

Investigating the diversity of Venom Allergen-like Proteins expressed in flatworms

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Scripting for Biologists Final Project
Bioinformatics Pipeline

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Overview

- 1 Motivation behind pipeline
- 2 Summary
- 3 Walk-through
- 4 Wrap-up

MS thesis pipeline

The evolution of (blood) parasitism in flatworms

What's VAP got to do with it?

Breanna Siple

Masters Thesis Seminar
Biological Sciences

Friday, June 28

10:00 AM

Funchess 332



- Revisit
- Improve
- Move
- Generalize

 @Breanna_Siple

Bioinformatics | Flatworms | Gene Tree | Parasites

Phyletica Lab | Biological Sciences

What are VAPs and why do we care about them?

Sterol-binding secretory proteins

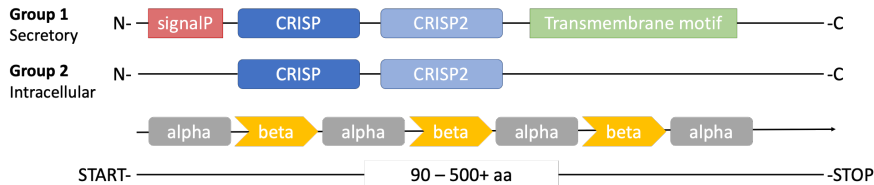


Figure: VAP domain architecture

Implications for parasitism

- Secreted by parasites
- Differentially expressed
- Induce vertebrate IgE

Why are flatworms an interesting system to study VAPs?

Large, ancient radiation of parasites*

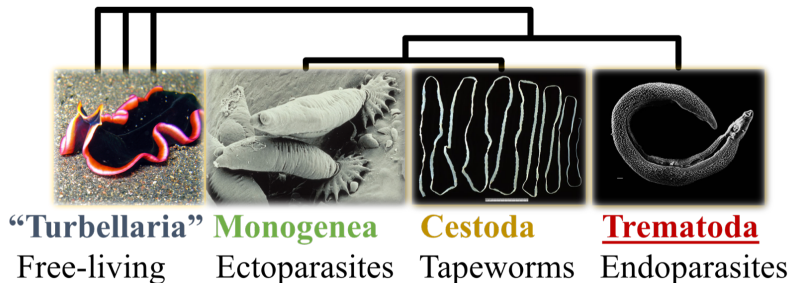


Figure: Simple flatworm phylogeny indicating single origin of parasitism

*Also, medical and economic value

Bioinformatics pipeline

Purpose

To survey the diversity of Venom Allergen-like Proteins (VAPs) expressed in *Schistosoma mansoni*

link: <https://github.com/Sipley/pipeline>



Summary

- Acquire a large dataset of sequences
- Pull out Gene Family of Interest from all sequences (non-redundant)
- Infer the best gene tree for your Gene Family of Interest
- Color best gene tree based on signal peptide predictions
- Compare average rates of amino acid substitutions

Walk-through

link: <https://github.com/Sipley/pipeline>

Wrap-up

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Questions?