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Data Article

The testes transcriptome of the New World Screwworm, *Cochliomyia hominivorax*

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ABSTRACT

The New World Screwworm (NWS), *Cochliomyia hominivorax*, is a pest insect that is endemic to subtropical and tropical regions of the Western Hemisphere. The female lays eggs in open wounds or orifices of warm-blooded animals. Upon hatching, the resulting larvae feed upon the host's living tissues, which can become infected and death can occur. The sterile insect technique was developed to eradicate this pest from North America and new female conditional-lethal strains that generate only male individuals are being developed for use in the eradication program. To facilitate the identification of useful transcripts and gene promoters for these new strains, we used an Illumina Hi-Seq protocol to sequence the testes transcriptome of NWS. We report the assembly of 4149 transcripts (≥ 200 nt) from testes dissected from NWS males obtained from the J06 strain used in the screwworm production plant in Pacora, Panama. Functional annotation resulted in 2060, 2031, 558, and 325 transcripts with assigned BlastX, Gene Ontology, Enzyme Codes, and KEGG pathway information, respectively. In the Gene Ontology annotations, 6% and 3% of the transcripts in the Biological Process Ontology were noted as Developmental Process and Reproduction, respectively. This data

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set will serve as a resource to facilitate studies of sex determination in the NWS and the development of recombinant vectors that can be used to create new male-only strains of NWS.

Specifications

Subject Area	Biology
More specific subject area	Insect genomics
Type of data	Transcriptome sequences and associated annotations
How data was acquired	2 × 54 paired-end read RNAseq of RNA isolated from testes dissected from NWS males
Data format	Raw FASTQ and processed FASTA sequence files
Experimental factors	Testes dissected from 100 male individuals into RNALater
Experimental features	Assembled transcriptome of testes tissue dissected from adult male NWS
Data source location	Strain of NWS used in the screwworm production plant in Pacora, Panama
Data accessibility	Data is with this article and also available at the National Center for BIotechnology Information (NCBI) Short Read Archive (SRA) through the direct link http://trace.ncbi.nlm.nih.gov/Traces/sra_sub/sub.cgi?subid=707563 or through SRA accession number SRP076734. The *C. hominivorax* testes transcriptome shotgun assembly project has been deposited at DDBJ/EMBL/GenBank under the accession GEVJ00000000. The version described in this paper is the first version, GEVJ01000000. The overall BioProject ID is PRJNA324578 and the BioSample accession is SAMN05213682.

Value of Data

- Testes-specific transcript sequences to supplement the available NWS transcriptomes previously reported for embryos, larvae, adult male, and adult female [1].
- Resource for investigations of sex-specific gene expression and sex determination pathways.
- Provides candidate protein coding regions and gene promoters for the development of recombinant vectors that can be used to create new male-only strains of NWS.

1. Data

Testes were dissected out of male NWS from Pacora, Panama. Following RNA isolation, 1 lane of 2 × 54 paired end RNAseq reads were obtained, *de novo* assembled and annotated. The raw reads are accessible at NCBI's SRA through the direct link http://trace.ncbi.nlm.nih.gov/Traces/sra_sub/sub.cgi?subid=707563 or through SRA accession number SRP076734. The assembled transcriptome shotgun assembly project has been deposited at DDBJ/EMBL/GenBank under the accession GEVJ00000000. The version described in this paper is the first version, GEVJ01000000. The overall BioProject ID is PRJNA324578 and the BioSample accession is SAMN05213682.