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ORIGINAL ARTICLE

Identification and functional analysis of six *DNAJ* genes from *Myzus persicae* (Hemiptera: Aphididae) in response to UV-B stress

Long-Chun He[1,*], Jian-Yu Meng[2,*], Guy Smagghe[1], Chang-Li Yang[1], Xue Tang[1] and Chang-Yu Zhang[1,]**

[1] Institute of Entomology, Guizhou Provincial Key Laboratory for Agricultural Pest Management of the Mountainous Region, Guizhou University, Guiyang, Guizhou 550025, China; e-mails: helongchun0303@gmail.com, guysma9@gmail.com, yangchangli@126.com, aneira1994@163.com, gzuzcy1121@126.com

[2] Guizhou Tobacco Science Research Institute, Guiyang, Guizhou 550081, China; e-mail: mengjy0417@163.com

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Abstract. Ultraviolet B (UV-B) is a significant environmental factor affecting insect development, survival, and reproduction. DNAJ proteins are molecular chaperones found ubiquitously in insects that are crucial for their adaptation to environmental stresses. This study aimed to elucidate the roles of *DNAJ* genes in the response of *Myzus persicae* to UV-B stress. Herein, we identified six *DNAJ* genes in the aphid *M. persicae*, a devastating agricultural pest. We analyzed their expression profiles at different stages of development, in different tissues and for various durations of UV-B exposure. The expression levels of *MpDNAJC30*, *MpDNAJC11*, *MpDNAJC2*, and *MpDNAJC3* were highest in wingless adults, while *MpDNAJC9* and *MpDNAJC17* were highest in second- and third-instar nymphs, respectively. Six *MpDNAJ*s had higher expression levels in the epidermis and embryos, and lower levels in the head. Additionally, the expression levels of all genes increased significantly under different durations of UV-B exposure. Knockout of the *DNAJ* genes using RNA interference caused a significant decline in the survival rate, weight, body length, and body width of *M. persicae* exposed to UV-B radiation. Our research provides valuable insights into the stress response mechanisms of *M. persicae*, highlighting the importance of *DNAJ* genes in mediating their adaptation to UV-B stress.

1. INTRODUCTION

Ultraviolet (UV) radiation is a significant factor, which is classified into UV-A (315–400 nm), UV-B (280–315 nm), and UV-C (200–280 nm) based on its wavelength (Paul & Gwynn-Jones, 2003; Tang et al., 2023). UV-B has detrimental effects on various living organisms, including insects (Van Atta et al., 2015). Excessive UV-B radiation causes oxidative stress via the production of reactive oxygen species that can damage DNA, membrane lipids, and proteins, seriously affecting the growth and population structure of living organisms (Adams & Shick, 2001; Hideg et al., 2013; Guo et al., 2019). UV-B irradiation can decrease the survival rate of larvae and the fecundity of adult *Cadra cautella* (Alwaneen et al., 2019). UV-B has also been shown to increase the mortality of *Tribolium castaneum* larvae, thus prolonging the egg-hatching period. UV-B exposure can delay the development of larvae and pupae (Sang et al., 2016; Guo et al., 2019). Increased UV-B exposure to specimens of *Osmia bicornis* caused decreases in body weight and carbohydrate content, leading to malformations and increased mortality (Wasielewski et al., 2015).

Insects possess several antistress mechanisms involving photo-protective pigments, antioxidants, apoptosis, heat shock proteins (Hsps), and DNA repair mechanisms, in order to effectively alleviate the deleterious effects of UV-B radiation (Vandenbussche et al., 2018; Villena et al., 2018). Hsps, widely distributed in living organisms, are crucial in combatting exposure to extreme environmental factors, including high temperatures, coldness, oxygen deprivation, UV radiation, and overcrowding (Mahroof et al., 2005; King & MacRae, 2015). Based on their size (in kDa), Hsps are categorized into large Hsps, Hsp90, Hsp70, Hsp60, Hsp40 and small Hsps (Hu et al., 2022). Hsp40, also called DNAJ, has a conserved J domain and can function autonomously as a molecular chaperone or in conjunction with Hsp70 as a co-chaperone (Kampinga et al., 2019). The DNAJ protein can be transported to specific organelles and regulates the polymerization of protein complexes as well as being involved in protein folding and

* These authors contributed equally to this work.

** Corresponding author; e-mail: gzuzcy1121@126.com

unfolding process (Stark et al., 2014; Sopha et al., 2023). Additionally, as a chaperone protein for Hsp70, it promotes the ATPase activity of Hsp70 (Rodriguez et al., 2008). Previous studies have elucidated the pivotal role of *DNAJ* in insect growth, development, and response to stressors. *AdomHsp40* is indispensable for the wing-shed of *Acheta domesticus* as its silencing significantly reduced the occurrence of wing-sheds (Chen et al., 2019). *DNAJ* is involved in the development, oviposition, and female reproduction of *Nilaparvata lugens* (Chen et al., 2021). Silencing *NlDNAJB9* increases honeydew excretion and fecundity in *N. lugens* (Gao et al., 2023). The expression of *AccDnaJC3*, essential for various stress responses in *Apis cerana cerana*, is induced under stress conditions, such as extreme cold and heat, and exposure to H_2O_2, heavy metals, UV radiation, and pesticides (Zhang et al., 2019).

Myzus persicae is a globally distributed polyphagous pest exhibiting a broad host range and specificity, and it can cause damage on over 400 species (Weber, 1985; Wang et al., 2021). This aphid damages plants through direct feeding and as an indirect vector for the transmission of numerous viral diseases (Kirchner et al., 2005). Numerous studies have demonstrated that *M. persicae* spreads over 100 plant viruses, such as cucumber mosaic (CMV), potato virus Y (PVY), and tobacco etch virus (Lai et al., 2017; Ahmed et al., 2018). *Myzus persicae* is constantly exposed to direct sunlight and environmental UV-B stress throughout the year. However, the precise mechanisms underpinning the response of these aphids to UV-B stress remain elusive. In this study, we identified six *DNAJ* genes in *M. persicae* and analyzed their expression patterns. RNA interference (RNAi) was employed to reveal the role of *DNAJ* genes in *M. persicae* for mitigating UV-B stress. Our investigations on the adaptive molecular mechanism of aphid to UV-B stress will contribute to our understanding of insect response strategies to physical factors, enabling the development of novel control strategies for aphids.

2. MATERIALS AND METHODS

2.1 Insect

The *M. persicae* specimens were originally collected from Guizhou, China (longitude: 106.96, latitude: 27.06). An *M. persicae* colony was established at the Tobacco Research Institute of Guiyang City, Guizhou Province. Tobacco seedlings were used as host plants for continuous rearing under standard conditions of 25°C ± 1°C, relative humidity of 65% ± 5%, and alternating 14-h light and 10-h dark cycle.

2.2 Sequence analysis of *MpDNAJ* genes in *M. persicae*

We cloned the open reading frames (ORFs) of *DNAJ* genes using the primers listed in Table S1. The target gene sequences were subsequently verified using polymerase chain reaction (PCR). Total RNA was extracted from *M. persicae* as described by Huang (2023) and then reverse-transcribed into cDNA. Then, the target *DNAJ* gene fragments were amplified using PCR, purified, recovered, cloned, and sequenced. Homologous gene sequences were identified using the Basic Local Alignment Search Tool from the National Center for Biotechnology Information website (https://blast.ncbi.nlm.nih.gov/Blast.cgi). ORFs were detected using ORF finder (https://www.ncbi.nlm.nih.gov/orffinder/). The molecular weight and isoelectric point of *DNAJs* were predicted using the Expasy ProtParam tool (https://web.expasy.org/protparam). Phylogenetic analyses were performed by MEGA 6.0 using the neighbor-joining (1000 replicates) method to construct a phylogenetic tree of insect *MpDNAJs.*

2.3 Collection of different developmental stages and tissue samples of *M. persicae*

Samples comprising the following developmental stages of *M. persicae* were collected: 1st instar (n = 100), 2nd instar (n = 80), 3rd instar (n = 60), 4th instar (n = 40), wingless adults (n = 30), and winged adults (n = 60). Three biological replicates were performed for each sample (n = 3).

Tissues, including head, gut, epidermis, and embryos, were dissected from adult *M. persicae* (n = 200) using phosphate-buffered saline (Ye et al., 2019). Each treatment included three biological replicates (n = 3). Total RNA was extracted from each sample and stored at −80°C.

2.4 UV-B treatment

One-day-old wingless adults (n = 30) were collected and acclimatized in the dark for 2 h and then irradiated with UV-B rays (280–315 nm) using a UV-B lamp (Nanjing HuaQiang Electronic Engineering, Nanjing, China) at an intensity of 300 W/cm^2 for different durations: 0 (CK), 30, 60, 90, 120 and 150 min. Each treatment included 30 aphids with three biological replicates. Total RNA was extracted and stored at −80°C.

2.5 RNAi

Primers were designed using the FlyRNAi website (https://www.flyrnai.org/cgi-bin/RNAi_find_primers.pl) (Table S1). The dsRNA was synthesized using the 5× MEGAscript T7 Kit (Invitrogen, USA) and introduced into *M. persicae*. The gene encoding green fluorescent protein (GFP) was used as the control. Nanocarriers were mixed with dsRNAs at a 1:1 mass ratio (final concentrations of 320 ng/μL for each dsRNA). Then, detergent was added (at 0.5% of the total volume) to form a complex of dsRNA, nanocarriers, and detergent (Yang et al., 2022). The compound was applied to the back of the abdomen of a 1-day-old adult insect. After 48 h, 15 live aphids were collected and tested for RNAi efficiency using qRT-PCR. Three biological replicates were performed.

2.6 Survival rate analyses upon UV-B exposure and RNAi of *DNAJ* genes

For functional validation, we selected genes that were highly expressed under short-term (30 min) or long-term (120 min) exposure to UV-B. The corresponding genes ds*MpDNAJC2*, ds*MpDNAJC9*, ds*MpDNAJC30,* ds*MpDNAJC3*, ds*MpDNAJC11*, and ds*MpDNAJC17* were synthesized as described above. Adults (n = 30) were treated with dsRNA for 48 h, and then irradiated with UV-B for 4 days. The survival rate was recorded daily. Aphids treated with ds*MpDNAJC2*, ds*MpDNAJC9*, and ds*MpDNAJC30* were exposed to UV-B for 30 min daily, whereas those treated with ds*MpDNAJC3*, ds*MpDNAJC11*, and ds*MpDNAJC17* were exposed to UV-B for 120 min daily. After 3 days of UV-B treatment, the body length, width, and weight of 60 surviving adult aphids were measured. The average body weight was measured using a group containing five aphids (n = 12). The body length and width of the aphids were measured using the Nikon SMZ1270 stereomicroscope (Nikon Corporation, Tokyo, Japan).

2.7 qRT-PCR

After extracting the total RNA from all collected samples, we performed electrophoresis using 1% agarose gels and detected the bands with a UV spectrophotometer. After synthesizing the first-

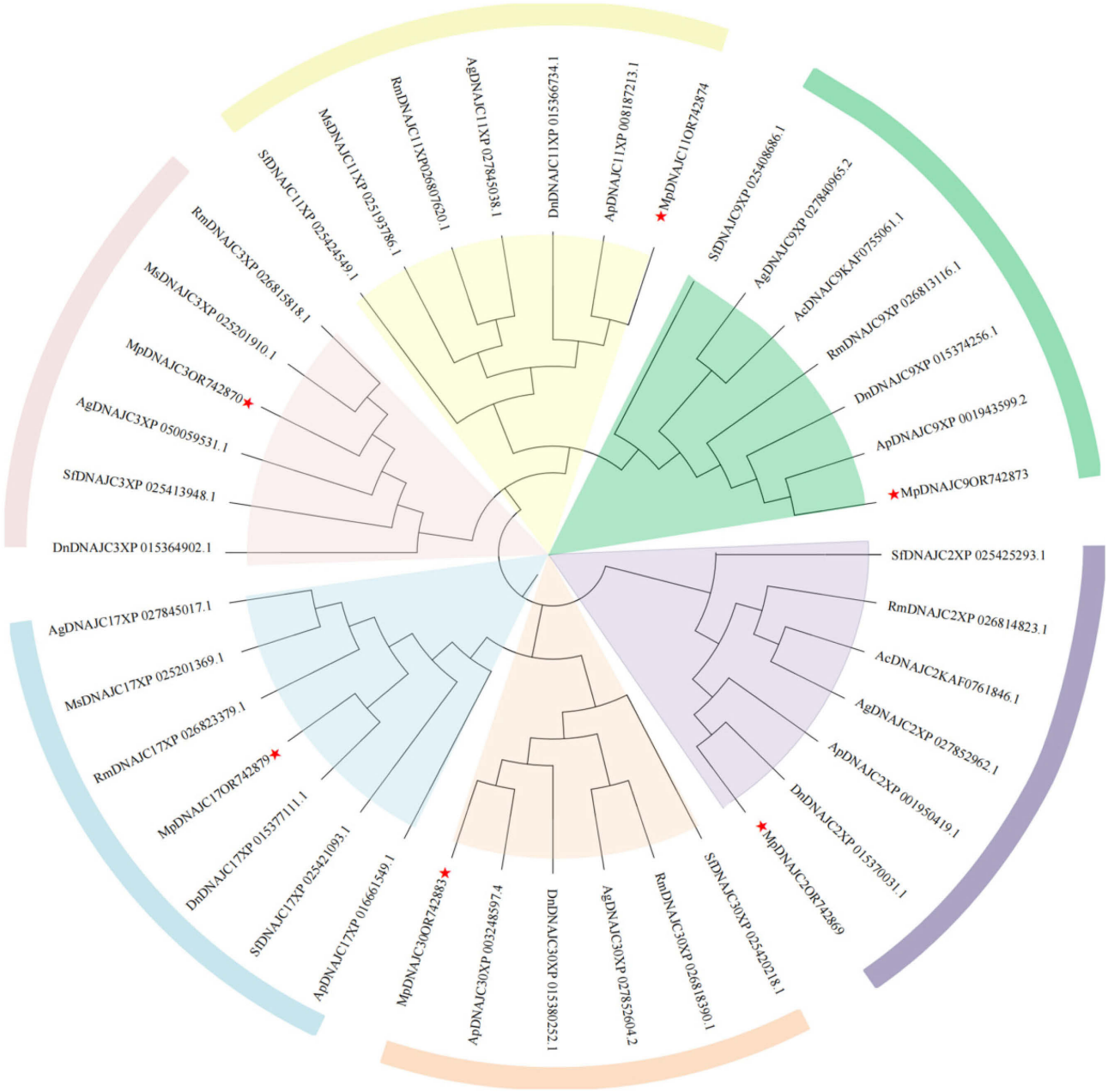

Fig. 1. Phylogenetic analysis of *MpDNAJ* genes from different aphid species: *Acyrthosiphon pisum* (Ap), *Aphis craccivora* (Ac), *Rhopalosiphum maidis* (Rm), *Diuraphis noxia* (Dn), *Aphis gossypii* (Ag), and *Sipha flava* (Sf). An unrooted phylogenetic tree was constructed from six insect species (showing node support based on 1000 bootstrap replicates) with MEGA6.0 using the neighbor-joining method.

strand cDNA, real-time quantitative PCR using the SYBR Green Supermix dye method was carried out. Sangon Biotech (Shanghai, China) synthesized the primers used as shown in Table S1.

2.8 Statistical analysis

All data statistics were compiled using Microsoft Excel 2010. The expression levels of *M. persicae* genes were quantitatively analyzed using the $2^{-\Delta\Delta CT}$ method (Livak & Schmittgen, 2001). qRT-PCR data (*MpDNAJC3* from UV-B treated samples) were transformed using the natural log to increase the homogeneity of variance. The data for *MpDNAJC9* from UV-B treated samples were analyzed using nonparametric tests. The Student's *t*-test was used to test the difference in expression level between the two experimental treatments. Other data were subjected to one-way analysis of variance (ANOVA) and Tukey's honest significant difference (HSD) test for multiple comparison analysis using IBM SPSS Statistics for Windows, version 19.0 (IBM Corporation, Armonk, NY, USA). A level of $P < 0.05$ was used to determine statistical significance.

3. RESULTS

3.1 Identification and analysis of *MpDNAJ* genes

The gene accession numbers for *MpDNAJC2*, *MpDNAJC3*, *MpDNAJC9*, *MpDNAJC11*, *MpDNAJC17*, and *MpDNAJC30* are OR742869, OR742870, OR742873, OR742874, OR742879, and OR742883, respectively. The DNAJ proteins were found to contain 621–1731 amino acids, with predicted molecular weights of 24.52–67.51 kDa, isoelectric points of 6.3–9.57, and stability coeffi-

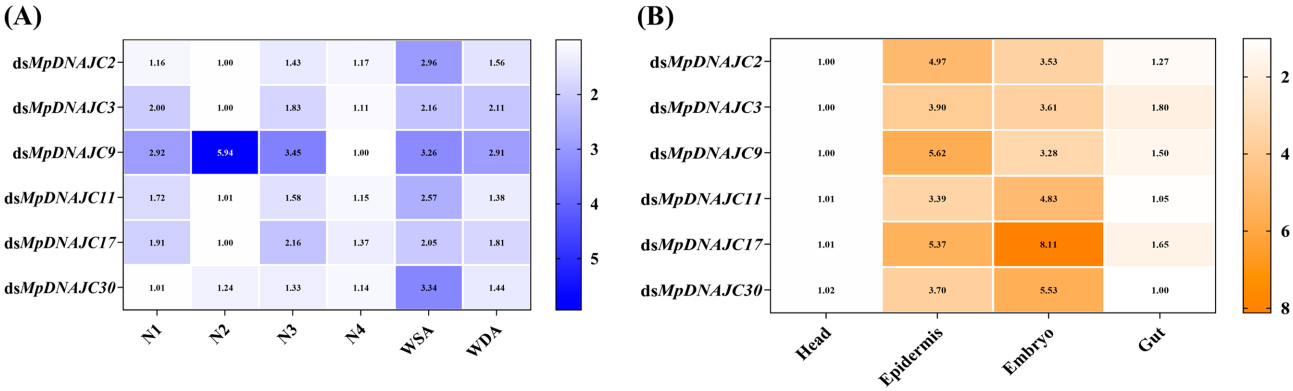

Fig. 2. Expression of *MpDNAJ* genes in *M. persicae* at different developmental stages (A) and in various tissues (B). Developmental stages: N1–N4: first- to fourth-instar nymph stages; WSA – wingless adult; WDA – winged adult.

cients of 31.01–47.19. Table 1 lists the GenBank search numbers.

Phylogenetic trees (Fig. 1) showed that the *DNAJ* genes of *M. persicae* were highly clustered with those of other Hemiptera aphids and were most closely related to those of *Acyrthosiphon pisum*, suggesting that *M. persicae DNAJ* was conserved during evolution.

3.2 Expression of *MpDNAJ* genes in different developmental stages and tissues

The expression levels of *MpDNAJ* genes varied with *M. persicae* developmental stages (Fig. 2A). The expression levels of *MpDNAJC30*, *MpDNAJC11*, *MpDNAJC2*, and *MpDNAJC3* were highest in wingless adults, whereas the expression of *MpDNAJC9* and *MpDNAJC17* were highest in the second- and third-instar nymphs, respectively. The expression levels of *MpDNAJC3*, *MpDNAJC11*, *MpDNAJC2*, and *MpDNAJC17* were lowest in the second-instar nymphs, whereas those of *MpDNAJC9* were lowest in the fourth-instar nymphs, and *MpDNAJC30* were lowest in the first-instar nymphs. Additionally, the relative expression levels of most *MpDNAJ* genes were the lowest in the head, whereas those of *MpDNAJC11*, *MpDNAJC17*, and *MpDNAJC30* were highest in the embryo. Further, the expression of *MpDNAJC2*, *MpDNAJC3*, and *MpDNAJC9* were highest in the epidermis (Fig. 2B).

3.3 Expression level of the *MpDNAJ* genes under UV-B radiation stress

We examined the expression levels of six *MpDNAJ* genes under UV-B stress at different durations (0, 30, 60, 90, 120, and 150 min) (Fig. 3). The expression of *MpDNAJ* genes increased significantly at different treatment times. The expression levels of the *MpDNAJC2*, *MpDNAJC9*, and *MpDNAJC30* genes peaked after UV-B exposure for 30 min and then gradually declined. The expression levels of *MpDNAJC3*, *MpDNAJC11*, and *MpDNAJC17* peaked after UV-B exposure for 120 min and then started to decrease. In general, we observed that under UV-B exposure, the expression pattern of *MpDNAJ* genes increased initially and then gradually reduced.

3.4 Expression level of *MpDNAJ*s after RNAi and the survival rate, body length, and body weight of *M. persicae* after UV-B exposure

After 48 h of dsRNA treatment, the expression of ds*MpDNAJC2*, ds*MpDNAJC30*, ds*MpDNAJC3*, ds*MpDNAJC17*, ds*MpDNAJC9* and ds*MpDNAJC11* were significantly inhibited (Fig. 4A). After 4 days of continuous UV-B exposure, the survival rate of RNAi-treated aphids was significantly lower than that of ds*GFP*-treated control aphids (Figs 4B). After 3 days of continuous UV-B exposure, the body length and width of *M. persicae* treated with ds*MpDNAJs* reduced significantly, and the body weight was also evidently decreased compared to the ds*GFP*-treated control group (Figs 5A–C). Moreover, after 3 days of UV-B exposure, the bodies of the aphids appeared browner after treatment with ds*MpDNAJC2*, ds*MpDNAJC11*, and ds*MpDNAJC30* compared to the controls (Fig. 5D).

4. DISCUSSION

UV-B radiation is an inevitable environmental factor in the natural habitat, seriously affecting the development, survival, and reproduction of various organisms. Hsps can regulate physiological activities and contribute to responses under various biotic and abiotic stresses. DNAJ, a kind of heat shock protein, is an important regulator of insect survival that plays a crucial role in resisting stress environments. Herein, we identified six *MpDNAJ* genes in *M. persicae*, a significant agricultural pest. All the genes had a

Table 1. Characteristics of the *MpDNAJ* mRNAs of *M. persicae*

Gene	ORF (bp)	Protein length	Molecular weight (kDa)	Isoelectric point (IP)	Instability index (II)	GenBank accession no.
MpDNAJC2	1731	576	67.51	8.71	47.19	OR742869
MpDNAJC3	1467	488	56.68	6.30	37.06	OR742870
MpDNAJC9	774	257	30.27	8.60	34.20	OR742873
MpDNAJC11	1710	569	64.59	7.19	41.72	OR742874
MpDNAJC17	918	305	34.65	9.17	31.01	OR742879
MpDNAJC30	621	206	24.52	9.57	40.22	OR742883

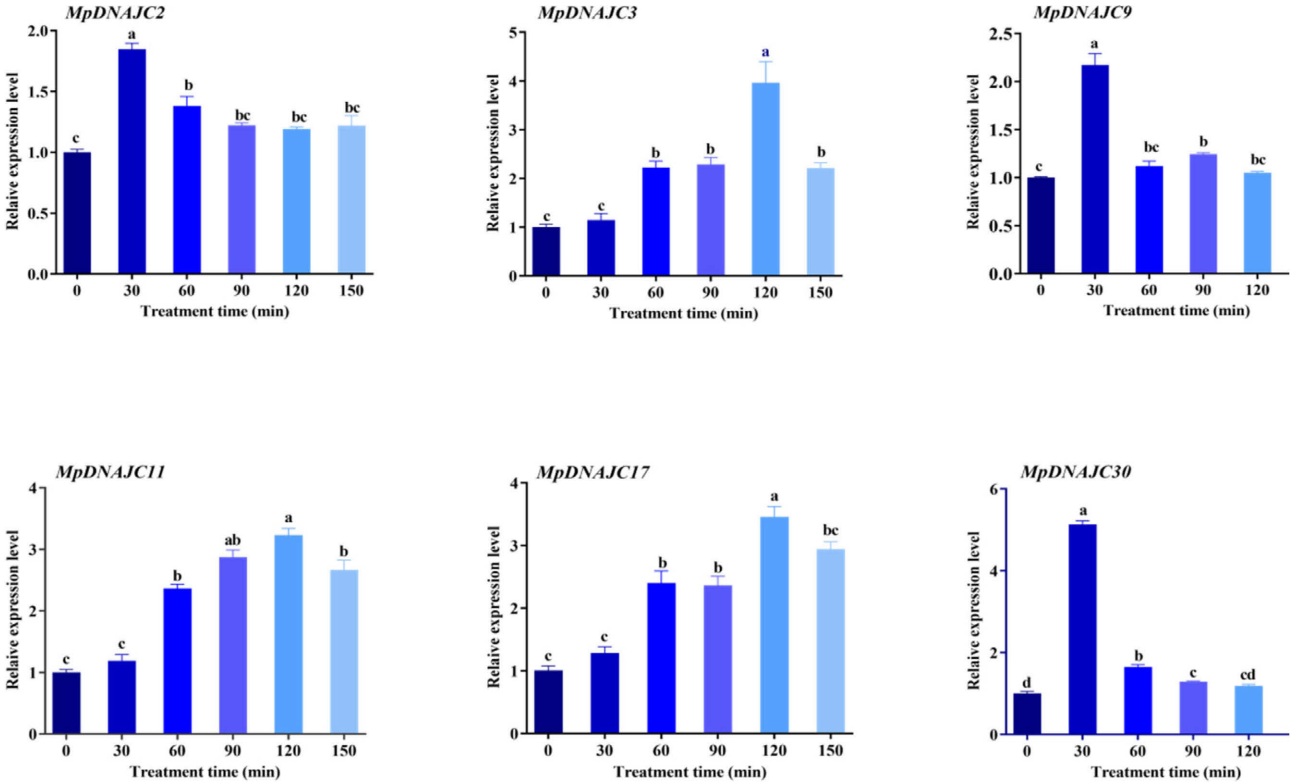

Fig. 3. Expression of *MpDNAJ* genes in *M. persicae* under UV-B exposure for different time periods (0, 30, 60, 90, 120 and 150 min). Different letters above the bars indicate significant differences between treatment durations based on one-way ANOVA ($P < 0.05$, Tukey's HSD test for multiple comparison analysis).

conserved J domain with a highly conserved His-Pro-Asp (HPD) motif. This motif interacts with Hsp70 to stimulate its ATPase activity, thereby promoting the correct folding of peptides (Young, 2010). Phylogenetic analyses showed that *MpDNAJ* genes formed corresponding branches with homologous proteins in other species. In organisms, many proteins are prone to misfolding and aggregation because of molecular crowding and external stimuli. The DNAJ proteins can regulate protein folding in the endoplasmic reticulum to enable the release of newly synthesized proteins into the cytoplasm and mitochondria. They also prevent protein aggregate formation (Karademir & Sari-Kaplan, 2018). The *M. persicae MpDNAJ* genes are expressed at different developmental stages, suggesting that *DNAJ* is indispensable for the growth and development of *M. persicae*. However, the expression patterns of *DNAJ* genes vary across the developmental stages of *M. persicae*, suggesting that *DNAJ* might have different roles. *CpHSP40* genes exhibited differential expression at various developmental stages, indicating their pivotal role in the development and

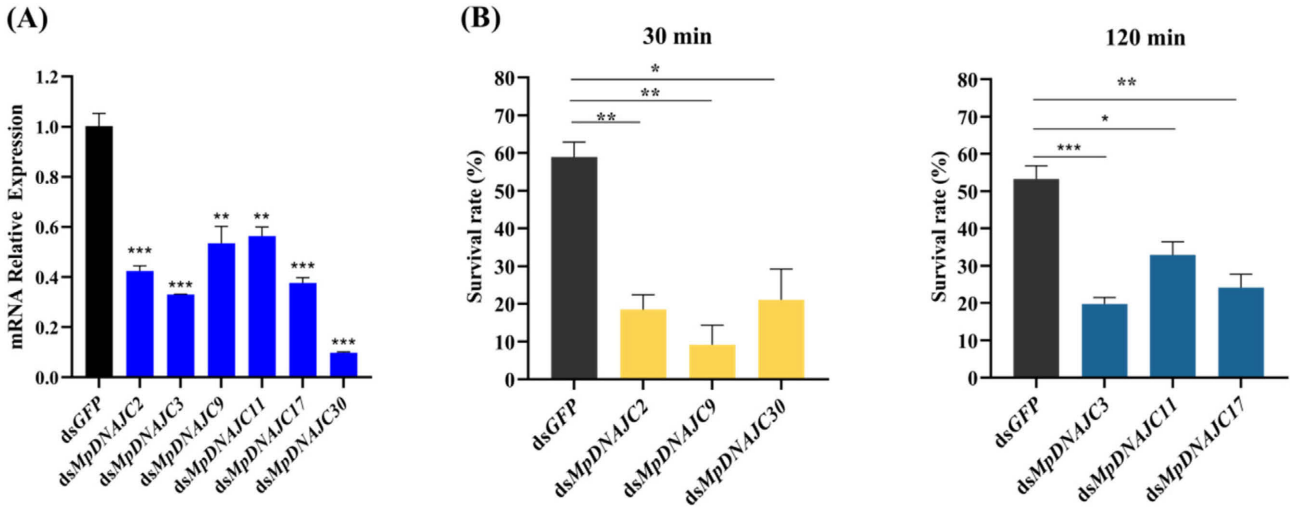

Fig. 4. (A) Detection of *MpDNAJ* gene expression 48 h after delivery of ds*MpDNAJ* to *M. persicae* using nanomaterials. Data are expressed as mean ± standard error of three collections (Student's *t*-test, $^{**}P < 0.01$ or $^{***}P < 0.001$). (B) Survival of *M. persicae* after 4 days of UV-B irradiation at 30 and 120 min per day after 48 h of RNAi treatment. Data are expressed as mean ± standard error of three collections (Student's *t*-test, $^{*}P < 0.05$ $^{**}P < 0.01$ or $^{***}P < 0.001$).

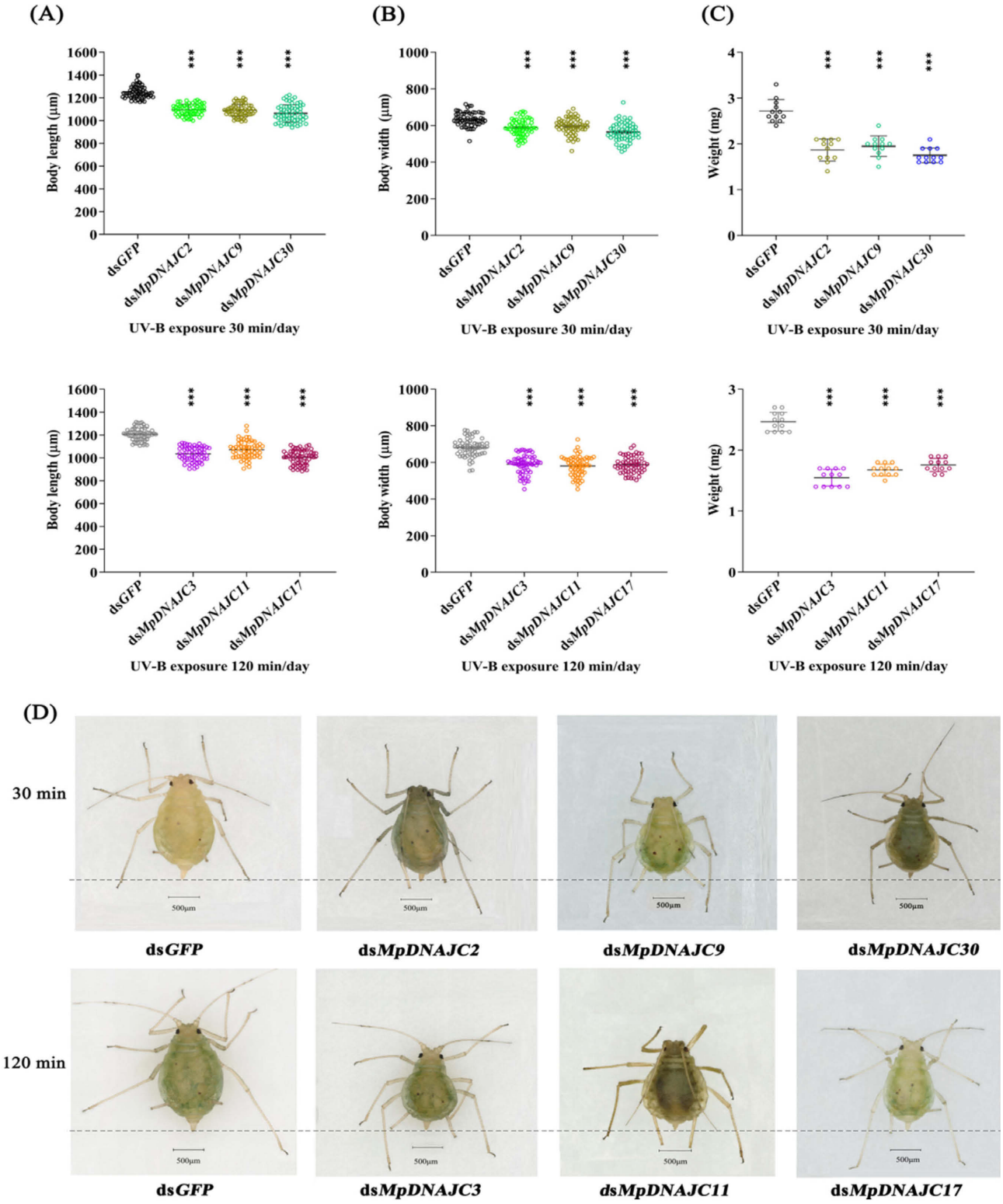

Fig. 5. Body parameters of RNAi-treated *M. persicae* after 3 days of UV-B exposure. (A) Body length, (B) body width, and (C) body weight of surviving *M. persicae*. Data are expressed as mean ± standard error (n = 60) (Student's *t*-test, ***$P < 0.001$). (D) After 48 h of RNAi treatment, UV-B irradiation of adult aphids for 30 and 120 min per day resulted in phenotypic changes after 3 days.

life cycle of *Cydia pomonella* (Yang et al., 2016). The expression levels of most *DNAJ* genes are highest in adult *M. persicae*, which is consistent with the findings of Chen (2021) in *N. lugens*. Furthermore, the expression pattern of *MpDNAJ* genes varied among tissues. The expression levels of *MpDNAJC2*, *MpDNAJC3*, and *MpDNAJC9* were highest in the epidermis, perhaps because the epidermis is the primary barrier against environmental stress. Further, the expression levels of *MpDNAJC11*, *MpDNAJC17*, and *MpDNAJC30* were highest in the embryo, indicating the involvement of these genes in the embryonic development of *M. persicae*.

In this study, we investigated the expression patterns of the six *MpDNAJ* genes in *M. persicae* under UV-B stress. The results showed that the expression level of six *MpDNAJ* genes increased at first and then decreased with prolonged UV-B exposure. Previously, similar results were observed in *A. cerana cerana* (Li et al., 2018, 2022). In insects, Hsp70 is typically upregulated in response to stressors to help refold or degrade damaged proteins and maintain cellular homeostasis. However, prolonged or severe stress can cause cellular damage that cannot be mitigated by Hsp70, resulting in a decrease in Hsp70 transcription (Kim et al., 2011). The mRNA expression levels of six *MpDNAJ* genes first increased and then decreased, suggesting these genes might be regulated by a negative feedback mechanism in order to prevent the accumulation of harmful substances. The upregulation of Hsps is a ubiquitous physiological response to environmental stressors to cope with diverse stresses, such as extreme temperatures, hypoxia, and radiation (Colinet et al., 2010). Previous research has shown that increased levels of *Hsp40* proteins during winter enhance the cold tolerance of *Eurosta solidaginis*, contributing to the insect's survival (Zhang et al., 2011). *Hsp40* was shown to improve the ability of flies to withstand UV-A radiation, as demonstrated by the significant increase in the expression of *DmHsp40* after exposure to UV-A for 0.5 to 3 h (Wang et al., 2014). Based on these studies, we hypothesize that *MpDNAJ* genes might be involved in the response to UV-B stress in *M. persicae* and its resistance to environmental stress.

In RNAi assays, dsRNA is used to silence specific insect genes to investigate their function (Huvenne & Smagghe, 2010; Cooper et al., 2019). dsRNA delivered via nanocarriers can effectively silence key genes in aphids (Yan et al., 2020). In the present study, the silencing of *MpDNAJC2*, *MpDNAJC9*, *MpDNAJC11*, *MpDNAJC30*, *MpDNAJC3*, and *MpDNAJC17* significantly reduced the survival rate of *M. persicae* under conditions of persistent UV-B exposure. The body length and width of dsRNA-treated *M. persicae* under UV-B exposure were decreased. Moreover, the body color of *M. persicae* turned light brown. These changes suggest that *MpDNAJ* genes are important for UV-B resistance and survival in *M. persicae*. Similar results have been observed for UV-B-induced *Hsp70* genes in *M. persicae*. In a previous study, the knockout of *Hsp70* genes significantly altered the length, weight, and color of the bodies of *M. persicae* under UV-B stress (Yang et al., 2022). Other studies have similarly revealed the biological function of Hsps in response to stressful environments. For instance, Ding et al. (2022) reported that the silencing of *DNAJC1* significantly increased mortality in *M. persicae* after exposure to trans-anethole. Chen et al. (2021) showed that the silencing of *NlDNAJC5* and *NlDNAJC22* caused mortality of *N. lugens* before or during molting, suggesting that these proteins are essential for the growth and development of the brown plant hopper. Li et al. (2018) found that in honeybees (*A. cerana cerana*), the knockdown of *DnaJB12* and *DnaJC8* reduced their resistance to the insecticide lambda-cyhalothrin and heat stress. There is a potential relationship between Hsp70 and DNAJ proteins. Hsp40 and Hsp70 form an Hsp70/Hsp40 complex to achieve synergistic actions (Kampinga & Craig, 2010; Ajit Tamadaddi & Sahi, 2016; Craig & Marszalek, 2017). *TID1*, a *DNAJ* gene, interacts with *Hsp70* genes in *Drosophila* to maintain embryonic cell survival (Lo et al., 2004). Studies on Hsps in *N. lugens* have revealed that the functions of most *DNAJ* genes are partially consistent with those of *Hsp70* genes (Chen et al., 2021). Therefore, *DNAJ* and *Hsp70* genes might perform similar functions within the organism or work synergistically. However, this hypothesis should be further investigated in insects. Exploring these mechanisms in beneficial insects, such as pollinators (bees) and natural enemies of pollinators exposed to UV-B light daily might reveal potentially novel adaptation mechanisms in these insects to different stressors in our complex environment.

In conclusion, UV-B is an important environmental stress factor for various organisms, it has been proved that it is directly harmful to insects. Understanding the biological effects and adaptive mechanisms of *DNAJ* genes under UV-B stress will provide insights into the survival strategies and adaptive mechanisms of insects in response to UV-B radiation and prevent the damage associated with it. In pest management strategies, insecticides targeting *DNAJ* genes could be used to disrupt the survival of this species under UV stress. These findings might also facilitate agricultural pest management and ecological studies.

AUTHORSHIP CONTRIBUTION. L.-C. He: Writing – original draft, Investigation, Formal analysis, Data curation, Conceptualization. J.-Y. Meng: Investigation, Formal analysis, Data curation. C.-L. Yang: Validation, Methodology. X. Tang: Methodology, Conceptualization, Writing – original draft. G. Smagghe: Validation, Methodology. C.-Y. Zhang: Writing – review & editing, funding acquisition.

DATA AVAILABILITY. The sequences derived from this study are deposit in Genbank accession numbers OR742869, OR742870, OR742873, OR742874, OR742879, and OR742883.

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Table S1. The primers used in this experiment.

Application of primers	Primers name	Forward primer (5′–3′)	Reverse primer (5′–3′)
Gene cloned	*MpDNAJC2*	TTCGAATTGCTTGAGGTCCTG	TCTATTTGGAGGGCACTGGA
		GTGATCAACTTTCTGCCATACAAC	AAGTTGCTGCCTACATTGTGTC
	MpDNAJC3	TGTTCAGACACCGTTCGCTT	GCGCTGACTGACTGTCTACT
		TCCAAGCCGATGATACAGACG	GACACAGCCTTTTGAACCCT
	MpDNAJC9	TCATCCTCAAATCCCGACCC	TAGCCCTGCTCACAATCCAAT
	MpDNAJC11	ATGGATTCCAATTCGGAAAACGA	TCAAGATGGCGGTGTAGCAG
	MpDNAJC17	ATGGATTCTGATTTGAAAGATTTA	TCATAATACCCAAGGTTCTTT
	MpDNAJC30	TTTGAACACTGAGGTAATTCTGAAG	AGGTGTCCGTTGTGAGGTAA
Quantitative real-time PCR	*MpDNAJC2*	TCGTTTCTACAATTCTTGGTATGGT	TCAGCTTAGTACGATTTGCACG
	MpDNAJC3	CTTGATGGCCTTGCCTACGA	AGGAGCCCAAGGACAATGTT
	MpDNAJC9	GCTCTGCTCAATGATGCTGATA	TGAACTCCAATAGGTTTCCCAAG
	MpDNAJC11	GCAATCTATGACTGCGTCGG	CGATCCCTTGCTAACGCTTCA
	MpDNAJC17	TGAGATCCAACAGTCGGCTAC	AGCTGCTTTGGGATTATCGGG
	MpDNAJC30	TAAAGGAAGTGAAGAAGCTGCAA	TTCTTTGACGGACATTTCCCAAG
	18S	TCAACACGGGAAACCTCACCA	CACCACCCACCGAATCAAGAA
	Actin	AGTGCGACGTTGACATCAGA	GCTTGGAGCTAAGGCAGTGA
dsRNA synthesis	*MpDNAJC2*	CAGCTGTGAAACAAGCCAAA	TTCTATTTGGAGGGCACTGG
	MpDNAJC3	ATAATGGACTTGCGGACAGC	TCGTCAAACATTGAGTTGGC
	MpDNAJC9	GATGATGCTGGATGTGTTGG	TTTTGCACTGGGCTTCTTCT
	MpDNAJC11	GGTGCCCGAACTACTGGTTA	GCTTCTTGACGCAATTCTCC
	MpDNAJC17	GCAGCACGATCAGCTTATGA	CTTGTCCGTAATCCCCAAGA
	MpDNAJC30	ATCTTGGGAAATGTCCGTCA	TGAATTTTGTCGTGCTGCAT
	dsMpDNAJC2	T7+CAGCTGTGAAACAAGCCAAA	T7+TTCTATTTGGAGGGCACTGG
	dsMpDNAJC3	T7+ATAATGGACTTGCGGACAGC	T7+TCGTCAAACATTGAGTTGGC
	dsMpDNAJC9	T7+GATGATGCTGGATGTGTTGG	T7+TTTTGCACTGGGCTTCTTCT
	dsMpDNAJC11	T7+GGTGCCCGAACTACTGGTTA	T7+GCTTCTTGACGCAATTCTCC
	dsMpDNAJC17	T7+GCAGCACGATCAGCTTATGA	T7+CTTGTCCGTAATCCCCAAGA
	dsMpDNAJC30	T7+ATCTTGGGAAATGTCCGTCA	T7+TGAATTTTGTCGTGCTGCAT

T7: TAATACGACTCACTATAGGG