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Abstract (oral session)

Molecular epidemiology of the capsular locus of serogroup 11 *Streptococcus pneumoniae* isolates from Italy: identification of the newly described serotype 11E

R. Camilli*, F. D'Ambrosio, M. Moschioni, F. Berti, M. Del Grosso, M. Monaco, M.A. Barocchi, A. Pantosti (Rome, Siena, IT)

Objectives: Recent studies have demonstrated that the capsular locus of *S. pneumoniae* serotype 11A is associated with a high degree of genetic heterogeneity. A new serotype, named 11E, was discovered among strains previously identified as serotype 11A, carrying a capsular locus with a mutated or disrupted *wcjE* gene. In addition, the genomic analysis of 3 serotype 11A pneumococcal strains revealed a discordance between the serotype and the capsular locus, which corresponded to that associated with the 11D serotype. The aim of this study was to verify which capsular locus was present in serotype 11A pneumococcal strains circulating in Italy. **Methods:** 31 pneumococcal strains serotyped as 11A according to the Quellung reaction and obtained from invasive diseases in Italy in the years 1997-2010, were analysed. Since most of the nucleotide diversity between capsular loci 11A, 11D and 11E, resides in *wcjE*, coding for a putative O-acetyl transferase, the entire gene was amplified and sequenced. **Results:** Out of 31 strains, 2 carried a *wcjE* gene 100% identical to 11A and 20 carried a *wcjE* gene 99-100% identical to 11D. Among the latter, 2 strains carried an amino acid substitution due to distinct single nucleotide polymorphisms (SNPs). The remaining 9 strains showed a disrupted *wcjE* gene, being consistent with serotype 11E. In particular, 5 strains showed a *wcjE* gene disrupted by transposable elements (IS1515 insertion in 4 strains and IS1167 insertion in 1 strain) while 4 strains showed unique mutations including duplications, insertions and SNPs resulting in either late start codon or premature stop codon with respect to the wild type sequence. These mutations have not been previously described. **Conclusions:** This study highlighted that in Italy the more prevalent capsular genotype, associated with serotype 11A, corresponds to 11D. In addition, the presence of isolates with an 11E genotype has been demonstrated, suggesting that conventional serotyping could have masked the real epidemiology of this serogroup. It is likely that the 11 serogroup typing scheme would be reconsidered in the near future. Further studies on larger serogroup 11 pneumococcal collections are needed to investigate if a change in genotype prevalence could have occurred in recent years, as a possible effect of the widespread use of pneumococcal vaccines.