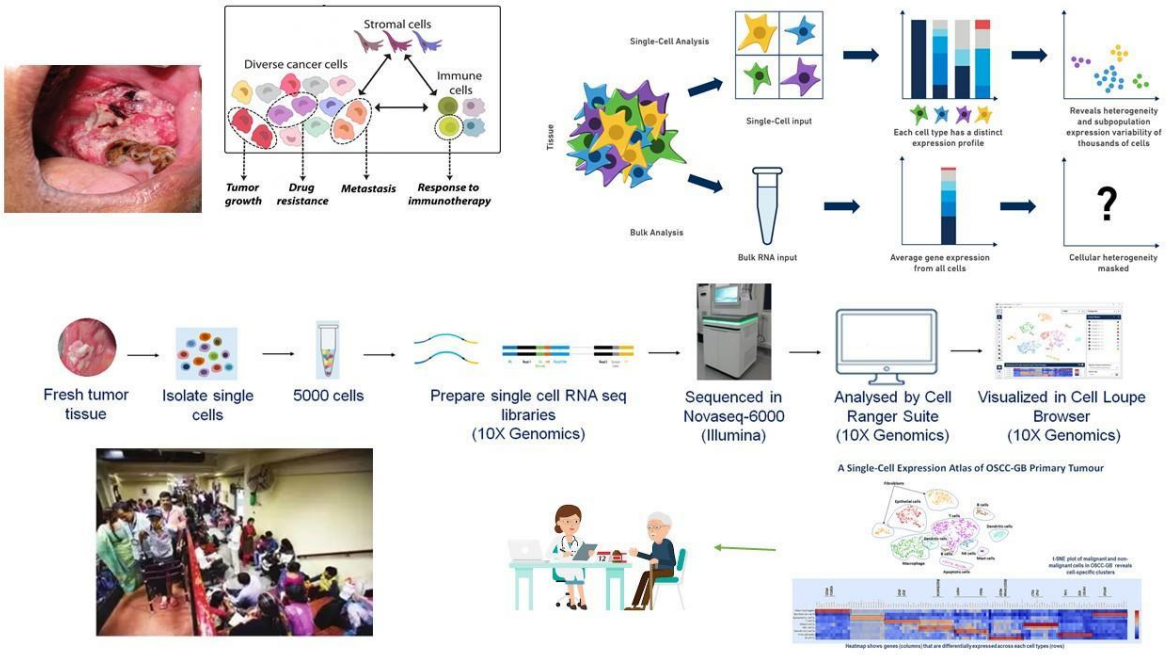
DBT-NIBMG scientists seek to understand cellular heterogeneity of Tumour Ecosystem

New Delhi, May 14**:** Cancer is caused by changes in the genome. In most cancers, such changes are caused during the lifetime of the individual by environmental and lifestyle risk factors. Oral cancer is the most predominant cancer type in men in Indian subcontinent. It is mostly caused in this part of the globe by chewing of tobacco or related products, and betel leaf and areca nut which causes changes in the squamous cells, a type of cells lining the oral cavity. Scientists have identified many such somatic changes in the DNA in oral cancer patients in India. They have also identified the genes in which they are located, as these somatic mutations lead to either inactivation or other changes in the function of the proteins coded by these genes. However, the relationship of such information with clinical results e.g. the ability of the patient to be cured after surgery or treatment or the possibility of recurrence of the tumour is yet to be delineated. Addressing these intricacies can result in improved understanding of the initiation and progress of the tumour and help clinicians manage and treat cancer patients more efficiently. In recent times, tumours are understood to be ecosystems of multiple and diverse types of cells. There is an expectation that this diversity in the cell types, each of which behave differently in the ecosystem, and which vary from one patient to another, might hold vital clues for prediction of clinical outcome of the cancer patient. However, sequencing the bulk tumour tissue for investigating gene expression and other genomic changes averages out the signal from individual cells. Hence, a group of scientists at DBT- National Institute of Biomedical Genomics have undertaken a study in which they are harnessing cutting edge methods to profile gene expression of individual cells of the tumour ecosystem obtained from each oral cancer patient. They aim to use this data to understand the cellular heterogeneity between oral tumours obtained from different patients and illuminate the relationship of such heterogeneity with clinical outcome. They expect the results to provide valuable information which can be translated in the clinics for improved management and treatment of oral cancer patients.



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