

TOLL IMMUNE PATHWAY IN THE MOSQUITO *Aedes aegypti*

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The availability of the *A. aegypti* genome enables researchers to perform comparative and functional analyses of the *A. aegypti* immune system. Transgenic approach, in combination with the RNAi technique is being used to elucidate the regulation of Toll immune pathway in the mosquito *Aedes aegypti*. By creating gain-of-function and loss-of-function transgenic *Aedes* strain we have shown that AaREL1, a homolog of *Drosophila* Dorsal, is a key regulator of Toll immune pathway in the adult mosquito *A. aegypti*. The Toll receptor and its ligand, Spätzle (Spz), links extracellular immune signals to the Toll intracellular transduction pathway. Genome analysis has shown that in the mosquito *Ae. aegypti*, there are five homologues of the *Drosophila* Toll (Toll1) receptor and three homologues of the *Drosophila* cytokine Spätzle (Spz). The transgenic approach, in combination with the RNAi technique, has shown that AeToll5 and Spz1C function as cytokine-receptor systems specific to the Toll receptor-mediated immune response following fungal challenge in the mosquito fat body. High throughput microarray analyses that focus on the determination of the REL1 regulated gene repertoire are being performed using gain-of-function REL1 transgenic mosquitoes.

Key words: *Aedes aegypti*, Toll pathway, microarray