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Molecular cloning, characterization and functional analysis of *GluCl* from the oriental armyworm, *Mythimna separata* Walker



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ABSTRACT

Glutamate-gated chloride channels (GluCls) mediate inhibitory synaptic transmission in invertebrate nervous systems, and only one *GluCl* gene has been found in insects. Therefore, insect *GluCls* are one of the major targets of insecticides including avermectins. In the present study, a 1347 bp full-length cDNA encoding a 449-amino acid protein (named *MsGluCl*, GenBank ID: MK336885) was cloned from the oriental armyworm, *Mythimna separata*, and characterized two alternative splicing variants of *MsGluCl*. The protein shares 76.9–98.6% identity with other insect GluCl isoforms. Spatial and temporal expression analysis revealed that *MsGluCl* was highly expressed in the 3rd instar and adult head. Dietary ingestion of dsMsGluCl significantly reduced the mRNA level of *MsGluCl* and decreased abamectin mortality. Thus, our results reveal that *MsGluCl* could be the molecular target of abamectin and provide the basis for further understanding the resistance mechanism to abamectin in arthropods.

1. Introduction

Glutamate-gated chloride channels (GluCls), a type of neurotransmitter receptor, are members of the cysteine-loop ligand-gated ion channel family. In the nervous system of invertebrates, GluCls play a critical role in inhibitory synaptic transmission (Cleland, 1996; Jones and Sattelle, 2006). There are five subunits in GluCls and each subunit contains an extracellular N-terminal domain including the glutamatebinding site and four transmembrane (TM) α -helices that form a channel domain. To date, GluCl channels have been described only in invertebrates, which have different numbers of orthologous GluCl genes (Jones and Sattelle, 2006; Wolstenholme and Rogers, 2005; Dermauw et al., 2012a). In contrast to other invertebrates, insects such as Drosophila melanogaster, Apis mellifera and Tribolium castaneum have only one GluCl gene (Jones and Sattelle, 2007; Knipple and Soderlund, 2010). Because GluCls are only found in invertebrates, they are regarded as ideal insecticide targets with high selectivity (Janssen et al., 2007).

Abamectin belong to the class of macrocyclic lactone insecticides, which have nematocidal, acaracidal and insecticidal activity (Lasota and Dybas, 1991) and now are widely used in the agricultural, veterinary and pharmaceutical fields to control pests (Geary, 2005; Copping and Duke, 2010). GluCls together with gamma-amino butyric acid (GABA)-gated chloride channels have been identified as the primary targets of abamectin in arthropods (Duce et al., 1995; Bloomquist, 2003; Hüter, 2011). To date, most of the information about targeting of GluCls by insecticides has come from studies in model nematodes and insects. (Cully et al., 1994; Kane et al., 2000). The mutations in GluCls have been found to increase resistance to abamectin in the diamondback moth *Plutella xylostella* and the two-spotted spider mite *Tetranychus urticae* (Kwon et al., 2010; Dermauw et al., 2012b; Wang et al., 2016; Liu et al., 2014). In addition, studies have reported that the α subunit is important for the action of glutamate and abamectin in insects, but, in *C. elegans*, both α and β subunits are required for the actionproviding strong evidence that avermectins act on one or more subunits of GluCls (Cully et al., 1994).

The oriental armyworm, *Mythimna separata* Walker is a devastating pest of > 300 types of food and industrial crops, such as corn, rice, and sugarcane (Zhang et al., 2012; Jiang et al., 2014; Wang et al., 2018a). In addition, *M. separata* is a migratory pest with outbreaks in specific years and result in substantial economic damage to local crops (Wang et al., 2006; Jiang et al., 2011). The most common and efficient way to

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control M. separata is by applying chemical treatments including abamectin; however, frequent application of insecticides often results in serious environmental problems and the development of insecticide resistance (Song et al., 2017). Characterization and detailed analysis of the full-length GluCl cDNA is fundamental for understanding the molecular mechanism underlying insecticide resistance. While no significant abamectin resistance M. separata population was found in the field, studies need to done before resistance occurred. Therefore, to fill the gap in knowledge about the mechanism of insecticide resistance in M. separata, we investigated the relationship between MsGluCl and susceptibility to abamectin. We cloned and characterized a full-length GluCl cDNA (named MsGluCl) from M. separata and profiled the mRNA expression pattern of MsGluCl. In order to explore the molecular targets of abamectin in M. separate, we studied the influence of RNAi-mediated knockdown effect on MsGluCl expression and investigated the susceptibility of M. separata to abamectin after RNAi.

2. Materials and methods

2.1. Insects

The oriental armyworm *M. separata* was originally purchased from Henan Jiyuan Baiyun Industry Company (Jiyuan, Henan, China), and the colony was maintained in the laboratory for 10 years without exposure to insecticides. The insects were kept on an artificial diet under laboratory conditions at 26 \pm 1 °C, with 70% relative humidity and a 16 h:8 h (L:D) photoperiod.

2.2. RNA extraction and cDNA synthesis

Total RNA was extracted from several developmental stages (eggs, 1st to 6th instar larvae, pupae and adults) and from different tissues (integument, gut and head) from 6th-instar larvae with the RNeasy Micro Kit (Qiagen, Hilden, Germany) according to the manufacturer's instructions. Then the remaining genomic DNA was removed, and the first-strand cDNA was synthesized from 1 µg total RNA using the Prime Script[™] 1st Strand cDNA Synthesis Kit with gDNA Eraser (Perfect Real Time) (TaKaRa, Dalian, China) for reverse transcription-polymerase chain reaction (RT-PCR) and quantitative RT-PCR (qRT-PCR).

2.3. Cloning and sequence analysis

The open reading frame (ORF) of the GluCl transcript (obtained from our unpublished transcriptome data) was predicted using the tool ORF Finder (http://www.ncbi.nlm.nih.gov/gorf/gorf.html). Then, three specific primers (MsGluCl-1-3) were designed to amply the GluCl coding region (Table S1) from M. separata, the clones were sent to Biosune Co. ltd (Fuzhou, China) for sequencing. The amplified sequences were assembled and aligned with DNAMAN (DNAMAN 5.2.2, Lynnon BioSoft). The gene specific primer (MsGluCl) was used for clone the whole ORF and verify assembled sequence (Table S1). The isoelectric point (pI) and molecular weight (MW) of the deduced protein sequences were analyzed using the ExPASy Proteomics Server (http:// cn.expasy.org/tools/pi_tool.html). The BioEdit (https://bioedit. software.informer.com) was used for analysis protein similarity. The mature GluCl protein sequences from M. separata and other pest species were aligned using ClustalX 1.83, and a phylogenetic tree was constructed in MEGA 6.0 using the neighbor-joining method with 1000 bootstrap resampling. The signal peptide in MsGluCl was predicted using the SignalP 4.1 server (http://www.cbs.dtu.dk/services/SignalP/), and TM domains were predicted using TMHMM 2.0 (http://www.cbs. dtu.dk/services/TMHMM-2.0/). Putative motifs were predicted using ExPASy ScanProsite (http://prosite.expasy.org/scanprosite/) or by aligning to other published GluCls.

2.4. qRT-PCR analysis of MsGluCl expression profiles

The relative transcription levels of MsGluCl at different developmental stages (eggs, 1st to 6th instar larvae, pupae and adults) and in different body parts (integument, gut and head) from 6th-instar larvae were determined using qRT-PCR, which was performed for three biological replicates using gene-specific primers (Table S1) and SYBR Premix EX Taq[™] (TaKaRa, Dalian, China) on the ABI 7500 system (Applied Biosystems, CA, USA). Each 20-µl reaction contained 1.0 µl cDNA (200 ng/ul), 10 µl SYBR Premix Ex Taq[™], 0.4 µl forward primer $(10 \,\mu\text{M})$, $0.4 \,\mu\text{l}$ reverse primer $(10 \,\mu\text{M})$, $0.4 \,\mu\text{l}$ Rox Reference Dye II, and 7.8 µl nuclease free water. The thermal cycling conditions were: 95 °C for 30 s. 40 cvcles of 95 °C for 5 s. 62 °C for 34 s. After the cvcling protocol, a melting curve analysis from 60 °C to 95 °C was performed for all reactions to verify the amplification of a single PCR product. The amplification efficiency was estimated using the equation, $E = 10^{-1}/$ slope, where the slope was derived from a plot of cycle threshold (Ct) value versus copy number for five serially diluted template concentrations. Quantification of MsGluCl transcript level was conducted using the $2_{-\wedge\wedge Ct}$ method (Pfaffl, 2001) and the housekeeping genes β -actin and $EF-\alpha$ were used as controls to correct for sample-to-sample variation. The expression of MsGluCl at different stages and in various body parts was analyzed using one-way ANOVA followed by Tukey's HSD test for multiple comparisons in SPSS 18.0(George and Mallery, 1998).

2.5. Bioassay

Twenty-five 2nd instar larvae were selected and starved for 12 h before being fed an artificial diet containing an 100 μ l solution of various doses of abamectin (Shijiazhuang Ruitian Biochemical Co., Ltd., China; 0.1 mg/L, 0.5 mg/L, 1 mg/L, and 5 mg/L) using acetone as the carrier solvent (Song et al., 2017). The criterion to determine death is larval could not move after touching with brush. After 48 h, the mortality rate was recorded, and the corresponding LC₅₀ was calculated by Probit analysis in SPSS 18.0. Each concentration was replicated for three times in this experiment.

2.6. RNAi in M. separata

The templates for *in vitro* transcription, a fragment of *MsGluCl* (202 bp) and a fragment of the enhanced green fluorescent protein gene *egfp* (414 bp), were generated by PCR using specific primers (Table S1) conjugated with the T7 RNA polymerase promoter (TAATACGACTCA CTATAGGG). Then double stranded RNAs were synthesized using the T7 Ribomax TM Express RNAi System (Promega, Madison, WI, USA) as described in the manual.

Thirty late 1st instar larvae were fed on an artificial diet containing 100 µg dsRNA (dsMsGluCl or dsEGFP) in a 24-well plate continuous for 3 days, with fresh dsRNA supplied each day. A diet with the same amount of ddH₂O (100 µl) was used as the control. After 3 days, larvae molted to the 2nd instar stage, and five living larvae in each group (control, *MsGluCl*-dsRNA, and *egfp*-dsRNA) were extracted for total RNA. Then approximately left 20 larvae in each group were used for bioassay test with a dose of 1.7 mg/L (LC₅₀) as described above (section 2.5). Two days after avermectin application, the number of dead larvae were recorded. The experiment was replicated three times.

3. Results

3.1. Analysis of the MsGluCl amino acid sequence and alternative splicing

Three sets of primers were designed to amplify the ORF of *MsGluCl* based on the transcript obtained from *M. separata* transcriptome data. Finally a set of primer was used to amplify the whole ORF and verify the assembled sequence. The assembled ORF consisted of 1347 bp of contiguous sequence and encoded 449 amino acids. This sequence was



Fig. 1. Alignment of nine insect GluCls. The four transmembrane domains (TM1–4) and four cysteine residues are indicated by black lines and black triangles, respectively. The Cys-loop, the signature domain of neurotransmitter-gated ion-channels, is indicated by a dotted line.

submitted to NCBI under GenBank ID: MK336885.

The predicted MsGluCl protein has a MW of ~51.3 kDa and a pI of 8.71. The MsGluCl amino acid sequence was analyzed for putative regulatory domains. Alignments of insect GluCl proteins showed that there were four typical hydrophobic TM domains in the COOH-terminal region of MsGluCl at positions 253–269 (TM1), 281–302 (TM2), 315–334 (TM3), and 422–442 (TM4) (Fig. 1). In addition, four cysteine residues (C1–C4) in the extracellular domain were found. The sequence motif, CPMNLKLYPLDKQTC, which was identified between C1 and C2 and constitutes part of the neurotransmitter-gated ion-channel signature domain, the Cys-loop, was highly conserved in MsGluCl (165–179) and eight other insect GluCls (Fig. 1).

Alignment of the sequences of multiple cDNA clones revealed one alternative splicing site in the *MsGluCl* transcript, which is predicted to result in the deletion of amino acid residues 372–385 (Fig. 2).

3.2. Phylogenetic relationships of insect GluCl family members

The amino acid sequence identities between GluCl proteins from several orders of insects are shown in Table 1. MsGluCl shared the greatest identity with GluCls from the lepidopteran species *Helicoverpa* armigera (HaGluCl, 98.6%) and *P. xylostella* GluCl (PxGluCl, 93.7%), and also shared a high level of identity with the GluCls from *Tribolium*

castaneum (82.3%), D. melanogaster (81.3%), and Laodelphax striatellus (80.7%). MsGluCl shared the lowest identity with GluCl from Aedes aegypti (76.9%).

In a phylogenetic tree of GluCl proteins from 20 species, the insect GluCls were separated from the nematode GluCls (Fig. 3). MsGluCl was clustered with GluCls from the four other lepidoptera species, and GluCls from other species in the same order, such as Diptera, Lepidoptera, Coleoptera, Hymenoptera and Hemiptera, were grouped together.

3.3. Spatial and temporal expression of MsGluCl

Analysis of expression at different developmental stages revealed that *MsGluCl* was expressed at all life stages; *MsGluCl* was most highly expressed in the egg and 1st and 3rd instars, while the expression level during the 4th instar to pupae stage was much lower than that at the other stages. Compared with the 1st instar, the relative expression level of *MsGluCl* mRNA was 1.06-, 0.21-, 1.15-, 0.16-, 0.05-, 0.08-, 0.14- and 0.24-fold higher in the egg, 2nd, 3rd, 4th, 5th, and 6th instar larvae, pupae, and adults respectively (Fig. 4A). *MsGluCl* was highly expressed in the head, while to our surprise, we could not detect *MsGluCl* expression in intestinal tissue (Fig. 4B).

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Fig. 2. Sequence alignments of MsGluCl alternative splicing variants.

3.4. Toxicity of abamectin to M. separata

The toxicity of abamectin to *M. separata* was determined using the feeding method. Based on bioassay results (Table S2), 1.7 mg/L of abamectin (the LC₅₀ dose) was used to treat *M. separata*.

3.5. Effect of dsMsGluCl on MsGluCl expression and abamectin tolerance

After 3 days of continuous ingestion of dsMsGluCl, the late 1st instar molted to the 2nd instar. The levels of *MsGluCl* mRNA in the treated larvae were significantly lower (46.7%) compared with those in corresponding controls. Three days of ingestion of dsRNA killed few larvae. The surviving larvae that had been exposed to CK (ddH₂O), dsEGFP, or dsMsGluCl diets were used for further bioassay experiments.

Approximately 20 larvae in each treatment were fed with further abamectin treatment (LC_{50} dose). Larval mortality in both the CK and dsEGFP treatment groups (47.1% and 41.5%, respectively) was much higher than that in the dsMsGluCl treatment group (32.4%, Fig. 5B).

4. Discussion

Avermectin insecticides are widely applied in several crop fields because of its efficient and eco-friendly. In addition, Fluxametamide, another novel wide-spectrum insecticide, which also target to *GluCl* (Asahi et al., 2018). Even though no studies have documented *M. separata* resistance to abamectin, the lack of knowledge about the relationship between the structure and function of *M. separata* GluCl and the potential resistance risk will make it difficult to figure out the

Table 1

Comparison of GluCl sequences from different insects.

	M. sepereta	H. armigera	P. xylostella	D. melanogaster	M. domestica	A. aegypti	A. mellifera	L. striatellus	T. castaneum
M. sepereta H. armigera P. xylostella D. melanogaster M. domestica A. aegypti A. mellifera	-	0.986 -	0.937 0.941 -	0.813 0.811 0.809 -	0.798 0.796 0.794 0.943 -	0.769 0.767 0.768 0.862 0.86 -	0.789 0.789 0.781 0.778 0.759 0.728	0.807 0.807 0.803 0.786 0.769 0.731 0.784	0.827 0.825 0.823 0.828 0.839 0.782 0.806
L. striatellus T. castaneum								-	0.817 -

The species and their corresponding GenBank IDs are: Mythimna separata (MsGluCl), this study; Laodelphax striatellus (LsGluCl), AEE39458.1; Musca domestica (MdGluCl), BAD16657.1; Plutella xylostella (PxGluCl), ACT09139.1; Tribolium castaneum (TcGluCl), NP_001107775.1; Drosophila melanogaster (DmGluCl), ABG57261.1; Aedes aegypti (AaGluCl), XP_021704264.1; Apis mellifera (AmGluCl), NP_001071277.1; Helicoverpa armigera (HaGluCl), XP_021191010.1.



Fig. 3. Phylogenetic tree of the deduced amino acid sequences of MsGluCl and known GluCls from different species.

resistance mechanism when it occurs.

We cloned the full-length *GluCl* coding sequence from *M. separata*, phylogenetic analysis indicated that the MsGluCl amino acid sequence is homologous to that of different insect GluCls. Known domains were

also identified in the MsGluCl protein: four cysteine residues within the N terminal region and four transmembrane domains near the C-terminus (Fig. 1). The three TM regions were mostly conserved among insects from different orders including Diptera, Lepidoptera,



Fig. 4. Spatial and temporal expression of *MsGluCl* mRNA. (A) Relative expression levels of *MsGluCl* mRNA at nine development stages were determined: egg, 1–6 instar nymphs (L1-L4), pupae and adults compared to L1. (B) *MsGluCl* mRNA levels in 6th instar larvae body parts compared to Head. Different lowercase letters (a, b and c) indicate significant differences (p < 0.05) based on one-way ANOVA followed by Tukey's HSD test for multiple comparisons. Means ± standard error from three replicates are shown. NE indicates no expression.



Fig. 5. Effect of the dietary introduction of dsMsGluCl on the relative *MsGluCl* transcript level (A) and mortality of 2nd instar larvae (B). Larvae were continuously fed dsRNA for three days, and mortality was evaluated two days after avermectin or water treatments (CK). Different lowercase letters (a, b and c) indicate significant differences (p < 0.05) based on one-way ANOVA followed by Tukey's HSD test for multiple comparisons. Means \pm standard error from three replicates are shown.

Coleoptera, Hymenoptera, and Hemiptera, but TM4 was less conserved (Dong et al., 2013; Shi et al., 2014; Meyers et al., 2015). Amino acid sequence alignment showed that MsGluCl shares 76.9–98.6% similarity with other insect GluCl homologs. Phylogenetic analysis showed that insect GluCls are genetically conserved and clearly diverged from the three nematode GluCls, and insect GluCls also clustered together based on insect order (Fig. 3).

GluCls have been found only in invertebrates (Wolstenholme, 2011), hence these proteins are potential targets for the development of pesticides. Several studies have confirmed that mutations GluCl are associated with avermectins resistance. Both electrophysiology and homology modelling studies have demonstrated that three mutations are associated with target-site resistance to abamectin: A309V in *P. xylostella* GluCl (PxGluCl), G323D in *Tetranychus urticae* GluCl1 (Tu-GluCl1) and G326E in TuGluCl3 (Wang et al., 2016; Wang et al., 2017). In addition, a 36-bp deletion in *P. xylostella* GluCl contributes to target-site resistance to abamectin (Liu et al., 2014). None of the abovementioned mutations were detected in our *MsGluCl* sequence. Therefore, our work provides valuable data for further studies aimed at detecting the relationship between the mutation and abamectin resistance in the *M. separata*.

Alternative splicing is a key posttranscriptional processing mechanism for generating protein diversity. Two splicing variants were detected in *M. separata*, similar to what has been observed in the insects *D. melanogaster* (Semenov and Pak, 2010), *A. mellifera* (Jones and Sattelle, 2006), *N. vitripennis* (Jones et al., 2010) and *P. xylostella* (Wang et al., 2016). In contrast, three alternative splicing variants of *GluCl* were found in *T. castaneum*, *Laodelphax striatellus* and *Musca domestica* (Hassani et al., 2012; Wu et al., 2017; Eguchi et al., 2010).

To begin to understand physiological roles of GluCl in *M. separata*, we investigated the temporal and spatial expression patterns of *MsGluCl* using qRT-PCR. We found that *MsGluCl* is expressed at all development stages, *MsGluCl* mRNA was the most abundant in the head, in accordance with data from other insects, such as *M. domestica* (Kita et al., 2013), *L. striatellus* (Wu et al., 2017), *B. mori* (Furutani et al., 2014), *B. tabaci* (Wei et al., 2018) and *A. gambiae* (Meyers et al., 2015). It has been reported *GluCl* is expressed in the membranes of the corpus allatum, which synthesizes and releases juvenile hormone and plays an important role in insect metamorphosis (Liu et al., 2005). The *MsGluCl*, which is highly expressed in head tissue, we infer it might play a role in *M. separata* development process. Through the analysis of temporal expression, we found that *MsGluCl* mRNA was highly expressed in the eggs and early larvae except the 2nd instar and was lowly expressed in the L5 and the L6 instars. This expression pattern is similar to, but not

exactly the same, as that observed in carmine spider mite *Tetranychus cinnabarinus* (Xu et al., 2017), the silkworm *B. mori* (Furutani et al., 2014) and the small plant hopper *L. striatellus* (Wu et al., 2017). However, not all insect *GluCls* share the same expression pattern as *MsGluCl*. The *GluCl* is highly expressed in adults in *M. domestica* (Kita et al., 2013) and in *B. tabaci* (Wei et al., 2018), and expression of *BtGluCl* was significantly lower in eggs and larvae. Therefore, the temporal expression of *GluCl* varies among insect species.

Theoretically, the change in mRNA expression levels of the target gene should affect the sensitivity of insects to insecticides, and this theory has been confirmed by an increasing number of studies. For example, in the greenbug Schizaphis graminum, the amount of acetvlcholinesterase mRNA in an organophosphate resistant strain was approximately 1.5-fold higher than that in the susceptible population based on northern blot analysis (Gao and Zhu, 2002). In a laboratory flubendiamide-selected P. xylostella strain, the expression level of PxRyR was 2.93-fold higher than that in the susceptible strain (Yan et al., 2014). RNAi technology has been widely used to identify or validate insecticide target genes (Kim et al., 2015). Therefore, to confirm the role of GluCl in abamectin resistance, we tested sensitivity of M. separata larvae to abamectin after targeting MsGluCl with dsMsGluCl. Ingestion of dsMsGluCl for 3 days significantly reduced the level of MsGluCl mRNA in treated 2nd instars by 53.3%, and greatly decreased abamectin -induced mortality. Our result suggests that MsGluCl encodes a functional GluCl that mediates toxicity of abamectin to M. separata. Consistent with our finding, knockdown of GluCl in P. xylostella (Shi et al., 2012), B. tabaci (Wei et al., 2018) and T. cinnabarinus (Xu et al., 2017) also decreased avermectins -induced mortality.

GluCls play important roles in insect development (Hassani et al., 2012; Kita et al., 2013; Boumghar et al., 2012; Chiang et al., 2002) and have been reported to be involved in the control of locomotion, feeding and sensory input (Wolstenholme, 2011). We previously demonstrated that injection of dsHzGluCl negatively affected egg hatching in corn earworm *Helicoverpa zea* (Wang et al., 2018b); however, we did not observe any negative effects of dsMsGluCl on larval growth during the 3 days of ingestion. Therefore, further work is needed to test the negative effects of dsMsGluCl, and explore the physiological roles of *MsGluCl*.

In the current study, we cloned and characterized the *GluCl* gene from *M. separata* and investigated the function of *GluCl* in abamectin. Further work should be done to reveal the structure and pharmacological characteristics of insect GluCls to provide a basis for understanding the remarkable selectivity of this insecticide towards lepidoptera and the mechanism of resistance.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.pestbp.2019.02.004.

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