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Abstract (oral session)

Integrating functional genomics with phenomics to better understand the mechanisms of host adaptation amongst serovars of Salmonella enterica subspecies enterica

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Objectives: To better understand the mechanisms maintaining the non-overlapping distribution of different Salmonella enterica serovars amongst common livestock species. Methods: Two serovars of Salmonella enterica subspecies enterica with distinct isolation frequencies from livestock production in the UK between 2000 and 2010 were selected for study. Serovar S. Derby was most frequently isolated from turkeys and pigs, while the serovar S. Mbandaka was most commonly isolated from chickens and cattle. Both annually caused approximately 50 clinical cases. Two isolates of each serovar were selected to undergo full genome sequencing, functional annotation, metabolic reconstruction and phenomic profiling using Biolog(tm) PM technology. The results of functional genomic analyses were used to inform the design of additional laboratory experiments. Results: The genome sequence of S. Derby D1 and D2 contained 102 unique ORFs that were absent from the genome sequences of S. Mbandaka M1 and M2, all of which were of hypothetical status. Biolog PM technology showed that D-galacontic acid gamma-lactone and L-tartaric acid, common components of plant material, were only utilised as carbon sources by S. Mbandaka. A new putative Salmonella pathogenicity island, SPI-23, was described from the chromosomal sequence of S. Derby. S. Derby isolates also showed increased adhesion and invasion of IPEC-J2 cells, a higher degree of antimicrobial resistance to commonly used drugs and the ability to express type 1 fimbriae at 37 o^C. S. Mbandaka possessed the ability to form biofilms at 25 o^C. Conclusion: The results suggest that S. Derby is better adapted to infection and persistence within a porcine host than S. Mbandaka, whereas S. Mbandaka appears to be better adapted to persist in the external environment. These adaptations may reflect niche partitioning during the cyclic process of pathogenesis and re-infection.