## Additional Study of Sp RNA Interaction with Key Regressor FMTO, Recurrence in Rhabdomyosarcoma (MGC) – MoJo

Authors: William Lee Melinda Morrison Kelsey Holder Robert Hopkins Stephen Crane

Published Date: 09-09-2014

Alaska Pacific University

School of Environmental Studies

Epigenetic mechanism causing increased or decreased expression of the key transcription factor specificity protein (Sp) RNA transcripts, detailed this week in the journal Cancer Research.

Patients with glioblastoma multiforme (GBM) or breast cancer have been suffering from high rates of rhabdomyosarcoma. These rare forms of cancer have often been treated with controversial therapies in the form of radiation therapy, radiation-induced lymphadenopathy and antitumor chemotherapy or targeted therapy. There is an increased risk of recurrence when treatment is discontinued.

Sp DNA transcription factors are the key promoters of the growth and differentiation of cells, tissue, and tumor. Increasing expression of Sp transcript factors in cancer cells can induce inhibition of cell/tumor growth by protein-forming transcription factors. In human rhabdomyosarcoma, Sp RNA transcript factors have been shown to interfere with the proliferation of the cancer cells. Promoters of Sp transcription factors include RAS, YH5, and IDH1, which are activated when the expression of other human transcription factors (IPFs) is inhibited. In total, over 650 binding partners of Sp RNA for the many genes are known to be active in the human body.

Researchers at the Broad Institute of MIT and Harvard describe the roles of four key-sp transcript factors (1) in cell and tumor growth and development and (2) in protein-forming networks. Their study evaluated the functional translation capacity of each of these transcription factors and how its levels are linked to cell function, in response to depletion of them and the levels of other key transcription factors.

The investigators examined three methods of silencing the Sp transcript factors: methylation (non-functional silencing), silencing either the RAS transcription factor or the IDH transcription factor. The study provides the first elucidation of silencing mechanisms of these key transcription factors, which likely have important effects on the development of tumor cells. They also found that silencing reduced transcription of MGC cells and emphasized the role of MPCP in regulating gene expression.

There is great need for more understanding of Sp transcription factors, which the Broad Institute researchers describe in detail, in this multi-jurisdictional, research collaboration with University of Texas M.D. Anderson Cancer Center.

This work was funded by the National Cancer Institute.

This study was co-authored by: Steven A. Arnold, Ery S. Alvart, Hari Hariharan, Sathya T.D. Vasudevan, Laura McClain, Satyajit Bajaj, Karim Anavy, Richard Platts-Mills, Jesse Kleinfeld, Ngoc-Yung Kim, Eric J. Ozmans, Robert Sobol, Kyounghyun Kim, Lajdeep Singh Chauhan, Daniel Offenberg, William B. Carrels, Silvia Negreiro, Greg Keach, Angie L. Spratt, Junwen Dai, Andrew S. Jaffe, Megan R. Larson, Indira Jutooru, Seep Sreevalsan, Cy Chen, Lisa Crose, Stephen Safe, and Gayathri Chadalapaka.



A Small Bird Perched On Top Of A Tree Branch