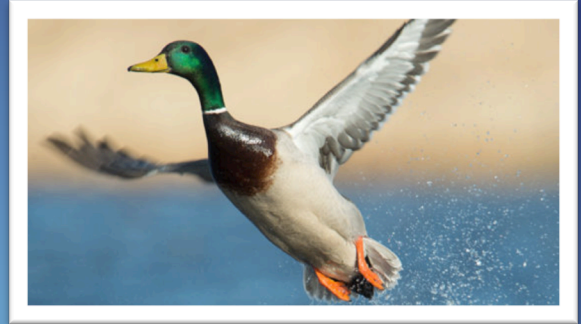


FAANG-Europe



“Understanding the genotype-phenotype interaction in Anseriformes underpinning variation in susceptibility to influenza infection”

My research addresses the molecular evolution of the immune gene repertoire in natural populations of birds, also known as the “immunome”. Wild and domesticated birds are exposed to many pathogens, and diseases can easily be carried over great distances by migrating species. Waterfowl, most prominently ducks, are an economically important livestock while also serving as a potential reservoir for avian influenza. The outbreak of avian influenza (H5N8 virus) in 2016 showed different susceptibility in mallard and tufted duck. While mallards can carry the virus without getting seriously ill, tufted ducks are very sensitive to infection and usually die within hours. I would like to understand if there is a genetic basis to that, and therefore I am mostly interested in a fully annotated immunome, preferably in combination with expression patterns in different tissues. Usually, immune genes are poorly annotated, because the proper splice structure is frequently unknown due to their high variability. Full length transcriptomes may help to find the correct isoforms of these genes.

**Ralph Muller, Max Planck Institute for Ornithology & University of Konstanz,
Department of Migration and Immuno-Ecology, Germany**

Host: Lel Eory, The Roslin Institute, Edinburgh, UK

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