**Spina Bifida** is the most common birth defect characterized by a failure of the neural tube to fuse properly during embryonic development.[1] It is complex to treat and often leads to lasting disability.[2] Several single nucleotide polymorphisms (SNPs) in the maternal ***MTHFR* gene** have been identified and the C677T SNP is associated with modest increased risk of having a baby with spina bifida if heterozygous and significant increased risk if homozygous.[3] The **MTHFR** enzyme converts 5,10 methylenetetrahydropholate into 5-methyltetrahydrofolate which is the primary circulatory form of folate and a necessary compound for cellular production of methionine.[4] *Although this individual SNP has been shown to cause small to modest increases risk of a spina bifida, it is not understood how multiple SNPs in* ***MTHFR*** *and other genes in the folate metabolic pathway interact to impact the risk of developing spina bifida.*

The **long term goal** of this project is to develop a polygenic risk profile for the development of spina bifida in order to implement effective preventative prenatal care. My **primary objective** for this project is to characterize the impact of multiple SNPs in ***MTHFR*** on the risk of developing spina bifida. My **hypothesis** is that the presence of increasing numbers of SNPs in MTHFR will have an additive effect and contribute to proportionally lower enzymatic functioning, increasing the risk of developing spina bifida. A mouse (*Mus musculus*) model will be used to investigate this hypothesis due to the similarity of mouse and human neurulation and the 90% identity between human and mouse ***MTHFR***.[5]

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