



INSTITUTIONEN FÖR KEMI OCH MOLEKYLÄRBIOLOGI

**Molecular biology of barnacle  
*Balanus improvisus* settlement**

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## ABSTRACT

The aim of this thesis was to investigate molecular mechanisms of various aspects of barnacle settlement, using the acorn barnacle *Balanus improvisus*. This barnacle is a common fouling species and a model organism for studies in settlement biology, in particular in relation to antifouling research.

In order to facilitate the development of genomic resources in this species, we conducted a pilot study for the sequencing of the *B. improvisus* genome and performed an initial genomic characterization. The analysis revealed that *B. improvisus* genome has an extremely high genetic diversity, with about 5% nucleotide diversity in coding regions. In addition, we experimentally estimated the *B. improvisus* genome size, based on DNA staining and flow cytometry measurements, resulting in a haploid genome size of 738 Mbp.

To investigate molecular changes during the settlement process, transcriptomes of four different settlement stages, ie free-swimming, close-search, attached and juvenile, were compared. We identified several key genes involved in the hormonal regulation of molting and metamorphosis, including the broad complex, ecdysone receptor and retinoid X receptor, adding a new level of insight to the molecular mechanisms involved in settlement. Furthermore, we used two types of surfaces with different wettability to test if differences in surface preferences are reflected in gene expression. The results revealed that exploration of the "favourable" hydrophobic surface induced more genes and with larger changes in expression than on hydrophilic suggesting a stronger transcriptional response.

We also investigated two specific aspects related to barnacle chemical communication during settlement - sensory receptors and pheromones. Analysis of the transcriptome of cyprid antennules resulted in the identification of two receptor classes, the chemosensory ionotropic receptors and mechanosensory receptors represented by several TRP subfamilies. We identified and characterized six homologs of the waterborne pheromone WSP in *B. improvisus* that showed differential expression during settlement. These results suggest the existence of a pheromone mix, where con-specificity might be determined by a combination of sequence characteristics and the concentration of the individual components.

With the aim to further establish *B. improvisus* into a potent marine model system, a detailed protocol was developed for an all-year-round culturing of *B. improvisus* and adapted at Tjärnö Marine Laboratory.

Finally, I summarise current knowledge on the molecular mechanisms of barnacle settlement and outline new research directions to further improve our understanding of the settlement biology of this species.

**Keywords:** barnacles, settlement, transcriptomics, ecdysone cascade, chemosensory receptors, waterborne pheromones