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Molecular characterisation of gastric tumours in a south Indian cohort and their clinical correlation

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The prevalence of gastric cancer is high in Asian countries. There is a gross heterogeneity in the clinical outcomes and recurrence patterns due to varied molecular mechanisms driving differences in cancer aggressiveness and treatment outcomes. The developments in next generation sequencing platforms has enabled the genome-scale identification of molecular dysregulations and the possible genomics-guided stratification of tumors for prognosis and eventually targeted therapeutics.

Our aim was to stratify gastric tumours into novel genomic subtypes based on the differential activation of 21 oncogenic signalling pathways and look for its association with histological characteristics and clinical outcomes.

Patients who underwent surgery at Meenakshi Mission Hospital tumour bits were sent to genetics lab and Genome-wide expression profiling was performed. The tumor samples were then subtyped into eight different groups based on oncogenic signaling pathways. The histopathological features of the samples intraoperative details were collected along with follow up data for a period of 1 year.

On analysis of these 21 oncogenic signalling pathways, the gastric cancer from 52 gastrectomy samples in south Indian could be subdivided into eight different subtypes. The mortality (V-0.85% & VII -0.88%) and rate of metastasis (0.9% & 0.77%) has been high in genomic subtypes V and VII (p value <0.001 and 0.002 respectively). The local infiltration rate observed intraoperatively was high for the genomic subtype II (0.72%) (p value - 0.002).

Numerous whole-genome profiles decoding the landscape of molecular determinants of gastric tumors have been established from Japan, South Korea and China. However, such larger profiles of gastric tumors are largely lacking from India. In this study, we profiled 50 gastric tumors from a South Indian cohort and they were analyzed for any possible clinical correlation.