ORAL ABSTRACTS

125. Single Nucleotide Polymorphisms Drive Phenotypic Diversity Among Sequence Type 1 Group B *Streptococcus*, An Emerging Cause of Invasive Disease in Adult Humans

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Background. Over the past 20 years, the rates of invasive group B streptococcal (GBS) disease in non-pregnant adults have markedly increased with the majority of adult infections now due to serotype V strains.

Methods. Multi-locus sequence typing (MLST) was performed on 233 serotype V GBS bloodstream isolates from non-pregnant adults in the United States and Canada collected from 1992 -2013. An ST-1 GBS genome was completed and used for whole genome comparative analyses of 201 ST-1 isolates. Analysis of gene specific polymorphism frequency was used to identify genes under positive selection. The impact of observed polymorphisms on strain phenotypic variation was assessed by capsule level measurements, pilus protein assays, or global transcriptome analysis using RNA-seq.

Results. 211/233 isolates (>90%) were ST-1 or a single nucleotide variant of ST-1. The completed ST-1 reference genome showed multiple, significant differences in cell surface components critical to GBS host-pathogen interaction compared to the previously published GBS serotype V ST-110 genome. Whole genome sequence analyses revealed significant recombination in 8 strains. ST-1 strains differed by an average of 97 single nucleotide polymorphisms (SNPs) over the 2.1MB genome. Phylogenetic analyses revealed a temporally dependent mode of genetic diversification consistent with the relatively recent introduction of ST-1 GBS into humans. Thirty-one GBS genes were found to be under positive selective pressure for variance including capsule, pilus proteins, and key transcriptional regulators. Antimicrobial resistance elements were widespread among ST-1 strains, with the majority of strains harboring both tetracycline (97%) and macrolide (70%) resistance determinants.

Conclusion. These data provide the first dense genomic level insight into GBS population structure and reveal that phenotypic diversity among ST-1 GBS is mainly driven by small genetic changes rather than recombination. Our data provide novel information on GBS loci contributing to host-pathogen interaction in adult invasive infections which influences GBS preventive strategies, and more globally elucidate the molecular diversification of emerging bacterial pathogens recently introduced into humans.

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