



Contribution ID: 45

Type: **Talk**

Immunology going wild: genetic variation and immunocompetence in ducks

Monday, September 24, 2018 1:30 PM (20 minutes)

Wild animals are vectors and reservoirs of emerging infectious diseases with major implications on human health. Still little is known about the interactions of these pathogens and their main hosts in their natural environment. In my PhD project I studied several aspects of the immune and its interactions between the mallard duck and its pathogens. The methods ranged from gene expression profiling by RNA sequencing of experimentally immune-challenged mallards to large-scale re-sequencing of >100 immune genes in 96 wild duck samples of mallards and related duck species. To analyse these large data sets of genomic and transcriptomic nature I utilised the HPC systems of the HPCC5 in several ways. By combining population-scale genomic information and experimentally induced transcriptomic responses to pathogens with further approaches to measure physiological parameters of mallards I arrived at a comprehensive view on the interaction of diseases and their hosts in the wild.

Abstract (optional)

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Session Classification: Session 2

Track Classification: Scientific Track