Towards unravelling the potential of red macroalgae for human health: a molecular approach

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As food requirements are shifting towards promoting human health and avoiding disease, seaweed has attracted much interest as a natural source of bioactive compounds, which, due to their supposed health benefits, attract attention for economic exploitation. Currently there are few to none studies available that have investigated the molecular mechanisms behind the production of these metabolites. Omics tools, including transcriptomics, can potentially bridge this knowledge gap and can help in understanding the interactions between complex metabolic pathways and environmental conditions, as they sample entire transcriptomes rather than focusing on a limited set of genes.

Therefore, in this project we aim to unravel the underlying molecular pathways involved in the production of three of those identified bioactive metabolites, i.e., floridoside, phycoerythrin and phycocyanin, in the Atlantic red seaweed species Palmaria palmata, one of the most common red macroalgae on rocky shores in the Northern Hemisphere.

In this project, we have subjected the macroalgae to two different constant temperatures: 12 and 14 °C at neutral days (12 h:12 h light:dark) for two different exposure durations (i.e. two and ten days of exposure, representing an acute and sustained exposure period, respectively), with 4 replicate tanks for each exposure scenario. In addition to quantifying the concentration of the bioactive compounds of interest, we sequenced the transcriptome and studied differences in the seaweed's gene expression as the molecular processes underpinning the studied phenotypic effects. We mainly focused on the carbohydrate metabolic pathways, underpinning the production of the studied bioactive compounds, in addition to typical stress responses of the seaweed. The results obtained from this study set a base line for future studies, as we are beginning to gain crucial insights into how environmental factors influence the seaweed metabolism in addition to developing quantitative relationships linking molecular endpoints (omics) to the nutritional value of seaweed.

Keywords

Seaweed; Nutraceuticals; Bioactive compounds; Transcriptomics; Gene expression