



Comparative transcriptome analysis of Nile tilapia (*Oreochromis niloticus*) in response to alkalinity stress

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ABSTRACT. To identify genes of potential importance to alkalinity tolerance, RNA sequencing (RNA-Seq) was performed to survey gill transcriptome profiles from freshwater (FW) and alkaline water (AW) exposed Nile tilapia (*Oreochromis niloticus*). A total of 22,724,036 (AW)/16,461,040 (FW) single-end reads were generated in which 20,304,348 (AW)/14,681,290 (FW) reads (90.0/89.72%) were aligned to the reference genome. Differential expression analysis revealed 302 up-regulated and 193 down-regulated genes between AW- and FW-exposed fish. These differentially expressed genes were enriched in several Gene Ontology (GO) terms related to “stress response”, “heme binding”, and “carbonate dehydratase activity”. Meanwhile, significant KEGG pathways were enriched in energy metabolism, including nitrogen and sulfur metabolism. These results demonstrate the response of Nile tilapia exposed to alkaline-water and might provide valuable information to further understand the molecular mechanisms of adaptation of fish to alkaline environments.

Key words: Alkalinity stress; Nile tilapia; Transcriptome; Carbonate