Original

We previously demonstreton that two immune signaling pathways, Toll and IMD, were concomitantly activated in the model beetle *Tribolium castaneum* by challenges to their immune system by several species of microbes, including Gram-positive and -negative bacteria as well as yeast. This contrasts with the Drosophila immune system in which more specific pathway activation depending on the type of microbe is well established. We suggest that the activation of an indiscriminate immune pathway in *T. castaneum* are due in part to an unselective recognition of pathogen-associated molecular patterns by the extracellular sensing modules of the two pathways. In order to obtain a more detailed understanding of the *T. castaneum* immune pathway, we investigated whether potential components of the *T. castaneum* IMD pathway, Caspar, DREDD and FADD, are involved in immune reactions triggered by microbial challenges. A sequence analysis of these three genes with the orthologues of other species, including insects, mouse and human, indicated that *T. castaneum* Caspar, DREDD and FADD functioned as immune signal transducers, which are usually induced by microbial challenges. However, these genes were not induced by microbial challenges. To establish whether these genes are involved in immune reactions, we used RNA interference-mediated knockdown of these genes to assess the microbial inducing vels of the representative read-out antimicrobial peptide genes of the respective classes. The results indicated that these genes encode the canonical constituents of the IMD pathway of this beetle. DREDD and FADD infl uenced the induction of Toll-dependent antimicrobial peptide genes, providing novel crosstalk points between the two immune pathways, which appears to support indiscriminate pathway activation in *T. castaneum.* Furthermore, the phenotypes of DREDD or FADD knockdown pupae challenged by the two model bacterial pathogens correlated with AMP gene induction in the respective knockdowns, indicating that these intracellular factors contributed to antibacterial host defenses.