



Category: Functional Genomics

# Gene expression program of regeneration in *Eisenia fetida*: a transcriptomics study

Aksheev Bhambri<sup>1,2</sup>, Neeraj Dhaunta<sup>1</sup>, Surendra Singh Patel<sup>1,2</sup> and Beena Pillai<sup>1,2\*</sup>

<sup>1</sup>CSIR – Institute of Genomics and Integrative Biology, Mathura Road, New Delhi 110025, INDIA

<sup>2</sup>Academy of Scientific & Innovative Research (AcSIR), Mathura Road, Delhi 110 025, INDIA

\*Corresponding author: [beena@igib.in](mailto:beena@igib.in)

## Abstract

Annelids form a connecting link between segmented and non-segmented organisms. In other words, phylogenetically, the segmented body pattern starts from Annelida, a phylum that consists of thousands of species, including marine worms, freshwater leeches and earthworms that inhabit deep layers of soil to environmental niches in forests and cultivated land. We are using *Eisenia fetida* (Indian isolate) a top dwelling, vermicomposting worm due to its ability to regenerate its posterior after damage, injury or complete removal. On average, *Eisenia fetida* has 100-110 segments. We separated the anterior (upto 55-60<sup>th</sup> segment) and posterior of the worm, and allowed it to regenerate. In this model, only the posterior could be regenerated after injury. We isolated RNA from the regenerated tissue and the immediate adjacent old tissue at 15 days, 20 days and 30 days during regeneration. We carried out transcriptome sequencing and analysis. With the aim of identifying specific factors which promote nerve regeneration, we have annotated the differentially expressed genes. In all organisms which possess a segmented body, the expression pattern of the Hox cluster is conserved. Hox gene expression, a conserved developmental phenomenon in establishment of body plan has been studied by comparative genomics of other annelids like the marine worm *Capitella telleta*, the leech *Helobdella robusta*. We have used a combination of high-throughput sequencing based techniques and validation through cell and molecular biology to identify key aspects of the gene expression program of regeneration in this worm. Besides the transcriptome, we have also done whole genome sequencing, miRnome and metagenome sequencing of this terrestrial annelid.

**Citation:** Bhambri, A., Dhaunta, N., Patel, S.S. and Pillai, B. Gene expression program of regeneration in *Eisenia fetida*: a transcriptomics study [Abstract]. In: Abstracts of the NGBT conference; Oct 02-04, 2017; Bhubaneswar, Odisha, India: Can J biotech, Volume 1, Special Issue, Page 108. <https://doi.org/10.24870/cjb.2017-a94>