

Transcriptomic analysis of physiological effects for acute salinity change on Antarctic fish

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In the Antarctica peninsula region, the melting glaciers and sea ice contributes freshwater to the surface waters seasonally, and it could affect the physical and biological environment. The rate of melting glaciers and sea ice in the Antarctica is speeding up dramatically caused by global warming and climate change. However, the potential impacts of the environmental changes on marine organisms are not well characterized. Along the significant increase of air temperature, decreased salinity cause the discharging freshwater can influence the marine ecosystem including phytoplankton, diatom, and fish. In teleost, Notothenioids have evolved successfully to adapt to specific Antarctic marine ecosystems, and Antarctic bullhead notothen, *Notothenia coriiceps*, a typical Antarctic notothenioid teleost, is one of the main Antarctic fish in the Southern Ocean having higher abundant in the Antarctica peninsula. In order to improve our understanding on direct biological effects of Antarctic marine organism on the acute salinity change, transcriptomic analysis performed by RNA-Seq analysis after exposing *N. coriiceps*, to diluted salinity series (25 and 15‰) comparing control (35‰) respectively for 6 and 24 hours. Four tissues (gill, head kidney, intestine, and skin) were dissected from the fish in each group of treatment. The next-generation sequencing transcriptome library was constructed using RNA extracted the tissues. A differential expression analysis and a quantitative real-time RT-PCR was performed. The results could help to grasp biological strategies of polar marine teleost to the extreme environment.

References

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