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.

Temporal and spatial transcriptional programs in murine kidney development.

G. Challen, B. Gardiner, G. Caruana, X. Kostoulias, G. Martinez, M. Crowe, D. F Taylor, J. Bertram, M. Little, and S. M Grimmond. Physiol Genomics. 2005 Jul 5; [Epub ahead of print].

http://www.ncbi.nlm.nih.gov/pubmed/15998744?dopt=Abstract

Development of the mouse kidney, including induction of the ureteric bud (UB) and metanephric mesenchyme (MM), is still only partially understood. Global expression profiling is required to measure both temporal and spatial changes during development. However, both the number of developmental stages and number of genes identified in these studies is limited.

In this study, researchers performed expression profiling throughout all stages of kidney development using several experimental strategies. Using oligonucleotide arrays, the temporal profiles of the MM were monitored at 24-hour intervals from 10.5dpc through the neonatal period. Early metanephric development was further studied by directly comparing RNA from 10.5 vs. 11.5 vs. 13.5dpc kidneys. Spatial profiling was performed by comparing MM (10.5dpc) to adjacent intermediate mesenchyme.

The data were analyzed by applying B statistics at a threshold of 0.0, a Welch ANOVA test ($p<0.005$), and a Benjamini/Hochberg correction. IPA and the Ingenuity Knowledge Base were used for pathway analysis and network classification. It was shown that temporal and spatial profiles have high concordance with the published rat array data using GeneSpring gene tree analysis. The results were validated by in situ hybridization using mouse tissues.

There were 3600 genes identified in the temporal experiment by statistical analysis. All were imported into IPA. A total of 813 upregulated genes were identified and classified into six top scored networks using the Ingenuity Knowledge Base. Pathway analysis characterized the genes in kidney development: cell cycle, DNA replication and RNA post transcriptional genes in early development, and biosynthetic and immune response genes in later development. IPA identified several signaling pathways not identified by other methods. Genes involved in these pathways include Wnt, Tgfß, IGF, VEGF, and insulin signaling during early kidney development, Erk Map signaling in early nephrogenesis, and PPAR and other metabolism genes in later kidney development.