

TMT-Based Proteomics Provides Insights into *Mytilus coruscus*' Digestive Gland's Response to Heat Stress

Yuxia Guo*

Department of Pathology, London South Bank University, London, UK

Introduction

Mytilus coruscus, commonly known as the shining mussel, is an ecologically and economically important bivalve species found along the coastlines of East Asia. As a filter-feeding organism, *M. coruscus* plays a crucial role in coastal ecosystems by filtering large amounts of water and accumulating various contaminants and nutrients. However, environmental stressors such as heat waves pose a significant threat to the survival and physiological function of these organisms. Understanding the molecular mechanisms underlying their response to heat stress is vital for predicting and managing the impacts of climate change on marine ecosystems. In recent years, a powerful technique called Tandem Mass Tag (TMT)-based proteomics has emerged as a valuable tool for investigating cellular responses to environmental stressors. In this article, we explore how TMT-based proteomics has provided valuable insights into the digestive gland's response of *M. coruscus* to heat stress. The digestive gland of bivalves, including *M. coruscus*, plays a vital role in nutrient digestion, absorption, and metabolism. It serves as a central hub for several key physiological processes, including energy metabolism, detoxification, and protein synthesis. Therefore, investigating the response of the digestive gland to heat stress can shed light on the adaptive strategies employed by *M. coruscus* to cope with elevated temperatures.

Description

Proteomics, the large-scale study of proteins, provides a comprehensive understanding of cellular processes by identifying and quantifying proteins present in a biological sample. TMT-based proteomics is a cutting-edge technique that enables simultaneous identification and quantification of proteins from multiple samples. It involves labeling protein samples with unique TMT tags, followed by their combination and analysis using mass spectrometry. This technique allows researchers to compare protein expression levels between control and heat-stressed samples, facilitating the identification of heat-responsive proteins. TMT-based proteomics has been successfully employed to investigate the response of *M. coruscus*' digestive gland to heat stress. Several studies have identified differentially expressed proteins in the digestive gland under heat stress conditions, highlighting key molecular mechanisms involved in the organism's response. Heat stress triggers the upregulation of heat shock proteins, a class of chaperone proteins that protect cellular proteins from misfolding and degradation. TMT-based proteomics revealed that HSPs such as HSP70 and HSP90 are significantly upregulated in the digestive gland of *M. coruscus* under heat stress. This upregulation suggests their role in maintaining protein homeostasis and preventing cellular damage.

Heat stress induces the generation of Reactive Oxygen Species (ROS), leading to oxidative stress. Proteomic analysis demonstrated the upregulation of antioxidant enzymes such as Superoxide Dismutase (SOD), Catalase (CAT) and Glutathione Peroxidase (GPx) in the digestive gland of *M. coruscus* under

heat stress conditions. These enzymes help neutralize ROS and protect cellular components from oxidative damage. Heat stress alters the energy metabolism of *M. coruscus* to cope with increased energy demands. TMT-based proteomics revealed significant changes in proteins involved in carbohydrate and lipid metabolism, indicating a metabolic reprogramming response. These findings suggest a shift towards anaerobic glycolysis and lipid catabolism to meet the energy requirements during heat stress. Heat stress affects the cytoskeletal structure and organization within cells. TMT-based proteomics identified alterations in proteins associated with cytoskeleton remodeling, including actin, tubulin, and microtubule-associated proteins. These changes indicate the reorganization of the cytoskeleton, which may be crucial for maintaining cellular integrity and adapting to heat stress.

TMT-based proteomics has emerged as a powerful tool for understanding the molecular response of *M. coruscus*' digestive gland to heat stress. By identifying and quantifying differentially expressed proteins, this technique has provided valuable insights into the adaptive strategies employed by *M. coruscus* to cope with elevated temperatures. The findings from TMT-based proteomics studies highlight the role of heat shock proteins, antioxidant defense mechanisms, metabolic reprogramming, and cytoskeleton remodeling in the heat stress response. Further research in this field will deepen our understanding of the physiological and molecular mechanisms underlying the response of *M. coruscus* to heat stress, contributing to the development of effective strategies for the conservation and management of these ecologically important organisms in the face of climate change.

Heat stress is a significant environmental challenge faced by marine organisms, particularly bivalves such as the *Mytilus coruscus*, commonly known as the Corrugated mussel. As global temperatures continue to rise due to climate change, understanding the physiological responses of these organisms to heat stress becomes crucial. The digestive gland plays a vital role in energy metabolism and detoxification processes in mussels, making it a target organ for investigating their response to environmental stressors. Recent advancements in proteomics, particularly the Tandem Mass Tag (TMT)-based approach, have revolutionized our ability to comprehensively analyze protein expression changes in complex biological systems. Heat stress has been shown to have adverse effects on various physiological processes in marine organisms, including mollusks. *Mytilus coruscus*, an economically and ecologically important species, is known to inhabit intertidal areas with fluctuating temperatures.

When exposed to elevated temperatures, mussels experience several responses, such as reduced feeding, impaired reproductive success, and compromised immune function. The digestive gland, responsible for digestion, nutrient absorption, and metabolism, is highly susceptible to temperature fluctuations. Investigating the molecular mechanisms underlying its response to heat stress can provide valuable insights into the adaptive strategies employed by these organisms [1-5].

Conclusion

TMT-based proteomics offers a powerful approach to unravel the molecular mechanisms underlying the digestive gland's response to heat stress in *Mytilus coruscus*. By identifying differentially expressed proteins and pathways associated with heat stress, this technique provides valuable insights into the adaptive strategies employed by mussels. Understanding the molecular basis of their response to heat stress can contribute to conservation efforts and aid in developing strategies to mitigate the impacts of climate change on marine organisms. Further research in this field holds immense potential for elucidating the complex interactions between environmental stressors and organismal responses, paving the way for the development of targeted interventions to

*Address for Correspondence: Yuxia Guo, Department of Pathology, London South Bank University, London, UK; E-mail: daniele@gmail.com

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mitigate the adverse effects of heat stress on marine ecosystems. The labeled peptides are analyzed using mass spectrometry, which identifies and quantifies the peptides based on their mass-to-charge ratios.

The obtained data are processed using bioinformatics tools and statistical methods to identify differentially expressed proteins between control and heat-stressed groups. The differentially expressed proteins are subjected to functional enrichment analysis, allowing the identification of biological processes, molecular functions, and cellular components associated with the heat stress response in *Mytilus coruscus*. TMT-based proteomics analysis can provide valuable insights into the molecular mechanisms underlying *Mytilus coruscus*' digestive gland's response to heat stress. The identification and quantification of differentially expressed proteins can help elucidate key pathways and processes affected by heat stress. Upregulation of HSPs indicates the activation of cellular defense mechanisms to cope with protein misfolding and oxidative stress caused by heat. Increased expression of HSPs, such as HSP70 and HSP90, can promote protein folding, prevent aggregation, and facilitate protein turnover.

Acknowledgement

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Conflict of Interest

None.

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