NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE

Evidence of horizontal gene transfer between *Wolbachia* and *Aedes aegypti*

Darian Labrosciano* , Ariana Rivera and Vinayak Mathur

Abstract

Horizontal gene transfer (HGT) is the non-vertical movement of genetic material among organisms and is believed to be an important factor driving evolution. A key question regarding these horizontally transferred genes is the functional role they play in the organism. In the past, HGT studies have focused on prokaryotes, but now there are a number of studies documenting functional HGT in a wide range of eukaryotes. In this study we focused on *Aedes aegypti*, the yellow fever mosquito, which is a known vector for several diseases. Using information from the NCBI database and the BLAST search tool we found evidence of horizontal gene transfer between Wolbachia and *Aedes aegypti*. The *Wolbachia* protein identified in our study is an uncharacterized conserved RhaS protein that has 28 RHS repeats. Using comparative genomics tools and a phylogenetics approach we were able to create the evolutionary relationship between these two organisms. The ProgressiveMauve software was used to generate a synteny analysis of this genomic region where we compared several *Wolbachia*, and Mosquito species to understand the pattern of HGT. Based on our findings, we want to further investigate the functional role of the horizontally transferred genomic regions and expand our study to other mosquito species.

Introduction

- Horizontal Gene Transfer (HGT) is the nonsexual transmission of genetic material from species to species (Wybouw, Pauchet, Heckel, & Van Leeuwen, 2016) .
- HTG has a known significance in prokaryotes but the impact in eukaryotes is not yet fully known (Wybouw, Pauchet, Heckel, & Van Leeuwen, 2016).
- *Wolbachia* is one of the most common endosymbiotic bacteria that is known. *Wolbachia* effects may range from costs in fitness to the benefits of fitness (Dutra et al., 2016).
- *Aedes aegypti* is mainly responsible in the transmission of Dengue disease. However, the transmission of the disease strongly depends on the fitness of the host(Dutra et al., 2016).
- *Wolbachia* is not naturally present in *Aedes aegypti,* but the bacteria has been found in the mosquito (Dutra et al., 2016).
- When *Wolbachia* is present in *Aedes aegypti,* the mosquito's fitness is greatly affected. This is turn limits the transmission rate of dengue virus from the mosquito (Walker et al., 2011)

Methods

Accession Numbers were assessed through the use of reference articles. The accession numbers were evaluated through NCBI and a BLAST search was carried out, revealing a possible relationship between Wolbachia and *Aedes aegypti*. MegaX was used to observe the evolutionary relationship between the species. The relationship was finally assessed through a Syntenty analysis which consisted of Wolbachia, *Aedes aegypti,* and two other mosquito species that were relevant in our BLAST search.

Conclusions

Our results can conclude there is Horizontal Gene Transfer between *Wolbachia* and *Aedes aegypti.* Overall, there seems to be evolutionary relationships between the two species that can be seen on the phylogenetic tree, along with the similarities in the nucleotide sequences from the synteny analysis. In the future, we plan to analyze other mosquito species and their relationship with *Wolbachia*.

Results

	BLAST Results for Wolbachia Protein				
	Accession #	Perc. Identity	E value	Query Cover	Descriptions
Foward BLAST	EAT44460.1	50.09	0	96	uncharacterized protein LOC5564242 in yellow fever mosquito (UNKNOWN FUNCTION)
Reverse BLAST	WP_138264814.1	50.12	0	99	Uncharacterized conserved protein RhaS, contains 28 RHS repeats

Table 1: The forward and reverse blast results when the Wolbachia protein (WP_138264814.1) was inputted into the BLAST software.

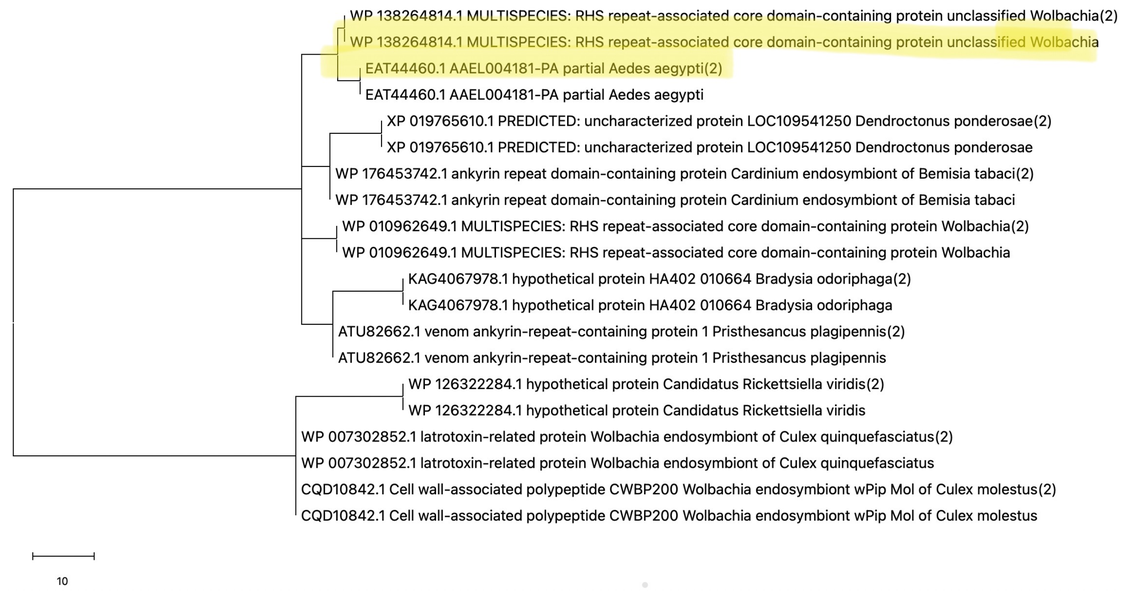

Figure 1: The phylogenetic tree analysis of *Aedes aegypti* and Wolbachia. This figure shows the evolutionary relationship between the two species being on the same clade.

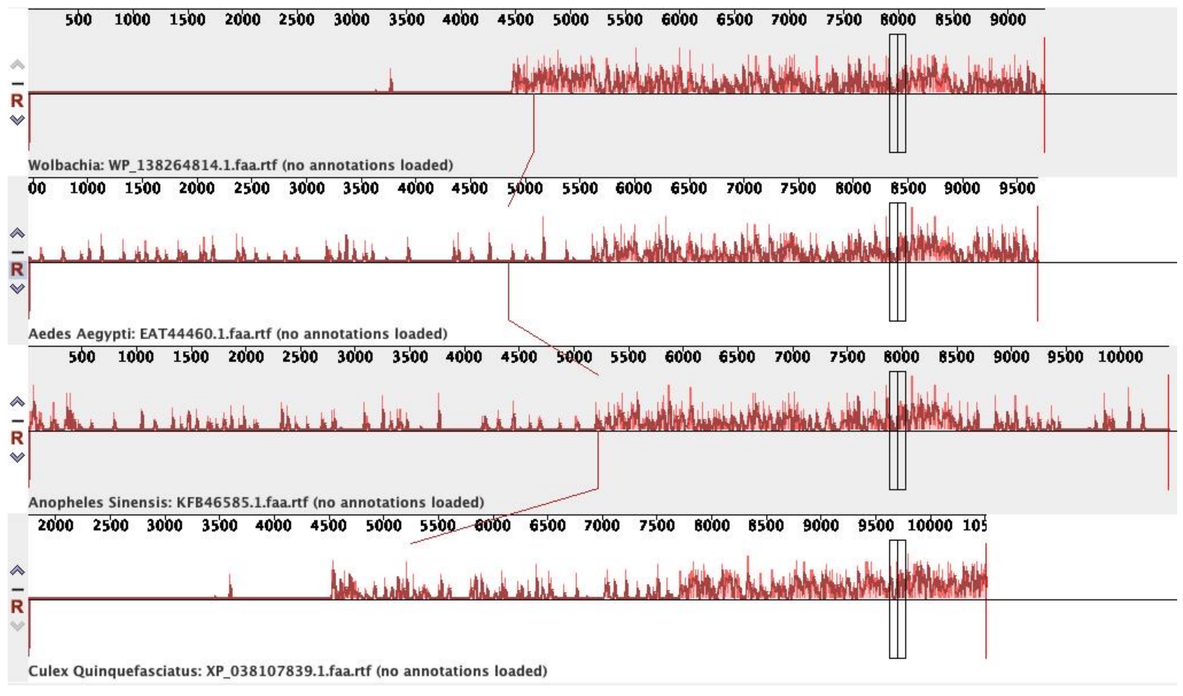

Figure 2: Synteny analysis of Wolbachia, *Aedes aegypti,* and two other mosquito species from BAST results.

NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE NO PRINTING ZONE