Genotyping Mouse Models

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INTRODUCTION

- Animal models are an important approach to study human diseases and develop therapies. When using animal models, it is essential to distinguish the diseased animals and the wild-type animals. Genotyping is a widely used technique to identify the genetic background of different animals. This is an important process because it allows scientists to determine what types of genetic traits are coded for by the genome. In this project, two mouse models are used to study two human brain disorders: intellectual disability and Alzheimer's disease. Mutations in Heparan Sulfate 6-O-Sulfotransferase 2 (HS6ST2) cause intellectual disability in human patients. We have generated mouse models to disrupt HS6ST2 in mice to study HS6ST2-associated intellectual disability. We also have the 5xFAD mice, which are a widely used mouse model of Alzheimer's disease. By performing genotyping for the two mouse models, we can determine if the organisms are wild-type, heterozygous, or homozygous for the mutation. Overall, this process allows us to categorize mice into different groups.

METHODS

- Tail samples are obtained from several groups of mice for each of the two mouse lines studied in the project.
- The DNA from each tail sample was isolated.
- Then a PCR mixture for each DNA sample is prepared and placed in the PCR machine.
- A gel electrophoresis is run for each type of mouse model.
- Results are visualized under ultraviolet light.

We Need to Know the Genetic Background of Organisms

Figure 1

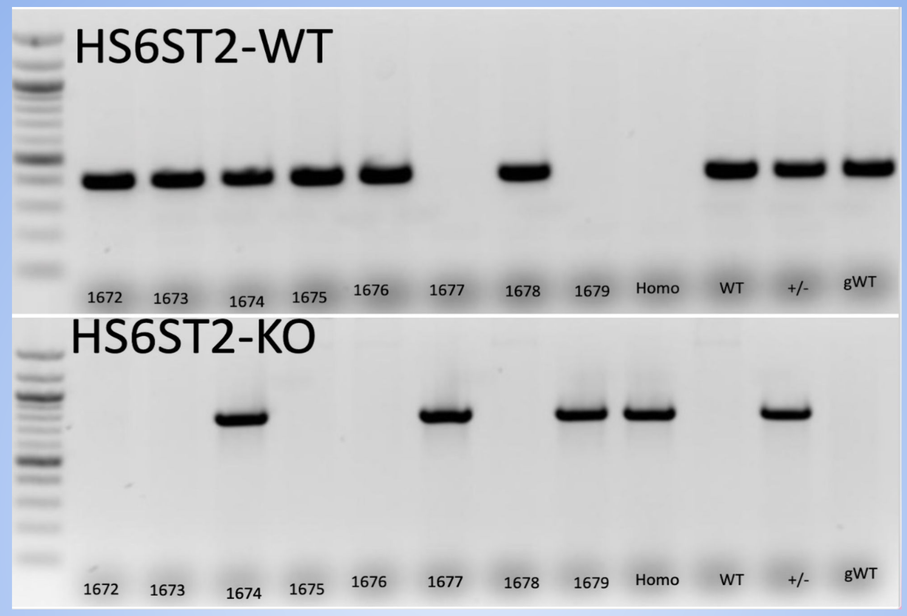
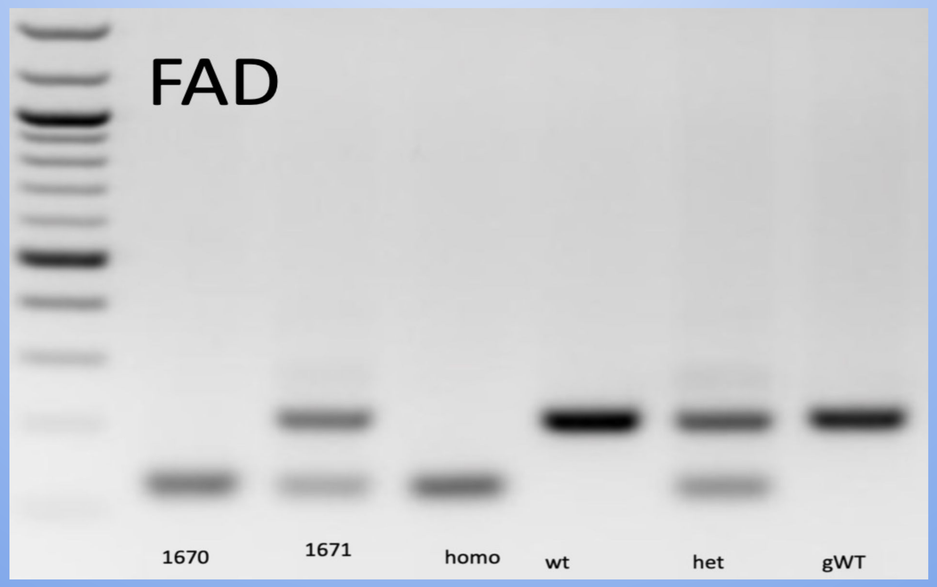


Figure 2



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RESULTS FOR THE GENOTYPES

Figure 1:

- Figure 1 shows a gel electrophoresis that was run to find the genetic background for mice for the gene, HS6ST2. The figure reveals an image taken under UV light where each column represents the genotype of a different mouse.
- It can be observed that wild-type mice had a singular band that was around 375 base pairs. The mutated (diseased) mouse had a singular band that was around 800 base pairs. A mouse that was heterozygous (inherited one diseased allele and one wild-type allele) had two bands: one at 375 base pairs and one at 800 base pairs.

Figure 2:

- Figure 2 is a gel electrophoresis run to find the genetic background for each mouse for the gene, FAD. In the picture, each column represents the genotype of a different mouse.
- The picture shows that the wild-type mouse had a singular band that was approximately 216 base pairs. The mutated (diseased) mouse had a singular band that was approximately 129 base pairs. A mouse that was heterozygous had two bands: one at 216 base pairs and one at 129 base pairs.

CONCLUSION

- This process is vital in order to further study these two mouse lines. This is because knowing the genetic background allows scientists to perform other experiments that can increase our understanding of these neural disabilities. Increased knowledge of these disorders will potentially lead to the development of new therapeutics that can help millions of people in the future.