

Transcriptome sequencing and De novo analysis of the Antarctic copepod *Boeckella poppei*

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Despite their species abundance and primary economic importance, genomic information about copepods is still limited. In particular, genomic resources are lacking for the Antarctic freshwater copepod *Boeckella poppei*, which is a dominant species in shallow freshwater lakes located in the Antarctic Peninsula. In this study, we performed de novo transcriptome sequencing to produce a large number of expressed sequence tags for the copepod *B. poppei*. Using illumina sequencing, a total of 5.7 Gb were obtained, which were assembled into 42,988 high quality expressed sequence tags. Based on their sequence similarity to known proteins, about 31,160 different genes were identified. Our data provide the most comprehensive transcriptome resource available for *B. poppei*. This resource allowed us to identify genes associated with primary physiological processes, which facilitated the quantitative analysis of differential gene expression. These data should provide foundation for future genetic and genomic studies of this and related species.