

Ingenuity[®] Science Spotlight:

Articles featured in the Ingenuity Science Spotlight represent some of the best and most diverse examples of how IPA[®] has contributed to research across multiple platforms, research areas, and research goals.



Genomic analysis of increased host immune and cell death responses induced by 1918 influenza virus.

Kash JC, Tumpey TM, Proll SC, Carter V, Perwitasari O, Thomas MJ, Basler CF, Palese P, Taubenberger JK, García-Sastre A, Swayne DE, Katze MG. *Nature*. 2006 Oct 5;443(7111):578-81

<http://www.ncbi.nlm.nih.gov/pubmed/17006449>

A research team led by John Kash and Michael Katze of the University of Washington School of Medicine's Department of Microbiology has combined global gene expression analysis IPA to understand the molecular basis of the extreme host response induced by the 1918 influenza virus.

The team used gene expression analysis in order to get a global view of the host response in infected mice, and analyzed the data in IPA to understand the functional consequences of those gene expression changes. Utilizing IPA's Canonical Pathway and Network features, the team was able to conclude that infection with the 1918 influenza virus resulted in significant activation of pro-inflammatory and cell death responses, and that activation of these pathways may be major contributors to the severe immunopathology seen in mice infected with the 1918 virus. A comparison analysis run in IPA went on to reveal that the biological responses most significantly induced by infection with non-lethal strains of the virus included cell-cycle and glutathione metabolism pathways, both of which may contribute to the less severe immunopathology seen in mice infected those strains.

The combined genomics and Ingenuity Pathways Analysis approach in this study contributes to our understanding of the molecular basis of host response to virulent influenza, and may eventually lead to identification of novel antiviral therapies.