VanWoRM

Vancouver Worm Research Meeting

Wednesday, January 23rd, 2008

5:00 pm

Michael Smith Building

Lecture Theatre

2185 East Mall, UBC

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Advancing through Genomics

Itinerary:

5:00 pm - Introduction

Update from the NRRR Committee

5:10 pm – Talks

Andrew C. Giles - A Multi-Worm Tracker for a Genetic Screen for Abnormal Habituation in *C. elegans*

Ismael A. Vergara - Comparative analysis of worm genomes using Orthocluster

6:00 pm - Food/Beverages

Pizza (courtesy of Macrogen)

Drinks (courtesy of Invitrogen)

Abstracts:

A Multi-Worm Tracker for a Genetic Screen for Abnormal Habituation in *C. elegans*

Andrew Giles (Rankin Lab)

Using a candidate gene approach to study short-term habituation in *C. elegans* has been useful in the past to elucidate clues to understand the molecular mechanisms involved; however, the number of suitable candidate genes is relatively small, and it is very time consuming when the outcome is merely a null result. For this reason, performing a genetic screen to find novel genes that play a role in habituation is very attractive. Until now this has been a daunting task because it takes a long time to analyze an individual genetic line (approx. 40 hours by manual behavioural analysis; 6 hours using an automated system that tracks individual worms). We have developed a system that is capable of simultaneously analyzing multiple worms (as many as 50 reliably). This lowers the time needed to assess an individual strain to 10 minutes, making a genetic screen temporally feasible. The tracking system can score the frequency, magnitude, and duration of responses to tap as well as the average speed of the response. We have validated the system by demonstrating a number of essential habituation characteristics, such as the interstimulus interval dependence on both the rate and asymptotic level of habituation in wild-type worms. We have also tested several previously identified mutants, such as *dop-1* and *cat-2*, which show altered short-term habituation and found that the system is capable of reproducing the same phenotypes as previously reported. We are currently optimizing the system for use in a genetic screen to identify genes that affect different characteristics of habituation.

Comparative analysis of worm genomes using Orthocluster

Ismael A. Vergara (Chen Lab)

Genes within a genome are not randomly distributed. Compelling evidence suggests that genes expressed in same tissue types or genes that are co-transcriptionally regulated form clusters in a genome. Such gene clusters may be functionally important and are under evolutionary constraints since blocks of genes have been found to be conserved across many different genomes. To extensively understand the arrangements of genes in the entire *Caenorhabditis elegans* genome and the functional implication of such arrangements, we undertake to analyze synteny blocks and genome rearrangement events in multiple worm species whose genomes have been recently sequenced and analyzed. In particular, we will compare the genomes of *C. elegans* and three of its sister species *C. briggsae*, *C. remanei*, and *C. brenneri*, and of the filarial nematode *Brugia malayi*. To facilitate the comparative analysis, we have developed an effective and flexible computer program, Orthocluster, which is capable of identifying synteny blocks, as well as various types of genome rearrangement events including reciprocal translocations, inversions, transpositions and insertions/deletions. In this talk, I will present the algorithm underlying Orthocluster and its application to comparing the genomes of four *Caenorhabditis* species and *Brugia malayi*. In particular, I will overview synteny blocks in these worm species with a focus on the conservation of operon structures, segmental duplications within each species, and the improvement of ortholog assignment as well as different rearrangements rates.