Category: Cancer Genomics

Delineation of HIF1α mediated transcription program and the oncogenic signaling pathways in gastric tumors

Dhanasekaran Rathinam and Kumaresan Ganesan*

Unit of Excellence in Cancer Genetics, Department of Genetics, School of Biological Sciences, Centre for Excellence in Genomic Sciences, Madurai Kamaraj University, Madurai 625021, INDIA

*Corresponding author: kumar@oncocellomics.org

Abstract

HIF1α is a transcription factor activated under hypoxic condition in many cancer types and has been implicated in cancer cell proliferation, invasion and energy metabolism. Towards understanding the role of HIF1α mediated transcription in gastric cancer, the HIF1α gene signatures established to date were analyzed for their expression across the mRNA profiles of gastric tumors. HIF1α regulated genes were identified to involve and associated with the signaling pathways and processes such as integrin signaling, Wnt, P53, EGF, FGF, VEGFA, PI3K, TGFβ and NFkB signaling pathways. The HIF1α genes were identified to play a significant role in energy metabolism including glycolysis, drug resistance due to epithelial to mesenchymal transition and cancer cell survival. In gastric tumors, the HIF1α regulated genes were observed to express in diffuse, poorly differentiated and stage-3 tumors. The analyses reveal i) activation of HIF1 in a sub-set of gastric tumors, ii) the pathways associated with the HIF1 activation in gastric tumors, and iii) genes involved in HIF1α mediated transcription in gastric cancer. We are further investigating the drugs that would best suit for this sub-set of tumors with activated HIF1α.

References


Citation: Rathinam, D. and Ganesan, K. Delineation of HIF1α mediated transcription program and the oncogenic signaling pathways in gastric tumors [Abstract]. In: Abstracts of the NGBT conference; Oct 02-04, 2017; Bhubaneswar, Odisha, India: Can J biotech, Volume 1, Special Issue, Page 69. https://doi.org/10.24870/cjb.2017-a56