The Trich of the matter: Temporary title for Trichinella spiralis project

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Abstract

Introduction

De Novo Genome Assembly

Premise:

Currently the best genome assemblies for *Trichinella spiralis* are at ~98% complete depending upon the species, mostly using Illumina and a few used PacBio RSII (ick). We plan to use Oxford Nanopore for ultra long reads assembly to further complete the genome, possibly incorporate some Illumina for hybrid correction.

- Also look at methlyation of ONT reads?

Target information

- Genome size: ~50-65Mb
- 3 Chromosomes

One flowcell would generate ~100-200X coverage raw.

Protocols

Extraction/Size selection

Recent PacBio paper [1] simply used phenol/chloroform extraction followed by Covaris G-tube. Previous papers [2,3] for Illumina sequencing appear to use classic Qiagen or phenol/chloroform as well.

Requires >2ug HMW DNA

De Novo Transcriptome

Premise:

Annotation of genes can be done in several ways- one of which is pure computational prediction. Since *T. spiralis* is eukaryotic- we cant exclude alternative splicing playing a role here as well, which Im not sure anyone else has looked at yet. Nanopore direct RNA-sequencing will capture spliceforms and improve genome annotation.

Target information

- 15k-20k genes/transcripts per genome
- Primarily should be polyA+

Go after non-polyA too?

Protocols

Extraction/Size selection

TBD polyA tagging of non-polyA RNAs. **Requires >500ng polyA+ RNA for direct nanopore sequencing**

Vesicle RNA

Premise:

The crux of this project- *T. spiralis* transcripts have been found in vesicles, leading to immune modulation and neuronal alterations. Believed to be to benefit the worm, but also providing benefits to autoimmune and neurodegradation disorders. By using the stronger genome/transcriptome, we can try to identify the collection of transcripts in vesicles.

Target information

Protocols

Extraction/Size selection

TBD polyA tagging of non-polyA RNAs. **Requires >500ng polyA+ RNA for direct nanopore sequencing**

References

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