Name: - Naaila Tamkeen

Topic of Research: - Modeling and analysing the gene regulatory networks for Spina Bifida to identify potential therapeutic targets.

Supervisor: - Dr. Nadeem Ahmad

Department: - Department of Biosciences

Notification No.:- 555/2024

Notification Date: - : 20-03-2024

In the first part of the study, a manually curated set of genes from the literature that are reported to be involved in Spina Bifida (SB) was analyzed using graph theory to identify the key regulatory (KR) genes of SB. In the second part, the identification of the common key candidate genes and pathways for SB and Wilm's Tumor (WT) was done using an integrative bioinformatics analysis aimed at their concurrent therapeutic management. In the third part of the study, SB and Myelomeningocele (MMC) microarray datasets were analyzed for the key regulatory genes by employing a network-based approach. In the last part, we searched in the literature if there are single nucleotide polymorphisms (SNPs) in the KR genes identified through the first three parts of our study. MTHFR, PTCH1, and TNIP1 KR genes were found to have SNPs reported to be involved in SB. Molecular dynamics simulation studies showed that there were slight fluctuations found due to the corresponding polymorphism in the MTHFR protein structure, while polymorphisms in PTCH1 and TNIP1 genes resulted in considerable fluctuations in the PTCH1 and TNIP1 protein structures respectively, indicating that these SNPs might be involved in the occurrence of SB.