



Transcriptome profiling of the crofton weed gall fly *Procecidochares utilis*

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ABSTRACT. *Procecidochares utilis* is a tephritid gall fly, which is known to be an effective biological agent that can be used to control the notoriously widespread crofton weed *Eupatorium adenophorum*. Despite its importance, genetic resources for *P. utilis* remain scarce. In this study, 1.2 Gb sequences were generated using Illumina paired-end sequencing technology. *De novo* assemblies yielded 491,760 contigs, 90,474 scaffolds, and 58,562 unigenes. Among the unigenes, 34,809 (59.44%) had a homologous match against the National Center for Biotechnology Information non-redundant protein database by translated Basic Local Alignment Search Tool (BlastX) with a cut-off E-value of 10^{-5} . Among the unigenes, 57,627 were classified in the Gene Ontology database, 15,910 were assigned to Clusters of Orthologous Groups, and 38,565 were found in Kyoto Encyclopedia of Genes and Genomes. In addition, 5723 simple sequence repeats (SSRs) were discovered based on the unigene sequences. The transcriptome sequences and SSRs obtained represent a major molecular resource for *P. utilis*, which will extend our knowledge of the comparative and

functional genomics of this organism and enable population genomic and gene-based association studies of the gall fly.

Key words: Gall fly; *Procecidochares utilis*; Transcriptome; Simple sequence repeat marker; Illumina sequencing