Characterisation of ESBLs conferring resistance to \( \beta \)-lactams in multi-drug resistant \textit{Salmonella} Concord

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BACKGROUND

- Treatment of salmonellosis using first line antibiotics such as the \( \beta \)-lactam antibiotics ampicillin and amoxicillin have failed 1
- \textit{Salmonella} Concord infections is emerging in children adopted from Ethiopia now living within Europe and United States 2
- The \( S. \) Concord isolates in this study are ESBL producers and predominantly multi-drug resistant (MDR) which is a major concern for treatment
- Positive correlation has been observed in the significant rise in the number of \( S. \) Concord infections in adopted Ethiopian children from 2004 and the resistance against extended-spectrum cephalosporins 3

AIMS:

- Determine the multi-drug resistant regions in \( S. \) Concord isolates that have been sequenced by Whole Genome Sequencing (WGS) using bioinformatics, which has not been undertaken fully before.
- Furthermore, phenotypic susceptibility testing was done on all \( S. \) Concord isolates, following the guidelines provided by European Committee on Antimicrobial Susceptibility Testing (EUCAST)

METHODS

- Bioinformatic analysis was performed on three Ethiopian isolates 527, 537 and 408 that were known to be multi-drug resistant
- Due to incomplete assembly of sequence data, location of the ESBL genes, either on plasmids or chromosome cannot be determined, only partial characterisation of the drug resistant region can be completed

RESULTS

- Genotypic analysis was performed on three Ethiopian isolates 527, 537 and 408 that were known to be multi-drug resistant
- Due to incomplete assembly of sequence data, location of the ESBL genes, either on plasmids or chromosome cannot be determined, only partial characterisation of the drug resistant region can be completed

DISCUSSION AND CONCLUSION

- Resistance to ESBL in 8 isolates is shown phenotypically and is due to the presence of \( \text{bla}_{\text{TEM-1}} \) and \( \text{bla}_{\text{SHV-12}} \)
- Current bioinformatics tools are not able to confirm that the mechanisms causing ESBL resistance in this study are plasmid-mediated or chromosomal, due to the short reads produced by the use of Illumina Sequencing on the three highly resistant Ethiopian isolates
- Despite displaying a large resistance profile (with all strains appearing sensitive to fosfomycin only), not all resistance genes to these antibiotics were found during genomic analysis
- In conclusion, multi-drug resistance, especially resistance to \( \beta \)-lactams is a problem for treatment of \( S. \) Concord
- The possible mechanisms causing spread of ESBL resistance in \( S. \) Concord is most likely due to acquisition of plasmids or drug resistance cassettes from \( E. \) coli, Klebsiella and other \textit{Salmonella} spp., through horizontal gene transfer. Further work must be conducted to confirm this
- Investing in surveillance systems is required to establish antimicrobial resistance trends and determine the mechanism by which resistance determinants are transferred within and between bacterial species
- This will aid public health interventions

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REFERENCES