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## Genome-Wide Association Analysis of adaptation to oxygen variations in Nile Tilapia (*Oreochromis niloticus*)

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Tilapia is one of the most abundant species in aquaculture for their relative ease of culture. Global production of Tilapia has increased rapidly driven by improvement of selection in breeding program. However, due to high stocking, high density and high biomass per cubic meter in pond systems, a low oxygen environment arises especially at the end of the night in many farms, which leads to a high mortality. Growth traits are treated as indicators of hypoxia stress in previous studies, but little is known about adaptation to chronic low oxygen levels in Nile Tilapia. To investigate the genetic architecture of hypoxia adaptation, a Genome Wide Association Study (GWAS) was applied based on genotyping-by-sequencing in the 16<sup>th</sup> generation GIFT (Genetically Improved Farmed Tilapia) population, consisting of 2,300 fish. Fish were measured from stocking to harvest for body weight (BW) in aerated (normoxia) and non-aerated (hypoxia) environment. A GWAS was performed in order to identify candidate variants that are associated with growth under different oxygen conditions. Result shows that 36 genome-wide significant and suggestive SNPs associated with early (BW1) to latest (BW5) timepoints in the growth period. Six SNPs between 19.48 Mb and 21.04 Mb on Linkage group (LG) 8 attained a genome-wide significant level with body weight at BW1, BW2 and BW3 in hypoxia environment. The effect of two SNPs (LG1: 30766342, LG1:30766336) reached suggestive levels from BW3 to BW5. 48 and 31 genes were identified in the early and later growth stage separately. Intriguingly, candidate genes *rora*, *adamts3* and *efna3a* are reported related to hypoxia in other species. In contrast, 29 unique significant and suggestive SNPs were found across growth period in the normoxia environment. The significance of those SNPs declined from BW1 to BW3. In a meta-analysis on hypoxic and normoxic environments together, 31 SNPs were significantly associated with growth. Genes such as *rara*, *tbc1d24*, *rora*, and *bahcc1* were involved in both environments. Our findings provide candidate genes involved in growth under normal and oxygen-depleted growth conditions.