What Are The Genes That Cause Male Sterility in Hybrid Offspring Between *Drosophila mauritiana* and *Drosophila simulans*?

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What Are The Genes That Cause Male Sterility in Hybrid Offspring Between Drosophila mauritiana and Drosophila simulans

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WHAT WE LEARNED

Finding genes that cause sterility in hybrid males between D. mauritiana and D. simulans will help us better understand evolution at the molecular level.

A genetic component related to sterility is near the 7.10 Mb region, but more research is needed to identify the gene or genes contributing to sterility.

This will expand on the current understanding of speciation and shed light onto mechanisms of male sterility in insects that may help solve the challenges of insect disease vectors.

BACKGROUND

Research has found that the genes causing sterility in interspecific hybrids have a higher chance of residing on the X chromosome; this pattern is called the ‘large X-effect’. Therefore this study focuses on the X chromosome and not the autosomes. The mechanisms underlying the large X-effect are not well understood. Previous research has demonstrated that the X-chromosome evolves faster than the autosomal chromosomes and regulatory phenomena such as spermatogenic X inactivation and dosage compensation can contribute to sterility within species, but further research is needed in order to better understand their effects on hybrid sterility. Researchers have used genetic approaches as well as studying species incompatibilities and have been successful. Other researchers have used different species of Drosophila and have discovered genes that may be responsible for the sterility in the male hybrid, but they have only discovered a few genes thus making this field an area of needed attention.

INTRODUCTION

The purpose of this research project is to better understand speciation - the process by which new species arise. To better understand how species form we will investigate how sterility within species, but further research is needed in order to better understand their effects on hybrid sterility. Researchers have used genetic approaches as well to studying sterility in hybrid offspring between D. mauritiana and D. simulans alleles at each of the regions 6.20 Mb, 7.10 Mb, 8.02 Mb and 9.74 Mb. The P-value obtained for the regions 6.20 Mb was 0.85, for the region 8.02 Mb the P-value was 0.078 and for the region 9.74 Mb the P-value was 0.96. Since all of these values are >0.05, it means that the differences between the total average fertility score of both D. mauritiana and D. simulans were not significant at those regions. This means that the null hypothesis was accepted. The P-value for the region 7.10 Mb was 1.04E-06 which is below 0.05 therefore the null hypothesis can be rejected. Thus statistically there is a significant difference between the total average fertility score of genotypes that carry D. mauritiana and D. simulans alleles at the 7.10 Mb region on the 2P3 X-chromosome. Figure 5 shows the difference between the fertility scores at all four markers. The graph shows that there is a difference in the fertility of the DNAs depending on whether they are D. simulans or D. mauritiana for 7.10 Mb region while the other regions show very little difference. Figure 6 shows that the 7.10 Mb region of the DNAs with the D. mauritania DNA are very light in color, ranging from yellow to light blue indicating low fertility scores. This means that the gene or genes of interest may be very close to the 7.10 Mb region. The next step will be to design primers that increase the precision of estimates of the recombination break points to confirm and extend the results of this research.

METHODS

• Hybrid females were backcrossed to D. simulans males in order to move small chromosomal regions from one species to another
• Qualitative Polymerase Chain Reaction was used to determine if the DNA that was genotyped was either D. mauritiana or D. simulans at specific regions of the 2P3 X-chromosome.
• DNA Extraction was conducted to extract DNA from frozen hybrid flies that were previously generated.
• Gel Electrophoresis was used to separate and analyze the DNAs
• Data collection consisted of determining whether the DNA was D. mauritiana or D. simulans at the regions 6.20 Mb, 7.10 Mb, 8.02 Mb and 9.74 Mb. The average fertility scores for all the DNAs that consisted of both species were obtained for each region. Then a t-test was conducted in order to determine how significant the differences between the total average fertility score were.

RESULTS

The data obtained starts with Figure 3, which explains how the hybrid male sterile flies were obtained. The 2P3 X-chromosome has dark orange eyes while the 1P3 X-chromosome has light orange eyes. A-t-test was conducted on the fertility scores for DNAs with D. mauritiana and D. simulans alleles at each of the regions 6.20 Mb, 7.10 Mb, 8.02 Mb and 9.74 Mb. The P-value obtained for the regions 6.20 Mb was 0.85, for the region 8.02 Mb the P-value was 0.078 and for the region 9.74 Mb the P-value was 0.96. Since all of these values are >0.05, it means that the differences between the total average fertility score of both D. mauritiana and D. simulans were not significant at those regions. This means that the null hypothesis was accepted. The P-value for the region 7.10 Mb was 1.04E-06 which is below 0.05 therefore the null hypothesis can be rejected. Thus statistically there is a significant difference between the total average fertility score of genotypes that carry D. mauritiana and D. simulans alleles at the 7.10 Mb region on the 2P3 X-chromosome. Figure 5 shows the difference between the fertility scores at all four markers. The graph shows that there is a difference in the fertility of the DNAs depending on whether they are D. simulans or D. mauritiana for 7.10 Mb region while the other regions show very little difference. Figure 6 shows that the 7.10 Mb region of the DNAs with the D. mauritania DNA are very light in color, ranging from yellow to light blue indicating low fertility scores. This means that the gene or genes of interest may be very close to the 7.10 Mb region. The next step will be to design primers that increase the precision of estimates of the recombination break points to confirm and extend the results of this research.

Citations