Author's response to reviews

Title: Identification of Transcriptional Regulatory Networks Specific to Pilocytic Astrocytoma

Authors:

Hrishikesh Deshmukh (hdeshmuk@gmail.com)
Jinsheng Yu (JYu@path.wustl.edu)
Jahangheer Shaik (jshaik@path.wustl.edu)
Tobey J MacDonald (tmacdona@cnmc.org)
Arie Perry (aperry@pathology.wustl.edu)
Jacqueline E Payton (jpayton@wustl.edu)
David H Gutmann (gutmannnd@neuro.wustl.edu)
Mark A Watson (watsonm@wustl.edu)
Rakesh Nagarajan (rakesh@wustl.edu)

Version: 2 Date: 30 September 2010

Author's response to reviews:

September 17, 2010

To the Editors of BMC Medical Genomics –

Attached, please find our manuscript entitled, “Identification of Transcriptional Regulatory Networks Specific to Pilocytic Astrocytoma” which we hope that you will consider for publication in BMC Medical Genomics. This report describes a bioinformatics approach that uses meta-analysis of gene expression microarray data coupled with empirically derived transcription factor (TF) – gene promoter interaction data to synthesize predictive gene regulatory networks. This approach has been applied to human pilocytic astrocytoma tumor specimens. Because the number of defined genetic alterations in this particular tumor type are rare and under-reported, our approach represents a novel and perhaps more sensitive strategy to identify possible “genetic reprogramming” in this tumor type. Moreover, we demonstrate that the transcriptional regulatory networks identified are specific to the cell lineage of this tumor type, relative to other types of gliomas such as oligodendroglioma and glioblastoma.

We believe that this report will be of general interest to readers in the fields of medical genomics because of the relative novelty of our analytical approach. We also believe that the report will be of interest to researchers in the field neuron-oncology because of the application of this analytical approach to the genomic analysis of pilocytic astrocytomases, a tumor that is not nearly as well characterized as other CNS tumors such as glioblastoma multiforme.
In addition to the primary results presented in this study, we are interested in contributing the gene expression microarray data sets from pilocytic astrocytoma that are described in this report, to the genome research community at large. Together with the demonstrated biological applicability of our PAP tool, which we have previously reported on and have provided freely to the research community, we believe that this data set and the analysis described in our report will be a valuable resource for many other investigators.

We also declare that we have no competing interests originating from this manuscript and its contents.

Thanks in advance for your consideration.

Sincerely yours,

Mark A. Watson, M.D., Ph.D.

Associate Professor of Pathology and Immunology