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DE NOVO TRANSCRIPTOME ANALYSIS FOR MECHANISTIC STUDY OF ORGANOTIN-MEDIATED ENDOCRINE DISRUPTION IN *REISHIA CLAVIGERA*

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Many endocrine disrupting compounds are bioaccumulative and toxic to a wide range of marine organisms, leading to reproductive impairment, development of cancer and abnormal metabolism. For instance, organotin compounds (OTs) such as tributyltin and triphenyltin can induce the development of imposex (i.e., superimposition of male sexual organs) in females of over 200 gastropod species. OTs have been widely used as biocides in antifouling paints and industrial applications. Thus they have been released into the marine environment, posing risks to non-target marine organisms and human health. Although many studies have been conducted to examine the underlying mechanism of imposex development in marine gastropods over the past 40 years, the question has not yet been satisfactorily addressed. This study aims to elucidate the imposex mechanism by comparing the transcriptomic profiles among females of the intertidal whelk, *Reishia clavigera*, of different imposex stages. We first established a *de novo* transcriptome of *R. clavigera* using Illumina sequencing. A total of 453,422 assembled transcripts were obtained, with 51,316 transcripts annotated with at least a BLAST hit, 34,759 transcripts assigned with at least one well-defined Gene Ontology (GO) and 8,596 transcripts involved in 337 different Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways. Currently, we are using RNA sequencing data to identify genes and pathways possibly related to imposex development in *R. clavigera* which were exposed to various treatments of OTs for four months under laboratory conditions. The extensive sequence data generated from this study will also provide valuable molecular resources for facilitating similar mechanistic studies of other chemical pollutants.