Antimicrobial resistance profile and genetic diversity of *Salmonella enterica* serotypes Typhimurium and Muenchen

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**Summary:** The aim of this study was to compare the antimicrobial resistance pattern and genetic diversity of *Salmonella enterica* serotypes Typhimurium and Muenchen from human and swine. Previously, we reported two predominant multi-drug resistant (MDR) patterns common among *Salmonella* isolates from swine. In this study we report serovar Muenchen, to have MDR pattern similar to Typhimurium and with expanded spectrum in swine (AmCmStSuTeKm). This pattern is more frequent among isolates from swine (with 46% frequency) while most of isolates from human were pansusceptible (only one isolate with MDR to 10 antimicrobials). Genotyping using PFGE revealed swine and human isolates clustered separately from each other. We identified class-I integrons among nine *S. Muenchen* isolates from swine and single isolate from human using polymerase chain reaction (PCR). We propose that interserovar exchange of resistance genes might be responsible for emergence of MDR strains among serovars not previously showing MDR. Further molecular investigations are underway.

**Keywords:** Multidrug resistance, genotyping, pigs, fingerprinting, integrons

**Introduction:** Multidrug resistant (MDR) strains of *Salmonella* Typhimurium have been isolated from pigs (Gebreyes and Altier, 2002). Another important serotype is Muenchen, which is in humans and accounts for 1.6% of the cases in the United States (CDC, 1997). Also, foodborne disease outbreak have been traced to improperly processed pork products or primarily linked to pig farms (Murase et al., 2000). Therefore, we decided to ascertain the antimicrobial resistance profile between the *S. Typhimurium* and Muenchen isolates from humans and swine and compare genotypes from different sources in order to understand their genetic similarity and/or diversity.

**Materials and Methods:** We tested *S. Typhimurium* isolated from 365 human clinical, 56 swine clinical and 484 swine non-clinical isolates and *S. Muenchen* from 40 human and 28 swine isolates. The isolates were tested for 14 antimicrobials by Kirby-Bauer and/or Vitek calorimetric methods using the NCCLS standards for Enterobacteriaceae family. The antimicrobials with their abbreviation used are: ampicillin (Am), amoxicillin-clavulanic acid (Ax), amikacin (An), chloramphenicol (Cm), ceftriaxone (Cro), ciprofloxacin (Cip), cephalothin (Cf), gentamicin (Gm), kanamycin (Km), Piperacillin (Pip), streptomycin (St), sulfamethoxazole (Su), tetracycline (Te) and trimethoprim –sulfamethoxazole (Ts). Genotyping was done by Pulsed field gel electrophoresis (PFGE) and fingerprint analysis was done by using the Bionumerics software. PCR was used to detect the presence of integrons, *bla* _PSE1_, *bla_ TEM, *aphA1_, _lab, tetA_ and _tetB_ genes.

**Results:** *S. Typhimurium* isolates from swine had a higher frequency of resistance but the human clinical isolates showed resistance to more antimicrobials. Resistance was also seen against ceftriaxone (1.6%) and ciprofloxacin (single isolate) among the human isolates.
PfGE of the three groups showed isolates from clinical cases clustered together and separate from the research isolates. Twelve isolates out of 13 S.Muenchen isolates tested for 12 antimicrobials from swine showed AmCmStSuTeAxKm resistance pattern. The human isolates were susceptible to most of the antibiotics (Figure: 1). Dendrogram revealed the swine isolates grouped together in a cluster and separate from the human isolates. PCR detected the presence of integron in 9 swine isolates. We also detected aphA1-tetB genes from swine and blaPSE1 gene in one human isolate.

Discussion and Conclusions: Integron detected among S.Muenchen isolates seen in this study in swine has never been reported so far. This resistance pattern is similar to the one found above in Typhimurium though Muenchen had both kanamycin and chloramphenicol resistance at the same time. This indicates that both the serotypes are capable of exchanging resistance genes among each other. Detailed molecular studies are being carried out at present. Though most of the human isolates were susceptible, a single isolate was resistant to 10 out of 12 antibiotics and also had the gene for integron. Fingerprinting analysis showed separate cluster formation between the swine and human clinical isolates showing genetic diversity based on host. The most common resistance pattern and phage type in swine non-clinical isolates was not seen at all in the clinical cases. Based on fingerprinting results, we observed phenotypic and genotypic dichotomy based on the type of isolate (clinical or non-clinical) and not on the host involved. This indicates that the predominant MDR strains of Typhimurium from swine may not be important causes of foodborne illnesses in humans and that there are other foci of infections as supported by recent model.

References: