



De novo assembly and transcriptome characterization of the freshwater prawn *Palaemonetes argentinus*: Implications for a detoxification response



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ABSTRACT

Palaemonetes argentinus, an abundant freshwater prawn species in the northern and central region of Argentina, has been used as a bioindicator of environmental pollutants as it displays a very high sensitivity to pollutants exposure. Despite their extraordinary ecological relevance, a lack of genomic information has hindered a more thorough understanding of the molecular mechanisms potentially involved in detoxification processes of this species. Thus, transcriptomic profiling studies represent a promising approach to overcome the limitations imposed by the lack of extensive genomic resources for *P. argentinus*, and may improve the understanding of its physiological and molecular response triggered by pollutants. This work represents the first comprehensive transcriptome-based characterization of the non-model species *P. argentinus* to generate functional genomic annotations and provides valuable resources for future genetic studies.

Trinity *de novo* assembly consisted of 24,738 transcripts with high representation of detoxification (phase I and II), anti-oxidation, osmoregulation pathways and DNA replication and bioenergetics. This crustacean transcriptome provides valuable molecular information about detoxification and biochemical processes that could be applied as biomarkers in further ecotoxicology studies.

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