Deciphering the Genetic Blueprint of Salinity Resilience in Taiwan Tilapia Oreochromis spp Unlocking Osmoregulatory Networks for Next Generation Breeding

Chung-Ping Chiang[1], Pei-Yun Chu[1,2], Te-Hua Hsu[1,2], Hong-Yi Gong[1,2], and Chang-Wen Huang*†[1,2]

[1]Department of Aquaculture, National Taiwan Ocean University, Keelung 202301, Taiwan – Taïwan
[2]Center of Excellence for the Oceans, National Taiwan Ocean University, Keelung 202301, Taiwan – Taïwan

Résumé

Salinity tolerance is a critical trait in aquaculture, particularly for *Oreochromis spp.*, where genetic variation significantly influences the capacity for adaptation to high-salinity environments. In this study, we investigated the genetic composition and transcriptomic adaptation of a salinity-tolerant (ST) strain of Taiwan tilapia to elucidate the molecular mechanisms underlying salinity adaptation. Mitochondrial DNA PCR-RFLP analysis confirmed that the ST population predominantly belongs to *O. mossambicus*, whereas microsatellite markers (UNH899, UNH896, UNH773, and UNH155) indicated introgression from *O. niloticus*, revealing a complex hybrid genetic background. Transcriptome analysis identified differentially expressed genes (DEGs) associated with osmoregulation, including significant upregulation of *inositol monophosphatase 1* (IMPA1) in the brain (5.51-fold), gill (6.67-fold), and head kidney (6.55-fold), suggesting its pivotal role in long-term osmotic stress adaptation. Comparative analysis highlighted significant enrichment of the AMPK signaling pathway, which may compensate for the downregulation of immune-regulatory pathways observed in seawater-adapted strains. Salinity tolerance tests demonstrated that ST progeny exhibited higher survival rates at 32 psu compared to hybrid (SH) and salt-intolerant (SS) strains, confirming the heritability of this trait. Microsatellite marker analysis identified candidate loci associated with salinity resilience, including *MHC class II antigen (Orni-DAB)*, suggesting a potential interaction between immune modulation and osmoregulation. These findings provide a comprehensive understanding of the genetic basis of salinity tolerance in Taiwan tilapia, offering valuable insights for marker-assisted selection (MAS) and the development of high-salinity aquaculture strains. The identified molecular markers and candidate genes represent a powerful resource for enhancing selective breeding programs, thereby promoting sustainable aquaculture in saline environments.

Mots-Clés: Salinity tolerance, Transcriptomics, Microsatellite markers, AMPK signaling pathway, Tilapia breeding

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*Intervenant

†Auteur correspondant: cwhuang0116@gmail.com