

Poster A-1
Comparative genomics of *Ciona savignyi* and *Ciona intestinalis*



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Short Abstract: The studies of *Ciona* species may provide insights to the origins and evolutions of chordate phylum, from which all vertebrates sprouted. To this end, the genome sequence and annotation of an as yet unpublished *Ciona savignyi* assembly was compared to that of *Ciona intestinalis* using comparative genomics approaches and a number of interested findings were identified and reported.

Long Abstract:

Species from *Ciona* genus have the smallest genomes of any chordate that can be manipulated experimentally [1]. As the members of the urochordates (the most primitively branching clade of chordates), *Ciona* species are good candidates for investigating the origins and evolutions of the chordates phylum, from which all vertebrates sprouted.

The draft assembly and analysis of protein-coding portion of *C. intestinalis* genome was firstly reported by Dehal et al. in 2002 [1]. The *C. intestinalis* genome at the DOE Joint Genome Institute (JGI) has a genome size of 173Mb and includes a total of 14,728 genes, which account for 41.6% of the whole genome (Version 2.0, March 2005).

The genome of *C. savignyi* was shotgun-sequenced by the Broad Institute, MIT and assembled using Arachne2, which consists of 374 contigs (Genome size 174Mb). The *Ciona savignyi* annotation project (initialized in Nov. 2002) is a collaborative effort between Temasek Life Sciences Laboratory (TLL, Singapore), Stanford University Medical Center (USA) and Telethon Institute of Genetics and Medicine (TIGEM, Italy). Many rounds of annotations were done with the new *C. savignyi* assembly with the facilitation of Biopipe [2]. Currently, 27.9% of the genome is annotated as genic regions, which are composed of 11,693 genes (protein-based annotation) compared to 14,728 genes in the *C. intestinalis* genome (Version 2.0, September 2005).

The availability of genome sequences and annotations of *C. savignyi* and *C. intestinalis* allows for the comparative analysis of these two genomes. In this study, the comparison of the genomes of *C. savignyi* and *C. intestinalis* were undertaken particularly in the unannotated portions of both genomes. More than 1,000 transcripts were found to be unique to *C. savignyi*. A comparable number of transcripts in *C. intestinalis* were not identified in *C. savignyi*. Further comparison between the unannotated regions of the two *Ciona* genomes reveals ultra-conserved regions. Differences in gene content were analyzed to account for the discrepancy in gene annotations. We report on strong evolutionary signals present in these two *Ciona* species and discuss their occurrence relative to other extant vertebrate

species.

1. Dehal, P., et al., The draft genome of *Ciona intestinalis*: insights into chordate and vertebrate origins. *Science*, 2002. 298(5601): p. 2157-2167.
2. Hoon, S., et al., Biopipe: a flexible framework for protocol-based bioinformatics analysis. *Genome Research*, 2003. 13(8): p. 1904-1915.