Objectives: *Streptococcus agalactiae* or Group B streptococcus (GBS) is an important pathogen of people and cattle, inducing mastitis and milk production losses in the latter species. In the 20th century, *S. agalactiae* was almost eradicated from the dairy industry in Finland and Sweden but it is now re-emerging. Based on genetic and genomic studies of human and bovine *S. agalactiae*, different host species appear to be affected by distinct subpopulations, although the host-association is not absolute. The objective of the current study was to obtain contemporaneous human and bovine isolates of *S. agalactiae* from both countries and to determine whether they constitute distinct subpopulations, as described in the literature, or similar subpopulations, suggesting potential for transmission between humans and animals.

Methods: Cross-sectional study of human and bovine *S. agalactiae* isolates obtained via hospitals and veterinary diagnostic laboratories in Finland and Sweden between 2011 and 2013. Human isolates were obtained from one hospital per country and included a convenience sample of carriage and disease-associated isolates for which a clear classification by disease status and organ system was available. Bovine isolates were obtained from milk samples submitted for bacteriological culture from individual animals with clinical or subclinical mastitis. Per herd, a single isolate was included in the analysis. Isolates were subjected to multilocus sequence typing, molecular serotyping, and pilus-island typing using published methods.

Results: 80 human and 78 bovine *S. agalactiae* isolates were characterized. More than half of the isolates (n=82 or 52%) belonged to 5 sequence types (STs) that were shared between people and cattle. Four of 5 shared STs were represented by more than 10 isolates in the study. Of 30 STs that were unique to one host species, only 2 were represented by more than 10 isolates. Fourteen new STs were identified. They all differed by a single SNP from known STs, demonstrating that MLST diversity in this area has almost been mapped completely. For STs that were shared between host species, the same molecular serotype (MS) dominated in both host species, i.e. MS Ib, II, IV and V for ST8, 12, 196 and 1, respectively. The only exception was ST23, where human isolates belonged exclusively to MS Ia whereas bovine isolates included equal numbers of MS Ia and MS III. Pilus island profiles were strongly correlated with STs but did not differ between human and bovine isolates.

Conclusion: In contrast to what has been reported in the literature, human and bovine *S. agalactiae* from Sweden and Finland have highly similar genetic profiles, implying that there is no clear host-species barrier and that there is potential for zoonotic transmission between people and cattle. This may contribute to the pathogen's re-emergence in dairy cattle and pose a risk for public health.