A Resource for Experimental Data Investigating Host Factor Responses to Viral Infection at the Influenza Research Database (IRD) and Virus Pathogen Resource (ViPR)

Introduction

Host cell responses to viral infection can be monitored by a variety of different high throughput experimental methodologies in order to understand the biological systems involved. For instance, gene expression studies can be used to identify cellular systems involved in the antiviral response. The Influenza Research Database (IRD) and Virus Pathogen Resource (ViPR) developed by the J. Craig Venter Institute provide access to such data and tools to explore and analyze these data. The IRD is a freely accessible web-based resource providing a comprehensive collection of experimental data that have been analyzed to discover patterns in the data from early time points and visualized using KEGG pathway information.

Figure 1: In order to validate these host factor data, we evaluated the intersection between experiments that had the same virus strain and similar study design. A) When comparing studies of pandemic H1N1 in human Calu-3 cells, in this case experiments ICL006-R and ICL010-R, we found 60-80% overlap of differentially expressed genes. B) Similar observations were made when comparing studies of HPAI H5N1 in Calu-3 cells (ICL004, ICL011, ICL012) where an 80-90% overlap was found.

Figure 2: We were interested in understanding the early transcriptional changes in cells infected with the highly pathogenic avian influenza A/Vietnam/1203/2004 (VN1203). A) First we browsed Host Factor Experiments via a faceted criteria such as "viral Agent" (VN1203 (H1N1)) and found experiment ICL004-R. B) After selecting ICL004-R (H1N1) followed by the "View Associated Resources" link, we were able to view the 778 DAVID IDs and 1517 Up genes for this experiment. C) We focused on patterns for ICL004-R highlighting up-regulated probes for the first two time points of H1N1 infection (+). D) After acquiring the gene list for (+), we performed an enrichment analysis at DAVID. E) We then visualized enrichment results for the KEGG RIG-I pathway and found that both IFN alpha and beta are upregulated early after infection with VN1203, which would predict the up regulation of interferon stimulated genes (ISGs) at later time points.

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References

