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Research article

Characterization and analysis of myosin gene family in the whitefly (*Bemisia tabaci*)

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Abstract: Myosin is an actin-based motor protein that widely exists in muscle tissue and non-muscle tissue, and myosin of a diverse subfamily has obvious differences in structure and cell function. Many eukaryotes and even some unicellular organisms possess a variety of myosins. They have been well characterized in human, fungi and other organisms. However, the myosin gene family in *Bemisia tabaci* MEAM1 (Middle East-Asia Minor1 species) is poorly studied. In the study, we identified 15 myosin genes in *B. tabaci* MEAM1 based on a genome database. Myosin genes can be divided into ten classes, including subfamilies I, II, III, V, VI, VII, IX, XV, XVIII, XX in *B. tabaci* MEAM1. The amounts of myosin in Class I are the largest of the isoforms. Expression profiling of myosins by quantitative real-time PCR revealed that their expression differed among developmental stages and different tissues of *B. tabaci* MEAM1. The diversely may be related to the development characteristics of *B. tabaci* MEAM1. The *BtaMyo-IIIb-like X1* was highly expressed in nymphs 4 instar which may be related to the development process before metamorphosis. Our outcome contributes to the basis for further research on myosin gene function in *B. tabaci* MEAM1 and homologous myosins in other biology.

Keywords: myosin; phylogenetic analysis; expression profiles; *Bemisia tabaci*

1. Introduction

Myosin is a kind of multifunctional protein, whose main function is responsible for the actin-based motility and contraction [1]. As one of three major families of motor proteins, myosins bind to actin filaments and converts chemical energy into mechanical force by hydrolyzing ATP to participate in various kinds of cellular processes [2]. The Myosin superfamily is a large and varied protein family which can be divided into many classes [3], and diverse classes of myosin motors afford several types of cellular functions [4].

In insects, the study of these four subfamilies (class I, II, V and IX) is relatively clear. Class I participates in the cell membrane and the cytoskeleton-interaction process. Some Class I myosins can binds to acidic phospholipids by a tail homology 1 (TH1) domain [5]. Most Class I myosins can be divided into two distinct forms, amoeboid and short, and the two forms differ in their C-terminal tail domain. The C-terminal tail domain of the amoeboid form in the Class I has a polybasic domain, a GPA domain, and SH3 domain; whereas the tail domain of the short form only has a one polybasic region. The amoebic forms are a relatively conserved class of actin-based motor proteins, and they play important roles in powering pseudopod extension or vesicle transport. For instance, two type of Class I are reported to be involved in pseudopod formation process in *Dictyostelium discoideum* [6,7]. Myosin II consists of heavy chains, the essential light chain and the regulatory light chain. The head domain of each heavy chain at the N-terminal consists of an actin binding site and ATPase site, followed by light chains. The combined long α-helical light chain-binding site and light chains form rigid lever bar to generate movement [8]. Non-muscle myosin II plays a role in many fundamental cellular processes including cell adhesion, migration, cytokinesis, and epithelial barrier function [9,10]. Most non-muscle cells express multiple myosin II motor proteins including myosin IIA, myosin IIB, myosin IIC [11]. Myosin II also can change biochemical signaling through changes in the actin-associated proteins that regulates the gene transcription process [12]. Myosin V is characterized by its long tail composed of the coiled-coil region and C-terminal globular tail domain (GTD). Myosin V can recognize numerous cellular cargos through its GTD, which is critical for cargo binding and actin cable organization. Additionally, phosphorylation plays an important role in class V myosin cargo choice process [13,14]. Class IX myosins are consist of a motor region, a light-chain-binding region and a tail region. In invertebrates, Class IX only have one member, whereas mammals contain two IX myosins that called myo9a and myo9b. Myo9a is mainly involved in the regulation of epithelial cell morphology and differentiation, while myo9b is critical to the regulation of macrophage morphology and movement [15].

The whitefly (*Bemisia tabaci*) is a polyphagous pest widely distributed in all regions of the world, causing great damage to crop through direct harm (feeding) and indirect harm (spreading the virus) [16]. The whitefly is a cryptic species complex that consists of at least 36 cryptic species, and most of them are difficult to distinguish morphologically [17]. Among these cryptic species, the MEAM1 type of *B. tabaci* is listed as one of the world's most dangerous invasive pests. Moreover, *B. tabaci* (MEAM1) has a higher resistance to both parathyroid and permethrin [18]. The myosin gene structure, gene location, sequence characteristics, and gene expression profile were analyzed, providing a basis for further exploring the relationship between myosin genes and stress energy metabolism or viral transmission.

2. Materials and methods

2.1. Insect cultures and sample preparation

The group of *B. tabaci* MEAM1 was maintained on cotton plants, kept at a temperature of 26–28 °C. The photoperiod was 16 hours of light following by 8 hours of darkness, and the relative humidity was 60%–70%. The purity of species was monitored by the mitochondrial cytochrome oxidase I gene (mtCOI) [19]. Sample of tissue-specific (head, thorax, abdomen) and temporal-specific (egg, 1st and 2nd instar nymph, 3rd instar nymph, 4th instar nymph females, males) were collected from the *B. tabaci* MEAM1 population and rapidly stored at –80 °C until to use.

2.2. Genome-wide identification and sequence analysis of the myosin genes

To identify the putative myosin gene in the *B. tabaci* MEAM1 genome (assembly ASM185493v1), we have downloaded the genome information of *B. tabaci* MEAM1 population from National Center for Biotechnology Information (https://www.ncbi.nlm.nih.gov/). We also downloaded the HMM profile of the Myosin head (PF00063) from the Pfam database (https://pfam.sanger.ac.uk/). To search for the protein that matched the Pfam HMM profile of myosin in the *B. tabaci* MEAM1 genome database by hmmsearch (HMMER software, version 3.1b1) [20]. The non-redundant protein sequence was deleted using CD-HIT (sequence identity 90%) [21,22]. The Myosin head domains of the candidate protein were further identified through the SMART online website (http://smart.embl-heidelberg.de/) [23]. The chromosomal location information was obtained from National Center for Biotechnology Information (http://www.ncbi.nlm.nlh.gov/). The gene location information was showed through TBtools software. The theoretical molecular weight and isoelectric point of 15 myosin genes in *B. tabaci* MEAM1 were predicted through the Ex-PASy Proteomics website (http://web.expasy.org/protparam). Meanwhile, the predicted myosin protein genes were manually annotated by online BLASTP searches against the non-redundant protein database in NCBI (https://www.ncbi.nlm.nih.gov/). Exon-intron structure information of myosin genes was obtained from the consensus gene set (Gff File) from National Center for Biotechnology Information. The information was showed by the GSDS 2.0 online tools. Conserved domain analyses were performed by the online program SMART.

2.3. Phylogenetic analysis

To comprehensively annotate the evolutionary relationship of the myosin genes of *B. tabaci* MEAM1, a phylogenetic tree was constructed based on the putative myosin genes of *B. tabaci* MEAM1 and myosin genes from different insects. All the myosin genes protein sequences were aligned using the program ClustalW, and further to generate a phylogenetic tree with the neighbor-joining (NJ) method in MEGA 7.1 software with 1000 boostrap replicates [24].

2.4. Total RNA isolation and cDNA synthesis

The samples from different tissues (heads, thorax, abdomen) and different development stages (egg, nymphs 1–2 instar, nymphs 3 instar, nymphs 4 instar, females, males) of *B. tabaci* MEAM1

were isolated with the TRIzol reagent (Invitrogen, Carlsbad, CA, USA), following the manufacturer's instructions. The total RNA was quantified by spectrophotometer, and its quality was checked on a 1% agarose gel. Three samples were used as biological replicates. The reverse transcription reaction was performed using PrimeScrip RT Reagent Kit with gDNA Erase (TaKaRa, Dalian, China) to synthesize the first strand of cDNA, according to the manufacturer' s protocol. The cDNA was stored at –80 °C until used.

2.5. Expression profile of myosin genes

RT-qPCR was conducted using an ABI QuantStudio 3 real-time PCR system. All qPR-PCR analyses included three technical replications for each of three biological replications. The TUB gene was selected as the reference gene [25]. RT-qPCR was carried out in a 20 μl volume of mixture containing 10 μL of 2× TB Green Premix Ex Taq II, 0.4 μL of 50× ROX reference dye, 0.8 μL of forward primer, 0.8 μL of reverse primer, 2.0 μL of cDNA, and 7.6 μL of RNase-free ddH2O, following the instructions of the TB Green® Premix Ex Taq™ II (SYBR Green) Kit (TaKaRa, Dalian, China). The PCR procedure was as follows: 95°C for 30 s, followed by 40 cycles of 95 °C for 5 s, and annealing at 57 °C for 34 s. The transcript levels of the target genes were analyzed by the 2-ΔΔCt method [26]. RT-qPCR data were analysed by SPSS 19.0.

3. Results

3.1. Identification and sequence analysis of myosin genes

Table 1. *B. tabaci* MEAM1gene encoding proteins with myosin head domains.

Class	Gene name	Accession	Protein length (aa）	N. W. (kDa)	pI	Location
I	BtaMyo-IA	XP_018899154.1	1012	116.0	9.3	NW_017547203.1
	BtaMyo-Ia X1	XP_018907049.1	1078	125.7	8.97	NW_017548382.1
	BtaMyo-Ia X2	XP_018907050.1	1058	122.2	8.94	NW_017548382.1
II	BtaMyo HC X1	XP_018907939.1	1981	228.7	5.37	NW_017549105.1
	BtaMyo HC X17	XP_018918184.1	1970	224.9	5.92	NW_017547120.1
III	BtaMyo-IIIb-like X1	XP_018914102.1	1361	155.9	9.21	NW_017563186.1
V	BtaMyo-Va X1	XP_018910252.1	1843	213.0	8.87	NW_017551919.1
VI	BtaMyo HC 95F	XP_018907135.1	1256	144.0	9.07	NW_017548708.1
VII	BtaMyo-VIIa X1	XP_018899711.1	2166	250.0	9.03	NW_017547225.1
	BtaMyo-VIIa	XP_018910382.1	2284	260.3	8.06	NW_017547107.1
IX	BtaMyo-IXa-like X1	XP_018913812.1	2027	231.0	9.26	NW_017562455.1
	BtaMyo-IXa-like	XP_018913814.1	1959	223.2	9.24	NW_017562455.1
XV	BtaMyo-XV	XP_018915199.1	2698	305.2	8.77	NW_017565251.1
XVIII	BtaMyo-XVIIIa X2	XP_018902235.1	2130	305.2	8.77	NW_017547285.1
XX	BtaMyo-I HC	XP_018907729.1	1120	121.9	9.03	NW_017549038.1

To identify myosin proteins in *B. tabaci* MEAM1, we retrieved the HMM profile of the Myosin head (PF00063) from the Pfam database and searched all the candidate myosin genes by using HMMER 3.1 software. Protein domains of all candidate genes myosin were confirmed with Simple

Modular Architecture Research Tool. A Total of 15 non-redundant myosin protein sequences were identified in the *B. tabaci* MEAM1 genome. The 15 myosin genes in *B. tabaci* MEAM1 genome are divided into 10 subfamilies including Class I, Class II, Class III, Class V, Class VII, Class XV, Class IX, Class VI, Class XVIII, Class XX. *B. tabaci* MEAM1 myosin genes varied greatly in length and physicochemical properties. The amino acid sequence ranged from 4330 to 11680 residues in the length. The molecular weights ranged from 33.3 kDa to 248 kDa. The predicted isoelectric point ranged from 5.5 to 9.7 (Table 1).

Molecular weight (M.W.) and isoelectric point (pI) were determined using the ExPASy compute pI/Mw tool avaliable at https://web.expasy.org/protparam/.

Table 2. Phylogenetic distribution of myosin classes in *B. tabaci* MEAM1 and other species. Black circles indicate the presence of orthologs of a myosin class in a particular lineage.

	Homo sapiens	Bemisia tabaci	Danaus plexippus	Tribolium castaneum	Drosophila melanogaster	Caenorhabditis elegans
I	●	●	●	●	●	●
II	●	●	●	●	●	●
III	●	●	●		●	●
V	●	●			●	
VI	●	●	●	●	●	●
VII	●	●	●	●	●	
IX	●	●		●		●
XV	●	●	●			
XVIII	●	●	●	●	●	●
XX		●	●	●	●	
Classes	9	10	8	7	8	6

Myosin heavy chain generally consists of three domains, an N-terminal head region, a neck, and a C-terminal tail domain [27]. The putative domains or motif were identified by Pfam and SMART databases (http://smart.embl-heidelberg.de/) with the default parameters. It is well known that gene duplication is important for species-specific adaptations and for the evolution of new functions since it provides organisms with genetic material [28]. A total of 15 myosin proteins were present by in *B. tabaci* MEAM1 myosin genes (Figure 1). All the myosin protein contained the MYSc domains in *B. tabaci*. Among these subfamily, Class I myosin protein only contain one MYSc and one IQ motif; Class VII myosin protein has two MyTH4 and B41 domain which is located in the tail domain; Class III protein contains one kinases domain, one MYSc and three IQ motifs; the XV myosin protein contain one MYSc, one IQ motifs, one MyTH4s and one coiled-coils domains; and Class V myosin protein consist of one MYSc, six IQ motifs, two coiled-coils domains and DIL domain in *B. tabaci* MEAM1.

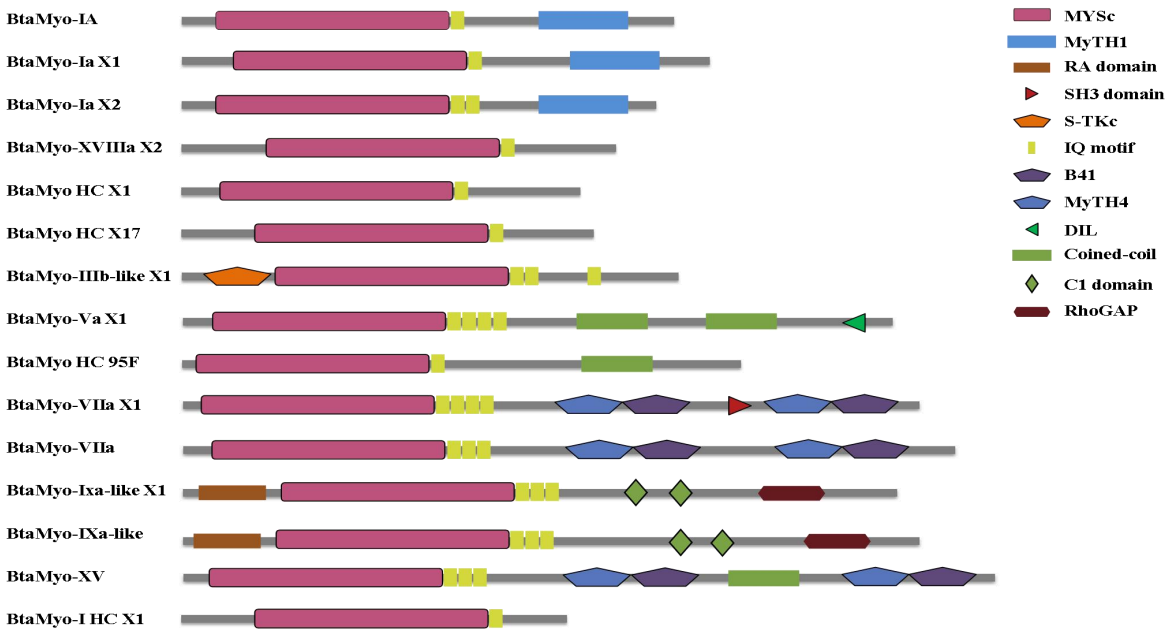

Figure 1. Schematic diagram of the domain structures of myosin proteins *B. tabaci* MEAM1. A color key to the domain names and symbols are given on the right. The abbreviations for the domains are as follows: MYSc, myosin head domains; MyTH1, Unconventional myosin tail, actin- and lipid-binding; RA domain, Ras association (RalGDS/AF-6) domain; SH3 domain, src homology 3 domains; S_TKc, serine/threonine protein kinases, catalytic domain; IQ motif, short calmodulin-binding motif containing conserved Isoleucine and Glutamine residues; B41, band 4.1 homologues; MyTH4, myosin tail homology 4; DIL, DIL domain; C1 domain, protein kinase C conserved region 1 (C1) domains (Cysteine-rich domains); RhoGAP, GTPase-activator protein for Rho-like GTPases.

To determine the distribution and contexts of the myosin genes family on *B. tabaci* MEAM1, a "myosin distribution map" was constructed based on the chromosomal coordinates extracted from National Center for Biotechnology Information (https://www.ncbi.nlm.nih.gov/). Among them, 15 identified genes of myosin genes were distribution to 13 Scaffold (Figure 2). The size of the scaffolds ranged from 148 kbp to 9260 kbp, there is a great difference among the sizes of the scaffolds. Most of myosins in *B. tabaci* MEAM1 were dispersed on different Scaffold, but *BtaMyo-IXa-like* and *BtaMyo-IX-like X1* and *BtaMyo-Ia X1* and *BtaMyo-Ia X2* were respectively assigned to two same Scaffold, suggesting that these genes probably originated from a common ancestral by gene duplication. The alterations in exon and intron structure are critical in gene function divergence, especially in duplicate genes [29]. The exon-intron structures of myosin were determined via GSDS, using comparison of the cDNA sequence to the genomic sequences. The exon-intron structures of 15 myosin genes showed a high degree of structural divergence in the *B. tabaci* MEAM1. The exon numbers range from 12 (*BtaMyo-IA*) to 37 (*BtaMyo HC X17*) in *B. tabaci* MEAM1 myosin genes. Compared to the conserved exon size, the lengths of introns were more divergent (Figure 3).

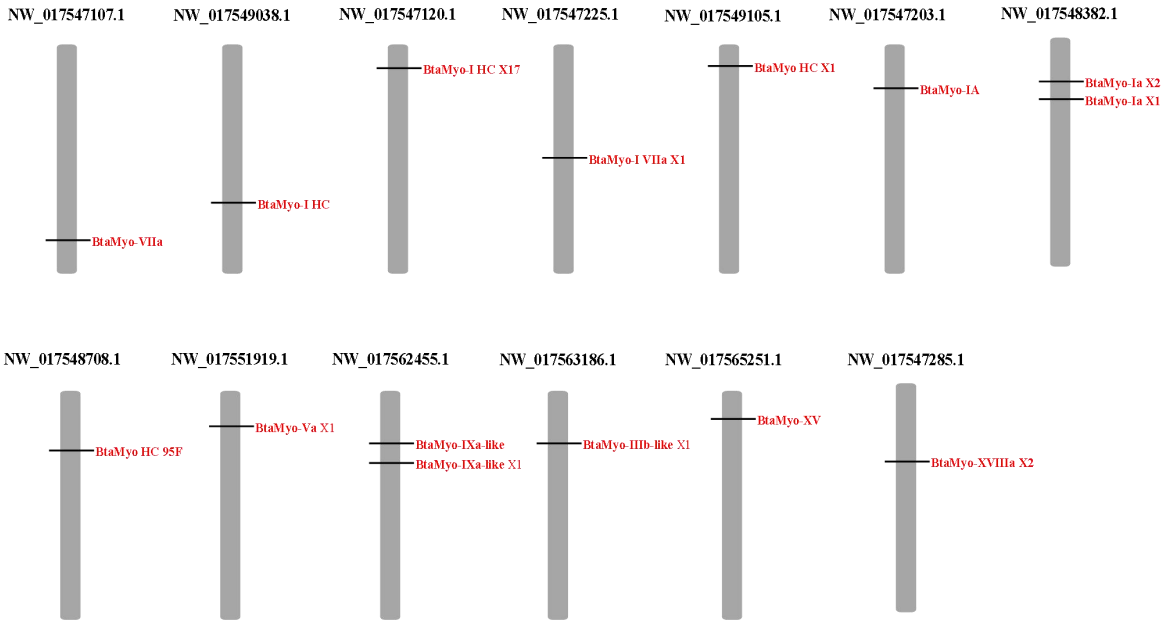

Figure 2. The relative physical positions of myosin genes on scaffolds of the *B. tabaci* MEAM1 genome. The 15 myosin genes in *B. tabaci* are located on 11 Scafford.

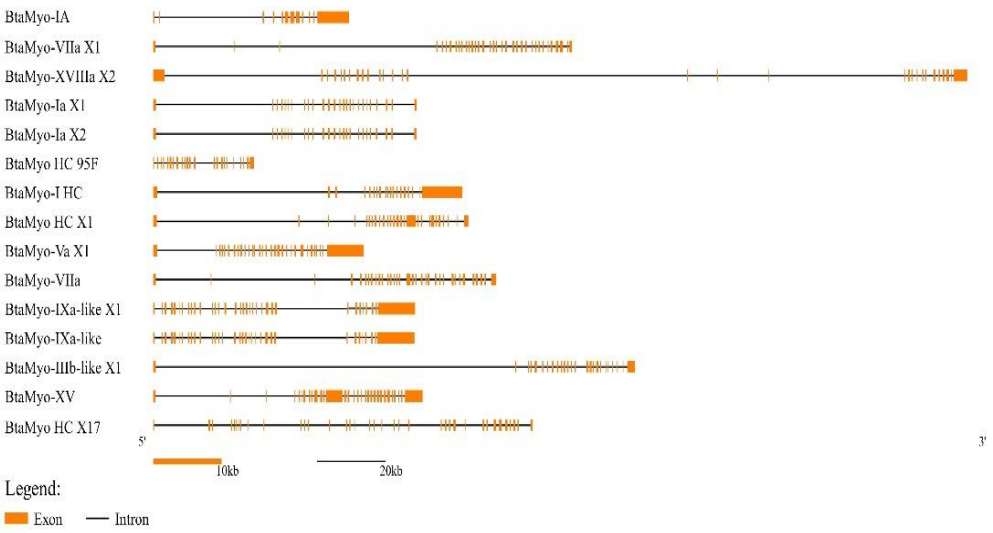

Figure 3. Structures of the myosin genes in *B. tabaci* MEAM1. Exons and introns are indicated by orange boxes and black lines, respectively.

3.2. Phylogenetic analysis

To further classify the 15 putative myosin genes in *B. tabaci*, phylogenetic analysis was performed. Deduce amino acid sequence of myosin genes in *B. tabaci* and five other species (*D. melanogaster*, *D. plexippus*, *T. castaneum*, *H. sapiens*, *C. elegans*) were aligned and analyzed. Protein sequences were the subjected to phylogenetic analysis using the neighbor-joining (NJ) method with MEGA 7 software (Figure 4). These myosin genes from six species were clustered into ten subfamilies. However, there are significant differences between species (Table 2), such as myosin

genes in *H. sapiens* and *B. tabaci* comprise more than eight subfamilies, while *C. elegans* only has six subfamilies. The number of subfamilies in *D. plexippus* and *D. melanogaster* is the same. It is interesting that Class XX is only found in four insect species, which may be related to species-specific evolution and environment

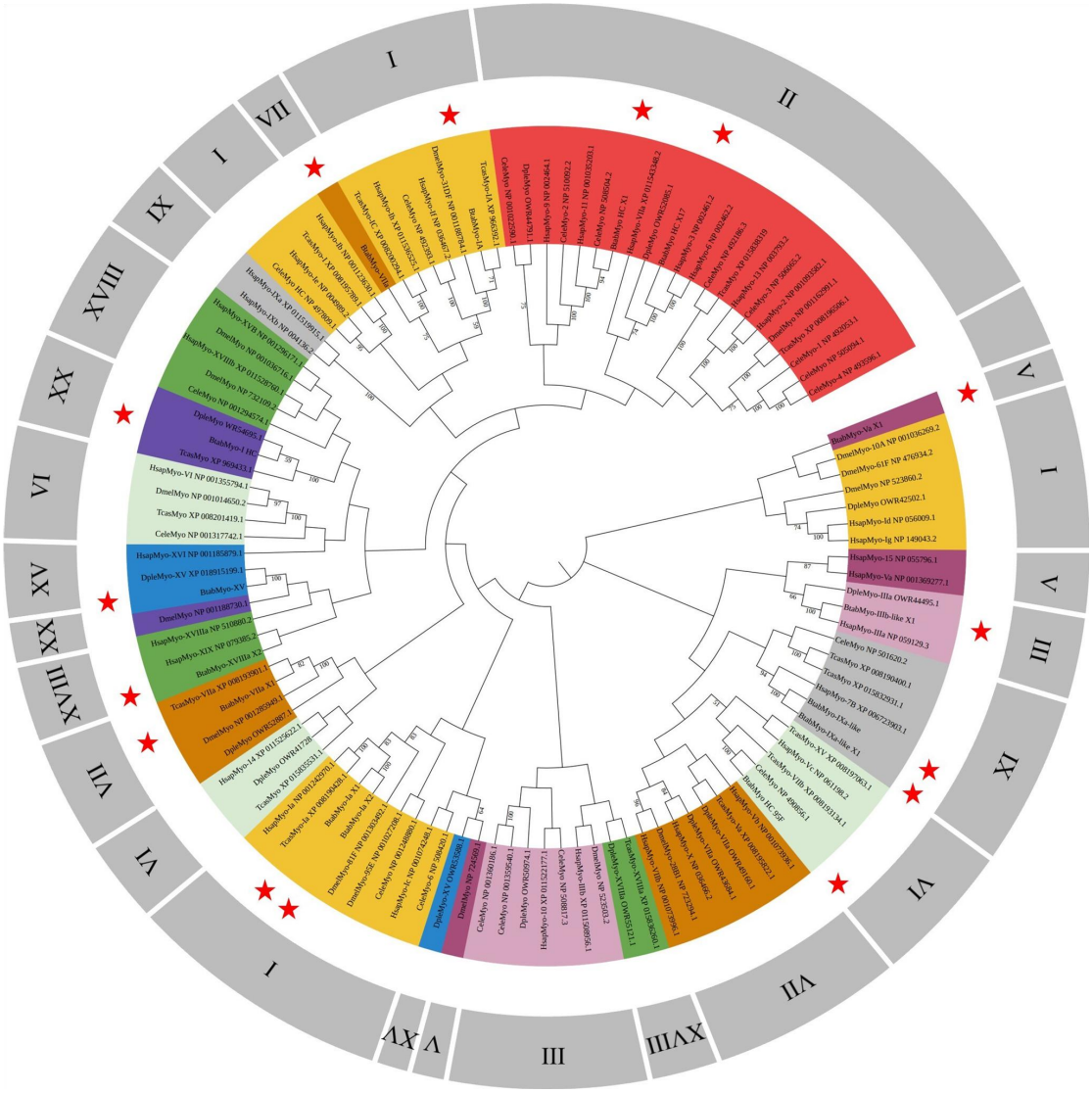

Figure 4. Phylogenetic analysis of the myosin gene family in *B. tabaci* MEAM1 and other species. The phylogenetic tree was constructed with the neighbor-joining method in MEGA 7.0. Numbers at the nodes are bootstrap values of 1000 replicates. *Btab* = *Bemisia tabaci*, *Dmel* = *Drosophila melanogaster*, *Dple* = *Danaus plexippus*, *Tcas* = *Tribolium castaneum*, *Hsap* = *Homo sapiens*, *Cele* = *Caenorhabditis elegans*.

Classification of the myosins is based on the phylogenetic relationship of the motor domains of the myosins [30,31]. myosin class present in separate clades has also been reported in several other papers [32]. In the phylogenetic tree of *B. tabaci* MEAM1 myosin genes, Class I contains three genes and accounting for 20% of all *B. tabaci* MEAM1 myosin members; Class II, Class VII and Class IX each contains two myosin genes in each group whereas six classes (III, V, VI, XV, XVIII

and XX) only have one. This showed these subfamily (Class I, Class II, Class VII, Class IX) have expanded more than the other isoform during the evolution of the myosin superfamily in *B. tabaci* MEAM1.

3.3. Spatial and temporal expression profile of the myosin genes in B. tabaci MEAM1

To further study the expression profile of myosin genes in *B. tabaci* MEAM1, quantitative real-time PCR was conducted for these 15 myosin genes. We performed RT-qPCR from egg to adult periods in *B. tabaci* MEAM1 to investigate the temporal expression profile of myosin genes in all life stages (Figure 5). *BtaMyo-IIIb-like X1* exhibit high expression level in the nymphs 4 instar stages. *BtaMyo-VIIa*, *BtaMyo-VIIa X1*, *BtaMyo-Ia X1*, *BtaMyo-IA*, *BtaMyo-Va X1*, *BtaMyo-XVIIIa X2*, *BtaMyo-IXa-like X1*, *BtaMyo-Ia X2* were not expressed or expressed low during nymph stages, indicating that they might not be associated with metamophosis in *B. tabaci* MEAM1. Interestingly, most myosin genes (*BtaMyo-XV*, *BtaMyo-VIIa*, *BtaMyo-VIIa X1*, *BtaMyo-XVIIIa X2*, *BtaMyo-IXa-like X1*, *BtaMyo HC X17*, *BtaMyo-IXa-like*, *BtaMyo-Va X1*, *BtaMyo-IIIb-like X1*, *BtaMyo HC 95F*, *BtaMyo-I HC*, *BtaMyo-Ia X1*, *BtaMyo-Ia X2*, *BtaMyo-IA*) had different expression level between female and male whiteflies.

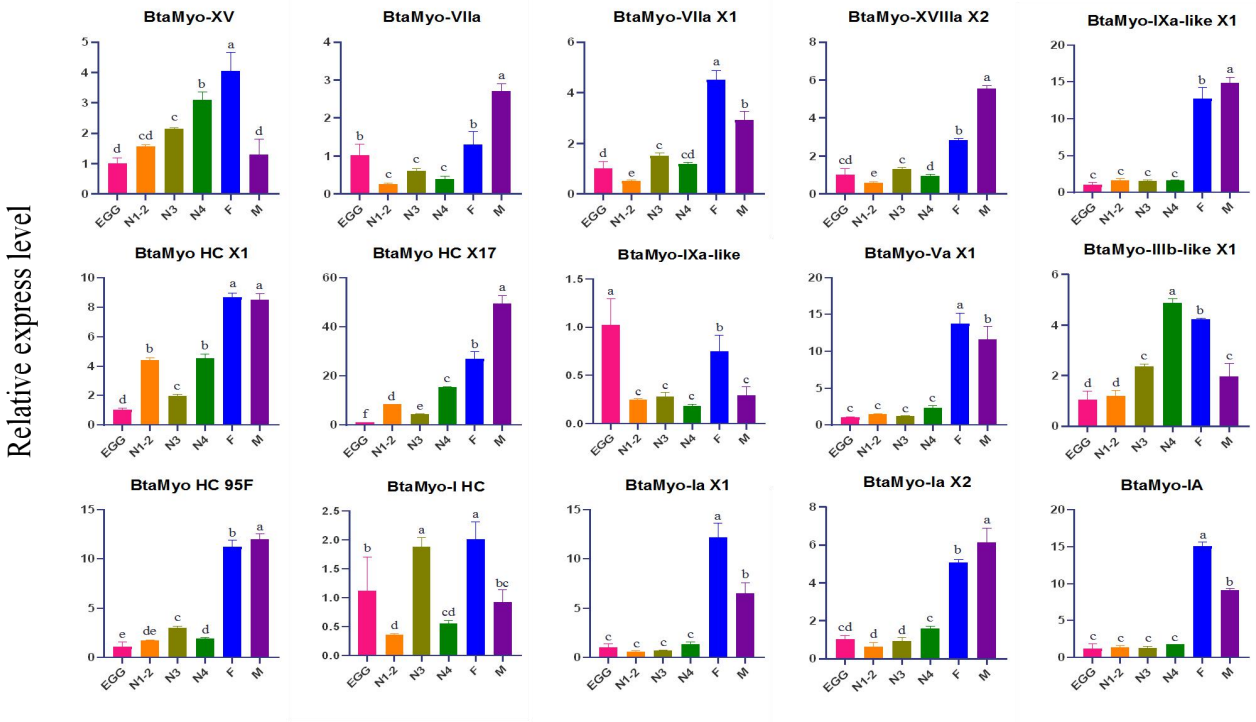

Figure 5. Temporal expression profiling of myosin genes during *B. tabaci* MEAM1. The expression of 15 myosin genes in different stages of *B. tabaci* MEAM1 as determined by qPCR analysis. E, egg; N1-2, 1st and 2nd instar nymphs; N3, 3rd instar nymphs; N4, 4th instar nymphs; F, female; M, male. RT-qPCR results were analyzed by the 2-ΔΔCt method. Values are means with standard deviation (n=3). Bars annotated with same letters are not significantly different, $P < 0.05$.

Our investigation also found that Myosin genes were specially expressed in various tissues

(Figure 6). The seven genes (*BtaMyo HC X17*, *BtaMyo-IIIb-like X1*, *BtaMyo HC 95F*, *BtaMyo-I HC*, *BtaMyo-Ia X1*, *BtaMyo-Ia X2*, *BtaMyo-IA*) were with low expression level in head, whereas the remaining eight myosin genes were highly expressed in head. The high expression level of *BtaMyo HC X17* was found in thorax. The results also showed that the seven myosin genes (*BtaMyo-Va X1*, *BtaMyo-IIIb-like X1*, *BtaMyo HC 95F*, *BtaMyo-I HC*, *BtaMyo-Ia X1*, *BtaMyo-Ia X2*, *BtaMyo-IA*) were highly expressed in abdomen of *B. tabaci* MEAM1 than in the head and thorax, and the other eight genes showed low level of expression in abdomen.

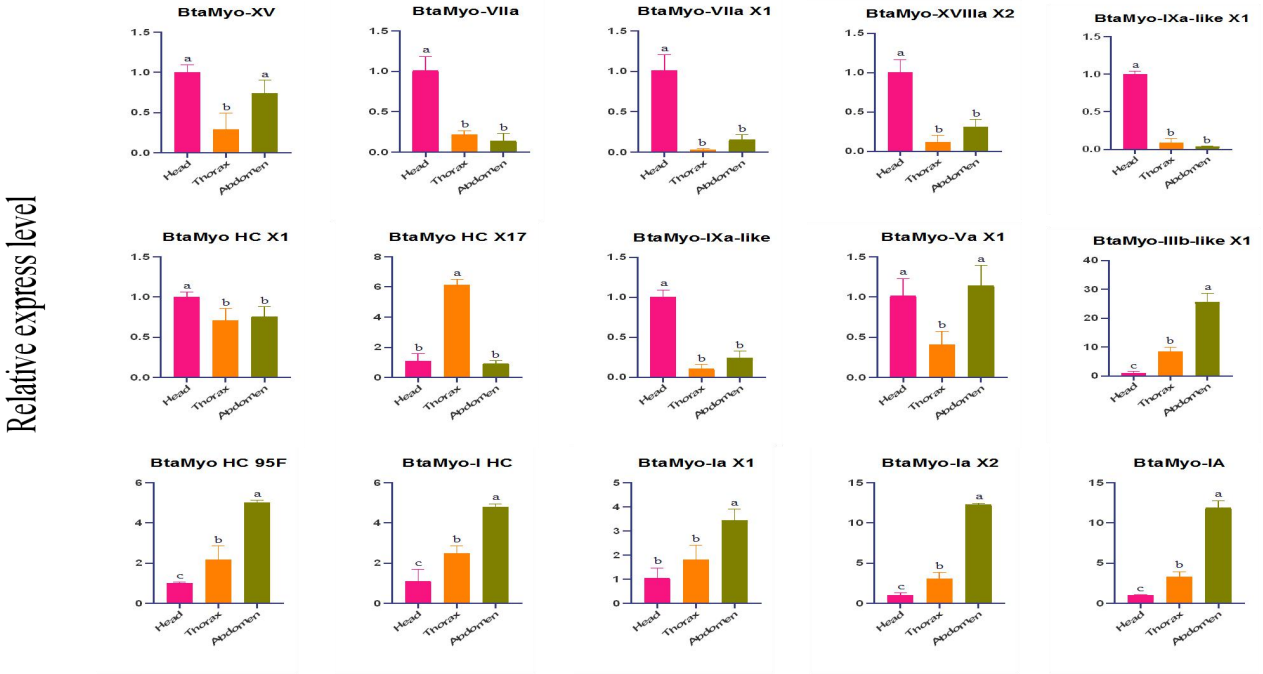

Figure 6. Spatial expression profiles of myosin genes in *B. tabaci* MEAM1. The expression of 15 myosin genes in different body segments of *B. tabaci* MEAM1 as determined by qPCR analysis, including the head, thorax, and abdomen. RT-qPCR results were analyzed by the 2-ΔΔCt method. Values are means with standard deviation (n=3). Bars annotated with same letters are not significantly different, $P < 0.05$.

4. Discussion

Bemisia tabaci is a one of most major crop pest in worldwide [33]. It causes extensive damage by direct feeding or transmitting plant virus ways [34]. Because *B. tabaci* MEAM1 is the most widely distributed population, a comprehensive understanding of *B. tabaci* MEAM1 myosin genes will contribute to study physiology features. In this study, we identified and analyzed the putative myosin gene superfamily in *B. tabaci* MEAM1. A total of 15 putative myosin genes were identified in the *B. tabaci* MEAM1 genome by bioinformatics analysis. This number was similar to the myosin genes in other insect species [35]. The expression profiling of myosin genes in diverse development stages and different body segments was showed by RT-qPCR.

The myosin motor powers diverse cellular functions, including cytokinesis, membrane trafficking, organelle movements, and cellular migration. Myosin is a major structural protein in skeletal muscle, which is essential for muscle contraction [36,37]. It is a multimeric protein including one or two heavy chain and variable number of light chains. There are more than 40 known classes

of myosin gene in human, but *B. tabaci* MEAM1 myosin genes only have ten classes of them. We found that *B. tabaci* MEAM1 had a larger Class I subfamily in all myosin genes. The Class I are monomeric motor protein which is different to Class II in structural [38]. Previous studies have showed Class I isoform have multiple function including cell endocytosis, cell exocytosis, cell shape and membrane elasticity [39]. The Class I is required for over-lapping function in various cellular processes and cell elasticity [40,41]. Mutations in the *D. melanogaster* myosin I homologue cause situs inversus in the abdomen. The knock down of TbMyosin 1 in Trypanosoma brucei decreases in endocytic activity and cessation in cell division, finally causing cell death [42]. In B cells, myo1g is a main regulator in different membrane and cytoskeleton-dependent processes. When myo1g was deficient, the adhesion ability and chemokine-induced directed migration of lymphocytes occurred abnormalities [43]. The Class II genes are an essential role in the synaptic vesicle mobility at the neuromuscular junction, junctional contraction, cell migration, cell adhesion, cytokinesis in eukaryotes [44–48]. Whether the expansion of the myosin genes in *B. tabaci* MEAM1 is related to its development characteristics for some of these genes needs to be further investigated.

Gene expression profiling characterization provides important information for understanding biological function [49]. The expression profile of the myosin genes at different development stages of *B. tabaci* MEAM1 showed that myosin genes might be involved in many processes of growth and development. We detected highly expression of most myosin genes in adult stages of whiteflies. The expression levels of myosin gene differ between males and females throughout development, suggesting that they could be considered within the sexed-biased genes. The *BtaMyo-IIIb-like X1* of Class III was highly expression in 4th instar nymphs, indicating it may be related to the developmental process before metamorphosis. Myosin III was found to bind espin 1, suggesting that it plays a role in transporting espin 1 [50]. However, the molecular function of Class III myosin genes in *B. tabaci* MEAM1 are still unknown. Thus, the function analysis of Class III myosin genes in *B. tabaci* MEAM1 requires further study. The *BtaMyo-IXa-like* gene, which belongs to the Class IX isoform, was expressed at low level in the adult stage but highly expressed in the egg stage. We speculate that this gene may be involved in early developmental process in *B. tabaci* MEAM1.

Among all the myosin genes, the Class II and Class V have been best characterized in neurons and are related in a wide range of cellular functions in the nervous system, including neuronal morphogenesis, synaptic and sensory function, neuronal migration, growth cone motility, neuronal morphogenesis in *D. melanogaster* [51]. The spatial expression profile showed that *Btamyo HC X1* and *BtaMyo-Va X1* exhibited highly expression in the head, and we speculate that it has a potential function in *B. tabaci* MEAM1 sensory systems. Non-muscle myosin II plays a part in regulating the mechanical properties of the peripheral epithelium [52]. Therefore, it can help withdraw from the wing imaginal disc columnar tissue. Moreover, myosin light chain-2 was related to wing bear frequency, indirect flight muscle contraction kinetics, flight in *Drosophila* [53]. In *H. sapiens*, A previous study have suggested that the myosin genes are critical for hearing function, and the mutation of the unconventional myosin XVa protein and other unconventional myosin VI protein leads to hearing impairment [54]. The mutations of the myosin IIIA genes in *D. melanogaster* cause the progressive hearing loss [55]. *BtaMyo-HC 95F* of Class VI was highly expressed in the abdomen of *B. tabaci* MEAM1, which may participate in egg chamber morphogenesis and sperm individualization process. Such as in *Bactrocera dorsalis*, myosin VI is necessary for follicle cell epithelial development. The deficiency of myosin VI causes defects in sperm individualisation in D. melanogaster [56]. Further study is needed to verify the myosin genes and their exact function in

diverse aspects in *B. tabaci* MEAM1.

Most studies have suggested that the myosin gene has an important role in virus movement [57,58]. In this study, we provide an overview of genome sequence features of myosin genes in *B. tabaci* MEAM1. Further work includes identifying how different classes of myosin genes interact with the virus proteins and influence virus transmission.

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Conflict of interest

The authors declare no competing or financial interests.

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