Animal Welfare in Aquaculture

EFFECTS OF INCREASING SALINITY ON MARAENA WHITEFISH *COREGONUS MARAENA* IN THREE DIFFERENT FARMING SYSTEMS

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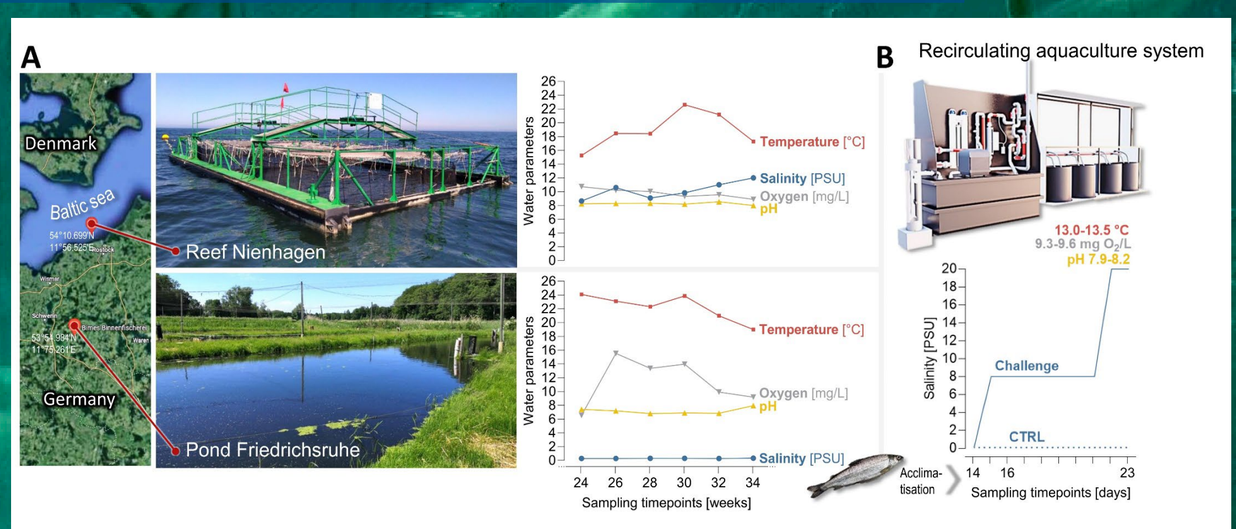
- A qPCR panel of salinity biomarkers has been adapted for maraena whitefish
- *Atp1a1a* levels in the gills of whitefish reflect adaptation to higher salinities
- *Eef2*, *ghr* and *wasf1* dominate transcriptional salinity response across tissues
- Maraena whitefish was not negatively affected by salinities up to 20 PSU

Introduction

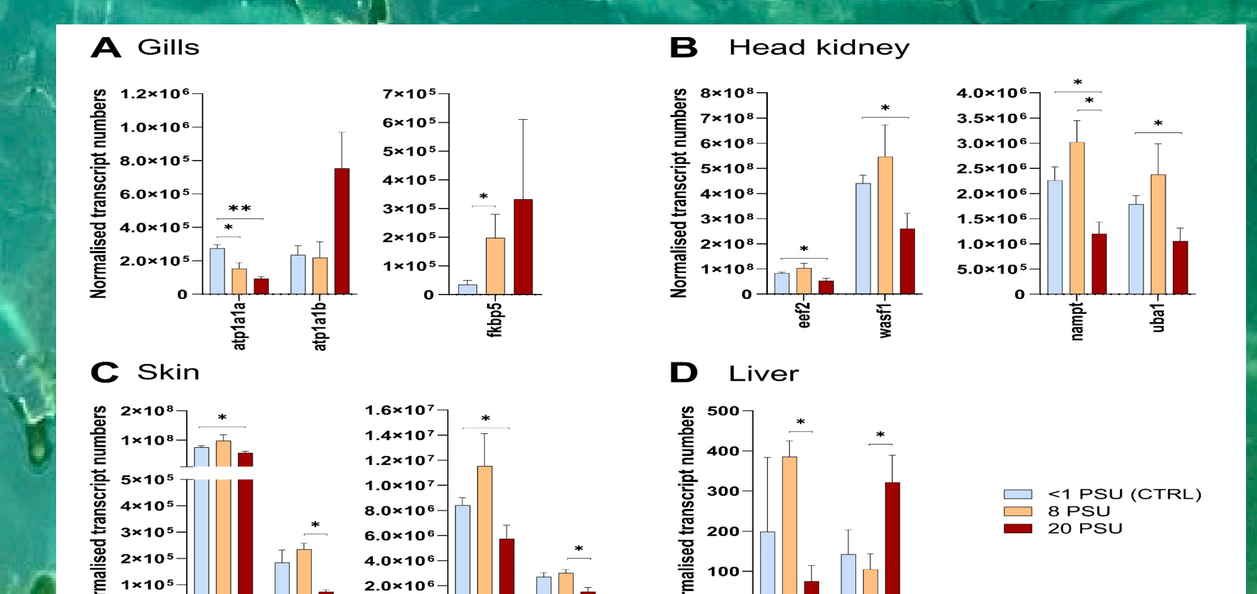
The present study investigated the influence of salinity fluctuations on gene-expression patterns in maraena whitefish (*Coregonus maraena*) from three aquaculture facilities. We monitored the expression of an established panel of seawater-tolerance biomarkers in four tissues of whitefish over a period of ten weeks. Fish were kept in a natural reef in the South-western Baltic Sea with locally rapidly changing salinity conditions and compared to conspecifics from a freshwater-pond system. The largely consistent expression profiles across whitefish from both habitats provided only sporadic modulations of most genes. A principal component analysis revealed that these differential expression patterns were dominated by *eef2*, *ghr* and *wasf1*. A subsequent salinity experiment was carried out in a recirculating aquaculture system under constant environmental conditions.

Results

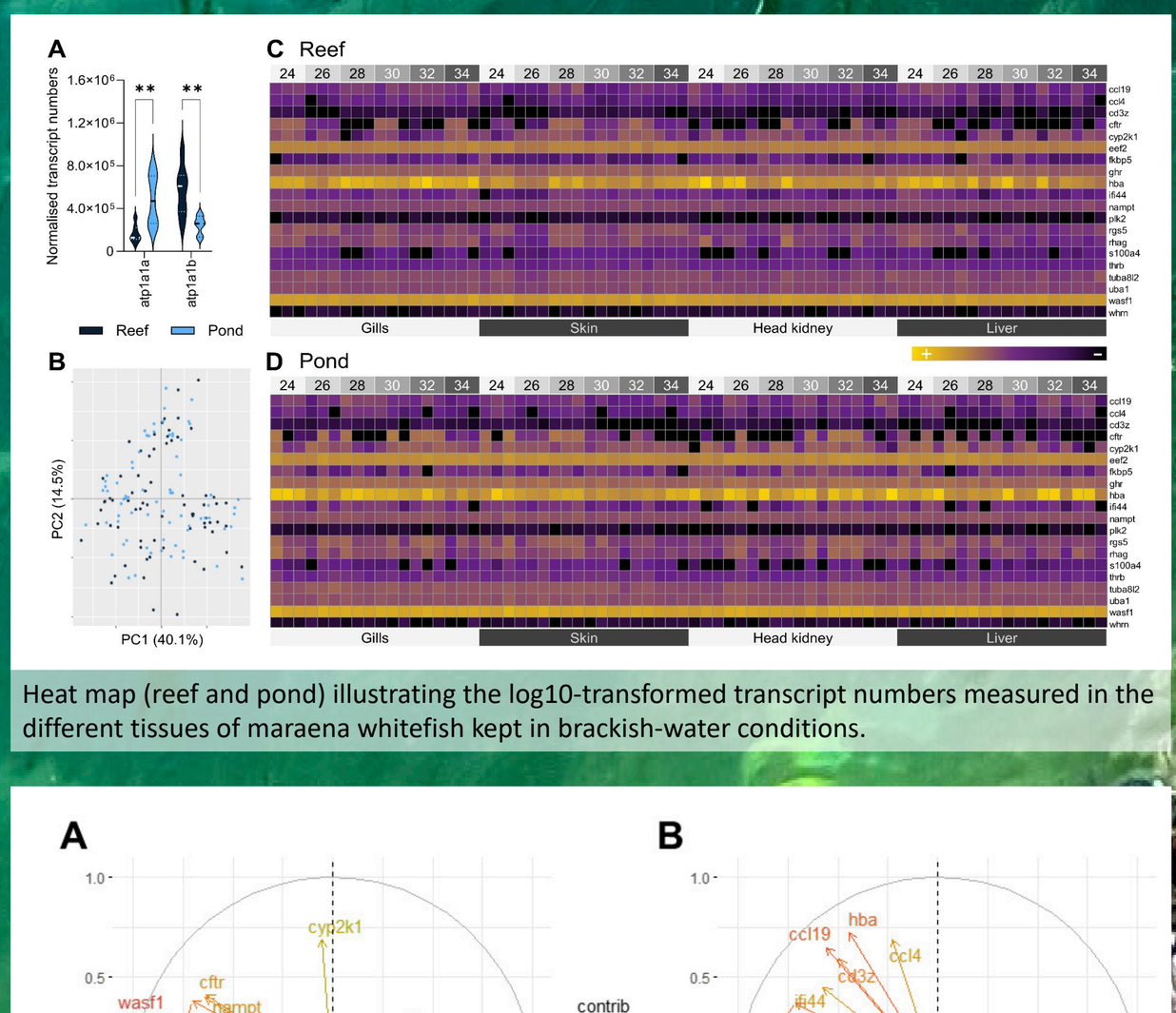
The elevation of salinity from 0 to 8 PSU was only indicated by the significantly increased *fkbp5* and *atp1a1a* transcript levels in the gills of whitefish. The reduced levels of *eef2*, *ghr*, *wasf1*, nampt, and *uba1* in the head kidney or skin or both tissues indicated the response mechanism to higher salinity (20 PSU). Altogether, only the quantification of the *atp1a1a* gene provided the most reliable evidence of the successful acclimation from low- to higher-salinity water in all three facilities investigated. Based on the overall transcriptional data and the generally good physical constitution, we assume that maraena whitefish was not negatively affected by salinities up to 20 PSU, but were capable of acclimating well to changing brackish-water conditions.



Overview of whitefish sampling facilities and selected local physicochemical parameters.



Bar plots of selected genes differentially expressed in the **(A)** gills, **(B)** head kidney, **(C)** liver and **(D)** skin of each three maraena whitefish exposed to salinity of <1 PSU (blue bars), 8 PSU (orange bars) or 20 PSU (red bars).



Heat map (reef and pond) illustrating the log10-transformed transcript numbers measured in the different tissues of maraena whitefish kept in brackish-water conditions.

Factor maps representing the contribution of the 20 genes analyzed to the overall separation of the PCA on maraena whitefish **(A)** exposed to <1, 8 and 20 PSU in the RAS and **(B)** fish from the reef versus pond facility.

Left: Ronald Brunner, Fabian Swirplies and Frederike Schmachtl at our experimental aquaculture facility from Kunststoff-Spranger GmbH. **Right:** Maraena whitefish for tissue sampling harvested from the pond system.

Conclusions

Good growth is crucial for the economic production of maraena whitefish. Since the start of the experiment at the brackish water Nienhagen reef site, the maraena whitefish has shown low growth rates, indicating the presence of external stressors that have apparently not affected the parallel maraena whitefish cohort from the pond management or flow-through system. Our experimental data show that European whitefish are not negatively affected by varying salinities up to 20 PSU, but are able to adapt well to fast changing brackish water conditions. During the observation period, the salinity at Nienhagen Reef in 0-5 m water depth did not exceed 12 PSU and was thus in the optimal range for coregonids. We conclude that salinity challenges are not environmental key factors that cause the low growth performance of maraena whitefish at the reef site.

References

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