

Transcriptomic response patterns of hornyhead turbot (*Pleuronichthys verticalis*) dosed with polychlorinated biphenyls and polybrominated diphenyl ethers

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To evaluate the impact of environmental contaminants on aquatic health, extensive surveys of fish populations have been conducted using bioaccumulation as an indicator of impairment. While these studies have reported mixtures of chemicals in fish tissues, the relationship between specific contaminants and observed adverse impacts remains poorly understood. The present study aimed to characterize the toxicological responses induced by persistent organic pollutants in wild-caught hornyhead turbot (*P. verticalis*). To do so, hornyhead turbot were interperitoneally injected with a single dose of PCB or PBDE congeners prepared using environmentally realistic mixture proportions. After 96-hour exposure, the livers were excised and analyzed using transcriptomic approaches and analytical chemistry. Concentrations of PCBs and PBDEs measured in the livers indicated clear differences across treatments, and congener profiles closely mirrored our expectations. Distinct gene profiles were characterized for PCB and PBDE exposed fish, with significant differences observed in the expression of genes associated with immune responses, endocrine-related functions, and lipid metabolism. Our findings highlight the key role that transcriptomics can play in monitoring programs to assess chemical-induced toxicity in heterogeneous group of fish (mixed gender and life stage) as is typically found during field surveys. Altogether, the present study provides further evidence of the potential of transcriptomic tools to improve aquatic health assessment and identify causative agents.

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