Abstracts from poster sessions (by alphabetical order of first author)

Molecular epidemiology of multidrug resistant *Salmonella enterica* serovar Typhimurium isolated from swine and humans

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Background: Previously, we reported that multidrug resistant (MDR) *Salmonella enterica* serovar Typhimurium with two distinct resistance phenotypes: AmCmStSuTe and AmKmStSuTe were common among isolates from swine particularly, the latter R-type. In this study, we analyzed genotypes and genetic determinants to compare isolates from human and swine and characterized strains based on genetic diversity and identified virulence factors to discern explanation why distinct MDR strains are common in swine but not among human clinical isolates.

Methods: We used pulsed field gel electrophoresis (PFGE) and amplified fragment length polymorphism (AFLP) to determine genotypic diversity of 202 swine isolates and 215 human isolates as recommended by the CDC. We also tested for the carriage of *Salmonella* plasmid virulence genes *spvA*, *spvB*, *spvC*, *spvD* and a regulator gene *spvR*.

Results: More than 80% of the human isolates were susceptible to all antimicrobial agents tested. None of the MDR types among diagnostic specimens (human as well as swine) exhibited the R-type, AmKmStSuTe, which is common in healthy swine as shown in our previous research. Using PFGE analysis, we were able to discriminate that there is genotypic dichotomy between diagnostic and research isolates irrespective of the host involved. PCR analysis of *spv* genes also clearly showed that *spvR* is present in diagnostic isolates but not in the common AmKmStSuTe research isolates. AFLP fingerprinting analysis using the Pearson-pair-wise algorithm and UPGMA clustering also resulted in 16 clonal groups.

Conclusion: Our study indicates that the most common MDR types found in healthy swine are distinctly different from the ones commonly found in clinical cases (swine and human) as determined by molecular epidemiology analysis. This can be explained partially by the lack of important virulence factors such as *spvR*, which at the same time make the most common MDR strain among healthy pigs more fit for survival in the gastrointestinal tract.

Typing and characterization of *Leishmania* sub-clinical isolates from Nuba Mountain, west of Sudan

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The proved PCR positive field samples (The Green Valley Village, Nuba Mountain, west of Sudan, August 1995, February 1996 and October 1996 collections) using leishmania specific primers AJS3 & DB8; total of 32 samples (Barker, Cambridge) were tested for typing and characterization of the parasite using different genes targeted PCR which include: the mini-exon (ME), glucophosphate (gp63), internal transcript spacer (ITS), and random amplified polymorphic DNA (RAPD). Selected genes targeted PCR proved to be not sensitive to detect clinical samples collected by filter paper blood spotted samples, compared with cultured WHO reference samples, but ITS, GP63 and RAPD tools showed promising results in identification and typing of parasites encountered specially if probing technique used. For specification various non-donovani samples were included. Gene targeted PCR studies were performed in LSH & TM, UK (Prof. Miles unit).

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Keywords: *Leishmania*; Polymerase chain reaction (PCR); Typing; Characterization

The ecology and genetics of a host-shift: *Microbotryum* as a model system

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The need to prevent and cure emerging diseases often precludes their continuing study in situ. We present studies on the process of disease emergence by host-shifts using the model system of anther-smut disease (*Microbotryum violaceum*) on the plant genus *Silene* (Caryophyllaceae). This system has little direct social impact, and it is readily amenable to experimental manipulation. Our