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Characterization of *Streptococcus pneumoniae* from the solithromycin global clinical trial programme in community acquired pneumonia

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Background: *Streptococcus pneumoniae* is the major bacterial cause of pneumonia globally. Vaccines have been introduced to prevent these infections, however their coverage is not universal. We examined isolates of *S. pneumoniae* from two global community acquired pneumonia clinical trials examining serotype, genotype and antibiotic susceptibility.

Material/methods: Two global randomized, prospective community acquired pneumonia trials were undertaken between 2011-2014. Isolates of *S. pneumoniae* were serotyped by Quellung reaction, and a subset was genotyped to establish current epidemiological patterns. Susceptibility data to solithromycin were also collected using CLSI M100-S25 methods.

Results: The etiologic agent was detected in 785 of 1719 (45.7%) patients. Among 352 patients with *S. pneumoniae* recovered by culture, there were 219 typeable isolates comprising 45 different serotypes, with an additional 17 being non-typeable. The most common serotypes were type 3 (11.4%), 19F (5.0%) and 19A (4.6%). Overall, 62.3% of the serotypes are included in the PPSV23 vaccine, and 44.6% in the PCV13 vaccine.

Forty four macrolide resistant isolates were genotyped. The most common macrolide resistance gene detected was *ermB* (25 isolates, 56.8%), followed by *ermB* & *mefE* (8 isolates, 18.2%), *mefE* (6 isolates, 13.6%), and one each of *mefA* and *ermB* & *mefA* combined (2.3%). One isolate was negative for all macrolide resistance genes tested. The solithromycin MIC₉₀ was 0.03 mg/l (range 0.002-1.0 mg/l) among 205 isolates tested.

Conclusions: *S. pneumoniae* was isolated in approximately 20% of community acquired pneumonia infections. More than one third of the isolates recovered are not included in current pneumococcal vaccines. Solithromycin was highly active in vitro against macrolide susceptible and resistant strains, among which *ermB* was most common resistance mechanism.