SIgN Immunology Seminar



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Proteomics Informed by Transcriptomics - everything you need to know in one go!

Host
Dr Lisa Ng
Singapore Immunology Network,

Date
Friday
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Time
11am – 12pm

Venue
SIgN Seminar Room
Immunos Building
Level 4
Biopolis

We have pioneered an integrated high throughput analysis technique called Proteomics Informed by Transcriptomics or PIT analysis (Nature Methods 9, 1207–1211 2012). In this approach, cell lines are analysed by combining deep sequencing of the cellular mRNA alongside very high throughput quantitative mass spectrometry based proteomics. We use the data from deep sequencing of the mRNA to derive a theoretical list of the proteins that could be in the sample and use the mass spectrometry data to determine which proteins are real (typically 5000 - 6000 proteins in a single experiment). Significantly, this approach is an "open" system and works even if the genome of the target species is not known/poorly annotated and it will also detect any known or unknown pathogens present. Thus it enables any species to be studied by high throughput methods with the same kind of bioinformatic depth as humans. For example, we have studied the widely use insect cell line aag2 to discover previously uncharacterised persistent virus and transposable elements in this cell line. In addition, the approach gathers quantitative data over time on both gene expression and protein abundance. This integrated analysis allows us to compare changes in gene expression alongside changes in protein abundance to highlight post transcriptional anomalies that are worthy of further investigation (e.g. where a gene is switched on but the corresponding protein abundance falls).

We have used this PIT approach to study a number of viruses including adenovirus, dengue, respiratory syncytial virus and, in collaboration with the Australian Animal Health Laboratories, Hendra Virus. Hendra virus illustrates another advantage of the PIT approach as were were able to follow infection of human and bat cell lines side by side. We were also able to improve the annotation of the bat genome and highlight differences in how bat and human cells respond to this highly dangerous BSL4 pathogen. Hendra Virus is apparently asymptomatic in bats but has a ~50% case fatality rate in humans. We are currently funded to study the newly emerging MERS virus in bats, humans and camel cell lines and are extending our ability to generate system wide data on viral infections of cell lines, primary cells and, in the longer term more complex substrates.