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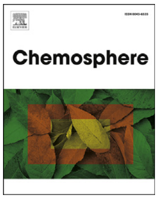

De novo transcriptome assembly and differential gene expression analysis of the calanoid copepod *Acartia tonsa* exposed to nickel nanoparticles

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HIGHLIGHTS

- A *de novo* assembled transcriptome of *A. tonsa* was generated.
- The transcriptome of *A. tonsa* consisted of 53,619 unigenes.
- Mostly genes were downregulated in copepods exposed to nickel nanoparticles.
- The down regulated genes are involved in protein turnover.

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ABSTRACT

The calanoid copepod *Acartia tonsa* is a reference species in standardized ecotoxicology bioassay. Despite this interest, there is a lack of knowledge on molecular responses of *A. tonsa* to contaminants. We generated a *de novo* assembled transcriptome of *A. tonsa* exposed 4 days to 8.5 and 17 mg/L nickel nanoparticles (NiNPs), which have been shown to reduce egg hatching success and larval survival but had no effects on the adults. Aims of our study were to 1) improve the knowledge on the molecular responses of *A. tonsa* copepod and 2) increase the genomic resources of this copepod for further identification of potential biomarkers of NP exposure. The *de novo* assembled transcriptome of *A. tonsa* consisted of 53,619 unigenes, which were further annotated to nr, GO, KOG and KEGG databases. In particular, most unigenes were assigned to Metabolic and Cellular processes (34–45%) GO terms, and to Human disease (28%) and Organismal systems (23%) KEGG categories. Comparison among treatments showed that 373 unigenes were differentially expressed in *A. tonsa* exposed to NiNPs at 8.5 and 17 mg/L, with respect to control. Most of these genes were downregulated and took part in ribosome biogenesis, translation and protein turnover, thus suggesting that NiNPs could affect the copepod ribosome synthesis machinery and functioning. Overall, our study highlights the potential of toxicogenomic approach in gaining more mechanistic and functional information about the mode of action of emerging compounds on marine organisms, for biomarker discovering in crustaceans.

1. Introduction

Copepods, the most abundant invertebrates and the dominant taxa in aquatic environments, constitute almost 70% of the ocean's biomass with approximately 14,000 known species (Huys and Boxshall, 1991). Due to their relevant role in the aquatic food web copepods are commonly used as model organisms in ecotoxicology

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