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Indirect Evidence of Transposon-Mediated Selection of Antibiotic Resistance Genes in Aquatic Systems at Low-Level Oxytetracycline Exposures

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Abstract:

Subinhibitory levels of antibiotics can promote the development of antibiotic resistance in bacteria. However, it is unclear whether antibiotic concentrations released into aquatic systems exert adequate pressure to select populations with resistance traits. To examine this issue, 15 mesocosms containing pristine surface water were treated with oxytetracycline (OTC) for 56 days at five levels (0, 5, 20, 50, and 250 $\mu\text{g L}^{-1}$), and six tetracycline-resistance genes (*tet(B)*, *tet(L)*, *tet(M)*, *tet(O)*, *tet(Q)*, and *tet(W)*), the sum of those genes (*tet^R*), “total” 16S-rRNA genes, and transposons (Tn916 and Tn1545) were monitored using real-time PCR. Absolute water-column resistance-gene abundances did not change at any OTC exposure. However, an increase was observed in the ratio of *tet^R* to 16S-rRNA genes in the 250 $\mu\text{g L}^{-1}$ OTC units, and an increase in the selection rate of *Tc^r* genes (relative to 16S-rRNA genes) was seen when OTC levels were at 20 $\mu\text{g L}^{-1}$. Furthermore, *tet(M)* and Tn916/1545 gene abundances correlated among all treatments ($r^2 = 0.701$, $p = 0.05$), and there were similar selection patterns of *tet^R* and Tn916/1545 genes relative to the OTC level, suggesting a possible mechanism for retention of specific resistance genes within the systems.

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