

Molecular Characterization and Oxidative Stress Response of a Cytochrome P450 Gene (*CYP4G11*) from *Apis cerana cerana*

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Cytochrome P450 proteins, widely distributed multifunctional enzymes, are mainly involved in biosynthetic and degradative pathways of endogenous compounds and the detoxification of xenobiotics in insects. Moreover, these enzymes exhibit peroxidase-like activity, therefore they may be involved in protecting organisms against the toxicity of reactive oxygen species (ROS). In the present study, we cloned a *CYP4G11* gene – *AccCYP4G11* – from the Chinese honey-bee (*Apis cerana cerana*). The open reading frame of the cDNA was 1656 bp long and encoded a 551 amino acids polypeptide, which shared high sequence identity with homologous cytochrome P450 proteins. In the genomic DNA sequence, a 5'-flanking region consisting of 1168 bp was obtained, and some putative transcription factor binding sites were predicted. Quantitative polymerase chain reaction (Q-PCR) revealed that the level of *AccCYP4G11* was higher in the epidermis than in other tissues, and *AccCYP4G11* was expressed in all stages with the highest level in two-week-old adult worker honey-bees. Moreover, the expression patterns under oxidative stress indicated that *AccCYP4G11* transcription was significantly influenced by external factors, such as temperature challenges, ultraviolet (UV) light, and insecticide treatment. *AccCYP4G11* was regulated differentially in response to oxidative stress and may be involved in protecting honey-bees from oxidative injury.

Key words: *Apis cerana cerana*, *CYP4G11*, Q-PCR, Oxidative Stress