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Impact of molecular methods in the analysis of the invasiveness of *Streptococcus pneumoniae*

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JUSTIFICATION

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Streptococcus pneumoniae is one of the most important pathogens in bacterial pneumonia, sepsis and meningitis worldwide. The polysaccharide capsule of the pneumococcus is the major virulence factor, from which about 97 different types have been identified. Despite this high diversity not all of them are capable of causing invasive pneumococcal disease (IPD). Some serotypes are more prone to cause invasive disease than others. The invasive disease potential indicates the capacity of the serotypes to cause invasive disease or to be asymptomatic colonizers of the nasopharynx. In 2000, a pneumococcal conjugate vaccine (PCV) was licensed including the seven pneumococcal serotypes responsible for the main burden of the disease in the United States. The introduction of PCV7 caused an important reduction of IPD in the EEUU and in several other countries where the vaccine was implemented. This reduction was reported by several epidemiological studies that analyzed the changes experienced in the serotypes causing IPD and in the serotypes found in the nasopharynx of healthy carriers after the introduction of PCV7. Unfortunately, non vaccine serotypes started to increase filling the empty ecological niche left by the vaccine serotypes. The surveillance of the invasive disease potential of pneumococci has been traditionally performed using standard methods based on culture for both the detection and the capsular identification.