JAMES RENNIE BEQUEST
REPORT ON EXPEDITION/PROJECT/CONFERENCE

Expedition/Project/ Conference Title: 2012 Meeting on Evolution of Caenorhabditis and other Nematodes, and 2012 NemaSym Meeting

Travel Dates: 03-April-2012 to 06-April-2012

Location: Cold Spring Harbor Laboratory, New York

Group member(s): Sujai Kumar

Aims:
1. To present my current research in poster format
2. To meet principal scientists in the field and explore post-doc opportunities
3. To discuss progress on a large multi-institution paper on Caenorhabditis genome evolution

OUTCOME (not less than 300 words):-

The 2012 Evolution of Caenorhabditis and other Nematodes meeting was held at Cold Spring Harbor Laboratory (CSHL), New York, from April 3 to April 6, 2012. CSHL is situated in an isolated campus on Long Island, and has an excellent reputation for intense meetings and courses.

This year, the main meeting was preceded by a one-day meeting of the NemaSym Research Coordination Network on Nematode-Bacterium Symbioses, which I also attended. Mark Blaxter, my supervisor, presented the keynote address. His talk summarised the state of the art in genomic methods and studies of nematode-bacterium symbioses, and cited some of my contributions as well.

The main nematode evolution meeting was organised in 3-hour sessions, each with 12 talks. The sessions generally started at 9am each day and went on till 1030pm, with breaks only for meals and coffee. Normally, one might imagine that so many talks would be exhausting. However, in this case, because the topic of nematode evolution is central to my PhD research, I enjoyed almost all of the talks. About a fourth of the 105 presentations were directly relevant to my specific PhD topic of the evolutionary genomics of nematodes. Although I am not a biologist by training (my previous education was in Informatics), I found the biology-only talks fascinating from a scientific perspective, and learnt a lot about the morphology, genetics, ecology, embryology, and behaviour of nematodes in a very short time. Meeting the leaders and students in the field during the breaks was also very enjoyable and I enjoyed the chance of getting to know them and their work personally. On the last two days of the meeting, I also live-tweeted some of the core ideas of the talks (https://twitter.com/#!/search/%23worms12) for the benefit of others who could not attend the meeting.

At the poster session, I presented my research (poster attached) to several people in the 2 hour session. I had long discussions with five researchers and they all provided valuable suggestions for extending my work. I also participated in a special session with about 30 other researchers on a large-scale multi-institution study on the analysis of 8 Caenorhabditis genomes to which I have contributed the assembly and annotation of one species, and an analysis of the evolution of noncoding regions.

In summary, this was an intense and highly productive meeting in a beautiful location. I would highly recommend CSHL meetings and courses because the campus and the people inspire scientific learning and collaboration. Standing next to James Watson at the lunch buffet and seeing the labs where some of the path-breaking genetic experiments were carried out was an added bonus, and I am very grateful to the James Rennie Travel Bequest that made it possible for me to attend these two meetings.

Q. Mammals and Fish share Genome Resident Elements. Do Nematodes?

A. No.

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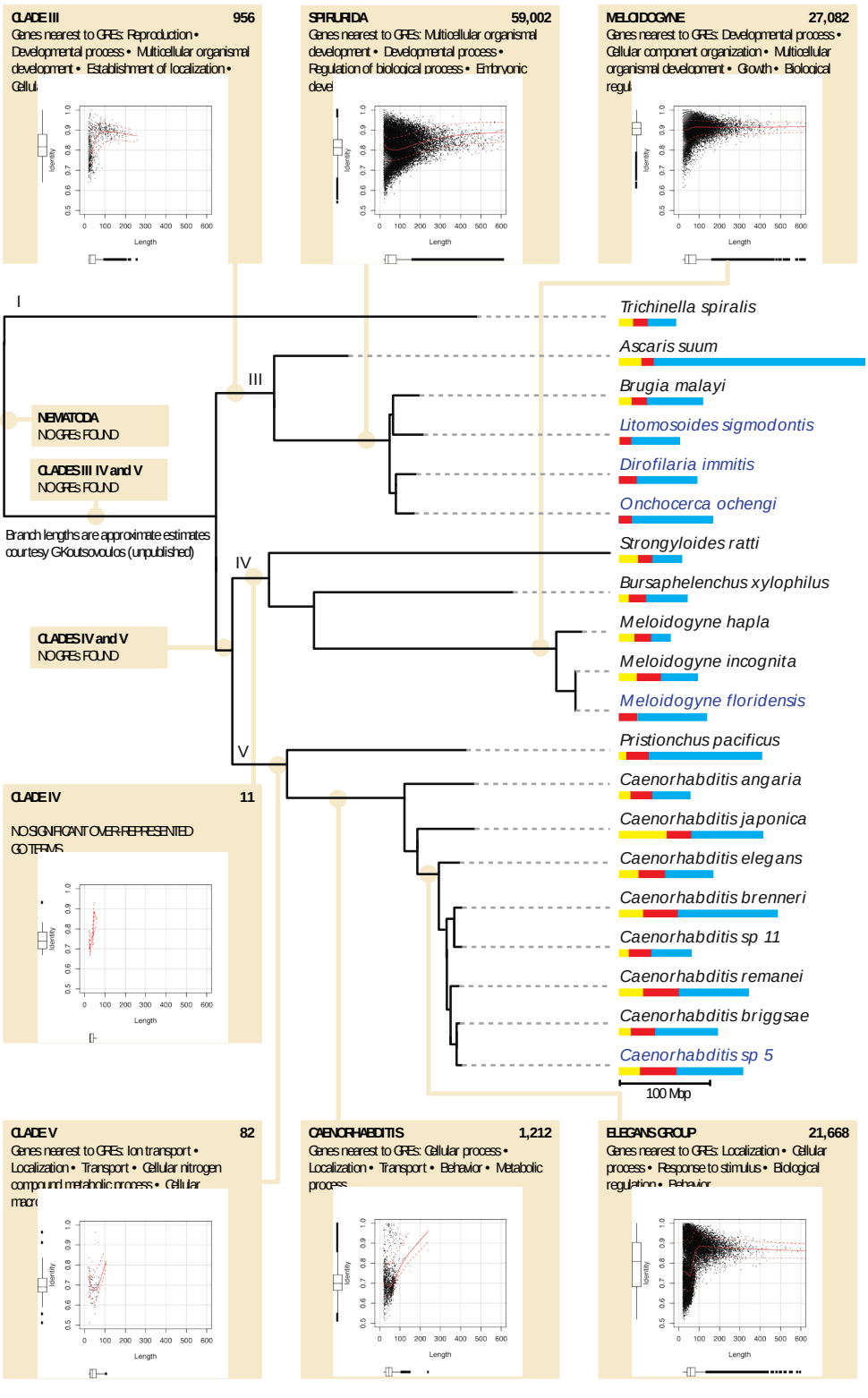
Number, length, and identity of GREs shared across all species at that node. The top 5 over-represented gene-ontology (GO) terms for the genes nearest to the GREs are shown:



1. WHY STUDY GENOME RESIDENT ELEMENTS

We use the term Genome Resident Elements (GREs) to describe conserved functional DNA elements that do not encode an RNA or protein product. GREs are identified by first performing whole-genome alignments and then looking for highly conserved elements that do not code for proteins or RNA.

Previous studies on such elements in vertebrates[1,2,3] have concluded that they are *cis*-regulatory elements located near developmental genes. Similar elements have been found near orthologous genes in alignments of five insect and three *Caenorhabditis* genomes in the past, although the elements did not share any identity across phyla, leading to the speculation that such elements may somehow be related to the phylum body plan.

In this study, we extend the study of GREs from three *Caenorhabditis* species to the breadth of the phylum Nematoda using 20 complete genomes.

2. WHAT WE FOUND

A. There are no Nematoda-wide GREs and no GREs were conserved across clades.

B. The genes nearest to GREs are related to development only in Clade III and Meloidogyne, but not in Clade V.

Therefore, the development of the nematode phylum body plan is probably not correlated with highly conserved GREs as previously hypothesised.

A and B are important negative results, because they demonstrate that inferences of processes that drive the evolution of genomic structures derived from a few *Caenorhabditis* genomes may not be true for all Nematoda.

3. HOW GREs WERE IDENTIFIED

- 15 finished and draft genomes were obtained from WormBase WS230[4].
- 5 draft genomes were assembled and annotated at the Blaxter Lab.
- Repeat regions were masked. Pairwise whole-genome alignments were performed using LAST[5].
- Multi-genome alignments were created using TBA/MULTIZ[6] for each node marked with a dot in the tree.
- Protein and RNA coding regions were identified using GFF files, alignments to nematode protein sequences, tRNAscan[7], and Rfam[8].
- These regions were removed from the whole-genome multi-alignments.
- Nearest genes were identified using BEDTools[9].
- GO terms were assigned to all gene sets using the same BLAST2GO settings.[10]

Sizes indicate relative proportions of:
Repeat masked regions
Protein or RNA coding regions
Noncoding regions

4. POTENTIAL PROBLEMS

- Only elements present in copy numbers of one per genome were identified.
- Not all coding regions can be identified.
- Nearest gene may not reflect cis-regulatory function.
- Differences in nearest gene annotations could be due to uneven gene predictions.

5. WHAT NEXT

- Improve gene predictions and annotations for new draft genomes.
- Perform multiple whole-genome alignments using pipelines that are not restricted to single-coverage elements.

REFERENCES

1. Woolfe, A. et al. Highly conserved non-coding sequences are associated with vertebrate development. PLoS Biology 3, e7+
2. Vavouri, T. et al. Parallel evolution of conserved non-coding elements that target a common set of developmental regulatory genes from worms to humans. Genome Biology 8, R15+
3. Siepel, A. et al. Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. Genome Research 15, 1034-1050
4. Yook, K. et al. WormBase 2012: more genomes, more data, new website. Nucleic Acids Research 40, D735-D741
5. Kielbasa, S. M. et al. Adaptive seeds tame genomic sequence comparison. Genome Research 21, 487-493
6. Blanchette, M. et al. Aligning multiple genomic sequences with the threaded blockset aligner. Genome Research 14, 708-715
7. Lowe, T. M. et al. tRNAscan-SE: A program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Research 25, 955-964
8. Gardner, P. P. et al. Rfam: Wikipedia, clans and the "decimal" release. Nucleic Acids Research 39, D141-145
9. Quinlan, A. R et al. BEDTools: a flexible suite of utilities for comparing genomic features. Bioinformatics 26, 841-2
10. Götz, S. et al. High-throughput functional annotation and data mining with the Blast2GO suite. Nucleic Acids Research 36, 3420-3435

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COLLABORATORS

L. sigmodontis: Judith Allen, Simon Babayan • *D. immitis*: Pascal Maeser, Christelle Peret, Daniel Neilsson, Georgios Koutsovoulos • *O. ochengi*: Ben Makepeace, Alistair Darby • *M. floridensis*: David Lunt, Etienne Danchin • *C sp 5*: Asher Cutter, Erich Schwarz, Marie-Anne Félix, Michael Paulini

SEQUENCING

the gene pool
FASTERIS

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