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Poster Session II
Molecular diagnostic methods in bacteriology - miscellaneous

GROUP B STREPTOCOCCAL INFECTIONS AMONG ADULTS IN ICELAND: 1978-2012 SURVEILLANCE

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Objectives: We undertook the analysis of 134 group B streptococci (GBS) isolates recovered from cases of invasive infection in adults in Iceland, between 1978 and 2012, with the aim of documenting the prevalence of serotypes, genetic lineages and antimicrobial resistance patterns.

Methods: All isolates were serotyped and assigned to clones according to their pulsed-field gel electrophoretic (PFGE) profiles and MLST-based sequence types. Susceptibility to penicillin, erythromycin and clindamycin was tested by disk diffusion according to the CLSI guidelines. Presence of the surface protein genes *bca*, *alp2*, *alp3*, *alp4*, *eps* and *rib* and of pilus islands PI-1, PI-2a and PI-2b was tested by PCR.

Results: The isolates were grouped into 11 PFGE clusters. Serotype Ia was the most frequently found (23%) but was closely followed by serotypes V, III, Ib and II, all showing similar prevalence (14-19%). Although serotype V was not the dominant serotype in Iceland, it was represented mainly by a single PFGE cluster defined by ST1/*alp3*, similarly to what has been described among invasive isolates recovered from non-pregnant adults in most European countries and the USA. On the other hand, the more frequent serotype Ia isolates were distributed across several PFGE clusters and genetic lineages, mainly ST23/*eps*, but also ST24/*bca* that has been found mostly in the Mediterranean region. Additionally, we identified a genetic lineage associated with invasive disease in fish, ST7/*bca* and carrying PI-1+PI-2b, a combination of pilus islands almost exclusively found in the neonatal 'hypervirulent' clone III/ST17. The combination PI-1+PI-2a was found in 66% of all isolates. All isolates were susceptible to penicillin. The overall rate of erythromycin and clindamycin resistance was 6.0% and 9.0%, respectively, and an overrepresentation of erythromycin resistance was observed in serotype V/ST1/*alp*3 genetic lineage ($p<0.05$).

Conclusions: The population of GBS causing invasive infections in Iceland revealed that several distinct lineages were present over a significant time-span. In contrast to what has been documented elsewhere, where serotypes V or Ia are responsible for the majority of invasive disease cases in non-pregnant adults, in Iceland there is no significant dominance of a particular serotype or genetic lineage, but instead several serotypes and genetic lineages cause significant disease. Our data emphasizes the need for continued surveillance of GBS invasive infections in non-pregnant adults in Iceland to determine the reasons behind the diversity of the circulating genetic lineages.