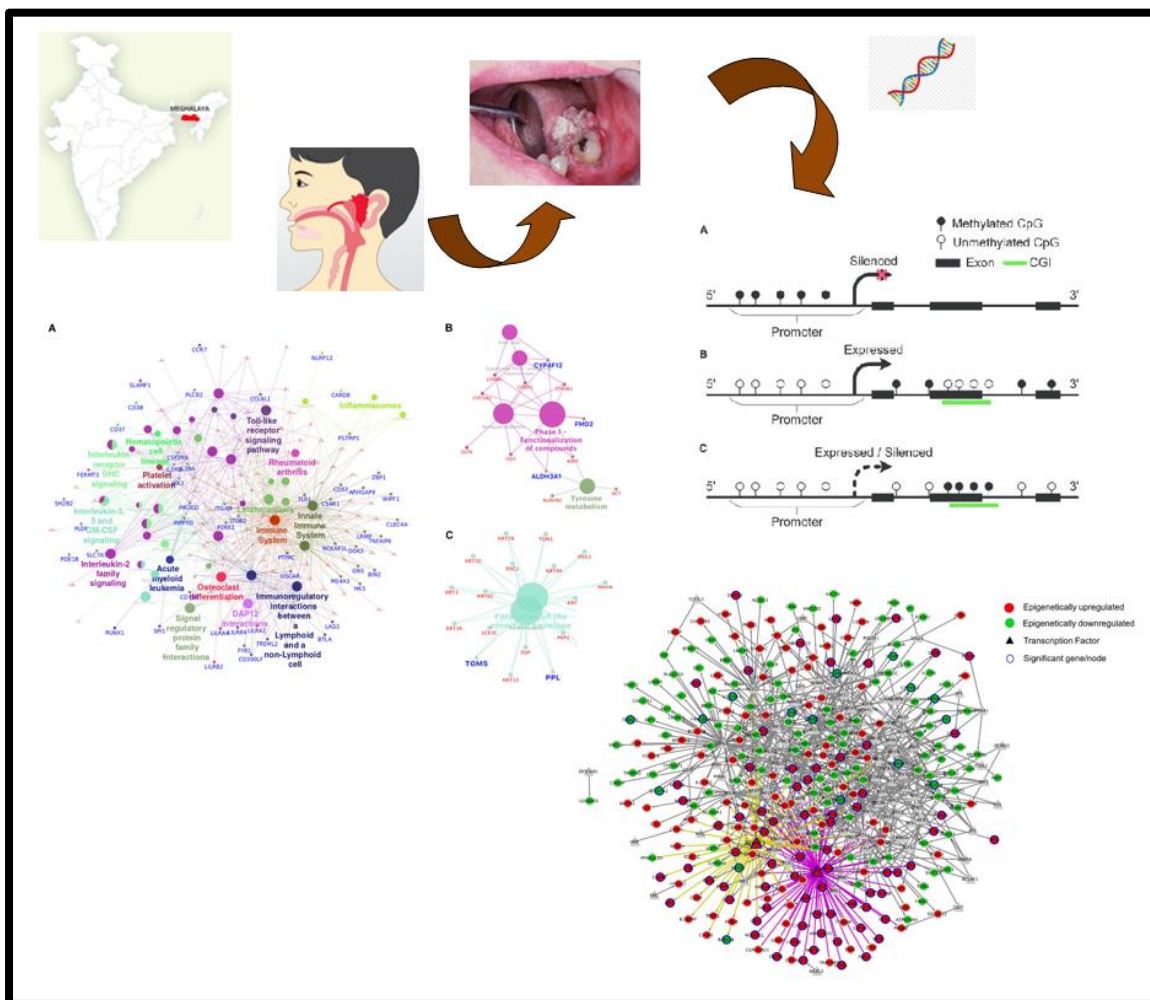


## DBT-NIBMG study gets new insights into Oropharyngeal cancer

New Delhi, Nov 11: Oropharyngeal cancer is a subtype of head and neck squamous cell carcinoma that is associated with unique risk exposures like chewing of tobacco and arecanut and is highly prevalent in the northeastern region of India, especially Meghalaya. However, the underlying epigenetic and transcriptomic changes in this cancer type is yet to be delineated.



A Twinning Research Grant, funded by the Department of Biotechnology, Ministry of Science and Technology, Govt. of India, enabled National Institute of Biomedical Genomics (NIBMG), Kalyani, North-eastern Hill University (NEHU) and North Eastern Indira Gandhi Regional Institute of Health and Medical Sciences (NEIGRIHMS), Shillong to collaboratively investigate the epigenetically altered gene expression changes in this cancer type.

The team analyzed genome wide DNA methylation changes and whole transcriptome changes in paired tumour and adjacent normal tissue samples obtained from patients using a DNA microarray-based platform and RNA sequencing respectively. By using integrative approaches, they have identified 194 epigenetically silenced and 241 epigenetically overexpressed genes in the tumor tissue of these patients. Pathways that are significantly enriched by these genes include the pathways of immune systems, such as the interleukin signaling pathways and Toll-like receptor signaling pathway. Also, osteoclast differentiation pathway was found to be epigenetically upregulated. The pathways enriched by the epigenetically downregulated genes were found to be predominantly those involved in xenobiotic metabolism and keratinization. Two major transcription factors – SPI1 and RUNX1 were identified as epigenetically dysregulated, which further modulates 129 downstream genes.

Comparison of these observations with the head and neck cancer data from TCGA revealed distinct DNA methylation and gene expression landscapes which might be specific for oropharyngeal cancer. The results obtained in this study might provide improved understanding of the disease. The study has been published in *Frontiers of Genetics* (<https://www.frontiersin.org/articles/10.3389/fgene.2020.00986/full>).

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