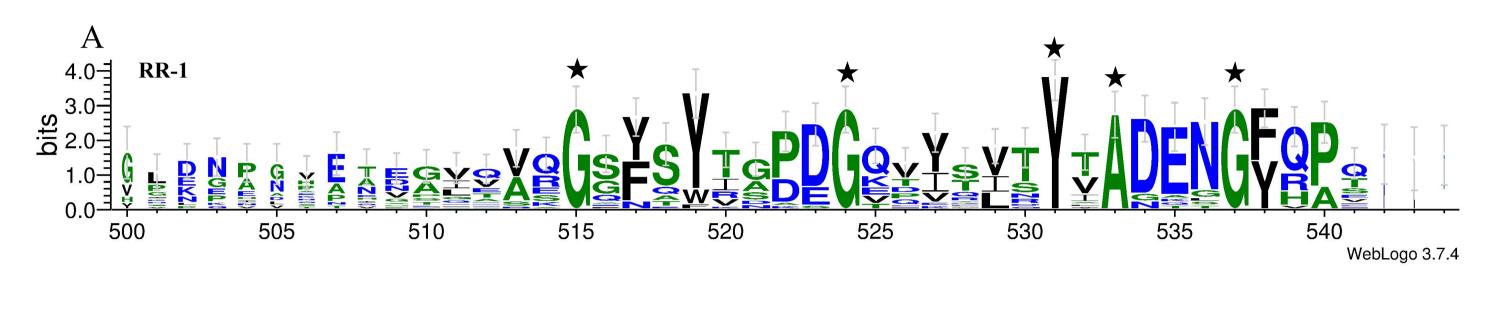
# Identification of cuticular protein genes in *Glyphodes* pyloalis (Walker) and expression patterns under stress of insecticides

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# INTRODUCTION

- *Glyphodes pyloalis* Walker (Lepidoptera: Pyralidae) is one of the major destructive agricultural pests, which is widely distributed in the main mulberry planting areas in eastern China and other countries<sup>[1]</sup>. This pest has been suppressed excessively dependent on commonly used insecticides.
- Insect cuticle is composed mainly of structural proteins and
- Two types of GpCPR protein have been identified: RR-1, and RR-2. Four of GpCPRR proteins contains the RR-1 cuticular protein motif and three GpCPRR-2 proteins were identified.

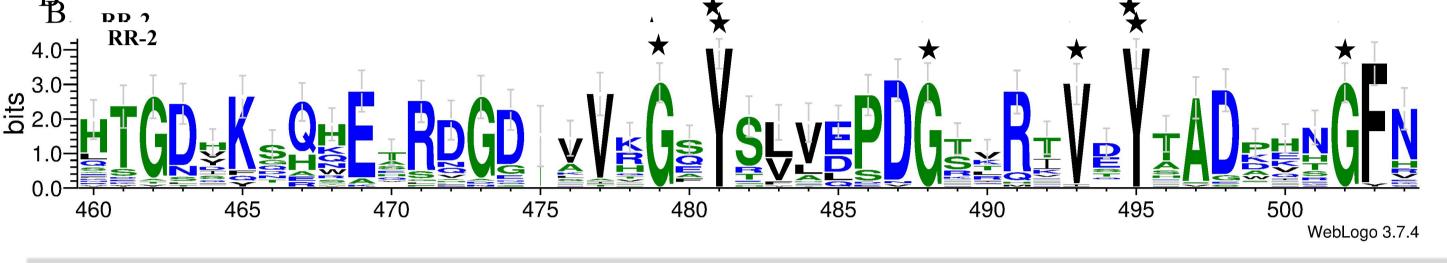


the polysaccharide chitin.Cuticular proteins have effects on shaping insect bodies and influencing insect development stages.The CPR family is the largest family of cuticle proteins (CPs), which can be further divided into two subgroups based on the presence of one of the presumptive chitin-binding sequence motifs<sup>[2]</sup>.

• However, the exact roles of CPRs in insecticides tolerance in *Glyphodes pyloalis* still receive less attention.

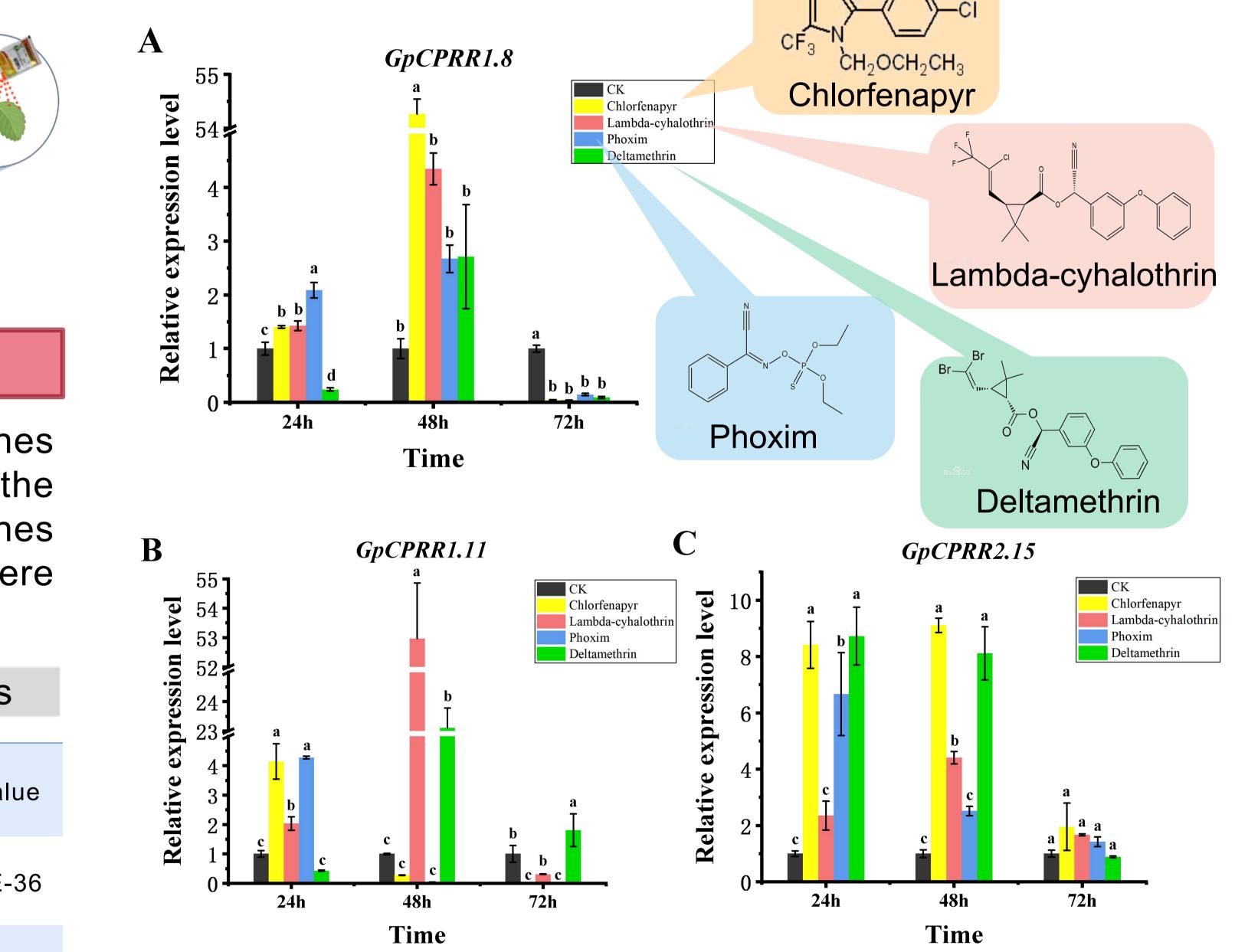
# METHODS

- The genes of *G. pyloalis* were identified from transcriptome constructed previously<sup>[3]</sup>.NCBI, ORFfinder, PFAM, and ExPASy was used to analyse bioinformation.
- The 4th instar *G. pyloalis* larvae were treated by four common chemical insecticides using a leaf-dipping bioassay.Total RNA was extracted from the whole larvae and RT-qPCR was used to characterize expression patterns of *Glyphodes pyloalis* insect cuticle protein genes (*GPCPs*).



**Fig.1** Conserved motif analysis of RR-subfamily proteins of *Glyphodes pyloalis* (Walker) **A:** RR-1 subfamily **B:** RR-1 subfamily

• Compared with the control, the expression of *GpCPRR1.11* was significantly up-regulated after 48h exposure to two contact toxicity insecticides lambda-cyhalothrin and deltamethrin. Four insecticides all have significant effects on the expression of *GpCPRR2.15* and the upregulation level depended on exposure time.



## **RESULTS & DISCUSSION**

• In the present study, we identified several *GpCPRR* genes incluing *GpCPRR1.11,GpCPRR1.8,GpCPRR2.15* from the transcriptome database of *G. pyloalis*. All GpCPRR genes contained full-length open reading frames (ORF) and were relatively high similar with CPR proteins of other insects.

#### **Table 1** Sequence information of identified GpCPRR genes

Clan	Gene Name	ORF (aa)	Blastp Results	E value
GpCPRR-1	GpCPRR1.8	310	Larval cuticle protein LCP-30-like [Ostrinia furnacalis]	2.4E-36
	GpCPRR1.11	128	Larval cuticle protein LCP-14-like [Ostrinia furnacalis]	3E-28
	GpCPRR1.14	105	Flexible cuticle protein 12-like [Ostrinia furnacalis]	2E-35
	GpCPRR1.23	73	Larval cuticle protein 1-like [Galleria mellonella]	5.4E-23
GpCPRR-2	GpCPRR2.11	183	Cuticle protein 7 [Ostrinia furnacalis]	4.7E-64
	GpCPRR2.15	177	Cuticle protein 7-like [Ostrinia furnacalis]	6E-52
	GpCPRR2.17	171	Cuticular protein RR-2 motif 130 [Antheraea pernyi]	4.7E-84

**Fig.2** Relative expression level of **(A)** *GpCPRR1.8*, **(B)** *GpCPRR1.11* and **(C)** *GpCPRR2.15* after exposing to **chlorfenapyr, lambda-cyhalothrin, phoxim and deltamethrin** 

# CONCLUTIONS

### ACKNOWLEDGEMENT

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- Under stress of insectcides, the expression of three GpCPR genes decreased continuously with increasing exposure time. The results provide a basis for further functional investigation of CPR implied in insecticide stress in *G. pyloalis*.

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