

CHRNA5 is a receptor subunit which mediates signal transmission. Single nucleotide polymorphisms (SNPs), have been associated with susceptibility to nicotine dependence. It is crucial to understand CHRNA5's expression in the development of therapies for individuals struggling with nicotine consumption. To date, the mechanism through which the decreased function of CHRNA5 increases nicotine intake is not well understood. As of now, there have been several GWAS studies that have evaluated the variants in CHRNA5. There has been minimal research done in other aspects, such as the effects of in utero nicotine exposure through maternal smoking. Maternal smoking during pregnancy exposes the developing fetus to nicotine and as a higher chance of dealing with nicotine dependency. Carriers of the risk variant may be at elevated risk of struggling with smoking cessation during pregnancy. The literature review and experimental proposal aim to evaluate the impact of CHRNA5 variants on nicotine dependence and its relationship to alcohol and nicotine addiction in adolescence.

Although tobacco has been growing in the Americas for around 8,000 years, it was not up until around 2,000 years ago that indigenous people began chewing and smoking tobacco during cultural and religious ceremonies (Cancer Council NSW, n.d.). The spread of tobacco from the Americas around the world began shortly after the start of European colonization. In the 1600s, tobacco became widespread in Europe, and by the 1700s it was already established as a worldwide developed industry. Although risks associated with smoking were reported as early as the 1600s, it was not until the 1960s that the link between smoking and cancer was established. It is even more interesting to note that in the period between the 1930s and

Single nucleotide polymorphisms (SNP) variants in the gene are associated with an increased risk for tobacco dependence. The way that polymorphisms in this case work is that they alter the receptor composition and the binding of nicotine to the receptor. This, in fact, leads to changes in functional and behavioral outcomes (Chaity et al., 2022). Therefore, investigating into the CHRNA5 gene is of crucial interest in learning more about human nicotine dependency.

To date, there have been many human genome-wide association studies (GWAS) that have identified SNPs associated with nicotine dependence. For example, a GWAS by Lassi et al. (2016) identified a SNP on chromosome 15 that is associated with nicotine dependence. Another GWAS by Hong et al. (2020) identified a SNP on chromosome 10 that is associated with nicotine dependence. These studies have contributed to determining the risks of nicotine dependency depending on the location where people live. In a research paper by Hong et al. (2020), the results indi-

H3: Adolescent mice D with in utero nicotine exposure will consume the third most alcohol at both concentrations.

H4: Adolescent mice D without in utero nicotine exposure will consume the least alcohol at both concentrations.

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As of current literature review and my personal research, there has } [c h a ^ A } A a e } A ^ P } A i a { ^ } c h c @ a e c A @ a • A c ^ • c A a A c @ A A ^ A & c h [- A a e | & [@ [] A & [] • ~ {] - c i [] A a } A [•] i a } * A , i c @ A c @ A A P A c a e i a e } c e A V @ A ^ - [! A e A c @ i • A ^ P } A i a { ^ } c h i • A } [c A A and contributes to the topic of adolescent addiction. The results of this experiment will help to better understand the mechanism of the CHRNA5 gene and its impact on addiction in mice. The results of this experiment & [~] a A a A A [• • i a | ~ A ~ • A a A c [A [a • A i c A c @ A A ^ A & c h a } A c @ A A @ ~ { a e } A [] [~] a e c A [] E

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After collecting the data of the consumption from the three a a ^ ! ^ } c A a [c c | ^ • e A c @ A A ! ^ • ~ | c A , a i | A a A a e c A ! a e ~ A a A a e } a A a e } a e | ~ : A a A ~ • i } * A a e } A C E P U X C E A c ^ • c e A a e | [[, a } * A c [A & [{] a e ! A A c @ A A - [~ ! A a i ^ ! ^ } c h ^ P } A i a { ^ } - t a l groups. The goal of the analysis will be to examine the relation between the groups and to observe whether it will be statistically con- , ! { A a A c @ a e c A } i & [c i } A A a e } a A a e | & [@ [] A a A } a A } & ~ A & a e } A a A A & [! : A \