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Transcriptome Profiling in Gastric Cancer

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Gastric cancer (GC) is the fifth most common cancer and third most common cause of cancer-related mortality in the world. The symptoms of GC occur in the late stages making early diagnosis a challenging task compromising disease management. Therefore, efforts are underway to develop effective biomarkers for early diagnosis of the disease and to identify new targets of drug development. Recently, Next Generation Sequencing (NGS) based RNA Seq approach have provided a cutting edge over traditional methods in understanding molecular pathogenesis of human diseases and disorders. We have performed comparative transcriptome profiling of tumor and normal tissues using Illumina RNA-Seq to identify differentially expressed genes (DEGs) and single nucleotide polymorphisms (SNPs) involved in the occurrence of gastric tumorigenesis. Over 390 million high quality reads covering 90% of total reads were obtained from twelve libraries, six each for tumor and normal tissue. We identified 2034 differentially expressed genes in cancerous tissue in comparison to normal tissue. The top ten upregulated and downregulated genes were *CDH3*, *DKC1*, *NAT9*, *KRT5*, *CDCA5*, *BATF2*, *GNA15*, *ENG*, *KRT16*, *LAMP3* and *LIPF*, *PRKAR2B*, *VIT*, *SLC28A2*, *FBLN2*, *ACACB*, *MAP7D2*, *MTURN*, *SASH3*, *CDS1*, respectively. The DEGs were accommodated in various ontology categories including digestion, digestive system processes, and digestive system and digestive tract development. The level of expression of selected DEGs in tumor tissues has been validated through real-time PCR. Our findings contribute towards understanding molecular events occurring during gastric tumorigenesis and useful leads for developing future strategies management of gastric cancer.

Biography:

Prof. Prakash Chand Sharma has teaching and research experience of over 35 years in the field of genetics, molecular biology and biotechnology. He has contributed significantly towards development and use of molecular markers, particularly microsatellite markers, for diverse applications in different crop plants. Recently, his group has exploited NGS-based transcriptome profiling to identify abiotic stress responsive elements in seabuckthorn, an important medicinal plant, and to understand molecular pathogenesis of early phase hypobaric hypoxia and gastric cancer. Dr. Sharma has published over 100 research papers, executed a number of research projects, and supervised a large number of Ph.D., M.Phil., M.Sc., B.Tech./M.Tech. students.