Using hierarchical cluster analysis to investigate the relationships among *Salmonella* Typhimurium DT 104 isolates from humans and animals in Scotland (1990-2004)

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Introduction and Methods

A surveillance system managed by the Scottish Salmonella Reference Laboratory (SSRL) and Health Protection Scotland (HPS) reported 30% of Scottish Salmonella submissions were *Salmonella* Typhimurium definitive type (ST DT104). The resistance profile of each isolate was identified in the SSRL by the Bauer-Kirby disk diffusion method. The resistance patterns (R-types) against thirteen antibiotic treatments used in SSRL, viz., ampicillin (Ap); gentamicin (Gm); kanamycin (Ka); streptomycin (St); sulfonamide (Su); tetracycline (Te); trimethoprim (Tm); Chloramphenicol (Cl); nalidixic acid (Na); netilmicin (Ne); spectinomycin (Sp); furazolidone (Fz) and ciprofloxacin (Cp), were used to analyse the relationships among the ST DT104 isolates from human and animal datasets, respectively. The hierarchical cluster analysis package in SPSS 14 was used to group the 2,796 human and 2,439 animal isolates using their resistance pattern to the 13 antibiotics. The dendrograms were constructed with the "between-group-linkage" method and the square Euclidean distance measurement. The dendrograms were divided into three hierarchical level groups. The proportions of each group are presented in figure 1. The R-types which have less than 5 percentages are not shown.

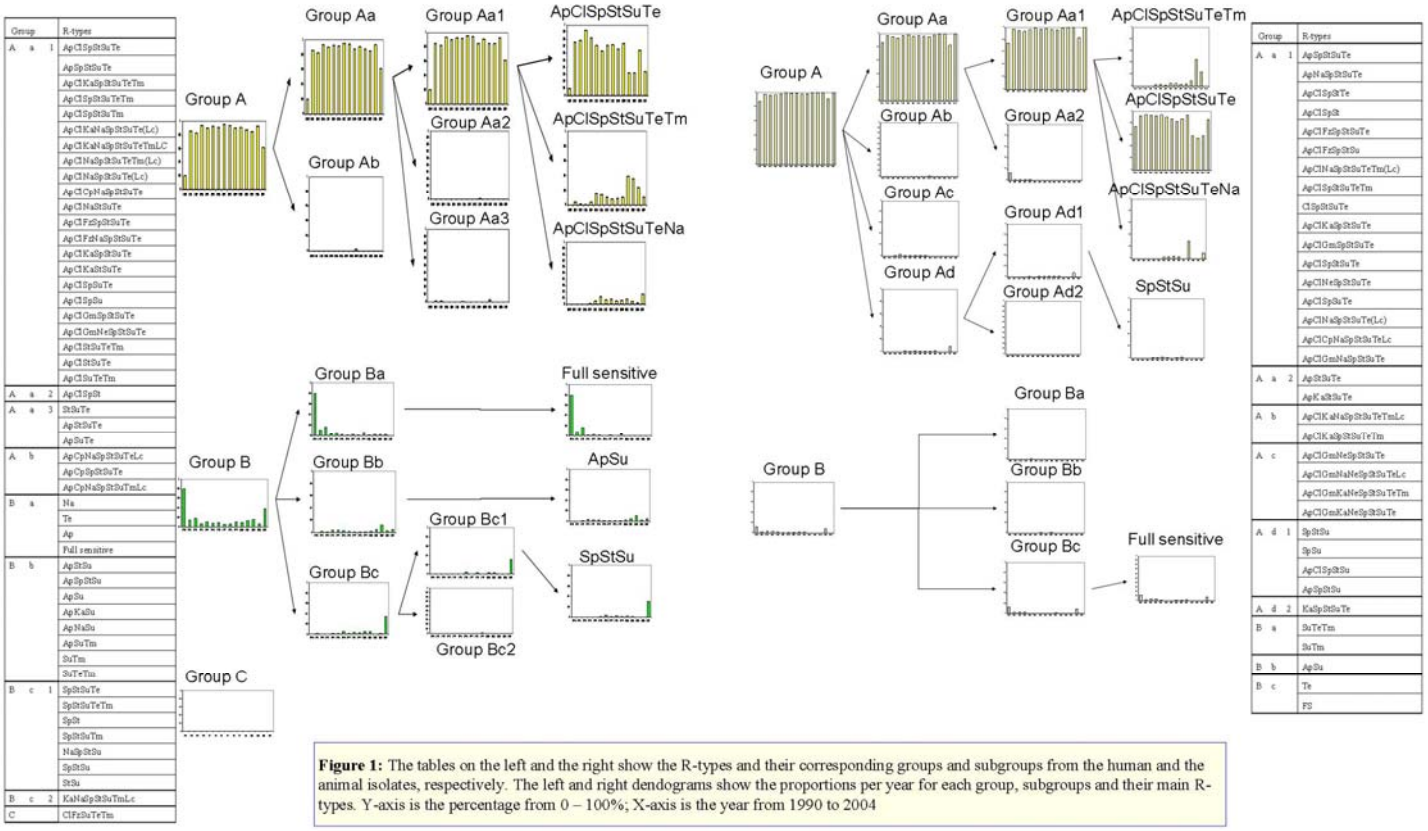

Figure 1: The tables on the left and the right show the R-types and their corresponding groups and subgroups from the human and the animal isolates, respectively. The left and right dendograms show the proportions per year for each group, subgroups and their main R-types. Y-axis is the percentage from 0 – 100%; X-axis is the year from 1990 to 2004

Results and Conclusion

Two major first level clusters were identified, and 6 and 5 main R-types for humans and animals. respectively. The ApClSpStSuTe R-type, with its associated resistance patterns, ApClSpStSuTeTm and ApClSpStSuTeNa R-types, dominated the trend throughout the study period. The ApSu R-type emerged in 1992. The SpStsu R-type was first isolated in 1996. In the animal dataset, the proportion of fully sensitive R-type was about 10% in 1990 and 2003. The proportion of the SpStSu R-type was very low throughout the study period. The ApSu R-type was also identified in 1994 but the proportion was less than 5% in any single year. The emergence of ApClSpStSuTeNa R-type has been postulated to be related to the licensing of quinolone drugs for veterinary usage [1]. However, in Scotland, resistance was co-emergent in humans and animals. The increased prescription of trimethoprim in both humans and animals may play a role in the emergence of ApClSpStSuTeTm R-type [2]. As many as 22 R-types were common to both human and animal datasets supporting the assumption that relationships exist between the two microbial populations. However, there was no consistent temporal association between the emergence in humans and animals suggesting that the ecological and epidemiological direction of the relationships is complex. The relationships between R-types and their corresponding genotypes requires further investigation.

Reference List

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2. Enne, V. I., Livermore, D. M., Stephens, P., Hall, L. M. Persistence of sulphonamide resistance in *Escherichia coli* in the UK despite national prescribing restriction. *Lancet* 2001;357:1325-8.