

## Ingenuity<sup>®</sup> Science Spotlight:

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



### **Systems biology approach predicts immunogenicity of the yellow fever vaccine in humans.**

Querec TD, Akondy RS, Lee EK, Cao W, Nakaya HI, Teuwen D, Pirani A, Gernert K, Deng J, Marzolf B, Kennedy K, Wu H, Bennouna S, Oluoch H, Miller J, Vencio RZ, Mulligan M, Aderem A, Ahmed R, Pulendran B. Nat Immunol. 2009 Jan;10(1):116-2.

<http://www.ncbi.nlm.nih.gov/pubmed/19029902>

In order to identify gene signatures that may predict vaccine efficacy, researchers from Emory University and the Institute for Systems Biology used gene expression profiling to measure the innate immune responses in humans after vaccination with yellow fever vaccine YF-17D. From two independent trials, they were able to select a common subset of 65 genes that were differentially expressed over time for further analysis and characterization of YF-17D vaccine responses. Using IPA, they were able to identify a network of antiviral genes that is induced by YF-17D vaccination. IPA Network Analysis revealed a closely interacting network of 50 interferon and antiviral genes including IRF7, OAS1, OAS2, OAS3 and OASL; genes involved in viral recognition including TLR7, DDX58, IFIH1, DHX58 and EIF2AK2; and genes mediating antiviral immunity, such as CXCL10, MX1, and the complement genes SERPING1 and C3AR1. The ability to analyze gene signatures of early immune response to vaccination in the context of relevant molecular networks and pathways will help address a major challenge in vaccine development – the ability to predict vaccine efficacy.

Additional computational analysis, performed to understand variations in CD8+ T Cell and neutralizing antibody responses to YF-17D, identified two distinct gene signatures. One signature including C1qB and many stress response pathway genes correlated with, and predicted, YF-17D CD8+ T Cell responses. The other, including B cell growth factor TNFRS17, predicted the neutralizing antibody response with up to 100% accuracy. This demonstrates that systems biology approaches not only help researchers gain a global understanding of vaccine induced innate immune responses but also enable prediction of subsequent adaptive immune responses