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Escherichia coli tetracycline-resistant-genes relative to antibiotics overuse and their impact on the environment

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etracycline resistance (Tc^r) is dramatically increasing, causing serious worldwide environmental problems. One hundred and eighteen antibiotic resistant Escherichia coli strains from chicken intestine, human feces and treated-sewage-effluent (TSE) were isolated and identified biochemically. Out of these strains, 55% E. coli strains were Tc^r. For the latest comparison with the new technologies, the Tc^r isolates were re-identified by their protein patterns using MALDI-Biotyper and their identity were confirmed by the 16S rRNA sequencing. Single and multiplex PCR were applied to screen isolates for 14 tet genes and were found to be positive for seven tet genes (A, B, C, M, Q, W, 32). The genes were sequenced and their identities were confirmed using BLAST, NCBI. Among the resistant isolates, tet A was the most similar gene (83% identity) followed by tet B (78.5% identity) and tet 32 (38.5% identity) while the rest tet determinants occurred at a very low frequency. Many strains contained multiple Tcr determinants. Some strains contained

4 resistant genes *tet* (A/B/C/32) and *tet* (A/B/M/32). The 4 *tet* gene-combination is reported for the first time in this study. The Tcr isolates showed a high variation of *tet* gene combination. The increase in the resistance of tetracycline with high divarication is an indication of the abuse of this antibiotic and its serious impact on the environment. Strict regulation enforcement in this region is urgently needed to control and prevent the spread of resistant strains.

Speaker Biography

Mahmoud W Yaish is a Canadian Scientist. He finished his PhD degree from the University of Leon, Spain in 2002. He worked at the University of Waterloo, Canada as Post-doctoral Researcher during the period between 2003 and 2006, then he moved to the University of Guelph, Canada and worked as a Post-doctoral fellow between 2006 and 2009. After that, he obtained a faculty position at Sultan Qaboos University, Oman. His major research interest focused on studying the contribution of endophytic microbiome in salinity tolerance mechanisms of plants. During his scientific journey, he has published more than 23 scientific papers in prestigious journals.

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