

## **ImmuNov: genomics and epigenomics of immune innovations in insects**

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With the project ImmuNov, my aim is to understand how novel genes, and genes with a novel function, can integrate into pre-existing highly conserved gene networks and how their expression is regulated. As a functional model, I will use the innate immune system of insects, which is both highly conserved in its core set of genes and signaling pathways, and one of the fastest evolving biological functions, displaying a high rate of gene gains and losses across the insect phylogeny. To achieve this, I will perform a screen of immune-induced gene expression across phylogenetically diverse insect species, through experimental infections with two opportunistic pathogens, to identify common sets of immune genes and novel, taxon-specific immune-induced genes. I will test the role of chromatin accessibility as an epigenomic mechanism to control the expression of immune genes in response to infections and identify the cis-regulatory elements that govern the expression pattern of immune-induced genes. Finally, I will reveal the evolutionary history of immune-induced genes and test whether taxon-specific immune genes exhibit specific epigenetic signature. The recent development in molecular and computational technologies offers the possibility to design for the first time a large-scale comparative study of immune-induced transcriptomes couple with epigenomics in a controlled fashion to identify novel genes and reveal their regulatory mechanisms. This innovative project will provide insights into fundamental functional aspects of the genomic and epigenomic basis of immune innovation in insects beyond the *Drosophila* model, insights which are not attainable with comparative genomics alone.