

GENETIC SELECTION OF PERCIFORM FISHES: FUNCTIONAL GENOMIC POTENTIAL OF NATURAL AND CULTURED POPULATIONS

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With a growing world population and recurrent problems of hunger and malnutrition, food security is of major societal and international concern. The growing need for nutritious and healthy food will increase the demand for fishery resources. Unfortunately, the production of marine capture fisheries is close to the maximum ecosystem productivity and cannot be increased substantially in the future. Therefore, the interest in aquaculture has grown substantially the last 40 years. To ensure a sustainable development of aquaculture, the selection criteria have to lead to an improvement in production efficiency and a greater adaptability of the selected animals. The rapid advances of genomic technologies that lead to large amounts of genomic information will show the way for a selection procedure solely based on the genotype. In this project we exploit the large amount of available genomic data of fish species to identify, both between and within species, functionally important regions and selection-sensitive areas. Our main objective is the study of functional genomic regions susceptible to positive selection in sea bass. The project has four major objectives: 1) identification of potential selection-sensitive areas by an in silico comparison of three fully sequenced Perciform genomes (stickleback, Nile tilapia and sea bass); 2) Development of genetic markers for a genome scan of natural and cultured populations of sea bass; 3) Genome scan and candidate gene analysis in natural populations of sea bass, and 4) Genome scan and candidate gene analysis in cultured sea bass populations.