

IDENTIFICATION AND CHARACTERIZATION OF SEX-SPECIFIC PROTEINS AND GENES IN THE BROWN ALGA *ECTOCARPUS SILICULOSUS*

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Fertilization patterns in seaweeds are of great interest from a molecular and ecological perspective. Successful reproduction in many species depends on a delicate equilibrium between biotic and abiotic conditions. Among the factors affecting fertilization rate, we find those triggering gamete release (including water movement and light) and those affecting gamete viability, but the first and crucial step of successful reproduction is gamete recognition.

Gamete recognition in sexual eukaryotes is mediated by sex-specific proteins that are unique to the gender and species, which assures that the mating occurs between correct individuals. The sex-recognition genes show outstanding divergence, suggesting a unique selection pattern acting upon them during the speciation process. Therefore studies of the sex-specific proteins and their evolution may provide a useful insight into species isolation and diversification.

Ectocarpus siliculosus is a brown, filamentous alga that can be found in all temperate climate zones. Small size, easiness of culturing in laboratory conditions, completion of life cycle in less than 3 months and its high fertility makes it a model organism for brown algae. The life cycle of *Ectocarpus* includes both, asexual and sexual reproduction. Sexual reproduction appears in the form of isogamy, where flagellated gametes are morphologically, but not physiologically, identical. The gamete recognition in *Ectocarpus* is known to be mediated by lectin-glycoprotein complexes associated with gamete outer membranes.

The aim of this study is to isolate and characterize sex related agglutinins and explore the differences between male and female gametes on a gene expression level. We apply chromatography techniques to isolate lectins and glycoproteins basing on their specificity and Mass Spectrometry measurements to identify retained proteins. To study differential expression patterns, we have prepared a transcriptome library for both male and female gametes, using Next Generation Sequencing platform. The analysis of obtained data revealed many gender-specific and sex-regulated transcripts. Combining the two approaches mentioned above will help better understand the complex matter of sexual reproduction and speciation in brown algae.