

Abstract 43:

Genomic selection and introgression signatures resulting from adaptation to high salinity: a case study on an Indonesian farmed tilapia (Sukamandi) strain

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Background: Tilapia is currently the most important fish in aquaculture in the tropics and subtropics. Originally a freshwater species, it is cultured in a wide range of conditions. Among the most challenging is when high salinity is involved, e.g. culturing in estuaries or high salinity ponds in polyculture with shrimp. Optimized tilapia strains generally do not tolerate high salinity well. Although the physiological adaptation for osmoregulation is reasonably well understood, it is less clear how selection results in salinity tolerance. Here we investigate one such strain that was bred to perform well in brackish water. Specifically, we infer signatures of selections in the genome. In addition, since the salinity tolerance in the strain was hypothesized to be derived from another species, we also inferred signatures of introgression between species.

Results: The local Indonesian farmed tilapia (Sukamandi) strain, is based on four generations of selection in water salinity varying from 15 to 58 ppt. We compared the genome of this Sukamandi strain to that of Nile tilapia (*Oreochromis niloticus*) and blue tilapia (*Oreochromis aureus*), the latter a putative donor of the salinity tolerance. Our results indicate that the Sukamandi strain is genetically much more similar to Nile tilapia (*Oreochromis niloticus*) ( $F_{st}=0.042$ ) than to blue tilapia (*Oreochromis aureus*) ( $F_{st}=0.386$ ). Analysis of genes located in genetically differential regions showed significant involvement of ion transmembrane transport processes, such as MAPK3 activity, potassium ion homeostasis, ATPase activity and response to calcium ions. Combining genome-scale scanning for selection and introgression revealed that salinity tolerance related genes, such as *caprin1a*, *nucb2a*, *abcb10*, *cacna1ab*, *ulk2*, *slc25a24* and *cdh1* were strongly selected. While the genome of the Sukamandi strain appears to be overwhelmingly of Nile tilapia origin, some introgression from blue tilapia may have conferred some of the observed salinity tolerance.

Conclusion: Artificial selection and inter-species introgression in the tilapia Sukamandi strain, have resulted in a non-random retainment of genes derived from the introgressed species. Introgression also increased standing variation in the target trait, while directional selection enhanced the adaptivity of the introgressed individuals. Our findings support further selective breeding of tilapia tolerant to high salinity conditions.