

Reconstruction of whole-genome metabolic model of Atlantic salmon *Salmo salar* (SALARECON)

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Introduction: Atlantic salmon *Salmo salar* is Norway's main livestock and the biggest export commodity after the oil. Currently, the plant feedstock is the main feed for the farming salmon, consequently, it influences both growth rate and quality of the fish biomass. The whole-genome (WG) metabolic model of *S. salar* (SALARECON) will allow multifactorial optimization of the fish growth conditions by means of a diet for the application in salmon farming. Special interest will be paid to the optimization of fat yield and growth limitations due to dietary amino acids. The reconstruction of WG metabolic model requires integration of available genomic, biochemical and physiological information.

Methods: The genome and metabolic information are available at NCBI and KEGG. The SALARECON is the integrated stoichiometric model that describes steady state growth of the biomass. The reconstruction workflow includes: (1) Gene-Protein-Reaction associations (GPRs) using in-house SAPP system; (2) network setup and network topological analyses; (3) Flux Balance Analysis for optimization of the network using Insilico Discovery package. The model allows integration of high-throughput experimental omics-data (transcriptomics, proteomics, metabolomics).

Results and Discussion: The model integrates all important biochemical reactions/pathways that lead to polymerization of major biomass constituents: proteins, carbohydrates, fats/lipids, polynucleotides. The modeling methodology is based on energy-centric approach because energy- and redox-balances in different subcellular compartments play a central role in coupling and harmonizing activities of different metabolic modules and pathways. The energy costs for the ion balance is one of the main contributor to the maintenance costs. The model will be optimized for two osmotic scenarios: fresh and sea waters.

Currently, the SALARECON integrates 311 transformer steps (performed by products of 931 genes), 255 balanced compounds belonging to 56 pathways which are allocated in 3 compartments. For the network reconstruction, the in-house developed SAPP system is used to predict GRP associations as well as subcellular compartment localizations of the corresponding biochemical reactions.

The model aims to optimize a whole range of possible diets of farmed salmon. Exact formulation of the biomass composition (model's output) defines the input fluxes through the network of reactions, which are compared with experimentally measured dietary requirements. The model is validated using variety of experimental omics-data.