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Poster Session VI

Epidemiology with molecular typing

**COMPARATIVE ANALYSIS OF STREPTOCOCCUS AGALACTIAE ISOLATES CAUSING INFECTIONS IN CATTLE AND HUMANS IN ICELAND**

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**Objectives:** *Streptococcus agalactiae* (Group B streptococcus, GBS) was first described as a causative agent of bovine mastitis and only later acknowledged as a leading cause of neonatal disease and associated with invasive infections in adults. The aim of this study was to compare GBS isolates recovered from human infections and bovine mastitis in Iceland.

**Methods:** We compared 24 isolates recovered from cases of bovine mastitis with 134 GBS isolates recovered from invasive infections in adults. All isolates were serotyped and assigned to clones ( $n \geq 3$  isolates) 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. The 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 most frequent serotype among the isolates recovered from bovine mastitis was V (29%), non-typable isolates were equally prevalent, and serotypes Ib, II, III and IX were also found. No isolates of serotype Ia were identified in this collection, in contrast to the human isolates among which it was the most frequent serotype (23%). The isolates were grouped into 13 PFGE clusters, with 14 of the 24 bovine isolates grouping into clones together with human isolates and 2 grouping with a human isolate. The remaining 8 were included in minor PFGE groups or had unique profiles with no clones grouping exclusively bovine isolates. Accordingly, the same genetic lineages dominated in both human and bovine isolates, namely V/ST1/*alp3*, III/ST23/*alp2*, and Ib/ST8/*bca*. Surprisingly, the PI-1+PI-2b combination, associated with ST17 having a proposed bovine origin, was not the most frequent but instead the PI1+PI-1a combination predominated (92%) similarly to human isolates. All isolates were susceptible to penicillin and erythromycin resistance was significantly associated with the serotype V/ST1/*alp3* genetic lineage ( $p < 0.05$ ) in both human and bovine isolates.

**Conclusions:** Over half of the bovine isolates clustered together with those causing invasive infections in humans. Our data indicates there is only limited differentiation between the two GBS populations, raising the possibility of ongoing GBS transmission between humans and their cattle. Continuous surveillance is needed to clarify this possibility.