

2<sup>nd</sup> Indo-Global Summit & Expo on

# Veterinary

October 26-28, 2015 Hyderabad, India

## Metagenomic sequencing for pathogen identification and pathogen discovery

**Chitra Pattabiraman**

National Centre for Biological Sciences, India

Outbreaks of Ebola, HIV-1, SARS, H1N1, West Nile virus and more recently MERS have brought home the realization that emerging pathogens are a huge threat to humans and animals. Many of the emerging/re-emerging pathogens (between 60-70%) are of zoonotic origin. In an attempt to identify pathogens that are in the early phases of adaptation to the human host, in a collaborative effort, we have built a deep-sequencing based pipeline for pathogen identification and discovery. In this approach, we extract RNA/DNA from clinical material, make sequencing libraries and perform sequencing at medium depths (about 15-20\*10<sup>6</sup> sequences/sample). Pathogen identification involves bioinformatic removal of host sequences followed by aligning the remaining sequences to known databases. Such methods can be applied to detect the emergence of novel viruses/pathogens.

### Biography

Chitra Pattabiraman is currently a Post-doctoral Fellow at the National Centre for Biological Sciences, TIFR; Bangalore, India. Her current research interest is to discover novel pathogens circulating in India, particularly in the context of acute fevers and acute encephalitis. Her PhD thesis, carried out under the guidance of Professor Sudhir Krishna, examined the link between the Human Papilloma Virus life cycle and cellular sub-sets in cervical cancer.

[pattabiraman.chitra@gmail.com](mailto:pattabiraman.chitra@gmail.com)

Notes: