

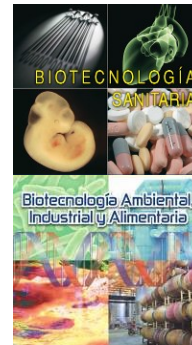
## Talk

## Identification of the lncRNA signature related to Sorafenib effectiveness in liver cancer cells

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### ABSTRACT

Hepatocellular carcinoma is the most common form of primary liver cancer being globally recognized as the fourth cause of cancer-related death [1]. The impact of risk factors on HCC has a variable geographic distribution, including hepatitis C (HCV) and B (HBV) virus infection, alcohol, aflatoxin B1, metabolic-associated steatotic liver disease (MASLD), tobacco and congenital diseases. Patients with advanced stage of HCC who lack preserved liver function, as well as vascular disorders and high blood pressure cannot benefit from the first-line systemic therapies (Atezolizumab-Bevacizumab and Durvalumab-Tremelimumab), and they are recommended to receive Sorafenib. Sorafenib is an orally administered multityrosine kinase inhibitor approved by the FDA for the treatment of HCC in 2008 [2, 3]. Among non-coding RNA, miRNAs, lncRNAs and circRNAs have been related to the initiation, progression and metastasis in HCC [4]. The group has recently shown that miR-512-3p exerts oncogenic role, and miR-200c-3p exert antitumoral properties under Sorafenib treatment in vitro, in vivo and in two independent cohorts of patients [5]. In this study we focus on lncRNA, a ncRNA molecule of more than 200 nucleotides. lncRNAs carry out many biological processes, including the regulation of proliferation, invasion, differentiation and metastasis. lncRNA also regulate gene transcription and translation by modifying the microRNA and mRNA signature in cells [6]. We have identified the lncRNA signature in response to Sorafenib in two liver cancer cell lines. In silico analysis of RNAseq data highlighted the differential expression of 11 Sorafenib-regulated lncRNAs in both cell lines. In vitro functional study validated the results obtained in silico. Sorafenib decreased the expression of 9 lncRNAs and increased the expression of 1 lncRNA. We will carry out specific experimental approaches to determine the functional role of these selected lncRNAs in cell invasion and migration. The final outcome of the project would be to determine whether the lncRNA signature might be a new biomarker of disease prognosis and treatment responsiveness.

### REFERENCES

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