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ANTIBIOTIC RESISTANCE POLLUTION IN PHARMACEUTICAL WASTEWATER BIOLOGICAL TREATMENT SYSTEMS

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Abstract

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To investigate the effects on resistance development under long-term antibiotic selection pressures, wastewater and biomass samples from antibiotic production wastewater (APW) treatment plants as well as antibiotic production wastes were taken and analyzed. Clone libraries, real-time PCR, and a high-throughput functional gene array (GeoChip 3.0) analyses were used to evaluate the functional structure of microbial communities from two plants, which treat APW containing high concentrations of oxytetracycline (OTC). Eleven tetracycline resistance genes (tet) and three mobile elements were detected by PCR. Eight frequently reported tet genes (tet(A), tet(C), tet(L), tet(M), tet(O), tet(Q), tet(W) and tet(X)), Class 1 integrons (Int11), and transposon Tn916/1545 were successfully quantified by real-time PCR. The relative abundances of tet genes and Int11 in the treated effluent and activated sludge were higher than those in the OTC production wastes, and were 1-4 log higher than those from sewage treatment plants, showing that it may be necessary to regulate the discharge of the effluents and sludge from APW treatment plants. A high release of Int11 was also found in the effluent and sludge. According to GeoChip analysis, antibiotic resistance and transporter genes (559 genes) were abundant in bacteria and gene signal intensity positively correlated with antibiotics in APW biological systems. A total of 29.0% of the microbial community variation could be explained by antibiotics. This study provides insights into microbial functional gene structure in APW biological treatment systems, revealed the relative high antibiotic resistance gene discharge from APW biological systems.