



Identification and characterization of two CYP9A genes associated with pyrethroid detoxification in *Locusta migratoria*

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Cytochrome P450s (CYPs) constitute one of the largest gene super families and distribute widely in all living organisms. In this study, the full-length cDNA sequences of two LmCYP9A genes (LmCYP9AQ1 and LmCYP9A3) were cloned from *Locusta migratoria*. We analyzed the expression patterns of two LmCYP9A genes in various tissues and different developmental stages using real-time quantitative PCR. Then we evaluated the detoxification functions of the two LmCYP9A genes by testing mortalities with four kinds of pyrethroid treatment after RNA interference (RNAi), respectively. Combining with docking structure of two LmCYP9A genes, their detoxification properties were extensively analyzed. The full-length cDNAs of LmCYP9AQ1 and LmCYP9A3 putatively encoded 525 and 524 amino acid residues, respectively. Both LmCYP9A genes were expressed throughout the developmental stages. The expression of LmCYP9AQ1 in the brain was higher than that in other examined tissues, whereas the LmCYP9A3 was mainly expressed in the fat body. The mortalities of nymphs exposed to deltamethrin and permethrin increased from 27.7% to 77.7% and 27.7% to 58.3%, respectively, after dsLmCYP9A3 injection. While the mortalities of nymphs exposed to fluvalinate increased from 29.8% to 53.0% after LmCYP9AQ1 was silenced using RNA interference. Our results suggested that the two LmCYP9A genes may be involved in different pyrethroid insecticide detoxification in *L. migratoria*.