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Comparative transcriptomics in Gadus morhua and Boreogadus saida under different temperatures and PCO2 levels



Biosciences - Integrative Ecophysiology

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ties for acclimation determined by different evolutionary backgrounds.

cular genetic signatures of adaptation profils in relation to physiological per-tures and dynamics in Boreogadus in Boreogadus saida and Gadus formance parameters under combined saida and Gadus morhua over time morhua to qualify their different capaci- PCO, and temperature treatments to and possibly in relation to transcriptoevaluate species' fitness under future mic data, to project future distribution climate change projections.

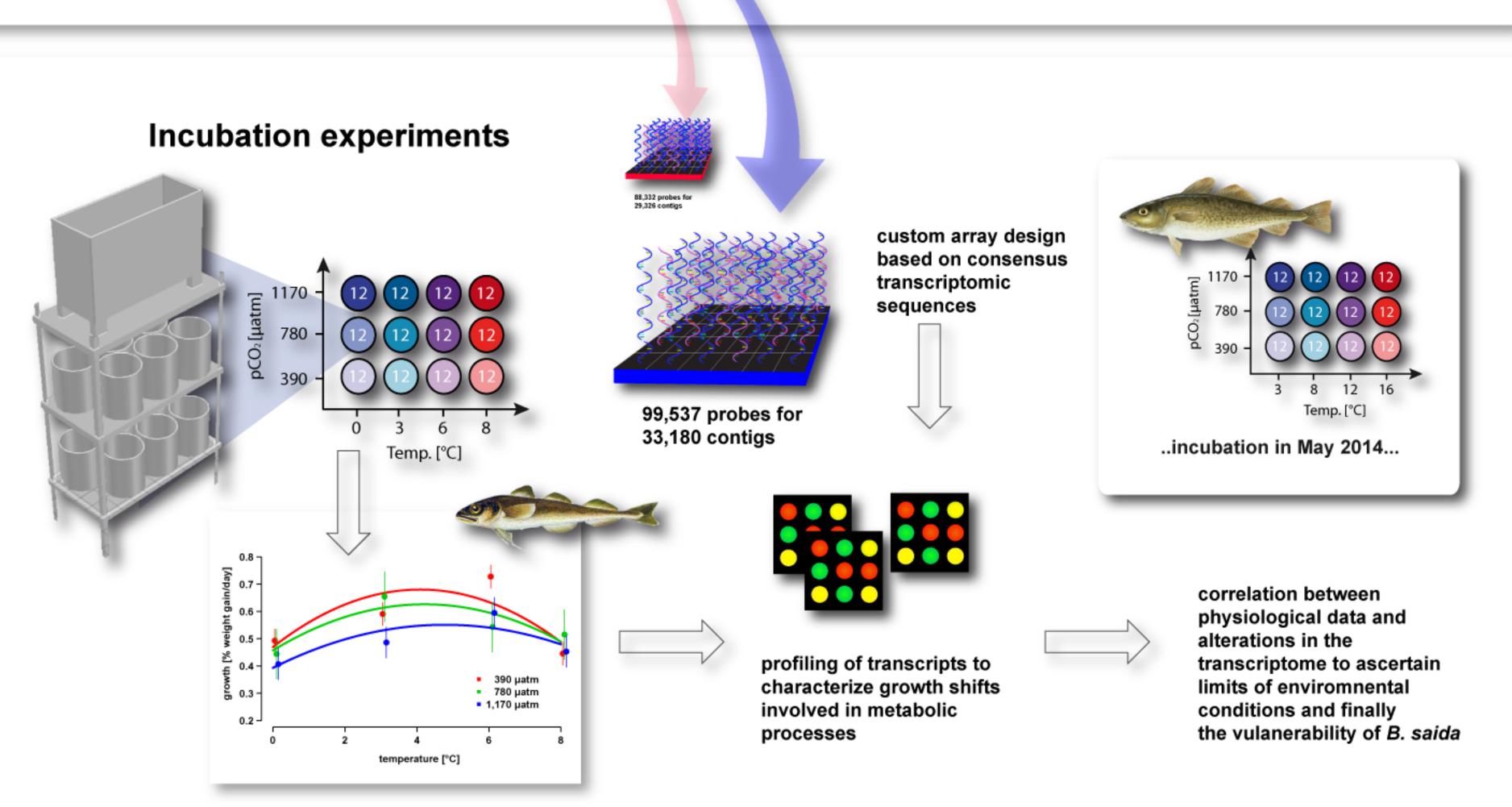
Objectives 1. Investigation of mole- 2. Characterization of gene expression 3. Characterization of population strucpatterns and species interaction.

Sequence comparisons

DNA/RNA sequences as well as their respective translations of both cod species are being compared through analyses of normalized transcriptomic cDNA libraries. Orthologous sequences are used for codon and amino acid usage profiles as well as for the construction of a gadid-specific array. Moreover, as both libraries were built from 6 specimen (3 male + 3 female) we are able to localize SNPs in the transcriptome. A set of these polymorphisms will be used for population genetic studies.

G. morhua Function unknown B. saida workflow General function prediction only Secondary metabolites biosynthesis, transport and catabolism Q paired - end sequencing 3.8 Gb 2.5 Gb G. morhua and Trinity assemblies best peptide models 174,209 145,706 Carbohydrate transport and metabolism G per gene blastp vs ENSEMBLE 46,857 37,281 Gmor 1.73 pep.all Cell wall/membrane/envelope biogenesis M core-set of 11,902 orthologous sequences in both species Cell cycle control, cell division, chromosome partitioning D Chromatin structure and dynamics B core peptide alignments, sequence selection for analyses of amino acid usage gadid-specific microarray RNA processing and modification A Translation, ribosomal structure and biogenesis core cDNA alignments, analyses of codon usage 34,956 counts of fiNOGs in COG (categories of orthologous goup) 11,901 25,380 9,368 Functional characterization of sequences by assigning transcripts with fish-specific 1,432 Non-superwised orthologous groups (fiNOGs)

Transcriptomic profiling The effects of combined temperature and CO, treatments will be assessed after long-term incubation in several tissues of B. saida and G. morhua at the transcriptomic level. Together with physiological performance parameters we will be able to characterize species' fitness as well as their vulnerability. To this end, a gadid-specific microarray is under construction to track changes of biological processes, cellular components and molecular functions under different conditions.



Population genetics

The composition of different cod populations will be analyzed through microsatellite and SNP analyses giving information about dynamics of stock development over time. For G. morhua data from beginning 1990ies are available, for B. saida data over longer time scales are scarce. Recent catches from 2012-2013 are depicted in the two maps.

