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Molecular Strategies of Cadmium Detoxification in the Marine Diatom Phaeodactylum tricornutum: A Transcriptomic Perspective

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ABSTRACT: Cadmium (Cd) is a hazardous heavy metal increasingly contaminating marine ecosystems, posing risks to primary producers such as microalgae. This study investigates the physiological and transcriptomic responses of the marine diatom Phaeodactylum tricornutum to cadmium stress, with the goal of elucidating detoxification mechanisms and assessing its bioindicator potential. Cultures of P. tricornutum were exposed to 123 μg/L and 1230 μg/L Cd for 96 hours. Physiological assessments included growth rate, chlorophyll content, ROS levels, and cell viability. Concurrently, RNA-seq was performed to identify differentially expressed genes (DEGs) and enriched gene ontology (GO) terms associated with Cd stress. Results revealed that exposure to 1230 μg/L Cd caused substantial physiological impairments: decreased growth and chlorophyll content, elevated ROS accumulation, and reduced cell viability. Transcriptomic profiling showed marked upregulation of genes associated with metal efflux (ATPase5-1B), vacuolar sequestration (VIT1, CCC1), and oxidative stress mitigation (SOD, GSH1, HSP70). Enriched GO terms included "oxidative stress response" and "metal ion transport," indicating activation of detoxification and stress adaptation pathways. The findings demonstrate that P. tricornutum employs a coordinated molecular defense strategy involving metal transport and antioxidant pathways, conferring resilience under high cadmium exposure. These adaptive responses support its use as a sensitive bioindicator species for marine cadmium pollution. This integrative approach enhances understanding of diatom detoxification strategies and offers practical applications in ecotoxicological monitoring.

Keywords: Cadmium, Phaeodactylum Tricornutum, Transcriptomic s, Oxidative Stress, Heavy Metal Detoxification, Bioindicator, Marine Microalgae.

INTRODUCTION

Cadmium (Cd) is a heavy metal of significant environmental concern due to its toxicity, persistence, and increasing presence in marine ecosystems. Its entry into aquatic systems is largely attributed to anthropogenic activities, including industrial discharges, mining runoff, and agricultural leaching (Sung et al., 2022). In marine waters, cadmium concentrations vary spatially, typically ranging from 0.1–0.5 nmol Cd^{2+}/kg in surface waters and rising to approximately 1.0 nmol Cd^{2+}/kg in deeper regions (Srivastava et al., 2021). These variations are influenced by geological features and interactions with biological and particulate matter, which modulate cadmium's bioavailability (Bourne et al., 2018).

Marine microalgae are among the first organisms affected by metal pollutants. These photosynthetic microorganisms form the base of the marine food web and are critical to nutrient cycling and primary productivity. Cadmium disrupts various physiological processes in microalgae, including photosynthesis, membrane integrity, and metabolic stability. Sublethal exposures typically induce oxidative stress, resulting in increased reactive oxygen species (ROS) production, reduced chlorophyll content, and altered growth rates (Lavoie et al., 2016). Lethal exposures exacerbate these effects, causing widespread cellular damage and reproductive failure (Díaz-Cruz et al., 2020).

Experimental studies using model organisms such as Chlamydomonas reinhardtii have provided a foundation for understanding metal toxicity at cellular and molecular levels (Penen et al., 2019). However, marine diatoms such as Phaeodactylum tricornutum offer ecologically relevant alternatives due to their prevalence in coastal waters and involvement in carbon sequestration, nutrient cycling, and food web dynamics (Pikula et al., 2022). P. tricornutum not only contributes to primary production but also plays an essential role in recycling trace metals, including cadmium, through its metabolic and decay processes (Hollister et al., 2020).

Detoxification mechanisms in microalgae encompass both cellular and molecular strategies. At the molecular level, microalgae upregulate proteins such as metallothioneins and phytochelatins to bind and neutralize metal ions (Ohta et al., 2019). These proteins reduce cadmium toxicity by facilitating intracellular compartmentalization and sequestration. In addition, microalgae often undergo broad metabolic reprogramming, adjusting energy metabolism and enhancing antioxidant defenses to mitigate oxidative stress (Penen et al., 2017).

Transcriptomic analysis has emerged as a powerful tool to investigate the complexity of microalgal responses to environmental stressors. Techniques such as RNA sequencing (RNA-seq) allow researchers to map genome-wide changes in gene expression, enabling the identification of critical pathways involved in metal tolerance (Kumar & Sharma, 2019). These high-throughput approaches provide insights into gene networks and regulatory mechanisms underlying adaptive responses to cadmium.

Despite the recognized vulnerability of diatoms to heavy metal stress, detailed transcriptomic investigations of their responses to cadmium remain limited. This study aims to fill this gap by assessing the transcriptomic profiles and physiological changes in P. tricornutum exposed to two environmentally relevant Cd concentrations: 123 μg/L (low) and 1230 μg/L (high). The goal is to identify differentially expressed genes (DEGs) and molecular pathways associated with detoxification and stress adaptation. We hypothesize that high-dose cadmium exposure will trigger a robust transcriptomic response involving upregulation of metal efflux transporters, vacuolar sequestration genes, and oxidative stress-related proteins. By elucidating these mechanisms, this research contributes to a deeper understanding of diatom resilience and supports the application of molecular tools in marine pollution monitoring.

METHOD

This study employed a multifaceted experimental design to evaluate the physiological and transcriptomic responses of Phaeodactylum tricornutum to cadmium (Cd) exposure. The methodology was developed in accordance with established protocols for marine microalgae toxicology and transcriptomics (Li et al., 2016).

Culture Conditions and Exposure Design

Axenic cultures of P. tricornutum were grown in sterile f/2 medium under controlled temperature and light conditions. Cultures were acclimated before exposure. Three Cd treatments were administered: 0 µg/L (control), 123 µg/L (low concentration), and 1230 µg/L (high concentration), representing environmentally relevant and elevated levels, respectively. Each treatment was replicated in triplicate and maintained for 96 hours. Growth rates, chlorophyll content, reactive oxygen species (ROS) levels, and cell viability were measured at the endpoint.

Physiological Assessments

Growth was monitored using optical density (OD750). Chlorophyll content was determined spectrophotometrically. ROS levels were quantified using fluorescence assays, while cell viability was measured via trypan blue exclusion method. These indicators collectively reflect the impact of cadmium on cell health, photosynthetic efficiency, and oxidative stress (Li et al., 2017).

RNA Extraction and Sequencing

Total RNA was isolated using an algal-optimized extraction kit to overcome challenges posed by diatom silica frustules and potential contaminants (Zhao et al., 2025). RNA integrity and concentration were verified using Nanodrop and Bioanalyzer systems. High-quality RNA samples were used for library preparation and sequencing on the Illumina platform, targeting a depth sufficient for transcriptome-wide analysis. Samples included at least three biological replicates per condition.

Transcriptome Analysis

Raw reads were processed for quality using FastQC and trimmed for adapters and low-quality sequences. Reads were aligned to the P. tricornutum reference genome using HISAT2. Differentially Expressed Genes (DEGs) were identified using DESeq2 with thresholds set at log2 fold change > 1 and adjusted p-value < 0.05 (Ma et al., 2018).

Functional Enrichment and Network Analysis

DEGs were annotated and analyzed for enrichment using g:Profiler, which mapped gene functions to Gene Ontology (GO) categories, including biological processes, molecular functions, and cellular components (Kolberg et al., 2020). Pathway-level interactions among DEGs were explored using STRING, providing insight into molecular networks and stress response mechanisms (Chujan et al., 2023).

This integrative approach enabled a comprehensive assessment of how P. tricornutum modulates physiological functions and gene expression in response to cadmium stress.

RESULT AND DISCUSSION

Physiological Response

Cadmium exposure elicited marked physiological changes in Phaeodactylum tricornutum, particularly at 1230 µg/L. Growth rate declined significantly, accompanied by reductions in chlorophyll content and cell viability. This decrease is indicative of impaired photosynthetic capacity, as supported by similar findings in Bayçu et al. (2018). Concurrently, ROS levels increased sharply, pointing to oxidative stress, which is a recognized cadmium biomarker in marine diatoms (Sozoniuk et al., 2019). These patterns suggest a dose-dependent toxicological response typical of cadmium's impact on membrane integrity, chlorophyll biosynthesis, and cellular redox balance (Dai et al., 2018).

Table 1. Physiological Parameters of P. tricornutum Under Cd Exposure

Parameter	Control (0 µg/L)	123 µg/L	1230 µg/L
Growth rate (OD750)	1.00	0.96	0.55
Chlorophyll (µg/mL)	5.2	5.1	3.2
ROS level (A.U.)	1.0	1.2	2.5
Cell viability (%)	98	95	76

Transcriptomic Response

Transcriptome analysis identified 4403 DEGs under high Cd treatment, with major changes observed in metal detoxification and oxidative stress pathways. P1B-type ATPases, such as ATPase5-1B, were significantly upregulated, aligning with their known role in cation efflux and vacuolar sequestration of cadmium (Tiwari et al., 2016). Other metal-handling genes including VIT1 and CCC1 were also induced, reinforcing their importance in intracellular Cd management (Yu et al., 2018; Luo et al., 2018). Genes involved in oxidative stress mitigation, such as SOD, CAT, GSH1, and HSP70, showed elevated expression, reflecting the organism’s effort to stabilize redox homeostasis (Xu et al., 2020).

Table 2. Representative DEGs in P. tricornutum at 1230 μg/L Cd

Gene	Annotation	log2FC	Function
ATPase5-1B	P1B-type ATPase	+3.1	Cd efflux
VIT1	Vacuolar transporter	+2.8	Cd sequestration
CCC1	Cation channel protein	+2.4	Metal ion transport
SOD	Superoxide dismutase	+2.2	ROS detoxification
GSH1	Glutathione synthetase	+1.9	Antioxidant biosynthesis
HSP70	Heat shock protein	+2.0	Protein stabilization

Functional Enrichment

Gene Ontology (GO) enrichment analysis revealed significant overrepresentation of terms related to stress responses and metal detoxification. Categories such as "oxidative stress response," "metal ion transport," and "cellular detoxification" were among the top enriched terms (Coakley et al., 2021). Key detoxification pathways, such as glutathione biosynthesis and phytochelatin production, were prominently activated (Guo et al., 2017). These enriched processes highlight the strategic upregulation of protective pathways over growth-related functions a classic trade-off under metal stress conditions (Ye et al., 2017).

Table 3. Enriched GO Terms in Upregulated Genes

GO Term	Fold Enrichment	p-value	Description
Oxidative stress response	4.3	<0.001	ROS detoxification and redox balance
Metal ion transport	3.9	<0.005	Heavy metal homeostasis
Antioxidant activity	3.5	<0.01	ROS mitigation pathways
Cellular detoxification	3.0	<0.05	Defense against toxic compounds

These findings demonstrate that P. tricornutum mounts a robust and multifaceted molecular response to cadmium, reallocating cellular resources toward survival through detoxification, ion transport, and antioxidant protection.

The transcriptomic profile of Phaeodactylum tricornutum under cadmium stress reflects both conserved and unique molecular responses compared to other marine microalgae. Consistent with previous studies, P. tricornutum upregulated genes involved in metal ion transport, antioxidant defense, and detoxification processes. These shared responses include the increased expression of phytochelatin synthase, metallothioneins, and antioxidant enzymes, reinforcing the existence of a common stress-response core across microalgal taxa (Ashworth et al., 2016). However, P. tricornutum also demonstrates lineage-specific transcriptomic features, likely shaped by its evolutionary adaptations to fluctuating marine environments (Huang et al., 2016).

Notably, the distinct expression of transporters such as ATPase5-1B and vacuolar-associated proteins like VIT1 and CCC1 suggests a well-coordinated metal sequestration strategy unique to P. tricornutum. This strategy supports enhanced tolerance and rapid physiological adjustments, attributed to the species' ability to thrive under variable environmental conditions (Carvalho &

Bowler, 2020). The modulation of photosynthesis- and respiration-related pathways during cadmium exposure also underscores the metabolic plasticity of this diatom, allowing energy reallocation toward detoxification and survival.

From an ecological perspective, the observed transcriptomic responses have broader implications. As a key component of marine primary production, any cadmium-induced physiological and metabolic disruption in P. tricornutum can cascade through trophic levels. Decreased chlorophyll content and reduced growth imply lower biomass availability for grazers, potentially impairing energy transfer efficiency in the food web (Yazdanabdad et al., 2021). Furthermore, cadmium stress can influence nutrient cycling by altering diatom contributions to silica and carbon processing, ultimately affecting ecosystem productivity and stability (Li et al., 2016).

Transcriptomic plasticity serves as a survival advantage for microalgae exposed to environmental stressors. P. tricornutum exemplifies this adaptability by activating detoxification pathways and restructuring its metabolism to maintain viability under cadmium stress. The rapid transcriptional shifts enable the organism to respond to oxidative challenges, sustain ATP production, and preserve cellular homeostasis despite metal toxicity (Islam et al., 2020). This molecular agility enhances resilience and ensures ecological persistence in polluted habitats.

The findings from this study highlight the potential of P. tricornutum as a bioindicator for marine heavy metal pollution. Its ability to bioaccumulate cadmium, coupled with a well-characterized and quantifiable molecular response, supports its use in environmental monitoring applications. The integration of transcriptomic data offers an advanced dimension to bioindicator frameworks, capturing both exposure levels and the physiological impact of contaminants in real-time (Ashworth et al., 2016). This approach aligns with modern environmental assessment strategies that prioritize functional biomarkers over chemical quantification alone.

CONCLUSION

This study provides comprehensive insights into the molecular and physiological responses of Phaeodactylum tricornutum to cadmium (Cd) stress, highlighting key mechanisms that underlie its detoxification strategy. Exposure to high Cd concentrations (1230 μg/L) resulted in substantial physiological disruptions, including reduced growth, chlorophyll content, and cell viability, as well as elevated reactive oxygen species (ROS). These findings confirm the metal's toxicity and its capacity to impair essential cellular functions in marine diatoms.

Transcriptomic analyses revealed a robust reprogramming of gene expression in response to cadmium, involving the upregulation of transporters such as ATPase5-1B, VIT1, and CCC1, which mediate Cd efflux and vacuolar sequestration. Additionally, genes associated with oxidative stress defense, including SOD, GSH1, and HSP70, were significantly induced, indicating the organism's activation of antioxidant pathways to mitigate redox imbalance. These molecular adaptations are central to the survival of P. tricornutum under heavy metal exposure.

The study contributes to a growing body of evidence supporting the use of marine diatoms as bioindicators for metal pollution. P. tricornutum demonstrates both sensitivity to cadmium and transcriptomic plasticity, making it a suitable sentinel species for monitoring environmental metal stress. The integration of physiological and transcriptomic data offers a holistic view of stress responses, bridging molecular changes with ecological implications.

In conclusion, the observed transcriptomic patterns underscore a conserved yet flexible detoxification response in P. tricornutum, characterized by metal transport, compartmentalization, and oxidative stress regulation. These findings enhance our understanding of diatom resilience and inform strategies for using microalgal systems in marine ecotoxicology and environmental assessment.

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