

Session C. Sarcoma

C03 Into the Wild of long non-coding RNAs in Gastrointestinal Stromal Tumors (GISTs) to explore new prognostic/predictive biomarkers

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Background: Long Non-coding RNAs (lncRNA) are emerging as essential regulators of genetic and epigenetic networks, and their deregulation may underlie complex diseases, such as carcinogenesis. Several studies have described lncRNAs alterations in patients with solid tumors. In particular, in Gastrointestinal Stromal Tumors (GIST),

upregulation of HOTAIR has been associated with aggressiveness, metastasis, and poor patients' survival. In order to gain more detailed insight on the molecular role of lncRNAs in GIST, we analyzed *in vivo* the expression levels of lncRNAs H19 and MALAT1 in surgically resected patients.

Material and methods: The expression of the lnc-RNAs H19 and MALAT1 was evaluated in primary tumor tissue from 20 GIST patients undergoing surgical resection, and paired normal mucosa samples, using quantitative real-time reverse transcriptase qRT-PCR. The result was considered reliable if the tumor tissue harboured at least 70% of cancer cells.

Results: H19 was evaluable in 20 patients, MALAT1 in 8 patients. H19 was overexpressed in 66% (12/20) cancer tissue from GIST patients, and the difference of expression between the two groups (tumor tissue vs normal tissue) was found to be statistically significant ($P=0.0496$). MALAT1 was overexpressed also in 100% (8/8) cancer tissue from GIST patients.

Conclusions: H19 and MALAT1 appear frequently upregulated in GIST patients. Further analyses are needed to confirm these data, and evaluate the potential role of such lncRNAs, as prognostic/predictive biomarkers.