

Title: Genetic diversity of serotype 3 *Streptococcus pneumoniae* isolates in the post vaccine period in Southern region of Brazil

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Abstract:

The introduction of 10-valent pneumococcal conjugated vaccine (PCV10) in Brazilian national immunization program in 2010 generated a selective pressure in the population dynamics of this microorganism. An increase in incidence of non-vaccine serotypes, as described in other countries where the PCV has been previously introduced is expected. Serotype 3 is not covered by the PCV10 formulation and is well documented as a serotype associated to an elevated number of complicated cases in the post vaccine period. The aim of this study was to evaluate the genetic diversity of serotype 3 *Streptococcus pneumoniae* isolates obtained after the introduction of the PCV10 in Porto Alegre, Southern region of Brazil. Isolates were obtained from patients with pneumococcal disease from 2010 to 2014, and serotyped by multiplex PCR. Molecular relationship among isolates was determined by MLVA (*Multiple-Locus Variable Number Tandem Repeats Analysis*) and the genetic profiles were analyzed by Bionumerics 7.1 software. A total of 503 pneumococci were isolated in the post vaccine period, of which 38 (7.55%) belong to serotype 3. The most commons specimens were blood and sputum (11/38). The mean age of the patients was 54.03 and 13 patients were ≥ 65 years old. The molecular analysis using the MLVA technique generated 13 distinct profiles but all isolates were clustered in the same clonal group, with 75% of similarity or higher, considering clonal group as isolates that have the same number of repetitive units in 12 out of 18 loci. Our results suggest that pneumococcal disease caused by serotype 3 isolates after PCV10 can be genetically characterized by MLVA as a conserved single clonal group. This observation deserves further studies considering the important role of this serotype in the post PCV10 era.

Keywords: pneumococcus, vaccine, MLVA, genotyping, serotype 3.

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