

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.



“My group used IPA to understand genetic variation at genomic and geographic levels. Using F_{ST} (population differentiation measures) analysis, we identified SNPs with major population differentiation and linked this information with ontological annotation and functional networks/pathways. We followed the target genomic regions using IPA network/pathway analysis to characterise the main functional networks/pathways underlying genes with substantial population differentiation and elucidate their roles and functional implications in human genetic variations and diseases. We innovatively used IPA to demonstrate whether recursive partitioning (RP) based gene-gene interactions are part of an integrated and interconnected biological networks that involved in genes that have functional commonalities. The result indicated that genes in RP based analysis are related to biological activities and shown functional commonalities, indicating the utility of IPA to validate statistical based interactions.”



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Researchers used IPA to identify differences in candidate gene association between European ancestry and African American asthmatic children

PLoS ONE 6(2): e16522. Tesfaye M. Baye, Melinda Butsch Kovacic, Jocelyn M. Biagini Myers, Lisa J. Martin, Mark Lindsey, Tia L. Patterson, Hua He, Mark B. Ericksen, Jayanta Gupta, Anna M. Tsoras, Andrew Lindsley, Marc E. Rothenberg, Marsha Wills-Karp, N. Tony Eissa, Larry Borish, Gurjit K. Khurana Hershey.

Dr. Tesfaye Baye Mersha and his team apply ancestry variation and population genetics/genomics to find genes in common disease studies. They used IPA to confirm that the recursive partitioning (RP) interacting genes are part of an integrated and interconnected biological network. IPA further helped them to identify the most enriched canonical pathways in Caucasians, and then in African Americans. IPA helped reveal different gene networks and pathways associated with asthma in children with European ancestry versus African Americans. Their work suggests that there may be distinct mechanisms underlying the pathogenesis and expression of asthma in different human populations and provides valuable insights into the pathways that may predispose asthma in individuals with European versus African ancestry. Dr. Tesfaye Baye Mersha and his group published their research in PLoS ONE.

To read the full article, go to: <http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0016522>