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Fate of Tetracycline Resistance Genes in Aquatic Systems: Migration from the Water Column to Peripheral Biofilms

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Abstract:

Antibiotic resistance genes (ARGs) are emerging contaminants that are being found at elevated levels in sediments and other aquatic compartments in areas of intensive agricultural and urban activity. However, little quantitative data exist on the migration and attenuation of ARGs in natural ecosystems, which is central to predicting their fate after release into receiving waters. Here we examined the fate of tetracycline-resistance genes in bacterial hosts released in cattle feedlot wastewater using field-scale mesocosms to quantify ARG attenuation rate in the water column and also the migration of ARGs into peripheral biofilms. Feedlot wastewater was added to fifteen cylindrical 11.3-m^3 mesocosms (some of which had artificial substrates) simulating five different receiving water conditions (in triplicate), and the abundance of six resistance genes (*tet*(O), *tet*(W), *tet*(M), *tet*(Q), *tet*(B), and *tet*(L)) and 16S-rRNA genes was monitored for 14 days. Mesocosm treatments were varied according to light supply, microbial supplements (via river water additions), and oxytetracycline (OTC) level. First-order water column disappearance coefficients (k_d) for the sum of the six genes (tet^R) were always higher in sunlight than in the dark (−0.72 d^{-1} and −0.51 d^{-1}, respectively). However, water column k_d varied among genes (tet(O) < tet(W) < tet(M) < tet(Q); tet(B) and tet(L) were below detection) and some genes, particularly tet(W), readily migrated into biofilms, suggesting that different genes be considered separately and peripheral compartments be included in future fate models. This work provides the first quantitative field data for modeling ARG fate in aquatic systems.