transferability were 50% and 28%, respectively (Tractz *et al*., 2012). Therefore, the tested markers were not suitable for genetic variability analyses of *D. sturtevanti* natural populations, requiring more tests with other primers or the use of strategies for obtaining and synthesizing specific primers for this species.

Keywords: saltans group, molecular markers, genetic variability, microsatellite DNA, transferability.

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Drosophilids from the Font Groga site (Barcelona, Spain): a new collection.

Rosselló, M., R. Madrenas, V. Ojeda, and F. Mestres*. Dept. Genètica, Microbiologia i Estadística, Universitat de Barcelona, Barcelona (Spain); *Corresponding author: fmestres@ub.edu.

On 6th October 2015, we obtained a new collection of drosophilids from the Font Groga site (Barcelona, Spain). This location presents excellent environmental conditions for the study of drosophilid diversity, and a complete description can be found in Araúz *et al.* (2009). This research completes the studies of Canals *et al.* (2013), Pineda *et al.* (2014), and Esteve and Mestres (2015). The results of our collection are presented in Table 1.

Table 1. Number and percentage for each species and sex collected from Font Groga site (Barcelona, Spain) on 6th October 2015.

Species	Number	Percentage
D. subobscura (♂)	107	3.14
D. subobscura (♀)	155	4.55
D. simulans (♂)	836	24.52
D. melanogaster (♂)	16	0.47
D. menalo/simulans (♀)	1953	57.29
D. suzukii (♂)	86	2.52
D. suzukii (♀)	220	6.45
D. cameraria (♂)	13	0.38
D. cameraria (♀)	20	0.59
D. phalerata (♂)	1	0.03
D. buzzatii (♀)	1	0.03
Scaptomyza sp.	1	0.03
Total	3409	100

Comparing these data with those previously obtained in 2012, 2013, and 2014 (Canals *et al.*, 2013; Pineda *et al.*, 2014; and Esteve and Mestres, 2015), it is worth noting the large fluctuation of the frequency of species belonging to *melanogaster* group (*D. melanogaster* and *D. simulans*). This frequency was high in 2012 (81.01%) and again in the present sample (82.28%), whereas it was 32.14% and 38.94% in 2013 and 2014, respectively. Usually, a hot and dry summer produces an increase of this group frequency during autumn. However, *D. subobscura* shows the opposite behavior, being abundant in autumn if the summer has been relatively cold and humid. It was scarce in the present sample (7.69%) and in 2012 (6.85%), but reached 62.60% and 30.53% in 2013 and 2014, respectively. It is interesting to observe the relative abundance of the invasive species *D. suzukii*, presenting similar values in the present research (8.97%) and also in 2012 (9.20%) and 2013 (7.98%). However, its frequency had a peak in 2014 (20.35%). Finally, commenting that for the first time we didn't find *D. immigrans* in the Font Groga site, but a *D. buzzatii* female was sampled for the first time.

With data of Table 1, we computed the *H'* (Shannon diversity index) and *J* (Shannon uniformity index), their values being 0.62 and 0.35, respectively. These values are the lowest recorded in our time series

at the Font Groga site. Likely, this is due to the relative high abundance of individuals belonging to the *melanogaster* group.

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Metabolic activity of diuron by *Zea mays* detected through the wing spot assay in *Drosophila melanogaster*.

Peraza-Vega, Ricardo, América N. Castañeda-Sortibrán, and Rosario Rodríguez-Arnaiz*. Laboratorio de Genética y Evolución, Departamento de Biología Celular, Facultad de Ciencias, Universidad Nacional Autónoma de México; *E-mail: rosario.rodriguez@ciencias.unam.mx

Abstract

Diuron is a phenylurea herbicide compound amply used in agriculture to control a wide variety of annual and perennial broadleaf and grass weeds, algae, and mosses. The aim of the present study was to evaluate the genotoxicity of diuron in the wing spot assay of *Drosophila melanogaster* after metabolic activation of an aqueous extract from the roots of *Zea mays* treated with different concentrations of the herbicide. Bentazone was used as positive control. The wing spot assay that assesses for somatic mutation and recombination events was carried out with standard (ST) and high-bioactivation (HB) crosses given chronic treatment to third instar larvae. Results showed that larvae treated with the aqueous extracts caused a similar positive response in both crosses.

Introduction

Diuron is an herbicide used to control a wide variety of weeds affecting maize, sugarcane, cotton, sorghum, among other crops and for fallow and idle cropland use. Diuron also has a widespread use in non-agricultural applications like industrial and rights of way uses. Due to its chemical structure, diuron has been classified as a substituted phenylurea compound. This compound can be readily taken from soil by the root system of plants and translocated into stems and leaves moving primarily via the xylem. The mechanism of action of diuron is through inhibiting photosynthesis by blocking the electron transfer at photosystem II (Wessels and van der Veen, 1956). This compound is able to bind to D-1 protein located at the reactive center of photosystem II (Arnaud *et al*., 1994; Duke, 1990).

The basic metabolism of phenylureas include N-demethylations followed by oxidation of aromatic groups (Engelhardt *et al*., 1972). In mammal cells, diuron is mainly metabolized through de-alkylation of methyl-urea groups (Abass *et al*., 2007). Diuron is capable of increasing cytochrome P450 enzymes (CYPs) activity as well as other enzymes including glutathione-S-transferase, epoxide hydrolase, and UDP-glucuronyl transferase (Schoket and Vincze, 1985, 1990). In plants, phenylureas are metabolized through N-demethylation of the nitrogen atom and hydroxylation of the aromatic group (Fonné-Pfister and Kreuz, 1990). It has been demonstrated that some enzymes belonging to CYP71 and CYP76 families are involved in diuron metabolism in plants (Fonné-Pfister and Kreuz, 1990; Höfer *et al*., 2014; Robineau *et al*., 1998; Siminszky *et al*., 1999).

Many pesticides are promutagens and become active after metabolic biotransformation by plants (Plewa, 1978). Herbicides and their metabolites represent potential health risks to humans since they are applied to food crops and may exert a genotoxic effect when they are consumed by the population. The US Environmental Protection Agency has listed diuron as a likely human carcinogen (US EPA, 1997, 2004). Also, several studies have demonstrated that diuron is a genotoxic and carcinogenic compound (Akcha *et al*.,