Analysis of DNA Methylation at Dlk1 during Embyronic and Neonatal Development

Epigenetics is the study of heritable changes in gene expression caused by mechanisms other than changes in the DNA sequence itself. These changes made to the chromatin structure can affect gene expression and cellular phenotype. Our research focuses on a sub-discipline of epigenetics, which is the study of genomic imprinting. This is a phenomenon by which the allele that is expressed is parent-of-origin, and this imprinted expression essential to mammalian growth and development. I will be looking into differences in the epigenetic modifications, such as DNA methylation and histone modification, on the paternally and maternally inherited alleles that allow them to be distinguished from one another. More specifically, I will be analyzing the DNA methylation acquisition at the Dlk1/Gtl2 locus during embryonic growth and neonatal development. Dlk1 and Gtl2 are linked imprinted genes that share a common differential methylation regulatory element, the IG-DMR. In addition, there are two more DMRs in this region: Dlk1-DMR and Gtl2-DMR. Since these DMRs are located within the same chromosomal region, I hypothesize that they will be similarly regulated. To test this hypothesis, I will determine when the Dlk1 gene is methylated and how many sites are methylated at each stage of development in both the maternal and paternal alleles and compare the results to those of the Gtl2-DMR. Through this research, one can gain a better understanding of gene imprinting as a whole, as well as lead to further studies in the direction of similarities in methylation acquisition for linked genes.