

**DNA barcoding and morphotaxonomic analyses of  
mosquitoes collected from Chittagong Metropolitan  
area**



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**June, 2018**

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**Md. Suruzzaman Sarkar**

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***The Author***

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## **Dedication**

To my ever loving parents

**Md. Sarbesh Ali Sarkar**  
and  
**Mazeda Begum**

## Table of contents

Contents	Page no.
<b>Authorization</b>	<b>ii</b>
<b>Signature page</b>	<b>iii</b>
<b>Acknowledgements</b>	<b>iv</b>
<b>Dedication</b>	<b>v</b>
<b>Table of contents</b>	<b>vi-vii</b>
<b>List of tables</b>	<b>viii</b>
<b>List of figures</b>	<b>ix</b>
<b>List of abbreviation</b>	<b>x</b>
<b>Abstract</b>	<b>xi</b>
<b>Chapter-1: Introduction</b>	<b>1-2</b>
Objectives	2
<b>Chapter-2: Review of Literature</b>	<b>3-8</b>
2.1. Vector importance of mosquitoes	3-4
2.2. Mosquitoes of Bangladesh	4
2.3. Morphotaxonomy of mosquitoes	5-7
2.3.1. <i>Aedes aegypti</i>	5
2.3.2. <i>Aedes albopictus</i>	5-6
2.3.3. <i>Culex pipiens</i>	7
2.4. DNA barcoding and mosquito characters	7-8
<b>Chapter-3: Materials and Methods</b>	<b>9-12</b>
3.1. Study area	9
3.2. Study period	9
3.3. Collection of sample	9
3.4. Microscopic examination	9
3.5. DNA barcoding	10
3.6. DNA extraction	10-11
3.7. Amplification of COI gene and DNA sequencing	11
3.8. Gel electrophoresis	11-12

<b>Chapter-4: Results</b>	<b>13-30</b>
4.1. Morphology study	13-23
4.2. Molecular study	23-34
4.2.1. Sequence analyses	23-24
4.2.2. Sequencing and phylogenic analyses	24
4.2.3. Phylogenic analysis of <i>Aedes aegypti</i> , <i>Aedes albopictus</i> and <i>Culex pipiens</i>	24-32
4.2.4. Bioinformatic analyses	33
<b>Chapter-5: Discussion</b>	<b>34-37</b>
<b>Chapter-6: Conclusion</b>	<b>38</b>
<b>Chapter-7: References</b>	<b>39-43</b>
<b>Appendix-I</b>	<b>44</b>
<b>Appendix-II</b>	<b>45-47</b>
<b>Appendix-III</b>	<b>48</b>

## List of tables

<b>Table no.</b>	<b>Topic</b>	<b>Page no.</b>
Table-1	Primer name	11
Table-2	Morphological characteristics of mosquitoes	11-18
Table-3	Similarities of our identified species with the species of different parts of the world	25-29
Table-4	NCBI retrieved sequences of COI of <i>Aedes aegypti</i> from different parts of the world	44
Table-5	The GenBank accession numbers of nucleotide sequences provided by NCBI	48

## List of figures

Figure	Topic	Page no.
Figure-1	Entovisioin Microscopes (3D Microscope) used during this study	9
Figure-2	Preparation of PCR reaction (A and B)	12
Figure-3	Vortexing of PCR reaction	12
Figure-4	Denaturation of PCR reaction by five cycle	12
Figure-5	Preparation of gel	12
Figure-6	Adding of PCR reaction into the gel	12
Figure-7	<i>Aedes aegypti</i>	18
Figure-8	Head of <i>Aedes aegypti</i>	18-19
Figure-9	Thorax of <i>Aedes aegypti aegypti</i>	19
Figure-10	Wing of <i>Aedes aegypti</i>	20
Figure-11	Fore leg of <i>Aedes aegypti</i>	20
Figure-12	Mid leg of <i>Aedes aegypti</i>	20
Figure-13	Hind leg of <i>Aedes aegypti</i>	21
Figure-14	Hind tarsi of <i>Aedes</i>	21
Figure-15	Abdomen of <i>Aedes aegypti</i>	21
Figure-16	<i>Aedes albopictus</i>	22
Figure-17	<i>Culex pipiens</i>	22
Figure-18	Head of <i>Culex pipiens</i>	22
Figure-19	Wing of <i>Culex pipiens</i>	23
Figure-20	Abdomen of <i>Culex Pipiens</i>	23
Figure-21	PCR amplification of COI gene (520 bp) of the <i>Culex pipens</i> , <i>Aedes albopictus</i> and <i>Ae. aegypti</i> mosquito pure-line (Sample-13 as CVASU13, Sample-14 as CVASU14, Sample-21 as CVASU 21, Sample-24 as CVASU24, Sample-26 as CVASU26).	24
Figure-22	Evolutionary relationships of taxa	30
Figure-23	Evolutionary relationships of taxa	31
Figure-24	Evolutionary relationships of taxa	32

### List of abbreviation

Sample-13	CVASU-13
Sample-14	CVASU-14
Sample-21	CVASU-21
Sample-24	CVASU-24
Sample-26	CVASU-26
Cox-I	Cytochrome oxidase subunit-I

## Abstract

Mosquitoes are important vectors for a wide variety of pathogens and parasites. Identification of different mosquito species are crucial for their eventual control. We have used the classical morphometry and modern molecular methods like DNA barcoding approach for reliable identification of mosquitoes that were collected from different locations of Chittagong Metropolitan area of Bangladesh. A total of 20 randomly collected specimens were included in this study. Different morphological features of head, clypeus, vertex, antenna, maxillary palp, thorax, wings, legs and abdomen of the mosquitoes were examined using three-dimensional microscopy. The morphological characteristics of the mosquitoes observed under stereo binocular microscope in the laboratory shown highly similarity with the *Aedes aegypti* species. Genomic DNA was extracted from all of the 20 samples using commercial kits and specific primers were used for amplification of partial cytochrome oxidase genes for molecular characterization. PCR products were then sequenced and further bioinformatics analyses was accomplished. Sequence similarity based BLASTn and phylogenetic analyses (MEGA 6) of the sequence indicated similarity with three different species namely *Aedes aegypti*, *Culex pipiens* and *Aedes albopictus*. Among these 5 samples, 3 samples were *Aedes aegypti*, 1 sample was *Aedes albopictus* and 1 sample was *Culex pipiens*. The findings were compatible with the morphological data and reliably characterized the mosquito species. The study was first DNA barcoding analyses on mosquito in the country and showed the feasibility of using molecular tools for their characterization. Further study about the origin and vector potential of these mosquitoes will enhance our capacity to improve existing vector surveillance and control program.



