UDP-glucosyltransferases potentially contribute to the pesticide detoxification of insect parasitoids.

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Introduction

Integrated Pest Management (IPM) emphasizes a holistic approach to optimizing the control of pests by coordinating use of multiple suppressive tactics (agronomical, physical, chemical and biological strategies) in an ecological and economical matter. As a crucial component of sericulture, mulberry is the specific supplement plant to silkworm but has been destroyed by numerous pest insects. Until now, broad-spectrum, highly toxic and shortly residual insecticides have still been applied to depress and regulate the pest insects in mulberry field, in view of greater susceptibility of silkworm toward novel pesticides and the security of silkworm rearing. Whereas, some pest insects like *Spodoptera litura* (Fabricius) and *Glyphodes pyloalis* (Walker) have become major destructive agricultural pests in eastern China and other countries and been suppressed excessively dependent on commonly used insecticides, such as phoxim, cypermethrin and chlorfenapyr*. Meteorus pulchricornis* (Wesmael) (Hymenoptera: Braconidae) is a predominant endoparasitoid of Lepidoptera pests. Extensive application of insecticides puts parasitoid wasps under threat and endangers their behavior and physiology. Therefore, it is necessary to evaluate the susceptibility of wasps under exposure to insecticides in the agroecosystem to improve the compatibility between chemical and biological tactics. Detoxification enzymes are essential for survival of insects under exposure to insecticides. In insects, UDP-glycosyltransferases (or glucuronosyltransferases) (UGTs, EC2.4.1.17), are regarded as minor detoxification enzymes compared with major enzymes implicated in detoxification and metabolism in insects, such as cytochrome P450s (P450s), glutathione transferases (GSTs) or carboxyl/ cholinesterases (CCEs). Although several studies have documented that insect UGTs were involved in the evolution of insecticide resistance in Lepidopteran, the precise roles of UGTs towards insecticides in parasitoid wasps still remain unknown.

Table 1 Sequences information of the verified *M. pulchricornis* UGTs.

Gene name	Acc.no	ORF (aa)	pI	Mw (kDa)	BLASTX best hit		
					Gene description	E-value	Identity (%)
MpulUGT403G1	MW584269	535	9.13	60.39	PREDICTED: UDP-glucuronosyltransferase 2B15	0.00E+00	67.03%
MpulUGT332G1	MW584273	525	8.89	59.72	PREDICTED: UDP-glucuronosyltransferase 2C1-like	0.00E+00	61.64%
MpulUGT334AA1	MW584277	447	5.89	51.48	UDP-glucuronosyltransferase 2B20	0.00E+00	66.36%

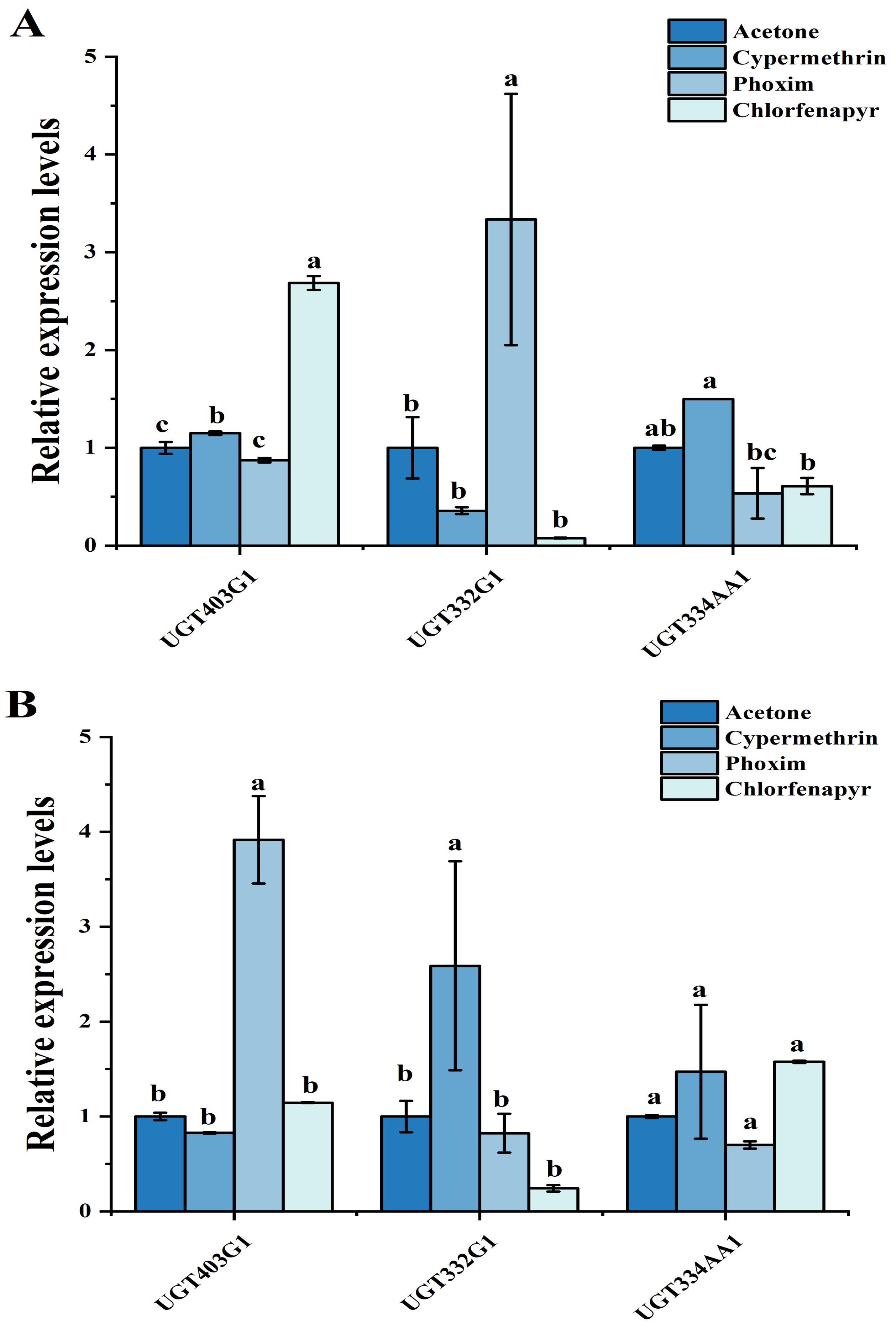

Figure 1 Relative expression profiles of MpulUGTs toward Cypermethrin, Phoxim and Chlorfenapyr post-treatment at 24h(A) and 48h(B). The transcriptional levels of each gene insecticide-treated individuals were normalized relative to that in acetone-treated(control) individuals. Different lowercase letters indicate significant differences (P<0.05)

Results

The resent study indicated that several UGT genes were detected from the transcriptome database of *M. pulchricornis*. All UGT genes contained full-length open reading frames and shared relatively high identity with other homologous Hymenopteran insects. UGT protein sequences alignment predicted conversed functional domains and catalytic residues. Phylogenetic analysis revealed that order-specific gene diversification and inter-species conversation in *M. pulchricornis* UGTs. qRT-PCR validation demonstrated UGT genes were up-regulated after the *M. pulchricornis* adults under exposure to phoxim, cypermethrin and chlorfenapyr.

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