



GÖTEBORGS UNIVERSITET

**From Geography to Genes:  
Evolutionary perspectives on salinity tolerance in the  
brackish water barnacle *Balanus improvisus***

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Akademisk avhandling för filosofie doktorsexamen i Biologi, som med tillstånd från  
Naturvetenskapliga fakulteten kommer att offentligt försvaras fredagen den 21  
februari 2014 kl. 14.00 i hörsalen, vid Institutionen för biologi och miljövetenskap,  
Lovécentret – Tjärnö, Hättebäcksvägen 7, Strömstad.

ISBN: 978-91-628-8901-2

## ABSTRACT

How species respond to changes in their environment is a fundamental question in biology. This has become an increasingly important issue as anthropogenic effects of climate change and biological invasions have major impacts on marine ecosystems worldwide. In this thesis I investigated the role of salinity tolerance from an evolutionary perspective, using a wide range of techniques, spanning from population genetics and common-garden experiments to characterizing potential genes involved in osmoregulation in barnacles. I used the acorn barnacle species *Balanus (Amphibalanus) improvisus*, which displays a remarkably broad salinity tolerance, to investigate how this trait has influenced the species' potential to establish in new environments, and respond to projected near-future salinity reductions in coastal seas. I also examined physiological and molecular mechanisms that may be involved in osmoregulation in *B. improvisus*. I further analysed population genetic structure using microsatellites and mitochondrial DNA, and related the results to anthropogenic and natural dispersal dynamics on both global and regional (Baltic Sea) scales. I found high genetic diversity in most populations, with many shared haplotypes between distant populations. This supports the hypothesis that maritime shipping is an important vector for the dispersal of the cosmopolitan species *B. improvisus*. Nonetheless, natural larval dispersal is also important on smaller geographical scales, such as within the Baltic Sea. Marked genetic differentiation between northern and southern Baltic Sea populations raises the question whether there is restricted gene flow within the Baltic Sea, creating potential for local adaptations to evolve. To investigate the extent to which the broad distribution of *B. improvisus* along the Baltic Sea salinity gradient is explained by local adaptation *versus* physiological plasticity, I performed a common-garden experiment in which multiple populations were exposed to different salinities and multiple fitness-related phenotypic traits were recorded. The experiment confirmed that phenotypic plasticity, rather than local adaptation, explained the broad distribution of the species along the salinity gradient. Interestingly, all populations of *B. improvisus* performed best at low and intermediate salinities in many fitness-related traits (survival, growth and reproduction), although other traits (e.g. shell strength and juvenile growth) indicated higher costs associated with low salinity. A candidate gene approach was used to investigate the molecular basis of broad salinity tolerance in *B. improvisus* by characterizing the Na<sup>+</sup>/K<sup>+</sup> ATPase (NAK) of *B. improvisus* – an ion transporter commonly involved in active osmoregulation in many species. We identified two main gene variants in *B. improvisus* (NAK1 and NAK2), and found that NAK1 mRNA existed in two isoforms that were differentially expressed in different life stages and adult tissues, suggesting an active role in osmoregulation. Lastly, I summarise current knowledge about salinity tolerance in barnacles and outline new research directions to further our understanding of the physiological and molecular mechanisms involved in salinity tolerance in barnacles.

**Key words:** *environmental change, salinity, evolution, phenotypic plasticity, marine invertebrates, population genetics, functional genomics, barnacles, osmoregulation*