	15.9	Chain E, superoxide dismutase	55 sequence: 15%	2	gi 349912
4	6.60	15.8	ATP synthase	73 sequence: 18%	2	gi 51479152
5	5.66	22.0	peroxiredoxin 2	158 sequence: 22%	4	gi 77744389

Score coverage: MOWSE scores greater than 48 are considered to offer high confidence of identification. Number of peptides indicates the number of peptides used to identify the protein.

In contrast, 2-dimensional gels of frontal homogenates of case 1 stored at 4°C for different time periods up to 50 hours and then frozen at -80°C disclosed marked differences in the silver staining of several spots. Interestingly, several spots progressively decreased in intensity until disappearance at the time point of 50 hours. Yet, other silver spots did not show differences in the intensity of staining (Fig. 3A, B).

Several spots at 2 hours 15 minutes and 50 hours were in-gel-digested and analyzed by mass spectrometry. The proteins resistant to postmortem delay were YWHAZ, G3PDH, malate dehydrogenase, and aldolase A. Several proteins were vulnerable to postmortem delay, including α -synuclein, β -synuclein, peroxiredoxin, ATP synthase, and superoxide dismutase 1 (Fig. 3C; Table 2). A semiquantitative study of selected proteins that are degraded with time is presented in Table 3, in which the percentage of reduction is expressed as a percentage of reduced density values in relation with a control protein (aldolase A), which is more stable during the period of the study.

Two-dimensional gels of frontal homogenates in case 4 in which samples were stored at room temperature (22°C) and then frozen disclosed several differences when comparing gels of 2 hours and 48 hours. Several proteins were identified as vulnerable to postmortem delay, including α -synuclein, β -synuclein, vacuolar proton ATPase, fructose-biphosphate

aldolase C, amphiphysin, and α -enolase (Fig. 4; Table 4). Other proteins, dihydropyrimidinase-like 2, manganese superoxide dismutase, G3PDH, 14-3-3, HSP90, and HSPgp96, were resistant. A semiquantitative study of selected proteins that are degraded with time is presented in Table 5, in which the percentage of reduction is expressed as a percentage of reduced density values in relation with a control protein (protein 14-3-3), which is more stable in these experimental circumstances during the period of the study.

Posttranslational Modifications in Alzheimer Disease: Phospho-tau Pattern in Sarkosyl-Insoluble Fractions

Blots of AD samples at 2 hours stored at 4°C revealed 3 bands of 68, 64, and 60 kDa, several bands between 60 kDa and 24 kDa, and a band of approximately 22 kDa for up to 26 hours in one case, but the phospho-tau bands were markedly decreased at the same time period in another case. Phospho-tau degradation, as revealed by reduction or near disappearance of the bands, was observed at 50 hours postmortem (Fig. 5A, B). More marked and rapid degradation was seen in samples obtained at 6 hours and stored at room temperature for different time periods when compared with the same tissue frozen at 6 hours after death (Fig. 5C). Interestingly, the lower bands were barely visible in this condition. Finally, poor

TABLE 3. Percentage of Reduction Through Time of Selected Proteins in Samples Stored at 4°C for 2, 5, 8, 23, and 50 Hours and then Frozen at -80°C (case 1)

	2 Hours	5 Hours	8 Hours	23 Hours	50 Hours	Percent of Reduction (between 2 and 50 hours)
Aldolase A	100	88.6	84.7	79.3	74.2	26
α -synuclein	81.1	27.5	1.5	0.4	0.3	99.6
α -synuclein	93.4	40.4	20.2	1.6	3.1	96.7
SOD1	32.1	27.9	40.5	21.2	4.8	85
ATP-synthase	12.5	8.9	3.2	1.5	3.4	72.8
Peroxiredoxin	21.3	6.6	11.4	11.9	4.7	77.9
14-3-3	110	91.6	107	102	76.6	30.4

Aldolase A (optical density arbitrarily considered as 100%) is chosen because its preservation was good up to 50 hours postmortem. Numbers in the table express the percentage of optical density when compared with the optical density of aldolase at every time point. Densitometric measurements were obtained by drawing a monodimensional transect across the spot and measuring the optical density along the transect.

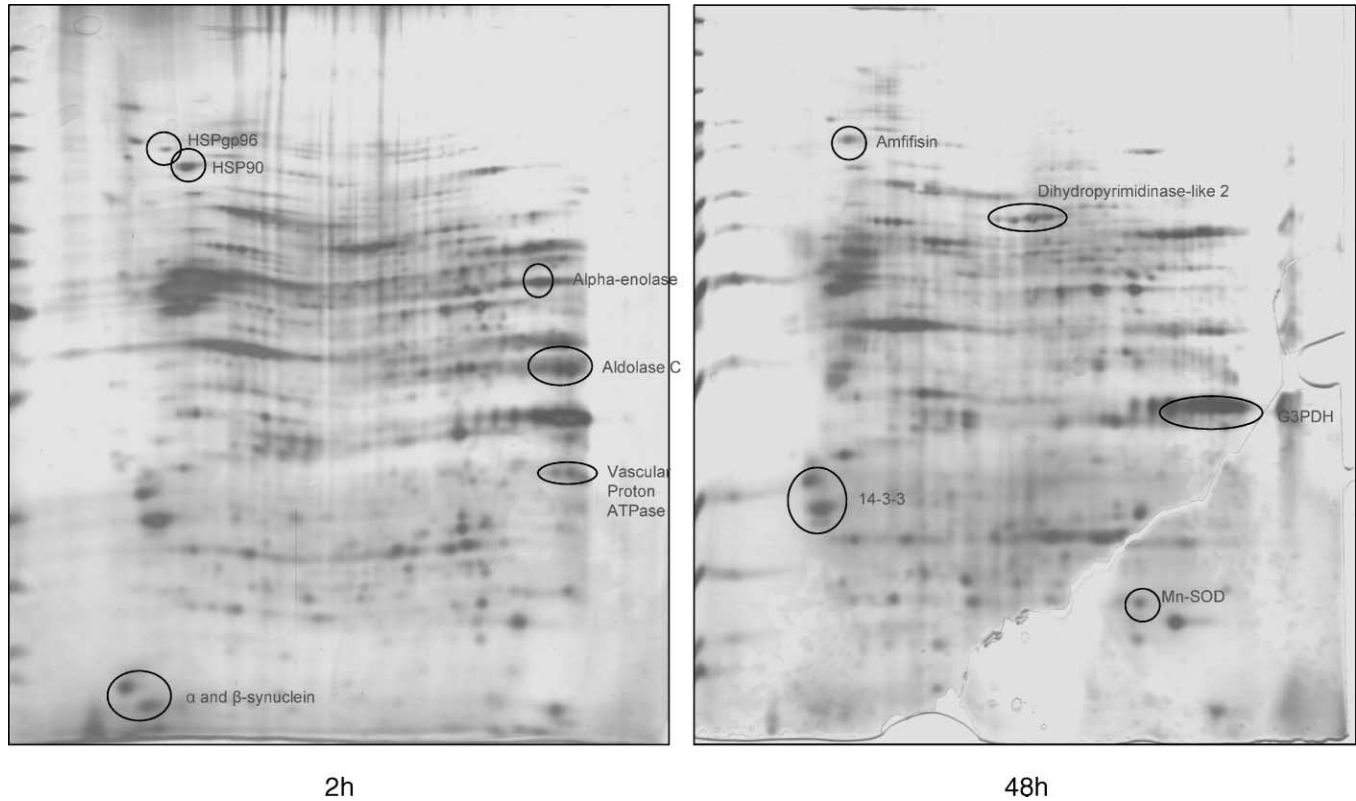


FIGURE 4. Two-dimensional gels of frontal cortex homogenates, stained with silver, of case 4 frozen at 2 hours after death or stored at room temperature (22°C) until 48 hours and then frozen. Labeled spots in the left panel correspond to proteins no longer present in samples stored at room temperature for 48 hours. Spots circled in the right panel correspond to proteins that are still present in samples at 48 hours. Vulnerable proteins are α -synuclein, β -synuclein, vacuolar proton ATPase, aldolase C, amphiphysin, and α -enolase. Resistant proteins are dihydropyrimidinase-like 2, manganese superoxide dismutase, G3PDH, 14-3-3, HSP90, and HSPgp96.

results were found in samples obtained at 8 hours after death (with the corpse maintained at room temperature) and then frozen. Moreover, no signal was seen in thawed samples further maintained at room temperature for variable periods and then frozen until use (Fig. 5D).

DISCUSSION

This study was designed to learn the effects of delay and temperature during the postmortem period in human brain

tissue. Other factors such as premortem metabolic status and agonal state were minimized in the present study. The pH of the tissues was neutral at the first time postmortem; thus, further indicating no major metabolic disturbances related with prolonged hypoxia and acidosis before death.

By using monodimensional gel electrophoresis and Western blotting to selected proteins, the present results support the concept that postmortem delay can affect protein levels by selective decay of vulnerable proteins.

TABLE 4. Identification of Proteins Vulnerable to Postmortem Delay in Samples Stored at Room Temperature (22°C) for 50 Hours and Then Frozen at -80°C (case 4)

Spot	Calculated pI	KDa Nominal mass	Protein	Score Coverage	Number of Peptides Matched	GI Accession Number
1	4.67	14.45	α -synuclein	628 sequence: 54%	15	gi 80475099
2	4.41	14.3	α -synuclein	78 sequence: 16%	2	gi 48255903
3	8.45	26.3	Vacuolar proton ATPase	85 sequence: 34%	8	gi 313014
4	6.41	39.8	Fructose-biphosphate aldolase C	82 sequence: 21%	6	gi 78070601
5	4,58	76,4	Amphiphysin	208 sequence: 23%	14	gi 4502081
6	7.01	47.5	α -enolase	292 sequence: 39%	16	gi 14530765

Score coverage: MOWSE scores greater than 48 are considered to offer high confidence of identification. Number of peptides indicates the number of peptides used to identify the protein.

TABLE 5. Percentage of Reduction Through Time of Selected Proteins in Samples Stored at Room Temperature (22°C) for 2, 5, 8, 23, and 50 Hours and Then Frozen at -80°C (case 4)

	2 Hours	5 Hours	8 Hours	23 Hours	50 Hours	Percent of Reduction (between 2 and 50 hours)
14-3-3	100	75.6	75.3	70.4	67.1	32.9
α-synuclein	91.1	47.2	42.8	56.9	0.5	99.5
β-synuclein	45.3	53.7	36.8	35.9	1.1	97.6
Vacuolar proton ATPase	84	85.2	83.2	73.5	1.4	93.3
α-enolase	74.4	37.2	43.1	8.8	1.2	98.4
Amphiphysin	13.7	12.8	5.4	5.3	0.3	97.8
Aldolase C	108	79.4	34.8	36.4	1	99

Protein 14-3-3 (optical density arbitrarily considered as 100%) is chosen because its preservation was good up to 50 hours postmortem. Numbers in the table express the percentage of optical density when compared with the optical density of 14-3-3 at every time point. Densitometric measurements were obtained by drawing a monodimensional transect across the spot and measuring the optical density along the transect.

Moreover, reduced temperature during the postmortem period is vital for protein preservation. Although the number of assays was limited, similar observations were obtained in

the several laboratories participating in this study, thus indicating that the present observations are applicable to different settings.

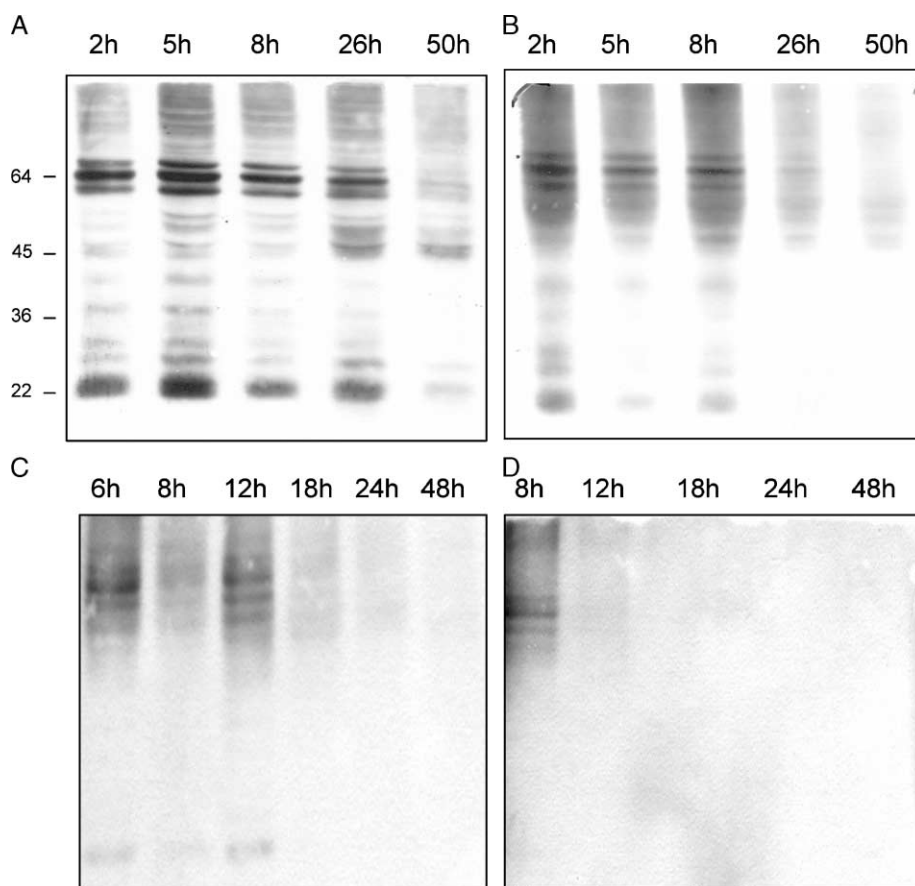


FIGURE 5. Effects of artificial postmortem delay in Alzheimer disease as revealed by gel electrophoresis and Western blotting of sarkosyl-insoluble fractions immunostained with specific anti-phospho-tau Ser 422 antibodies. **(A)** Bands of 68, 64, and 60 kDa, several bands between 60 kDa and 24 kDa, and a band of approximately 22 kDa are seen in samples obtained 2 hours after death and then frozen or stored at 4°C at 5, 8, and 26 hours and then frozen. Immunoreactivity decays at 50 hours in one case (case AD1). **(B)** The same apparent conditions result in reduced phospho-tau expression at 26 hours in another (case AD2). **(C)** Reduced immunoreactivity is found in samples obtained 6 hours after death and maintained at room temperature (23°C) and then frozen at progressive time periods. No signal is seen at 18, 24, and 48 hours of artificial postmortem delay (case AD3). **(D)** Very poor results are obtained in postmortem samples obtained at 8 hours and then frozen and later thawed and refrozen at 12, 18, 24, and 48 hours after death (case AD4).

The variable vulnerability of proteins to postmortem delay in the human brain is in line with histochemical and immunohistochemical observations in mice. Hilbig et al studied the effects of postmortem delay and storage temperature on the detection of antigens (13). They found that some proteins were more sensitive to storage temperature, other proteins were more sensitive to postmortem delay, and yet other proteins were always stable under their experimental conditions. The present findings also confirm previous observations on certain proteins such as the relative vulnerability of PLC β 1 (14) and the variable vulnerability of synaptic proteins (4). Synaptophysins are resistant proteins, whereas synucleins are not. It is worth noting that the present study is focused on normal brains and the vulnerability of synucleins refers to "normal" synuclein. It is likely that pathologic proteins forming aggregates such as α -synuclein in Lewy bodies in Lewy body diseases and glial cytoplasmic inclusions in multiple system atrophy are more resistant to degradation, a feature that permits their identification by immunohistochemistry. Reduced protein levels with postmortem may have implications in forensic pathology. Imidazole receptor-binding protein immunoreactivity is reduced with postmortem delay, a feature that has implications in the post-mortem study of depressed suicide victims (15). The effects of postmortem temperature here observed in the human brain are also in accordance with previous one-time studies showing that hypothermia reduces the postmortem degradation of MAP2, whereas normothermia makes MAP2 progressively undetectable with increasing postmortem interval in the rat (16).

Protein degradation in relation to increasing postmortem delay and storage temperature has been further analyzed by 2D gel electrophoresis, in-gel digestion, and mass spectrometry in the human brain. Spots corresponding to α -synuclein and β -synuclein gradually disappear with increasing postmortem intervals. Chain E, superoxide dismutase, ATP synthase, and peroxiredoxin 2 are no longer observed at 48 hours. Interestingly, aldolase A and malate dehydrogenase remain unaltered at 50 hours. Storage of the sample at room temperature further disclosed proteins, in addition to synucleins, which were vulnerable to postmortem delay. Vacuolar proton ATPase, fructose-biphosphate aldolase C, amphiphysin, and α -enolase were in this group. Why some proteins are more resistant than others is not clear. It can be suggested that housekeeping proteins are less vulnerable to postmortem delay, whereas proteins related to receptors and certain cytosolic proteins are more prone to degradation. However, this suggestion has to be validated with a more extensive sampling and identification of more proteins.

Postmortem-dependent variable reduction in the levels of proteins has implications not only in the identification of quantitative changes related with pathology in neurologic diseases, but may also have an impact on the study of the function of proteins in the postmortem brain. Preserved levels and activity of cathepsin D are stable for long periods at room temperature in human and mouse postmortem brain (17). Similarly, the expression levels of proteasome subunits are resistant to postmortem delay, and this resistance is accompanied by preserved proteasomal activity in human

and mouse brains (18). However, the study of ATP synthase activity in human postmortem samples stored at room temperature for 24 hours can be assumed to be unreliable as deduced from the observed decreased expression levels of the protein at this time point.

Postmortem delay in tissue processing is accompanied by decreased intensity of phospho-tau bands (9). Also, postmortem delay in tissue processing affects the phospho-tau band pattern in AD. This deleterious effect is markedly related with the temperature. Preservation of the samples at room temperature for more than 12 hours makes the biochemical study less reliable. This observation may not be limited to AD, but rather is probably applicable also to the study of other tauopathies. As a marginal note, thawed tissue stored at room temperature and then refrozen is definitely no longer usable for biochemical studies.

Together, these results confirm that the control of brain (body) temperature and the postmortem delay are crucial in the study of proteins in human postmortem samples. The present observations based on mono- and bidimensional gel electrophoresis, Western blotting, and mass spectrometry are useful in determining, on a large scale, the degradation of a brain sample. Therefore, it is probably prudent to carry out preliminary studies mimicking increased postmortem delay under conditions similar to those applied to the sample in question when analyzing the expression of proteins with unknown postmortem preservation (19, 20). Brain banks, as providers of tissue samples for research, as well as neuroscientists, must be concerned about the possibilities and limitations of the human postmortem material available for study.

ACKNOWLEDGMENT

The paper reflects only the authors' views and the community is not liable for any use that may be made of it. The authors thank T. Yohannan for editorial assistance.

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Low molecular weight species of tau in Alzheimer's disease are dependent on tau phosphorylation sites but not on delayed post-mortem delay in tissue processing

Low molecular weight species of tau in Alzheimer's disease are dependent on tau phosphorylation sites but not on delayed post-mortem delay in tissue processing

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Received 22 October 2005; received in revised form 6 January 2006; accepted 18 January 2006

Abstract

Gel electrophoresis and Western blotting of sarkosyl-insoluble fractions enriched in hyper-phosphorylated tau in Alzheimer disease (AD) have been used to analyze the pattern of phospho-tau by using different antibodies directed to the amino-terminal, core and carboxyl terminus of tau, and by using samples with increased artificial post-mortem delay in order to gain understanding on the characteristics of the band pattern and its vulnerability to post-mortem degradation. In addition to the typical profile of three major bands of 68, 64 and 60 kDa, several bands of lower molecular weight have been distinguished in frontal cortex homogenates in four AD cases stage V of Braak and Braak in optimal samples with 2 h of post-mortem delay. Lower bands, ranging from 60 to 22 kDa, are best seen with antibodies directed to the core of tau protein and, particularly, to the carboxy-terminus, thus suggesting the presence of truncated or cleaved forms of tau containing the C-terminal region. This pattern is not the result of post-mortem degradation, as artificial post-mortem delay of the same sample does not reveal the appearance of new bands with time. On the contrary, tau degradation, manifested as a reduction in the number and intensity of the bands, may occur between 8 and 26 h post-mortem and is universal in samples with post-mortem delays of 50 h.

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Keywords: Alzheimer disease; Tau; Truncated tau; Post-mortem delay; Brain bank

One of the pathological hallmarks of Alzheimer's disease (AD) is the intracellular accumulation and aggregation of hyper-phosphorylated microtubule-associated protein tau in the form of paired helical filaments (PHF) and straight filaments localized in neurofibrillary tangles, neuropil threads and dystrophic neurites surrounding β -amyloid plaques. Accumulation of hyper-phosphorylated tau is also a common feature in other tauopathies including progressive supranuclear palsy (PSP), corticobasal degeneration, argyrophilic grains disease, Pick's disease and frontotemporal dementia and parkinsonism linked to mutations in the tau gene [15]. Tau is found in the brain in six isoforms generated by alternative splicing from a single gene which is located in chromosome 17q21, with N-terminal inserts of 0 (0N), 29 (1N) or 58 (2N) amino acids, in combination with three (3R) or four (4R) microtubule-binding repeat regions at the C-terminal region [1,9–11]. In AD, gel electrophoresis and Western blot-

ting of fractions enriched in PHFs have classically disclosed a pattern of three bands of 68, 64 and 60 kDa, often accompanied by a weak fourth band of about 72 kDa in advanced cases, as revealed with several phospho-specific anti-tau antibodies. These bands derive from the six full-length tau isoforms in their insoluble form detected after dephosphorylation. In addition to these bands, other bands of lower molecular weight have been recognized with a variety of anti-tau antibodies [9,14,16–18]. Although the nature of these bands appears to be related to truncated tau, it is not clear whether they correspond to amino-terminal or C-terminal fragments (or both), and whether these bands are influenced by fragmentation of tau during the process of post-mortem delay.

The present study is geared toward increasing understanding of the banding profile of tau from sarkosyl-insoluble fractions in AD considering two variables: antibodies directed against different regions of tau, and effects of post-mortem interval between death and tissue processing.

Studies were carried out in the frontal cortex of four AD cases stage V of Braak and Braak, artificially subjected to increasing

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post-mortem delay. Clinically, the patients had suffered from severe dementia of Alzheimer type following the diagnostic criteria of the NINCDS-ADRDA, and all of them had a clinical dementia rating scale stage 3. Brain tissues were obtained as the result of a generous donation for research to the Institute of Neuropathology following strict criteria of full disclosure and approval by the Ethics Committee of the IDIBELL-Hospital Universitari de Bellvitge. The post-mortem neuropathological examination was carried out on multiple and representative formalin-fixed, paraffin-embedded sections which were stained with haematoxylin and eosin, Klüver-Barrera, and immunohistochemistry to phospho-tau (antibody AT8), β -amyloid ($A\beta_{1-40}$ and $A\beta_{1-42}$), α -synuclein, ubiquitin, phosphorylated neurofilament epitopes, glial fibrillary acidic protein, α B-crystallin and *Lycoperium esculentum* lectin for microglia. AD was the only relevant brain pathology which was staged following the instrumental criteria of Braak and Braak [3]. Samples were excluded based on evidence of fever, seizures, infection, metabolic disturbances and drugs after revision of the clinical records.

Brain samples were obtained 2 h after death and rapidly frozen at -80°C until use, or stored at 4°C and then frozen at 3, 6, 24 and 48 h of additional artificial post-mortem interval (in fact 5, 8, 26 and 50 h of post-mortem). The pH of the brain samples was between 6.8 and 7.1. Frozen samples of about 2 g from the frontal cortex (area 8) were gently homogenized in a glass tissue grinder in 10 volumes (w/v) with cold suspension buffer (10 mM Tris-HCl, pH 7.4, 0.8 M NaCl, 1 mM EGTA, 10% sucrose). The homogenates were first centrifuged at $20,000 \times g$ and the supernatant (S1) was retained. The pellet was re-homogenized in 5 volumes of homogenization buffer

and re-centrifuged. The two supernatants (S1 + S2) were then mixed and incubated with 0.1% *N*-lauroylsarkosylate (sarkosyl) for 1 h at room temperature while being shaken. Samples were then centrifuged at $100,000 \times g$ in a Ti70 Beckman rotor. Sarkosyl-insoluble pellets (P3) were re-suspended (0.2 ml/g starting material) in 50 mM Tris-HCl (pH 7.4). Protein concentrations were determined with the BCA method. Equal amounts of protein (75 μg) were loaded onto 10% sodium dodecylsulfate polyacrilamide gel electrophoresis and then electrophoretically transferred to nitrocellulose membranes (Hybond-C Extra, Amersham, Freiburg, Germany) at 400 mA/gel at 4°C . The membranes were blocked for 1 h at room temperature with 5% skimmed milk in Tris-buffered saline containing 0.1% Tween 20 (TTBS) and were then incubated with the primary antibodies. After washing with TTBS, blots were incubated with the secondary antibody (anti-mouse/anti-rabbit IgG conjugated with horseradish peroxidase 1:1000, DAKO, Denmark) for 45 min at room temperature. Immunoreactive bands were visualized by chemiluminescence using the ECL method (Amersham). Western blot analysis was carried out using several anti-tau antibodies. The monoclonal antibody tau-13 (MBL, Nagoya, Japan) is raised against the amino-terminal domain of tau (2–18 residues from the longest tau isoform), and was used at a dilution of 1:1000. The goat polyclonal antibody N-terminus (Chemicon International, Hampshire, UK), used at a dilution 1:2000, is directed against amino acids 1–16 of the human tau protein. Rabbit polyclonal phospho-specific antibodies to tau Thr212 and tau Ser214, both used at a dilution of 1:500, were used to map the core of phospho-tau. Rabbit polyclonal phospho-specific antibodies to tau tauSer396 and tauSer422, both used at

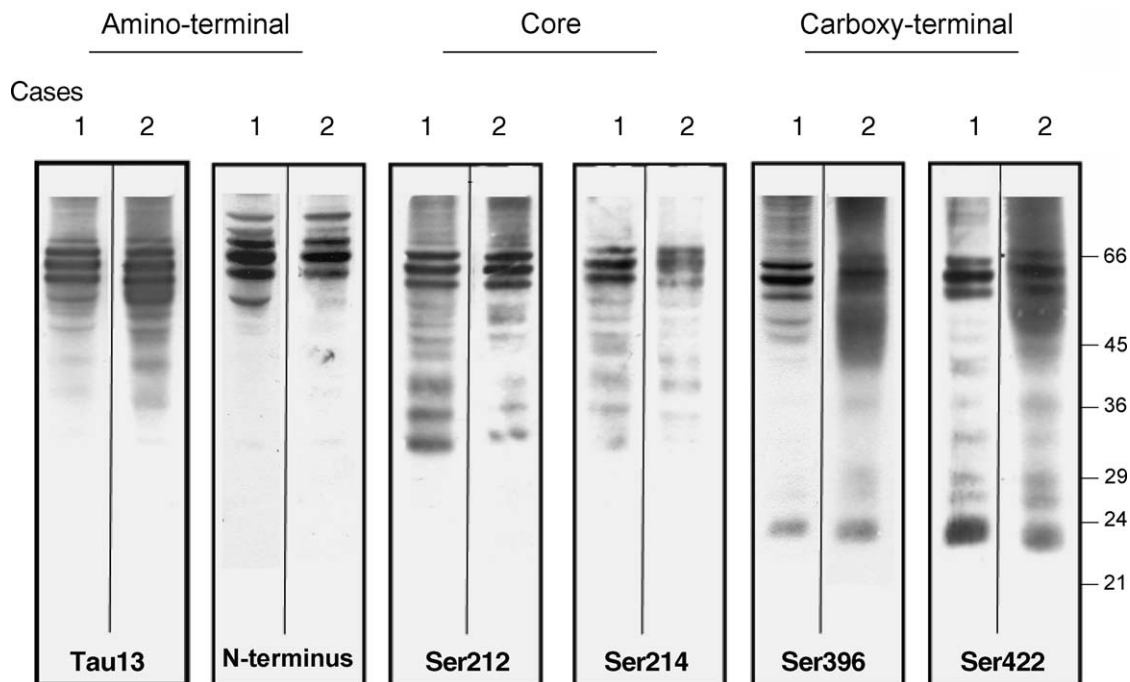


Fig. 1. Western blots of frontal cortex (area 8) homogenates from two cases (1 and 2) of AD, Braak and Braak stage V, at 2 h of post-mortem delay analysed with antibodies to the amino-terminal, core and carboxy-terminal regions of tau. The typical three-band pattern of 68, 64 and 60 kDa is found independently of the antibody used. However, the number of bands increases when using phospho-tau antibodies directed to the core region. The carboxy-terminal band of 22 kDa is only observed with phospho-specific anti-tauSer396 and Ser422 antibodies.

a dilution of 1:1000, were used to detect de C-terminal domain of phospho-tau protein. All phospho-specific anti-tau antibodies were purchased from Calbiochem (La Jolla, CA, USA).

Two different antibodies for N-terminal, core and C-terminal regions of tau protein were used in order to detect duplicates of possible differences in the tau profile banding, depending on target regions of tau. The examination of samples with optimal preservation (2h) revealed that all the antibodies detected the same three-bands at 68, 64 and 60 kDa (Fig. 1). In addition, the antibodies tau-13 and N-terminus, which are directed to the amino-terminus, detected a few weak bands between 60 and 36 kDa. However, antibodies to phospho-tauThr212 and phospho-tauSer214, directed to the core of phospho-tau protein, detected several bands between 60 and 29 kDa. The lower molec-

ular weight species of about 37, 32 and 29 kDa were moderately immunoreactive. Finally, antibodies to phospho-tauSer396 and phospho-tauSer422, both directed against the carboxyl terminus, detected several bands between 60 and 24 kDa. A well-defined band of about 22 kDa was only recognized with these two anti-phospho-tau antibodies directed to the C-terminal domain of phospho-tau (Fig. 1).

To test whether these patterns were modified with post-mortem delay (a common scenario when using human post-mortem material), the effects of post-mortem delay were examined by processing, in parallel, samples with post-mortem delays of 2, 5, 8, 26 and 50h, using antibodies directed to the amino-terminal (tau-13), core (phospho-tauThr212) and carboxy-terminus (phospho-tauSer422).

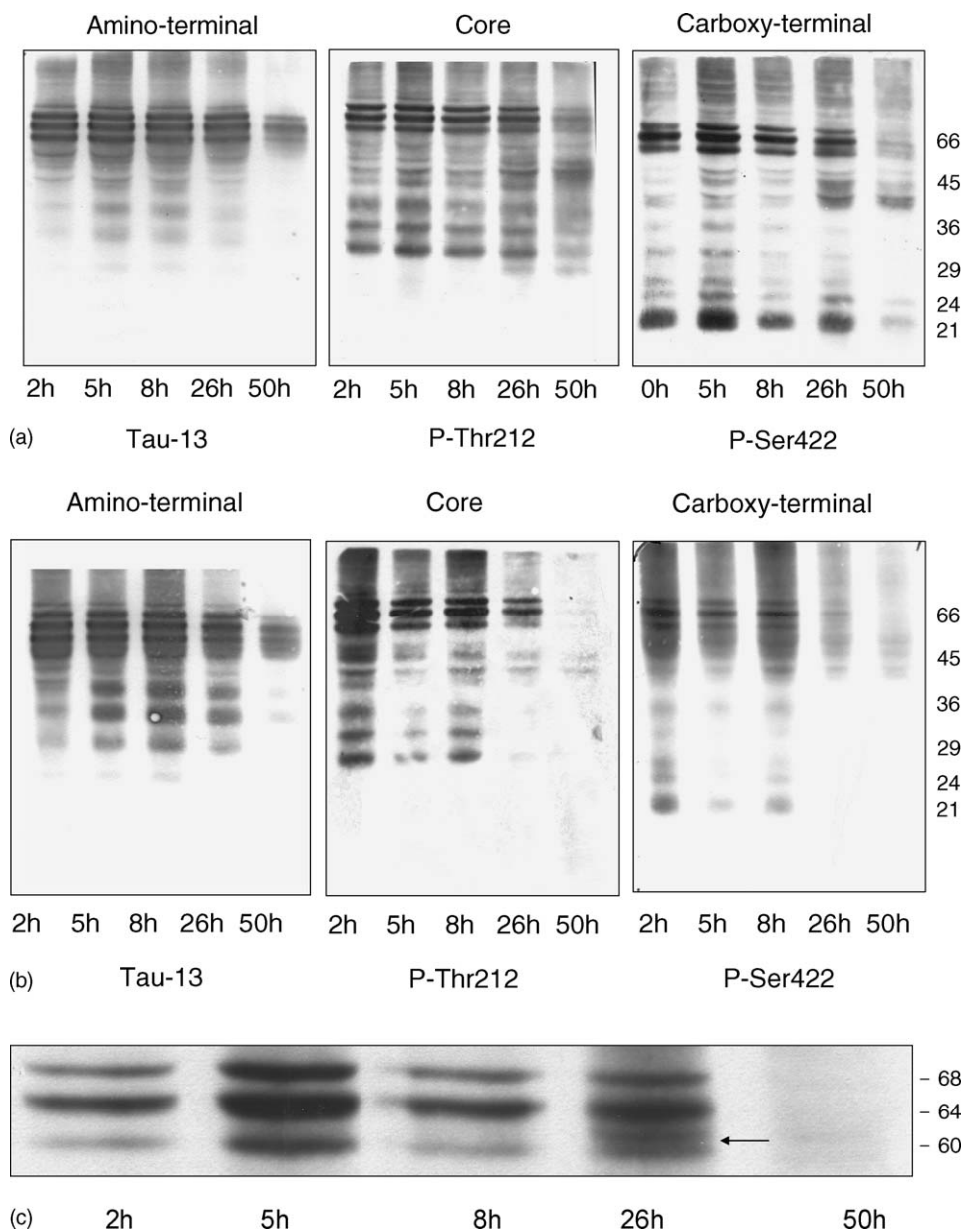


Fig. 2. Effect of artificial post-mortem delay in tau banding pattern in two AD cases. Samples of 2, 5, 8, 26 and 50h of post-mortem delay are processed in parallel with the antibody tau-13 and phospho-specific antibodies raised against phospho-tauThr212 and phospho-tauSer422. (a) This case shows a degraded tau profile at 48 h. (b) This case shows marked tau degradation at 26 and 50h. (c) High magnification of the first case to show a doublet of 60–62 kDa at 26h.

Tau degradation, as revealed by the reduction or near disappearance of the bands, occurred in every case with 50 h of post-mortem (Fig. 2a). However, degradation was already observed at 26 h of post-mortem delay in some cases (Fig. 2b). Modifications over time in the banding pattern were more marked when using phospho-specific anti-tau antibodies than with pan-tau antibodies, suggesting that phospho-tau is subjected to post-mortem degradation of endogenous phosphatases.

The typical three bands of 68, 64 and 60 kDa were well defined in all non-degraded samples in every case, but a double-band of 60–62 kDa was observed at 26 h in one case (Fig. 2a and c). This band was detected with all anti-phospho-tau antibodies, but not with the antibody tau-13, thus suggesting that this doublet is the result of partial tau dephosphorylation with increasing post-mortem time.

The present findings show that tau profile bands are dependent on the phospho-specific anti-tau antibody. Antibodies directed against C-terminal epitopes detect more bands than those directed to the core or the N-terminus. The strong immunoreactive band of 22 kDa is detected only with phospho-tau antibodies raised against the carboxy terminal of phospho-tau.

Recent studies have shown enzymatic cleavage of tau in AD by several proteases such as caspase 3, caspase 6, calpain-1 and thrombin [2,7,8,12]. As a result of these observations, it has been proposed that abnormal phospho-tau proteolysis may alter tau turnover, thereby triggering intracellular accumulation [13]. Other studies point to the neurotoxicity of certain tau cleavage products, particularly those related with the C-terminal region [4–6]. Moreover, PHFs are composed of a protease-sensitive coat and a protease resistant core [21]. The core is enriched in C-terminal fragments of tau, and the minimum protease-resistant fragment of tau is found around the glutamic acid at position 391 [18,20]. Together, these findings are consistent with the idea that the band profile of phospho-tau in AD is more complex and functionally relevant than previously supposed.

The present observations in AD are similar to those recently described in PSP [19] in which complex band patterns are partly related with the phospho-specific anti-tau antibody used, thus indicating variable products of truncated or cleaved tau as common features in tauopathies.

Finally, the present observations show that the complex band pattern is not dependent on post-mortem degradation, as no differences were seen between 2 and 8 h of post-mortem delay. In fact, reduced numbers of bands of low molecular weight rather than newly appearing bands are seen with sub-optimal preservation. These findings may have practical implications in the study of phospho-tau profiles in other tauopathies.

Nonetheless, longer post-mortem delays may affect phospho-tau examination, as degrading phospho-tau is currently observed at 50 h and may also be present in samples with artificial post-mortem delay of 26 h. It is, however, worth stressing that the present paradigm refers to samples obtained at 2 h of post-mortem in cases in whom the body was maintained at room temperature from the time of death until the autopsy. Then, selected brain samples were stored at 4 °C and frozen at progressive intervals. This scenario is not frequent in the common

practice in which the body is usually kept at room temperature for longer periods. Therefore, one might predict a more rapid protein degradation in these cases.

Acknowledgements

This work was supported in part by BrainNet II and FIS grants (PI030032, PI040998). G. Santpere is the recipient of a Fundació IDIBELL grant. We thank T. Yohannan for editorial assistance.

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3

Expression of transcription factors c-Fos, c-Jun, CREB-1 and ATF-2, and caspase-3 in relation with abnormal tau deposits in Pick's disease.

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Expression of transcription factors c-Fos, c-Jun, CREB-1 and ATF-2, and caspase-3 in relation with abnormal tau deposits in Pick's disease

Received: 25 July 2005 / Revised: 22 October 2005 / Accepted: 22 October 2005 / Published online: 23 February 2006
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Abstract Hyper-phosphorylated tau deposition in Pick bodies and neuron loss are major hallmarks of Pick's disease (PiD). However, there is no regional correlation between neuron loss and Pick bodies, as illustrated in dentate gyrus, where Pick bodies are present in almost every neuron, whereas cell death, if present, is not a major event. In order to better understand the possible role of selected transcription factors and members of the caspase family in cell death and cell survival, immunohistochemistry to c-Fos, c-Jun, CREB-1, ATF-2; c-Fos^P, c-Jun^P and CREB-1^P; and procaspase-8, procaspase-3 and active (cleaved) caspase-3 immunohistochemistry was carried out in the frontal cortex and hippocampus. Increased expression of c-Fos, c-Jun, CREB-1 and ATF-2 was observed in PiD cases. Increased c-Fos^P, c-Jun^P and CREB-1^P was also found in the nuclei of neurons in diseased brains. Interestingly, c-Fos but not c-Fos^P co-localized in many Pick bodies, as observed by double labelling-immunofluorescence and confocal microscopy. Pro-caspase-8 and pro-caspase-3 were increased in PiD. Moreover, granular active caspase-3 was observed in the nuclei as was aggregated active caspase-3 in the cytoplasm of neurons in PiD. Finally, double-labelling immunofluorescence and confocal microscopy disclosed co-localization of cytoplasmic active caspase-3 only in neurons with Pick bodies. Together, these findings show an increased expression of selected transcription factors and active (phosphorylated) forms in PiD, c-Fos

sequestration in Pick bodies, and increased active caspase-3 expression in relation with Pick bodies. Since all these findings were observed equally in neurons of both vulnerable regions (frontal cortex) and resistant regions (dentate gyrus), it may be suggested that transcription factors are only barely related with cell death. Active caspase-3 is associated with tau deposition in Pick bodies, but it is not a marker of cell death in the dentate gyrus in PiD. The present findings are in line with the previous studies showing tau products cleaved by caspase-3, as recognized by specific tau-cleaved antibodies, in Alzheimer's disease and other tauopathies.

Keywords Pick's disease · tau · c-Fos · c-Jun · CREB · ATF-2 · caspase-3

Introduction

Pick's disease (PiD) is a fronto-temporal dementia characterized by marked neuron loss, mainly in the upper cortical layers, and the appearance of typical phospho-tau-immunoreactive intraneuronal inclusions named Pick bodies principally in the dentate gyrus, CA1 region of the hippocampus and upper layers of the entorhinal cortex and neocortex, together with phospho-tau-immunoreactive inclusions in astrocytes and oligodendroglia [3, 6, 12, 29]. Intraneuronal inclusions do not match neuron loss; specifically, Pick bodies are encountered in the majority of, if not all, granule cells of the dentate gyrus, although these neurons are apparently preserved in terms of cell survival. The reasons for this selective vulnerability are not known although specific signals of cell death and cell survival are probably involved in this process.

Inducible transcription factors of the Jun and Fos families, and constitutive transcription factors activating transcription factor-2 (ATF-2) and calcium/cAMP response element binding protein (CREB), have been implicated in a large number of cellular events including

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regulation of cell survival, as derived from in vitro and in vivo paradigms [9, 20, 22, 23, 25, 37, 39].

Transcription factor activator protein 1 (AP1) composed of jun:jun dimers seems to play a pivotal role in the regulation of amyloid precursor protein (APP) production in Alzheimer's disease (AD) [28, 38]. Increased c-jun immunoreactivity has been associated with apoptosis in AD [2]. c-Fos immunoreactivity is increased in certain areas of the hippocampus in patients with AD [1, 30, 31, 41]. Yet practically nothing is known about transcription factors and PiD.

The present study is focused on the expression of c-Fos, c-Jun, CREB-1 and ATF-2 in the hippocampus (particularly in the dentate gyrus) and frontal cortex in PiD cases in order to gain insights concerning the association of these factors with cell survival. In addition, expression of pro-caspase-3 and 8, and cleaved (active) caspase-3 (17 kDa), which are crucial in apoptotic pathways [13], has been examined in the same regions to increase the understanding of the possible role of caspases in relation with tau deposits in PiD.

Materials and methods

Subjects

Samples of the hippocampus and frontal cortex (area 8 Brodmann) were obtained from four men with PiD and five control cases (two men and three women with no neurological disease), with ages ranging from 56 to 68 years, and from 55 to 73 years, respectively. The delay between death and tissue processing did not exceed 14 h in control or diseased brains. Human brain tissue in this study was provided by the Institute of Neuropathology and University of Barcelona/Hospital Clinic Brain Banks following the guidelines of the local ethics committees. At autopsy, half of the brain was fixed in 10% formalin for no less than 3 weeks, whereas the other half was cut in coronal sections 1 mm thick, frozen on dry ice and stored at -80°C until use. Control and diseased cases were processed in parallel. Clinical and neuropathological findings in PiD were in accordance with well-established criteria [6]. Optimal preservation of these samples for functional studies has been reported elsewhere [35]. Neurofibrillary tangles, senile plaques, and synuclein deposits were not observed in PiD cases. Control cases had no neurological or metabolic disease, and the neuropathological study was normal. The clinical and neuropathological findings of control and PiD cases are detailed elsewhere [10].

Gel electrophoresis and Western blotting

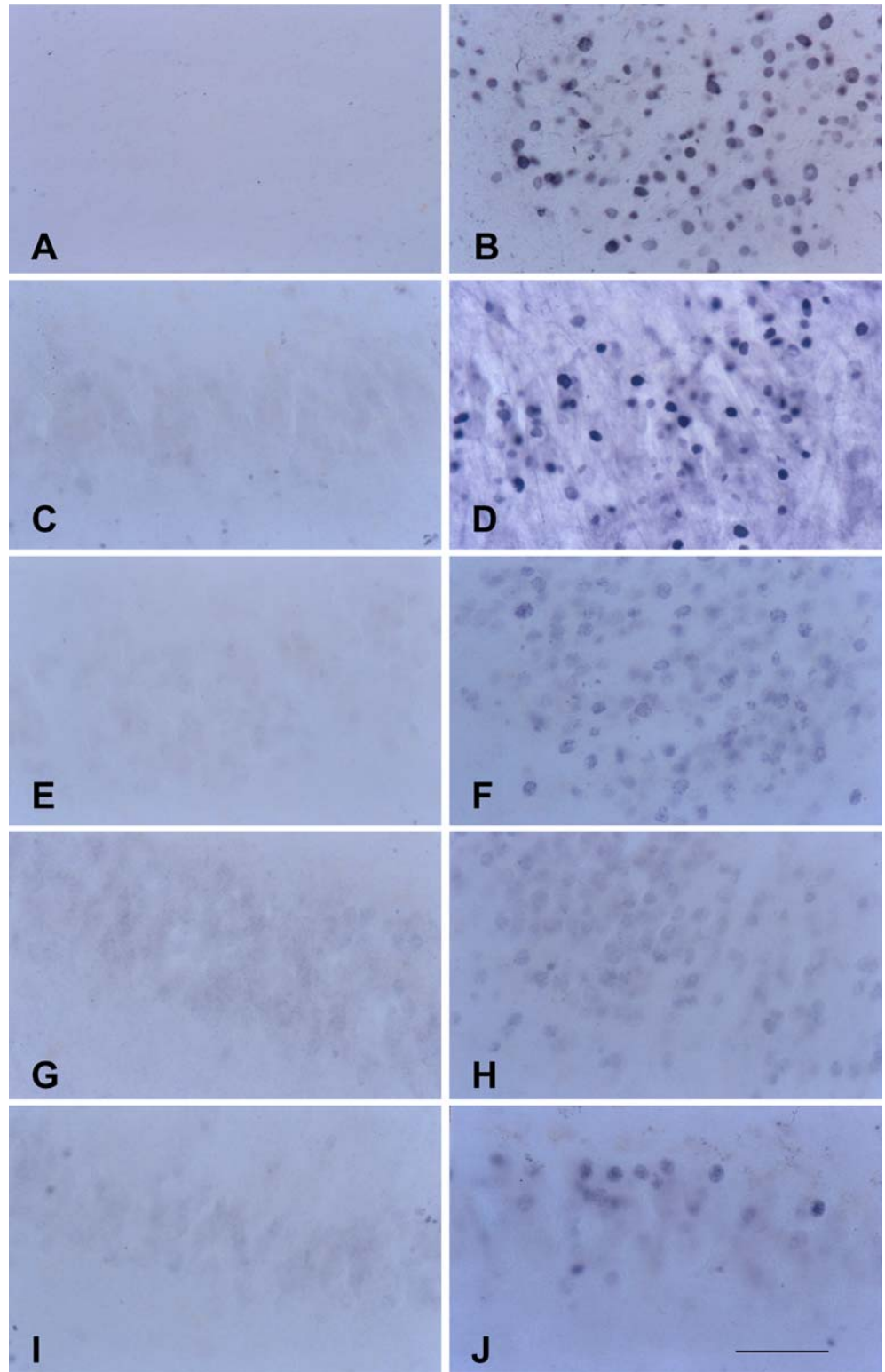
Western blots were carried out with total homogenates of the hippocampus from PiD and control brains processed in parallel. Samples about 1.5 g were dissected and homogenized in a glass homogenizer containing 1.5 ml

of PBS and a protease inhibitor cocktail (Boehringer Mannheim). The homogenates were then sonicated and centrifuged at $2,650 \times g$ at 4°C for 10 min and at $100,000 \times g$ at 4°C for 1 h. Supernatants of total homogenates were collected and protein concentrations were determined using the BCA method (Pierce) with bovine serum albumin as a standard. Equal amounts of protein (40–50 μg) were loaded onto 7.5–10% sodium dodecylsulfate polyacrylamide gels, and then proteins were electrophoretically transferred to nitrocellulose membranes (Hybond-C Extra, Amersham) at 200 mA/gel and 4°C . The membranes were blocked with 5% skimmed milk in Tris-buffered saline containing 0.1% Tween 20 (TTBS) for 1 h at room temperature and incubated with one of the primary antibodies, as follows: mouse anti-human PHF-tau (clone AT8, Innogenetics) at a dilution of 1:80; rabbit polyclonal anti-c-Fos (Santa Cruz Biotechnology) at a dilution of 1:200; anti c-fos (Oncogene science, Calbiochem) at a dilution 1:250; phospho-specific monoclonal anti-c-Fos^P (Ser³⁷⁴) (Calbiochem) at a dilution of 1:100; rabbit polyclonal anti-c-Jun (AB1, Oncogene) diluted 1:100; phospho-specific polyclonal rabbit anti-c-Jun^P (Ser⁶³) (Cell Signalling) diluted 1:100; rabbit anti-CREB-1 (Santa Cruz Biotechnology) at 1:500; phospho-specific rabbit anti-CREB-1^P (Ser¹³³) (Cell Signalling) at 1:100; rabbit anti-ATF-2 (Santa Cruz Biotechnology) at 1:200; and phospho-specific rabbit anti-ATF-2^P (Thr69/71) (Cell Signalling) at 1:100. After washing with TTBS, blots were incubated with the corresponding secondary antibody conjugated with horseradish peroxidase (Dako) at a dilution of 1:1000 for 45 min at room temperature. Immunoreactive bands were visualized by chemiluminescence using the ECL method (Amersham). The same membranes were incubated after stripping with anti- β -actin (Sigma) at a dilution of 1:1000 for the control of protein loading.

Immunohistochemistry

Sections 40 μm thick were processed free-floating with the labelled streptavidin–biotin method (Dako LSAB+ kit, Dako) following the instructions of the supplier. Briefly, after blocking endogenous peroxidases, sections were blocked in 10% normal horse serum for 2 h and then incubated overnight at room temperature with the same primary antibodies used for western blotting. In addition, rabbit anti-pro-caspase-3 at a dilution of 1:200, mouse anti-pro-caspase-8 at 1:200, and rabbit anti-cleaved caspase-3 (Asp¹⁷⁵) at 1:100 (all of them from Cell Signalling) were also employed. After washing, the sections were then incubated with LSAB and streptavidin–peroxidase for 15 min each at room temperature. The peroxidase reaction was visualized as a dark blue precipitate with NH_4NiSO_4 (0.05 M) in phosphate buffer (0.1 M), 0.05% diaminobenzidine, NH_4Cl and 0.01% hydrogen peroxide. Some sections were stained without the primary antibody to rule out non-specific immunoreactivity.

Fig. 1 Immunohistochemistry to phospho-tau, as revealed with the AT8 antibody (**a, b**), c-Fos (**c, d**), c-Fos^P (**e, f**), c-Jun (**g-h**) and c-Jun^P (**i-j**) in dentate gyrus of control (**a, c, e, g, i**) and PiD brains (**b, d, f, h, j**). Increased expression of TFs is observed in PiD cases. Strong c-Fos immunoreactivity seems to localize in globular structures reminiscent of Pick bodies. Moreover, phosphorylated c-Fos and c-Jun occur in the nuclei of dentate gyrus neurons in PiD cases. Cryostat sections, bar 25 μ m

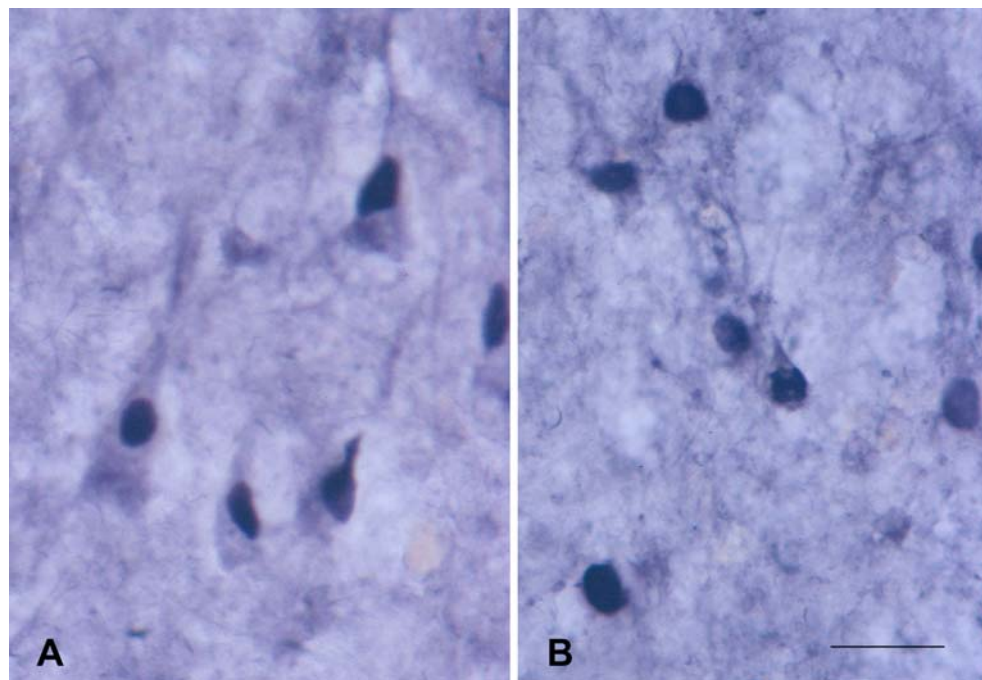


Double-labelling immunofluorescence and confocal microscopy

Sections 40 μ m thick were rinsed in PBS, mounted on glass slides, and stained with a saturated solution of Sudan black B (Merck) for 15 min to block the

autofluorescence of lipofuscin granules present in nerve cell bodies. After washing with 70% ethanol and distilled water, sections were washed in PBS, pH 7.5 and co-incubated at 4°C overnight with the monoclonal antibody to phospho-tau clone AT8 (1:50, Innogenetics), and the rabbit polyclonal anti-c-Fos

Fig. 2 Immunohistochemistry to c-Fos in the frontal cortex (a) and CA1 area of the hippocampus (b). c-Fos immunoreactivity is observed in globular structures reminiscent of Pick bodies. Cryostat sections, bar 25 μ m



(Santa Cruz Biotechnology) at a dilution of 1:200, or the rabbit anti-cleaved caspase-3 (Asp¹⁷⁵) antibody (Cell Signalling) at 1:100. After washing with PBS, the sections were incubated with a cocktail of secondary antibodies (in dark conditions) for 45 min at room temperature. Secondary antibodies were Alexa456 anti-mouse (red) and Alexa588 anti-rabbit (green) (1:400, Molecular Probes). Finally, the sections were washed with distilled PBS, mounted in immuno-Fluore Mounting medium (ICN Biomedicals), sealed and dried overnight at 4°C. All images were analysed with a Leica TCS-SL confocal microscope. Sections incubated only with the cocktail of secondary antibodies were used as controls. TO-PRO-3 (Invitrogen Life Technologies, Barcelona, Spain) was used to detect, in blue, the cell nuclei.

Results

Western blot analysis

Antibodies used in the present study recognized immunoreactive bands at the appropriate molecular weights in total hippocampal homogenates of control and diseased brains processed in parallel. In addition, several non-specific bands of lower and higher molecular weights were observed in both control and diseased hippocampus. None of these bands replicated the typical tau doublet of PiD [4, 7, 11, 42]. Most particularly, antibody to c-Fos recognized a single molecular band at the appropriate molecular weight. However, the phospho-specific rabbit anti-ATF-2^P (Thr69/71) antibody recognized two bands with identical molecular weight to those recognized with anti-phospho-tau antibodies (data not shown).

c-Fos and c-Jun immunohistochemistry

Anti-phospho-tau antibodies decorated Pick bodies in the expected regions. Pick bodies were stained with anti-phospho-tau antibodies, whereas no immunostaining was found in controls (Fig. 1a, b).

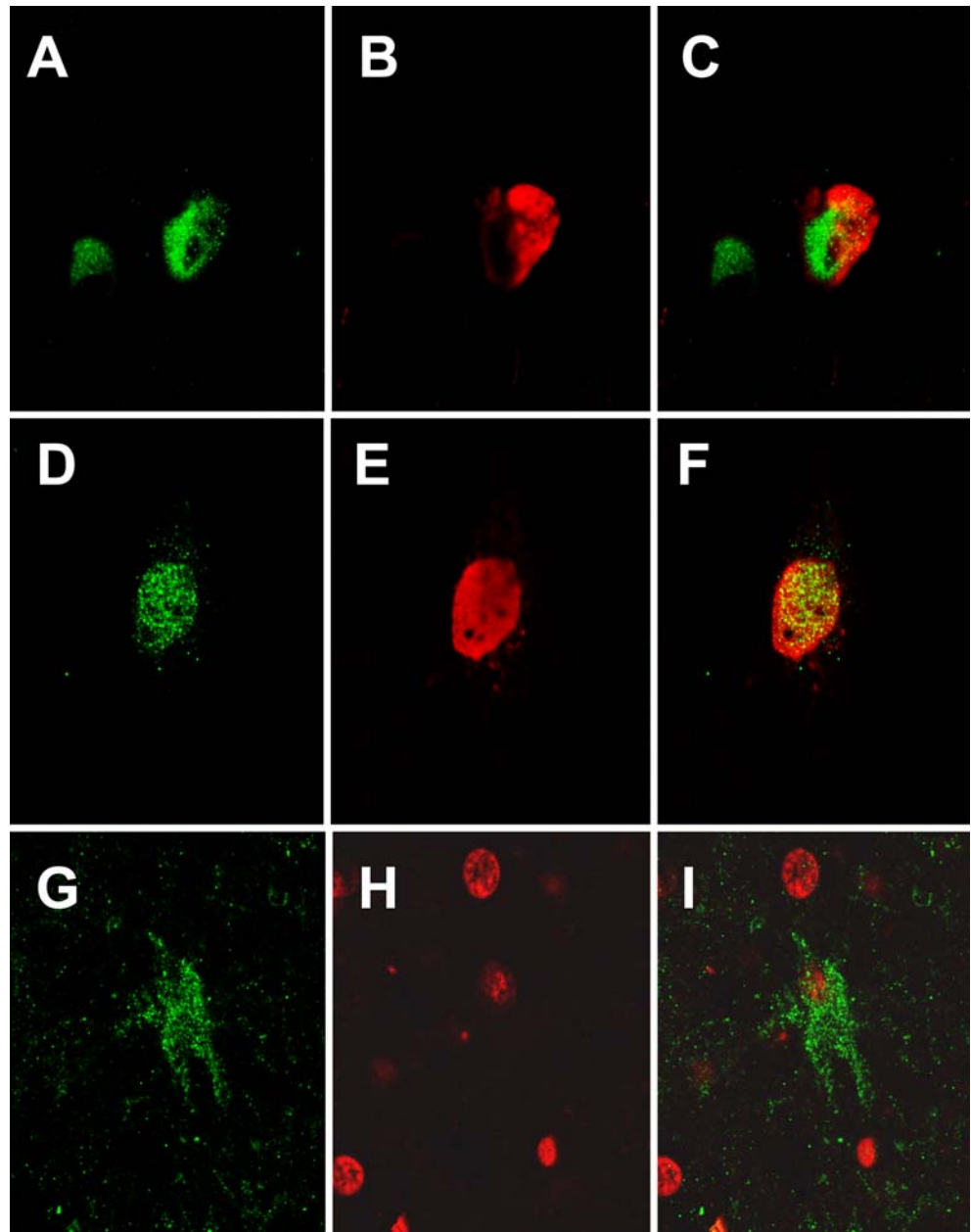
In normal brain, c-Fos weakly and diffusely stained the cytoplasm of a few neurons (Fig. 1c). Weak c-Fos immunoreactivity in PiD was found in the cytoplasm of neurons of the dentate gyrus and CA1 area of the hippocampus and dentate gyrus, but also as strong c-Fos immunoreactive deposits in the cytoplasm mimicking Pick bodies in the dentate gyrus (Fig. 1d). Similar findings were observed in the frontal cortex (Fig. 2a) and CA1 area of the hippocampus (Fig. 2b). Antibodies to c-Fos also stained scattered astrocytes. Antibodies to c-Fos^P rarely stained cells in control brains (Fig. 1e), but they revealed a nuclear staining in the frontal cortex, CA1 area of the hippocampus and dentate gyrus in PiD cases (Fig. 1f).

In control brains, weak c-Jun immunoreactivity was rarely seen in the cytoplasm of neurons and astrocytes (Fig. 1g). Moderate c-Jun immunoreactivity was seen in the nuclei of neurons in PiD cases (Fig. 1h). Weak c-Jun^P immunoreactivity was localized in a few scattered neocortical and CA1 neurons in controls, but was extremely rare in dentate gyrus (Fig. 1i). In contrast, moderate c-Jun^P immunoreactivity occurred in the nucleus of many neurons in PiD cases (Fig. 1j).

Double labelling immunofluorescence and confocal microscopy to c-Fos and phospho-tau

Double-labelling immunofluorescence and confocal microscopy disclosed co-localization of c-Fos and

Fig. 3 c-Fos (*green*) and phospho-tau (*red*) immunofluorescence in Pick bodies of the dentate gyrus (**a–c**) and CA1 area (**d–f**). c-Fos co-localizes phospho-tau in the majority of Pick bodies. In addition, scattered astrocytes are immunostained with anti-c-Fos and AT8 antibodies (**g–i**)



phospho tau (as revealed with the AT8 antibody) in the majority but not all neurons of the dentate gyrus and CA1 area of the hippocampus containing Pick bodies in PiD brains. In addition, a few astrocytes were also stained with anti-c-Fos and anti-phospho-tau antibodies (Fig. 3).

CREB-1 and ATF-2 immunohistochemistry

In control brains, weak CREB-1 immunoreactivity was localized in neurons (Fig. 4a). However, moderate nuclear CREB-1 immunoreactivity was observed in PiD neurons of the dentate gyrus (Fig. 4b), CA1 and frontal cortex. CREB-1^P immunoreactivity in controls was

rarely observed (Fig. 4c). Yet extensive and strong CREB-1^P immunoreactivity occurred in PiD, localized in the nuclei of nerve cells (Fig. 4d).

In control brains, weak ATF-2 immunoreactivity localized in the cytoplasm occurred in neurons of the frontal cortex and neurons of the CA1 area of the hippocampus, but the cytoplasm of neurons of the dentate gyrus was negative at the concentrations of the antibody used for the other regions (Fig. 4e). Increased ATF-2 immunoreactivity was found in the dentate gyrus in PiD cases; the immunoreaction decorated the nuclei of granule cells (Fig. 4f).

Pick bodies were stained with phospho-specific rabbit anti-ATF-2^P (Thr69/71) antibodies (data not shown).

Fig. 4 Immunohistochemistry to CREB-1 (a, b), CREB-1^P (c, d) and ATF-2 (e, f) in control (a, c, e) and PiD (b, d, f) dentate gyrus brains. Increased CREB-1, CREB-1^P and ATF-2, with predominant nuclear staining, is observed in PiD cases. Cryostat sections, bar 25 μm

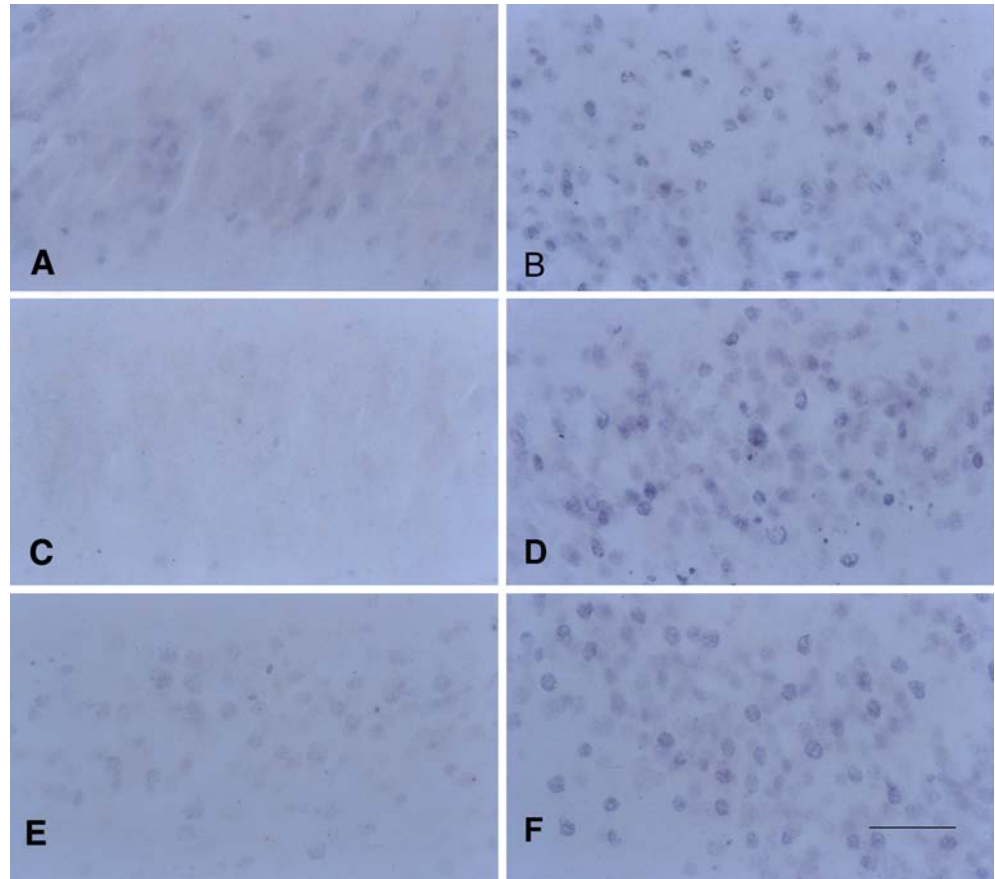
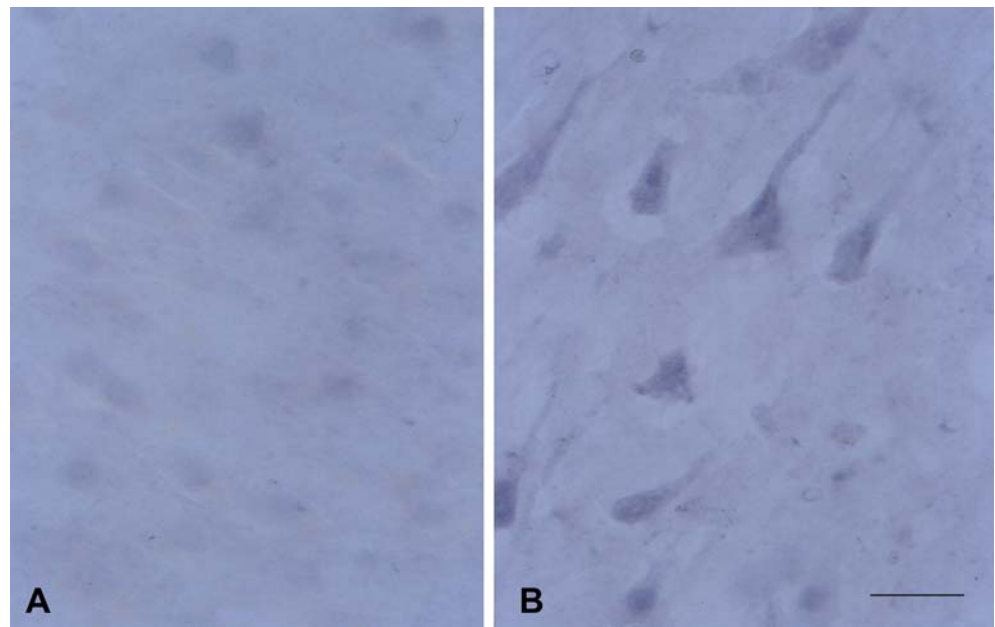


Fig. 5 Pro-caspase-8 immunohistochemistry in dentate gyrus of control (a) and PiD (b) brains. Pro-caspase-8 immunoreactivity is increased in diseased brains when compared with controls. Cryostat sections, bar 25 μm



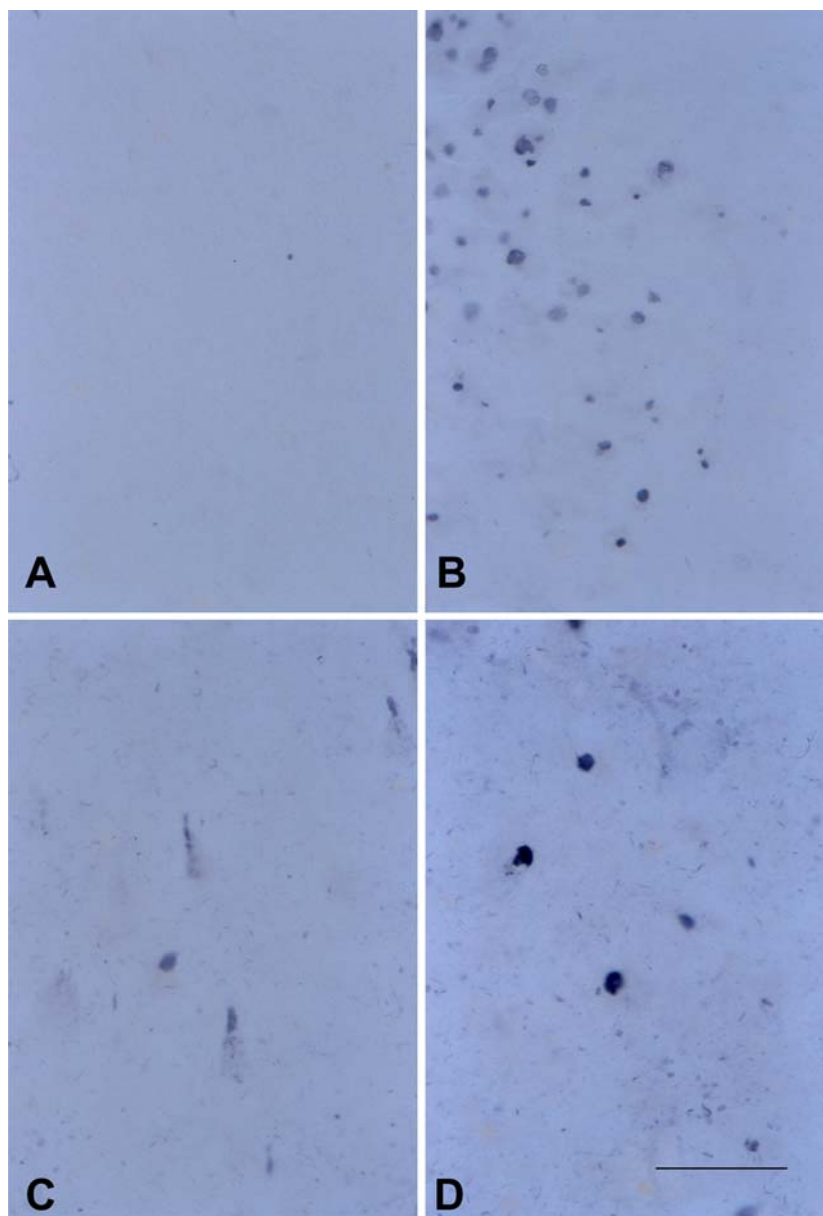
Pro-caspase-8, pro-caspase-3, and active caspase-3 immunohistochemistry

Pro-caspase-8 immunohistochemistry was practically negative in the frontal cortex, CA1 area and dentate gyrus in control brains (Fig. 5a). In contrast, moderate to strong

pro-caspase-8 immunoreactivity was found in the cytoplasm of nerve cells in PiD cases (Fig. 5b). Similar findings were observed with pro-caspase-3 antibodies (data not shown).

Active (cleaved) caspase-3 immunohistochemistry was negative in control brains. However, strong active

Fig. 6 Active caspase-3 immunohistochemistry in the dentate gyrus (**a, b**), CA1 (**c**) and frontal cortex (**d**) in controls (**a**) and PiD cases (**b–d**). Strong caspase-3-positive aggregates occur in the cytoplasm of neurons in PiD. Cryostat sections, bar 40 μ m



caspase-3 immunoreactivity was observed in the cytoplasm of neurons of the frontal cortex, hippocampus and dentate gyrus in PiD cases (Fig. 6). The number of labelled cells varied from one region to another. In the dentate gyrus, the number of positive cells ranged from 25% to 50% of the total number of neurons.

Double labelling immunofluorescence and confocal microscopy to active caspase-3 and phospho-tau

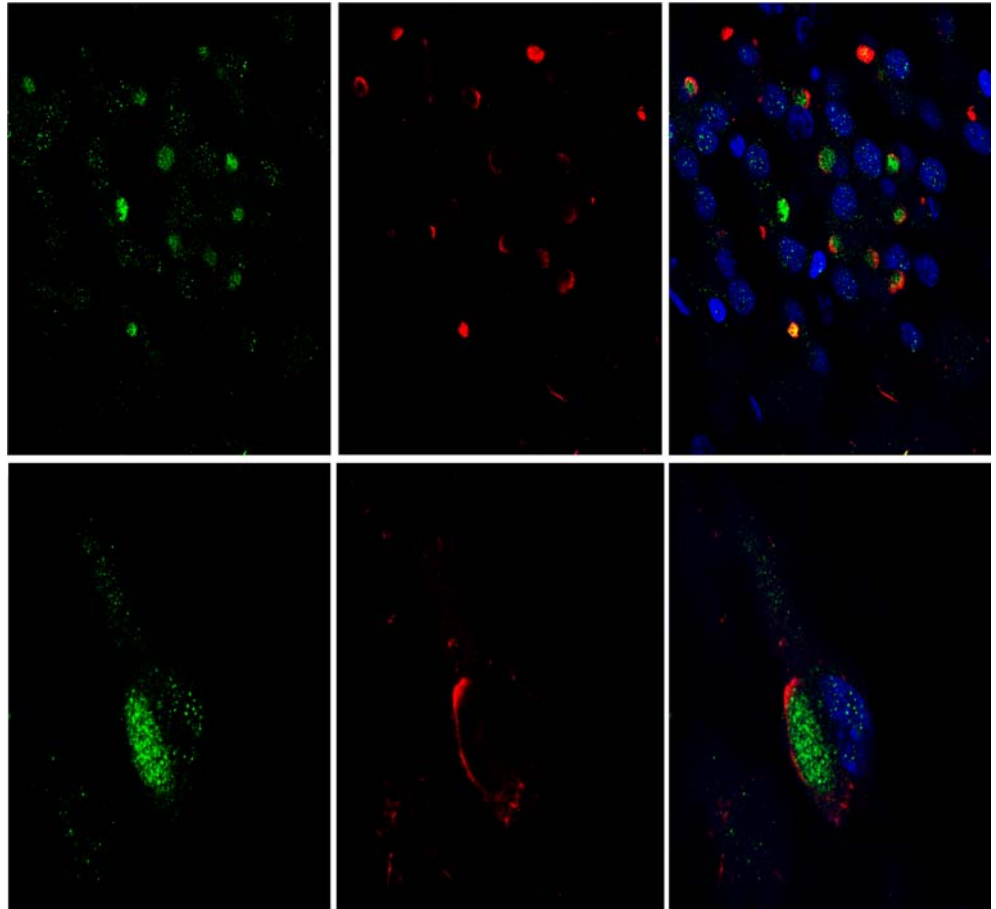
Double-labelling immunofluorescence revealed colocalization of caspase-3 and phospho-tau in Pick bodies of the dentate gyrus (Fig. 7). Not all Pick bodies were decorated with anti-phospho-active caspase-3 antibodies, but expression of active caspase-3 was restricted to Pick bodies. Interestingly, caspase-3 and AT-8 staining

did not overlap. Rather, the staining was complementary in most examples.

Discussion

The present study has shown increased expression of transcription factors c-Jun, c-Fos, CREB-1 and ATF-2 in neurons of the dentate gyrus, CA1 area of the hippocampus, and frontal cortex in PiD cases, when compared with age-matched controls with no neurological or metabolic disease and with no neuropathological abnormalities in the post-mortem study. Moreover, phosphorylated (active) c-Jun, c-Fos and CREB-1 (c-Jun^P, c-Fos^P and CREB-1^P) are markedly increased in the nuclei of neurons in all these regions, and particularly in granule neurons of the dentate gyrus.

Fig. 7 Active caspase-3 (green) and phospho-tau (red) immunofluorescence in Pick bodies of the dentate gyrus (upper panel) and CA1 area (inner panel). The nuclei are visualized with TO-PRO-3 (blue). Note granular caspase-3 immunofluorescence in the nuclei of granule cell neurons and aggregated caspase-3 immunoreactivity in association with Pick bodies



The phospho-specific rabbit anti-ATF-2^P (Thr69/71) (Cell Signalling) decorated Pick bodies and showed a two-band pattern in cortical homogenates of PiD cases which was the same as the pattern of phospho-tau. For these reasons, cross-reaction of ATF-2^P and phospho-tau was considered, and this antibody was no longer used in the study.

Based on these findings, it is clear that the activation of these transcription factors occurs in vulnerable neurons in PiD. Whether the presence of activated transcription factors is associated with cell death or with cell survival is not clear, because they are present in neurons in which neurons are sensitive, in terms of cell death, to PiD (i.e. frontal cortex), as well as in neurons typically resistant to the disease (i.e. granule cells of the dentate gyrus). Previous studies in a paradigm of kainic acid excitotoxicity, which selectively produces cell damage in the hippocampus accompanied by preservation of granule cells, have shown increased expression of c-Jun^P and CREB-1^P in granule cells of the dentate gyrus, thus suggesting association with cell survival [14]. Furthermore, phosphorylated CREB is associated with cell survival in resistant regions of the hippocampus after hypoxic insults [39]. c-Jun and c-Fos are also induced in neurons of the CA1 area and dentate gyrus that show delayed onset of pyknosis or complete resistance to hypoxic-ischaemic injury [19]. Following focal cerebral

ischaemia, CREB-1^P is reduced very early on in the core of the infarction, whereas phosphorylated transcription factors are expressed in the nuclei of neurons in the penumbra area [16].

Transcription factors are regulated by phosphorylation, and several mitogen-activated protein kinases (MAPKs), as well as stress kinase c-Jun-N-terminal kinases (SAP/JNKs) and p38-kinases, which regulate phosphorylation of transcription factors, have also been implicated in the control of cell death and cell survival in various scenarios [21, 27, 33, 34].

Interestingly, MAPKs, SAPK/JNK, and p38 also have the capacity to phosphorylate tau in vitro and in vivo, and active (phosphorylated) MAPKs, SAP/JNK and p-38 are expressed in AD, PiD, and other tauopathies in association with hyperphosphorylated tau deposits in neurons and glial cells [17]. Yet there is no relation between the expression of active kinases and cell death in these diseases [5, 14].

In spite of the ambiguity concerning the role of these factors in the regulation of cell death and cell survival, increased expression of c-Jun, c-Fos, CREB-1 and ATF-2, and, more importantly, of the active forms translocated to the nuclei, is probably associated with gene regulation related with the deposition of hyper-phosphorylated tau. Whatever the function of this increased expression may be, these results suggest active gene

transcription in PiD granule cells and other neurons sensitive to PiD. Similar conclusions have been suggested in AD [40].

A very interesting point is the localization of c-Fos (but not phosphorylated c-Fos) in many Pick bodies in the dentate gyrus and CA1 area of the hippocampus. Since Western blots disclosed no ambiguity on the unique band at the corresponding molecular weight recognized by the anti-c-Fos antibody, and c-Fos colocalized phospho-tau, as revealed with the AT8 antibody, in many but not all Pick bodies, a cross-reaction of c-Fos and AT8 seems very unlikely. It is feasible, however, that c-Fos is sequestered by protein aggregates in Pick bodies, as it happens in protein aggregates in many other neurodegenerative diseases. The reasons and the effects of this situation are largely unknown.

Another important aspect is the increased expression of pro-caspase-8 and pro-caspase-3 in PiD neurons of the frontal cortex, CA1 area of the hippocampus and dentate gyrus. More importantly, active (cleaved) caspase-3 is strongly expressed in the cytoplasm of neurons, including granule cells of the dentate gyrus in PiD brains. Furthermore, active caspase-3 is closely related with Pick bodies, as revealed by double labelling immunofluorescence and confocal microscopy.

In addition to the well-known involvement of caspases in apoptotic pathways, several studies have demonstrated the participation of caspases in several settings, including cellular proliferation, cell cycle regulation, and differentiation [8, 24, 26]. Furthermore, caspase-3 is probably involved in the cleavage of tau in neurofibrillary tangles in AD and other tauopathies [18, 36]. Therefore, it may be postulated that caspase-3 activation in PiD is associated, rather, with tau cleavage in Pick bodies. In this line, accumulation of Asp⁴²¹-caspase-cleaved tau (as recognized with the Δ Tau antibody) in Pick bodies in PiD, as well as in other tau deposits in distinct tauopathies [32], has been reported. Together, these findings support the idea that caspase-3 activation is involved in tau cleavage in Pick bodies.

Acknowledgments This work was supported by FIS grants G03-165 and PI040184. We wish to thank T. Yohannan for editorial assistance.

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4

Abnormal Sp1 transcription factor expression in Alzheimer disease and tauopathies

Abnormal Sp1 transcription factor expression in Alzheimer disease and tauopathies

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Received 31 October 2005; received in revised form 12 November 2005; accepted 30 November 2005

Abstract

Sp1 transcription factor expression was examined by immunohistochemistry, immunofluorescence and confocal microscopy in Alzheimer disease (AD), Pick disease (PiD), progressive supranuclear palsy (PSP), Parkinson disease (PD) and Dementia with Lewy bodies (DLB). Sp1 partly co-localizes with hyper-phosphorylated tau deposits in neurofibrillary tangles, dystrophic neurites of senile plaques and neuropil threads in AD, and in neurons, astrocytes and oligodendrocytes bearing hyper-phosphorylated tau in PiD and PSP. Sp1 is not found in α -synuclein inclusions in PD and DLB. These modifications are not associated with changes in the total expression levels of Sp1, as revealed with gel electrophoresis and Western blotting of brain homogenates. Furthermore, no co-immunoprecipitation of Sp1 and phospho-tau was observed in AD and PiD cases. Since Sp1 binding sites are present in the promoters of several genes involved in amyloid and tau, and Sp1 is regulated by oxidative stress, the present findings suggest that Sp1 deposition in hyper-phosphorylated tau deposits may have functional consequences in the pathology of AD and other tauopathies.

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Keywords: Alzheimer disease; Pick disease; Progressive supranuclear palsy; Parkinson disease; Sp1

Sp1 is a zinc finger transcription factor which binds to GC boxes of the promoters of several genes expressed in a wide variety of tissues [6,18]. The phosphorylation of Sp1 and the adaptor proteins which bind to Sp1 both regulate the positive and negative effects of Sp1 on gene expression [5,15]. Sp1 participates in many physiological processes including angiogenesis and cell cycle regulation [2,3].

Sp1 has also been related to Alzheimer Disease (AD). Major hallmarks of AD are the abnormal deposition of β -amyloid, which results from the combined cleavage of the β -amyloid precursor protein (APP) by β - and γ -secretases, in the form of β -amyloid or senile plaques, and the accumulation of hyper-phosphorylated tau comprising neurofibrillary tangles, dystrophic neurites surrounding amyloid plaques, and neuropil threads [10]. In vitro studies have shown that Sp1 is involved in the positive regulation of the TGF-beta-dependent expression of APP [9]. Sp1 also regulates the expression of BACE1, the major β -secretase involved in APP cleavage, and BACE2, a

homologue of BACE1 [4,22]. Finally, Sp1 regulates the expression of tau [13].

The present study examines the expression of Sp1 in AD and in the tauopathies Pick disease (PiD) and progressive supranuclear palsy (PSP), which are characterized by abnormal hyper-phosphorylated tau deposition in neurons, astrocytes and oligodendrocytes [1,12,19]. For comparative purposes, Sp1 expression was also examined in another group of diseases characterized by abnormal α -synuclein deposition in the form of Lewy bodies and neurites, Parkinson disease and Dementia with Lewy bodies [14,16].

The brains of AD ($n=7$, Braak stages V-VIC), PiD ($n=3$), PSP ($n=5$), PD ($n=4$), DLB ($n=6$) and age-matched controls ($n=6$) were obtained as a generous donation following the guidelines of the local ethical committee. The postmortem delay was between 3 and 10 h in control and diseased brains. One hemisphere was cut in coronal sections, immediately frozen and stored at -80°C until use. The other hemisphere was fixed in 4% buffered formalin for no less than 3 weeks. Samples of selected regions of the brain ($n=22$) were embedded in paraffin and the sections were examined for neuropathological study using current histological and immunohistochemical methods.

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Finally, samples of the frontal cortex (area 8), entorhinal cortex and hippocampal complex, and mesencephalon containing substantia nigra, were fixed in 4% paraformaldehyde in phosphate buffer for 24–48 h, cryoprotected and stored at -80°C until use. Control and diseased brains were processed in the same way. Pathological cases fulfilled the neuropathological criteria for the corresponding disease. Control cases did not have evidence of neurological or metabolic disease during life, and did not show morphological abnormalities in the neuropathological examination.

Paraformaldehyde-fixed cryostat sections, $15\ \mu\text{m}$ thick, were processed for Sp1 immunohistochemistry following the streptavidin LSAB method (Dako). After incubation with methanol and normal serum, the sections were incubated free-floating with rabbit polyclonal anti-Sp1 specific antibody raised to residues 750–785 (Serotec) or with anti-Sp1 antibody raised against full length Sp1 (Upstate) used at dilutions of 1:500 at 4°C overnight. Following incubation with the primary antibody, the sections were incubated with LASB for 1 h at room temperature. The peroxidase reaction was visualized with diaminobenzidine, NH_4NiSO_4 and H_2O_2 . Control of the immunostaining included omission of the primary antibody; no signal was obtained following incubation with only the secondary antibody.

Other sections in AD cases were stained with a saturated solution of Sudan black B (Merck) for 30 min to block the autofluorescence of lipofuscin granules present in nerve cell bodies,

rinsed in 70% ethanol and washed in distilled water. The sections were incubated, at 4°C overnight, with rabbit polyclonal anti-Sp1 specific antibody (Serotec) used at a dilution of 1:500 and monoclonal AT8 antibody (Innogenetics) used at a dilution of 1:50 in a vehicle solution composed of Tris buffer, pH 7.2, containing 15 mmol/L NaN_3 (Dako). After washing in PBS, the sections were incubated in the dark with the cocktail of secondary antibodies and diluted in the same vehicle solution as the primary antibodies for 45 min at room temperature. Secondary antibodies were Alexa488 anti-mouse (red) and Alexa546 anti-rabbit (green) (both from Molecular Probes), used at a dilution of 1:400. After washing in PBS, the sections were mounted in immuno-Fluore Mounting medium (ICN Biomedicals), sealed and dried overnight. Sections were examined in a Leica TCS-SL confocal microscope.

Weak Sp1 immunoreactivity in control brains was restricted to the nuclei of scattered neurons throughout the brain. Immunohistochemistry in AD cases showed Sp1 immunoreactivity in neurons with neurofibrillary tangles, as well as in dystrophic neurites of senile plaques and in neuropil threads (Fig. 1A and B). Astrocytes and oligodendrocytes were not labeled with anti-Sp1 antibodies in AD. No Sp1 immunoreactivity was observed in the vicinity of diffuse plaques as revealed in consecutive sections processed for β -amyloid immunohistochemistry using polyclonal antibodies to β_{1-40} and β_{1-42} (Dr. M. Sarasa, Zaragoza) used at dilutions of 1:500 and 1:2000, respectively.

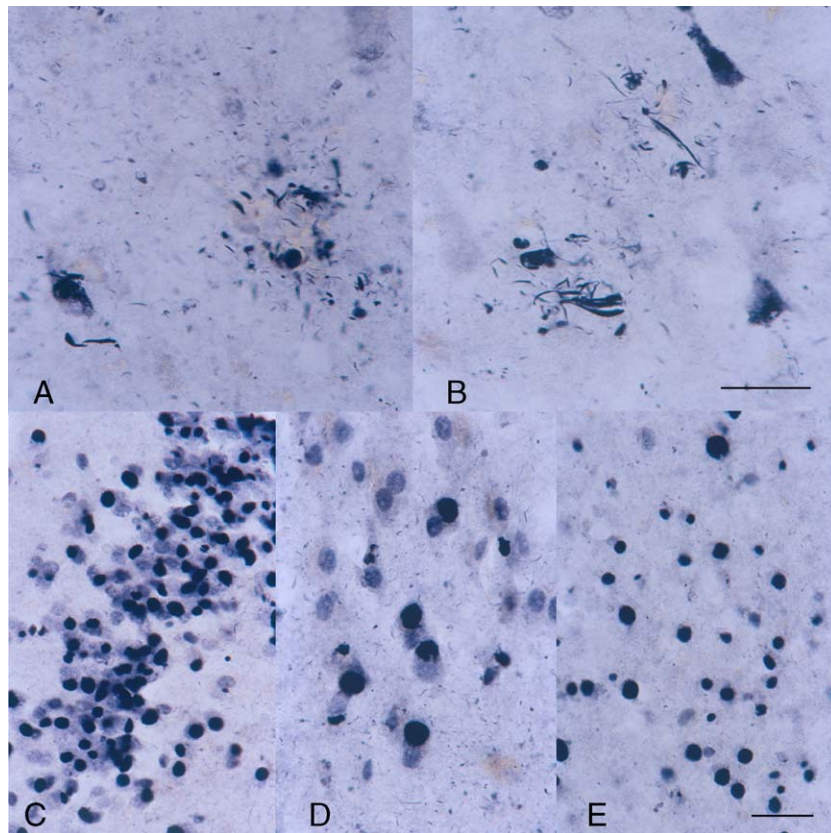


Fig. 1. Sp1 immunoreactivity in Alzheimer disease (A, B), and Pick disease (C–D). Sp1 decorates neurofibrillary tangles, dystrophic neurites and neuropil threads (A, B), and Pick bodies in the dentate gyrus (C), CA1 area of the hippocampus (D) and frontal cortex (E). Cryostat sections processed free-floating without haematoxylin counterstaining. Bar = $25\ \mu\text{m}$.

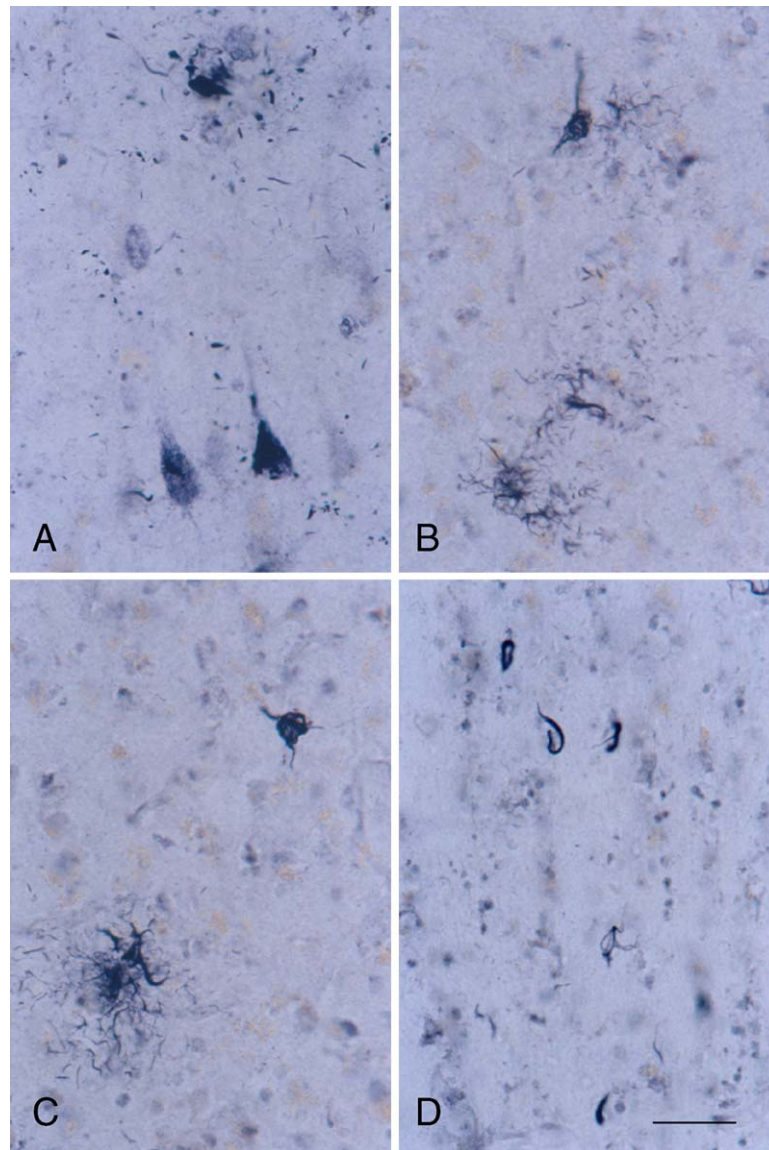


Fig. 2. Sp1 immunoreactivity in progressive supranuclear palsy. Sp1 decorates many neurons (A–C), astrocytes (B, C) and coiled bodies (D). Cryostat sections processed free-floating without haematoxylin counterstaining. Bar = 25 μ m.

Sp1 immunoreactivity also decorated cytoplasmic structures resembling Pick bodies in the dentate gyrus, CA1 area of the hippocampus, entorhinal cortex and frontal cortex in PiD. Sp1 immunoreactivity was also observed in scattered neurons in the cerebral cortex, diencephalic nuclei, selected nuclei of the brain stem, and astrocytes and coiled bodies in PSP (Fig. 2).

In contrast, Lewy bodies and neurites in PD and DLB were not stained with anti-Sp1 antibodies.

Double-labeling immunofluorescence using AT8 and anti-Sp1 antibodies, and confocal microscopy, disclosed partial co-localization of Sp1 and hyper-phosphorylated tau in neurofibrillary tangles and dystrophic neurites of senile plaques. Similarly, Sp1 co-localized hyper-phosphorylated tau in many Pick bodies in PiD (Fig. 3).

Gel electrophoresis and Western blotting was carried in the frontal cortex in AD cases and controls. No differences in the expression levels of Sp1 were found between control and dis-

eased brains. In order to understand whether abnormal tau in AD and tauopathies interacts with Sp1, immunoprecipitation studies were performed following the same methods described elsewhere [7]. No co-immunoprecipitation of Sp1 and phospho-tau was found in AD and PiD cases (Fig. 4).

The present observations suggest a sequestration of Sp1 by tau aggregates in AD and other tauopathies. Since no co-immunoprecipitation of Sp1 and phospho-tau was demonstrated, we cannot rule out this possibility. Sp1 might also be associated with intermediate molecules in NFTs. Whether Sp1 trapping by hyper-phosphorylated tau deposits may imply abnormal Sp1 function on target genes is a matter for speculation. Sp1 regulates the expression of BACE1, BACE2, APP and tau [4,9,13,22]. Sp1 is also dramatically increased in response to oxidative stress in embryonic cortical neurons [20], and it induces the expression of manganese superoxide dismutase (SOD2), which protects the mitochondrion from ROS-induced

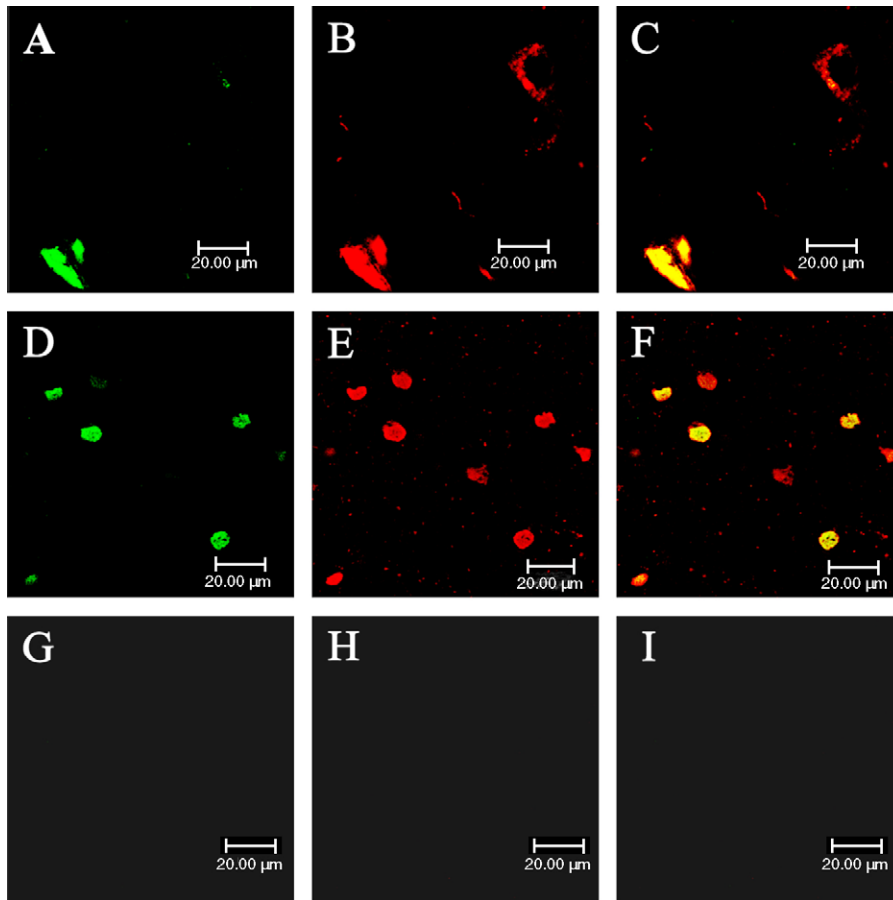


Fig. 3. Sp1 (green) partly co-localizes phospho-tau (red) in neurons with neurofibrillary tangles in AD (A–C), and in Pick bodies in Pick disease (D–F). Merge: yellow. G–I: negative controls incubated only with the secondary antibodies.

damage [23]. Therefore, possible targets of abnormal Sp1 distribution could be genes involved in amyloid and tau processing, and in mechanisms involved in the response to oxidative stress.

No relationship of Sp1 expression and cell death was seen in sections processed for Sp1 and active caspase 3 immunohistochemistry (Cell Signaling) (data not shown).

Huntington disease (HD) is a neurodegenerative disease, mainly involving the striatum and cerebral cortex, that is caused

by polyglutamine expansions in the huntingtin gene, the product of which accumulates in the cytoplasm and aggregates as intranuclear inclusion bodies [8]. Expansion of glutamine amino acids in mutant huntingtin binds to the glutamine-rich activation domains of Sp1 [11]. Intranuclear aggregates of huntingtin sequester Sp1 and one of its co-activators (TAF)II130, inhibiting its binding to gene promoters [17,21]. Studies are needed to elucidate whether Sp1 binding to specific gene promoters is also reduced in AD and tauopathies.

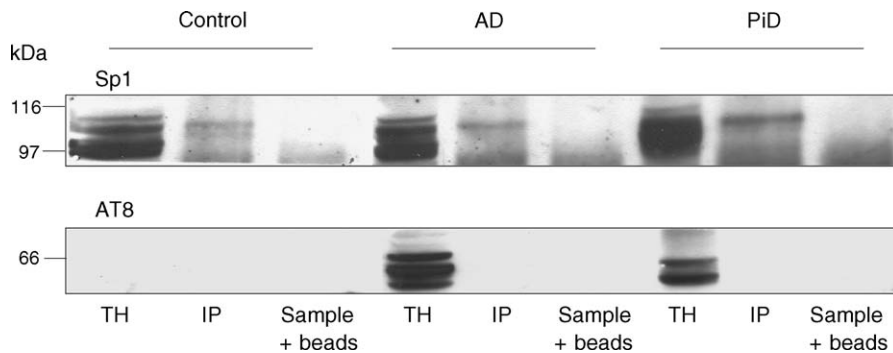


Fig. 4. Sp1 immunoprecipitation studies in control, Alzheimer disease (AD) and Pick disease (PiD) with anti-Sp1 (Upstate) blotted with anti-Sp1 (Serotec) show positive bands in the lanes corresponding to total homogenates (TH) and in the lanes of immunoprecipitates (IP), but not in control lanes with samples and beads but without the antibody. The same membranes blotted for AT8 show typical phospho-tau profiles in TH fractions in AD (three bands) and PiD (two bands), but not in IP fractions.

Acknowledgements

This study was carried out with the support of FIS grant PI030032. We wish to thank T. Yohannan for editorial assistance.

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5

Argyrophilic grain disease

REVIEW ARTICLE

Argyrophilic grain disease

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Argyrophilic grain disease (AGD) is a common sporadic neurodegenerative disease of old age characterized by the presence of argyrophilic grains (AGs)—dendritic-derived appendages as revealed with the Golgi method—together with pre-tangle neurons in the limbic system, which accounts for about 5% of all demented cases. AGs and pre-tangle neurons contain hyperphosphorylated 4R tau. This is associated with a typical 64 kDa and 68 kDa pattern, but also accompanied by tau truncated forms of low molecular mass, probably resulting from thrombin-mediated proteolysis. Hyperphosphorylated tau also accumulates in oligodendroglial-coiled bodies and in limbic astrocytes. Ballooning neurons in the amygdala are non-specific accompanying abnormalities. A new proposal for AG distribution considers four stages. Clinical symptoms largely depend on the extension of AGs together with the very common associated tauopathies, mainly Alzheimer's disease, progressive supranuclear palsy, corticobasal degeneration and synucleinopathies. Pathogenesis of AG and related lesions herein proposed includes oxidative stress that is followed by increased expression of oxidative response markers, and activation of stress kinases (stress activated protein kinase and p38). These kinases together with glycogen synthase kinase 3 β co-localize with hyperphosphorylated tau deposits in neurons and glial cells, thus indicating a link between oxidative stress and tau phosphorylation in AGD. Hyperphosphorylated tau, in turn, co-localizes with p62/sequestosome 1 and ubiquitin, thus pointing to activation of protein aggregation and protein degradation pathways, respectively. Finally, AGs and tangles co-localize with mutant ubiquitin (UBB⁺) resulting from molecular misreading of mRNA, thus supporting proteasome function impairment and, therefore, impelling accumulation of hyperphosphorylated tau in AGs and tangles. The sequestration of active kinases in AGs and tangles is an additional local cause of tau hyperphosphorylation.

Keywords: argyrophilic grain disease; Alzheimer's disease; tau; p62; ubiquitin; mutant ubiquitin; oxidative stress; stress kinases; GSK-3 β

Abbreviations: AD = Alzheimer's disease; AGD = argyrophilic grain disease; AG = argyrophilic grains; CBD = corticobasal degeneration; CJD = Creutzfeldt–Jakob disease; DLB = dementia with Lewy bodies; FTD = frontotemporal dementia; PD = Parkinson's disease; PiD = Pick's disease; PSP = progressive supranuclear palsy; RAGE = AGE receptor; UPS = ubiquitin-proteasome system

Received September 9, 2007. Revised November 17, 2007. Accepted November 19, 2007. Advance Access publication January 29, 2008

Introduction

Argyrophilic grain disease (AGD) was first described as a degenerative disease characterized by argyrophilic grains (AGs) in the entorhinal cortex, hippocampus, amygdala and neighbouring temporal cortex in a subset of patients who had suffered from adult onset dementia (Braak and Braak, 1987, 1989).

Although the seminal descriptions emphasized the lack of Alzheimer changes, subsequent studies have shown frequent association of AGD with other degenerative diseases of the nervous system, including Alzheimer's disease (AD), Pick's disease (PiD), progressive supranuclear palsy (PSP), corticobasal degeneration (CBD), dementia with only tangles, Creutzfeldt–Jakob disease (CJD) and

α -synucleinopathies such as Lewy body diseases [Parkinson's disease (PD) and Dementia with Lewy bodies (DLB)] and multiple system atrophy (Masliah *et al.*, 1991; Ikeda *et al.*, 1995; de Vos *et al.*, 1996; Martinez-Lage and Muñoz, 1997; Braak and Braak, 1998; Jellinger, 1998; Jellinger and Bancher, 1998; Kiwashima *et al.*, 1999; Seno *et al.*, 2000; Togo *et al.*, 2002; Ferrer *et al.*, 2003). Rare cases have been reported with combined association of AGD, Lewy body disease and motor neuron disease (Liang *et al.*, 2005; Klos *et al.*, 2005). As in AD, Lewy bodies are frequent in the amygdala in AGD (Popescu *et al.*, 2004). Finally, hippocampal sclerosis may be found in combination with AGD, as it occurs in other cases of dementia with tauopathy (Beach *et al.*, 2003; Probst *et al.*, 2007).

Together, these observations have raised cautionary comments about the reality of AGD as a distinct entity (Martinez-Lage and Muñoz, 1997; Ikeda *et al.*, 2000), while the opposing view is defended by others (Tolnay *et al.*, 2003; Tolnay and Clavaguera, 2004).

AGs are not uncommon structures in aged human brains (Davis *et al.*, 1997). Their presence has been estimated at 5–9% in adult autopsy series (Braak and Braak, 1998; Tolnay and Clavaguera, 2004). In our series of 1000 consecutive autopsy cases from an adult general hospital, the percentage of cases with AGs was 4%. There is a general agreement that the incidence of AGD increases with age (Braak and Braak, 1998; Tolnay and Clavaguera, 2004). This may explain AGs in 43% of cases in a series of very aged patients (Saito *et al.*, 2002) and the occurrence of AGD in 10 of 32 centenarians (Ding *et al.*, 2006). The mean age of onset is about 75–80 years (Braak and Braak, 1998; Jellinger 1998; Tolnay *et al.*, 2001; Tolnay *et al.*, 2003). In our series, the distribution of AGD for ages was: younger than 60 years, 10%; between 61 and 70, 17%; between 71 and 80, 30%; and older than 80 years, 43%. Both genders are equally affected.

The cause of AGD is not known. The disease appears to be sporadic. Genetic studies have failed to discover a sustained link of AGD with a particular gene locus. Interestingly, a single case bearing the *MAPT* S305I mutation had AGD-like neuropathology (Kovacs *et al.*, 2007). The frequency of apolipoprotein E ϵ 4 (ApoE ϵ 4) allele in AGD is similar to that of the general population (Tolnay *et al.*, 1998; Togo *et al.*, 2002). Yet the frequency of ApoE ϵ 2 is higher than that observed in AD and controls (Ghebremedin *et al.*, 1998). Polymorphisms of the low-density lipoprotein receptor-related gene protein and α 2-macroglobulin gene have also been implicated in AGD (Ghebremedin *et al.*, 2002), paralleling what is known in AD. Nevertheless, association of AGD with tau H1 haplotype is confusing, with both positive and negative results (Togo *et al.*, 2002; Miserez *et al.*, 2003). Further studies are obviously needed to elucidate genetic aspects of AGD.

Clinical symptoms

AGD may manifest with cognitive decline and dementia (Tolnay *et al.*, 2001; Saito *et al.*, 2002; Togo *et al.*, 2002; Tolnay and Clavaguera, 2004). Behavioural abnormalities, personality changes and emotional and mood imbalance have been noted in other cases (Braak and Braak, 1998; Ikeda *et al.*, 2000). Episodic memory loss has been noted in a majority of subjects in some series (Ikeda *et al.*, 2000).

Recent studies have shown that older AGD cases who were admitted to geriatric wards of mental hospitals had suffered from amnesia, irritability and agitation, followed by delusions, dysphoria and apathy (Togo *et al.*, 2005). Mild amnesic cognitive impairment is not uncommon as an initial manifestation of AGD (Jicha *et al.*, 2006; Petersen *et al.*, 2006).

A small number of patients present with progressive transcortical sensory aphasia, prominent abnormal behaviour and aggression, and moderate to severe cognitive impairment consistent with frontotemporal dementia (FTD) (Tsuchiya *et al.*, 2001; Ishihara *et al.*, 2005). These latter examples lend support to the proposal for considering AGD as one of the causes of FTD (Cairns *et al.*, 2007).

Although the variability of lesions and the common accompanying AD pathology make it difficult to assign clinical symptoms to AGs, it is necessary to emphasize the importance of clinical and pathological correlations in individual cases. It is clear that the involvement of the entorhinal cortex, hippocampus, neighbouring temporal cortex and amygdala may be the anatomical substrate for cognitive impairment and dementia in AGD. Using a logistic regression model, AGD has a significant effect on the development of dementia; demented AGD cases show lower stages of AD-related pathology than do pure AD cases, but higher stages than non-demented AGD patients (Thal *et al.*, 2005). Based on these and similar findings, it has been suggested that AGD acts as an additive pathology (Thal *et al.*, 2005; Josephs *et al.*, 2006). It is the presence of AGD plus mild-moderate AD-type pathology that results in dementia and not just the presence of AGD.

Although AGD may present as FTD, this is a very rare situation related with diffuse neocortical involvement (Hodges *et al.*, 2004). Most often, disorders of behaviour and mood imbalance and personality changes are symptoms accompanying AGD in very aged people.

There is no specific test for a clinical diagnosis of AGD. The involvement of structures similar to those affected in patients with mild cognitive impairment and AD makes it difficult to distinguish AD from AGD on the basis of neuroradiological data. Neuroimaging studies have shown atrophy of the anterior part of the temporal and frontal lobes or non-specific cerebral atrophy (Ferrer *et al.*, 2003; Ishihara *et al.*, 2005; Rippon *et al.*, 2005). Moreover, AGD and AD may occur in the same individual. Biological assays do not permit a clinical diagnosis of AGD.

Diagnosis follows neuropathological study of the post-mortem brain. Sometimes, as happened in two personal individual cases with a four-year history of personality changes, mood disorders and mild mental impairment leading to a fulminating disease with hallucinations, ataxia, dementia and sharp EEG complexes, the combination of AGD and CJD was not suspected during life.

Finally, AGD has been reported in 30% of brains from cognitive normal aged (aged 85.4 ± 5.4 years) individuals (Knopman *et al.*, 2003).

Neuropathology of AGD

According to seminal studies, AGs localize in transentorhinal and entorhinal cortex, CA1 area of the hippocampus, presubiculum, neighbouring temporal cortex, orbitofrontal

cortex, insular cortex, basolateral nuclei of the amygdala and hypothalamic lateral tuberal nucleus (Braak and Braak, 1989; Schultz *et al.*, 1998). Coiled bodies in oligodendrocytes are common additional findings (Braak and Braak, 1989) (Fig. 1).

Electron microscopy

AGs contain straight filaments or tubules measuring 9–25 nm (Braak and Braak, 1989; Itagaki *et al.*, 1989; Ikeda *et al.*, 1995). Similar structures have been obtained in sarkosyl-insoluble fractions in AGD cases (Zhukareva *et al.*, 2002). Coiled bodies are composed of accumulations of fibrils measuring 10–13 nm in diameter (Yamada and McGeer, 1990; Ikeda *et al.*, 1995).

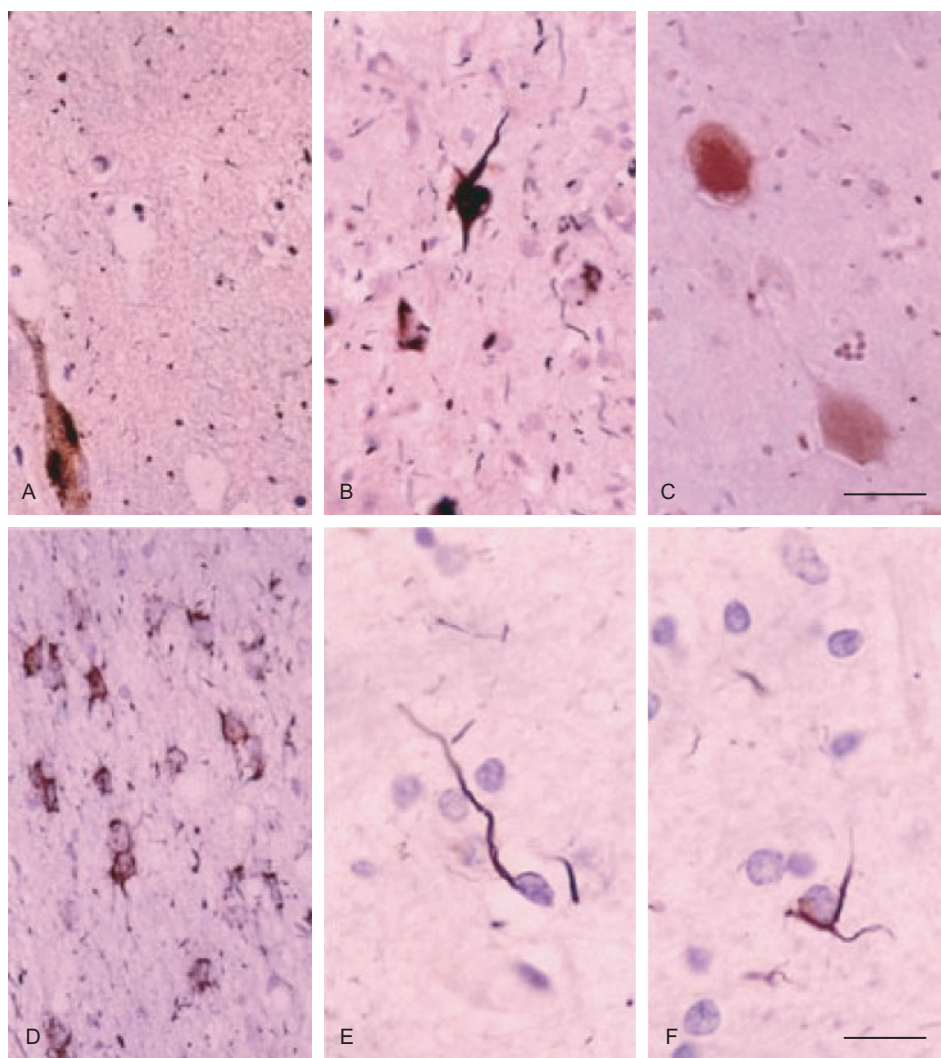


Fig. 1 AGD, Gallyas silver staining, showing argyrophilic tangles (**A, B**), grains (**A, B**), neuropil threads (**B**) in the CA1 region (**A**) and entorhinal cortex (**B**), periventricular astrocytes (**D**), and oligodendroglial coiled bodies in the white matter of the temporal lobe (**E, F**). Ballooned neurons in the amygdala show a diffuse pale coloration (Gallyas negative). Sections lightly counterstained with haematoxylin. **A–D**, bar in **C** = 25 microns. **E, F**, bar in **F** = 10 microns.

Immunohistochemistry

Early studies were mainly based on silver staining. However, the use of immunohistochemistry has greatly expanded the understanding of AGD pathology. The use of anti-tau antibodies has shown that phospho-tau deposition occurs in AGs, as well as in pre-tangle neurons (Gallyas-negative) and coiled bodies in oligodendrocytes. Most tau-containing astrocytes in the limbic system are Gallyas negative (Tolnay *et al.*, 1997a; Botez *et al.*, 1999; Spillantini *et al.*, 1999; Tolnay and Probst, 1999). Based on these crucial observations, AGD is now considered to be a tauopathy.

Grains

The term ‘argyrophilic grains’ is derived from their strong staining with the Gallyas silver iodide method. However, it is worth noting that not all silver methods permit the visualization of AGs (Uchihara, 2007).

Grains are small, about 4–8 microns, spindle shaped, rod-like, button-like or round bodies in the neuropil. Single and double-labelling immunohistochemistry has suggested that AGs are preferentially localized in dendrites and dendritic branches (Ikeda *et al.*, 1995; Schultz *et al.*, 1998; Tolnay *et al.*, 1998), although association of AGs with axons has also been reported (Tolnay and Clavaguera, 2004). The origin of grains is probably in pre-tangle projection neurons of the transentorhinal and entorhinal cortex, CA1 area of the hippocampus, neurons of the dentate gyrus and hilus, presubiculum, neighbouring temporal cortex, orbitofrontal cortex, insular cortex, basolateral nuclei of the amygdala and hypothalamic lateral tuberal nucleus (Tolnay *et al.*, 1998; Tolnay and Clavaguera, 2004).

Studies with the Golgi Cox (Tolnay *et al.*, 1998) and with the rapid Golgi method in the entorhinal cortex and hippocampus have permitted a clear visualization of AGs as small protrusions of apical, collateral and basilar dendrites of pyramidal cells (Fig. 2). These protrusions grow in normal-appearing dendrites filled with normal dendritic spines. Dendrites and dendritic spines have normal morphology distally to the protrusion. The surface of AGs is smooth, but often they are covered by a few spines or short thin processes (Fig. 2). Although rows of AGs can be seen in the CA1 area of the hippocampus, such rows have not been identified in Golgi-stained sections. These structures largely differ from varicosities, distal stumps and other dendritic abnormalities, as visualized with the Golgi method, in distinct neurological diseases (Ferrer *et al.*, 1990; Ferrer, 2000). AGs also differ from neuritic sprouts as seen in AD (Scheibel and Tomiyasu, 1978; Ferrer *et al.*, 1983; Probst *et al.*, 1983).

Pre-tangle neurons

Pre-tangle neurons are a constant finding in AGD, and their distribution is the same as that for AGs (Tolnay *et al.*, 2003; Tolnay and Clavaguera, 2004). Pre-tangle neurons are

immunostained with the same anti-tau phospho-specific antibodies that decorate AGs (Tolnay *et al.*, 1997a; Ferrer *et al.*, 2003). Tau-immunoreactive deposits in granule neurons of the dentate gyrus are a constant abnormality in AGD.

In agreement with previous observations, pre-tangle neurons in AGD do not apparently differ from neurons with early phospho-tau deposition in AD (Braak *et al.*, 1994; Bancher *et al.*, 1989; Tolnay *et al.*, 2003).

Coiled bodies

Coiled bodies are similar to those observed in many other tauopathies and they lack specificity (Chin and Goldman, 1996; Ikeda *et al.*, 1998; Komori, 1999). Yet coiled bodies are a constant finding associated with AGs (Tolnay *et al.*, 2003).

Tau-containing astrocytes

Astrocytes containing hyper-phosphorylated tau show granular immunoreactive cytoplasm rather than dense inclusions like those seen in tufted astrocytes in PSP. Rather, bush-like astrocytes show thin immunoreactive processes with anti-phospho-tau antibodies. Commonly, these delicate processes appear in clusters, thus being reminiscent of thin astrocytic plaques of CBD. In addition to bush-like astrocytes and thin astrocytic plaques in the amygdala, white matter of the temporal lobe, periventricular and subpial astrocytes, tufted astrocytes and small clusters of astrocyte processes reminiscent of astrocytic plaques are also present in some cases.

The presence of tau-containing astrocytes is variable from one case to another. Although usually confined to the limbic system, generalized astrocytosis in the subcortical white matter has been reported in some cases (Yamada *et al.*, 1992; Tsuchiya *et al.*, 2001). Whether these cases are pure AGD or different tauopathies with massive phospho-tau in astrocytes remains unresolved.

Ballooned neurons

Ballooned neurons (Gallyas-negative) expressing α B-crystallin are commonly observed in the amygdala (Tolnay and Probst, 1998), and they have been considered as a marker of AGD (Tolnay and Probst, 1998; Togo and Dickson, 2002). Variable numbers of ballooned neurons are also present in the presubiculum and middle layers of the basal temporal cortex in AGD (Tolnay *et al.*, 2003). Yet ballooned neurons in the limbic system would be more usefully interpreted as a non-specific lesions encountered in many familial and sporadic tauopathies (CBD, PiD, PSP) and AD (Fujino *et al.*, 2004).

The cause of neuron ballooning in AGD and related settings is not known. Ballooned neurons show reduced staining of the rough endoplasmic reticulum. They accumulate phosphorylated neurofilament epitopes, and

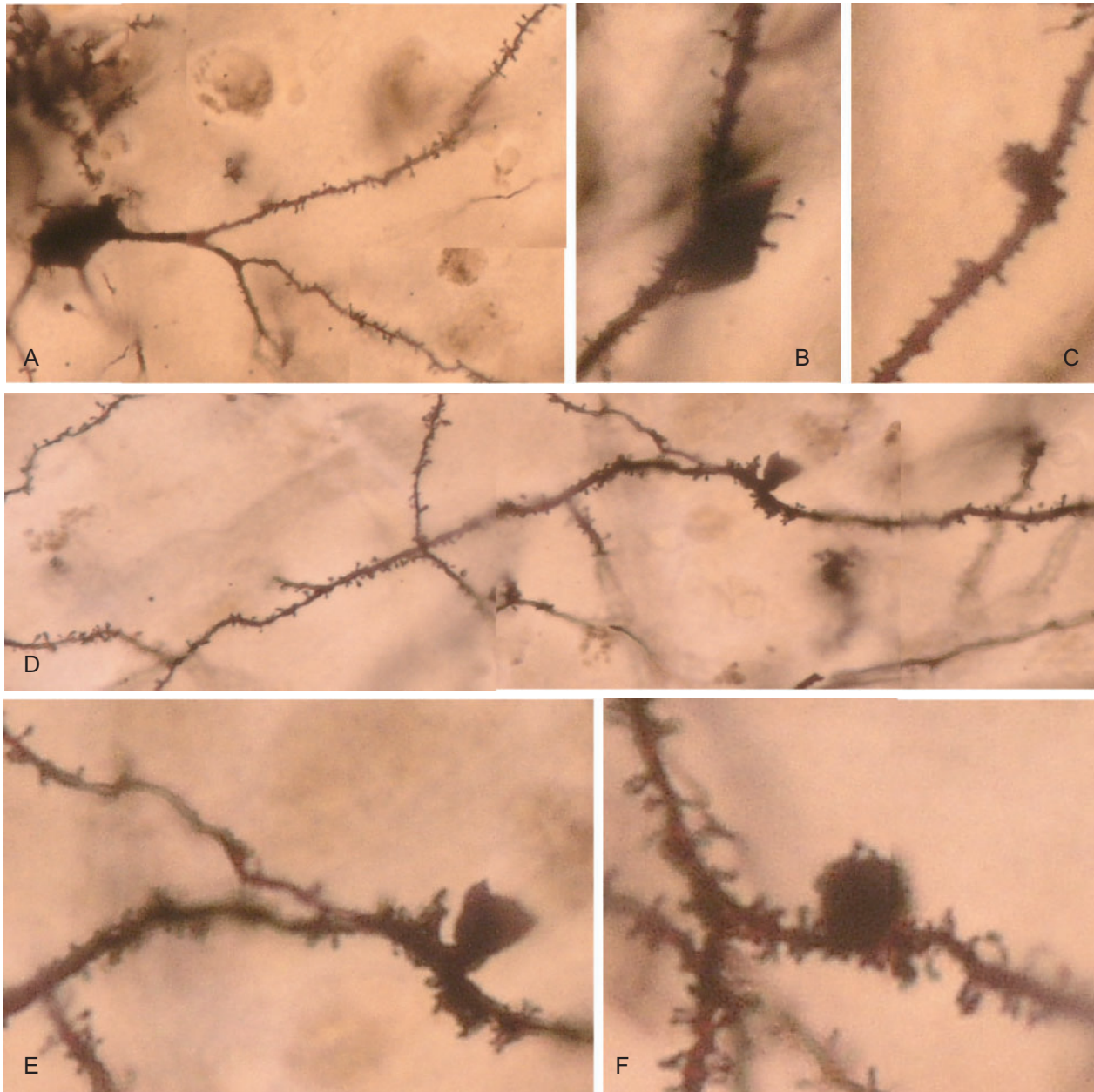


Fig. 2 AGD, Rapid Golgi method. **(A)** Neuron of the entorhinal cortex showing the normal morphology of dendrites and dendritic spines. **(B)** Spindle-shaped and **(C)** Round protrusions in dendrites. **(D)** Basilar dendrite with inverse-cone morphology with normal-appearing proximal (right) and distal (left) processes. **(E)** High magnification showing the smooth surface of the protrusion and the normal morphology of the spines in the mother dendrite. **(F)** Round protrusion covered with a few dendritic spines in a normal-appearing dendrite filled with dendritic spines.

they are decorated at the periphery with anti-phospho-tau antibodies. Ballooned neurons may be vacuolated. These characteristics show some resemblance to denervated neurons in other regions. The role played by α B-crystallin is also obscure, although recent studies point to its implication in the modulation of cytoskeleton proteins, including filaments and actin, and microtubule assembly (Ghosh *et al.*, 2007a; Gosh *et al.*, 2007b; Ohto-Fujita *et al.*, 2007; Singh *et al.*, 2007).

Tangles and neuropil threads

Variable numbers of tangles and neuropil threads may be present in the same regions as AGs and pre-tangle neurons. This has caused some confusion about the frontier between AGD with a few tangles and AGD with associated AD, and has led to consideration of AGD as a variant of AD (Cras and Perry, 1991). Yet AD changes (neurofibrillary tangles and neuropil threads) in AGD cases can be categorized following the guidelines of Braak and Braak

adapted to paraffin sections (Braak and Braak, 1999; Braak *et al.*, 2006).

The instrumental approach with separate consideration of AGs and AD-related changes is suitable, as this convention permits a general commitment for further studies in different settings.

In this line, Braak and collaborators have classified their own AGD cases as AGD + AD 0: 3; AGD + AD I-II: 79; AGD + AD III-IV: 41; AGD + AD V-VI: 2 (Braak and Braak, 1998). The apparently small percentage of AGs in advanced stages of AD must be interpreted cautiously, as the massive phospho-tau-immunoreactive pathology in such cases may hinder the visualization of AGs. This is particularly true when using the monoclonal AT8 antibody. Recent studies using 4R tau-specific antibodies, which highlight AGs, have shown a higher prevalence of AGs in advanced stages of AD (Fujino *et al.*, 2005).

Although often associated with AD, AGD is usually not accompanied by substantial β -amyloid deposits. In contrast to conventional AD cases, AGD brains show a very limited β -amyloid burden in the form of diffuse plaques; neuritic plaques are distinctively uncommon (Tolnay *et al.*, 1999).

Staging of AGs

Early observations indicated that the sole involvement of the anterior part of the CA1 region of the hippocampus was found in apparently normal individuals, whereas involvement of the posterior CA1 region occurred more commonly and more severely in demented cases (Tolnay *et al.*, 1997b). Other studies concluded that severe involvement of the ambient gyrus (the junction between the temporal lobe and the amygdala) differentiated AG with cognitive impairment and dementia from cognitively normal AGD (Saito *et al.*, 2002). More refined analysis has established a proposal for staging AGs (Saito *et al.*, 2004) which basically reflects a similar antero-posterior gradient of putative progression of the disease. Yet rare cases have shown widespread AGs throughout the temporal lobe, limbic system, frontal cortex and brain stem (Tsuchiya *et al.*, 2001; Maurage *et al.*, 2003; Ishihara *et al.*, 2005). The term diffuse AGD has been proposed as a subgroup of AGD to

differentiate these cases from the most common limbic AGD (Maurage *et al.*, 2003).

An up-dated staging based on previous descriptions (Braak and Braak, 1998; Saito *et al.*, 2004; Tolnay and Clavaguera, 2004; Ishihara *et al.*, 2005) and personal observations is shown in Table 1.

Staging of AGs does not include accompanying changes such as pre-tangle neurons, coiled bodies, bush-like astrocytes and ballooned neurons. The number and distribution of pre-tangle neurons parallels the distribution of AGs, whereas coiled bodies and tau-immunoreactive astrocytes have particular patterns in individual cases: large numbers of astrocytes may be encountered with relatively low numbers of AGs. Finally, the number of ballooned neurons in the amygdala shows important individual variation among cases with similar AG stage.

Consideration of the neuropathological diagnosis in AGD cases

Although silver stains have been useful in the past to discover AGD, the Gallyas method and other similar silver stains are not used in current practice. This is due in part to the variations in the quality of staining from one laboratory to another. Moreover, immunohistochemistry has been demonstrated to be a powerful tool with reproducible results in different laboratories (Alafuzoff *et al.*, 2006).

Lesions in AGD are best visualized with the help of any of the several commercial anti-phospho-tau antibodies available; good results are obtained with the AT8 antibody currently used in most laboratories and institutes. The best staining of AGs is achieved with anti-4R tau antibodies (Togo *et al.*, 2002; Fujino *et al.*, 2005). Combining these two antibodies allows the visualization of AGs, neurons with pre-tangles, neurofibrillary tangles, neuropil threads, coiled bodies and different tau-immunoreactive astrocytes.

Ballooned neurons are also mildly phospho-tau-immunoreactive although the best marker of ballooned neurons is anti- α B-crystallin.

The use of additional antibodies (e.g. anti- β A amyloid, α -synuclein, ubiquitin, TDP-43, protease resistant PrP) is obviously necessary to rule out combined pathologies.

Table 1 Argyrophilic grain (AG) staging

Stage I	Stage II	Stage III	Stage IV
Anterior entorhinal cortex; mild involvement of the cortical and basolateral nuclei of the amygdala; mild involvement of the hypothalamic lateral tuberal nucleus	Entorhinal cortex; anterior CA1; transentorhinal cortex; cortical and basolateral nuclei of the amygdala; presubiculum; hypothalamic lateral tuberal nucleus; dentate gyrus	Entorhinal cortex; CA1; perirhinal cortex; presubiculum; amygdala; dentate gyrus; hypothalamic lateral tuberal nucleus; mild involvement of CA2 and CA3; mild involvement of the subiculum; mild involvement of other nuclei of the hypothalamus (i.e. mammillary bodies); mild involvement of the anterior temporal cortex, insular cortex, anterior cingulate gyrus, orbitofrontal cortex, nucleus accumbens, septal nuclei; rare grains in the midbrain	Moderate to severe additional involvement of the neocortex and brainstem

Considering the high prevalence of other pathologies in association with AGs, it is probably prudent to consider a double or triple neuropathological diagnosis in the majority of AGD cases (i.e. AG + AD; AG + PSP; AG + CBD + PD). Staging of accompanying diseases may follow international agreement criteria (Braak and Braak, 1999; Braak *et al.*, 2003; McKeith *et al.*, 2005).

The majority of cases may be categorized, for example, as: AGs stage III + AD stage IIIA + PD stage 2, and probably including, as a note, the amount and distribution of tau-immunoreactive astrocytes and the presence of additional details. This complementary note may be useful as it may serve to describe early stages of tauopathies (PSP or CBD) that are commonly associated with AGs and for which there are not, at present, proposals for disease staging like those available for AD and PD.

Biochemistry of tau in AGD

Tau proteins are encoded by the *tau* gene in chromosome 17. Alternative splicing of exons 2, 3 and 10 results in six isoforms, which in turn give rise to six different mRNAs. The adult *tau* isoforms are proteins of 441 amino acids (2 + 3 + 10 +), 410 amino acids (2 + 3 + 10 –), 412 amino acids (2 + 3 – 10 +), 381 amino acids (2 + 3 – 10 –) and 383 amino acids (2 – 3 – 10 +); the fetal *tau* isoform is a protein of 352 amino acids (2 – 3 – 10 –). *Tau* proteins resulting from encoding exon 10 have four repeat regions (4R tau), whereas those lacking encoding exon 10 have three repeat regions (3R tau) (Goedert *et al.*, 1989; Himmler *et al.*, 1989). The function of *tau* largely depends on post-translational modifications including phosphorylation and dephosphorylation. Phosphorylation of *tau* is the result of a balanced action between protein kinases and protein phosphatases. Several kinases have been implicated in *tau* phosphorylation: glycogen synthase kinase-3 (GSK-3), cyclin dependent kinase-5 (cdk-5), mitogen-activated protein kinase, extracellular signal-regulated kinases (MAPK/ERK1 and MAPK/ERK2, p44 and p42), stress-activated protein kinases, c-Jun N-terminal kinase (SAPK/JNK) and p-38 kinase (p38), among others. These have the capacity to phosphorylate *tau* at specific sites (Hanger *et al.*, 1992; Mandelkow *et al.*, 1992; Goedert *et al.*, 1997; Lovestone and Reynolds, 1997; Reynolds *et al.*, 1997a; Reynolds *et al.*, 1997b; Goedert *et al.*, 1998; Jenkins *et al.*, 2000; Reynolds *et al.*, 2000; Buée-Scherrer and Goedert, 2002).

AGD is a 4R tauopathy

Early immunohistochemical studies disclosed several sites of tau phosphorylation in AGD (Tolnay *et al.*, 1997a; Ferrer *et al.*, 2003). Sites of tau phosphorylation in AGD do not differ from those in AD. Moreover, in contrast to results from early studies (Tolnay *et al.*, 1997a), tau phosphorylation at Ser262 has been found in AGs and pre-tangle

neurons (Tolnay *et al.*, 2002; Ferrer *et al.*, 2002b). Immunoreactivity of AGs and pre-tangle neurons to non-phosphorylation-dependent antibodies to N-terminal and C-terminal tau suggest that full tau is contained in these structures as well as in coiled bodies (Tolnay *et al.*, 1997a).

Gel electrophoresis of sarkosyl-insoluble fractions has been useful to recognize the band pattern of phospho-tau in AGD. In contrast to AD, characterized by bands of 68, 64 and 60 kDa often accompanied by an upper band of about 73 kDa, AGD is characterized by a double band of 68 and 64 kDa similar to that found in PSP and CBD (Togo *et al.*, 2002; Tolnay *et al.*, 2002; Ferrer *et al.*, 2003). Therefore, AGD is considered a 4R tauopathy (Togo *et al.*, 2002). The use of specific anti-4R antibodies has corroborated this biochemical observation (Togo *et al.*, 2002). Moreover, anti-4R immunohistochemistry has proved a very useful tool for the detection of AGD cases associated with AD changes (Fujino *et al.*, 2005). (Fig. 3).

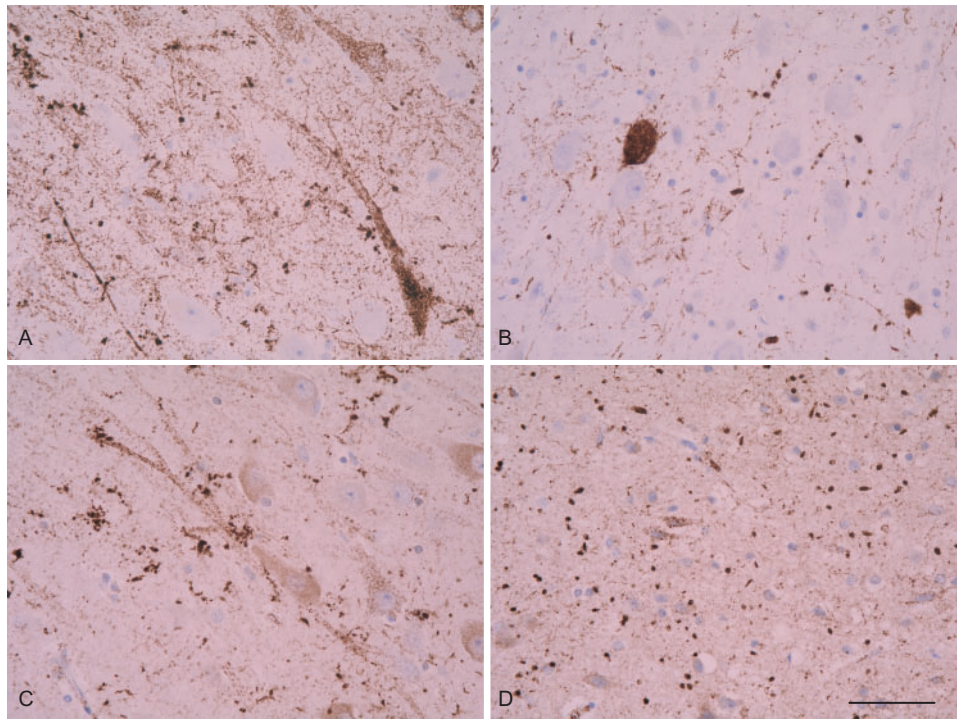
Interestingly, the presence of tangles and pre-tangles in the hippocampal CA2 area is associated with 4R tauopathy, and the most common is AGD (Ishizawa *et al.*, 2002).

In a particular series, three AGD cases showed a pattern similar to AD, but a 4R profile was found in two other cases (Zhukareva *et al.*, 2002). This example further illustrates the combination of AD and AGD changes in a number of AGD cases.

Truncated forms of tau in AGD

In addition to characteristic bands of 68 and 64 kDa in AGD, bands of lower molecular mass have been illustrated although not described in AGD (Tolnay *et al.*, 2002). This is an important point as bands of low molecular weight are concurrently present in sarkosyl-insoluble fractions in AGD (Fig. 4). These bands are not a post-mortem artefact due to delayed tissue processing (Santpere *et al.*, 2006), but rather they evidence truncated forms of tau (Novak *et al.*, 1991, 1993; Skrabana *et al.*, 2004). The presence of truncated tau may have implications in the pathogenesis of the disease, as truncated tau promotes polymerization of tau *in vitro* (Abraha *et al.*, 2000), drives neurofibrillary degeneration (Zilka *et al.*, 2006), induces oxidative stress in a rodent model of tauopathy (Cente *et al.*, 2006), and facilitates apoptosis *in vitro* under appropriate conditions (Fasulo *et al.*, 2000).

Among several proteases capable of cleaving tau, thrombin and prothrombin are present in neurons and accumulate in neurofibrillary tangles in AD (Arai *et al.*, 2005, 2006). By using double-labelling immunohistochemistry and confocal microscopy, co-localization of 4R tau and thrombin is found in AGs (Fig. 5), thus suggesting the participation of thrombin in tau truncation in AGs. In contrast, calpain-2 and active caspase-3 (17 kDa) are only substantially expressed in tangles but not in pre-tangle neurons and AGs in AGD (Fig. 5).



AGD. A: CA1 AT8; B: laterotuberal AT8; C: CA1 4R; D: ED 4R

Fig. 3 Strong 4R tau immunoreactivity is observed in pre-tangle neurons, tangles and grains. Paraffin sections, lightly counterstained with haematoxylin. Dilution of the 4R antibody (Upstate) 1:50. Bar = 25 microns.

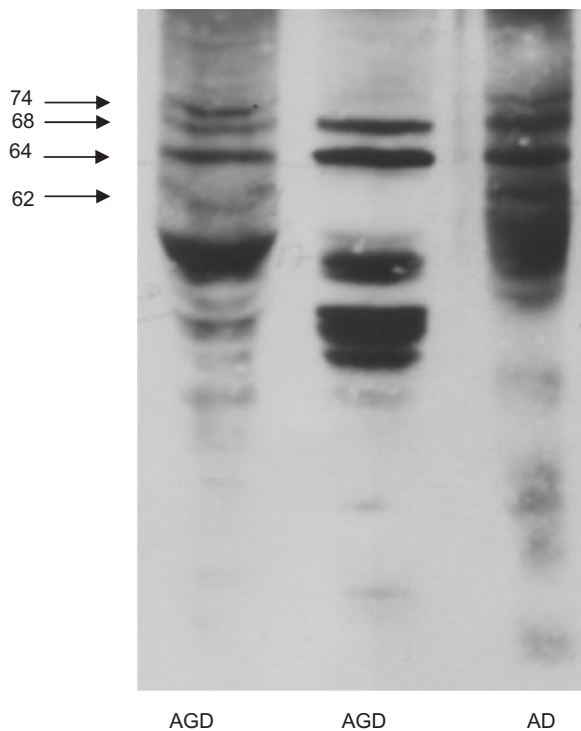


Fig. 4 Gel electrophoresis and western blotting of sarkosyl-insoluble fractions of the hippocampus in one case with AD (right), one pure AGD (middle) and one AGD combined with AD (left) processed in parallel. Four bands of 74, 68, 64 and 60/62 kDa are characteristic of AD. Two bands of 68 and 64 kDa are seen in AGD. In addition, several bands of lower molecular mass are found in AGD.

Tau phosphorylation and aggregation in AGD

Pre-tangle neurons contain phospho-tau, and straight filament and tubules, but do not develop paired helical filaments. Similarly, AGs are densely stained with anti-phospho-tau antibodies but they differ from neuropil threads in AD because of this particular structure. The reasons for these differences are barely known and our understanding of the factors that may distinguish pre-tangles and tangles is only fragmentary.

Kinases involved in tau phosphorylation in AGD

A few studies have shown increased expression of active tau-kinases in AGD (Ferrer *et al.*, 2003). These include mitogen activated kinase-extracellular signal-regulated protein kinase 1 and 2 (MAPK/ERK 1 and 2), stress-activated protein kinase (SAPK/JNK), kinase p38, glycogen synthase kinase-3 β (GSK-3 β) and calcium/calmodulin kinase (CaMK II). Phosphorylated active kinases co-localize with phospho-tau in pre-tangles, AGs, coiled bodies and astrocytes (Ferrer *et al.*, 2003) (Fig. 6). Detailed studies focused on GSK-3 β have shown early GSK-3 β activation preceding and accompanying the formation of pre-tangles, tangles and other tau-immunoreactive inclusions (Leroy *et al.*, 2007).

Expression levels of the different tau-kinases in pure AGD (that is, with no associated AD pathology) are similar

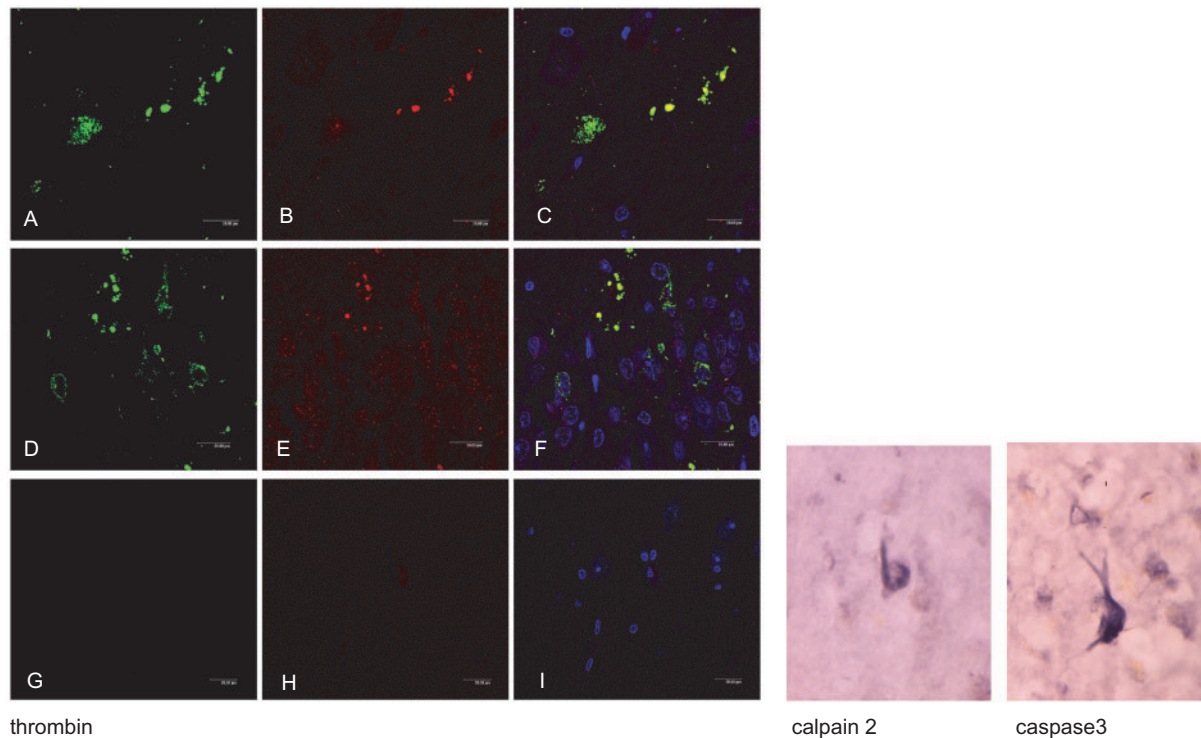


Fig. 5 Left panel: Double-labelling immunofluorescence and confocal microscopy showing co-localization of thrombin (green: **A, D**) and 4R tau (red: **B, E**) in grains (yellow: **C, F**) in CA1 area of the hippocampus (**A–C**) and dentate gyrus (**D–F**). (**G–H**): sections incubated without the primary antibodies serve as negative controls. Dilution of the thrombin antibody (American Diagnostica) 1:100 and 4R tau (Upstate) 1:50, respectively. TO-PRO counterstaining (blue) permits the visualization of nuclei. Right panel: calpain 2 (Calbiochem) 1:25 and active caspase 3 (17 kDa) (Cell Signalling) 1:25 immunohistochemistry. Immunoreactivity is restricted to neurofibrillary tangles.

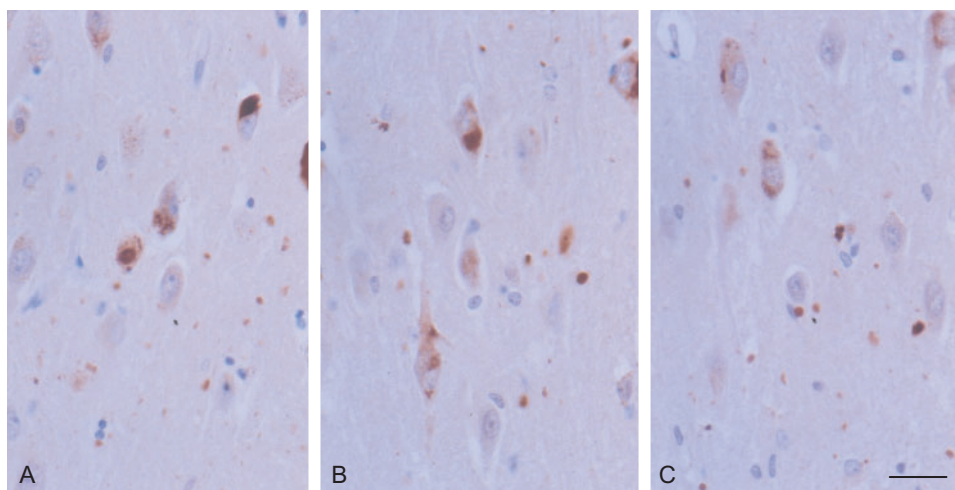


Fig. 6 GSK-3 (**A**), SAPK/JNK-P (**B**) and p38-P (**C**) immunoreactivity in the CA1 region of the hippocampus in AGD. Active tau-kinases are expressed in pre-tangle neurons, tangles and grains. Paraffin section lightly counterstained with haematoxylin. Dilution of the antibodies p38-PThr180/Tyr182 (cell Signalling) 1:200; SAPK/JNK-PThr183/Tyr185 (Cell Signalling) 1:150, GSK-3 β -P β 9 (Oncogen) 1:150. Bar = 25 microns.

in total homogenates and sarkosyl-insoluble fractions, a feature which is in contrast with the sequestering of several active kinases in the sarkosyl-insoluble fraction in AD (Ferrer, 2004; Ferrer *et al.*, 2005). Therefore, one of the

differential properties of tangles and pre-tangles is the sequestering of tau-kinases in tangles. Immunoprecipitation studies of tau-kinases from paired helical filament-enriched fractions in AD have shown the capacity to phosphorylate

specific substrates including recombinant tau, thus indicating that tangles have the ability to recruit tau for further phosphorylation (Ferrer *et al.*, 2002a; Ferrer, 2004; Ferrer *et al.*, 2005).

Components that differentiate pre-tangle neurons from tangles are tubulin (Puig *et al.*, 2005), and elevated levels of iron, ferritin and transferrin in tangles (Quintana *et al.*, 2006).

Sequestosome 1/p62

p62 is a protein for which a role in protein aggregation and degradation has recently been attributed (Seibenhener *et al.*, 2004). p62 is able to self-aggregate and it has high affinity for multi-ubiquitin chains (Vadlamudi *et al.*, 1996; Geetha and Wooten, 2002). Based on this evidence, it has been proposed that p62 may have a role both in promoting protein aggregation and in delivering polyubiquitinated proteins to the proteasome for their degradation (Kuusisto *et al.*, 2001; Nakaso *et al.*, 2004). Previous studies have shown the presence of p62 immunoreactivity in neurons with neurofibrillary tangles and in α -synuclein inclusions within the spectrum of Lewy body diseases (Kuusisto *et al.*, 2002, 2003; Zatloukal *et al.*, 2002). p62 also decorates AGs and to a lesser degree coiled bodies (Scott and Lowe, 2007). Further analysis of p62 expression has shown diffuse moderate p62 immunoreactivity in pre-tangle neurons, sometimes with a peri-nuclear reinforcement, as well as strong localized p62 immunoreactivity in tangles and strong p62 immunoreactivity in grains (Fig. 7A and B). These findings suggest that incorporation of p62 in pre-tangle neurons and grains is probably the same as the mechanism proposed for neurofibrillary tangles in AD (Kuusisto *et al.*, 2002).

Ubiquitin

The ubiquitin-proteasome system (UPS) plays a crucial role in non-lysosomal protein degradation under certain physiological conditions. Misfolded proteins or un-assembled subunits of larger protein complexes and retro-translocated proteins from the endoplasmic reticulum are also subject to rapid proteasomal degradation (Herschko and Ciechanover, 1998; Glickman and Ciechanover, 2002). The ubiquitin-proteasome pathway is initiated by the conjugation of ubiquitin to the substrate leading to poly-ubiquitination of the substrate. Most often, the 26S proteasome is composed of two caps or 19S complexes, which are responsible for recognition of ubiquitylated proteins, and the internal barrel 20S catalytic complex with three main peptidase activities: chymotrypsin-like, trypsin-like and peptidylglutamyl peptide hydrolyzing activities (Botchler *et al.*, 1999; Voges *et al.*, 1999; Herschko and Ciechanover, 1998; Glickman and Ciechanover, 2002).

The activity of the UPS is altered in many diseases characterized by aggregation of misfolded or abnormal proteins. Therefore, the proteasome has a crucial secondary role in the pathogenesis of several degenerative disorders

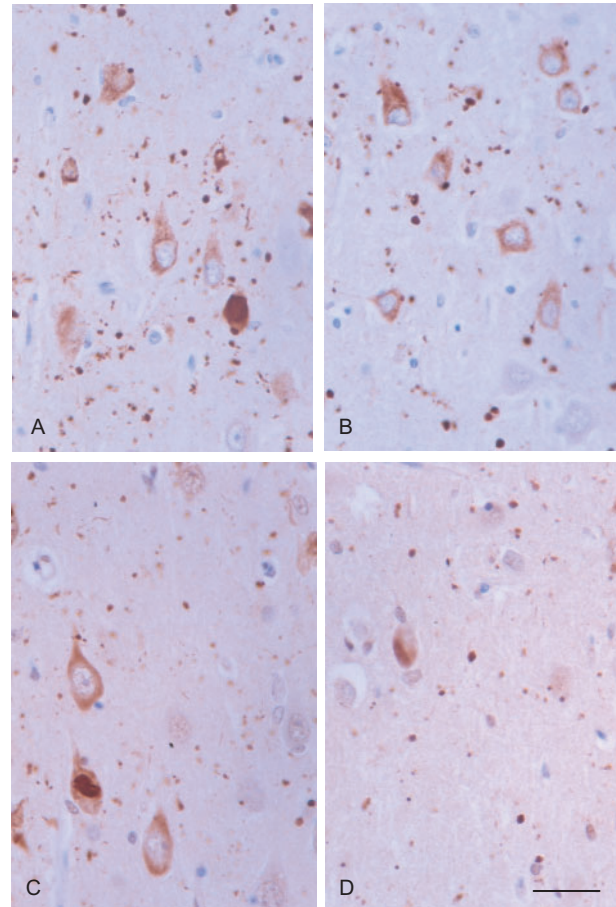


Fig. 7 p62 immunoreactivity (**A, B**) is found in pre-tangle neurons, tangles and grains in the CA1 region of two different AGD cases. Ubiquitin immunoreactivity (**C, D**) is also observed in pre-tangle neurons, tangles and grains in the same cases. Paraffin section lightly counterstained with haematoxylin. Dilution of anti-p62 C-terminal antibody (Progen) 1:100 and anti-ubiquitin (Dako) 1:500. Bar = 25 microns.

including AD, tauopathies and synucleinopathies (Layfield *et al.*, 2003). A common feature of these disorders is the accumulation of ubiquitin bound to non-degraded proteins.

Earlier studies have established that about 50% of AGs and coiled bodies are immunostained with anti-ubiquitin antibodies (Tolnay *et al.*, 2003). However, it is our experience that ubiquitin staining of these lesions is largely sensitive to sub-optimal tissue processing due to long formalin fixation, among other factors. Ubiquitin is present in a majority of AGs and coiled bodies, as well as in many pre-tangle neurons (Fig. 7C and D). Double immunofluorescence and confocal microscopy discloses co-localization of AT8 and ubiquitin in the vast majority of AGs (Fig. 8).

Mutant ubiquitin (UBB⁺¹)

UBB⁺¹ is generated by a non-DNA-encoded dinucleotide deletion occurring within UBB mRNA. The aberrant protein, resulting from molecular misreading, has a

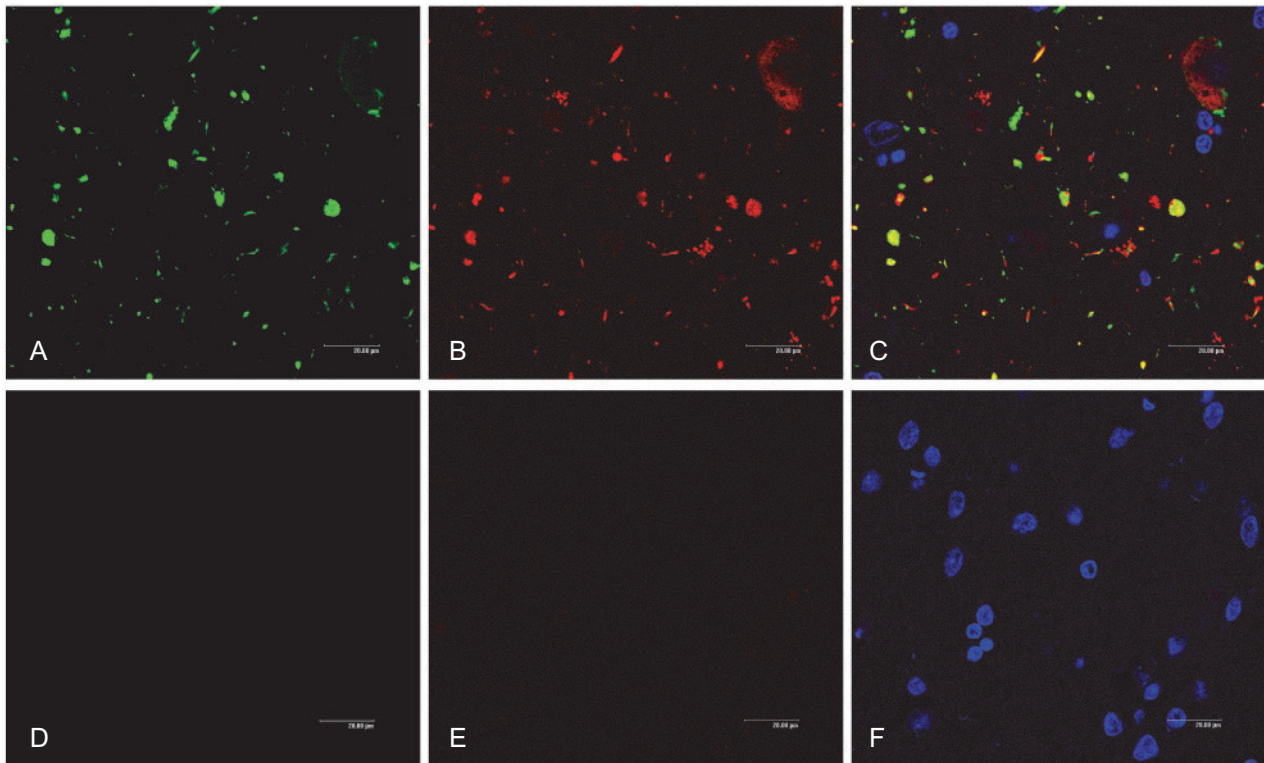


Fig. 8 Double-labelling immunofluorescence and confocal microscopy showing co-localization of tau AT8 (green: **A**) and ubiquitin (red: **B**) in the majority of grains (yellow: **C**). **G–H**: sections incubated without the primary antibodies serve as negative controls. Dilution of AT8 (Innogenetics) 1:50 and ubiquitin (Dako) 1:500. TO-PRO counterstaining (blue) permits the visualization of nuclei.

modified C-terminus and is unable to ubiquitinate other protein substrates (van Leeuwen *et al.*, 1998). UBB⁺ is itself ubiquitinated, and while at low expression levels it can be degraded by the proteasome, at high levels it can inhibit the proteasomal machinery (Lindsten *et al.*, 2002). Previous studies have demonstrated UBB⁺ in neurofibrillary tangles in AD (Fischer *et al.*, 2003). Moreover, UBB⁺ accumulates in the hallmark inclusions of Down syndrome and all other tauopathies. Therefore, the accumulation of UBB⁺ is considered a specific marker of proteasomal dysfunction in tauopathies and polyglutamine diseases (van Leeuwen *et al.*, 1998; Fisher *et al.*, 2003; de Pril *et al.*, 2004).

Consistent with these previous observations, UBB⁺ is expressed in neurons with tangles as well as in AGs in AGD (Fisher *et al.*, 2003). However, very low levels if any are noticed in pre-tangle neurons (Fig. 9). Since the inhibition of the proteasome activity by UBB⁺ is dose-dependent (van Tijn *et al.*, 2007), it can be suggested that low levels of UBB⁺ in pre-tangle neurons would not impede proteasomal function. High levels of UBB⁺ in tangles and grains make these structures barely vulnerable to degradation via the UPS.

It has been shown that paired helical filaments (the main component of neurofibrillary tangles) may further impair the proteasomal function (Keck *et al.*, 2003). It remains to be shown whether grains also have the capacity to collapse the proteasome.

Oxidative stress

Free radical production is a widespread phenomenon occurring under physiological aerobic metabolism in eukaryotic cells, and it is pronounced in the nervous system because of its primordial aerobic metabolism. A balance between oxidation and reduction reactions serves to maintain the physiological redox status. However, oxidative stress may cause deleterious metabolic effects when the generation of reactive oxygen species exceeds the level of antioxidant responses.

Oxidative stress plays a crucial role in the pathogenesis of AD (Moreira *et al.*, 2005; Zhu *et al.*, 2005; Nunomura *et al.*, 2006). One of the consequences of this is the lipoxidation, glycooxidation and nitration of certain proteins (Pamplona *et al.*, 2005; Butterfield *et al.*, 2006a; Butterfield *et al.*, 2006b; Sultana *et al.*, 2006a; Sultana *et al.*, 2006b; Sultana *et al.*, 2006c), which results in loss of function. Decline in the proteasome function in the earliest stages of AD is partially due to oxidative inactivation (Cecarini *et al.*, 2007). Another consequence is the activation of signal transduction cascades including stress kinases (Petersen *et al.*, 2007).

In spite of the important information about oxidative stress in AD, practically nothing is known about its role in AGD. Yet increased expression of advanced glycation end products (AGEs) and AGE receptor (RAGE) can be seen by immunohistochemistry in neurons of the hippocampus and

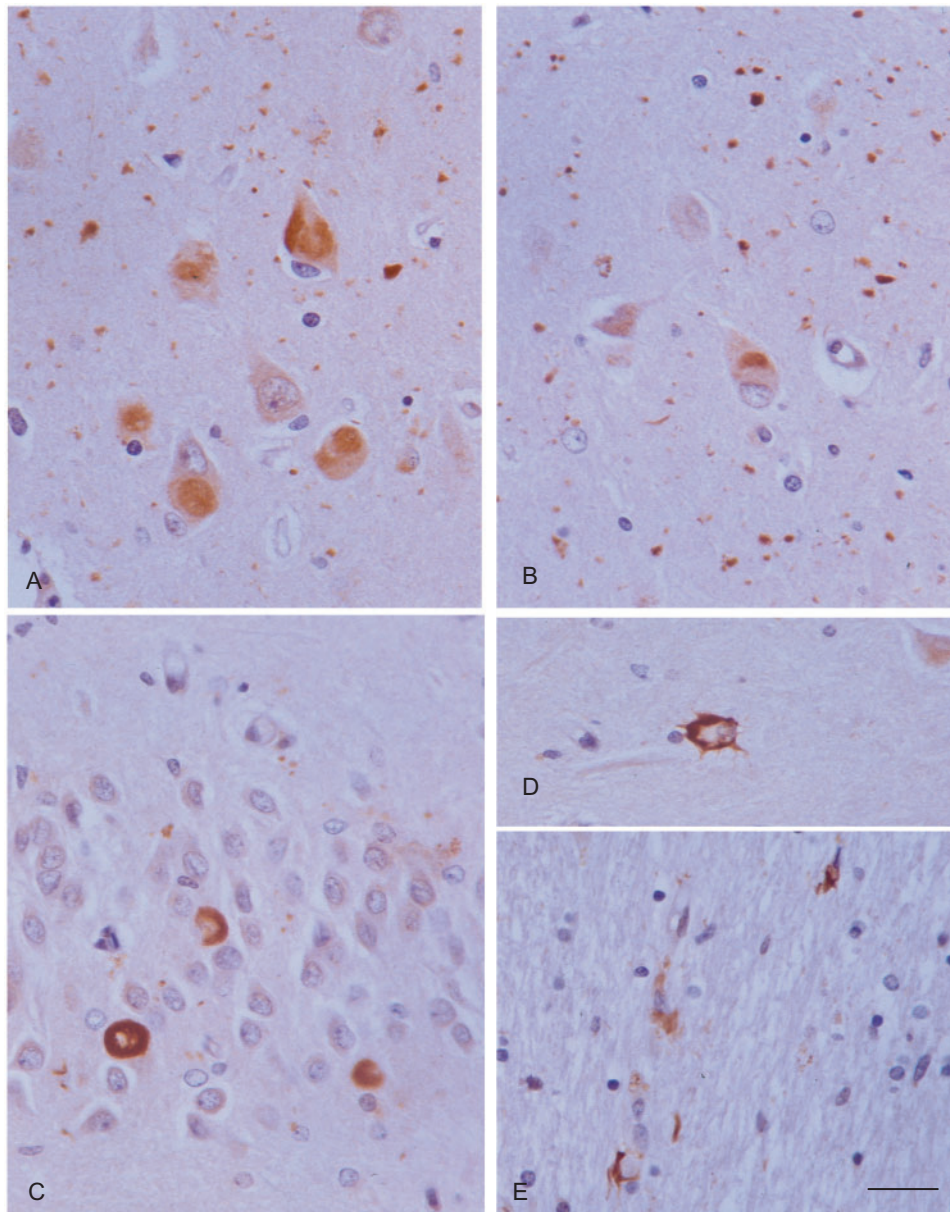


Fig. 9 Round elongated deposits of mutant ubiquitin (UBB^{+}) immunoreactivity in neurons of the CAI region (**A**), entorhinal cortex (**B**), and granule cells of the dentate gyrus (**C**), as well as in astrocytes (**D**) and coiled bodies (**E**). UBB^{+} immunoreactivity is clearly present in grains (**A**, **B**). Paraffin section lightly counterstained with haematoxylin. Dilution of the rabbit polyclonal UBB^{+} antibody (Dr Fred W. van Leeuwen, Ubi2+1, I40994, for details see Fisher *et al.*, 2003) 1:400. **A**, **B**, bar in **B** = 25 microns; **C**–**E**, bar in **E** = 10 microns.

entorhinal cortex in pure forms of AGD (data not shown). AGEs are carbonyl groups generated by secondary reaction of the primary amino group of lysine residues with reactive carbonyl derivatives produced by the reaction of reducing sugars or their oxidation products with lysine residues of proteins (glycation/glycoxidation reactions) (Dalle-Donne *et al.*, 2006). RAGE is a member of the immunoglobulin superfamily sensitive to the generation of reactive oxygen species that is crucial for many AGE-induced changes in cellular properties, including activation of protein kinase pathways (Lander *et al.*, 1997; Schmidt *et al.*, 2000). Anti-oxidant responses can also be determined by

immunohistochemistry to Cu/ZN superoxide dismutase I (SOD1) and Mn superoxide dismutase II (SOD2) in the AGD brain (data not shown). Increased SOD1 and SOD2 immunoreactivity is observed in neurons in vulnerable regions in parallel with AGs and pre-tangle neurons. These findings show that increased oxidative stress and increased oxidative responses occur in the hippocampus and entorhinal cortex in pure AGD, and, therefore, that these modifications are unrelated to typical AD changes.

Evidence of oxidative stress also suggests a link between free radical production, stress kinase (basically, SAPK/JNK and p38) activation, and tau phosphorylation in

AGD. Similar scenarios have been reported in AD and other human and murine tauopathies (Zhu *et al.*, 2000, 2001, 2003; Puig *et al.*, 2004; Ferrer, 2004, Ferrer *et al.*, 2005).

Neurotransmitters and receptors

Little is known about neurotransmitters and receptors in AGD. A single study reported normal cortical levels of choline acetyltransferase but markedly reduced levels of dopamine and its metabolites in the striatum (Yamada *et al.*, 1992). However, the description of these two cases is consistent with AGD associated with progressive subcortical gliosis.

Recently, increased adenosine receptor A (A1), but not A2A or A2B, together with increased levels of adenylyl cyclase, an effector of A1, and sensitization of this pathway, has been reported in the hippocampus but not in the frontal cortex in pure AGD (Perez-Buira *et al.*, 2007). This has been interpreted as a compensatory response geared to modulating glutamate neurotransmission and facilitating neuroprotection of this preferentially involved region in AGD.

Concluding comments

Although very common, AGD is still a poorly understood neurological disorder. However, the recent studies discussed above allow us to delineate a pathogenic scenario for some hallmark aspects of the disease. A summary of the pathways involved and suggested activation of metabolic cascades is shown in Fig. 10. Aging is the most important determinant factor. Oxidative stress plays a crucial role in the activation of stress-activated tau-kinases, which facilitate tau-hyperphosphorylation in a subset of neurons. Abnormal tau is aggregated after binding with p62 and subsequently ubiquitinated in grains, pre-tangle neurons and tangles. Incorporation of mutant ubiquitin, UBB⁺¹, blocks hyperphosphorylated tau degradation in grains and tangles. These structures sequester active tau-kinases, thus further promoting local tau hyperphosphorylation in AGs and tangles. Finally, thrombin accumulated in AGs and tangles may facilitate tau truncation, which is toxic for cells and which increases oxidative stress.

In spite of these achievements, several points remain obscure, such as: (i) original causes leading to oxidative

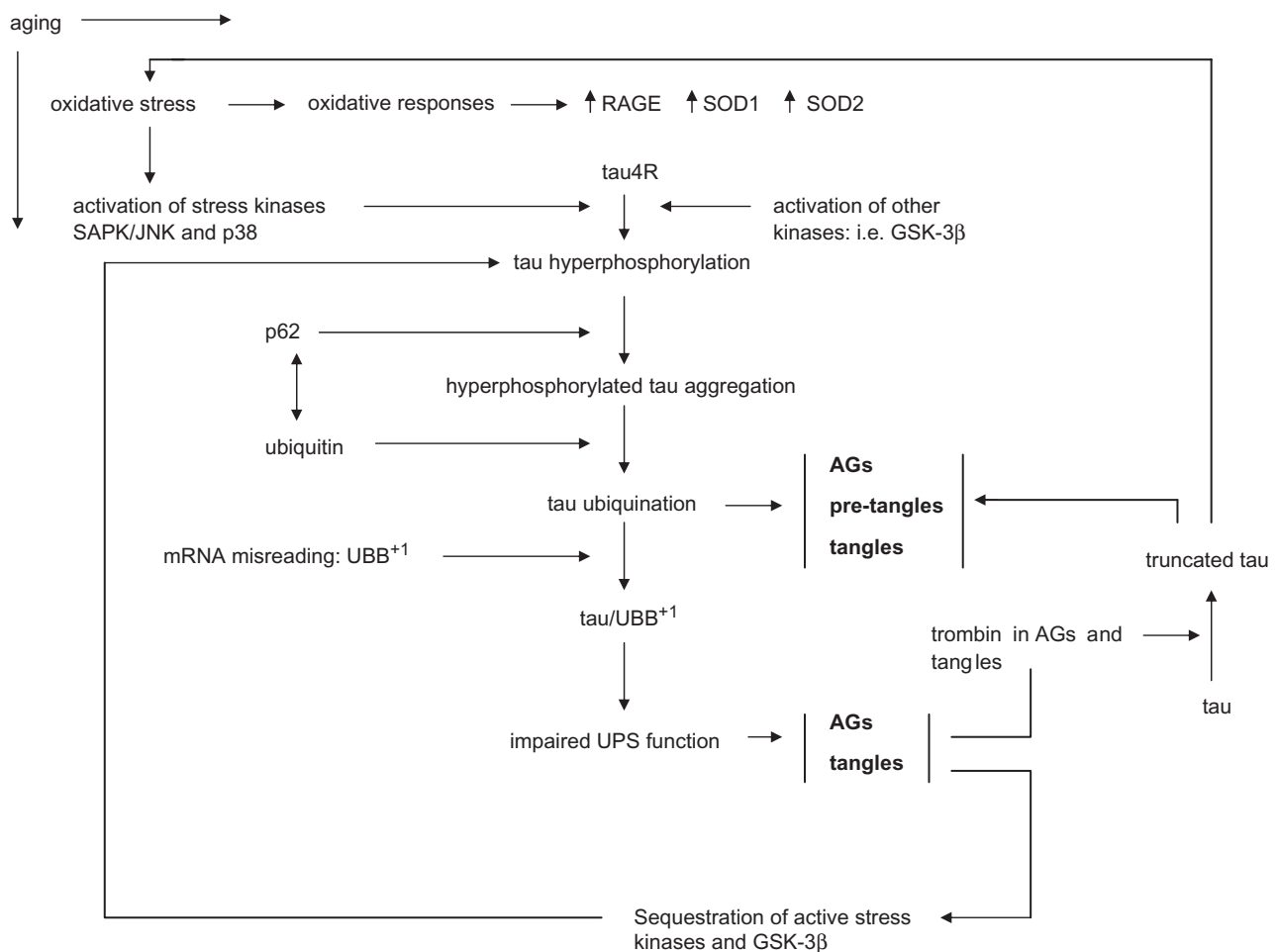


Fig. 10 Summary of pathologic events in AGD.

stress; (ii) targets of oxidative stress; (iii) role played by phosphatases; and (iv) reasons for selective tau 4R hyperphosphorylation, among others.

AGD is restricted to human beings, as no similar lesions have been reported under natural conditions in animals. Yet deafferentation of the hippocampus after lesions of the entorhinal cortex in rats is followed by the presence of small granules containing phospho-tau in the molecular layer of the dentate gyrus (Mudher *et al.*, 2001). Whether combined deafferentation and abnormal tau metabolism localized in vulnerable points of the dendritic arbour may be causative of grain architecture is a fascinating working hypothesis.

Acknowledgements

This study was supported in part by the Spanish Ministry of Health, Instituto de Salud Carlos III (PI05/1570 grant) and CIBERNED program, the European Commission, under the Sixth Framework Programme (BrainNet Europe II, LSHM-CT-2004-503039) and ISAO grant 06502. Brain samples were obtained from the Institute of Neuropathology and University of Barcelona Brain Banks following the guidelines and approval of the local ethics committees. We wish to thank Dr Jesús Ávila, Centro de Biología Molecular Severo Ochoa, Universidad Autónoma de Madrid, for providing the tau antibody 7.51; Rosa Blanco, Margarita Carmona (Institut de Neuropatologia) and Benjamín Torrejón-Escribano (Serveis Científico-Tècnics, Unitat de Biologia de Bellvitge) for technical assistance; and Tom Yohannan for editorial help.

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LRRK2 in neurodegeneration. A review.

LRRK2 and neurodegeneration

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Received: 9 November 2008 / Revised: 24 December 2008 / Accepted: 24 December 2008
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Abstract Mutations in leucine-rich repeat kinase 2 gene (*PARK8/LRRK2*) encoding the protein Lrrk2 are causative of inherited and sporadic Parkinson's disease (PD) with phenotypic manifestations of frontotemporal lobar degeneration, corticobasal degeneration and associated motor neuron disease in some patients, and with variable penetrance. Neuropathology is characterized by loss of dopaminergic neurons in the substantia nigra pars compacta in all cases with accompanying Lewy pathology, or tau pathology or without intraneuronal inclusions, thus indicating that mutations in *LRRK2* are not always manifested as Lewy body disease (LBD) or as α -synucleinopathy. Molecular studies have not disclosed clear association between nerve cell degeneration and modifications in the kinase activity of Lrrk2, and the pathogenesis of *LRRK2* mutations remains unknown. Several morphological studies have suggested that Lrrk2 is a component of Lewy bodies and aberrant neurites in sporadic PD and Dementia with Lewy bodies, whereas other studies have indicated that Lrrk2 does not participate in Lewy body composition. Likewise, some studies have shown Lrrk2 immunoreactivity in hyper-phosphorylated tau inclusions in Alzheimer's disease (AD) and other tauopathies, whereas other studies did not find Lrrk2 in hyper-phosphorylated tau inclusions. We have used three currently used anti-Lrrk2 antibodies (NB-300-268, NB-300-267 and AP7099b) and concluded that these differences are largely dependent on the antibodies used and,

particularly, on the interpretation of the origin of the multiple bands of low molecular weight species, in addition to the band corresponding to full-length Lrrk2, that recognize the majority of these antibodies. A review of the available data and our results indicate that full-length Lrrk2 is not a major component of Lewy bodies in LBDs, and of hyperphosphorylated tau inclusions in AD and tauopathies. Bands of low molecular weight are probably not the result of post-mortem artefacts as they are also present in cultured cells processed under optimal conditions. Truncated forms of Lrrk2 and additional transcripts related with *LRRK2*, in the absence of spliced forms of Lrrk2 may account for Lrrk2 immunoreactivity in distinct intraneuronal inclusions.

Keywords *LRRK2* · Parkinson disease · Alzheimer disease · Tauopathy · Lewy bodies

Parkinson disease

Parkinson disease (PD) is the second most prevalent neurodegenerative disease among the elderly population. Clinical features of PD are resting tremor, postural instability, akinesia and rigidity. Pathological findings are reduced pigmentation in the substantia nigra pars compacta due to loss of dopaminergic neurons. This is accompanied by intracytoplasmic proteinaceous inclusions in surviving neurons (Lewy bodies) and neurites [22]. Lewy bodies and aberrant neurites are composed of protein aggregates among which abnormal α -synuclein is a crucial component [88]. In addition to substantia nigra, neurons of other regions are affected, including several nuclei of the medulla oblongata, pons and midbrain, and the motor nuclei of the hypoglossal and vagal nerves, reticular formation and locus ceruleus, as well as the nucleus basalis of

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Meynert, amygdala, hippocampus, striatum and cerebral cortex [52].

The majority of PD cases (90%) are sporadic and their aetiology is unknown, but a number of mutated genes have been identified as the cause of the remaining, mostly familial, cases. Familial PD cases have been related with mutations, duplications and triplications in *SNCA* (α -synuclein)/*PARK1*, *UCHL-1* (ubiquitin carboxy-terminal hydrolase L1)/*PARK5*, parkin/*PARK2*, DJ-1/*PARK7*, PINK-1 (PTEN-induced putative kinase)/*PARK6*, ATP13A2 (p-type ATPase)/*PARK9*, HTRA2 (HtrA serine peptidase 2)/*PARK13* and *LRRK2/PARK8*. Other *PARK* loci have been identified: *PARK3*, *PARK10*, *PARK11* and *PARK12*; but the specific mutated gene is unknown. *LRRK2* mutations are by far the most abundant in autosomal dominant PD, and they may lead to late-onset PD in contrast to other PD-causative mutations which present more commonly as early onset PD [2, 94]. Expression of *LRRK2* mutations shows increased penetrance with age [34, 41, 43, 53]. The place of *LRRK2* in the pathogenesis of PD has been the subject of recent evaluations [6, 42, 45, 76, 96]. The present review deals with the role of *Lrrk2* in neurodegeneration, including PD, and covers controversial aspects such as the presence of *Lrrk2* in intraneuronal inclusions in α -synucleinopathies and tauopathies.

Mutations in *LRRK2*: clinical features and prevalence

A linkage study performed on a family with autosomal dominant PD revealed a region in chromosome 12 containing 116 genes segregating with the disease in all affected individuals. This region was called *PARK8* [23]. In 2004, the mutated gene causative of the disease was identified as *LRRK2* by two different groups [81, 109], and the encoded protein *Lrrk2* [81, 109] was named dardarin, from dardara which means tremor in Basque (several families analysed) [81].

About 30 different mutations have been identified in *LRRK2* gene. As a group, these mutations account for a maximum of 13% of familial PD and 5% of sporadic cases [9, 15, 18, 20, 24, 25, 31, 49, 53, 69, 78, 95, 105]. Most of these mutations are amino acid substitutions located in the C-terminal half of the protein [82]. It has been suggested that the most prevalent *Lrrk2* mutation in Mediterranean shores is G2019S, mainly in the Arab population of North Africa, representing 40% of familial and sporadic PD [3, 57, 58], and in the Ashkenazi Jewish population representing 30% of familial PD [79, 80]. However, population studies have indicated that such high prevalence is, probably, overestimated [19]. Other reported mutations include: R1441G, Y1699C, R1441C, I1122V, I2020T, R1441H and G2385R (see OMIM 609007 for further

details and references). *LRRK2* heterozygous R1628P and Gly2385Arg genotypes increase the risk of PD [95].

The majority of cases bearing *Lrrk2* mutations suffer from PD [12]. However, some cases have amyotrophy and ocular supranuclear palsy. Mutations in *LRRK2* are rarely manifested as a corticobasal syndrome, primary progressive aphasia and frontotemporal lobar degeneration [6, 13].

Varied pathology independent of mutation

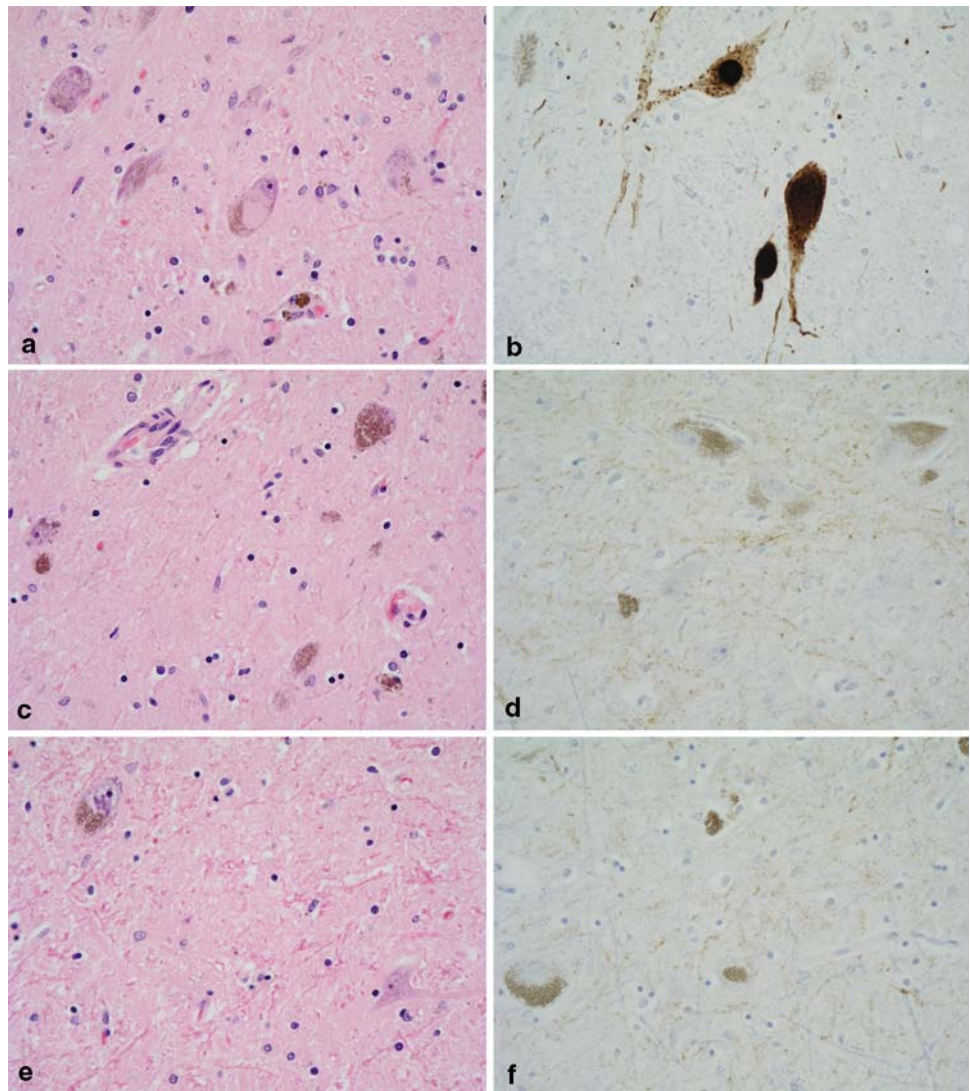
Mutations in *LRRK2* can lead to PD clinically indistinguishable from idiopathic PD and neuropathologically characterized by the presence of Lewy bodies, although no inclusions occur in other cases. I1371V, A1441C, Y1699C and G2019S mutations are accompanied by Lewy bodies [30–32, 54, 86, 104, 110] (Fig. 1). However, the same mutations are not always accompanied by Lewy bodies, as in one reported case bearing the T1699C mutation [104] and in another carrying the G2019S mutation [26] (Fig. 1). tau pathology and the absence of Lewy bodies occurred in one case with the G2019S mutation [85]. The only case examined with the R1441G (Basque) mutation had loss of dopaminergic neurons in the substantia nigra, free neuromelanin in the neuropil and absence of α -synuclein-, hyperphosphorylated tau- and ubiquitin-immunoreactive inclusions. The only accompanying feature was increased α B-crystallin immunoreactivity in isolated neurons [68] (Fig. 1). Intriguingly, the R1441C mutation in one family was manifested as an α -synucleinopathy (presence of Lewy bodies) in one member, as a tauopathy with neurofibrillary tangles and Progressive Supranuclear Palsy (PSP)-like distribution in a second affected member, and as loss of neurons with no intracytoplasmic neuronal inclusions in a third [109].

Other mutations are associated with motor neuron disease features, frontotemporal lobar degeneration and nuclear ubiquitin-immunoreactive inclusions [8, 13, 29]. This varied pathology suggests that *Lrrk2* is a protein which participates in different pathways and that mutated *Lrrk2* causes, primarily, loss of dopaminergic neurons and, secondarily, accumulation of abnormal proteins, together with ubiquitin, such as α -synuclein and hyper-phosphorylated tau [17].

Lrrk2 domains

LRRK2 is composed of 51 exons and encodes *Lrrk2*, a protein of 2,527 amino acids. From N-terminal to C-terminal, the domains identified in *Lrrk2* are named Ankyrin repeat (ANK), Leucine-Rich repeat (LRR), Ras of Complex (GTPase) (Roc), C-terminal of Ras (COR), kinase and WD40.

Fig. 1 Neuropathology of the substantia nigra in Parkinson's disease bearing the G2019S mutation showing the presence of Lewy bodies (**a, b**). Another unrelated case with the G2019S mutation with no Lewy bodies and other inclusions (**c, d**, [26]). A third case carrying the R1441G Basque mutation in *LRRK2* (**e, f** [68]) in whom neuron loss in the substantia nigra was not accompanied by Lewy bodies and neurites and hyperphosphorylated tau inclusions. **a, c, e** Haematoxylin and eosin; **b, d, f** α -synuclein immunostaining



ANK, LRR and WD40 are repeats separately found in several proteins and they confer platforms for protein interactions with different molecules such as cytoskeleton proteins, transcription factors, and signalling and cell cycle regulators. Because of this ability to bind different proteins, it has been suggested that *Lrrk2* may assemble a multi-protein signalling complex [70].

The kinase domain of *Lrrk2* belongs to the super-family of serine/threonine and tyrosine kinases, and is similar to the RIPK family (receptor-interacting protein kinase) which can regulate cell survival and cell death pathways in response to intracellular or extracellular stress signals [73].

The Roc and COR domains occur together as in the ROCO family of GTP-ases; the function of the COR domain is unknown, whereas the Roc domain is very homologous to members of the Rab-GTPase family [67]. This family is composed of more than 60 small GTP-ase proteins which regulate vesicle formation, actin- and

tubulin-dependent vesicle movement, and membrane fusion [93].

Functional domains

Lrrk2 is a GTP-ase which can bind and hydrolyse GTP and stimulate kinase activity, a property which suggests that the kinase domain of *Lrrk2* is activated by its own Roc domain [37]. The structure of Roc domain reveals a dimeric GTPase [16]. GTP binding is essential to the protein kinase activity of *Lrrk2* [50]. The ability of purified *Lrrk2* to autophosphorylate or to phosphorylate a generic substrate such as myelin basic protein appears to be low. Yet, it has been suggested that low kinase activity in vitro could be caused by the lack of the proper co-factor, lack of appropriate stimulus or abnormal protein folding in the assay conditions [70]. It has recently been shown that at least in vitro,

moesin, ezrin and radixin were substrates of phosphorylation by mutant Lrrk2-G2019S at the residues which regulate the binding of these proteins to actin [51].

How mutations affect Lrrk2 activity

Most of the identified Lrrk2 mutations are localized in kinase domain. Other mutations affect the GTPase (i.e. R1441C, R1441G, R1441H), the LRR (L1114L, I1122V) and Cor (Y1699C) domains. The G2019S mutation affects the kinase domain and increases kinase activity [35, 63, 100].

However, not all mutations in *LRRK2* lead to increased activity. R1441C and R1441G mutations affect the GTPase domain and they decrease GTPase activity [37, 59, 60]. Surprisingly, increased kinase activity has been reported to be associated with Lrrk2-R1441C and Lrrk2-R1441G mutants [38, 60]. However, these results were not reproduced in another study [51]. The Y1699C mutation, located in the Cor domain, seems not to be able to modify Lrrk2 kinase activity [51]. Furthermore, the T2356I mutation, affecting the WD40 domain, does not modify kinase activity. Finally, the R1941H and G2385R mutations inhibit the capacity of Lrrk2 for auto-phosphorylation, as well as for phosphorylation of MBP and moesin [51]. In contrast, increased kinase activity has been found in Lrrk2-Y1699C and Lrrk2-I2012T mutants [33, 101]. Understanding of these modifications is still fragmentary, probably due, in part, to methodological difficulties in the measurement of auto-phosphorylation [51].

Other properties of Lrrk2 may be affected depending on the site of the mutation [59]. Mutations in the residue 1441, although sited in the GTPase domain, are distant from the GTP hydrolysis region, but they are found in a region implicated in interaction with other proteins [93]. On the other hand, the G2385R mutation in WD40 domain involved in protein interaction is also able to inhibit kinase activity [44]. Finally, mutations in LRR and ankyrin domains may hamper Lrrk2-protein interactions [90].

Several small molecules may inhibit Lrrk2 activity and may have, therefore, therapeutic implications [10].

Lrrk2 interactions

Dimerization

Lrrk2 is predominantly found as a dimer in vivo. Dimerization occurs through the interaction of different regions of Lrrk2, including the ROC domain with several points in the LRR domain, a region close to ROC, WD40, and the N-terminal region [16, 36].

Cytoskeleton and proteins involved in trafficking

Most of the Lrrk2-interacting proteins identified to date are cytoskeleton and trafficking proteins. Lrrk2 has been found to interact in vitro with moesin, ezrin and radixin, which regulate β -actin binding to plasma membrane [51]. The ROC domain of Lrrk2 can also interact with α/β -tubulin heterodimers in microtubules, and co-localizes with them in primary hippocampal neurons [28]. Immunoprecipitation coupled with mass-spectrometry has permitted the identification of 14 potential Lrrk2-interacting proteins, among them clathrin and vimentin [14]. Finally, Lrrk2 appears to interact with Rab5a [87], thus being involved in endocytic vesicular transport between plasma membrane and early endosomes [7]. However, further studies are needed to learn whether protein interactions observed in vitro may occur in brain tissue.

Chaperones

Other putative interactors identified are proteins associated with phosphorylation, translation and chaperones [14]. Among these chaperones is Hsp90, which, together with its co-chaperone Cdc37, appears to play a crucial role in maintaining Lrrk2 stability [47].

Key proteins in neurodegenerative diseases

The interaction of Lrrk2 with proteins important in neurodegenerative diseases has also been tested. No interaction was found between Lrrk2 and α -synuclein, tau or Dj-1 [95]. However, the same study revealed interaction of Lrrk2 COR domain with parkin [92]. Parkin is the name of a E3 ubiquitin ligase which is found mutated in some cases of familial PD [2].

Expression and localization of Lrrk2

In the brain, *LRRK2* is expressed in neurons, and also in astrocytes and microglia [74]. It is also expressed in other tissues such as in liver, lung, kidney and heart [81, 109]. By using in situ hybridisation and immunohistochemistry, it has been shown that in normal brain *LRRK2* is expressed in several neuronal populations including cerebral cortex, caudate-putamen and hippocampus [27, 44, 45, 72, 89, 97, 102], as well as in dopaminergic neurons of the substantia nigra pars compacta [39, 44].

In cells, Lrrk2 is mainly found in the cytoplasm [30]. Lrrk2 is enriched in lipid raft, early endosomes, lysosomes, synaptic vesicles and plasma membrane [40, 87], as well as in the Golgi complex, endoplasmic reticulum and outer mitochondrial membrane [4, 40]. The association of Lrrk2 in

several membrane structures suggests a role for Lrrk2 in membrane trafficking [4, 40], which is further supported by the interaction of *LRRK2* with several cytoskeleton and trafficking-related proteins and with the function attributed to the RabGTPase family [93]. Moreover, with Rab5a and clathrin being possible interacting partners, a role for Lrrk2 in clathrin-mediated endocytosis was suggested and eventually demonstrated in vitro [87].

Accumulation of Lrrk2 has been observed in abnormal neurites of the substantia nigra pars compacta in one single case carrying the G2019S mutation [30]. Moreover, intracytoplasmatic Lrrk2-positive inclusions have been found in cultured cells bearing the R1441C and Y1699C mutations in Lrrk2 [35].

Biological effects of *LRRK2* mutations

In cells

In cell culture models, Lrrk2 can be toxic, depending on its kinase activity [35, 91]. Mutations in Lrrk2 associated with increased kinase activity increase apoptotic cell death in dopaminergic cell lines and primary neurons [62]. Decreased kinase activity, resulting from alteration of key residues in ROCO and kinase domains, reduces neuronal toxicity [91]. These observations led to the gain-of-function hypothesis to explain neurodegeneration in PD linked to mutations in *LRRK2*, particularly those associated with increased kinase activity such as G2019S.

Mutations affecting the kinase domain seem crucial also in neurite outgrowth, as expression of Lrrk2-G2019S, Lrrk2-I2010T and, to a lesser degree, Lrrk2-R1441G mutants in primary cortical neurons leads to dramatic reductions in neurite length and branching of axons and dendrites. Wild-type Lrrk2 over-expression in the same model does not alter cell morphology, whereas Lrrk2 shRNA-mediated knock-down leads to a gradual increase in neurite growth [64]. In retinoic acid-differentiated neuroblastomas, mutant Lrrk2 over-expression also causes neurite shortening in a process involving autophagy [84]. Interestingly, accumulation of Ser202 phosphorylated tau, but not of α -synuclein, was observed in spheroid-like aggregates, together with Lrrk2, within neurites in cells over-expressing Lrrk2-G2019S and Lrrk2-I2010T, and also, to a much lesser degree, in cells over-expressing wild-type *LRRK2* [64]. All these data suggest a role for Lrrk2 in the control of neurite length, ultimately regulated by its kinase activity.

Toxic effects of increased expression of Lrrk2 are probably level-dependent, as high levels of Lrrk2 over-expression produce cell death, whereas low levels of Lrrk2 over-expression are associated with impaired vesicle endocytosis [48, 87, 101]. Low Lrrk2 expression or

silencing *LRRK2* in rat hippocampal neurons results in kinase-independent altered vesicle endocytosis that can be rescued by co-expression of Rab5a [87].

Finally, RNA interference of *LRRK2* in SH-SY5Y cells results in differential regulation of 187 genes, with 94 transcripts being up-regulated and 93 transcripts down-regulated compared to scrambled control siRNA transfected cells [38].

In animal models

Lrrk2 has been studied in transgenic mice [60], pigs [55], worms [103] and flies [56, 61, 99].

Expression of Lrrk2-R1441C in mice is not accompanied by dopaminergic neuron loss [60], but degeneration of these neurons was observed following intracellular viral insertion of the Lrrk2 kinase domain fragment in rats [64].

Over-expression of wild type and human Lrrk2-G2019S in *Drosophila* results in retinal degeneration, selective loss of dopaminergic neurons, motor impairment and reduced lifespan [61]. Flies with the G2019S mutation show a significantly worse motor impairment than wild type, though this can be improved by administration of L-DOPA [61]. Previous studies in *Drosophila* expressing the CG5483 mutation, emulating human mutation R1441C, showed reduced integrity of dopaminergic neurons [56]. In contrast to these observations, no modifications of dopaminergic neurons were found in a *Drosophila* model in which the kinase domain of a Lrrk2 orthologue was removed [99]. Yet increased sensitivity to oxidative stress damage induced by hydrogen peroxide, but not with rotenone or paraquat, occurred in those transgenic flies [99]. Over-expression of wild Lrrk2 and mutated G2019S in *C. elegans* protects from toxicity mediated by rotenone, thus suggesting a role for Lrrk2 in mitochondrial physiology [103].

Observations in *C. elegans* and *Drosophila* must be considered with caution. Recent studies in cnidaria, deuterostomes (including human) and protostomes (including *Drosophila* and *C. elegans*) demonstrate a very ancient phylogenetic origin of human *LRRK2* (a bona fide orthologue of *LRRK2* is already found in cnidaria), which is lost in protostomes. Thus, *LRRK2* and *LRRK* genes in *Drosophila* and *C. elegans* are not real orthologues but rather paralogues [65, 66].

The presence of Lrrk2 in pathological brain

Lrrk2 immunoreactivity in α -synuclein inclusions

The presence or absence of Lrrk2 in Lewy bodies is controversial due to the distinct results obtained with different anti-Lrrk2 antibodies [5]. Antibodies AT106,

PA0362 and AP7099b, directed to functional domains of Lrrk2, fail to detect Lewy bodies [30, 44, 107]. However, antibodies NB-300-267 and NB-300-268, directed to the N-terminal and C-terminal regions of Lrrk2, respectively, do stain α -synuclein aggregates with variable intensity [1, 35, 44, 71, 74, 83, 107], and granular synuclein pathology in the brainstem of Parkinson's disease [1]. Currently, NB-300-268 stains the core and the halo of Lewy bodies, as well as aberrant neurites. In contrast, weak immunoreactivity, often decorating the halo, is usually obtained with the NB-300-267 antibody. The home-made antibodies JH5517, raised to the N-terminal part of *LRRK2* [44], ab04/11 [71] and EB06550 [1], raised to C-terminal domain of Lrrk2, also stain the halo of some Lewy bodies in PD. L955 Abgent antibody, which recognizes an epitope close to the one of NB-300-267, stains α -synuclein-immunoreactive oligodendroglial inclusions in multiple system atrophy (MSA) [46]. Based on these observations, the conclusions are divergent: (1) Lrrk2 is a component of Lewy bodies [35, 74, 83, 108], and (2) there is lack of evidence for Lrrk2 in α -synuclein pathological inclusions [11, 30].

A personal study has been carried out in order to compare results with those already available in control and diseased brains. A summary of cases examined is shown in Table 1.

We have tested the antibodies NB-300-268, NB-300-267 and AP7099b by using double-labelling immunofluorescence and confocal microscopy, and have corroborated that NB-300-268 antibody is able to stain Lewy bodies (Fig. 2), whereas Lewy bodies are barely stained with NB-300-267 and remain negative with AP7099b antibodies.

Table 1 Summary of cases examined in the present study

Diagnosis	Number of cases	Males/females	Mean age
Control	8	4/4	44-82
AD stage V/VIC	10	5/5	72
sPD	6	5/1	75
<i>LRRK2</i> G2019S	2	1/1	76
<i>LRRK2</i> R1441G	1	1/0	78
DLB	6	4/2	77
FTLD-tau P301L	3	3/0	56
FTLD-tau K317M	1	0/1	48
PiD	5	3/2	67
AGD	10	4/6	78

Control indicates cases with no clinical neurological deficits and normal neuropathological examination

AD Alzheimer's disease, sPD sporadic Parkinson's disease, *LRRK2* cases of PD with *LRRK2* mutations, DLB dementia with Lewy bodies, *FTLD-tau* frontotemporal lobar degeneration linked to mutations in the tau gene, PiD Pick's disease, AGD argyrophilic grain disease

We also tested the ab60937 antibody, which is raised against an epitope located in the C-terminal adjacent to the epitope recognized by NB-300-268. This antibody failed to stain α -synuclein inclusions.

Differences also occur between cortical-type and brainstem-type Lewy bodies [71] thus indicating that the composition of these inclusions is subject of regional differences.

Lrrk2-immunoreactive inclusions in other neurodegenerative diseases

The antibody NB-300-268 not only recognizes α -synuclein inclusions, but is also able to stain phospho-tau, huntingtin and ubiquitin inclusions in Alzheimer disease (AD), Parkinsonism dementia complex of Guam, multiple system atrophy, Pick's disease (PiD), Huntington disease, amyotrophic lateral sclerosis and frontotemporal lobar degeneration linked to mutations in tau gene (FTLD-tau) [74, 75]. We reproduced these results in AD, PiD and FTLD-tau using the same antibody (Fig. 3).

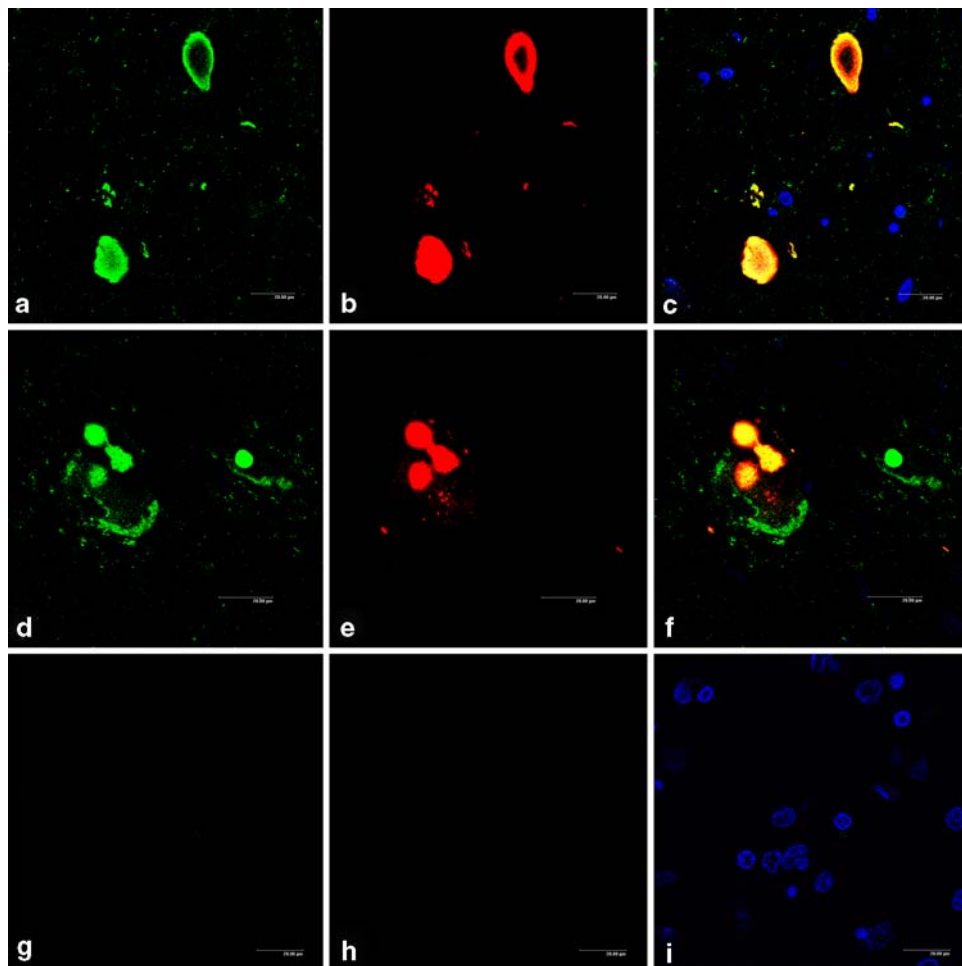
Interestingly, not all inclusions are stained equally with the NB-300-268 antibody. By using double-labelling immunofluorescence and confocal microscopy, a variable number of phospho-tau-immunoreactive inclusions were stained with NB-300-268 antibody (Fig. 4). To learn whether Lrrk2 immunostaining was dependent on tau conformation, antibodies to Alzh 50 and tau MC1 were analysed in combination with NB-300-268. Not all Alz 50- and tau MC1-immunoreactive inclusions were stained with NB-300-268 antibodies (Fig. 5). Our studies have shown that neurofibrillary tangles and phospho-tau-immunoreactive inclusions in AD and tauopathies were weakly stained with the antibody NB-300-267 and, rarely, with the ab60937 antibody.

In PiD, NB-300-267 Lrrk2 immunoreactivity was present in the cytoplasm of neurons usually independently of the presence of phospho-tau inclusions; Lrrk2 immunoreactivity was also present in Pick bodies (Fig. 6). Diffuse cytoplasmic staining was also observed in neurons in AGD. Yet AT8-immunoreactive grains were rarely stained with anti-*LRRK2* antibodies (Fig. 6).

In contrast, the AP7099b antibody fails to detect intracellular inclusions in AD, progressive supranuclear palsy (PSP), PiD or frontotemporal lobar degeneration/motor neuron disease (FTLD-MND) [30]. Likewise, the AP7099b antibody showed a punctuate immunoreactive pattern in the cytoplasm of neurons but did not stain hyper-phosphorylated-tau inclusions in AD and tauopathies, in our hands (Fig. 7).

As with α -synucleinopathies, there is no agreement about the presence of Lrrk2 in hyper-phosphorylated tau inclusions in AD and tauopathies. Lrrk2 is thought to be a

Fig. 2 Lrrk2 immunoreactivity in the substantia nigra in Parkinson's disease (a–c) and in Dementia with Lewy bodies (d–f) using the NB-300-268 antibody directed to the C-terminus. Lrrk2 immunoreactivity (green) co-localizes with α -synuclein (red) in Lewy bodies and neurites (merge, yellow). g–i Sections processed without the primary antibodies are negative. Nuclei were stained with TO-PRO-3-iodide



component of tau-immunoreactive inclusions by some authors [74, 75], but not by others [83].

Several reasons may explain many of these differences, covering differences in the type of sample (paraffin vs. frozen sections), method (immunohistochemistry or immunofluorescence), pre-treatment procedures for antigen retrieval, as well as dilution of the antibody among other conditions. Table 2 summarizes protocols, antibodies and results used by different authors regarding the most commonly used Lrrk2 antibodies that may help to have a comprehensive view of observations so far reported.

Lrrk2 antibodies in Western blots

A major point of discussion is the specificity of Lrrk2 antibodies. In principle, the primary sequences of immunogenic peptides directed to the C-terminal (TEGTQKQKEIQSCLTVVDINLPHEVQNLEKHIEVRKELAEKMRRTSVE for ab60937 and PHEVQNLEKHIEVRKELAEKMRRTSVE for NB-300-268) do not match with known sequences of other proteins. However, Western blot studies have shown that the NB-300-267 and NB-300-268 antibodies detect

several bands in human brain tissue and cell homogenates, and that the band corresponding to the predicted molecular weight of Lrrk2 (about 250 kDa) is very weak when compared with the other bands [1, 71, 74]. AP7099b antibodies disclose a clear band at about 250 kDa and a few bands of lower molecular weight in Western blots [30]. A number of studies show a band of about 250 kDa with several anti-Lrrk2 antibodies-in some instances only detected when 100 μ g of total protein of brain homogenates was used [108]. Yet Western blots are cut at the level of 150 or 100 kDa [1, 44, 108], thus making the observation of possible bands of lower molecular weight impossible. A varying number of bands of low molecular weight are practically observed with all the anti-Lrrk2 antibodies used [11].

The possible effect of post-mortem delay in the generation of Lrrk2 fragments has been assessed in freshly dissected mouse brain. The study showed that post-mortem intervals higher than 12 h were accompanied by a decrease in full-length Lrrk2 at 250 kDa together with the appearance of lower bands of about 120 and 150 kDa [30]. Our experience is that the bands detected with the NB-300-268 and NB-300-267 antibodies are already present after very short

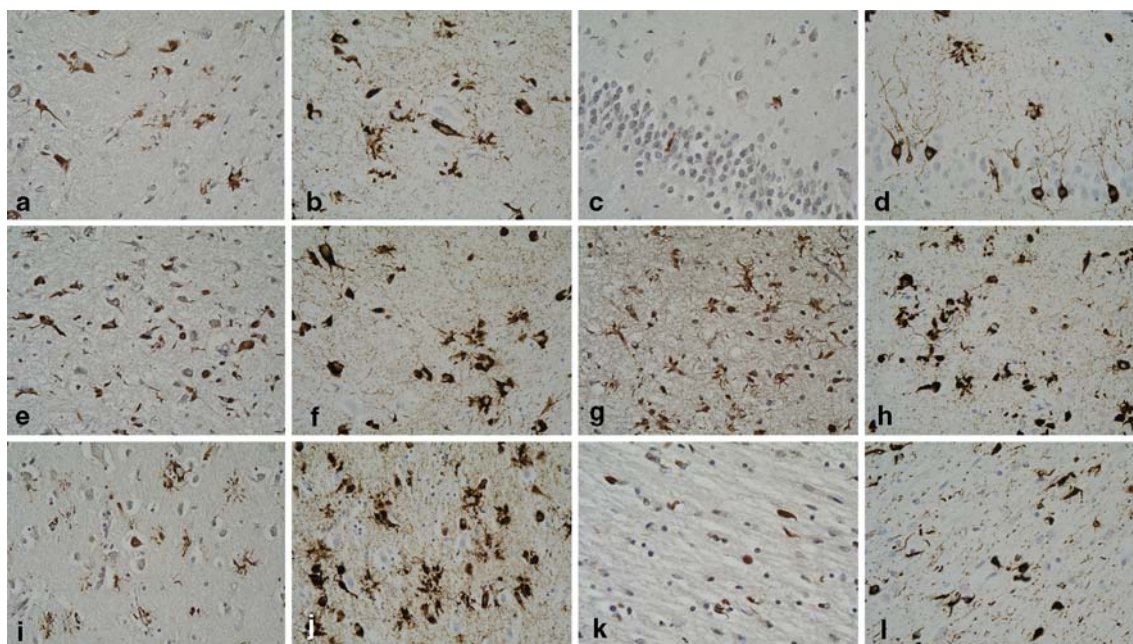


Fig. 3 Frontotemporal lobar degeneration due to K317M mutation in *MAPT* [106]. **a, c, e, g, i, k** Lrrk2 immunoreactivity using the NB-300-268 antibody. **b, d, f, h, j, l** hyper-phosphorylated tau inclusions

depicted with the antibody AT8. **a, b** CA1; **c, d** dentate gyrus; **e, f** entorhinal cortex; **g, h** temporal cortex (T3); **i, j** dorsomedial nucleus of the thalamus; **k, l** subcortical white matter, coiled bodies

post-mortem delays between death and tissue processing, and that progressive artificial post-mortem delay applied to human brain samples is accompanied by a reduction in the intensity of the bands due to protein degradation (data not shown). Strong immunoreactive bands of low molecular weight were also observed in cultured cells using NB-300-268 antibodies, giving further support to the lack of a relation between the bands of low molecular weight and delay of processing (Fig. 8). Therefore, these results point to other causes distinct from post-mortem delay-related truncation of Lrrk2 as the origin of the lower bands.

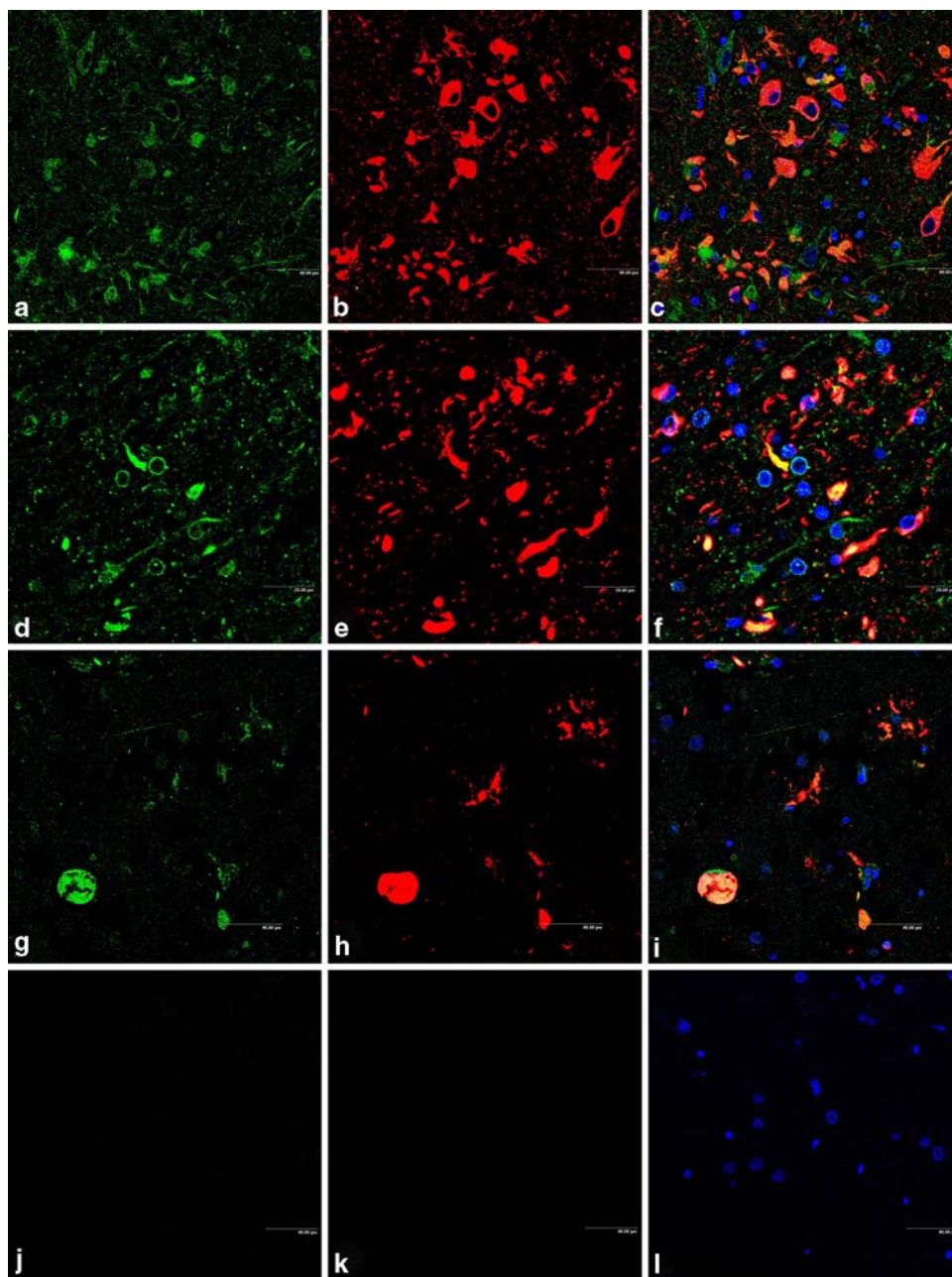
Interestingly, immunoprecipitation of Lrrk2 expressed in cells and analysed by SDS-PAGE coupled to mass spectrometry has revealed four bands in addition to the full-length one which corresponds to truncated species of Lrrk2 [14]. Whether these truncated forms exist in vivo and accumulate in Lewy bodies and hyper-phosphorylated tau inclusions in AD and tauopathies is not known.

Taking into consideration the truncation hypothesis, it can be suggested that C-terminal (and, to a lesser degree, N-terminal) truncated Lrrk2 species are detected within α -synuclein and hyper-phosphorylated tau inclusions when using NB-300-267 and NB-300-268 antibodies, while full-length Lrrk2 (apparently recognized by antibodies raised against the medial regions) is not. Alternatively, medial regions of Lrrk2 can be masked once trapped inside the inclusions, and therefore, antibodies raised against these medial regions fail to detect Lewy bodies.

Alternatively, anti-Lrrk2 antibodies do not stain Lrrk2 exclusively, but they do recognize a variegated number of other molecules as well. We have tested by Western blot the antibody NB-300-268 in sarkosyl-insoluble fractions in AD and other tauopathies to assess the possible cross-reaction of this antibody with hyper-phosphorylated tau. We found that the band of about 250 kDa was very weak in every case, a feature in striking contrast with the presence of several strong bands of lower molecular weight. No cross-reactivity with phospho-tau occurred as the molecular weight of Lrrk2-immunoreactive species did not match the molecular weight of phospho-tau in AD and other tauopathies (Fig. 9).

We also tested other anti-Lrrk2 antibodies in sarkosyl-insoluble fractions from frontal cortex in AD. The NB-300-267, NB-300-268 and ab60397 antibodies stained several bands of low molecular weight, and these bands differed depending on the antibody used in the same tissue samples processed in parallel (Fig. 10). Surprisingly, the AP7099b antibody, which was described as being highly specific for Lrrk2 [30], was not able, in our hands, to detect the band corresponding to Lrrk2 either in total homogenates or in sarkosyl-insoluble fractions from control and AD brains. However, AP7099b detected other strong bands at low molecular weight (Fig. 10). Finally, the ab60937 Abcam antibody recognized a band at about 250 kDa and an additional band at a lower molecular weight in total homogenates and sarkosyl-insoluble fractions (Fig. 10).

Fig. 4 Frontotemporal lobar degeneration due to K317M mutation in *MAPT*. Partial colocalization of Lrrk2 immunoreactivity (NB-300-268 antibody, *green*) and AT8 (*red*) is found in several but not all tau inclusions. **a–c** Frontal cortex; **d–f** white matter; **g–i** brain stem; **j–l** sections processed without the primary antibodies are negative. Nuclei were stained with TO-PRO-3-iodide

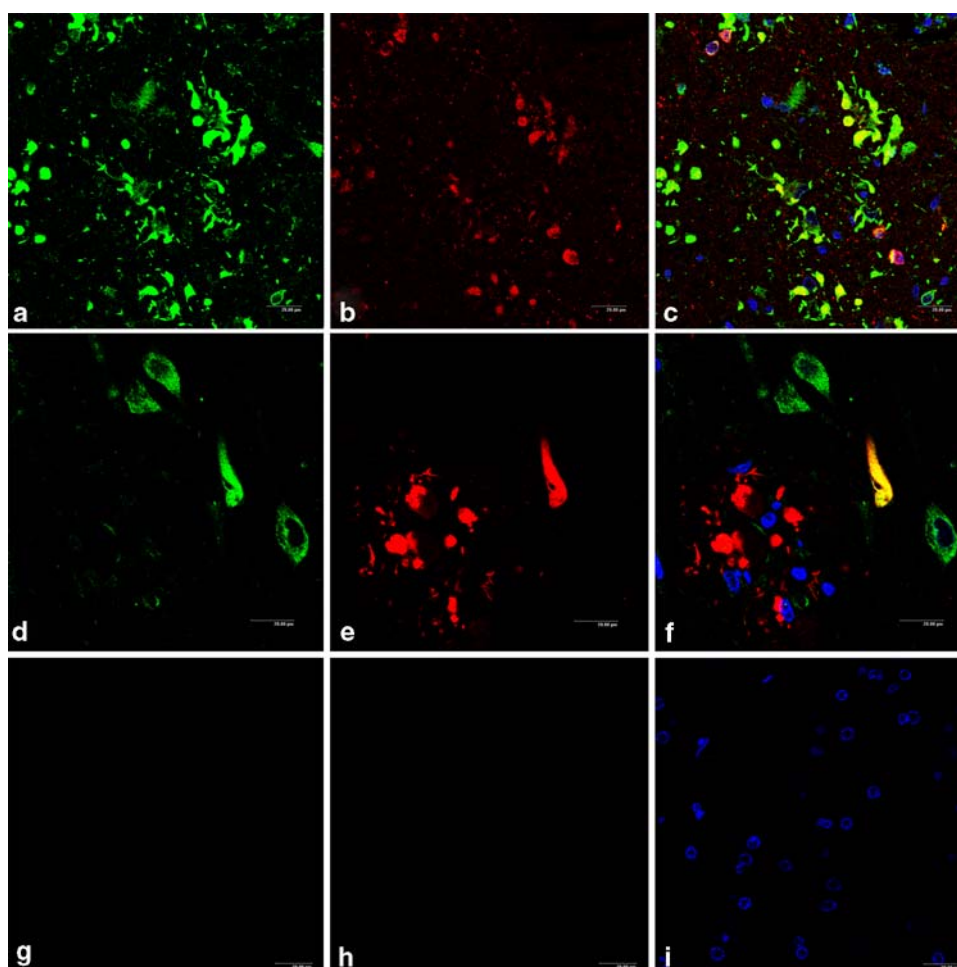


Finally, the band pattern differs from one case to another even using the same antibody (Fig. 10).

Taking together immunohistochemical and Western blot studies, it may be concluded that Lewy bodies in Parkinson's disease and related α -synucleinopathies, and hyperphosphorylated tau inclusions in AD and tauopathies, are recognized by anti-Lrrk2 antibodies depicting a weak or no band at the expected molecular weight of full-length Lrrk2 but strongly immunoreactive lower bands which do not cross-react with tau. In contrast, Lewy bodies and hyperphosphorylated tau inclusions in AD and tauopathies are not recognized by antibodies which show bands at the predicted molecular weight of Lrrk2. Therefore, full-length

Lrrk2 is apparently a minor component or not a component of Lewy bodies, or of hyper-phosphorylated tau inclusions in AD and tauopathies, although Lrrk2 is a component of cells. Moreover, antibodies show variegated band patterns depending on the antibody, but also the same antibody reveals different band patterns in cases with similar pathology (AD cases at the same Braak stage). Although not all neurons have tangles and neurons with phospho-tau deposits may have tangles or pre-tangles, the differences in the pattern of Lrrk2 bands with variable molecular weight in similar regions in AD cases at the same Braak stage cannot explain differences in tau composition and Lrrk2 burden, but rather on different Lrrk2 species.

Fig. 5 Frontotemporal lobar degeneration due to P301L mutation in *MAPT* [21] (a–c) and sporadic Alzheimer’s disease (d–f). Lrrk2 immunoreactivity (NB-300-268 antibody, green) co-localizes partially with Alz 50 (a–c) or tau MC1 (d–f) (red) in neurofibrillary tangles and dystrophic neurites. a–c Frontal cortex upper layers; d–f hippocampus; g–i sections processed without the primary antibodies are negative. Nuclei stained with TO-PRO-3-iodide



Alternative hypothesis of cross-reactivity

Although the sequences used in antigenic peptides do not match primarily with other known proteins, it cannot be ruled out that other proteins once folded may present sequences that can be bound to anti-Lrrk2 antibodies, as may be applied to all antibodies. Another possibility is that some anti-Lrrk2 antibodies recognize other possible translated Lrrk2-related transcripts.

No alternative splicing but one additional transcript with no biological significance was originally reported [100]. The possibility of transcripts of lower size than *LRRK2* was also suggested but not proved [109]. The Vertebrate Genome Annotation (VEGA) annotated transcripts in Ensembl OTTHUMT00000132847 and OTTHUMT00000132921, which are considered putative coding proteins, show maximum or high identity with RefSeq annotated proteins EAW57812.1, EAW57814.1 or EAW57815.1, respectively. EAW57812.1 (hCG1775001, isoform CRA_a) has an amino acid sequence identical to some regions of the N-terminal of *LRRK2*. EAW57814.1 (hCG39245, isoform CRA_a) and EAW57815.1 (hCG39245, isoform CRA_b)

almost entirely match the C-terminal half of the *LRRK2* protein sequence. The annotation of these three proteins is referred to the sequenced human genome [98]. Finally, VEGA transcript OTTHUMT00000132920 remits to AURA17 (Augmented in rheumatoid arthritis 17) protein, which matches a large portion of the N-terminal half of Lrrk2 amino acid sequence (Fig. 11). The existence of this protein remains at transcript level [77]. Whether these transcripts are translated and trapped in α -synuclein and hyper-phosphorylated tau inclusions in α -synucleinopathies, and AD and tauopathies, respectively, is not known. If present, antibodies directed to distinct Lrrk2 epitopes might also recognize *LRRK2*-related transcripts.

Concluding comments

LRRK2 is composed of 51 exons and encodes the protein Lrrk2 formed by a large N-terminal tail, followed by several domains named ANK, LRR, Roc, COR, kinase and WD40, and a short C-terminus. The gene contains several regions able to encode different transcripts, and the

Fig. 6 a–c Pick’s disease. Lrrk2 immunoreactivity (NB-300-267 antibody, *green*) occurs in the cytoplasm and Pick bodies as revealed with AT8-immunoreactivity (*red*) in the CA1 region. **d–f** AGD: the same antibody stains the cytoplasm of neurons, but rarely co-localizes in grains (*arrow*). **g–i** sections processed without the primary antibodies are negative. Nuclei were stained with TO-PRO-3-iodide

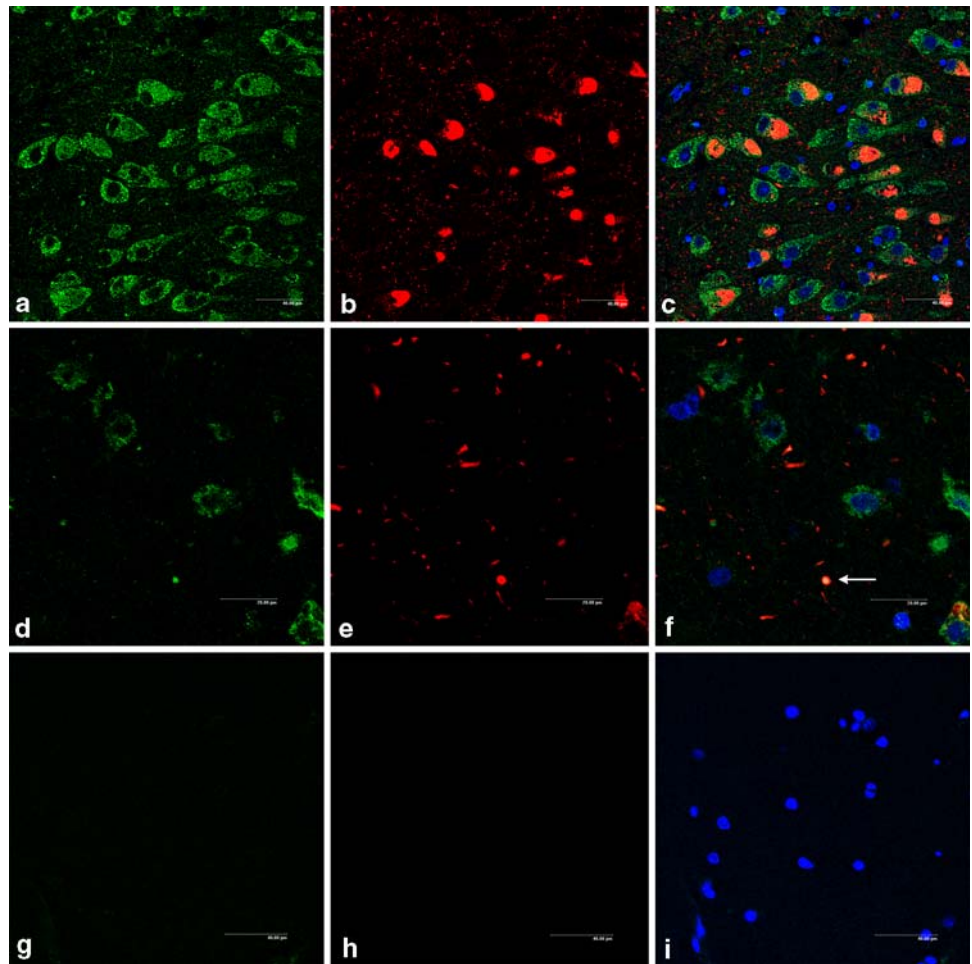


Fig. 7 Alzheimer’s disease. **a–c** Lrrk2 immunoreactivity as revealed with the AP7099b antibody does not co-localize with AT8-immunoreactive inclusions. **d–f** Sections processed without the primary antibodies are negative. Nuclei were stained with TO-PRO-3-iodide

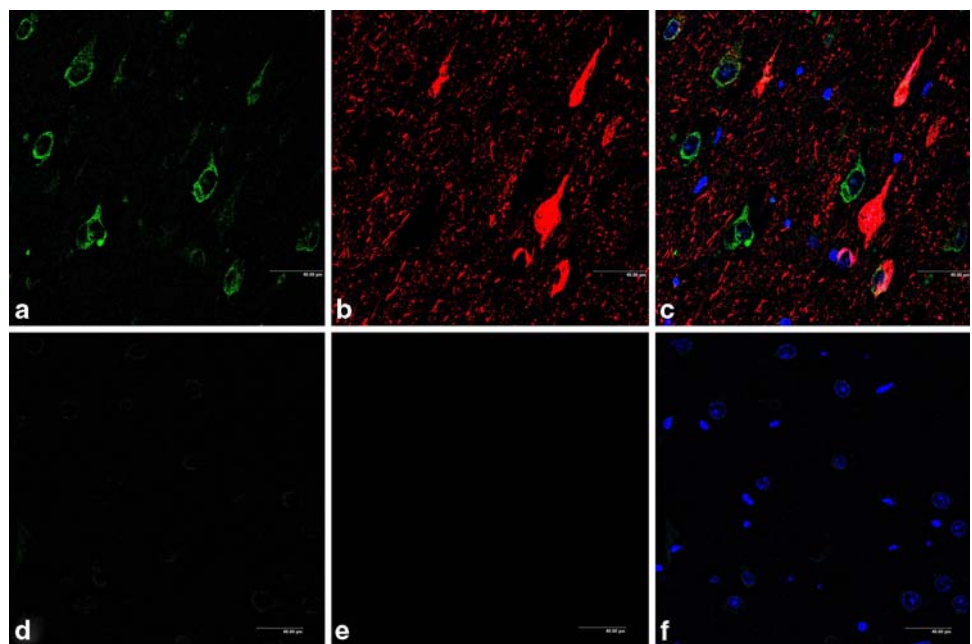


Table 2 Summary of antibodies (source and type), sections (paraffin: P, frozen: F, formalin: Form), epitope recognized, pretreatment, type of inclusions and corresponding references in different publications using Lrrk2 antibodies to the study of α -synuclein and phospho-tau-immunoreactive inclusions in α -synucleinopathies, Alzheimer's disease and tauopathies

Antibody Method	Source Dilution	Type	Epitope	α -syn inclusions	tau inclusions	References			
NB-300-268	Novus Biological	Rabbit polyclonal Frozen/paraffin section thickness (μ m)	2,500–2,527						
			Pretreatment						
			IHQ (DAB)	1:500	P 4	20' CB	PD, DLB	AD, PiD, FTLD-tau, AgD	This paper
			IF	1:500	P 4	20' CB*	PD, DLB	AD, PiD, FTLD-tau, AgD	This paper
			IHQ (DAB)	Not indicated	P 10	ME and CB 3'	GCI's MSA	–	[46]
			IHQ (DAB)	1:1,000	F 30	None/not indicated	PD, DLB, PDCG	AD, PiD, PDCG	[74]
			IF	1:300	F 30	None/not indicated	PD	AD, PiD	[74]
			IHQ (DAB)	1:1,000	F 30	None or 0.2% 5' Triton X-100	–	FTDP-tau (N279K)	[75]
			IF	1:1,000	F 30	None or 0.2% 5' Triton X-100**	–	FTDP-tau (N279K)	[75]
			IHQ (DAB)	1:300	Form 4–6	ME and CB 10' (some also with 0.1% Tryp.)	PD, DLB	–	[1]
IF	1:75	Form 4–6	ME and CB 10' (some also with 0.1% tryp.)	PD, DLB	–	[1]			
				IHQ (DAB)	1:500	P 5	10' CB	Some LB, DLB	–
IHQ (DAB)	1:100–1:200	P 6	None/not indicated	PD, DLB	–	[107]			
NB-300-267	Novus Biological	Rabbit polyclonal Frozen/paraffin section thickness (μ m)	920–945						
			Pretreatment						
			IHQ (DAB)	1:500	P 4	20' CB	Barely PD, DLB	Weak AD, PiD, FTLD-tau, AgD	This paper
			IF	1:500	P 4	20' CB*	Barely PD, DLB	Weak AD, PiD, FTLD-tau, AgD	This paper
			IHQ (DAB)	1:500	F 30	0.3% 60' Triton X-100	Faint halo some LBs PD	–	[44]
			IF	1:1,000	F 30	None/not indicated	Faint halo some LBs PD	–	[44]
			IHQ (DAB)	Not indicated	P 10	ME and CB 3'	GCI's MSA	–	[46]
			IHQ (DAB)	1:300	Form 4–6	ME and CB 10' (some also with 0.1% tryp.)	Halo some LBs PD, DLB	–	[1]
			IHQ (DAB)	1:200	Wax 7	CB 10'	Halo some LBs PD	–	[35]
			IHQ (DAB)	1:900	P 5	10' CB	Some LBs DLB	–	[71]
IHQ (DAB)	1:100–1:200	P 6	None/not indicated	PD and DLB	–	[107]			
AP7099b	Abgent	Rabbit polyclonal Frozen/paraffin section thickness (μ m)	1,246–1,265						
			Pretreatment						
			IHQ (DAB)	1:100	P 4	20' CB	No, in PD, DLB	No, AD, PiD, FTLD-tau, AgD	This paper
			IF	1:100	P 4	20' CB*	No, PD, DLB	No, AD, PiD, FTLD-tau, AgD	This paper
IHQ (DAB)	Not indicated	P 6	None, FA or ME, but not specified	No, PD, DLB, MSA	No, AD, PiD, PSP	[30]			
				IF	Not indicated	P 6	None, FA or ME, but not specified	No, AD, PiD, PSP	[30]

Table 2 continued

Antibody Method	Source Abgent Dilution	Type Rabbit polyclonal Frozen/paraffin section thickness (µm)	Epitope 1,246-1,265 Pretreatment		
IHQ (DAB)	Not indicated	P 6	None or FA, but not specified	No, PD + AD	[11]
IHQ (DAB)	1:100–1:200	P 6	None/not indicated	No, PD, DLB	[107]
Antibody Method	Source Abcam Dilution	Type Rabbit polyclonal Frozen/paraffin section thickness (µm)	Epitope 2,480-2,527 Pretreatment		
IHQ (DAB)	1:200	F 40	No	No, PD, DLB	This paper
IF	1:100	F 40	No*	No, PD, DLB	This paper
Antibody Method	Source Home-made Dilution	Type Rabbit polyclonal Frozen/paraffin section thickness (µm)	Epitope 334–347 Pretreatment		
IHQ (DAB)	1:200	F 30	0.3% 60' Triton X-100	Faint halo some LBs PD	[44]
IF	1:500	F 30	None/not indicated	Faint halo some LBs PD	[44]
Antibody Method	Source Abgent Dilution	Type Rabbit polyclonal Frozen/paraffin section thickness (µm)	Epitope 946–962 Pretreatment		
IHQ (DAB)	Not indicated	P 10	ME and CB 3'	GCI's MSA	[46]
IF	Not indicated	P 10	FA 3'	GCI's MSA	[46]
Antibody Method	Source Abgent Dilution	Type Rabbit polyclonal Frozen/paraffin section thickness (µm)	Epitope 2,008-2,027 region Pretreatment		
IHQ (DAB)	1:200	F 30	0.2% 5' Triton X-100	FTDP-tau (N279K)	[75]
Antibody Method	Source Everest Biotech Dilution	Type Goat polyclonal Frozen/paraffin section thickness (µm)	Epitope 2,015-2,026 Pretreatment		
IHQ (DAB)	1:1,000	Formalin 4–6	ME and CB 10' (some also with 0.1% tryp.)	Halo some LBs PD, DLB	[1]

Table 2 continued

Antibody ab04/11 Method	Source Non commercial Dilution	Type Rabbit polyclonal Frozen/paraffin section thickness (μm)	Epitope 2,507–2,527 Pretreatment		
IHQ (DAB)	1:3,000	P 5	10' CB	Few LBs DLB	[71]
Antibody PA0362 Method	Source Home-made Dilution	Type Rabbit polyclonal Frozen/paraffin section thickness (μm)	Epitope 2,507–2,527 Pretreatment		
IHQ (DAB)	1:250	P 5	10' CB	No, DLB	[71]
Antibody AB9704 Method	Source Chemicon Dilution	Type Rabbit polyclonal Frozen/paraffin section thickness (μm)	Epitope Property of Chemicon Pretreatment		
IHQ (DAB)	1:3,000	P 5	10' CB	Weak in few LBs DLB	[71]
Antibody AT106 Method	Source Alexis Biochemicals Dilution	Type Rabbit polyclonal Frozen/paraffin section/thickness (μm)	Epitope 1,838–2,133 Pretreatment		
IHQ (DAB)	1:100–1:200	P 6	None/not indicated	No PD, DLB	[107]

IHQ immunohistochemistry, IF immunofluorescence, CB citrate buffer, ME microwave exposure, FA formic acid, *+3 min or **15 min FA in double-labelling IF with α -synuclein, Tryp trypsin, DAB diamino benzidine, – not tested. PD Parkinson's disease, DLB dementia with Lewy bodies, AD Alzheimer's disease, PID Pick's disease, FTLD-tau frontotemporal lobar degeneration linked to mutations in the tau gene, AgD argyrophilic grain disease, GCI glial cytoplasmic inclusions, MSA multiple system atrophy. The variable terminology employed to designate Lrrk2 staining has been preserved from the original sources

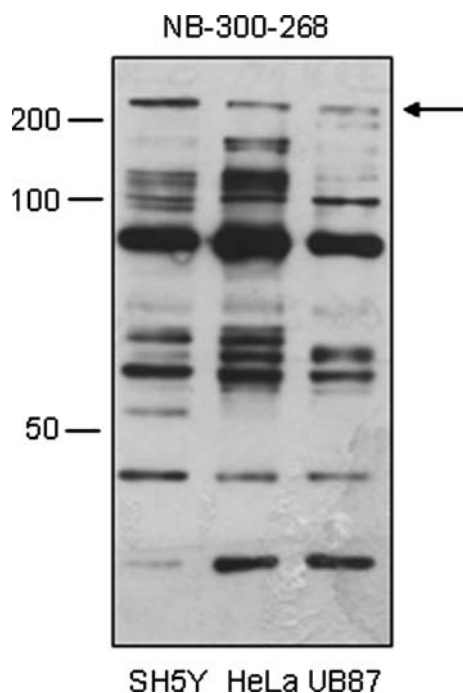


Fig. 8 Western blot analysis of three different cell lines (SH5Y, HeLa and UB87) using NB-300-268 antibodies shows weak staining of a band consistent with the predicted full-length Lrrk2 (arrows). In addition, several bands of lower molecular weight are detected with this antibody

domains ANK, LRR and WD40 are separately found in several proteins. Because of its ability to bind different proteins, Lrrk2 is thought to participate in multiple signalling pathways. The most dramatic evidence of Lrrk2 involvement in degeneration of the nervous system comes from the observation that mutations in *LRRK2* cause

degeneration of the human substantia nigra pars compacta clinically manifested as sporadic or familial parkinsonism with variable penetration. However, the functional consequences of the mutations are still poorly understood. Some mutations are accompanied by reduced kinase activity, whereas others are accompanied by increased kinase activity. Whether this might be due, in part, to methodological difficulties in the measurement of kinase activity is under discussion. The use of *Drosophila* and *C. elegans* as *LRRK2* mutant animal models is of limited value, as *LRRK2* in humans and rodents, and LRRK in flies and worms, are not real orthologues but rather paralogues. Moreover, studies in mice and rats expressing human *LRRK2* mutations have resulted in divergent results. Human mutations in *LRRK2* are manifested as different pathologies independently of the type of mutation; some cases are accompanied by Lewy bodies and neurites, others by hyperphosphorylated tau or ubiquitin-immunoreactive inclusions, while some of them do not have apparent inclusions in the remaining neurons of the substantia nigra. It is clear that *LRRK2* mutations may have an impact on common pathways resulting in degeneration of dopaminergic neurons, as well as on specific pathways involving α -synuclein modifications, tau hyperphosphorylation, and other proteins. Finally, whether Lrrk2 is a component of Lewy bodies and neurites in Lewy body diseases, and of hyper-phosphorylated tau inclusions in Alzheimer's disease and tauopathies, is not a subject of agreement because of the different results obtained using different anti-Lrrk2 antibodies. Other aspects are also important, as in addition to the predicted proper band at the corresponding molecular weight of Lrrk2, which is commonly weak, several strong bands of lower molecular

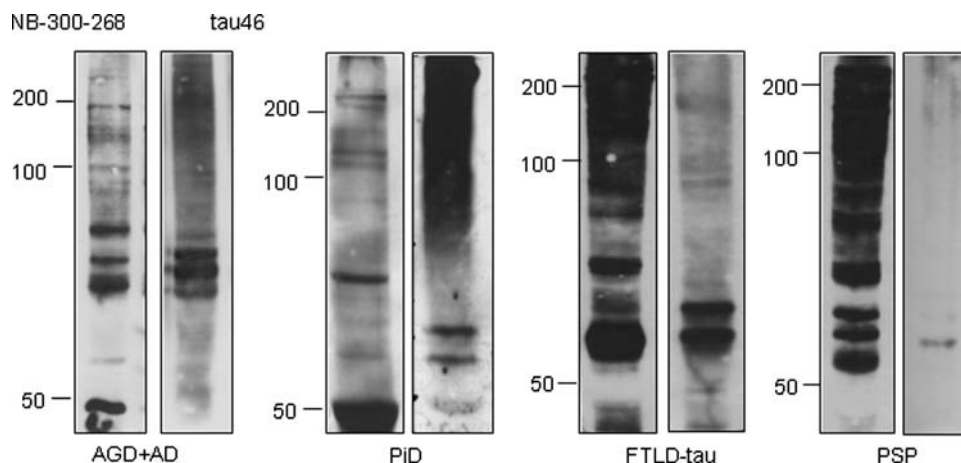


Fig. 9 Western blot of sarkosyl-insoluble fraction from brain samples of patients with different tauopathies immunostained with NB-300-268 antibody. *AGD + AD* Argyrophilic grain disease + Alzheimer's disease stage 3 of Braak, *PiD* Pick's disease, *FTLD-tau*: frontotemporal lobar degeneration linked to mutations in the tau gene, *PSP* progressive supranuclear palsy. The band consistent with full-

length Lrrk2 is hardly detected, whereas several lower bands are strongly immunoreactive. The pattern of these low bands differs among tauopathies. Re-incubation of the same membranes with an antibody against tau (tau46) reveals no match between Lrrk2 immunoreactivity and tau immunoreactivity, thus suggesting lack of cross-reactivity

Fig. 10 Western blots of sarkosyl-insoluble fractions in two AD cases (two columns per antibody) immunostained with NB-300-267, AP7099b, NB-300-268 and ab60937 antibodies. The four antibodies show different affinity to the predicted full-length Lrrk2, whereas all of them detect several bands at lower molecular weights. Antibodies display notably different band patterns. Moreover, the band pattern also differs, to a lesser degree, when comparing the two AD cases with the same antibody

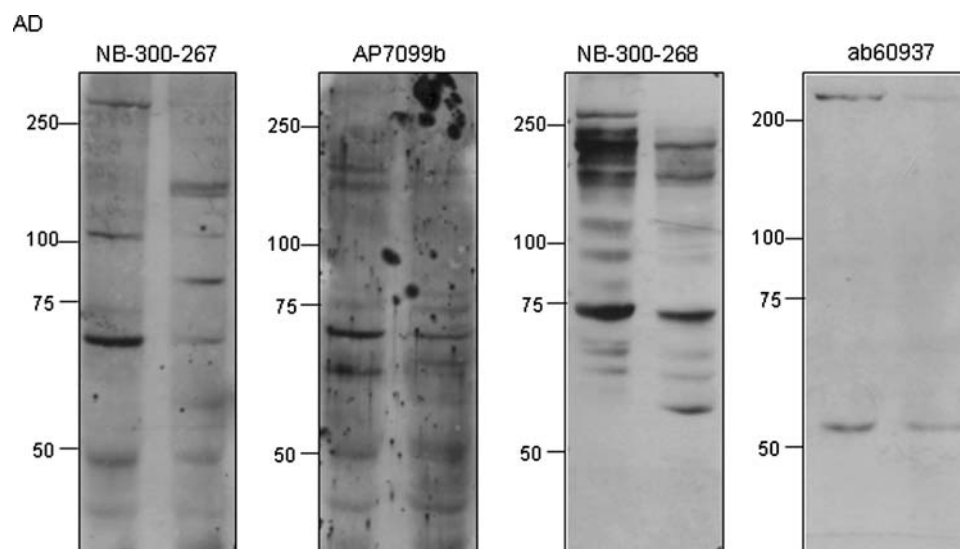
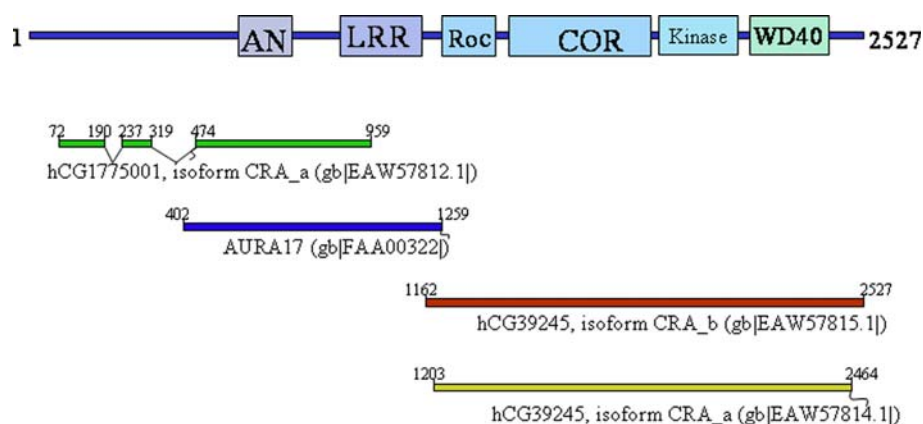


Fig. 11 Schematic alignment of GenBank-annotated proteins related to additional putative *LRRK2*-like transcripts



weight are seen after gel electrophoresis and Western blotting with the different available antibodies. Furthermore, some but not all inclusions are stained differentially with antibodies directed to the C-terminus and N-terminus, but they are not stained at all with antibodies directed to the middle regions of *Lrrk2*. Available data do not permit us, at present, to state that full-length *Lrrk2* is a major component of Lewy bodies in Lewy body diseases and hyper-phosphorylated tau inclusions in AD and tauopathies.

Acknowledgments Work carried out in the laboratory was funded by grant FIS PI080582 from the Spanish Ministry of Health, Instituto de Salud Carlos III, and supported by the European Commission under the Sixth Framework Programme (BrainNet Europe II, LSHM-CT-2004-503039) and INDABIP. We thank Professor Juan José Zarranz for stimulating comments, Sabine Hilfiker, Jordi Pérez-Tur and Carles Gaig for criticism and suggestions, Charles E. Chapple for help in bio-informatics, and Tom Yohannan for editorial assistance. Brain samples were obtained from the Institute of Neuropathology following the guidelines and approval of the local ethics committee. MC1 and Alz50 antibodies are a generous gift of Dr. Peter Davies, Albert Einstein College of Medicine, Bronx, NY.

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7

Oxidative damage of 14-3-3 zeta and gamma isoforms in Alzheimer's disease and cerebral amyloid angiopathy

OXIDATIVE DAMAGE OF 14-3-3 ZETA AND GAMMA ISOFORMS IN ALZHEIMER'S DISEASE AND CEREBRAL AMYLOID ANGIOPATHY

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Abstract—Previous studies have shown oxidative damage resulting from amyloid A β exposure to cultured cells and in murine models. A target of oxidation is 14-3-3 which comprises a group of proteins involved in kinase activation and chaperone activity. The present study shows glycoxidative damage, as revealed with mono and bi-dimensional gel electrophoresis and Western blotting, followed by in-gel digestion and mass spectrometry, in the frontal cortex in Alzheimer's disease (AD) and cerebral amyloid angiopathy (CAA), a neurodegenerative disease with deposition of A β in cerebral blood vessels and in diffuse plaques unaccompanied by intraneuronal hyper-phosphorylated tau deposition. malondialdehyde-lysine (MDA-Lys)-, but not 4-hydroxy-2-nonenal (HNE)-immunoreactive adducts, and N-carboxyethyl-lysine (CEL), but not N-carboxymethyl-lysine (CML)-products, were present in 14-3-3 involving zeta and gamma isoforms in both AD and CAA. These findings demonstrate that 14-3-3 glyco- and lipoxidation occurs in AD and CAA, probably as a direct consequence of A β deposition. © 2007 IBRO. Published by Elsevier Ltd. All rights reserved.

Key words: Alzheimer's disease, cerebral amyloid angiopathy, 14-3-3, A β , oxidative stress, lipoxidation.

Neurofibrillary tangles (NFTs) and amyloid plaques are the main neuropathological markers of Alzheimer's disease (AD). NFTs are mainly composed of aggregated and hyper-phosphorylated tau protein, which forms paired helical filaments (PHFs). Tau is a microtubule-associated protein which promotes and stabilizes the microtubule network through a balance between phosphorylation and dephosphorylation states. Abnormal phosphorylation of tau reduces its affinity to microtubules, and microtubule instability is a putative cause of nerve cell degeneration in AD (Spillantini and Goedert, 1998; Buee et al., 2000; Lee et al., 2001; Avila et al., 2002; Sergeant et al., 2005). Amyloid plaques are mainly composed of A β which is a product of the trans-membrane protein APP (amyloid precursor protein). Amyloid deposits are locally surrounded by abnormal cell processes, mainly aberrant neurites contain-

ing PHFs, and reactive microglia and astrocytes in neuritic plaques (Duyckaerts and Dickson, 2003; Masters and Beyreuther, 2003).

Recent evidence suggests that oxidative damage is an important early event, and a key factor, in the pathogenesis of AD (Butterfield et al., 2001; Cecchi et al., 2002; Chauhan and Chauhan, 2006; Pamplona et al., 2005; Nunomura et al., 2006; Butterfield et al., 2006). A $\beta_{(1-42)}$ has been shown to induce protein oxidation *in vitro* and *in vivo* (Boyd-Kimball et al., 2005; Butterfield and Lauderback, 2002; Varadarajan et al., 2000; Drake et al., 2003; Butterfield et al., 2006), whereas antioxidants such as vitamin E play a protective role against A β -mediated cytotoxicity in AD (Muñoz et al., 2005). Moreover, stress-activated protein kinases c-Jun N-terminal kinase (SAPK/JNK) and p38 pathways are activated in dystrophic neurites surrounding A β deposits and in neurons with abnormal tau accumulation in AD and related murine models (Zhu et al., 2000, 2001; Ferrer et al., 2001, 2005; Atzori et al., 2001; Pei et al., 2001; Puig et al., 2004).

Protein oxidation occurs physiologically as a consequence of aerobic life. Oxidized proteins appear to be degraded by an ubiquitin- and ATP-independent pathway ruled by the 20S proteasome (Davies, 2001). Yet excessive oxidative stress in the brain may render the proteolytic capacity of this system insufficient, and thereby facilitate the accumulation of abnormal proteins. In addition, oxidative damage of proteins is commonly associated with their loss of function (Davies, 1987; Oliver et al., 1987; Nishikawa et al., 2003; Sultana et al., 2006). Together, these circumstances promote the accumulation of abnormal and often disabled proteins, through covalent cross-linking reactions and increased surface hydrophobicity (Garrison et al., 1962; Davies, 2001).

The present study was undertaken in an attempt to identify oxidized proteins in sarkosyl-insoluble fractions in AD. N-carboxymethyl-lysine (CML) and N-carboxyethyl-lysine (CEL) were used as markers of glycoxidation and carbonyl production. Antibodies to 4-hydroxy-2-nonenal (HNE) and malondialdehyde-lysine (MDA-Lys) were used as markers of lipoxidation. Bi-dimensional (2D) electrophoresis and Western blotting linked to mass spectrometry revealed 14-3-3 (zeta and gamma isoforms) as a major target of glycoxidative and lipoxidative damage in sarkosyl-insoluble fractions in AD brains. In order to learn whether this was specifically related to AD, the study was extended to cases with amyloid angiopathy and A β plaques (cerebral amyloid angiopathy, CAA) without NFTs.

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Abbreviations: AD, Alzheimer's disease; BSA, bovine serum albumin; CAA, cerebral amyloid angiopathy; CEL, N-carboxyethyl-lysine; CML, N-carboxymethyl-lysine; HNE, 4-hydroxy-2-nonenal; MDA-Lys, malondialdehyde-lysine; NFT, neurofibrillary tangle; PHF, paired helical filament; TBS-T, 100 mM Tris-buffered saline, 140 mM NaCl and 0.1% Tween 20, pH 7.4; 2D, bi-dimensional.

EXPERIMENTAL PROCEDURES

Brain tissues

Brain tissues were obtained from the Institute of Neuropathology Brain Bank following the guidelines and approval of the local ethics committee. Four patients had suffered from severe (Global Deterioration Scale) dementia of Alzheimer type. Eleven cases were neurologically normal. The postmortem delay was between 3 and 20 h. Cases with and without clinical neurological disease were processed in the same way following the same sampling and staining protocols. At autopsy, half of each brain was fixed in 10% buffered formalin, while the other half was cut in coronal sections 1 cm thick, frozen on dry ice and stored at -80°C until use. In addition, samples of the frontal cortex were fixed in 4% paraformaldehyde in phosphate buffer for 24 h, cryoprotected in 30% saccharose and frozen at -80°C . The neuropathological study was carried out on de-waxed 4- μm -thick paraffin sections of the frontal (area 8), primary motor, primary sensory, parietal, temporal superior, temporal inferior, anterior cingulate, anterior insular, and primary and associative visual cortices; entorhinal cortex and hippocampus; caudate, putamen and pallidum; medial and posterior thalamus; subthalamus; Meynert nucleus; amygdala; mid-brain (two levels), pons and medulla oblongata; and cerebellar cortex and dentate nucleus. The sections were stained with hematoxylin and eosin, Klüver Barrera, and, for immunohistochemistry to glial fibrillary acidic protein, CD68 and *Lycopersicon esculentum* lectin for microglia, A β -amyloid, pan-*tau*, AT8 tau, phosphorylation-specific tau Thr181, Ser202, Ser214, Ser262, Ser396 and Ser422, and αB -crystallin, α -synuclein and ubiquitin. Following neuropathological examination, four cases were categorized as AD stages V/VIC of Braak and Braak (1999). Eight cases with no neurological involvement suffered from AD stages I/IIIA/B and were not included in the present study. The remaining three cases did not have neuropathological abnormalities and were considered as controls. In addition, two cases with CAA were included. All these had, in addition to amyloid angiopathy, A β diffuse plaques in the cerebral cortex consistent with stage B of Braak and Braak (1999). Hyper-phosphorylation of tau was restricted to aberrant neurites around rare neuritic plaques. A summary of the main clinical and neuropathological findings in the present series is shown in Table 1.

Brain tissue was further processed for biochemical studies and for 14-3-3 immunohistochemistry and Western blotting.

Sarkosyl-insoluble fraction extraction

Frozen samples of about 2 g of the frontal cortex (area 8) were gently homogenized in a glass tissue grinder in 10 vol (w/v) with cold suspension buffer (10 mM Tris-HCl, pH 7.4, 0.8 M NaCl, 1 mM EGTA, 10% sucrose). The homogenates were first centrifuged at 20,000 $\times g$ and the supernatant (S1) was retained. The pellet was re-homogenized in 5 vol of homogenization buffer and re-centrifuged. The two supernatants (S1+S2) were then mixed

and incubated with 0.1% N-lauroylsarcosinate (sarkosyl) for 1 h at room temperature while being shaken. Samples were then centrifuged at 100,000 $\times g$ in a Ti70 Beckman rotor. Sarkosyl-insoluble pellets (P3) were re-suspended (0.2 ml/g, starting material) in 50 mM Tris-HCl (pH 7.4). Protein concentrations were determined with the BCA method using bovine serum albumin (BSA) as a standard.

Mono-dimensional gel electrophoresis and Western blotting

For mono-dimensional gel electrophoresis, 30 μg of frontal cortex was mixed with reducing sample buffer and processed for 10% SDS-PAGE electrophoresis and then transferred to nitrocellulose membranes (400 mA for 90 min). Immediately afterward, the membranes were incubated with 5% skimmed milk in TBS-T buffer (100 mM Tris-buffered saline, 140 mM NaCl and 0.1% Tween 20, pH 7.4) for 30 min at room temperature, and then incubated with the primary antibody in TBS-T containing 3% BSA (Sigma, Madrid, Spain) at 4 $^{\circ}\text{C}$ overnight. The mouse monoclonal anti-CEL and anti-CML antibodies (TransGenic, Kumamoto, Japan) were used at a dilution of 1:1000. The goat polyclonal anti-MDA-Lys (BioMedical, Houston, TX, USA), rabbit polyclonal anti-MDA-Lys (Biomedical), rabbit polyclonal anti-HNE (Calbiochem, Barcelona, Spain) and rabbit polyclonal rabbit polyclonal anti-14-3-3 (Abcam, Cambridge, UK) were used diluted 1:1000. Subsequently, the membranes were incubated for 45 min at room temperature with the corresponding secondary antibody labeled with horseradish peroxidase (Dako, Barcelona, Spain) at a dilution of 1:1000, and washed with TBS-T for 30 min. Protein bands were visualized with the chemiluminescence ECL method (Amersham, Barcelona, Spain).

2D Gel electrophoresis

Samples of the frontal cortex (area 8) in AD, CAA and controls were homogenized in lysis buffer (40 mM Tris, pH 7.5, containing 7 M urea (9 M when using sarkosyl-insoluble fractions), 2 M thiourea and a cocktail of protease and phosphatase inhibitors, and centrifuged at 9700 r.p.m. for 10 min. The pellet was discarded and the concentration of protein of the resulting supernatant was determined with the BCA method. Equal amounts of protein were mixed with 0.2% Byolites (v/v), 4% CHAPS (Bio-Rad, Barcelona, Spain), 2 mM tributylphosphine solution (TBP), 50 μl 8 M urea and Bromophenol Blue in a final volume of 150 μl . In the first dimension electrophoresis, 150 μl of sample solution was applied to an immobilized 7 cm pH 3–10 nonlinear gradient ReadyStrip IPG strip (Bio-Rad) at both the basic and acidic ends of the strip. The strips were actively re-hydrated for 12 h at 50 V and the proteins were focused at 300 V for 1 h, after which time the voltage was gradually increased to 3500 V within 6 h. Focusing was continued at 3500 V for 12 h and at 5000 V for 24 h. For the second dimension separation, IPG strips were equilibrated for 10 min in 50 mM Tris-HCl (pH 6.8) containing 6 M urea, 1% (wt/v)

Table 1. Summary of the main clinical and pathological findings in the present series

	Age	Gender	Postmortem delay	Clinical diagnosis	Neuropathological diagnosis	Braak stage
1	73	F	5.5	Normal	No lesions	0
2	58	F	4	Normal	No lesions	0
3	73	F	7	Normal	No lesions	0
4	89	F	4	AD	AD	VC
5	78	F	3.5	AD	AD	VC
6	79	M	7	AD	AD	VC
7	61	F	4	AD	AD	VC
8	69	H	29		CAA	C
9	69	H	24		CAA	C

SDS, 30% (v/v) glycerol and 2% dithiothreitol, and then re-equilibrated for 10 min in the same buffer containing 2.5% iodoacetamide. The strips were placed on 10% polyacrylamide gels and electrophoresed at 100 V overnight. For gel staining, Coomassie Biosave staining (Bio-Rad) was used, as described by the manufacturer.

Two 2D electrophoreses were run in parallel in every case, one for Coomassie staining and the other transferred into a nitrocellulose membrane (200 mA for 1 h 30 min). After incubation with 5% skimmed milk in TBS-T buffer for 30 min at room temperature, nitrocellulose membranes were blotted with monoclonal anti-CEL and anti-CML (TransGenic), rabbit polyclonal anti-HNE (Calbiochem), and rabbit anti-MDA-Lys (Biomedical) or rabbit polyclonal anti-14-3-3 (Abcam) antibodies used at a dilution of 1:1000. Subsequently, the membranes were processed as previously indicated for mono-dimensional gels.

In-gel digestion

Proteins were in-gel digested with trypsin (sequencing grade modified, Promega, Barcelona, Spain) in the automatic Investigator ProGest robot of Genomic Solutions. Briefly, excised gels spots were washed sequentially with ammonium bicarbonate buffer and acetonitrile. Proteins were reduced and alkylated with 10 mM DTT solution for 30 min and 100 mM solution of iodine acetamide for 15 min, respectively. After sequential washing with buffer and acetonitrile, proteins were digested overnight at 37 °C with trypsin 0.27 nM. Tryptic peptides were extracted from the gel matrix with 10% formic acid and acetonitrile. The extracts were pooled and dried in a vacuum centrifuge.

Acquisition of MS and MS/MS spectra

Proteins manually excised from the 2D gels were digested and analyzed by CapLCnano-ESI-MS-MS mass spectrometry. The

tryptic-digested peptide samples were analyzed using on-line liquid chromatography (CapLC, Micromass-Waters, Manchester, UK) coupled with tandem mass spectrometry (Q-TOF Global, Micromass-Waters). Samples were re-suspended in 12 μ l 10% formic acid solution, and 4 μ l was injected for chromatographic separation into a reverse-phase capillary C18 column (75 μ m internal diameter and 15 cm in length (PepMap column, LC Packings, Amsterdam, Netherlands). The eluted peptides were ionized via coated nano-ES needles (PicoTip™, Woburn, MA, USA; New Objective). A capillary voltage of 1800–2200 V was applied together with a cone voltage of 80 V. The collision in the CID (collision-induced dissociation) was 25–35 eV, and argon was employed as the collision gas. Data were generated in PKL file format and submitted for database searching in MASCOT server (Matrix Science, Boston, MA, USA) using the NCBI database with the following parameters: trypsin enzyme, one missed cleavage, carbamidomethyl (C) as fixed modification and oxidized (M) as variable modification, and mass tolerance of 150–250 ppm.

Probability-based MOWSE score was used to determine the level of confidence in the identification of specific isoforms from the mass spectra. This probability equals 10 ($-\text{Mowse score}/10$). Mowse scores higher than 50 were considered to be of high confidence of identification.

14-3-3 Immunohistochemistry and Western blotting

Cryostat sections 7 μ m thick were processed free-floating with the LSAB method. The rabbit polyclonal antibody to 14-3-3 (ab6081, Abcam) was used at a dilution of 1:200. This antibody is directed to a synthetic peptide with the sequence DKSELVQKAEQAERYD, mapping to the amino terminal domain of human 14-3-3, and reacts with alpha, beta, zeta and theta isoforms. The rabbit polyclonal to 14-3-3 (phospho S) (ab14127, Abcam) was used at a dilution of 1:200. This antibody binds peptides and proteins containing a motif composed of phospho-Ser with proline at the +2

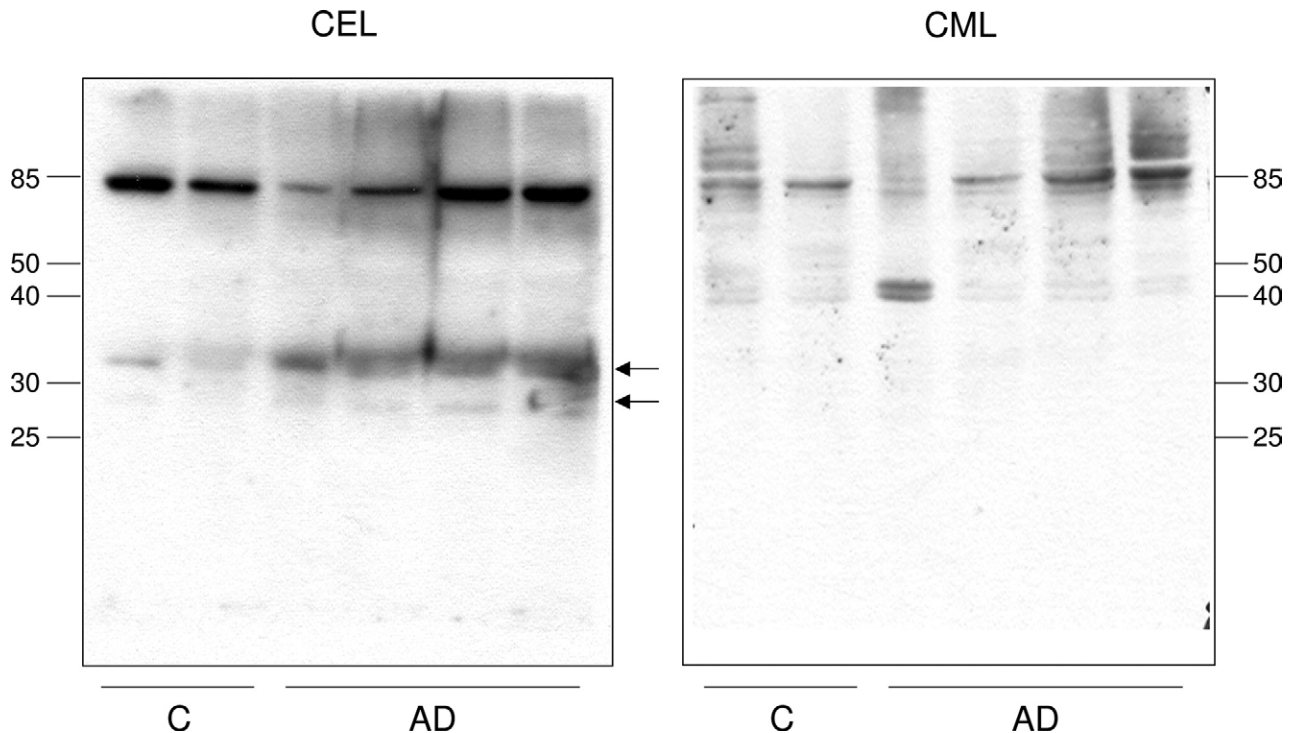


Fig. 1. Gel electrophoresis and Western blotting to CEL and CML in sarkosyl-insoluble fractions of the frontal cortex in two controls (C) and four cases of AD. Two strong bands of about 30 kDa are detected by CEL antibody in AD cases compared with age-matched controls. Note the presence of a band of about 85 kDa in control and AD cases. CML antibody detects several bands in C and AD. A doublet of about 40–50 kDa is present in one AD case.

position and arginine or lysine at the -3 position. Antibody binding is phospho-specific and largely independent of other surrounding amino acids. According to the supplier, the antibody recognizes a wide range of peptides containing the 14-3-3 binding motif and a large number of presumptive 14-3-3 binding proteins. Finally, the rabbit polyclonal anti-14-3-3 (18649, IBL, Gunma, Japan) was used at a dilution of 1:200. This antibody is raised against a synthetic peptide for a part of human 14-3-3 gamma, and may react to several human 14-3-3 isoforms. The sections were incubated with LSAB for 1 h at room temperature. The peroxidase reaction was visualized with NH_4NiSO_4 (0.05 M) in phosphate buffer (0.1 M), 0.05% diaminobenzidine, NH_4Cl and 0.01% hydrogen peroxide (dark blue precipitate). Some sections were incubated without the primary antibody. No immunoreactivity was found in these samples.

To test the specificity of these antibodies, membranes of sarkosyl-insoluble fractions in control and AD cases were blotted with anti-14-3-3 antibodies, and processed as indicated for conventional mono-dimensional gels. The rabbit polyclonal antibody to phospho-tauThr181 (Calbiochem; dilution 1:250) was used as a control of phospho-tau band pattern of sarkosyl-insoluble fractions in AD.

Double-labeling immunofluorescence and confocal microscopy

Cryostat sections, 7 μm thick, of the frontal cortex were stained with a saturated solution of Sudan black B (Merck) for 30 min to block the autofluorescence of lipofuscin granules present in nerve cell bodies, rinsed in 70% ethanol and washed in distilled water. The sections were incubated at 4 °C overnight with the mouse anti-AT8 antibody (Innogenetics, Barcelona, Spain) at a dilution of 1:50 and rabbit polyclonal anti-14-3-3 (18649, IBL) used at a dilution of

1:200. After washing in PBS, the sections were incubated in the dark with the cocktail of secondary antibodies, and then diluted in the same vehicle solution as the primary antibodies for 45 min at room temperature. Secondary antibodies were Alexa488 anti-rabbit (green) and Alexa546 anti-mouse (red) (both from Molecular Probes, Invitrogen, Barcelona, Spain), and these were used at a dilution of 1:400. After washing in PBS, the sections were mounted in Immuno-Fluore Mounting medium (ICN Biomedicals, Illrich, France), sealed and dried overnight. Sections were examined with a Leica TCS-SL confocal microscope. Nuclei were visualized in blue.

RESULTS

Mono-dimensional gel electrophoresis and Western blotting to glycosylated products

Two strong bands between 28 and 33 kDa were detected in sarkosyl-insoluble fractions from frontal cortex of AD cases, when compared with control samples, using anti-CEL antibodies. Although the intensity of the lower band was variable from one AD case to another, the intensity of the upper band was similar in every disease case. These antibodies also detected a band at 85 kDa, but no differences in the intensity of this band were observed between control and AD brains (Fig. 1).

Anti-CML detected the same band at 85 kDa and other bands between 40 and 120 kDa. None of them showed differences between controls and AD, except for a doublet between 40 and 50 kDa which was found in one AD case.

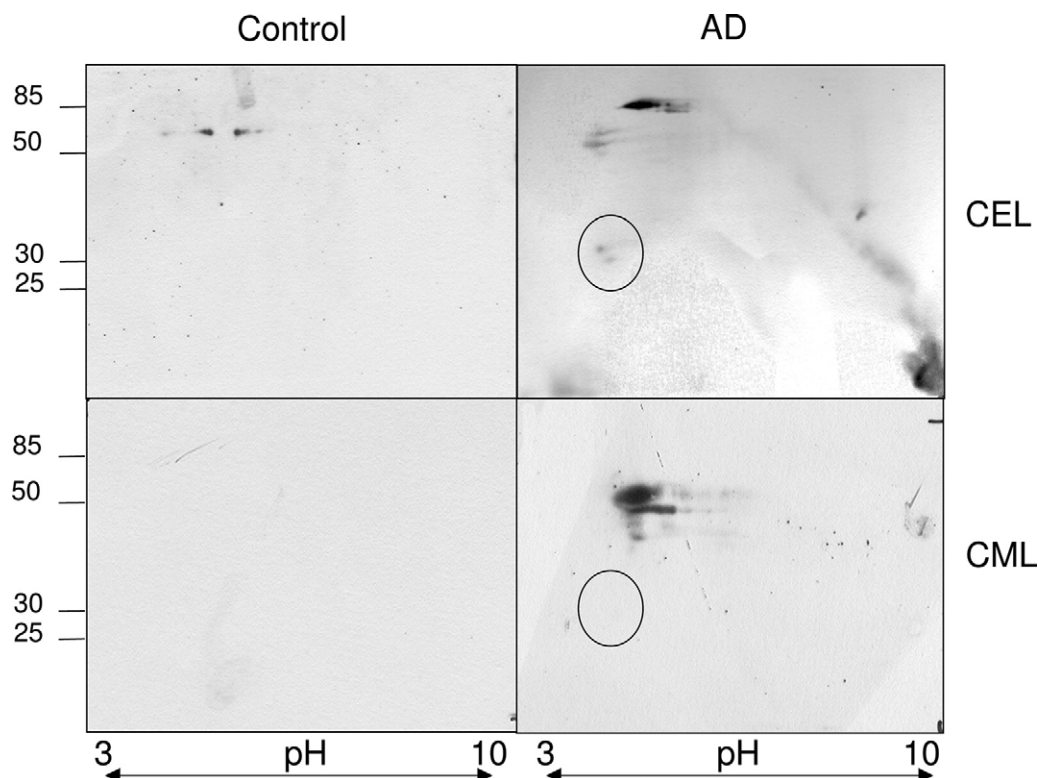


Fig. 2. 2D Gel electrophoresis and Western blotting to CEL and CML in sarkosyl-insoluble fractions of frontal cortex in control (C) and AD. CEL antibody reveals two spots of about 30 kDa which are not seen in control cases (circle). The CML antibody does not recognize spots of about 30 kDa (see inside circle) but a doublet of about 50 kDa (this case is the same as the first AD in Fig. 1).

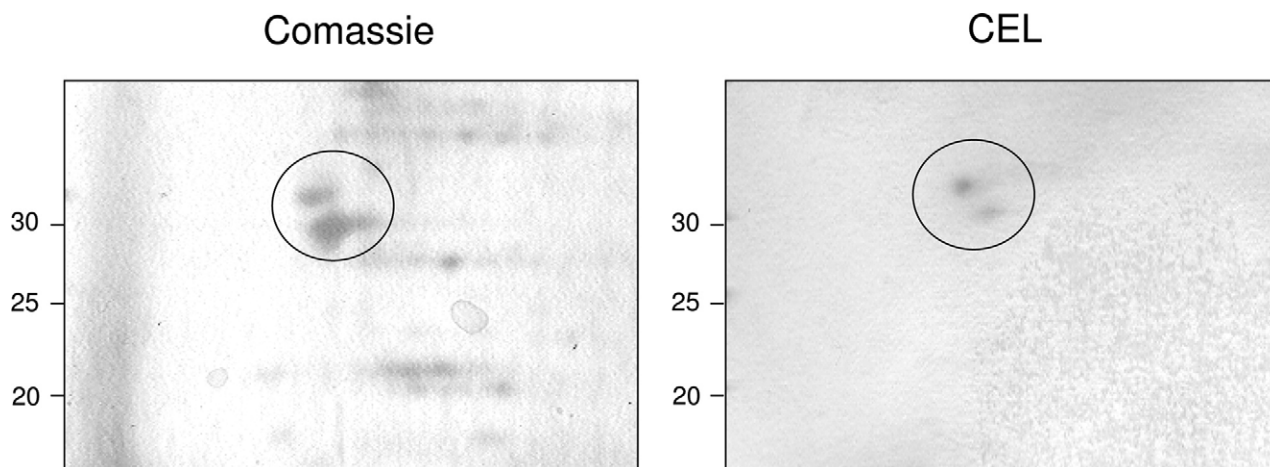


Fig. 3. CEL-immunoreactive oxidized spots of about 30 kDa (right panel) identified in Coomassie-stained 2D gels (left panel) processed in parallel (circles). The spots were excised from Coomassie-stained gels to perform the mass spectrometry analysis.

Yet the two bands around 30 kDa, detected with anti-CEL, were not detected with the CML antibody (Fig. 1).

2D Gel electrophoresis, Western blotting for oxidized proteins, and protein characterization in sarkosyl-insoluble fractions

AD. 2D Gels of sarkosyl-insoluble fractions of AD samples immunoblotted with anti-CEL antibody revealed oxidized spots at 85 kDa and 50 kDa, and two well-defined spots close to 30 kDa. In two controls, spots at 85 kDa were also observed. CEL-immunoreactive spots close to 30 kDa were not found in controls. 2D Gels of sarkosyl-insoluble fractions of AD samples immunoblotted with anti-CML disclosed several spots of high molecular weights but not the two spots around 30 kDa (Fig. 2). Therefore, 2D gels confirmed the presence of unique CEL-immunoreactive spots in AD brains within a molecular weight range of about 30–40 kDa. These spots were identified in Coomassie-stained 2D gels processed in parallel (Fig. 3) and excised. Mass spectrometry showed two 14-3-3 isoforms: zeta and gamma (Table 2).

The same membranes blotted for anti-14-3-3 (ab6081, Abcam) confirmed the localization of this protein in the corresponding spots (data not shown).

In order to assess lipoxidative damage of 14-3-3, additional 2D gels of sarkosyl-insoluble fractions were immunoblotted with anti-MDA-Lys and anti-HNE antibodies. Anti-MDA-Lys, but not anti-HNE, antibodies detected one spot at about 30 kDa. This spot was present only in AD and not in control samples (Fig. 4). The spot was identified in

Coomassie-stained gels run in parallel, in-gel digested, and identified following MS and data searching as 14-3-3 gamma isoform (data not shown).

CAA. 2D Gels of sarkosyl-insoluble fractions in CAA immunoblotted with anti-MDA-Lys or with anti-CEL antibodies recognized similar spots of about 30 kDa (Fig. 5). Western blots of the same membranes with anti-14-3-3 antibody revealed the spots corresponding to 14-3-3 at the same place as the spots detected by anti-MDA-Lys and anti-CEL antibodies (Fig. 5).

Total homogenates of AD and CAA

2D Gels of total homogenates from frontal cortex of AD were immunoblotted with anti-MDA-Lys antibodies. Anti-MDA-Lys antibody detected a pattern very similar to that of the sarkosyl-insoluble fraction in AD. Western blotting with the anti-14-3-3 antibody (ab6081, Abcam) revealed the spot corresponding to 14-3-3 at the same place as the spot detected by anti-MDA-Lys (Fig. 6). Interestingly the spot of 14-3-3 in AD cases was larger than the spot in controls thus suggesting higher amount of 14-3-3 protein in AD.

2D Gels of total homogenates from two cases of CAA showed similar spots of MDA-Lys and 14-3-3 proteins, using the corresponding specific antibodies (Fig. 6). These spots were identified in parallel Coomassie-stained 2D gels and excised. Mass spectrometry of MDA-Lys-modified proteins in CAA revealed two 14-3-3 isoforms: zeta and gamma (Table 3).

Table 2. Oxidized proteins excised from AD gels

Protein	Molecular weight	pI	MOWSE score ^a	Peptides matched	ID number
14-3-3 Protein gamma	28.3	4.8	41 (20%)	3	1433G_HUMAN
YWHAZ protein (14-3-3 zeta)	30.1	4.72	459 (33%)	11	gi 49119653

CEL-modified proteins in sarkosyl insoluble fractions in AD.

^a Sequence coverage shown in parentheses.

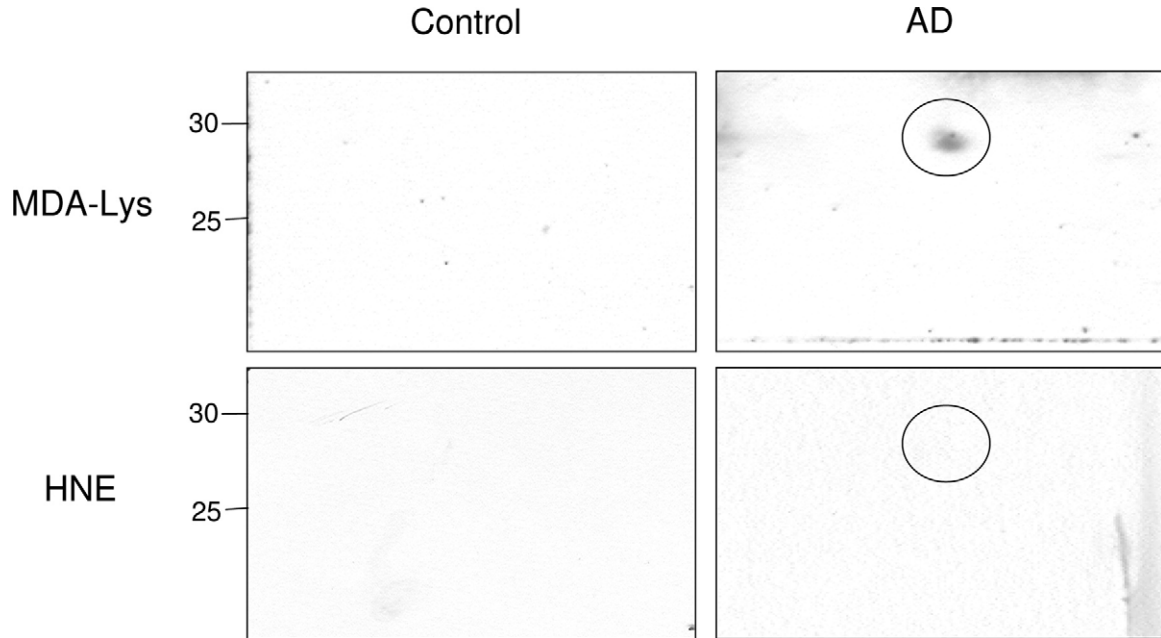


Fig. 4. 2D Gels and Western blotting of sarkosyl-insoluble fractions in one control and one AD case with anti-MDA-Lys and anti-HNE antibodies. MDA-Lys antibody reveals a spot of about 30 kDa. A similar spot is not recognized with anti-HNE antibodies (circles).

14-3-3 Immunohistochemistry, and 14-3-3 double-labeling immunofluorescence and confocal microscopy

Cryoprotected samples of the frontal cortex in control and diseased cases processed free-floating showed 14-3-3 immunoreactivity in the soma of neurons. By using antibodies

ab6081 (Abcam) and 18649 (IBL), immunoreactivity was present equally in neurons of control and AD cases. NFTs were not stained with these antibodies (Fig. 7). Yet immunohistochemistry with the antibody 14-3-3 (phospho S) (ab14127) revealed marked differences, as this antibody did not recognize constitutive 14-3-3 in the cytoplasm

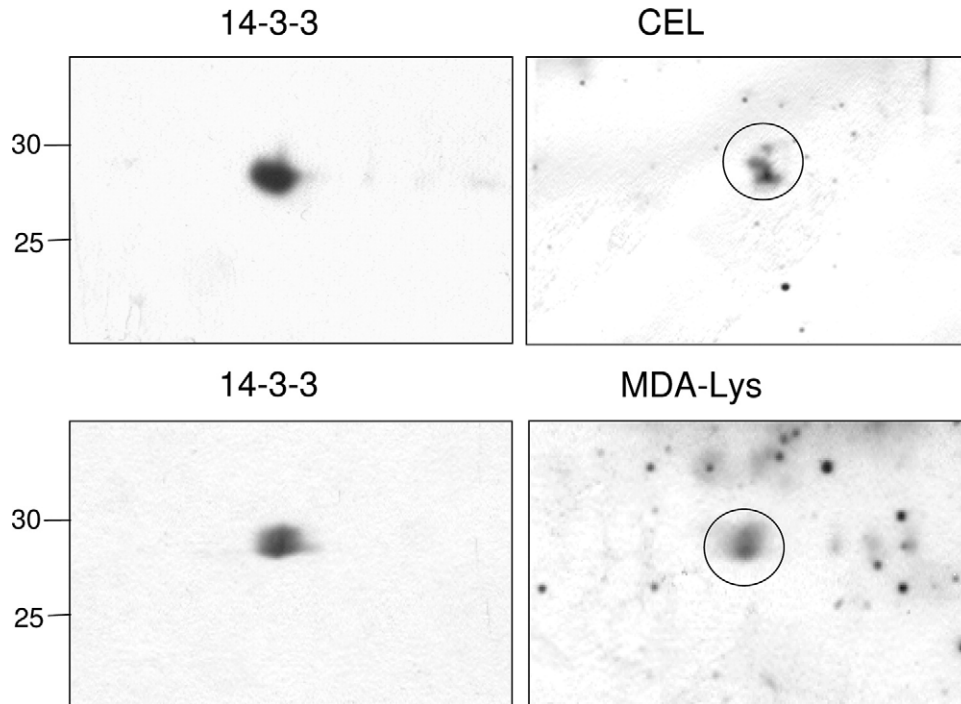


Fig. 5. 2D Gel electrophoresis and Western blotting of sarkosyl-insoluble fractions in CAA. Membranes were processed in parallel with anti-CEL or anti-MDA-Lys, and with anti-14-3-3. CEL and MDA-Lys immunoreactivity matches with 14-3-3-immunoreactive spots of about 30 kDa.

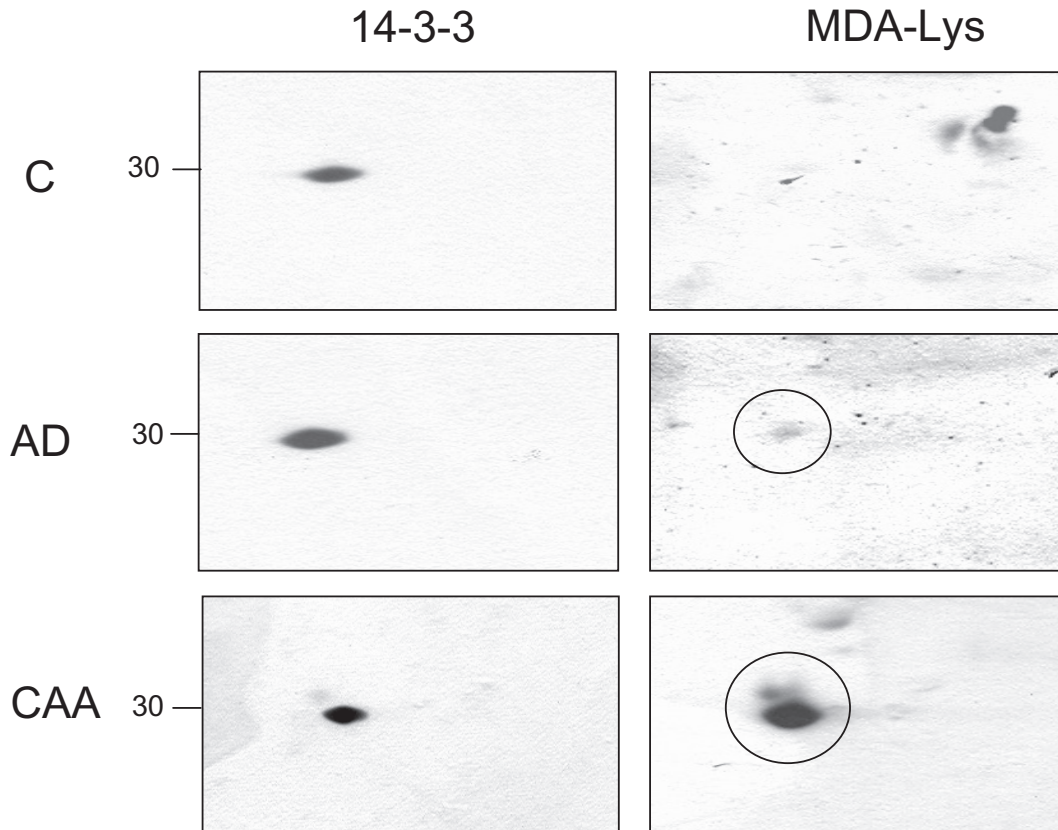


Fig. 6. 2D Gel electrophoresis and Western blotting of total homogenates from control, AD, and CAA with anti-14-3-3 and anti-MDA-Lys antibodies. MDA-Lys discloses spots of about 30 kDa corresponding to the spots which are also detected with the 14-3-3 antibody in AD and CAA (circles), but only barely in control cases.

of neurons but strongly immunostained NFTs, neuropil threads and dystrophic neurites of senile plaques. Consecutive sections immunostained with the AT8 antibody indicated that the majority of, if not all, NFTs were stained with the anti-14-3-3 (phospho S) antibody (data not shown).

Sections double-labeled with AT8 (anti-phospho tau antibody) and 14-3-3 disclosed that 14-3-3 protein was present in the cytoplasm of all neurons, whereas AT8 immunoreactivity was restricted to the subset of neurons with NFTs (Fig. 8). As a result, some neurons contained both 14-3-3 and phospho-tau, but the amount and the distribution of 14-3-3 in neurons with NFTs was the same as those in neurons without NFTs. Incubation without the primary antibodies revealed no immunoreactivity (Fig. 8).

Western blotting of 14-3-3 antibodies

To further identify the characteristics of the material recognized with these antibodies, Western blots of sarkosyl-

insoluble fractions were carried out in every case. Antibodies ab6081 (Abcam) and 18649 (IBL) recognized bands of about 30 kDa corresponding to 14-3-3 proteins (Fig. 9). In contrast, anti-14-3-3 (phospho S) antibody did not recognize bands of molecular weight consistent with 14-3-3 in control and diseased brains but, instead, several bands of 68, 64 and 60 kDa in AD cases only. These bands are the same as those obtained with anti-phospho-tau antibodies, and characterize the pattern of phospho-tau in AD (Fig. 9). Interestingly, similar bands were weakly immunostained with the 18649 (IBL) antibody. No bands were immunostained with the secondary antibody alone (data not shown).

DISCUSSION

14-3-3 is a family of acidic proteins composed of seven isoforms widely expressed in all tissues. This family of proteins is involved in kinase activation and chaperone

Table 3. Oxidized spots excised from CAA gels

Protein	Molecular weight	pI	MOWSE score ^a	Peptides matched	ID number
14-3-3 Protein gamma	28.3	4.8	64 (39%)	3	1433G_HUMAN
YWHAZ protein (14-3-3 zeta)	30.1	4.72	529 (39%)	12	gi 49119653

MAD-Lys-modified proteins in total frontal cortex homogenates in CAA.

^a Sequence coverage shown in parentheses.

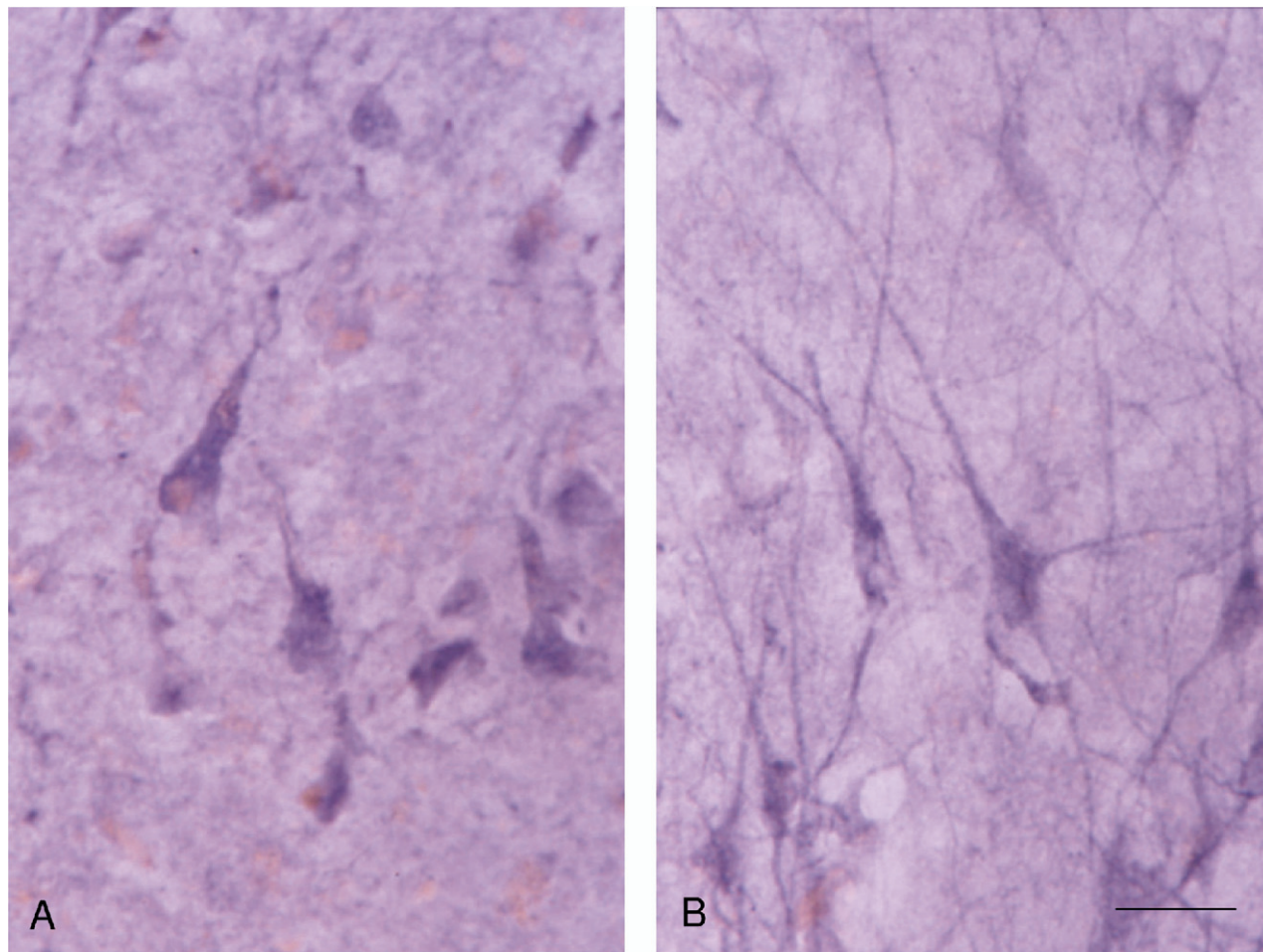


Fig. 7. Immunohistochemistry to 14-3-3 by using ab6081 (Abcam) (A) and 18649 (IBL) (B) in Alzheimer disease (B–D) cases. Antibodies recognize cytosolic 14-3-3 but not NFTs. Cryostat sections processed free-floating with no hematoxylin counterstaining. Scale bar=25 μm .

activity, among other functions related with signaling pathways, in addition to key roles in cell cycle regulation and development (Ferl, 1996; Muslin and Lau, 2005; Mhaweck, 2005; Darling et al., 2005; Hermeking and Benzinger, 2006; Aitken, 2006).

14-3-3 Proteins are highly expressed in the adult brain where they play important functions including protein interactions, protein folding and effects on protein kinases (Takahashi, 2003; Berg et al., 2003). In neurons, 14-3-3 is mainly found in cytoplasm and synapses (Fu and Subramanian, 2000). The fact that 14-3-3 proteins are phosphoserine/phosphothreonine-binding proteins implies important roles in cell signaling, and more than 100 binding partners have been identified (Dougherty and Morrison, 2004).

14-3-3 Zeta, gamma and epsilon are over-expressed in AD brain regions affected by tau pathology, and their levels correlate with disease progression (Fountoulakis et al., 1999; Soulié et al., 2004). 14-3-3 Gamma and epsilon isoforms are also over-expressed in the brains of cases with Down syndrome (Fountoulakis et al., 1999). Similar findings have been herein obtained in 2D gels.

Oxidative damage is increased by $A\beta$, as reported in several *in vitro* and *in vivo* studies (Butterfield and Lauderback, 2002; Varadarajan et al., 2000; Drake et al., 2003; Butterfield, 2003; Boyd-Kimball et al., 2005; Sultana et al., 2006).

In the present study, we have shown that 14-3-3, zeta and gamma isoforms are targets of oxidative damage in AD. Similar findings have been observed in every case. This is important, as monodimensional gels revealed individual differences in the intensity of the lower band of about 28 kDa, probably corresponding to oxidized levels of gamma isoform. The higher levels of MDA-Lys spots could reflect a larger content of this protein target in these pathological cases in agreement with previous observations showing 14-3-3 over-expression in AD (Fountoulakis et al., 1999). Thus, 14-3-3 oxidative damage in AD could be related to $A\beta$ -induced oxidative stress. To test this hypothesis, we studied the possible oxidation of 14-3-3 in CAA. We found that 14-3-3, zeta and gamma isoforms were also MDA-Lys- and CEL-modified in CAA, thus indicating a link between $A\beta$ pathology and 14-3-3 oxidation in AD and CAA.

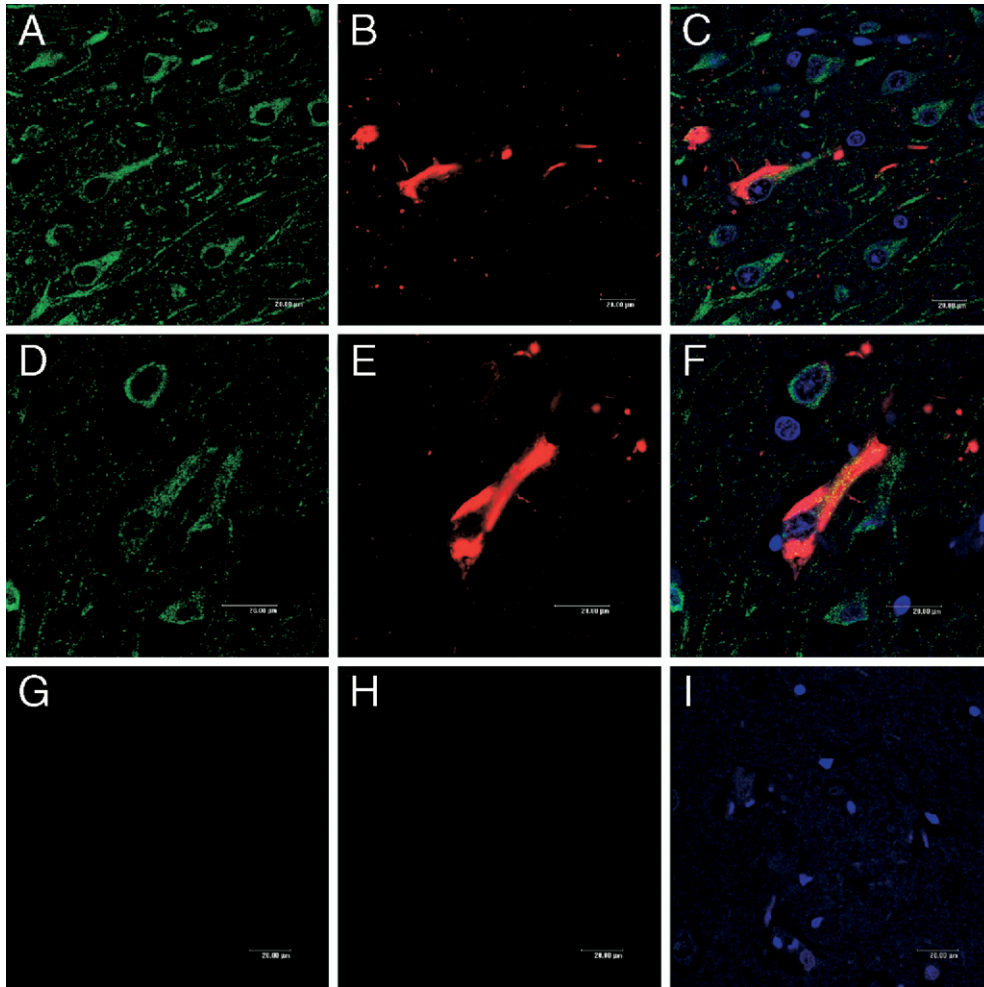


Fig. 8. Double-labeling immunofluorescence and confocal microscopy to 14-3-3 (green) and AT8 (red) in the frontal cortex in AD. Fine granular 14-3-3 immunoreactivity is found in the cytoplasm of all neurons and dendrites, whereas phospho-tau immunoreactivity (AT8) occurs only in neurons with NFTs. Note that 14-3-3 immunoreactivity is the same in neurons with NFTs as in neurons without NFTs. (A, D) 14-3-3; B and E: AT8; C and F: merge. (G–I) Incubation without the corresponding primary antibodies. Nuclei are visualized in blue.

Previous immunohistochemical studies have shown that 14-3-3 co-localizes with phospho-tau in NFTs in AD (Layfield et al., 1996; Umahara et al., 2004). In the first work, antibodies to sheep brain 14-3-3 were used for immunohistochemistry (Layfield et al., 1996); whereas in the second study, antibodies to human 14-3-3 common, and antibodies to 14-3-3 beta, gamma, epsilon and zeta were tested by Western blot and proved for immunohistochemistry, and double and triple fluorescence in AD brains (Umahara et al., 2004). No similar results were obtained in the present immunohistochemical and double-labeling immunofluorescence studies. Two different antibodies to 14-3-3 recognized cytosolic 14-3-3 but they did not stain NFTs. An additional 14-3-3-phospho antibody immunostained NFTs and other tau-bearing structures in AD cases. Yet this antibody identified only three bands of 68, 64 and 60 kDa which are typical of phospho-tau aggregates in AD. The later antibody was considered unsuitable for 14-3-3 immunohistochemistry because of the possible cross-reactivity of the antibody with phospho-

tau proteins. Lack of 14-3-3 immunoreactivity in relation with amyloid plaques in AD, but not in PrP plaques in CJD, was also emphasized in other studies (Richard et al., 2003).

Inconsistencies of immunohistochemical results do not undermine possible implications of oxidized 14-3-3 in AD and CAA

Some data point to the implications of 14-3-3 in tau phosphorylation: 1: tau interacts with zeta and beta but not with gamma and epsilon 14-3-3 isoforms (Hashiguchi et al., 2000); 2: dimers of 14-3-3 zeta can bind tau and GSK-3 β simultaneously, enhancing tau phosphorylation (Agarwal-Mawal et al., 2003); 3: 14-3-3 is able to bind the inactive form of GSK-3 β (GSK-3 β Ser9) and then preserve its activity (Yuan et al., 2004); 4: 14-3-3 zeta can stimulate the phosphorylation of tau at Ser(262)/Ser(356) through the cAMP-dependent protein kinase pathway (Hashiguchi et al., 2000); 5: a direct role for 14-3-3 zeta in tau fibril

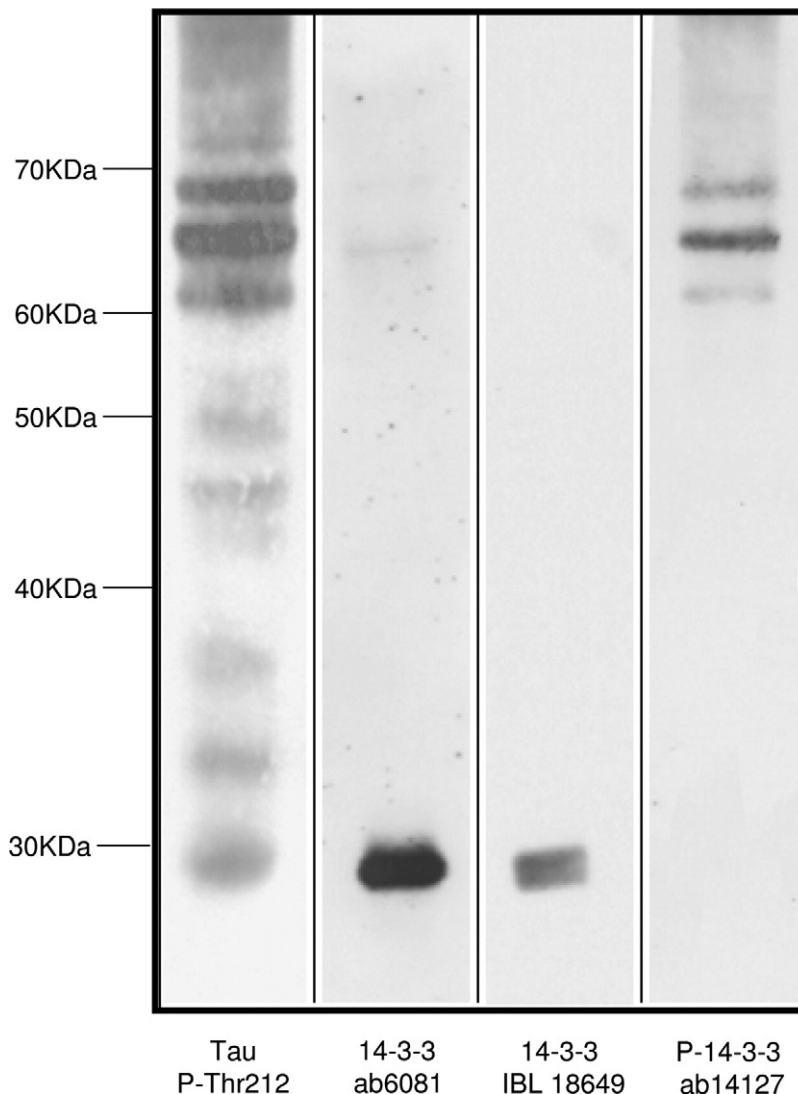


Fig. 9. Gel electrophoresis and Western blotting to 14-3-3 by using 18649 (IBL), ab6081 (Abcam) and 14-3-3 (phospho S) (ab14127, Abcam) antibodies in sarkosyl-insoluble fractions in AD. Anti-14-3-3 antibodies ab6081 and 18649 recognized a band of 30kDa. In contrast, 14-3-3 (phospho S) (ab14127), does not label bands at the predicted molecular weight of 14-3-3 but three bands of 68, 64 and 60 kDa corresponding to phospho-tau. Note that weak bands of high molecular weight are also seen with the IBL antibody.

formation has also been suggested (Hernández et al., 2004). Therefore, oxidized 14-3-3 may impact on tau phosphorylation in AD. Whether these possible effects are not apparently visualized in CAA is not known. Since 14-3-3 zeta is oxidized in AD and CAA, tau protein binding and tau phosphorylation may be modified in these disorders.

Additional implications of oxidized 14-3-3 in AD and CAA brains can be related to conformational changes of other proteins, abnormal scaffolding and physical occlusion of sequence-specific or structural protein features as reviewed elsewhere (Bridges and Moorhead, 2005; van Heusden, 2005; Coblitz et al., 2006). Additional studies are, however, needed to elucidate the exact impact of *in vivo* oxidized 14-3-3 in AD and CAA.

Acknowledgments—This work was funded by grants from the Spanish Ministry of Health, Instituto de Salud Carlos III PI040184

and PI05/1570, and supported by the European Commission under the Sixth Framework Programme (BrainNet Europe II, LSHM-CT-2004-503039). We thank Maria Antonia Odena and Eliandre Oliveira from the Plataforma de Proteòmica, Parc Científic Universitat de Barcelona for technical support. We thank T. Yohannan for editorial help.

There is no conflict of interest including financial, personal or other relationships with other people or organizations within the three years of beginning the work.

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(Accepted 8 March 2007)
(Available online 19 April 2007)

[doi:10.1016/j.neuroscience.2007.03.013](https://doi.org/10.1016/j.neuroscience.2007.03.013)

 Cite or Link Using DOI

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RETRACTED: Oxidative damage of 14-3-3 zeta and gamma isoforms in Alzheimer's disease and cerebral amyloid angiopathy

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Available online 19 April 2007.


This article has been retracted at the request of the editors and authors. Please see Elsevier Policy on Article Withdrawal (<http://www.elsevier.com/locate/withdrawalpolicy>).

Reason: After publication of their paper, the authors increased the number of control cases and carried out densitometric studies relating levels of malondialdehyde lysine (MDAL) immunoreactivity to levels of 14-3-3 immunoreactivity in comparative spots of membranes blotted with 14-3-3 and MDAL antibodies. Differences were not significant between Alzheimer's disease (AD) ($n=6$) and age-matched controls ($n=8$) when values of MDAL in 14-3-3 spots were corrected by values of total 14-3-3.

Therefore, the present data do not indicate significant differences between control and AD cases regarding total 14-3-3 and oxidised 14-3-3 levels in total homogenates, and the conclusion made in this article is invalidated.

In the article it was concluded that the 14-3-3 zeta and gamma isoforms are oxidatively damaged in the aged human brain. The latter conclusion is still valid.

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8

Delineation of Early Changes in Cases with Progressive Supranuclear Palsy-Like Pathology. Astrocytes in Striatum are Primary Targets of Tau Phosphorylation and GFAP Oxidation

RESEARCH ARTICLE

Delineation of Early Changes in Cases with Progressive Supranuclear Palsy-Like Pathology. Astrocytes in Striatum are Primary Targets of Tau Phosphorylation and GFAP Oxidation

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Keywords

argyrophilic grain disease, glial fibrillary acidic protein oxidative damage, progressive supranuclear palsy.

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Received 5 January 2008; accepted 19 February, 2008.

doi:10.1111/j.1750-3639.2008.00173.x

Abstract

Progressive supranuclear palsy (PSP) is a complex tauopathy usually confirmed at post-mortem in advanced stages of the disease. Early PSP-like changes that may outline the course of the disease are not known. Since PSP is not rarely associated with argyrophilic grain disease (AGD) of variable intensity, the present study was focused on AGD cases with associated PSP-like changes in an attempt to delineate early PSP-like pathology in this category of cases. Three were typical clinical and pathological PSP. Another case presented with cognitive impairment, abnormal behavior and two falls in the last three months. One case suffered from mild cognitive impairment, and two had no evidence of neurological abnormality. Neuropathological study revealed, in addition to AGD, increased intensity and extent of lesion in three groups of regions, striatum, pallidus/subthalamus and selected nuclei of the brain stem, correlating with neurological impairment. Biochemical studies disclosed oxidative damage in the striatum and amygdala. Together the present observations suggest (i) early PSP-like lesions in the striatum, followed by the globus pallidus/subthalamus and selected nuclei of the brain stem; (ii) early involvement of neurons and astrocytes, but late appearance of tufted astrocytes; and (iii) oxidative damage of glial acidic protein in the striatum.

INTRODUCTION

Progressive supranuclear palsy (PSP) is a rare neurodegenerative disease, with an age-adjusted prevalence of 6.4 per 100 000 (43), clinically manifested by movement disorders and cognitive deficits. These include bradykinesia, postural instability with falls (usually backwards), parkinsonism, nuchal dystonia and gaze supranuclear palsy. Frontotemporal impairment and dementia can follow the appearance of movement disorders (20, 39).

Clinical diagnosis of PSP is based on both inclusion and exclusion criteria of other neurodegenerative diseases with similar clinical features as Parkinson's disease (PD), corticobasal degeneration, multiple system atrophy and Lewy body disease (28, 29). Progressive Supranuclear Palsy Rating Scale and Staging system permits an approach to the clinical staging and prognosis of the disease (19).

The main neuropathological findings in PSP are neuronal loss, astrocytic gliosis, and hyperphosphorylated-tau accumulation in neurons, astrocytes and oligodendrocytes. Cortical and subcortical structures are affected at the terminal stages of the disease. The globus pallidus, striatum, subthalamic nucleus, nucleus basalis of Meynert, colliculi, tegmentum, periaqueductal gray matter,

substantia nigra, red nucleus, reticular formation of the midbrain and pons, basis pontis, and dentate nucleus are involved in the majority of cases; the cerebral cortex, locus ceruleus, oculomotor complex and inferior olive are variably affected (29, 21, 22). Tau-positive aggregates in PSP are neurofibrillary tangles (NFT) and pretangles in neurons, neuropil threads, coiled bodies in oligodendroglial cells, and heterogeneous inclusions in the cytoplasm of astrocytes that are subdivided into thorn-shaped or bush astrocytes and protoplasmic tufted astrocytes (4, 26, 46, 47). Hyperphosphorylated tau in PSP is mainly composed of 4R-tau isoforms that are resolved in two phospho-tau bands of 68 kDa and 64 kDa in Western blots of sarkosyl-insoluble fractions (11, 14).

In contrast with other degenerative diseases of the nervous system, as Alzheimer's disease (AD) or PD, practically nothing is known about early changes in PSP. This is because, in part, of the rarity of PSP in comparison with AD and PD. Yet PSP is often associated with argyrophilic grain disease (AGD) (31, 49), another tauopathy much more common than PSP. AGD was first described as a degenerative disease characterized by argyrophilic grains in the entorhinal cortex, hippocampus, amygdala and neighbouring temporal cortex in a subset of patients who had suffered from adult onset dementia (7, 8). However, AGD is frequently asymptomatic

depending on the extension of the lesions (42, 52); the presence of AGD has been estimated at 5%–9% in adult autopsy series (9, 50). The main neuropathological findings in AGD are tau hyperphosphorylation and accumulation in grains, pretangle neurons, tangles, neuropil threads, coiled bodies, and cytoplasm of astrocytes. Gel electrophoresis of sarkosyl-insoluble fractions has shown that AGD is characterized by a double band of 68 kDa and 64 kDa (16, 18, 49, 53, 54). The use of specific anti-4R tau antibodies has further categorized AGD as a 4R-tauopathy (49).

The neuropathological screening of AGD is relatively easy with the use of phospho-tau immunohistochemistry in a single section of the anterior hippocampus, and this method is routinely carried out in many laboratories because it also permits the screening of AD. Following this procedure, we have found 45 AGD cases, which represent 4% of the total autopsies, in a consecutive autopsy series in a general adult hospital. Seven cases had additional lesions of mild, moderate or severe intensity that resembled those seen in PSP. Three of them had suffered from typical clinical symptoms of PSP for 4–6 years—the neuropathological changes were also typical of terminal PSP—and these cases were diagnosed as PSP with associated AGD. Another case presented with cognitive impairment, abnormal behavior and two falls in the last 3 months. One case had suffered from mild cognitive impairment with no motor abnormalities. The remaining two cases had no evidence of neurological deficits according to the clinical report and the neurological examination.

The present study is focused on the neuropathology of the four cases with AGD and associated lesions that were evaluated as consistent with early PSP-like changes. It is worth considering that in spite of certain similarity of lesions in these cases to those encountered in advanced PSP, we will never know whether these individuals would have suffered from clinical PSP if they had survived for a long time. Therefore, the present study is geared to increase understanding about possible steps of PSP-like pathology in certain subjects rather than to establish a rigid and universal scheme of PSP stages of disease progression. In addition to the neuropathological study, gel electrophoresis and western blotting to glycoxidative and lipoxidative markers, as well as 2D gel electrophoresis and mass spectrometry, have been carried out to evaluate whether oxidative damage is an early event associated with PSP-like pathology.

MATERIAL AND METHODS

Cases

A summary of the cases studied is shown in Table 1.

Case 1: The patient was a 68 years old man who was admitted in the hospital because of fever, respiratory insufficiency, pancytopenia, lung infiltrates and positive cultures to pseudomona. He was diagnosed of chronic lymphocytic leukemia, bilateral pneumonia, septic shock and multiorganic failure. He died 7 days later. No clinical evidence of neurological disorder was recorded in the clinical file. An interview to the relatives after the neuropathological diagnosis was made further excluded major neurological deficits, including abnormal behavior and cognitive impairment.

Case 2: The patient was a 79 years old man with chronic respiratory insufficiency currently visited in the hospital. No evidence of neurological symptoms and signs was recorded in the clinical files. He was admitted in the hospital because of sudden respiratory failure caused by a lobar pneumonia. He died 48 h later.

Case 3: The patient was a 66 years old woman with loss of recent memory and cognitive decline during the last 2 years. The last CT examination carried out 3 months before her admittance in the hospital showed mild global cerebral atrophy. At the same time, the neurological examination did not reveal motor or sensory disturbances, gait disorders or motor ocular anomalies. The patient was admitted because of sudden respiratory failure caused by pulmonary thromboembolism and she died 4 h later.

Case 4: The patient was a 68 years old woman with progressive cognitive decline, abnormal behavior with irritability and emotional instability for the last 4 years, clinically categorized as possible Alzheimer's disease. Two falls were recorded in the last 3 months. The patient also suffered from arterial hypertension and renal failure under clinical study. The neurological examination 1 month before her admittance to the hospital revealed slight tremor and a discrete disorder of the gait; the motor ocular movements were not affected. The patient came to the hospital because of urinary infection and sepsis.

Case 5: The patient was a 75 years old man with progressive cognitive beginning at the age of 70 and characterized by loss of memory, impaired orientation and progressive aphasia, personality

	Age	Gender	p.-m. delay	Neurological diagnosis	Neuropathological diagnosis
1	68	Man	12 h	Normal	AGD + tauopathy
2	79	Man	4 h	Normal	AGD + tauopathy
3	66	Woman	6 h	MCI	AGD + tauopathy
4	68	Woman	16 h	MCI + falls	AGD + PSP-like
5	75	Man	18 h	PSP	PSP + AGD
6	54	Man	3 h	Normal	No lesions
7	35	Man	8 h	Normal	No lesions
8	82	Woman	11 h	Normal	A few diffuse plaques
9	75	Woman	6 h	Normal	No lesions
10	80	Woman	3.5 h	Normal	A few diffuse amyloid plaques; NFTs in EC
11	73	Woman	7 h	Normal	No lesions
12	58	Woman	4 h	Normal	No lesions

Table 1. Summary of the clinical and neuropathological diagnosis in the present series. Abbreviations: MCI = mild cognitive impairment; PSP = progressive supranuclear palsy; AGD = argyrophilic grain disease; NFTs = neurofibrillary tangles; EC = entorhinal cortex; p.-m. delay = post-mortem delay (h).

changes with apathy, frequent changes of mood, irritability, and insomnia. He also suffered from the last 3 years of frequent falls, tremor, abnormal gait, facial hypomimia and motor ocular disturbances, including slowness of saccadic movements and difficulties to look upward. The patient was admitted in the hospital because of respiratory insufficiency caused by lobar pneumonia.

Cases 6–12: No neurological abnormalities were recorded in these patients. Causes of death were respiratory infections (3), cardiac infarction (1), disseminated cancer (2) and pulmonary thromboembolism (1).

Neuropathological methods

The time between death and tissue processing was between 2 and 14 h.

The left hemisphere was immediately cut on coronal sections, 1-cm thick, frozen on dry ice and stored at -80°C until use. For morphological examination, the brains were fixed by immersion in 10% buffered formalin for 2 or 3 weeks. The neuropathological study was carried out on dewaxed 4- μm thick paraffin sections of the frontal (area 8), primary motor, primary sensory, parietal, temporal superior, temporal inferior, anterior gyrus cinguli, anterior insular, and primary and associative visual cortices, entorhinal cortex and hippocampus, caudate, putamen and globus pallidus, medial and posterior thalamus, subthalamus, Meynert nucleus, amygdala, midbrain (two levels), pons and bulb, and cerebellar cortex and dentate nucleus. The sections were stained with haematoxylin and eosin, Klüver Barrera, and, for immunohistochemistry to glial fibrillary acidic protein (Dako, Barcelona, Spain dilution 1:250), CD68 (Dako, dilution 1:100), βA -amyloid (Boehringer, Ingelheim, Germany, dilution 1:50), tau AT8 (Innogenetics, Gent, Belgium, dilution 1:500), tau 4R and tau 3R (Upstate, Gent, Belgium, dilution 1:200 and 1:2 000, respectively), phosphorylation-specific tau Thr181, Ser202, Ser214, Ser262, Ser396 and Ser422 (all of them Calbiochem, LaJoya, CA, USA, dilution 1:100, except Thr181 1:250), and αB -crystallin (Abcam, Cambridge, UK, dilution 1:100), α -synuclein (Chemicon, Millipore, MA, USA, dilution 1:500) and ubiquitin (Dako, dilution 1:200). AD stages were established according to the amyloid deposition burden and neurofibrillary pathology following the nomenclature of Braak and Braak (10). Stages of amyloid deposition refer to initial deposits in the basal neocortex (stage A), deposits extended to the association areas of the neocortex (stage B), and heavy deposition throughout the entire cortex (stage C). Stages of neurofibrillary pathology correspond to transentorhinal (I–II), limbic (III–IV) and neocortical (V and VI). AGD stages were established following the nomenclature of Saito *et al* (42), slightly modified (18). Stage I is characterized by mild involvement of the anterior entorhinal cortex, cortical and basolateral nuclei of the amygdala, and hypothalamic lateral tuberal nucleus. Stage II is defined by moderate involvement of the entorhinal cortex, anterior CA1, transentorhinal cortex, cortical and basolateral nuclei of the amygdala, presubiculum, hypothalamic lateral tuberal nucleus and dentate gyrus. Stage III involves the entorhinal cortex, CA1, perirhinal cortex, presubiculum, amygdala, dentate gyrus, hypothalamic lateral tuberal nucleus. In addition, there is mild involvement of CA2 and CA3, subiculum, other nuclei of the hypothalamus (ie, mam-

illary bodies), anterior temporal cortex, insular cortex, anterior gyrus cinguli, orbitofrontal cortex, nucleus accumbens and septal nuclei.

Sarkosyl-insoluble fraction extraction

Frozen samples of about 2 g of the amygdala and striatum were gently homogenized in a glass tissue grinder in 10 vol (w/v) with cold suspension buffer (10 mM Trishydroxymethylaminomethane (TRIS-HCl), pH 7.4, 0.8 M NaCl, 1 mM Ethylene-glycol tetraacetic acid (EGTA), 10% sucrose). The homogenates were first centrifuged at 20 000 g, and the supernatant (S1) was retained. The pellet was rehomogenized in 5 vol of homogenization buffer and recentrifuged. The two supernatants (S1 + S2) were then mixed and incubated with 0.1% N-lauroylsarcosinate (sarkosyl) for 1 h at room temperature while being shaken. Samples were then centrifuged at 100 000 g in a Ti70 Beckman rotor. Sarkosyl-insoluble pellets (P3) were resuspended (0.2 mL/g, starting material) in 50 mM TRIS-HCl (pH 7.4). Protein concentrations were determined with the Bradford method using bovine serum albumin (BSA) as a standard.

Brain homogenates

Brain samples (0.1 g) of the striatum and amygdala of cases 2, 3 and 5, and controls 6, 7 and 8 were homogenized in 1 mL of lysis buffer (40 mM Tris, pH 7.5, 7 M urea, 2 M thiourea, 4% 3-[(3-Cholamidopropyl)dimethylammonia]-1-propanesulphonate (CHAPS) (BioRad, Barcelona, Spain) and complete protease inhibitor cocktail (Roche Molecular Systems, Barcelona, Spain), and centrifuged at 15 000 rpm for 10 minutes at 4°C . The pellets were discarded and protein concentrations of the supernatants were determined by Bradford method with bovine serum albumin (BSA) (Sigma, Barcelona, Spain) as a standard.

Western blot

For monodimensional gel electrophoresis, 20 μg of each sample from total homogenates, 250 μg from sarkosyl-insoluble fraction of case 2 and 150 μg from the same fraction of case 3 and case 5 were loaded for 10% SDS-polyacrylamide gel electrophoresis (SDS-PAGE) electrophoresis and then transferred to nitrocellulose membranes (400 mA for 90 minutes). Mini-protean system (BioRad) was used for brain homogenates, and maxi-protean system (16 \times 20 cm) was used for sarkosyl-insoluble fractions. Immediately afterwards, the membranes were incubated with 5% skimmed milk in tris buffered saline Tween 20 (TBS-T) buffer (100 mM Tris-buffered saline, 140 mM NaCl and 0.1% Tween 20, pH 7.4) for 30 minutes at room temperature, and then incubated with the primary antibody in TBS-T containing 3% BSA (Sigma, Madrid, Spain) at 4°C overnight. The mouse monoclonal anti-carboxy-ethyl-lysine (CEL) and anti-carboxy-methyl-lysine (CML) (TransGenic, Kumamoto, Japan), the mouse-monoclonal anti-advanced glycation end products (AGE) (TransGenic), and the rabbit polyclonal anti-malondyaldehyde-lysine (MDA-L) (Bio-medical, Houston, TX, USA) antibodies were used diluted 1:1000. The rabbit polyclonal anti-glial fibrillary acidic protein (GFAP) (Dako) was used at a dilution of 1:4000. The monoclonal antibody to β -actin (Sigma) was used at a dilution of 1:30 000 as a control of

protein loading. In sarkosyl-insoluble fractions, rabbit polyclonal antiphospho-tau(Ser422) (Calbiochem) was used at a dilution of 1:1000. Subsequently, the membranes were incubated for 45 minutes at room temperature with the corresponding secondary antibody labeled with horseradish peroxidase (Dako) at a dilution of 1:1000, and washed with TBS-T for 30 minutes. Protein bands were visualized with the chemiluminescence ECL method (Amersham, Barcelona, Spain).

Control and diseased cases were processed in parallel.

2D gel electrophoresis

A 150- μ g protein was mixed with 2% Byolites (v/v), 2 mM tributylphosphine solution and bromophenol blue in a final volume of 150 μ L. In the first-dimension electrophoresis, 150 μ L of sample solution was applied to an immobilized 7-cm pH 3–10 nonlinear gradient ReadyStrip immobilized pH gradient (IPG) strip (Bio-Rad) at both the basic and acidic ends of the strip. The strips were actively rehydrated for 12 h at 50 V, and the proteins were focused at 300 V for 1 h, after which time the voltage was gradually increased to 3500 V within 6 h. Focusing was continued at 3500 V for 12 h and at 5000 V for 24 h. For the second dimension separation, IPG strips were equilibrated for 10 minutes in 50 mM Tris-HCl (pH 6.8) containing 6 M urea, 1% (wt/v) SDS, 30% (v/v) glycerol and 2% dithiothreitol, and then reequilibrated for 10 minutes in the same buffer containing 2.5% iodoacetamide. The strips were placed on 10% polyacrylamide gels and electrophoresed at 0.02 A. For gel staining, Coomassie Biosave staining (Biorad) was used as described by the manufacturer.

Two 2D gels for every case were run in parallel, one for Coomassie staining and the other transferred to a nitrocellulose membrane (200 mA for 1 h 30 minutes). Diseased cases were processed in parallel with control cases. After incubation with 5% skimmed milk in TBS-T buffer for 30 minutes at room temperature, nitrocellulose membranes were blotted with mouse monoclonal anti-AGE (TransGenic). Membranes were stripped by two incubations of 20 minutes at 64°C with stripping buffer (0.1 mM B-mecap, 2% SDS, 62.5 mM Tris HCL pH 6.8) and incubated with 5% skimmed milk in TBS-T buffer for 30 minutes at room temperature. Membranes were then incubated with rabbit polyclonal anti-GFAP (Dako) used at a dilution of 1:4000. Subsequently, the membranes were processed as previously indicated for monodimensional gels. Several combinations of disease cases with at least three control cases were performed in order to prove reproducibility.

In-gel digestion

Proteins were in-gel digested with trypsin (sequencing grade modified, Promega, Barcelona, Spain) in the automatic Investigator™ ProGest robot of Genomic Solutions, Michigan, USA. Briefly, excised gel spots were washed sequentially with ammonium bicarbonate buffer and acetonitrile. Proteins were reduced and alkylated with 10 mM DTT solution for 30 minutes and 100 mM solution of iodine acetamide for 15 minutes, respectively. After sequential washing with buffer and acetonitrile, proteins were digested overnight at 37°C with trypsin 0.27 nM. Tryptic peptides were extracted from the gel matrix with 10% formic acid and acetonitrile. The extracts were pooled and dried in a vacuum centrifuge.

Acquisition of Mass spectrometry (MS) and MS/MS spectra

Proteins manually excised from the 2D gels were digested and analyzed by CapLCnano-ESI-MS-MS mass spectrometry. The tryptic digested peptide samples were analyzed using on-line liquid chromatography (CapLC, Micromass-Waters, Manchester, UK) coupled with tandem mass spectrometry (Q-TOF Global, Micromass-Waters, Manchester, UK). Samples were resuspended in 12- μ L 10% formic acid solution, and 4 μ L was injected for chromatographic separation into a reverse-phase capillary C18 column [75- μ m internal diameter and 15 cm in length (PepMap™ column, LC Packings, Amsterdam, The Netherlands)]. The eluted peptides were ionized via coated nano-ES needles (PicoTip™, New Objective, Woburn, MA, USA). A capillary voltage of 1800–2200 V was applied together with a cone voltage of 80 V. The collision in the collision-induced dissociation was 25 to 35 eV, and argon was employed as the collision gas. Data were generated in PKL file format and submitted for database searching in Mascot server (Matrix Science, Boston, MA, USA) using the NCBI database with the following parameters: trypsin enzyme, one missed cleavage, carbamidomethyl (C) as fixed modification and oxidized (M) as variable modification, and mass tolerance of 150–250 ppm.

Probability-based Mowse score was used to determine the level of confidence in the identification of specific isoforms from the mass spectra. This probability equals 10 (-Mowse score/10). Mowse scores higher than 50 were considered to be of high confidence of identification.

RESULTS

Neuropathology

Representative lesions are shown in Figure 1. Characteristic lesions in individual cases 1, 2, 3 and 5 are shown in Figure 1S–4S (supplementary data).

AGD pathology was characterized by the presence of grains and pretangles in the entorhinal cortex, CA1 region of the hippocampus and amygdala in every case, although the intensity of lesions was variable depending on the presence of associated lesions. The amygdala was slightly damaged in cases 1 and 2, but it was severely affected in cases 3, 4 and 5. Grains and pretangles, together with deposits in dentate gyrus neurons, were also seen in the temporal cortex and subiculum in cases 3, 4 and 5. Astrocytic inclusions and coiled bodies were noticed in every case, although with variable intensity.

On the basis of neuropathological data, staging of AGD was established as follows: case 1: early stage 2, case 2: stage 2, and cases 3, 4 and 5: stage 3.

Neurofibrillary tangles in the same regions were categorized as stage I in cases 1, 2 and 4; and stage II in case 5. A few diffuse plaques were seen in the temporal and orbital cortices in case 3 (stage A of Braak and Braak).

PSP-like pathology was examined in three different groups of regions: caudate/putamen, globus pallidus/subthalamic nucleus, and brain stem nuclei (substantia nigra, locus ceruleus, colliculi, periaqueductal gray matter and ventral pons).

Lesions in the caudate/putamen were characterized by astrocytic gliosis, as revealed with GFAP-immunostaining, and gel electro-

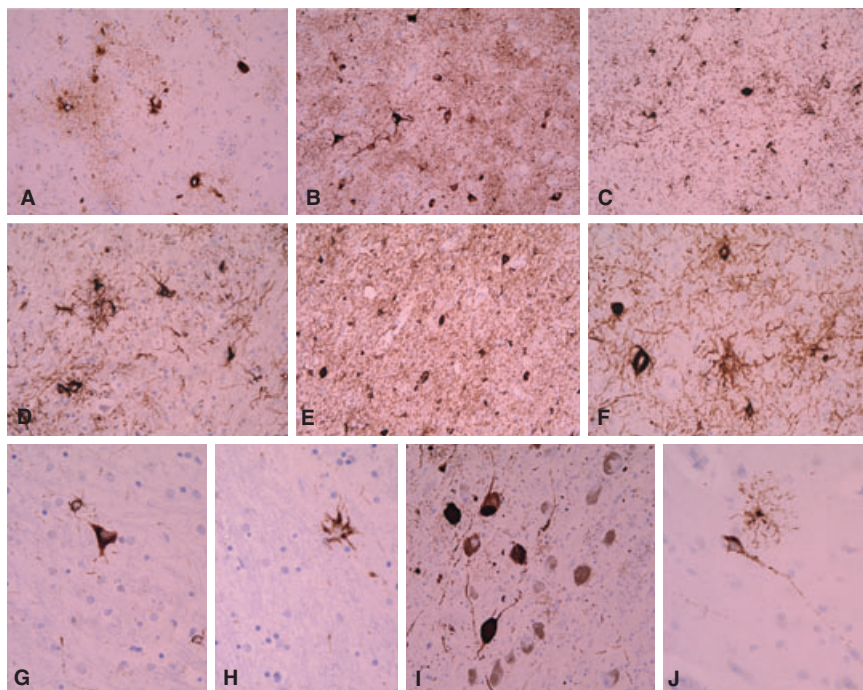


Figure 1. Phospho-tau pathology in cases with AGD and PSP-like pathology. **A.** caudate, case 2. **B.** amygdala, case 3. **C.** globus pallidus, case 5. **D.** CA1, case 3. **E.** subthalamus, case 5. **F.** superior colliculus, case 5. **G.** ventral pons, case 3. **H.** midbrain, case 3. **I.** locus coeruleus, case 3. **J.** gyrus cinguli, case 3. Paraffin section slightly counterstained with haematoxylin. Abbreviations: AGD = argyrophilic grain disease; PSP = progressive supranuclear palsy.

phoresis and GFAP immunoblotting (Figure 2), phospho-tau-immunoreactive astrocytes, and phospho-tau-immunoreactive neurons. These lesions were present in every case, although with variable intensity. The intensity of lesions was mild in case 1 and 2, moderate in cases 3 and 4, and severe in case 5.

Lesions in the globus pallidus and subthalamic nuclei were scanty in cases 1, 2 and 3, moderate in case 4 and severe in case 5. Neuronal pathology rather than astrocytic pathology predominated in these regions.

Lesions in the brain stem were characterized by neurofibrillary tangles and phospho-tau-immunoreactive inclusions in astrocytes. Discrete lesions were restricted to the ventral pons and ceruleus in cases 1 and 2. The intensity of lesions increased in these nuclei and the distribution of lesions extended to the substantia nigra, colliculus, red nucleus and peri-aqueductal gray matter in case 3 and particularly in case 4. Severe phospho-tau deposition in neurons and astrocytes was found in case 5.

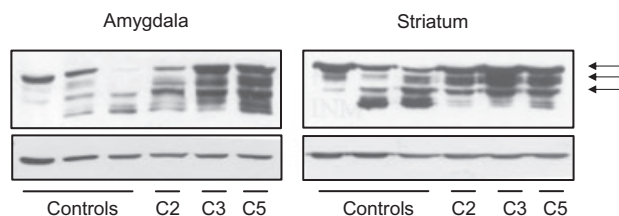


Figure 2. Monodimensional gel electrophoresis and western blotting to GFAP in the amygdala and striatum in cases 2, 3 and 5, and age-matched controls. Several bands of high molecular weight and strong density (arrows) are seen in diseased cases when compared with controls. Abbreviation: GFAP = glial fibrillary acidic protein.

Interestingly, in spite of the substantial numbers of phospho-tau-immunoreactive astrocytes, tufted astrocytes were absent in case 1, exceptional or very rare in cases 2 and 3, occasional in case 4 and frequent in case 5.

Coiled bodies in these regions were absent in cases 1 and 2, they were mild in case 3, moderate in case 4 and severe in case 5. These lesions were stained with anti-4R-tau antibodies. 3R-tau immunoreactivity was restricted to small numbers of tangles in the entorhinal cortex, thus suggesting combined stage I–II AD (data not shown).

Mild involvement of the Meynert nucleus occurred in cases 1 and 2, moderate in cases 3 and 4, and severe in case 5. The frontal cortex was involved in cases 3, 4 and 5, the parietal cortex was additionally involved in case 4, and the occipital cortex in case 5.

A summary of neuropathological observations is shown in Table 2, whereas individual changes in cases 1–5 are shown in the corresponding Tables 1S–5S (supplementary data).

No lesions were seen in cases 6–12. More explicitly, tau, α -synuclein and ubiquitin inclusions, and β -amyloid plaques were absent, excepting a few diffuse plaques in the orbital and temporal cortex in two cases and a few neurofibrillary tangles in the entorhinal cortex in one.

Tau banding pattern in sarkosyl-insoluble fraction

Western blots of sarkosyl-insoluble fractions incubated with antiphospho-tau(Ser422) antibody revealed a double band of 68 kDa and 64 kDa in the striatum and amygdala in case 3 and in case 5 (established PSP). In addition to these two bands, other bands of about 50 kDa and lower were detected in the striatum

Table 2. Summary of main neuropathological findings related with tau pathology. Involvement of three combined regions, presence of tufted astrocytes and AGD changes are expressed semiquantitative ly. +: mild; ++: moderate; +++: severe; +/- indicates lack of involvement of one of the mentioned regions. Abbreviation: AGD = argyrophilic grain disease.

Cases/region affected	1	2	3	4	5
Caudate/putamen	+	+	+	+	++
Globus pallidus/subthalamus	+/-	+/-	++/+	+	++
Substantia nigra/coeruleus/colliculi/ventral pons	+/-	+/-	+	++/+	+++/>++
Tufted astrocytes	no	exceptional	very rare	occasional	very common
AGD stage	2	2	3	3	3

and amygdala (Figure 3). Similar bands representing full-length 4R tau and truncated forms of tau have also been described in PSP and AGD (18, 38). The pattern in case 2 was lightly different because the two upper bands appeared to be composed of doublets. The reasons are not clearly understood, but the signal in this case was low when compared with case 3 and canonical PSP. The protein needed was higher in case 2 (250 µg) than in case 3 (50 µg).

Oxidative stress markers (MDA-L, AGE, CML and CEL)

Gel electrophoresis was carried out in total homogenates of the amygdala and striatum in three controls (cases 6, 7 and 8), and

diseased cases 2, 3 and 5. Membranes were immunoblotted with anti-MDAL, AGE, CEL and CML antibodies. Control and diseased cases were run in parallel.

Several bands were obtained in the amygdala in control and diseased cases with the different antibodies. Yet a band of about 50 kDa was detected with the four antibodies in cases 3 and 5. This band was not detected, or it was very faint in the three controls and in case 2. However, anti-AGE antibodies recognized a band of about 70 kDa only in case 2 (Figure 4, upper panel).

Several bands were also present in the striatum in control and diseased cases. Yet an AGE band of about 50 kDa was increased only in diseased brains, but not in controls (Figure 4, lower panel). A band of higher molecular weight (about 70 kDa) was also present in case 2. The intensity of MDA-L, CEL and CML bands was similar in disease cases and controls, thus indicating a preferential damage related with advanced glycation end products.

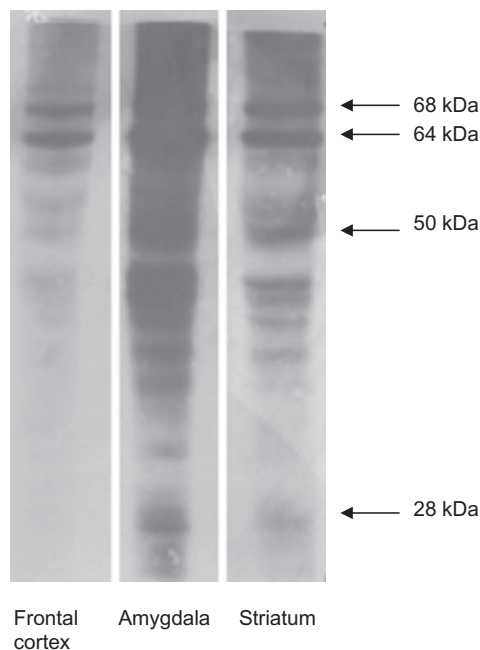


Figure 3. Western blots of sarkosyl-insoluble fractions in the amygdala and striatum in case 3 stained with the antiphospho-tau(Ser422) antibody. Bands of 68 kDa and 64 kDa together with bands of about 50 kDa and lower are present in the amygdala and striatum. These bands are similar to those currently found in PSP and AGD cases. Abbreviations: PSP = progressive supranuclear palsy; AGD = argyrophilic grain disease.

2D gel electrophoresis, western blotting and mass spectrometry

Amygdala

2D gels stained with Coomassie revealed three spots close to 50 kDa in case 3 when compared with controls. Parallel membranes blotted for AGE disclosed AGE immunoreactivity in these spots. The three spots were excised from the gels and identified by mass spectrometry as glial fibrillary acidic protein. Mowse scores higher than 50 (96, 204 and 273) were considered of high confidence of identification (Table 3).

Validation was carried out in 2D gels of one control and case 3 run in parallel and processed for Western blot with anti-GFAP antibody. Increased expression of GFAP was found in case 3 as three spots of high density and about 50 kDa of molecular weight.

No differences were seen between controls and case 2 (data not shown).

Striatum

2D gels stained with Coomassie revealed five spots (three from case 2, two from case 3) close to 50 kDa in cases 2 and 3 when compared with controls. The five spots were excised and identified by mass spectrometry as glial fibrillary acidic protein (GFAP) (Table 3). All the spots excised were consistent with GFAP. No other proteins or negative results were obtained in

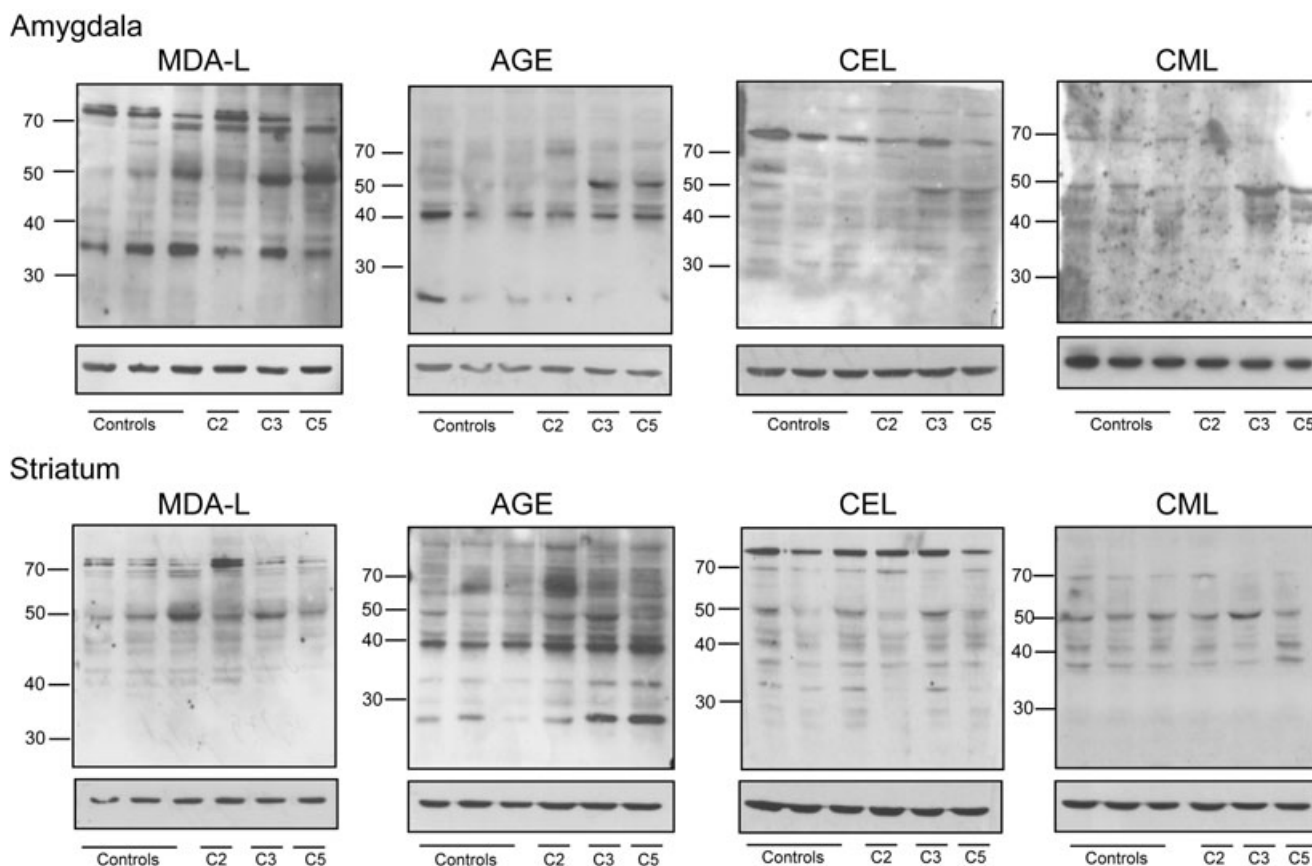


Figure 4. Monodimensional gel electrophoresis and western blotting to MDA-L, AGE, CEL and CML in the amygdala and striatum in three controls, and in cases 2, 3 and 5. Increased density of one band of about 50 kDa is found in the amygdala in cases 3 and 5, and in the striatum in cases 2, 3 and 5 with in membranes processed with anti-AGE antibody.

ies. Lower intensity of the band in the striatum in case 5 when compared with case 2 and 3 can be related with the longer post-mortem delay in this case. Abbreviations: MDA-L = malondyaldehyde-lysine; AGE = advanced glycation end products; CEL = carboxy-ethyl-lysine; CML = carboxy-methyl-lysine.

the present study. Mowse scores varied from 222 to 377, and they were considered to be of high confidence of identification (above 50).

Parallel membranes of cases 2 and 3, and corresponding controls showed the five spots immunoreactive for AGE and for GFAP (Figure 5).

DISCUSSION

The present study was carried out in an attempt to delineate neuropathological modifications consistent with early changes in PSP. As this is a small number of cases, and they have been selected from a series of AGD with associate PSP-like pathology, we can not

Table 3. Excised spots from 2D gels in the amygdala in case 3 and in the striatum in cases 2 and 3. Mowse scores higher than 50 are considered of high confidence of identification. Abbreviation: GFAP = glial fibrillary acidic protein.

Protein	Molecular weight	pI	Mowse score	Number of peptides matched	ID number
Amygdala case 3					
GFAP	49.7 kDa	5.42	204	12	gil38566198
GFAP	47.6 kDa	5.4	96	5	gil119571954
GFAP	49.7 kDa	5.42	273	16	gil38566198
Striatum case 2					
GFAP	49.7 kDa	5.42	286	22	gil38566198
GFAP	49.7 kDa	5.42	226	21	gil38566198
GFAP	49.7 kDa	5.42	222	17	gil38566198
Striatum case 3					
GFAP	49.7 kDa	5.42	377	22	gil38566198
GFAP	49.7 kDa	5.42	279	21	gil38566198

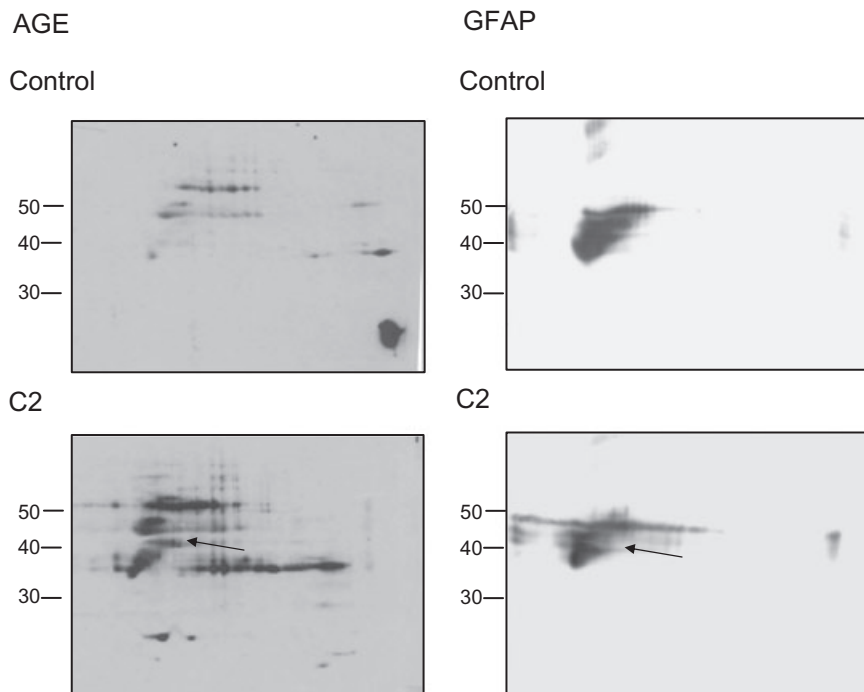


Figure 5. 2D gel electrophoresis and western blotting to AGE shows the presence of differential spots in case 2 when compared with the corresponding control run in parallel (arrows). Parallel membranes blotted for GFAP show that AGE-immunoreactive spots are also GFAP positive. Abbreviations: AGE = advanced glycation end products; GFAP = glial fibrillary acidic protein.

exclude certain bias in their selection and therefore that results of the present series may be not universal for PSP. This remark is even more relevant considering the heterogeneity in terms of clinical manifestations and neuropathological findings in established PSP (6, 12, 24, 36, 44, 55). As stated at the beginning, the present observations do not attempt to establish a rigid and universal scheme of PSP progression, but rather to increase our understanding about early changes related with PSP-like pathology.

Categorization of AGD pathology was carried out following established criteria (18, 42). Cases 1 and 2 were considered as stage 2, and cases 3, 4 and 5 as stage 3. Previous studies have shown that early stages in AGD are usually asymptomatic, and this is also observed in cases 1 and 2. AGD stage 3 is often associated with a variety of clinical symptoms, including cognitive decline, dementia, behavioral abnormalities, personality changes, and emotional and mood imbalance (8, 23, 41, 48–51). Cognitive and behavioral abnormalities were also present in cases 3 and 4, and these changes were ascribed to AGD. Cognitive impairment in case 5 was considered as a combined result of AGD and PSP.

For instrumental purposes, three main groups of regions were considered in the study of PSP-like pathology: (i) caudate/putamen; (ii) globus pallidus/subthalamus; and (iii) substantia nigra/ceruleus/colliculi/ventral pons.

The most remarkable lesions in cases 1 and 2 were astrocytic gliosis and hyperphospho-tau accumulation in caudate and putamen. Changes increased in intensity in case 3, where involvement of the globus pallidus and subthalamus, together with mild involvement of brain stem structures, was also observed. The intensity of lesions, ranging from mild to moderate, augmented in all three groups of regions in case 4. All these regions were severely affected in case 5 (prototypical PSP).

No motor deficits were present in cases 1, 2 and 3. The neurological examination carried out at the time of admission was not

relevant in cases 1 and 2. Cognitive impairment in case 3 was considered consistent with AGD. Mild motor deficits were present in case 4. Two falls in the last 3 months was the only additional complaint in this patient. However, the neurological examination disclosed, in addition to memory loss and cognitive impairment, slow saccadic eye movements and slight tremor in the upper extremities, as well as certain loss of stability. Motor symptoms and signs we considered the consequence of PSP-like pathology. Finally, neurological deficits and neuropathological findings in case 5 were typical of PSP.

Together, these observations point to early involvement in the caudate/putamen in cases with PSP-like pathology, followed by globus pallidus/subthalamus and selected nuclei of the brain stem. It may be postulated that clinical symptoms appear as the intensity of lesions increase in these regions from a determinate threshold in a particular individual. Yet it is noteworthy that mild or moderate lesions in the caudate/putamen, even associated with mild tau pathology in the globus pallidus/subthalamus and selected nuclei of the brain stem, are not accompanied by significant clinical deficits, at least those discriminated in the current clinical practice.

Interestingly, midbrain hypometabolism has been identified as an early diagnostic sign in PSP (32), and dopaminergic dysfunction has been characterized in subclinical familial PSP (45). More pertinent in the present context is the observation of early striatal abnormalities in nonaffected individuals in a large kindred with autosomal dominant PSP linked to 1q31.1, as revealed by 18F-dopa and 18-fluorodeoxyglucose positron emission tomography (15, 37, 40). Together, neuropathological and imaging data point to the caudate/putamen as the initial vulnerable region in PSP, followed by brain stem and globus pallidus/subthalamus.

Accumulation of phospho-tau in neurons and astrocytes occurred in cases consistent with early stages of PSP-like pathology, whereas coiled bodies in oligodendrocytes were rarely seen.

Moreover, abnormal astrocytes rarely had the morphology of tufted astrocytes. Early astrocytic lesions were rather characterized by fine tau-immunoreactive networks and tau-immunoreactive astrocytes. Tufted astrocytes were absent in case 1, exceptional or very rare in cases 2 and 3, and occasional in case 4. On the one hand, these findings suggest that tufted astrocytes and coiled bodies appear later in the course of the disease. On the other, these observations also indicate that astrocytes are early targets of abnormal tau phosphorylation in the caudate and putamen in cases with early PSP-like pathology. These observations are in line with previous studies suggesting that tau accumulation (and pathology) in astrocytes is a degenerative rather than a reactive process in PSP (47).

Previous studies have shown increased lipid peroxidation, as revealed by increased tissue levels of MDAL and HNE in the subthalamic nucleus, midbrain and superior frontal cortex in PSP brains (1, 2, 30, 34). Moreover, the activity of antioxidant systems such as superoxide dismutase and reduced glutathione is increased in multiple brain regions of PSP with reactive gliosis (13). Finally, stress-related proteins, as stress-activated protein kinase (SAPK/JNK) and p38SAPK, are activated and expressed in neurons and glial cells in PSP (3, 17). In line with these findings, evidence of oxidative stress damage was also observed in the amygdala (selected as a vulnerable region in AGD) and striatum (selected as a susceptible region in cases with PSP-like pathology). Single gel electrophoresis and western blotting showed increased lipoxidative and glycoxidative damage in diseased cases when compared with controls. Changes were observed in the amygdala and striatum thus showing that oxidative damage affects regions vulnerable to AGD and PSP-vulnerable regions as well.

2D gel electrophoresis, western blotting, in gel digestion and mass spectrometry revealed GFAP as a major target of oxidative damage in the striatum in conventional PSP and in the two cases with PSP-like pathology. GFAP was also oxidized in the amygdala in AGD associated with conventional PSP and in one case (case 3) with PSP-like pathology. GFAP has been found modified by oxidation in AD (27, 35) and Pick's disease (33). GFAP oxidation has also been reported in conditions not associated with tau pathology as in aceruloplasminemia (25) and diabetic retina (5). Whether GFAP oxidation is the result of phospho-tau deposition or an unrelated event in astrocytes associated with PSP-like pathology is not solved.

Oxidative damage to GFAP is associated with increased expression of GFAP, as revealed with western blotting and with increased astrogliosis as shown by immunohistochemistry. The present findings further support the concept of early involvement of astrocytes (increased numbers, increased GFAP levels and increased astrogliosis (increased numbers, increased GFAP levels and increased astrogliosis tau phosphorylation), and of GFAP as a target of oxidative damage in cases with PSP-like pathology.

ACKNOWLEDGMENTS

This work was funded by grants from the Spanish Ministry of Health, Instituto de Salud Carlos III (PI040184 and PI05/1570), and supported by the European Commission under the Sixth Framework Program (BrainNet Europe II, LSHM-CT-2004-503039). We thank B. Puig for criticism and suggestions, and T. Yohannan for editorial help.

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SUPPLEMENTARY MATERIAL

The following supplementary material is available for this article:

Figure 1S. Case 1: GFAP (A) and AT8 (B–D) immunoreactivity in the caudate (A,B), globus pallidus (C) and subthalamic nucleus (D). Moderate gliosis is observed in the caudate together with phosphor-tau accumulation in neurons and glial cells. Only rare neurons are immunoreactive with the AT8 antibody in the globus pallidus and subthalamus. Paraffin section slightly counterstained with haematoxylin. A, bar = 50 μ m; B–D, bar in D = 50 μ m.

Figure 2S. Case 2: AT8 immunoreactivity in the caudate (A), amygdala (B), CA1 region of the hippocampus (C) and dentate gyrus (D). Tau immunoreactivity is observed in astrocytes and in neurons in every region. In addition, grains are clearly visible in CA1. Paraffin section slightly counterstained with haematoxylin. Bar = 25 μ m.

Figure 3S. Case 3: AT8 immunoreactivity in the putamen (A), caudate (B), amygdala (C), CA1 region of the hippocampus (D), dentate gyrus (E), nucleus basalis of Meynert (F), ventral pons (G), midbrain (H), ceruleus (I) and gyrus cinguli (J). Tau immunoreactivity is observed in astrocytes and in neurons in every region. Note grains in the CA1 region and amygdala. Rare tufted astrocytes are seen in the caudate (A) and midbrain (H). Paraffin section slightly counterstained with haematoxylin. Bar = 25 μ m.

Figure 4S. Case 5: AT8 immunoreactivity in the putamen (A), amygdala (B), globus pallidus (C), dorsomedial nucleus of the thalamus (D), subthalamus (E), superior colliculus (F), ventral pons (G), frontal cortex (H) and CA1 region of the hippocampus. Paraffin section slightly counterstained with haematoxylin. A–G, I, bar in I = 25 μ m; C, E, H, bar in H = 50 μ m.

Table 1S. Summary of neuropathological findings in case 1. AGD classification: early stage 2. AD classification: ADI; no β -amyloid deposition

Table 2S. Summary of neuropathological findings in case 2. AGD classification: stage 2. AD classification: ADI; no β -amyloid deposition

Table 3S. Summary of neuropathological findings in case 3. AGD classification: stage 3. AD classification: ADIIA

Table 4S. Summary of neuropathological findings in case 4. AGD classification: stage 3. AD classification: ADI; no β -amyloid deposition

Table 5S. Summary of neuropathological findings in case 5. AGD classification: stage 3. No β -amyloid deposition

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Discussió

1-Sensibilitat del teixit cerebral humà als factors postmortem

1.1- Degradació de proteïnes

La utilització de teixit cerebral postmortem humà va lligada de manera inevitable a condicions de treball sub-òptimes. Això es deu principalment a l'interval de temps entre la necròpsia i la congel·lació del cervell, així com a la temperatura a la que es troba el cervell durant aquest interval.

Els efectes d'aquests factors ja fa més de 30 anys que es van plantejar i començar a estudiar (Kosik 1982), però la majoria dels estudis realitzats (resistència al postmortem de la seva estructura, activitat o modificacions post-traduccionals), fins la moment de la realització dels nostres experiments s'han dut a terme sobre proteïnes concretes i moltes vegades en models animals (Fountoulakis, 2001).

Per aquesta raó, el nostre disseny experimental va consistir en:

- 1- Sotmetre teixit cerebral (de l'escorça frontal) que ja de per si teni un postmortem molt curt (al voltant de les 2 hores) a diferents condicions de temperatura (1°C, 4°C i temperatura ambient) i durant diferents intervals de temps (2, 5, 8, 23 i 50 hores).
- 2- A partir d'aquí, per una banda es va seleccionar una sèrie de proteïnes (proteïnes sinàptiques, cinases, receptors de factors de creixement, del citosquelet, de membrana; així com proteïnes relacionades amb l'estrès oxidatiu, amb vies apoptòtiques o amb el sistema proteosomal) per tal d'estudiar la seva sensibilitat al postmortem. I, per altra banda, es va dur a terme un anàlisi més general mitjançant gels bidimensionals per tal d'analitzar el comportament de les proteïnes del cervell a "grosso modo".

Les dues aproximacions ens van portar a concloure la mateixa idea ja descrita anteriorment per altres autors (Hilbig et al., (Li et al., 1996), (Schwab et al., 1994), (Irving et al., 1997): a una determinada temperatura cada proteïna resisteix a la seva manera particular l'interval postmortem. Algunes són molt sensibles i es degraden ràpidament com l'alfa-sinucleïna, mentre que d'altres resisteixen fins al màxim de temps estudiat, com la 14-3-3. A nivell pràctic, això

implica que quan es treballa amb aquest tipus de material, és recomanable analitzar prèviament resistència de la proteïna d'interès al postmortem per descartar la possibilitat que es tracti d'una proteïna sensible a les poques hores. Depenent dels resultats l'investigador es pot permetre uns temps postmortem de les seves mostres o bé uns altres.

La temperatura també és un factor rellevant en la preservació de les proteïnes. Les condicions de menor temperatura, en el nostre cas 1°C, va acompanyada d'una menor degradació, on proteïnes especialment vulnerables, com la sinucleïna, es mantenen constants durant els intervals analitzats. Tenint en compte que la preservació del cos es produirà en el millor dels casos a 4°C i mai o quasi a 1°C, és esperable que la nostra mostra haurà estat subjecte a la degradació.

Posteriorment als nostres estudis sobre la degradació de les proteïnes n'han sorgit d'altres en la mateixa línia. Amb una aproximació similar, mitjançant gels bidimensionals però utilitzant mètodes amb més possibilitats de quantificació (DIGEs), es van identificar altres proteïnes sensibles al postmortem artificial (Crecelius et al 2008). A més de parar atenció a les proteïnes que disminueixen o que es mantenen, també es van llistar proteïnes que augmentaven la seva presència. El perquè hi ha augment de determinades proteïnes amb el temps postmortem és un enigma; però es podria deure a la creació de formes truncades, a un augment de síntesi o bé a una disminució de l'eliminació normal d'aquestes proteïnes.

A més de la degradació proteïca, altres estudis estant tractant la degradació de l'ADN o de l'ARN en les mostres postmortem preservades de diferent manera (incloses en parafina o congelades). A més, també s'ha estudiat la sensibilitat al temps postmortem de les principals modificacions epigenètiques de l'ADN: la metil·lació de CpGs, i l'acetil·lació d'histones.

1.2- Fosforil·lació i truncatge de la proteïna tau

En un segon estudi ens vam marcar l'objectiu d'estudiar els efectes del temps postmortem sobre una proteïna concreta de gran importància en la malaltia d'Alzheimer, la proteïna tau. En aquest cas, estàvem més interessats en

dos aspectes post-traduccionals de suma importància tant en MA com en altres taupaties, descrits en aquesta proteïna: la fosforil·lació i el truncatge. La fosforil·lació, però, està molt més estudiada que el truncatge.

Les fraccions enriquides en filaments de tau, de les mostres d'escorça frontal de malalts d'Alzheimer, sotmeses al postmortem artificial van mostrar que el triplet de tau hiperfosforil·lada pateix una modificació apreciable amb l'aparició d'una nova banda, de pes molt semblant, en algun moment entre les 6 i les 24 hores de postmortem. Aquesta banda podria ser resultat de l'acció de fosfatases endògenes, i posa de manifest que la fosforil·lació de les proteïnes és un fenomen sensible a l'interval entre la mort i la congelació. De totes maneres, la hiperfosforil·lació de tau en MA resulta ser més resistent que la fosforil·lació de la tau normal (la qual s'ha descrit que es desfosforil·la en qüestió de minuts després de la mort (Sorimachi et al. 1996)).

Els anticossos fabricats per reconèixer proteïna tau sovint detecten altres bandes de menor pes molecular. La naturalesa d'aquestes bandes no es coneix però s'hipotetitza que es podria tractar de fragments de tau. El model experimental anterior ens indica que les bandes de baix pes molecular, siguin o no fragments de proteïna tau, no són producte de la degradació postmortem pel fet que el patró de bandes baixes es troba present des del primer punt analitzat amb el menor temps postmortem possible.

1.3- Estrès oxidatiu i localització cel·lular

Altres estudis publicats s'han centrat en la preservació d'altres tipus de modificacions proteïques, presents a les malalties neurodegeneratives, com són les modificacions per estrès oxidatiu. La detecció d'adductes de lipo i glicoxidació en les proteïnes com MDAL, HNE, CEL o CML s'ha observat que es manté constant al llarg del postmortem artificial fins a les 8 hores. Al voltant de les 20 hores, algunes bandes augmenten i d'altres disminueixen. Això sembla indicar que durant el postmortem algunes proteïnes continuen essent oxidades mentre d'altres són degradades (Ferrer et al., 2008).

Per últim, les condicions de postmortem poden afectar la localització cel·lular de les proteïnes. En particular s'ha observat que factors de transcripció

que es troben en el nucli quan es fa una biòpsia de teixit (com c-fos, jun i factors de transcripció de la família Sp) , es troben en el citoplasma quan s'observen en el teixit postmortem (MacGibbon et al., 1997), (Boutillier et al., 2007).

Aquests tipus d'estudis tenen especial importància en bancs de teixit, on es dipositen i preserven mostres de cervell que han de servir per la recerca. És important que els protocols s'estandaritzin entre els diferents hospitals i bancs. La qüestió radica en identificar les limitacions que presenta la recerca amb aquest tipus de mostra i com, en alguns casos, es poden millorar les pràctiques per fer recular el màxim possible aquestes limitacions. És també rellevant la delimitació de l'efecte del postmortem en les diferents tècniques de preservació (congel·lació, parafina, etc) per tal de fer una correcta comparació dels experiments. Pot passar que un increment d'expressió observat en immunohistoquímica no s'observi per Western Blot pel fet que determinada proteïna es preserva de manera diferent en una mostra parafinada o congel·lada.

En algun grau o altre, la degradació de proteïnes sempre serà present en la recerca en malalties neurodegeneratives, perquè els factors pre-, peri- i postmortem es poden controlar només fins a cert punt. Mentre es fan aquest tipus d'estudi per tal acotar aquest problema, altres investigadors busquen possibilitats d'estudi alternatives. Una d'elles és, per exemple, estudiar la microglia, un factor important en la neuroinflamació present en la MA, a partir de les seves cèl·lules precursors de la sang, els monòcits de cada individu. Allunyant-se una mica del cervell, sortegen el problema de la degradació (Hamacher et al., 2007).

2- Tau en MGA, PSP i MA

2.1- Bandes de baix pes molecular

Un dels aspectes que vam voler analitzar en el nostre estudi és el patró per Western blot de la proteïna tau en les fraccions sarkosyl-insolubles (ens referim a la mateixa fracció que l'anomenem fracció enriquida en PHFs). Una de les preguntes que volíem resoldre, una vegada observat el fet que les bandes baixes de tau no semblen producte de la degradació post-mortem, era si aquest patró era igual entre totes les taupaties o, per contra, era específic de cada

malaltia. En aquests experiments es va incloure la MGA, que és una taupatia que acapara relativament poca atenció, encara que explica al voltant del 5% dels casos de demència i apareix molt freqüentment en combinació amb altres malalties neurodegeneratives.

Són molt pocs els estudis sobre el patró de bandes baixes de tau. En un d'ells, els autors proposaven que la taupatia 4R PSP es podia diferenciar de la també taupatia 4R DCB per la presència d'una banda forta a 37KDa en la PSP, i un doblet a 42KDa en la DCB (Arai et al., 2001, Arai et al., 2004). Un estudi posterior realitzat en el nostre grup va mostrar que tant la banda de 37KDa com el doblet de 42KDa estaven presents també en la PSP (Puig et al., 2005). En MGA es mostren però no es descriuen (Tolnay et al., 2002).

L'estudi del patró de bandes baixes de la MGA mostra que el patró resultant és molt similar al d'altres taupaties 4R com la PSP, la DCB i algunes DFTP-17. En canvi, el patró difereix del que es troba en la MA, on tant isoformes 3R com 4R es troben fosforil·lades. En el cas del malalt que presentem que patia al mateix temps MA i MGA, el patró és molt similar al de la MA.

En el conjunt dels treballs que presentem aquí en tres malalties diferents (MA, PSP i MGA) on s'han estudiat els patrons complets de tau, i d'altres reportats en la literatura, sembla que el patró de bandes baixes depèn en gran mesura de les isoformes que es veuen hiperfosforil·lades. Altres estudis realitzats pel nostre grup, però que no es presenten en aquesta tesi sobre DFTP-17 de tipus 4R donen el mateix patró que la resta de taupaties 4R, cosa que reforça la hipotesi que el patró de bandes baixes depèn de les isoformes hiperfosforil·lades.

A partir dels resultats obtinguts en el treball en MA, on estudiàvem el possible efecte del postmortem en la presència de bandes baixes, també podem afirmar que la regió de la proteïna cap on està dirigit cada anticòs també és un aspecte rellevant en el tipus de patró de bandes baixes que apareix. Com més cap al domini C-terminal està dirigit l'anticòs, major nombre de bandes baixes es reconeixen i també de menor pes molecular. Aquest resultat suggereix que aquestes bandes més baixes corresponen a fragments C-terminals de la proteïna.

2.2 Estudi de l'expressió de proteases de tau

Com dèiem a la introducció, la trombina és una proteasa que s'expressa al cervell i és capaç de tallar la proteïna tau. En els nostres experiments hem confirmat que s'acumula en els cabdells neurofibril·lars en diferents taupaties (incloent la MA i el cossos de Pick a la MPi) i vam voler comprovar si també ho feia en els grans argiròfils, i en les estructures pre-cabdell, característics de la MGA. També vam estudiar l'associació d'aquestes estructures amb altres proteases amb l'habilitat de tallar la tau, com la caspasa-3 o la calpaïna-2.

El resultat va ser que, mentre la trombina sí que es trobava present en els grans argiròfils i en els pre-cabdells, la calpaïna-2 i la caspasa-3 no. Aquestes últimes es trobaven present en el cabdells neurofibril·lars madurs, però no en els pre-cabdells ni als grans argiròfils. Per tant, si alguna proteasa pot ser candidata a tallar la tau *in vivo* en estadis primerencs de la formació de les inclusions i també en els grans, una d'elles pot ser la trombina.

Per altra banda, igual que ocorre en els cabdells ja formats, a la MPi hem trobat la caspasa-3 present en els cossos de Pick, la qual cosa suggereix la possibilitat de que aquesta proteasa estigui digerint la tau en aquestes inclusions.

3- Factors de transcripció en inclusions de tau

Els factors de transcripció són proteïnes que poden regular l'expressió de determinats gens unint-se a seqüències específiques dels seus promotors. Sovint, l'activació d'aquests factors de transcripció succeeix al citoplasma i posteriorment hi ha una translocació al nucli on finalment realitzen la seva funció. Algunes inclusions proteïques en diferents malalties neurodegeneratives atrapen factors de transcripció en el lloc de la inclusió, la qual cosa podem pensar que tindrà un efecte en la regulació dels gens que controla el factor de transcripció atrapat.

3.1 Sp1

Un exemple de l'efecte del segrest de factors de transcripció sobre l'expressió gènica el trobem en un experiment en cultiu cel·lular on s'estudia l'expressió de la proteïna huntingtina mutada, causant de les inclusions intranuclears de la malaltia de Huntington (DiFiglia et al., 1997). En aquest experiment *in vitro* s'observa que la huntingtina mutada efectivament segresta l'Sp1, i aquest ja no es pot unir al promotor del gen de NGFR (Nerve Growth Factor Receptor) suprimint així la seva expressió (Li et al., 2002).

Els nostres resultats mostren que, mitjançant immunohistoquímica i immunofluorescència, Sp1 es troba també a les inclusions intracitoplasmàtiques de tau a la MA, PSP i MPi, però no en les inclusions de sinucleïna de les sinucleïnopaties estudiades. Els efectes del segrest d'Sp1 observat en les cèl·lules que contenen inclusions encara són desconeguts. Però una possibilitat que es pot contemplar és el descontrol de l'expressió de proteïnes regulades per Sp1 entre les que poden tenir especial rellevància l'APP (Docagne et al., 2004), BACE 1 i 2 (Sun et al., 2005), tau (Heicklen-Klein and Ginzburg, 2000), caspasa-3 (Liu et al., 2002), IL-1beta (involucrades totes elles en la MA) o proteïnes relacionades amb la defensa contra l'estrès oxidatiu com la SOD-2 (Xu et al., 2002). De totes maneres, existeixen moltes altres proteïnes amb caixes Sp1 en els seus promotors, de manera que és difícil de saber la magnitud del dany que pot produir l'absència d'Sp1 al nucli quan se'l necessita. De fet, degut a la diversitat d'observacions sobre el seu efecte en diferents models, no hi ha consens en si es podria considerar l'Sp1 una diana terapèutica amb l'objectiu d'estimular-lo o d'inhibir-lo.

En el nostre estudi també vam tractar d'observar variacions en l'expressió d'Sp1 en els cervells de pacients de MA comparats amb els controls. Segons la nostra experiència, els nivells d'Sp1 eren similars en tots els casos. Posteriorment s'ha publicat que els nivells d'expressió a nivell de ARN missatger d'Sp1 són superiors en els cervells de malalts de MA comparats amb els controls; així com els dels cervells de ratolins transgènics per PSEN1 i/o APP comparats amb els Wt; en els ratolins la variació es descriu també a nivell de proteïna (Citron et al., 2008). El motiu d'aquesta discrepància no està clar i

caldran més experiments en aquest sentit per establir si els nivells d'Sp1 varien o no en la MA.

Finalment, un estudi recent es fixa en l'expressió en cervell de malalts de MA d'altres membres de la família Sp, com són Sp3 i Sp4. Els autors observen un forta presència d'aquests dos factors en els dipòsits de tau, igual que Sp1, i a més, un fort augment de la seva expressió (Boutillier et al., 2007). Els membres de la família Sp reconeixen el mateix motiu d'ADN i competeixen per la regulació dels gens diana. Tenint en compte això i que els factors de transcripció Sp regulen cadascú a la seva manera l'expressió gènica, és molt rellevant el ratio d'expressió d'uns respecte els altres (Li et al., 2004); però fa igualment molt difícil de predir l'efecte global sobre l'expressió gènica.

3.2 *c-Fos, c-Jun, ATF2 i CREB*

Quan s'estudia mitjançant tècniques d'immunohistiquímica la presència de proteïnes en inclusions de tau hiperfosforil·lada, especialment quan l'estudi es fa amb anticossos contra epítops fosforil·lats, és molt important descartar en la mesura possible la reacció creuada de l'anticos amb els múltiples epítops fosforil·lats de la pròpia tau. El què fem en aquests casos és provar els anticossos per Western blot sobre fraccions enriquides en filaments de tau de diferents taupaties i observar si l'anticos reconeix el patró de bandes de tau, a més de la banda pròpia de la proteïna. En el cas de l'anticos contra ATF2 fosforil·lat això és exactament el què vam observar, de manera que la presència d'ATF2 fosforil·lat a les inclusions de la MPI és probablement un artefacte, sobretot si tenim en compte que l'anticos contra ATF2 no fosforil·lat no tenyeix les inclusions.

En un estudi molt similar al de l'apartat anterior, a la MPI hem observat un augment d'expressió tant de *c-Fos*, com de *c-Jun*, *ATF2* i *CREB*. Aquesta sobreexpressió s'observa tant a l'escorça frontal com a l'hipocamp. Es ben conegut que la fosforil·lació juga un paper fonamental en l'activació d'aquests factors, i per això es van utilitzar anticossos contra les seves formes fosforil·lades i actives. El resultat va ser que els nuclis d'aquestes regions estudiades mostraven un augment de les formes fosforil·lades de *c-Fos*, *c-Jun* i

CREB. A més, c-Fos i ATF2 fosforil·lat es van trobar a l'interior dels cossos de Pick en colocalització amb la tau hiperfosforil·lada.

A priori es relaciona c-Jun amb mort neuronal per apoptosi, via l'alliberació del citocrom C o a través del control de l'expressió del gen del Fas-L (Kasibhatla et al., 1998, Ham et al., 2000). Els nostres resultats però, també mostren que aquest increment respecte els casos control es presenten tant en zones amb mort neuronal (l'escorça frontal), com en poblacions neuronals que tot i presentar patologia de tau (cossos de Pick) resisteixen i sobreviuen (les cèl·lules granulars del gir dentat de l'hipocamp). Es fa doncs complicat establir una relació directa entre l'activació i increment d'aquests factors i les respostes de supervivència o mort neuronal.

Estudis previs realitzats en el nostre laboratori havien mostrat que c-Jun i CREB s'expressaven de manera diferencial en models en rata d'excitotoxicitat per àcid kaínic (Ferrer et al. 2002). A l'escorça entorrinal, on les cèl·lules moren per l'acció del kaínic, hi havia una forta expressió de c-Jun fosforil·lat però no de CREB. Però de manera similar als resultats obtinguts ara en la MPi, c-Jun també es trobava augmentat en les cèl·lules del gir dentat, que si sobreviuen a la matança provocada per l'àcid kaínic (Ferrer et al., 2002). Els presents resultats en la MPi confirmen que la fosforil·lació de c-Jun no ha d'estar relacionada per força amb la mort neuronal. En el model de rata, CREB fosforil·lat es veia disminuït a l'escorça entorrinal i no variava els seus nivells en el gir dentat. En cervells de malalts de la malaltia de Creutzfeldt-Jakob, CREB també es troba disminuït, però a nivell d'expressió total, no només de CREB fosforil·lat (Rodríguez and Ferrer, 2007). A partir d'aquests treballs sembla que la disminució de CREB fosforil·lat es produeix en zones afectades amb mort neuronal i que en les resistents, o no varia o augmenta la seva expressió. En aquestes regions resistents de l'hipocamp CREB fosforil·lat augmenta els seus nivells en resposta a la hipòxia (Walton and Dragunow, 2000). Es podria pensar que el fet de trobar CREB fosforil·lat augmentat en MPi també a l'escorça frontal pot tenir relació amb el nivell d'afectació. En estadis tardans de malalties com el Creutzfeldt-Jakob de l'estudi citat, la disminució de CREB fosforil·lat podria explicar-se com a un esgotament de la resposta anti-apoptòtica o anti-excitotòxica protagonitzada per aquest factor de transcripció.

4- Aspectes patològics de la MGA

La revisió de la taupatia MGA ha inclòs experiments originals que han aportat noves dades sobre l'estrès oxidatiu, els patrons de bandes de tau, i la presència de p62, UBB+1, cinases i proteases a les inclusions; així com una proposta d'estadiatge de la malaltia i un paradigma integrador dels aspectes patogènics centrat en l'estrès oxidatiu, el segrestosoma (p62/UBB) i el truncatge de tau.

En resum, l'edat avançada, l'estrès oxidatiu i l'activació de cinases de tau com la GSK3-beta comporten un augment de la hiperfosforil·lació de tau. Aquesta s'associa a la p62 i a la UBB formant les inclusions patològiques en forma de cabdells, pre-cabdells i grans argiròfils. Paral·lelament, l'activació de proteases com la trombina tallen la tau tot formant fragments que participen també en la formació dels agregats i en augmentar l'estrès oxidatiu. A més, la presència de UBB+1 saturaria la capacitat del proteosoma de degradar la tau fosforil·lada i pre-agregada, participant també en la formació de les inclusions.

Cal dir que aquesta paradigma podria ser aplicable a altres taupaties donat el fet que l'edat, l'estrès oxidatiu i l'activació de cinases i proteases és un fenomen no exclusiu de la MGA. Per què en cada taupatia es fosforil·len unes isoformes específiques, es formen inclusions específiques, seguint uns estadiatges i unes regions diferents, és encara un misteri.

5- LRRK2 en taupaties

Entre els possibles components de les inclusions de tau n'hi ha un que és especialment interessant, l'Lrrk2. Aquesta proteïna acapara l'atenció desde que es va descobrir, pel fet que pot estar darrera de mecanismes comuns de neurodegeneració tant de sinucleïnopaties com de taupaties (Mata et al., 2006), tal i com s'ha comentat a la introducció.

El nostre objectiu va ser el de revisar tots els treballs on s'hagués estudiat la presència de Lrrk2 en les inclusions tant de sinucleïna com de tau, atès que existia una controvèrsia molt forta sobre aquest tema propiciada per l'obtenció de resultats diferents en funció dels anticossos utilitzats.

En la revisió presentem una sèrie d'experiments originals que inclouen la utilització de quatre anticossos comercials dirigits contra diferents epítops de la proteïna. Els anticossos es van utilitzar tant per anàlisi immunohistoquímica de diferents sinucleïnopaties i taupaties, com per Western blot en extractes de cultius cel·lulars (de tres línies diferents), o en homogenats totals i fraccions sarkosil-insolubles de diferents taupaties.

Els resultats obtinguts són consistents amb els obtinguts per la resta d'autors. *I.e.* els anticossos NB-300-268 i NB-300-267, dirigits contra epítops C-terminal i N-terminal respectivament, van ser els únics capaços de marcar les inclusions tant de sinucleïnopaties com de taupaties. En el grup de taupaties vam afegir la MGA, que no havia estat estudiada, i es va veure que aquests anticossos també marcaven els grans argiròfils. Per contra, l'anticòs AP7099b, dirigit contra epítops més interns de la proteïna i que havia estat descrit com un dels més específics (Giasson et al., 2006), no va ser capaç de marcar cap tipus d'inclusió.

Una de les hipòtesis que suggereixen alguns autors és que les inclusions estan enriquides en formes truncades de Lrrk2, o bé que els epítops interns queden emmascarats (Higashi et al., 2007). En el nostre cas però, vam utilitzar un anticòs que reconeix un epítop C-terminal molt proper al del l'anticòs NB-300-268, que tampoc va ser capaç de marcar cap inclusió.

Vist que tots aquests anticossos en major o menor grau detecten bandes addicionals a la de Lrrk2 sencera en Western blot, cal plantejar-se la possibilitat que els anticossos que tenyeixen les inclusions siguin inespecífics. Aquesta revisió té la intenció de servir de punt de partida pels propers anàlisis immunohistoquímics que es realitzin, coneixent quins han estat els resultats obtinguts fins ara, amb quines tècniques, amb quins protocols i sobretot, amb quins anticossos.

6- Estrés oxidatiu

Tal i com comentàvem a la introducció, sembla prou consistent l'afirmació de que l'estrés oxidatiu es troba incrementat en diferents malalties neurodegeneratives, i aquest increment s'observa amb diferents marcadors (de

glicooxidació, de lipoxidació, nitrotirosines o modificacions dels àcids nucleics). En els nostres estudis ens hem centrat en el dany oxidatiu que pateixen les proteïnes amb un objectiu: identificar quines proteïnes estan més oxidades en la patologia respecte les mostres que provenen de persones control. L'oxidació d'una proteïna pot afectar la seva activitat, de manera que identificar les proteïnes diana ens pot donar pistes per identificar les vies susceptibles o perjudicades a la malaltia.

6.1- Proteïnes oxidades en inclusions de tau a la MA

Un dels possibles efectes de l'adhesió d'adductes d'oxidació a les proteïnes és el de fer-les susceptibles a l'agregació (Garrison et al., 1962, Davies, 2001). En la MA s'acumula la tau hiperfosforilada a l'interior d'algunes neurones formant els cabdells neurofibril·lars. La nostra idea va ser intentar identificar proteïnes oxidades que poguessin estar atrapades en aquests cabdells de tau.

Per estudiar això vam realitzar el mateix protocol per tal d'enriquir en filaments de tau en fraccions sarkosil-insolubles, principal component dels cabdells neurofibril·lars, i provar diferents marcadors d'estrés (CML, CEL, HNE i MDAL) en gels monodimensionals. D'aquesta manera vam identificar dues bandes comparativament més oxidades en malalts d'Alzheimer, que mitjançant gels bidimensionals vam relacionar amb dues isoformes de la família de proteïnes 14-3-3 (la gamma i la zeta). Aquestes apareixien modificades tant per CEL com per MDAL (glico i lipoxidació, respectivament), però no per altres modificacions com CML o HNE.

Un cop realitzat aquest estudi, vam creure interessant saber si aquestes formes de 14-3-3 estaven situades en els cabdells quan s'analitzava mitjançant immunohistoquímica. Aquest aspecte ja havia estat estudiat per altres autors, com es comentava a la introducció, que havien trobat diferents isoformes i amb diferents anticossos, una col·localització amb la tau en les inclusions en la MA (Layfield et al., 1996, Umahara et al., 2004b); així com en els cossos de Pick a la MPi (Umahara et al., 2004a). Per contra, el nostre propi anàlisi immunohistoquímic convencional o amb immunofluorescència realitzat amb dos anticossos contra diferents epítops de 14-3-3 va mostrar només marcatge al citosol de les neurones, i no en els cabdells neurofibril·lars. Aquests dos

anticossos no presentaven gens ni mica de reactivitat creuada amb la tau quan es van provar en Western blot. No podem assegurar el mateix dels anticossos emprats pels dos equips anteriorment citats. La presència o no d'aquestes isoformes de 14-3-3 en les inclusions de tau, i l'origen de les discrepàncies al respecte, requerirà aprofundir més en aquest estudi.

La possibilitat que la 14-3-3 (la forma zeta en especial) estigui present pot basar-se en diverses observacions, principalment: que les isoformes zeta i beta de 14-3-3 poden interactuar amb la tau en extracte de cervell (Hashiguchi et al., 2000); que la 14-3-3 pot mantenir activa la forma inactiva d'una de les principals cinases de tau, la GSK3-beta (Yuan et al., 2004); que és capaç també de interaccionar simultàniament amb la GSK3-beta i la tau (Agarwal-Mawal et al., 2003); i que és capaç de promoure la fosforil·lació de tau estimul·lant la proteïna cinasa dependent d'AMPc (Hashiguchi et al., 2000). A més, també s'ha vist que la 14-3-3 zeta és capaç, *in vitro*, de facilitar l'agregació de la tau (Hernandez et al., 2004).

De totes maneres, tot i que les cinases amb les que la 14-3-3 pot interactuar es troben en els cabdells de tau i que tots aquests processos descrits fins ara recolzen la presència de 14-3-3 en el seu interior, res no impedeix suggerir que aquests mateixos processos es podrien estar produint fora dels cabdell o fins i tot abans de la seva formació.

Tornant a l'objectiu del nostre treball, la 14-3-3, estigui o no en els cabdells neurofibril·lars, apareix oxidada en les fraccions sarkosyl-insolubles. Per veure si aquesta oxidació afectava només a la 14-3-3 present en aquesta fracció o a tota la citosòlica, vam repetir l'experiment però utilitzant homogenats totals. Els nivells d'oxidació de 14-3-3 en aquesta fracció total eren indetectables amb CEL i pràcticament indistingibles dels controls, amb MDAL. Així doncs, tant si és perquè un cop oxidada s'associa als filaments de tau, o perquè forma altres agregats o conformacions més insolubles, la 14-3-3 (zeta i gamma) es troba més oxidada en la fracció sarkosyl-insoluble en la MA.

Poc abans de l'inici del nostre estudi, s'havia identificat la proteïna 14-3-3 zeta com una de les quatre proteïnes significativament oxidades en neurones després del tractament *in vitro* amb pèptid amiloide (Sultana et al., 2006). La 14-

3-3 zeta també apareix oxidada en sinaptosomes aïllats i tractats amb pèptid amiloide (Boyd-Kimball et al., 2005a), així com a l'hipocamp d'un model de rata al qual es realitza una injecció intracerebral del mateix pèptid (Boyd-Kimball et al., 2005b). Finalment, la 14-3-3 gamma s'ha trobat nitrada en estadis intermitjos de MA (III i IV de Braak i Braak) (Sultana et al., 2007). Realment, l'oxidació d'aquestes isoformes de 14-3-3 sembla estretament lligada a la presència d'amiloide, per això vam estudiar l'oxidació d'aquestes proteïnes en una malaltia que presenta acumul·lació d'amiloide però no de tau: l'angiopatia amiloidea (AAC). En el cas d'aquesta malaltia la 14-3-3 es va trobar oxidada per CEL només a les fraccions sarkosil-insolubles, mentre que amb MDAL també es trobava oxidada en les fraccions totals. Pel què fa a la glicooxidació per CEL, tan en la MA com en AAC, la 14-3-3 només queda marcada en les fraccions sarkosil insolubles, indicant que aquesta proteïna pateix un canvi de solubilitat que no ha de tenir res a veure amb els acúmuls de tau, els quals estan totalment absents en els casos de AAC.

En el transcurs de posteriors estudis sobre marcadors d'estrès oxidatiu, el nostre equip ha trobat moltes vegades un gran variabilitat entre els nivells d'oxidació dels casos control, que no només s'explica per les diferències d'edat. La tan subtil diferència entre els controls i el casos de MA en els nivells de MDAL dels homogenats totals ens van fer replantejar la possibilitat d'augmentar molt més el nombre de casos per establir més correctament aquest aspecte particular del treball. L'experiment va mostrar nivells similars d'expressió tant de MDAL com de la pròpia 14-3-3, la qual cosa va invalidar la nostra conclusió sobre els majors nivells d'oxidació per MDAL als homogenats totals. Es va advertir a la revista i l'article es va retirar. El fet que els nivells de 14-3-3 zeta siguin similar als controls a la MA contrasta amb certs treballs publicats que presenten una sobreexpressió de 14-3-3 zeta a nivell de transcripció (Soulie et al., 2004). També s'ha vist que les isoformes gamma i epsilon (Fountoulakis et al., 1999) estan més presents en regions afectades per tau en cervells de MA.

6.2- Estrés en estadis primerencs de malalties neurodegeneratives

Les malalties neurodegeneratives en estadis finals són incurables i el màxim interès es centra en identificar els canvis patològics que es produeixen

com més al principi millor de la malaltia, amb l'objectiu de millorar el diagnòstic precoç i de trobar dianes terapèutiques que l'aturin només començar.

Un dels aspectes que acapara l'atenció és la presència o no de formes d'estrès oxidatiu en etapes molt primàries de la malaltia, o en regions del cervell encara no afectades pels aspectes neuropatològics d'aquesta. Sobretot, el què a nosaltres ens interessa és la identificació de les proteïnes diana d'aquest estrès, que poden donar pistes de quines proteïnes perden la seva funció normal en les primeres etapes de cada malaltia.

Un exemple d'aquest tipus d'estudi és el que s'ha portat a terme en els darrers anys en l'espectre de sinucleinopaties que anomenem malalties amb cossos de Lewy (MP i DCL). En escorça cerebral de cervells amb MP o amb MP incidental (preclínica), on no hi ha presència de cossos de Lewy, s'han trobat ja augmentats marcadors de glicoxidació i lipoxidació, així com un increment de l'expressió del receptor d'AGEs (el RAGE) (Dalfo et al., 2005). Entre les proteïnes possiblement oxidades que s'han identificat fins al moment a l'escorça cerebral de cervells amb MP, hi ha: la pròpia alpha-sinucleïna (Dalfo and Ferrer, 2008), gamma-sinucleïna i SOD2 (Dalfo et al., 2005), SOD1 (Choi et al., 2005) i UCHL-1 (Choi et al., 2004). Recentment, s'ha trobat que un sèrie d'enzims del metabolisme energètic (aldolasa A, enolasa 1 i gliceraldehid deshidrogenasa) es troben marcats per l'adducte de lipoxidació HNE també en l'escorça frontal de MP incidental i MP (Gomez and Ferrer, 2008).

En el cas de la MA, alguns estudis s'han dedicat a analitzar els nivells d'oxidació en els cervells amb estadis intermitjos de la malaltia (III i IV de Braak i Braak), on la clínica es comença a manifestar d'una forma lleu amb discretes alteracions cognitives; estadi clínic que s'anomena MCI (de l'anglès, Mild Cognitive Impairment). Aquest estrès s'observa en forma d'un increment dels nivells d'HNE i d'un considerable llistat de proteïnes oxidades (Keller et al., 2005, Butterfield et al., 2006, Williams et al., 2006, Sultana et al., 2007). Molt recentment ha sortit el primer estudi sobre dianes proteïques d'estrès oxidatiu en estadis encara més primerencs de la malaltia (I i II de Braak i Braak). Aquest treball identifica la proteïna ATP-sintasa com a diana de lipoxidació a l'escorça entorrinal, així com una disminució de la seva activitat, amb possible conseqüències per la producció mitocondrial d'energia en aquesta primera etapa de la MA (Terni et al, 2009, en premsa).

6.2.1- Estadis primerencs de PSP

Aquí s'han presentat resultats referents a l'estrès oxidatiu en estadis primerencs de PSP, aspecte aquest que fins ara no havia estat mai analitzat. Un dels motius, és que la progressió de la PSP es coneix molt poc i no n'existeix un patró anotat com en el cas de la MA. El què se sap de l'inici de la PSP, com s'ha comentat a la introducció, prové de l'estudi d'una forma familiar autosòmica dominant de la malaltia on, mitjançant la tomografia per emissió de positrons (PET), s'ha assenyalat el caudat/putamen com el lloc que primer queda afectat, seguit del tronc i del globus pallidus/subtàlam (de Yebenes et al., 1995, Piccini et al., 2001, Ros et al., 2005).

Els nostres casos estudiats provenen d'una sèrie amb diversos estadis de MGA on s'hi va veure PSP associada. Les observacions no són, per tant, sobre casos purs de PSP i no podem afirmar que la MGA no representi un cert biaix. De tota manera, estem davant de casos inicials de PSP sense clínica rellevant.

L'estudi neuropatològic d'aquest casos es va realitzar sobre tres regions: caudat/putamen, globus pallidus/subtàlam i substància negra/ceruleus/colliculi/pons ventral. En els casos més primerencs, el caudat/putamen és el que es veia més afectat d'astrogliosi i acumulament de tau hiperfosforil·lada. En un cas més afectat, els canvis en aquesta regió eren més acusats però també es va observar l'alteració del globus pallidus/subtàlam, i també, però més lleugerament, de la tercera regió estudiada. El cas estudiat amb finalitat comparativa de PSP típica, amb tota la clínica present, mostrava afectació severa de les tres regions. Aquests resultats coincideixen en assenyalar el caudat/putamen com la primera regió afectada en la PSP, seguit del globus pallidus/subtàlam i de determinats nuclis basals. Els resultats també indiquen que el caudat/putamen pot estar afectat gliosi i de cert grau d'acumulament de tau sense presentar problemes clínics detectables en les proves habituals. A partir de quan les lesions comporten dèficits clínics no està ben establert i podria variar entre diferents individus.

Com s'ha comentat a la introducció, alguns astròcits en la PSP presenten tau hiperfosforil·lada formant inclusions de morfologia variable. També els oligodendròcits presenten acúmuls anomenats *coiled bodies*. Tant els *coiled*

bodies com un certa morfologia dels astròcits (tufted astrocytes) pràcticament es troben absents en els casos més primerencs de PSP. Aquestes lesions apareixen, per tant, més tard en el transcurs de la malaltia. Per altra banda, astròcits immunoreactius per tau hiperfosforil·lada si que es poden observar en el caudat/putamen en aquests casos més primerencs, la qual cosa suggereix que la fosforil·lació i acumulament de tau a la glia és un fenomen associat a la degeneració i no als processos reactius secundaris de la glia.

6.2.2- Gliosi i oxidació de la GFAP

En condicions normals els astròcits es dediquen al suport tròfic de les neurones, a regular els nivells extracel·lulars de glutamat, proveïr de factors tròfics i mantenir l'homeòstasi iònica; i també, com hem comentat a la introducció, ajuden a protegir de l'estrès oxidatiu. Quan parlem de gliosi, ens referim als canvis que experimenten els astròcits i la microglia. L'activació de la glia, o gliosi reactiva, és una fenomen comú en el cervell en cas de múltiples malalties o lesions. L'activació de la microglia produeix la resposta inflamatòria en el cervell. Les cèl·lules activades migren cap a la zona lesionada, proliferen i expressen factors proinflamatoris així com proteïnes del complex major d'histocompatibilitat; actuen com a cèl·lules presentadores d'antigen i es poden transformar al fenotip de cèl·lula fagocitària. L'alliberació de citoquines per la microglia com IL-1beta, TNF o TGF-beta tenen, no en exclusiva, la capacitat d'activar un astròcit. Quan parlem únicament de l'activació d'astròcits, ens referim a l'astrogliosi.

S'ha vinculat una activació desmesurada i sostinguda de la glia amb la neurodegeneració. Fins i tot, alguns autors li confereixen un paper capital en algunes malalties neurodegeneratives, a les que anomenen "gliodegeneratives" (Croisier and Graeber, 2006). aquesta activació d'astròcits està present en moltes malalties neurodegeneratives, inclosa la PSP.

Els astròcits reactius canvien la seva morfologia, la qual cosa està relacionada amb l'expressió de diferents gens. Alguns dels gens que augmenten la seva expressió en aquestes condicions tenen a veure amb els filaments intermedis, i són la GFAP (glial fibrillary acidic protein), la vimentina i la nestina

(Mucke and Eddleston, 1993). Els ratolins deficients en GFAP sembla que poden viure bé mentre no se'ls pertorbi el sistema nerviós (McCall et al., 1996), sota determinats estressors experimentals de tipus mecànic, aquests Knock Out resisteixen molt menys que els salvatges. Els filaments intermedis de GFAP tenen molta importància en mantenir mecànicament o estructuralment el sistema nerviós quan aquest rep estressors mecànics severes (Lundkvist et al., 2004, Pekny and Pekna, 2004). La funció d'aquests filaments intermedis s'està veient que va més enllà de la seva funció purament estructural i que determina estats funcionals de l'astròcit contra diversos estímuls perjudicials de tipus agut, mentre que poden perjudicar la regeneració dels sistema nerviós central si es perpetua la seva activació (Lepekhin et al., 2001, Pekny and Pekna, 2004). Altres funcions en les quals participa la GFAP són la de regular el volum dels astròcits (Ding et al., 1998) o lligar els receptors de glutamat a la membrana plasmàtica (Sullivan et al., 2007).

Els nostres resultats apunten a una tendència de la GFAP a veure's oxidada en el cervell ja en estadis primerencs de PSP. Mitjançant gels bidimensional i Western blot contra diferents marcadors d'estrès oxidatiu (CML, MDAL, AGE i CEL) es pot veure un increment d'una sèrie d'espots al voltant de 50 KDa, que la identificació per espectrometria de masses va revelar que es tractava de GFAP. Els Western monodimensional contra GFAP en diferents casos de PSP i els dos casos de PSP incidental comparats amb els controls mostra en les diferents àrees estudiades un augment dels nivells de GFAP en consonància amb els elevats nivells d'astrogliosi associats a la malaltia i observats en l'estudi neuropatològic. Els majors nivells d'oxidació que observem mitjançant Western blot sobre gels monodimensionals al pes de GFAP podrien correspondre no a un augment real d'aquests nivells sinó a un augment proporcional a l'augment d'expressió de GFAP. El Western contra CML, on s'observa la banda corresponent al pes de la GFAP en tots el casos, va permetren's un abordatge quantitatiu d'aquesta qüestió. Els nivells de CML a la banda de GFAP normalitzats amb actina dividits pels nivells de GFAP normalitzats amb actina ens va donar el ratio d'oxidació per CML de la GFAP en cada cas. Si l'oxidació fos únicament deguda als nivells d'expressió de GFAP el ratio hauria de ser el mateix entre els casos. Va resultar que el ratio era major en els cas de PSP incidental més afectat i més gran encara en el de PSP establerta, indicant una major oxidació de la GFAP independentment de la quantitat

d'aquesta. Aquest abordatge no es va poder realitzar amb els altres marcadors on no tot els casos mostraven la banda i per tant feien impossible la quantificació. Hem de tenir en compte, per tant, que l'augment observat amb certs marcadors pot estar únicament relacionat amb un augment d'expressió de GFAP.

L'oxidació de la proteïna GFAP s'ha pogut observar en altres malalties neurodegeneratives amb gliosi com la MA (Korolainen et al., 2005, Pamplona et al., 2005), la MPi (Muntane et al., 2006) o la DFT-Tau, DFT amb inclusions d'ubiquitina i les DFT-amb malalties de motoneurons (Martinez et al., 2008b); i també en altres malalties com l'aceruloplasminemia (Kaneko et al., 2002) o la malaltia de Huntington (Sorolla et al., 2008).

La GFAP presenta cinc isoformes conegudes (alpha, beta, gamma, delta i epsilon) (Nielsen et al., 2002). La isoforma més abundant i que més s'expressa quan comença l'astrogliosi és l'alpha. Fa cinc anys es va interrompre la creença de què la GFAP era una proteïna exclusivament glial. Es va veure que en regions dels cervell afectades per la MA, com l'escorça entorrinal o l'hipocamp, les neurones expressaven GFAP. A més, els mateixos autors van descobrir unes formes noves d'empalmament alternatiu dels transcrits de GFAP, dues de les quals eren "out-of-frame" i s'expressaven pràcticament només en les neurones de les zones afectades per la MA, es va anomenar GFAP+1 (com la UBB+1, deguda també a errors de lectura en la fabricació del transcrit) (Hol et al., 2003). Desconeixem quina de les cinc isoformes, o de les formes "out-of-frame", és la que nosaltres trobem incrementada i oxidada en els casos de PSP i PSP incidental estudiats. Creiem que el motiu és que les diferents formes (incluïdes les dues "out-of-frame"), que hem pogut comprovar al GeneBank o Ensembl, es diferencien en el seu extrem C-terminal. L'extrem C-terminal és particularment ric en lisines, de manera que la digestió amb tripsina, pas previ a l'espectrometria de masses, dona com a resultat pèptids massa petits per poder-se identificar correctament. La seqüència coberta pels pèptids identificats sempre s'ha situat en la part mitja-N-terminal de la proteïna.

No es coneix l'efecte que les modificacions oxidatives de la GFAP poden tenir en la seva funció, recanvi o localització. A més de l'oxidació se n'han identificat altres que podrien estar relacionats amb estats patològics com són la

O-glicosilació, la N-glicosilació o la fosforil·lació. En la MA, s'ha vist que tant la fosforil·lació com la N-glicosilació de la GFAP estan augmentades (Korolainen et al., 2005). Algunes d'aquestes modificacions, en especial la fosforil·lació, regulen la polimerització de la GFAP en la formació de filaments intermedis (Takemura et al., 2002). Però pràcticament res es coneix sobre aquests aspectes en la PSP.

Conclusions

Conclusions:

1.1) Les proteïnes són sensibles a l'interval postmortem i a la temperatura d'emmagatzematge en diferent grau i de manera particular. Algunes d'elles, com l'alfa-sinucleïna, són molt sensibles als dos factors i requereixen la utilització de teixit conservat en condicions de mínima temperatura i interval postmortem.

1.2) La fosforil·lació de la proteïna tau és sensible als factors postmortem. En l'estudi de modificacions post-traduccionals sobre teixit nerviós congel·lat ha de tenir-se molt en compte aquesta limitació.

2.1) Les bandes de baix pes molecular que mostren gran quantitat d'anticossos de tau no té relació amb la degradació postmortem, si en canvi, presenta certa associació amb la localització intramolecular dels epítops contra els quals han estat dirigits.

2.2) El patró de bandes de baix pes molecular reconegudes pels anticossos contra epítops C-terminal de la proteïna tau (o anticossos policlonals contra diversos epítops) presenta semblances entre les malalties que presenten només isoformes 4R hiperfosforil·lades i diferències amb les que presenten isoformes hiperfosforil·lades tant 4R com 3R.

2.3) La proteasa trombina es pot observar associada als grans argiròfils i als pre-cabdells neurofibril·lars en la MGA la qual cosa suggereix un paper per aquesta proteasa en el truncatge de tau en aquestes incisions. La calpaïna-2 i la caspasa-3 només estan presents als cabdells madurs en la MGA.

2.4) La proteasa caspasa-3 es troba present als cossos de Pick a la MPi, la qual cosa suggereix un paper per aquesta proteasa en el truncatge de tau en aquestes incisions.

3.1) El factor de transcripció Sp1 es troba anormalment localitzat a l'interior de les incisions de tau presents en diverses taupaties (MA, MPi i PSP), però no a les incisions d'alfa-sinucleïna en sinucleïnopaties (MP i DCL).

3.2) Els factors de transcripció c-Fos, c-Jun, ATF2 i CREB es troben sobreexpressats en hipocamp i escorça frontal de la MPi així com en col·localització amb la tau als cossos de Pick. Ni hi ha una relació clara entre l'activació d'aquests factors i les respostes de supervivència i mort neuronal en aquesta malaltia.

4) La proteïna p62 i la ubiquitina mutada estan presents en els grans argiròfils en la MGA. La qual cosa suggereix la formació del segrestosoma i també dificultats en la degradació proteosomal en la MGA.

5) La presència de LRRK2 a les inclusions d'alfa-sinucleïna i de tau depèn en gran mesura de l'anticòs util·litzat. Cal determinar l'especificitat dels anticossos comunament util·litzats abans de continuar extreient conclusions sobre el paper de LRRK2 basades en els estudis immunohistoquímics.

6) La proteïna 14-3-3 (gamma i zeta) es troba glico-oxidada (CEL) i lipo-oxidada (MDAL) en les fraccions sarkosil-insolubles en la MA i la AAC.

7.1) La proteïna GFAP es troba oxidada en diverses regions en estadis primerencs i pre-clínics de la malaltia PSP.

7.2) Els estadis primerencs de la PSP comencen a nivell neuropatològic amb la hiperfosforil·lació de tau en astròcits en el caudat/putamen, des d'on s'extén cap al globus pallidus/subtàlam i d'allà a certs nuclis basals.

Materials i mètodes

1- HOMOGENEÏTZACIÓ DEL TEIXIT

Tampó d'homogenat:

Per la major part d'experiments, els homogenats totals de teixit s'han realitzat amb tampó RIPA, que permet analitzar proteïnes citosòliques i de membrana i de l'interior d'òrgànuls, pel fet de portar detergents. La composició de RIPA utilitzat és:

Tris-HCl 10mM, NaCl 100mM, EDTA 10mM, 0,5% deoxicolat de sodi 0,5% NP40.

Ajustar el PH a 7´4.

Els inhibidors emprats sempre han estat per defecte:

1mM de PMSF (inhibidor d'algunes serina-proteases)

1 pastilla/10ml d'un còctel complet d'inhibidor de proteases (Roche)

1uM d'ortovanadat de sodi (Na₃VO₄) (inhibidor de fosfatases de tirosina i alcalines)

I en cas de voler detectar epítops fosforil·lats augmentem el nombre d'inhibidors de fosfatases:

25mM de fluorur sòdic (NaF) (inhibidor de fosfatases de serines i treonines)

20mM de beta-glicerofosfat (inhibidor de fosfatases de serines i treonines)

Procediment:

- S'homogenitza el teixit en aproximadament 10 volums de tampó. Empram tan homogenitzadors de vidre, com de plàstic com homogenitzadors per vibració.
- Centrifugar l'homogenat a unes 12.000rpm durant 5 min per tal de precipitar les restes cel·lulars no solubilitzades.
- El sobrenedant es guarda a -80°C o se'n mesura directament la concentració de proteïna mitjançant Bradford o BCA.

BRADFORD o BCA

En una placa de 96 pouets es pipetegen quantitats creixents d'albumina sèrica bovina (BSA). I les mostres es posen per duplicat en quantitat depenent del grau de turbidesa que s'observi, però sempre la mateixa quantitat per totes les mostres. S'afegeixen 200ul del reactiu Bradford, o BCA (una vegada mesclats els dos components en una relació 1:50), es deixa uns minuts que es produeixi la reacció i es llegeix la placa a l'espectrofotòmetre a la longitud d'ona a que emet cada reactiu.

2-ELECTROFORESI

La fabricació dels gels es realitza segons la recepta següent:

Gels d'acrilamida: (Bio-rad, 30%, 29:1)

RESOLVING (separació)

	8%	10%	12%	15%
Acrilamida	2'66ml	3.33ml	4ml	5ml
Tampó (R,S)	2'5ml	2'5ml	2'5ml	2'5ml
H ₂ O	4'69ml	4'02ml	3'35ml	2'35ml
Temed	10ul	10ul	10ul	10ul
AP	100ul	100ul	100ul	100ul

STACKING (concentració)

	4%
Acrilamida	1'3ml
Tampó (R,S)	2'5ml
H ₂ O	6'1ml
Temed	10ul
AP	100ul

SOLUCIONS:

Tampó R: 1'5M Tris HCl PH= 8'8 (18'7 grs Tris/ 100ml H₂O destil)
0'1% SDS

Tampó S: 0'5M TrisHCl PH= 6'8 (6'05 grs/ 100ml H₂O destil)

Amoni Persulfat: 0'1 mgrs/ml H₂O destil
TAMPÓ D'ELECTRODES (10x)

30'28 grs/l Tris (0'25M)
144'13 grs/l glicina (1'92M)
10 grs/l SDS (0'1%)

Les mostres es barregen amb el tampó de mostra següent:

TAMPÓ DE MOSTRA (SAMPLE BUFFER) 2X

4% SDS
10% 2-mercaptoetanol
20% glicerol
0.004% blau de bromofenol
0.125 M Tris HCl
Ajustar PH=6´8

Les concentracions del tampó de mostra més emprades han estat 2x i 4x. El beta-mercaptoetanol o el DTT, els agents reductors que trenquen els ponts disulfur que mantenen la forma nativa a les proteïnes, s'afegeixen al tampó abans de afegir-ho a la mostra, d'estar pre-mesclats amb el tampó de mostra es degradarien i perdrien l'efecte.

Un cop la mostra s'ha barrejat amb el tampó de mostra, es desnaturalitza la proteïna per calor en posar-ho a 95°C uns 5´. La mostra bullida es pot guardar al congelador de -20°C.

Un cop carregades les mostres al gel, connectar la font:

O bé marquem un voltatge constant de 60-70 volts mentre el front es troba a l'stacking, i després el pugem a 150 omés quan ja es troba al resolving; o bé, i això és completament equivalent, marquem l'amparatge constant a 20mA per gel durant tot el procés i el voltatge ja s'adequa sol als canvis de resistència del gel.

3- TRANSFERÈNCIA

2 papers whatman + membrana de nylon + gel + 2 papers whatman

Tot ha d'estar empapat de tampó de transferència. Treure les bombolletes amb un tub.

TAMPÓ DE TRANSFERÈNCIA GEL GRAN (SANDWICH):

250 mM Tris (Tris base) —————> 30´3 grs
1´92 mM Glicina —————> 144 grs

Enrassar a 1 l. No cal mesurar el pH.

Abans d'utilitzar, afegir 10% de metanol

Un cop feta la transferència, de forma rutinària posem la membrana en solució de Ponceau. Aquesta és capaç de tenyir de forma reversible les proteïnes de manera que ens permet assegurar dues coses: 1) que la transferència a sortit bé, i 2) que no hi ha hagut error de quantificació o de càrrega molt aparents.

I

4- IMMUNOBLLOT

TAMPÓ TBST (10x)

12´11 grs (100 mM) Tris

81´81 grs (1´4 M) NaCl

Ajustar el PH= 7´4 amb HCl i llavors afegir 1% de Tween-20

Enrasar a 1 l amb H₂O

Procediment:

- Bloqueig de les unions inespecífiques . 30´ amb TBSt-Ilet (TBST+ 5% Ilet)
- Anticòs primari dissolt en TBST-Ilet. Overnight a 4°C (o 1 hora a temperatura ambient si l'anticòs ho permet)
- 3 X 5 TBST-Ilet
- Anticòs secundari dissolt en TBST-Ilet a 1:1000. 45´
- 3 X 5´TBST-Ilet
- 3 X 5´TBST
- Revelar amb ECL

Revelador → 1:5 amb H₂O aixeta

Fixador → 1:5 amb H₂O aixeta

5- DESLLIGAMENT DE MEMBRANES

TAMPÓ DE DESLLIGAMENT:

3´78 grs de Tris en 500 ml H₂O destil. i ajustar PH= 6´8 amb HCl

10 grs SDS (2%)

3´48 ml beta-mercaptoetanol

Procediment:

- Netejar la membrana amb TBST
- Incubar 20´ la membrana amb el tampó de deslligament a 66°C aprox
- Canviar el tampó i tornar a incubar 20´ més
- 3 X 5´TBST
- Tornar a fer el bloqueig de les unions inespecífiques i continuar a partir d'aquí.

5- GELS BIDIMENSIONALS

Per tal de realitzar els gels bidimensionals quasi sempre partim de mostra lisada en un tampó amb urea, tiourea i CHAPS. En algunes ocasions, la mostra es trobava en algun altre tampó. Si la mostra està molt concentrada, es pot dissoldre en el tampó d'urea i ja està, però si no, val la pena precipitar-la amb TCA, acetona o metanol, i resuspendre-la en el tampó d'urea, a risc de perdre part de les proteïnes.

El tampó de lisi emprat més regularment és:

40 mM Tris, pH 7,5. 7M Urea (9M si es tracta de fraccions sarkosil-insolubles), 2M tiourea, 4% CHAPS (un detergent zwitteriònic molt apte per solubilitzar proteïnes sense desnaturalitzar-les), i els inhibidors de proteases i fosfatases.

Per la primera dimensió per tal de separar les proteïnes en funció del seu punt isoelèctric agafem:

150ug de la mostra en el tampó s'urea i afegim un 2% d'amfolits en el rang de pH que necessitem (p.e. 3-10). Els amfolits també són formes zwitteriòniques que serviran per establir un gradient estable de pH sobre la tira d'acrilamida de la primera dimensió. Afegim 2% de TBP com a agent reductor. No s'utilitza DTT perquè no és tan eficient en aquest cas pel fet de tenir un pl que el fa migrar. En migrar, és incapaç de reduir part de la mostra. Per últim, afegim blau de bromofenol per localitzar el front en la segona dimensió.

La mostra es col·loca sobre les tires d'acrilamida immobilitzades de gradient no lineal. Es comença per un procés de rehidratació a 50 V durant 12 hores. L'enfoc de les proteïnes en el seu pH s'aconsegueix amb 300V 1h, seguit d'un augment gradual durant 6h fins a 3500V, on s'atura en aquest voltatge durant 12h més. Per últim es deixen a 5000 V 24h. En aquest últim pas es pot interrompre el procés quan es considera que els volts/hora acumulats passen dels 10000-12000 volts.

Després les tires s'equilibren amb un tampó Tris 50mM, pH 6.8, Urea 6M, 1%SDS i 30% de glicerol. Primer s'afegeix al tampó un 2% de DTT i es posa a les tires 10min, i en acabat es canvia pel mateix tampó sense DTT però amb iodoacetamida que estableix el procés de desnaturalització unint-se a les cisteïnes de forma covalent i evitant que es tornin a produir els ponts disulfur prèviament trencats pel DTT.

Finalment la tira es col·loca sobre un gel sense stacking i es continua el procés exactament igual que amb els gels bidimensionals.

Sovint tenim els gels amb solució de Comassie col·loidal o plata, que ens permet la identificació dels spots i retallar-los per enviar al servei d'identificació de proteïnes.

6- IMMUNOPRECIPITACIONS (IP)

Cada immunoprecipitació és un món. El mètode correcte i l'anticòs més apte sovint es descobreix després d'un llarg camí d'assaig i error. Hem realitzat IPs amb boles de proteïna G/A, amb TrueBlot per evitar el reconeixement de les immunoglobulines del primari, amb uColumns amb matrius enganxades a suports magnètics amb boles magnètiques i amb gradetes magnètiques que permeten la precipitació de les boles i optimitzen l'eixugat i recuperació d'aquestes en cada rentat, sense necessitat de centrífuga.

En el cas de la IP que es presenta a la tesi, la d'Sp1, es va emprar el primer dels mètodes després d'un gran nombre d'intents.

Breument: 0,5 mg de mostra de cada cas es barregen amb 30 ul de boles netes d'etanol durant 1h-2h a 4°C en agitació orbital amb l'objectiu que arroseguin totes aquelles proteïnes que s'unirien de forma inespecífica a les boles sense necessitat d'anticòs primari. Després es centrifuga la mostra a 800g 3' per tal de fer baixar les boles sense trencar les interaccions i es recull el sobrenedant ja més net de inespecificitats. S'afegeix l'anticòs primari contra Sp1 a la concentració indicada per la casa comercial (si és així, sinó es tracta d'assaig/error altra vegada). Es deixa o/n a la nòria a 4°C.

L'endemà s'afegeixen les boles sobre la mostra amb el primari i es deixa a l'orbital 1-2h per deixar temps a formar-se el complex boles-primari-Sp1. Després, mitjançant centrífugues de 800 g 3' es realitzen els rentats (entre 10 i 15) amb PBS per tal d'eliminar les possibles unions inespecífiques que s'hagin pogut fer entre les boles i altres proteïnes de la mostra.

Després de l'últim rentat s'intenta deixar les boles el més seques possible i s'afegeix ràpidament el tampó de mostra (30ul o més d'1X). Es bull, es vorteja, es torna a bullir, i s'aconsegueix desfer la unió entre les boles i les Ig agafades a Sp1. Es centrifuga a màxima velocitat per baixar les boles i s'extreu el sobrenedant. Això ja es pot carregar directament en un gel.

Durant tot aquest procés s'ha realitzat exactament el mateix en paral·lel en un altre tub però sense anticòs primari. Quan es mostri el resultat del Western blot, aquest carril servirà per descartar inespecificitats.

7- PROTOCOL PER OBTENIR FRACCIONS SARKOSIL-INSOLUBLES

- ★ Homogeneïtzar el teixit (congelat a -70°C) en 10 vol de buffer

Buffer homogenat: 10mM Tris-HCl (PH= 7.4)

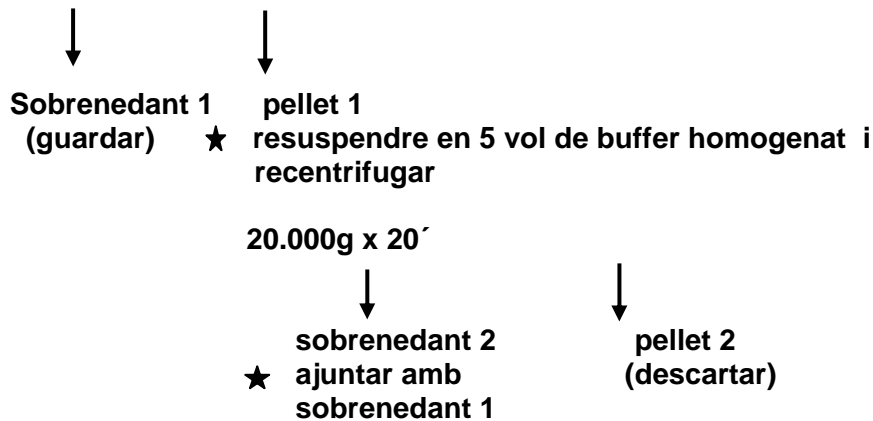
0.8M NaCl

1mM EGTA

10% sacarosa

+ tots els inhibidors de proteases i fosfatases descrits

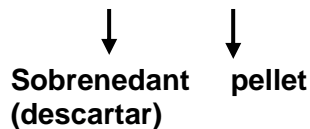
- ★ Centrifugar a 20.000 g x 20´



- ★ Afegir 0,1-1% (w/v) de N- laurosylsarcosinat

Incubar 1h a R.T. en agitació constant

- ★ Centrifugar a 100.000g 1h



- ★ Resuspendre en 50mM Tris-HCl (PH=7.4) (0.2 ml per gr de teixit del principi.

- ★ Guardar a 4°C

8- IMMUNOHISTOQUÍMICA EN PARAFINA

- Desparafinar i posar en aigua destil·lada
- Rentar 2x5' PBS
- Bloqueig de les peroxidases endògenes (70ml de PBS + 30ml de metanol + 1ml d'aigua oxigenada) 15'
- Rentat 5' aigua destil·lada
- Rentar 3x5' PBS
- Posar el tractament necessari per cada primari (saponina, tampó citrat, etc.)
- Rentat 5' aigua destil·lada
- Rentar 3x5' PBS
- Bloqueig de les unions inespecífiques amb sèrum normal durant 2h.
- Incubar amb l'anticòs primari o/n a 4°C diluït en sèrum normal.
- Atemperar
- Rentar 3x5' PBS
- Incubar amb el secundari biotinil·lat 10-15'
- Rentar 3x5' PBS
- Incubar amb streptavidina 10-15'
- Rentar 3x5' PBS
- Revelar. Amb DAB: 200ml de PBS + punta de pipeta Pasteur plena de DAB. Filtrar i afegir 50ul d'aigua oxigenada.
- Contrastar, si es vol, amb hematoxilina diluïda
- Deshidratar i muntar amb medi de muntatge

9- IMMUNOHISTOQUÍMICA EN FLOTACIÓ

- Seleccionar els talls i posar-los en PBS
- Rentar 3x5' PBS
- Bloqueig de les peroxidases endògenes (40ml d'aigua destil·lada, 5ml de metanol, 5ml d'aigua oxigenada)
- Rentar 6x5' PBS
- Bloqueig de les unions inespecífiques amb sèrum normal 2h a temp. amb.
- Rentar 3x5' PBS
- Anticòs primari o/n
- Atemperar
- Rentar 3x5' PBS
- 10' anticòs secundari
- Rentar 3x5' PBS
- 10' streptavidina
- Rentar 3x5' PBS
- Revelar amb DAB (0,05% + 30ul d'aigua oxigenada en 10ml de PBS)
- Rentar 3x5' PBS
- Muntatge en portes de polyisina al 5%
- Deixar aixugar, deshidratar i muntar

10- IMMUNOFLUORESCÈNCIA

El protocol segueix els mateixos passos que als apartats anteriors (segons s'utilitzi flotació o parafina), amb modificacions:

- S'ha de bloquejar la possible autofluorescència de determinades substàncies amb pigments (grànuls de lipofuscina). Ho fem amb una incubació amb negre de Sudan durant 30'.
- Els anticossos tenen un fluorocrom associat. El còctel d'anticossos després del primari assignen a cada primari un color. Existeixen secundaris i fluorocroms amb tots les possible combinacions: anti-ratolí vermell, anti-conill verd.
- Una vegada realitzada la immuno, el muntatge precisa d'un medi especial en el nostre cas Immuno-Fluore Mounting medium. Els cobre-objectes es segellen i es manté la preparació en la foscor fins el moment d'observar-la al microscopi de fluorescència amb els filtres corresponents.

11- Altres protocols realitzats:

Aquí enumero sense detallar altres tècniques que s'han dut a terme en múltiples experiments que han quedat fora de la tesi de diferents línees de recerca que han quedat interrompudes per motius diversos.

Estudi de la proteïna CSK (C-terminal Src Kinase)

Aquesta proteïna és capaç d'inhibir l'activitat de la família de tirosina-cinases Src (Src, Yes, Fyn, Lck...) una vegada és reclutada als rafts lipídics. Algunes d'aquestes cinases poden fosforil·lar directament tau (a l'epítol Tyr18, per exemple) o bé activar cinases de tau com la GSK3-beta. Ens va interessar veure diversos aspectes d'aquesta proteïna a la MA. A més de les tècniques abans esmentades vam utilitzar també :

- Immunomicroscopia electrònica de CSK sobre pellets de tau-PHF per confirmar la possible interacció, suggerida per la seva localització, observada amb immunohistoquímica, en inclusions de tau.
- Extracció de RNA, RT PCR i Real Time amb sondes TaqMan, per veure els nivells d'expressió de la proteïna.
- Extracció de rafts lipídics amb gradients de sacarosa, per estudiar els nivells d'expressió de CSK en la regió on desenvolupa la seva activitat.
- IP de CSK (mitjançant boles magnètiques) acoblada a una assaig d'activitat cinasa amb gamma-ATP32, per veure si la seva activitat estava disminuïda en la malaltia.
- Transfecció amb siRNA per silenciar l'expressió de CSK i comprovar el seu efecte sobre la fosforil·lació de tau en neuroblastomes, per tal de veure si el mecanisme hipotetitzat es complia en un model experimental.

Interacció de tau-PHF o tau citosòlica amb altres proteïnes

- Un altre objectiu va ser el d'utilitzar membranes d'arrais d'anticossos (Hipromatrix) de diferents tamany orientades a transducció de senyal. Es va provar en diferents malalties (MA, PSP i FTDP-17) amb tau de diferents fraccions (sarkosil-insoluble o citosòlica). L'arrai va mostrar un conjunt de proteïnes en tots els casos, algunes de les quals es van confirmar per immunohistoquímica i microscopia confocal i es va intentar validar per IP. Algunes d'elles, a més, es van provar de localitzar mitjançant immunomicroscopia electrònica sobre pellets enriquits en PHF.
- TAP system. Aquest sistema consisteix en clonar la proteïna (tau i tau amb diferents mutacions) en un vector que posseeix dos tags (d'unió a calmodulina i estreptavidina). La transfecció en neuroblastomes ens va permetre després realitzar els dos processos de purificació (mitjançant columnes) obtenint una fracció molt enriquida en tau. Aquesta fracció es va carregar en un gel gran i tenyir amb plata per tal de descobrir els interactors que arrossegava. Alguns d'aquests es van poder revelar mitjançant espectrometria de masses.
- Extracció d'inclusions de tau mitjançant microdissecció laser per tal de correr les inclusions en gels bidimensionals i identificar-ne els components. Aquest protocol pot resultar útil si es disposa d'una quantitat de temps enorme, motiu pel qual es va abandonar. En casos avançats de MA, si no es disposa del temps necessari, extirpar sota una lupa binocular la capa CA1 de l'hipocamp pot resultar molt més ràpid encara que molt menys precís.

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