Manual curation and phylogenetic analysis of chitinase family genes in the Asian citrus psyllid, *Diaphorina citri*

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Abstract

Chitinases are enzymes that digest the polysaccharide polymer chitin. Chitin is a major component of insect exoskeletons, which must be replaced multiple times during growth and development in a process known as molting. Insect genomes usually have multiple chitinase genes, some of which are required for molting and some whose functions are still unknown.

Since knockdown of the chitinases required for molting causes high levels of lethality, chitinase genes have drawn interest as targets for RNAi-based pest control methods. The Asian citrus psyllid, *Diaphorina citri*, carries the bacterium that causes Huanglongbing, also known as citrus greening disease, which is devastating the citrus industry worldwide. We have identified and annotated 12 chitinase family genes from *D. citri* as part of a community effort to create high quality gene models to facilitate the design of interdictory molecules for pest control. Using predicted protein domain content and phylogenetic analysis, we categorized the *D. citri* chitinases according to a previously established classification scheme and re-evaluated the classification of chitinases in other hemipterans. In addition to chitinases belonging to known groups, we identified a novel class of chitinases present in *D. citri* and several related hemipterans that appears to be the result of horizontal gene transfer.

Main Content

Data description

Background

During insect growth and development, the exoskeleton must be repeatedly shed and replaced. As part of this process, chitin, a polysaccharide polymer that is an important structural component of the cuticle, must be degraded [1]. Chitinases are enzymes that hydrolyze chitin into chitooligosaccharides that can then be recycled to synthesize new chitin molecules [1,2]. Restricting the degradation of chitin by inhibiting chitinases often results in lethality caused by molting defects (reviewed in [3]). Insect genomes usually contain 10-30 chitinase genes, with holometabolous insects generally having more than hemimetabolous insects [4]. These genes

are often expressed in different stages and tissues, suggesting that they may play distinct roles during the life of the insect [2]. The various chitinase genes also encode proteins with different structures, particularly with regard to the number of glycoside hydrolase 18 catalytic domains and chitin-binding domains (CBD). The most recent chitinase classification system, based on phylogenetic analysis and domain conservation of proteins from twenty species, divides chitinases into ten groups (I-X) [5]. Most of these groups appear to be quite ancient, with all but groups V and X being present in the ancestor of insects and crustaceans. This classification system has recently been applied to the chitinases of two hemipteran insects [6,7]. These studies concluded that almost all the chitinase groups are represented in at least some hemipterans. However, the Group IX chitinase seems to have been lost from the hemipteran lineage. Several hemipteran chitinase genes that could not be definitively classified have been tentatively assigned to Group IV.

Context

We are part of a community that is manually curating genes from the genome of the Asian citrus psyllid, *Diaphorina citri* (Hemiptera: Liviidae; NCBI:txid121845), the vector of *Candidatus* Liberibacter asiaticus (*C*Las), the bacterium that causes Huanglongbing (citrus greening disease) [8,9]. The primary goal of this project is to create high-quality gene models of potential targets for gene-based pest control. The essential role of some chitinases during insect development makes them promising pest control targets. Several putative chitinase genes have previously been reported in *D. citri*, but these have not been manually curated [10]. Here we report the annotation of the chitinase gene family in *D. citri*. We identified and annotated 11 chitinase

genes plus a gene encoding the related enzyme endo-beta-N-acetylglucosaminidase. We used phylogenetic and domain analyses to classify the chitinases according to the ten group system established by Tetreau et al. [5]. Our results indicate that *D. citri* has a similar complement of chitinase genes to other hemipterans, but also has an unusual chitinase that seems to have arisen from a horizontal transfer event. Our phylogenetic analysis indicates that several hemipteran chitinases previously assigned to Group IV are orthologous to this gene and should be reclassified.

Methods

D. citri chitinase genes were identified by BLAST analysis of *D. citri* sequences available on the Citrus Greening website [11] using orthologs from other insects as the query. To confirm orthology, we performed reciprocal BLASTs of the National Center for Biotechnology Information (NCBI) non-redundant protein database [12]. Genes were manually annotated in the *D. citri* v3 genome in Apollo (Apollo, RRID:SCR_001936; v2.1.0) using available evidence. A complete annotation workflow is available on protocols. io (Figure 1) [13].

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Annotating genes in Diaphorina citri genome version 3

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Figure 1: Protocol for *D.citri* genome community curation. [13]

Protein domains were identified using BLAST and InterPro (InterPro, RRID:SCR_006695) [14].

Phylogenetic analysis was performed with MEGA X (MEGA software, RRID:SCR_000667) [15]. Sequences were aligned with CLUSTALW (RRID:SCR_002909) [16] and trees were constructed by the neighbor-joining method with 1000 bootstrap replicates. Accession numbers for orthologs used in phylogenetic analysis are shown in Table 1. Counts for gene expression were obtained from the Citrus Greening Expression Network (CGEN) [17] and visualized using pheatmap (pheatmap, RRID:SCR_016418) [18] in R (R Project for Statistical Computing, RRID:SCR_001905) [19].

Table 1. Accession numbers of proteins used in phylogenetic analysis

Name in Tree	Order	Species	Accession
TcCht1	Coleoptera	*Tribolium castaneum*	XP_971647.1
TcCht2	Coleoptera	*Tribolium castaneum*	XP_970191.2
TcCht3	Coleoptera	*Tribolium castaneum*	EFA08056.1
TcCht4	Coleoptera	*Tribolium castaneum*	NP_001073567.1
TcCht5	Coleoptera	*Tribolium castaneum*	NP_001034524.1
TcCht6	Coleoptera	*Tribolium castaneum*	XP_967813.1
TcCht7	Coleoptera	*Tribolium castaneum*	NP_001036035.1
TcCht8	Coleoptera	*Tribolium castaneum*	NP_001038094.1
TcCht9	Coleoptera	*Tribolium castaneum*	NP_001038096.1
TcCht10	Coleoptera	*Tribolium castaneum*	NP_001036067.1
TcCht11	Coleoptera	*Tribolium castaneum*	NP_001038095.1
TcCht12	Coleoptera	*Tribolium castaneum*	XP_972802.2
TcCht13	Coleoptera	*Tribolium castaneum*	NP_001036034.1
TcCht14	Coleoptera	*Tribolium castaneum*	XP_973005.1
TcCht15	Coleoptera	*Tribolium castaneum*	XP_973077.1
TcCht16	Coleoptera	*Tribolium castaneum*	NP_001034515.1
TcCht17	Coleoptera	*Tribolium castaneum*	XP_972719.1
TcCht18	Coleoptera	*Tribolium castaneum*	XP_973161.2
TcCht19	Coleoptera	*Tribolium castaneum*	XP_973119.2
TcCht20	Coleoptera	*Tribolium castaneum*	NP_001034516.3
TcCht21	Coleoptera	*Tribolium castaneum*	NP_001034517.1
TcIDGF2	Coleoptera	*Tribolium castaneum*	NP_001038092.1
TcIDGF4	Coleoptera	*Tribolium castaneum*	NP_001038091.1
TcENGase	Coleoptera	*Tribolium castaneum*	EFA09314.2
DmCht1	Diptera	*Drosophila melanogaster*	NP_609190.2
DmCht10	Diptera	*Drosophila melanogaster*	EAA46011.1

DmCht11	Diptera	*Drosophila melanogaster*	NP_572361.1
DmCht12	Diptera	*Drosophila melanogaster*	NP_726022.1
DmCht2	Diptera	*Drosophila melanogaster*	NP_477298.2
DmCht4	Diptera	*Drosophila melanogaster*	NP_524962.2
DmCht5	Diptera	*Drosophila melanogaster*	NP_650314.1
DmCht6	Diptera	*Drosophila melanogaster*	NP_572598.3
DmCht7	Diptera	*Drosophila melanogaster*	NP_647768.3
DmCht8	Diptera	*Drosophila melanogaster*	NP_611542.2
DmCht9	Diptera	*Drosophila melanogaster*	NP_611543.3
DmIDGF1	Diptera	*Drosophila melanogaster*	NP_477258.1
DmIDGF2	Diptera	*Drosophila melanogaster*	NP_477257.2
DmIDGF3	Diptera	*Drosophila melanogaster*	NP_723967.1
DmIDGF4	Diptera	*Drosophila melanogaster*	NP_727374.1
DmIDGF5	Diptera	*Drosophila melanogaster*	NP_611321.3
DmIDGF6	Diptera	*Drosophila melanogaster*	NP_477081.1
DcCht5	Hemiptera	*Diaphorina* citri	Dcitr06g10380.1.1
DcCht7	Hemiptera	*Diaphorina* citri	Dcitr07g07740.1.1
DcIDGF1	Hemiptera	*Diaphorina* citri	Dcitr02g06220.1.1
DcIDGF2	Hemiptera	*Diaphorina* citri	Dcitr02g06220.1.1
DcIDGF3	Hemiptera	*Diaphorina* citri	Dcitr02g06590.1.1
DcCht6	Hemiptera	*Diaphorina* citri	Dcitr10g04150.1.1
DcCht11	Hemiptera	*Diaphorina* citri	Dcitr01g03820.1.1
DcCht3	Hemiptera	*Diaphorina* citri	Dcitr07g08380.1.1
DcENGase	Hemiptera	*Diaphorina* citri	Dcitr01g14510.1.1
DcChtPE	Hemiptera	*Diaphorina* citri	Dcitr11g03190.1.1
DcCht10-1	Hemiptera	*Diaphorina* citri	Dcitr02g11110.1.1
DcCht10-2	Hemiptera	*Diaphorina* citri	Dcitr12g04430.1.1
ApCht1	Hemiptera	*Acyrthosiphon pisum*	NP_001162142.1
ApCht2	Hemiptera	*Acyrthosiphon pisum*	XP_001943038.2
ApCht3	Hemiptera	*Acyrthosiphon pisum*	XP_029343203.1
ApCht4	Hemiptera	*Acyrthosiphon pisum*	XP_001950380.1
ApCht5	Hemiptera	*Acyrthosiphon pisum*	XP_008181779.1
ApCht6	Hemiptera	*Acyrthosiphon pisum*	XP_008182857.1
ApCht7	Hemiptera	*Acyrthosiphon pisum*	XP_008183766.1
ApCht8	Hemiptera	*Acyrthosiphon pisum*	XP_001945470.2
ApENGase	Hemiptera	*Acyrthosiphon pisum*	XP_016658011.1
NlCht1(partial)	Hemiptera	*Nilaparvata lugens*	AJO25036.1
NlCht2	Hemiptera	*Nilaparvata lugens*	AJO25037.1
NlCht3	Hemiptera	*Nilaparvata lugens*	AJO25038.1
NlCht4	Hemiptera	*Nilaparvata lugens*	AJO25039.1
NlCht5	Hemiptera	*Nilaparvata lugens*	AJO25040.1
NlCht6	Hemiptera	*Nilaparvata lugens*	AJO25041.1

NlCht7	Hemiptera	*Nilaparvata lugens*	AJO25042.1
NlCht8	Hemiptera	*Nilaparvata lugens*	AJO25043.1
NlCht10	Hemiptera	*Nilaparvata lugens*	AJO25045.1
NlIDGF	Hemiptera	*Nilaparvata lugens*	AJO25056.1
NlENGase	Hemiptera	*Nilaparvata lugens*	AJO25057.1
BtCht2	Hemiptera	*Bemisia tabaci*	MW699018*
BtCht3	Hemiptera	*Bemisia tabaci*	MW699019*
BtCht4	Hemiptera	*Bemisia tabaci*	MW699020*
BtCht5	Hemiptera	*Bemisia tabaci*	MW699021*
BtCht6	Hemiptera	*Bemisia tabaci*	MW699022*
BtCht7	Hemiptera	*Bemisia tabaci*	MW699023*
BtCht8	Hemiptera	*Bemisia tabaci*	MW699024*
BtCht9	Hemiptera	*Bemisia tabaci*	MW699025*
BtCht10	Hemiptera	*Bemisia tabaci*	MW699026*
BtCht11	Hemiptera	*Bemisia tabaci*	XP_018912124.1
BtIDGF1	Hemiptera	*Bemisia tabaci*	MW699027*
BtIDGF2	Hemiptera	*Bemisia tabaci*	MW699028*
BtIDGF3	Hemiptera	*Bemisia tabaci*	MW699029*
BtENGase	Hemiptera	*Bemisia tabaci*	MW699030*
TuXP015788124.1	Trombidiformes	*Tetranychus urticae*	XP_015788124.1
SfXP025409901.1	Hemiptera	*Sipha flava*	XP_025409901.1
DnXP015372246.1	Hemiptera	*Diuraphis noxia*	XP_015372246.1
MpXP022167894.1	Hemiptera	*Myzus persicae*	XP_022167894.1
ArCAF1372083.1	Bdelloida	*Adineta ricciae*	CAF1372083.1
BcXP037026665.1	Diptera	*Bradysia coprophila*	XP_037026665.1
CnXP031616960.1	Diptera	*Contarinia nasturtii*	XP_031616960.1
AcCht-h	Lepidoptera	*Agrius convolvuli*	BAE16588.1
BmCht-h	Lepidoptera	*Bombyx mori*	XP_037867787.1
DpCht-h	Lepidoptera	*Danaus plexippus plexippus*	XP_032522474.1
PxCht-h	Lepidoptera	*Papilio xuthus*	KPJ01281.1
SlCht-h	Lepidoptera	*Spodoptera litura*	XP_022815620.1
OfCht-h	Lepidoptera	*Ostrinia furnacalis*	XP_028158980.1

Ortholog names used in the phylogenetic tree (Figure 3), taxonomic order, species name and accession number are shown. * indicates that the GenBank entry is not yet public.

Data validation and quality control

We identified and annotated chitinase genes in the chromosome-level *D. citri* v3 genome (Table 2). BLAST analysis, domain content and phylogenetic analysis were used to determine the

orthology of annotated genes. We followed the established convention for naming chitinase genes, using the same name as the *Drosophila melanogaster* ortholog whenever possible [20].

Table 2. Manually Annotated Chitinase Family Genes from *D. citri*.

Group	**Gene/Isoform**	**OGSv3 ID**	**Evidence supporting annotation**			
			MCOT	**IsoSeq**	**RNASeq**	**Ortholog**
I	*Chitinase 5*	Dcitr06g10380.1.1	MCOT12176.1.CO	X	X	X
II	*Chitinase 10-1*	Dcitr02g11110.1.1	MCOT12469.0.CO		X	X
II	*Chitinase 10-2*	Dcitr12g04430.1.1	MCOT05985.1.CT			X
III	*Chitinase 7*	Dcitr07g07740.1.1	MCOT01854.1.CT	X	X	X
V	*Imaginal disc growth factor 1*	Dcitr02g06220.1.1		X	X	X
V	*Imaginal disc growth factor 2*	Dcitr02g06210.1.1	MCOT17201.0.CT		X	X
V	*Imaginal disc growth factor 3*	Dcitr02g06590.1.1		X	X	X
VI	*Chitinase 6*	Dcitr10g04150.1.1 Dcitr10g04150.1.2	MCOT02473.0.CO	X		X
VIII	*Chitinase 11*	Dcitr01g03820.1.1		X	X	X
X	*Chitinase 3*	Dcitr07g08380.1.1	MCOT14388.2.CO		X	X
ENGase	*endo-beta-N-acetylglucosaminidase*	Dcitr01g14510.1.1	MCOT20578.0.CT		X	X
ChtPE		Dcitr11g03190.1.1	MCOT00573.0.CT		X	X

The chitinase group, OGSv3 gene identifier and evidence types used during the annotation process are listed for each gene. MCOT identification numbers denote models from the Maker, Cufflinks, Oases and Trinity transcriptome [8].

Group I Chitinases

Group I chitinases contain one catalytic domain and one C-terminal CBD (Figure 2) [2]. Most insects have a single Group I chitinase (Table 3), which is typically named Chitinase 5 (Cht5). However, multiple Group I chitinase genes have been found in mosquitoes [21], as well as in several hemimetabolous insects [4,7,22,23]. Within the Hemiptera, *Acyrthosiphon pisum* and *Bemisia tabaci* have been found to have one *Cht5* ortholog while *Nilaparvata lugens* and *Sogatella furcifera* have two [4,6,7,23]. We identified only one *Cht5* gene in the *D. citri* genome (Tables 2 and 3, Figure 3). As expected, it encodes a protein with one catalytic domain and one CBD.

Table 3. Estimated number of chitinase genes in various insect species

Species	Chitinase Groups												
	I	II	III	IV	V	VI	VII	VIII	IX	X	ENGase	ChtPE	Tot
D. melanogaster	1	1	1	4	6	1	1	1	1	0	1	0	1
A. gambiae	5	1	1	8	2	1	1	1	1	0	1	0	2
T. castaneum	1	1	1	14	2	1	1	1	1	1	1	0	2
S. furcifera	2	1	1	0	2	1	1	1	0	1	1	0	1
N. lugens	2	2	1	0	2	1	1	1	0	1	1	0	1
B. tabaci	1	2	1	0	3	1	1	1	0	1	1	2	1
A. pisum	1	1	1	0	1	1	0	1	0	1	1	1	
D. citri	1	2	1	0	3	1	0	1	0	1	1	1	1

Chitinase groups are based on the classification system established by Tetreau et al [5], with the exception of ChtPE which is described in this work. *D. citri* gene numbers were determined based on our annotation of the *D. citri* v3 genome. Counts in other insects are based on the literature [4,6,7,21,23] and our phylogenetic analysis.

Group II Chitinases

Group II chitinases are typically named Chitinase 10 (Cht10) in insects [2]. These chitinases are high molecular weight chitinases that have multiple catalytic domains (some active and some

inactive) and several CBDs [2]. Most previously studied insects have only one *Cht10* gene (Table 3), although two were found in *N. lugens* (*NlCht10* and *NlCht1*) [23]. Two of the chitinases we annotated in *D. citri* cluster with the Cht10 proteins during phylogenetic analysis. One of these, Cht10-1, is a typical Cht10 protein. It is a large, 21-exon gene that encodes a protein containing five catalytic domains and two CBDs. The second protein identified as a potential Cht10 in *D. citri* is much smaller and only contains a catalytic domain. Despite the difference in size and domain content, phylogenetic analysis indicates this protein is most closely related to the Cht10 proteins, so we have named it Cht10-2. (Figure 3). Interestingly, the *B. tabaci* Cht4 protein, which had been tentatively placed in group IV [6], also has only a catalytic domain and clusters with the group II chitinases in our tree. Thus, we suggest that it be reassigned to group II (Table 3).

Group III Chitinases

The group III chitinases are typically named Chitinase 7 (Cht7) in insects [2]. Most insects have one Cht7 that contains an N-terminal transmembrane domain plus two catalytic domains followed by a CBD (Figure 2) [20]. In *D. citri* we identified one *Cht7* gene (Tables 2 and 3). As expected, the predicted protein contained two catalytic domains followed by one CBD (Figure 2). Like the *A. pisum* and *S. furcifera* group III chitinases, DcCht7 has an N-terminal signal peptide [4,7], suggesting that at least some hemipteran group III chitinases may be secreted and thus function differently than their orthologs in holometabolous insects that have an N-terminal transmembrane domain.

Group IV Chitinases

In holometabolous insects, group IV is the largest and most diverse group of chitinases [2]. These chitinases have the greatest variation in domain organization and are found in clusters in some insect genomes, suggesting duplication events. In hemimetabolous insects, group IV has previously been used as a catch-all group for chitinases that could not be clearly assigned to any group [6,23]. However, several of the hemipteran chitinases previously assigned to group IV have been reclassified recently as group X chitinases [6]. Moreover, in our phylogenetic analysis (Figure 3), no *D. citri* chitinases clustered with group IV and the other hemipteran chitinases that had previously been placed in group IV (*B. tabaci* Cht8 and Cht9) were part of a novel cluster discussed in more detail below. These observations suggest that hemipterans lack group IV chitinases.

Group V Chitinases

The group V Chitinases were first identified for their role in the growth of imaginal disc tissue in *Drosophila* and were named Imaginal disc growth factors (Idgf) [2,24]. *D. melanogaster* has six *Idgf* genes, but most insects have fewer (Table 3). Phylogenetic analysis suggests that independent duplications of *Idgf* genes have happened several times in insect lineages [4]. In *D. citri* we identified three *Idgf* genes (Tables 2 and 3), which we have named *Idgf1*, *Idgf2* and *Idgf3*. These genes are not one-to-one orthologs of the *Drosophila Idgf1*, *Idgf2* and *Idgf3* genes, as phylogenetic analysis suggests that *Idgf* genes have duplicated independently in these two insect lineages (Figure 3). All three *Idgf* genes in *D. citri* are located in a 1.25 Mb region of chromosome 2, with *Idgf1* and *Idgf2* adjacent to one another on the same strand. Idgf1 and

Idgf3 form their own clade in our phylogenetic tree, while Idgf2 is an outgroup to the other group V chitinases, suggesting it has diverged more extensively than the other two paralogs (Figure 3).

As seen in group V chitinases of other insects, all three *D. citri* Idgf proteins have only one catalytic domain and they do not contain a CBD (Figure 2). The catalytic domain of Idgf proteins is inactive due to a mutation that produces an aspartic acid to alanine substitution in conserved motif II [2,25]. This mutation is present in all three *D. citri Idgf* genes, confirming their identity.

Group VI Chitinases

In insects, the group VI chitinases are usually named Chitinase 6 (Cht6) [2]. In holometabolous insects, group VI chitinases have a similar domain structure to group I chitanases with an N-terminal catalytic domain and one CBD, but additionally have a long serine/threonine (S/T)-rich region at the C-terminus [2]. The hemipterans *N. lugens* and *A. pisum* each have a single group VI chitinase. These proteins differ from their holometabolous orthologs in that they have a second CBD near the C-terminus. [4,23]. In *D. citri*, we identified one *Cht6* gene that also encodes a protein with a second CBD (Figure 2). The *D. citri* Cht6 protein also contains a long stretch of amino acids between the CBDs which contains approximately 25% S/T residues, supporting its classification as a group VI chitinase. We identified two isoforms of Cht6 in *D. citri*, that differ only in the length of the S/T-rich region between the CBDs. Similar isoforms have been reported for *S. furcifera* Cht6 [7].

In contrast to the other chitinase groups, the group VI orthologs do not all cluster together in our phylogenetic tree (Figure 3). The hemipteran group VI proteins form one cluster, while the *T. castaneum* and *D. melanogaster* Cht6 orthologs are in a separate cluster with *N. lugens* Cht10, which has been classified in group I [23]. Moreover, *D. melanogaster* Cht8, considered a group IV member, is the closest outgroup to the hemipteran group VI proteins. These branches have low bootstrap values, however, so they may not represent the true relationships.

Group VII Chitinases

Group VII chitinases are typically named Chitinase 2 (Cht2) in insects [2]. Within hemipterans, the planthoppers *N. lugens* and *S. furcifera* have a group VII chitinase gene [7,23], but the sternorrhyncans *A. pisum* and *B. tabaci* do not (Table 3) [4,6]. Likewise, we did not find a group VII chitinase gene in the genome of *D. citri*, which is also a member of the Sternorrhynca. These results suggest that the group VII chitinase may have been lost after the divergence of the Sternorrhynca from other hemipterans.

Group VIII Chitinases

Group VIII chitinases are typically called Chitinase 11 (Cht11) in insects [2]. To our knowledge, all insects examined to date have only one group VIII chitinase gene. We too identified only one group VIII chitinase in the *D. citri* genome. Like several other group VIII chitinases, *D. citri* Cht11 has an N-terminal transmembrane domain and a catalytic domain, but no CBD [2,4].

Group IX Chitinases

Group IX chitinases appear to be an ancient group, since orthologs are found in organisms as distantly related to arthropods as sea urchins and nematodes [5]. However, no group IX chitinases have been found in hemipteran genomes thus far [4,6,7,23]. As expected, we were also unable to identify a group IX gene in *D. citri* (Table 3).

Group X Chitinases

Group X chitinases, most of which are named Cht3, were first recognized as a separate group by Tetreau et al [5]. Several members of this new group had previously been assigned to Group IV, although their membership in that group was always uncertain. Group X genes are found only in arthropods and seem to have been lost in the dipteran lineage [5]. The proteins encoded by Group X genes have a unique, highly conserved structure consisting of a single catalytic domain followed by two closely spaced CBDs, a long intervening region with many potential glycosylation sites and a third CBD near the C-terminus [5–7,23]. We identified and annotated one *Cht3* gene in *D. citri*. The encoded protein clusters with Group X members in our phylogenetic analysis (Figure 3) and shares the same domain structure (Figure 2).

ENGases

The endo-beta-N-acetylglucosaminidase (ENGase) proteins are part of the GH18 chitinase-like superfamily, and have therefore been included in recent phylogenetic analyses of chitinases [4,23]. Like the group V chitinases, these proteins lack chitinase activity because of a change in the catalytic domain. *ENGase* orthologs have been found across a wide variety of insects

including in hemipterans [4,6,7,23]. In the *D. citri* genome, we identified one *ENGase* ortholog (Tables 2 and 3).

Chitinase PE

D. citri has one chitinase gene that could not be classified based on the currently defined groups. In our tree, it clusters with *A. pisum* Cht7, which also has not been definitively classified [4] and *B. tabaci* Cht8 and Cht9, which had been tentatively included in Group IV [6].

The *A. pisum* and *D. citri* proteins have an unusual structure with an N-terminal signal peptide, a long N-terminal region where the only recognizable sequence is a PAN/Apple domain, a DNA/RNA non-specific endonuclease domain in the central portion of the protein, followed by the chitinase catalytic domain and multiple CBDs. We have named the *D. citri* gene *Chitinase PE* (*ChtPE*) to denote the presence of the PAN domain and endonuclease domain.

It had been previously noted that the three CBDs in *A. pisum* Cht7 are ChtBD1-type domains (typically found in plants and fungi) rather than the ChtBD2 type that is found in other insect chitinases [4]. We analyzed the domain structure of *D. citri* ChtPE and *B. tabaci* Cht8 and Cht9 and find that these proteins also have ChtBD1 domains, although the *D. citri* protein has only two.

BLAST analysis suggests that these novel chitinases have a very unusual phylogenetic distribution. Within the Hemiptera, they are present in several, but not all, of the sequenced

genomes from sternorrhyncans (aphids, psyllids and whiteflies). Orthologous genes encoding all the domains found in ChtPE are also found in a few other phylogenetically dispersed insects, as well as in several spider mites, springtails and rotifers.

The presence of plant/fungi-like CBDs and the limited phylogenetic distribution of the gene suggest that *ChtPE* may have arisen by horizontal gene transfer (HGT), although the source of the gene is not clear. There have been previous reports of HGT involving chitinases. Many lepidopterans have a *Cht-h* gene that seems to have been horizontally transferred from bacteria [5]. A separate instance of HGT of a bacterial chitinase has been reported in spider mites [26]. However, BLAST analysis, domain content and phylogenetic analysis show that these proteins are clearly distinct from ChtPE (Figure 3).

It is not clear how the odd phylogenetic distribution of *ChtPE*-like genes arose, since it would seem to require either horizontal transfer into multiple lineages or an ancient horizontal transfer followed by loss in most lineages. Neither scenario is particularly parsimonious. The presence of *ChtPE*-like genes in a number of sternorrhynchans, but very few other hemipterans suggests that there may have been a horizontal transfer event early in the sternorrhyncan lineage. However, it is not clear whether the *B. tabaci* genes *BtCht8* and *BtCht9* are really orthologous to *ChtPE*. *BtCht8* and *BtCht9* are unusual in that they are single exon genes [6], while the related *A. pisum* and *D. citri* genes have multiple exons. Moreover, the encoded *B. tabaci* proteins have the chitinase catalytic domain and the ChtBD1 domains, but lack the PAN/Apple and endonuclease domains. Regardless, of the number of HGT events, *A. pisum*

Cht7, BtCht8 and *BtCht9* belong with the HGT chitinases rather than in group IV where the *B. tabaci* proteins were previously placed [6].

Expression of Chitinase Genes in *D. citri*

We assessed expression of the chitinase genes in *D. citri* using the Citrus Greening Expression Network [17] found on the Citrus Greening website [11] (Figure 4, Table 4). This tool allows comparison of gene expression levels in a variety of publicly available *D. citri* RNA-seq datasets that vary by life stage, tissue, food source, and *C*Las exposure. In *D. citri*, *Cht5*, *Cht10-1*, and *Cht11* are expressed at highest levels in eggs with somewhat lower levels in nymphs, while *Cht3*, *Cht6*, and *Cht7* are most highly expressed in nymphs. The unusual group II gene *Cht10-2* is expressed at low to moderate levels in all stages and in most tissues. *IDGF2* expression is mostly restricted to eggs, while *IDGF1* and *IDGF3* are expressed at all stages but highest in adults. *ENGase* shows low levels of expression in all samples, with the highest expression in eggs and female abdomens. A few of the chitinases (*Cht5*, *Cht11*, *IDGF1* and *IDGF3*) show moderate expression in the gut. ChtPE is expressed in all stages and tissues, with the highest expression in head, thorax and midgut. These expression trends are consistent with reports from other hemipterans, particularly with respect to the stage showing the highest expression for each gene [4,6,7,23].

The generally conserved expression of the chitinase genes in hemipterans suggests that the genes may also have conserved functions. Based on expression data and RNAi studies in other insects, including several hemipterans [2,6,7,23], the *D. citri Cht5, Cht7 and Cht10* orthologs are

the most likely to be required for molting during development. Thus, these genes should be prioritized as potential targets for RNAi-based pest control. Knockdown of the other chitinase genes is likely to have only subtle effects, possibly because of redundancy, and understanding the function of these genes will require much more extensive analysis.

Table 4. Expression counts of *D. citri* chitinase genes

Gene ID	Cht5	Cht10-1	Cht10-2	Cht7	ChtPE	Idgf1	Idgf2	Idgf3	Cht6	Cht11	Cht3	ENG
Egg:C. macrophylla CLas-Whole body	80.44	17.67	5.15	181.38	6.15	185.72	110.96	461.11	22.37	108.89	17.17	15.8
Nymph:C. medica Clas+ Low infection Whole body	17	5.07	22.3	598.95	30.46	580.75	1.47	615.06	53.69	31.59	125.87	7.9
Nymph:C. sinensis Clas+ High infection Whole body	26.56	8.01	15.54	505.99	16.6	594.6	2.09	611.67	42.55	25.11	98.39	6.4
Nymph:C. sinensis Clas-Whole body	14.85	2.45	17.26	305.92	27.69	615.89	0.58	423.62	34.1	38.01	68.42	8.2
Nymph:C. macrophylla CLas-Whole body	12.88	4.14	53.68	471.04	33.3	356.48	1.19	350.74	19.36	51.44	135.21	4.1
Nymph	1.27	1.53	70.52	87.77	124.54	604.06	0.6	434.54	4.26	43.16	44.6	1.7

:Citrus spp. CLas- Whole body												
Nymph :Citrus spp. CLas+ Whole body	6.1	5.77	27.63	83.58	11	410.24	0.94	326.6	5	44.81	35.35	10.0
Adult:C. medica CLas- Gut	0.05	0.05	0.69	1.56	32.01	38.62	0	37.36	0	57.91	0.02	6.6
Adult:C. medica CLas+ Gut	0.07	0.03	1.25	0.57	39.99	30.13	0.03	37.35	0.02	72.09	0.03	6.4
Adult:C. medica CLas+ High infecti on Whole body	2.97	0.22	24.1	98.87	39.78	790.73	0.91	1123.6 4	6.69	38.29	20.34	8.6
Adult:C. medica CLas+ Low infecti on Whole body	2.98	0.28	33.97	104.33	30.33	735.91	1.16	846	6.79	40.08	19.07	11.8
Adult:C. medica CLas- Whole body	6.05	0.59	8.82	179.81	41.13	725.31	0.91	896.67	7.03	34.41	54.43	4.8
Adult:C. macro phylla CLas- Whole body	0.9	0.06	22.35	7.41	29.62	788.05	1.49	1098.3 2	1.34	49.79	2.32	13.0

Adult:Citrus spp. CLas- Whole body	0	0.09	11.7	2.99	88.19	533.99	1.42	368.82	0	42.11	0.86	6.8
Adult:Citrus spp. CLas+ Whole body	0	0.13	26.22	2.55	73.27	575.93	1.51	1055.86	0	44.96	0.51	9.0
Adult:Citrus spp. CLas- midgut	1.21	0.03	1.47	0.44	86.49	71.33	0	89.28	0.03	70.69	0.35	
Adult:Citrus spp. CLas+ midgut	0.53	0.03	2.27	4.83	140.65	186	0.08	116.46	0.1	40.18	1.46	10.0
Adult:C. reticulata CLas- Female abdomen	0.46	0.16	7.75	1.32	81.55	946.67	0.48	883.26	0.13	29.65	0.35	21.8
Adult:C. reticulata CLas- Female antennae	0	0	32.8	18.89	85.16	1723.19	0	1750.55	0.22	23.29	0.64	4.2
Adult:C. reticulata CLas- Female head	0.21	0	32.76	10.97	181.03	1662.39	0.18	1915.3	0.25	19.52	0.43	3.3
Adult:C. reticulata CLas- Female leg	0.02	0	8.5	2.73	69.41	1315.12	0	2022.88	0.18	20.17	0.27	12.8

Adult:C. reticulata CLas-Female terminal abdomen	0.64	0	89.66	6.12	47.48	609.54	0.16	1068.81	0	13.73	1.61	17.8
Adult:C. reticulata CLas-Female thorax	0	0	15.82	0.96	131.37	1221.78	0	1482.48	0.58	19.88	0.91	6.9
Adult:C. reticulata CLas-Male abdomen	0.48	0.09	5.75	2.3	75.05	1139.68	0.26	1490.21	0.1	37.33	1.02	6.3
Adult:C. reticulata CLas-Male antennae	0.33	0	14.25	37.15	55.26	1689.26	0.16	1918.4	0.52	30.12	1.69	2.7
Adult:C. reticulata CLas-Male head	0	0	31.07	9.79	136.84	1761.42	0	1936.55	0.31	28.17	0.76	3.1
Adult:C. reticulata CLas-Male leg	0	0	14.41	1.03	77.63	1994.31	0.5	2939.9	0.16	27.21	0.73	5.3
Adult:C. reticulata CLas-	1.83	0.02	13.6	8.5	24.59	823.39	0.37	1357.2	0.22	22.44	1.47	5.7

Male terminal abdomen												
Adult:C. reticulata CLas-Male thorax	0	0	12.45	0.37	203.18	1386.57	0.03	1798.49	0.31	22.61	0.82	6.2
Adult:C. reticulata CLas-Female antennae [27]	0.53	0	25	8.71	151.75	1835.97	0.49	2699.83	0.57	29.29	0.65	8.6
Adult:C. reticulata CLas-Female terminal abdomen [27]	0.77	0	12.95	1.87	61.81	980.79	0.37	1114.55	0.07	23.81	0.6	16.1
Adult:C. reticulata CLas-Male antennae [27]	0.44	0	23.52	20.19	140.14	2104.17	0.76	3582.55	1.36	37.96	1.61	5.2
Adult:C. reticulata CLas-Male terminal abdomen [27]	1.26	0.06	12.11	1.64	63.5	1132.34	0.98	1963.58	0	45.04	1.77	7.9

Expression values in transcripts per million (TPM) obtained from the Citrus Greening Expression Network [17] for annotated *D. citri* chitinase genes. Sample metadata including developmental stage, tissue, food source, and *C*Las exposure status are recorded in the first

column. Cht: Chitinase; IDGF: Imaginal disc growth factor; ENGase: endo-B-N-acetylglucosaminidase

Conclusions

We have annotated 12 genes of the chitinase family from the citrus greening vector *D. citri*. We used BLAST, domain content and phylogenetic analysis to assign the predicted chitinase proteins into groups according to the current classification system [5]. *D. citri* has members of all chitinase groups except groups IV, VII, and IX. We also determined that *D. citri* and several other sternorrhyncan hemipterans have a novel chitinase gene that appears to be the result of horizontal gene transfer.

Re-use potential

Our curation of chitinase gene models and classification of chitinase proteins will be helpful to scientists wishing to carry out additional research on these genes. Chitinases are considered good targets for gene-based pest control methods, but research in other insects has shown that not all chitinases are essential. Our analysis will help researchers choose the best genes to target and will provide accurately annotated genes as a foundation for their work.

Data availability

Sequences of the annotated genes described here are available in the GigaScience GigaDB repository. They will also be included in an updated official gene set (OGS) to be submitted to NCBI. Genome assembly, transcriptome and official gene set sequences are currently available

for BLAST and expression analysis on the Citrus Greening Solutions website [11] and will be available for download upon publication of the genome.

Declarations

List of abbreviations

Ac: *Agrius convolvuli*; Ag: *Anopheles gambiae*; Ap: *Acyrthosiphon pisum*; Ar: *Adineta ricciae*; Bc: *Bradysia coprophila*; Bm: *Bombyx mori*; Bt: *Bemisia tabaci*; CBD: Chitin binding domain; CGEN: Citrus Greening Expression Network; Cht: Chitinase; *C*Las: *Candidatus* Liberibacter asiaticus; Cn: *Contarinia nasturtii*; Dc: *Diaphorina citri*; Dm: *Drosophila melanogaster*; Dn: *Diuraphis noxia*; Dp: *Danaus plexippus plexippus*; ENGase: endo-beta-N-acetylglucosaminidase; HGT: horizontal gene transfer; Idgf: Imaginal disc growth factor; MCOT: Maker, Cufflinks, Oases and Trinity; Mp: *Myzus persicae*; NCBI: National Center for Biotechnology Information; Nl: *Nilaparvata lugens*; Of: *Ostrinia furnacalis*; OGS: official gene set; Px: *Papilio Xuthus*; RNA-Seq: RNA sequencing; Sf: *Sipha flava*; Sl: *Spodoptera litura*; S/T: serine/threonine; Tc: *Tribolium castaneum*; TPM: transcripts per million; Tu: *Tetranychus urticae*.

Ethical approval

Not applicable

Consent for publication

Not applicable

Competing interests

The authors declare that they have no competing interests.

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Authors' contributions

WBH, SJB, TD and LAM conceptualized the study; TD, SS, TDS and SJB supervised the study; SJB, TD, SS, and LAM contributed to project administration; SM, TDS, and BT conducted the investigation; PH, MF-G, and SS contributed to software development; SS, TDS, PH, and MF-G developed methodology; SJB, TD, WBH, and LAM acquired funding; TDS and SM prepared and wrote the original draft; SS, WBH and SJB reviewed and edited the draft.

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