Analysis of Transposable Elements in the Genome of a Black Widow Spider, *Latrodectus hesperus*

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Introduction

Latrodectus *hesperus*, also known as black widow spider, is a one of the 35 species in the Theridiidae family (Species List for Latrodectus) . The name "widow" originates due to the potential of female spider to eat males (known as sexual cannibalism) or siblings (sibling cannabalism) during rare circumstances with the intention of protecting their offspring. Females have potent venom which contains neurotoxin latrotoxin that is dangerous to humans, however, it has rarely caused any serious consequences or deaths. They are known as cobweb weaving species because they use their adhesive webs which contain glue to form a pattern like a web. L. *hesperus* is present in agricultural settings and may potentially affect the fruit. They are also found near residential areas such as garages, farms, and gardens, and mostly stay close to the ground (Vetter et al., 2012). Despite of huge diversity present among spiders in the arthropods group, the genetic variation that occurred during their evolution, which led to all kinds of adaptations and behaviors is still not largely known (Miles et al., 2024). Due to their complex genome and high variation among species, rare genomic studies have been performed and more studies are needed to explore this intriguing diversity of spiders. These studies can help advance the ways in which spiders can be used, and fought against to fulfill our goals, such as controlling their negative impact on crops through fertilizers. Additionally, their web is useful as it is composed of silk threads which are extremely durable, and lightweight, thus L. *hesperus* has huge biomedical and materials applications (Gatesy et al., 2001; Ayoub et al., 2007). Our study is aimed at exploring the genetic structure of L. *hesperus* and identifying the transposable elements, specifically DNA transposable elements, in the genome of this spider.

Figure 1: Latrodectus *hesperus,* black widow spider. Image credit: Timothy Boomer, WildMacro.com

LTR/Pao and LTR/Gypsy Elements

LTR, or long terminal repeats, form the retrotransposon characterized by the presence of identical pair of long sequences at either end of the DNA . These transposons work by reverse transcribing their mRNA to form cDNA, which is inserted into a different region of the DNA sequence . Pao and Gypsy comprise the main LTR subfamilies, thus it is important to analyze them as they play major role in the evolution due to the large number of mutations they can produce in a genome. The Bel/Pao and Gypsy elements are most abundant LTR elements and are similar in the domain arrangement as they both contain env gene (de La Chaux and Wagner, 2011). The length of the Pao elements is around 4.7-8.3 kb and their LTR sequences are usually 0.3-1.3 kb long. On the other hand, the Gypsy elements are usually 6-7 kb long and the length of their LTR sequences is around 200-400 nucelotides (nts) (Llorens et al., 2011).

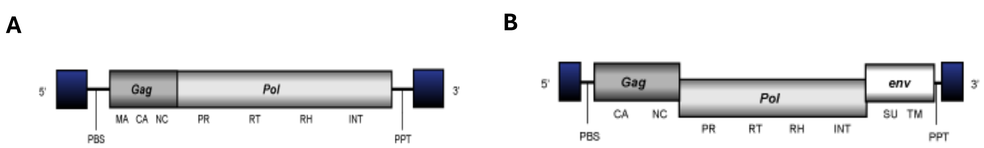

Figure 2: The genomic structure of two main subfamilies of LTR Retrotransposons, A. LTR/Pao, and B. LTR/Gypsy. Adapted from The Gypsy Database (GyDB) of Mobile Genetic Elements: Release 2.0.

Experimental Approach

The genome file was downloaded from the National center for biotechnology information (ncbi) website, and the genome structure was explored to determine the number of segments and the percentage of each of the nucleotides present, including A, C, T, G, and N. Then, the return characters were removed from the DNA sequence to ensure that header line and sequence line were separated. This was accomplished using the awk command which allowed us to determine the number of fragments in the genome. Later, the length of each fragment was determined, and the result was analyzed using a histogram and a box plot to identify the pattern for the majority of the fragments. Then, the BLAST run was performed with known transposable elements to identify the common locations within the genome that have matching patterns, and to determine which specific transposable elements match at specific locations.

Results

Analysis of the genome structure of L. *hesperus*:

Genome size: 1.2 Gb

There are 161595 segments within the genome.

Percentage of nucleotides:

A:15.56%, a: 19.99%, T: 15.54%, t: 19.98%,

C: 8.32%, c: 5.00%, G: 8.33%, g: 5.00%

N: 2.24% n: 0.05%

Number of fragments determined: 323190

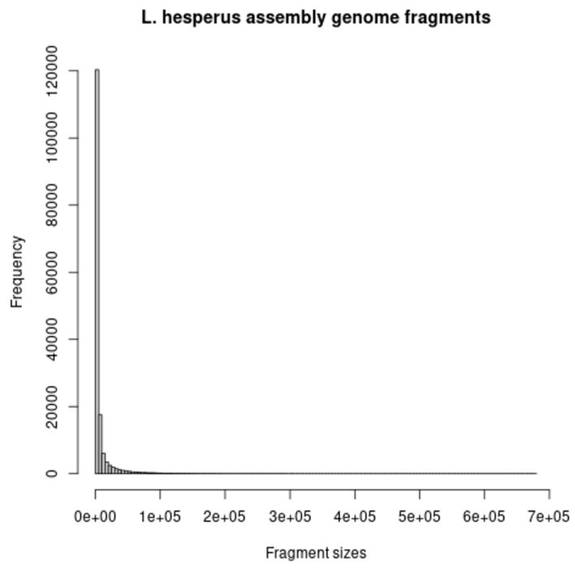

Figure 3: Histogram showing the frequency of fragment sizes within the genome of Latrodectus *hesperus*.

Results

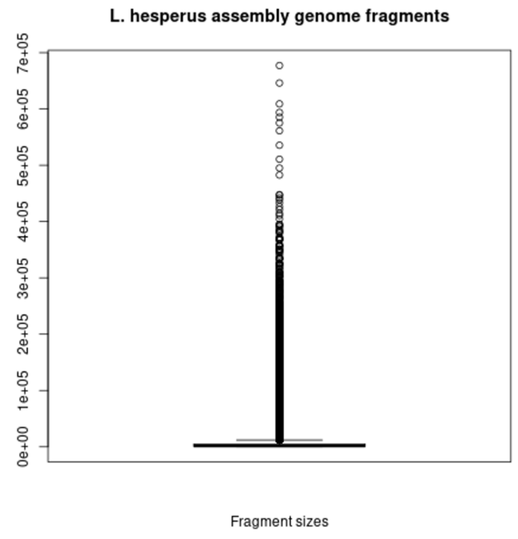

Figure 4: Box plot showing the distribution of fragment sizes within the genome of Latrodectus *hesperus*.

Transposable Element	Count
LTR/Pao	16
LTR/Gypsy	9

Figure 5: The number of LTR/Pao and LTR/Gypsy elements determined in the genome of Latrodectus *hesperus*.

Conclusion and Future Directions

The histogram shows that the data is highly skewed to the right, and most of the fragment sizes are extremely small (Figure 1). The second figure shows a box plot which is so skewed that only the top part can be observed (Figure 2). It shows that there are a number of large fragments for this genome which are about 650,000 bp in size. There is the presence of both LTR/Pao and LTR/Gypy transposable elements in the genome, where the Pao elements are more abundant than Gypsy elements. This project will be continued by other lab students who will further explore the genome of the Latrodectus *hesperus* by identifying the presence of various such types of subfamilies, and ultimately, help uncover the evolutionary history of this genome, and its related species.

Acknowledgements

With the guidance from Dr. Arensburger, the project was conducted, and progress was made by completing small tasks which were assigned in an organized way. ChatGPT was used to assist with writing commands to accomplish project goals.

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