

O061

Oral Session

Basic science: pathogenesis and epidemiology of Gram-positive bacteria

GENOMIC MONITORING OF WITHIN HOST EVOLUTION OF STREPTOCOCCUS PNEUMONIAE INDICATES STRONG SELECTIVE PRESSURE

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Objectives: Pneumococci are transient components of the human nasopharyngeal flora being involved in self-limited periods of asymptomatic carriage more frequent in children and with a seasonal peak in late winter. When giving rise to invasive infections bacteria change their physiology and are exposed to distinct environments and stresses. Our aim was to evaluate the selective pressure acting on pneumococci during bacteraemia in experimental models of infection

Methods: Blood cultures of mice infected by the intra venous route were subjected to whole genome sequencing of the whole pneumococcal population. Genome sequences were checked for single nucleotide polymorphisms (SNPs). Single clones with the identified polymorphisms were isolated and phenotypically characterised.

Results: Genomic analysis of clones derived from blood cultures of mice were shown to be generally monoclonal since characterised by one or two SNPs common to all bacterial cells growing in the blood culture. When infecting with strain TIGR4 the bacteraemia isolates were characterised by SNPs in multiple genes of the F0/F1 ATPase involved in maintenance of intracellular pH and proton gradient. Mutations were also detected in the potassium NADH dependent proton exchanger TrkA. When analysing bacteraemia isolates of other two pneumococcal strains a series of SNPs in the NAD biosynthesis pathway were detected. Pneumococci with mutated F0/F1 ATPase show altered mechanisms of pH stress response and mechanisms for managing membrane potential.

Conclusion: Our genomic data provide evidence for monoclonal origin of pneumococcal bacteraemia and indicate that the derived population underwent to a strong selective pressure within the host. Cumulative evidence from genomic analysis of infection series with three different pneumococcal strains point to selection of pH homeostasis related mechanisms involved fitness of pneumococci during invasive infection.