



A short note on comparative analysis of acetylcholinesterase genes in mosquito genome

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A short note on comparative analysis of acetylcholinesterase genes in mosquito genome

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Abstract

Acetylcholinesterase genes confer the organophosphate and carbamate resistance mechanism. A total of 46 acetylcholinesterase genes in the 24 mosquito genomes were identified. In this study, all the analysed mosquito genomes have the two acetylcholinesterase genes (*ace-1* and *ace-2*) except *Aedes albopictus* and *Anopheles sinensis-sinensis strain*. Phylogenetic tree showed the divergence of acetylcholinesterase genes among the mosquito genome. Phylogenetic tree confirmed that the *ace-1* and *ace-2* genes of each species were structurally different and they form the different clades. This provided data on acetylcholinesterase gene organization for 24 mosquito genome is possibly a first time and will be a starting point for the molecular characterization of the acetylcholinesterase genes which further helps to understand the organophosphate and carbamate resistance mechanism.

Introduction

Vector borne diseases are of the major public health problem due to insecticide resistance in mosquitoes. Organophosphates and carbamates kill insects by inhibiting acetylcholinesterase found in the central nervous system. Some species have *ace-1* gene and many other species has both *ace-1* and *ace-2* genes (Kozaki et al., 2008) but only *ace-1* gene involved in insecticide resistance mechanism (Liu 2015). It was reported that the mutations at codon 119 of the acetylcholinesterase (*ace-1*) gene that leads to a single amino acid substitution of glycine to serine may confer resistance to organophosphates and carbamates (Chang et al., 2014). In this study acetylcholinesterase genes in the 24 mosquito genome were analyzed.

Methodology

Anopheles gambiae acetylcholinesterase gene (Ranson et al., 2002) was blasted against the mosquito vector genome in VectorBase database (Giraldo-Calderon et al., 2015) using BLASTN tool.

The blast resulted sequences were retrieved and multiple sequence alignment was done by using MUSCLE tool (Edgar 2004). Phylogenetic tree was constructed for the sequences by using maximum likelihood module in MEGA 6 software (Benevides et al., 2016).

Result and Discussion

VectorBase database has 24 mosquito genomes namely *Aedes aegypti*, *Ae. albopictus*, *Anopheles albimanus*, *An. arabiensis*, *An. atroparvus*, *An. christyi*, *An. coluzzii*, *An. culicifacies*, *An. darlingi*, *An. dirus*, *An. epiroticus*, *An. farauti*, *An. funestus*, *An. gambiae*, *An. maculatus*, *An. melas*, *An. merus*, *An. sinensis-sinensis strain*, *An. sinensis-China strain*, *An. minimus*, *An. quadriannulatus*, *An. stephensi-Indian strain*, *An. stephensi-SDA 500 strain*, *Culex quinquefasciatus* (Giraldo-Calderón et al. 2015). A total of 46 acetylcholinesterase gene sequences were obtained from the blast results (Illustration 1). Two acetylcholinesterase genes each were present in all genome except *Ae. albopictus* and *An. sinensis-sinensis strain* are the two genome each has only one acetylcholinesterase gene similar to *Drosophila melanogaster* and *Musca domestica* species (Kozaki et al., 2008). Phylogenetic tree showed the divergence of acetylcholinesterase genes among the family members. Orthologous relationship is observed due to the conserved region in the genes, while paralogous relationship of the genes in the phylogenetic tree is observed due to the local gene duplication (Canoon and Young 2003). On the whole polyphyletic clades were observed in the phylogenetic tree. The species-wise observations inferred in the phylogenetic tree are explained below. Both *An. culicifacies* and *An. minimus* genes were orthologous to each other and paralogous to *An. funestus*. Similarly *An. stephensi* genes were orthologous among them and paralogous to *An. maculatus*. In case of *An. dirus*, *An. atroparvus* and *An. albimanus* genes were orthologous to *An. farauti*, *An. sinensis* and *An. darlingi* genes respectively forms the individual monophyletic clade. Whereas, *Aedes albopictus* gene was orthologous to *Ae. aegypti* gene and paralogous to *Culex quinquefasciatus* genes. The *gambiae* complex (Harbach 2013) species like *An. arabiensis*, *An.*

gambiae, *An. melas*, *An. merus* and *An. quadriannulatus* are orthologous and paralogous among each other but outside this clade *An. christyi* and *An. epiroticus* genes are presented as an outlier. It was observed in the phylogenetic tree that acetylcholinesterase gene 1 (*ace-1*) and Acetylcholinesterase gene 2 (*ace-2*) were structurally different, so they both formed different clades for the different species (Illustration 2).

Conclusion

This study reported the presence of acetylcholinesterase in the mosquito genomes. A total of 46 acetylcholinesterase genes in the mosquito vector were identified. All the mosquito genomes have the two acetylcholinesterase genes except *Ae. albopictus* and *An. sinensis-sinensis strain*. Phylogenetic tree confirmed that the *ace-1* and *ace-2* genes of each species were structurally different and they form the different clades. This provided data will be a starting point for the molecular characterization of the acetylcholinesterase genes which helps to understand the carbamate resistance mechanism.

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References

- Giraldo-Calderón GI et al. (2015). VectorBase: an updated bioinformatics resource for invertebrate vectors and other organisms related with human diseases. *Nucleic Acids Res.* 43:D707–D713
- Edgar RC. (2004). MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.* 32(5): 1792–1797.
- Benevides LDJ , Carvalho DSD, Andrade RFS , Bomfim GC and Fernandes FMDC. (2016). Evolutionary analysis of apolipoprotein E by Maximum Likelihood and complex network methods. *Genet Mol Biol.* doi-<http://dx.doi.org/10.1590/1678-4685-GMB-2015-0164>
- Ranson H et al. (2002). Evolution of supergene families associated with insecticide resistance. *Science.* 298: 179–181

Reddy BPN, Prasad GB, Raghavendra K. (2011). *In-silico* characterization and comparative genomic analysis of the *Culex quinquefasciatus* glutathione S-transferase (GST) supergene family. *Parasitol. Res.* 109: 1165–1177.

Harbach RE. (2013). Mosquito Taxonomic Inventory, <http://mosquito-taxonomic-inventory.info/>, accessed on 21st October, 2016.

Cannon SB, Young ND. (2003). OrthoParaMap: distinguishing orthologs from paralogs by integrating comparative genome data and gene phylogenies. *BMC Bioinformatics.* 4:35

Kozaki T, Kimmelblatt BA, Hamm RL, and Scott JG. (2008). Comparison of Two Acetylcholinesterase Gene cDNAs of the Lesser Mealworm, *Alphitobius diaperinus*, in Insecticide Susceptible and Resistant Strains. *Archives of Insect Biochemistry and Physiology.* 67:130–138

Chang X, Zhong D, Fang Q, Hartsel J, Zhou G, Shi L, Fang F, Zhu C, Yan G. (2014). Multiple Resistances and Complex Mechanisms of *Anopheles sinensis* Mosquito: A Major Obstacle to Mosquito-Borne Diseases Control and Elimination in China. *The PLOS Neglected Tropical Diseases.* doi: info:doi/10.1371/journal.pntd.0002967

Liu N (2015). Insecticide resistance in mosquitoes: impact, mechanisms, and research directions. *Annu Rev Entomol* 60: 537–59

Illustrations

Illustration 1

List of acetylcholinesterase genes (Vectorbase accession id) in 24 mosquito genome

<i>Aedes aegypti</i>	<i>Anopheles dirus</i>	<i>Anopheles minimus</i>
AAEL000511	ADIR001386-PA	AMIN005608-PA
AAEL012141	ADIR002455-PA	AMIN000542-PA
<i>Aedes albopictus</i>	<i>Anopheles epiroticus</i>	<i>Anopheles quadriannulatus</i>
AALF013932-PA	AEPI005838-PA	AQUA008010-PA
<i>Anopheles albimanus</i>	AEPI001137-PA	AQUA006538-PA
AALB002313-PA	<i>Anopheles farauti</i>	<i>Anopheles sinensis (China strain)</i>
AALB007715-PA	AFAF013551-PA	ASIC006247-PA
<i>Anopheles arabiensis</i>	AFAF012446-PA	ASIC005670-PA
AARA001814-PA	<i>Anopheles funestus</i>	<i>Anopheles stephensi (SDA 500 strain)</i>
AARA010659-PA	AFUN005694-PA	ASTE010565-PA
<i>Anopheles atroparvus</i>	AFUN011616-PA	ASTE007197-PA
AATE005176-PA	<i>Anopheles gambiae</i>	<i>Anopheles stephensi (Indian strain)</i>
AATE014052-PA	AGAP000466-PA	ASTEI01008-PA
<i>Anopheles christyi</i>	AGAP001356-PA	ASTEI07510-PA
ACHR009747-PA	<i>Anopheles maculatus</i>	<i>Culex quinquefasciatus</i>
ACHR005534-PA	AMAM010219-PA	CPIJ000662-PA
<i>Anopheles coluzii</i>	AMAM009185-PA	CPIJ006034-PA
ACOM033983-PA	<i>Anopheles melas</i>	
ACOM022771-PA	AMEC001981-PA	
<i>Anopheles culicifacies</i>	AMEC008403-PA	
ACUA020758-PA	<i>Anopheles merus</i>	
ACUA015087-PA	AMEM012321-PA	
<i>Anopheles darlingi</i>	AMEM004851-PA	
ADAC000367-PA	<i>Anopheles sinensis (sinensis strain)</i>	
ADAC000377-PA	ASIS006877-PA	

Illustration 2

Phylogenetic tree of acetylcholinesterase gene in 24 mosquito genome

