



Haplotype diversity and distribution pattern of *Oecophylla smaragdina* (Fabricius) (Hymenoptera, Formicidae) in Bangladesh based on mitochondrial COI genes

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ABSTRACT

Climatic oscillation often have influenced the present distribution and intraspecific genetic diversity *Oecophylla smaragdina* through its wide range of geographical distribution. Previous phylogeographic study of Asian weaver ant population denotes the evidence of distribution of Indian types in Indian, Sri Lanka and SE Asian types in South Asian countries including Bangladesh. However, recent phylogenetic analysis reveals the overlapping distribution of the Indian and South East Asian clades of *O. smaragdina* in Bangladesh. The present study aims to identify the haplotypes and its networking in Bangladesh based on extensive materials. Sampling was executed according to zonation of 5 areas, demarcated by 3 main rivers during the years 2013 to 2018. Adult *O. smaragdina* workers were collected from 71 colonies of 67 localities belonging to 47 districts of Bangladesh. A total of 25 haplotypes were identified in Bangladesh comprises 13 and 12 of Indian and SE Asian types, respectively from 93 sequences of Cytochrome c oxidase subunit I (COI) gene of 639 bp. The geographical distribution of this haplotype reveals that the Indian haplotypes are mostly located at the western part of Bangladesh while SE Asian haplotypes were dominated in the Eastern part of the country. Central part of Bangladesh has overlapped with the mixture of both Indian and SE Asian haplotypes. The results of the haplotype network give the evidence of recent expansion of *O. smaragdina* population in Bangladesh and clarify the evidence of presence of many missing haplotypes in refugee.

Introduction

Oecophylla, the weaver ant (Hymenoptera, Formicidae) is a relatively old genus in the subfamily formicinae. It has only two extant species, *Oecophylla longinoda* (Latreille) distributed in tropical Africa and *O. smaragdina* distributed from India through Southeastern Asia and Australia (Wheeler 1922, Bolton, 1995), including many tropical and subtropical western pacific Islands (Lokkers 1986). They formed pendulous bag like nest on tree canopy with diversified organizing behavior in the colony (Schlüns et al., 2009). Due to widespread distribution and evolutionary history, *O. smaragdina* was considered to be a valuable material for biogeographic study in tropical Asia. *O. smaragdina* has also an ancestral impact based on divergence time. According to the fossil records, *O. smaragdina* might have originated in the early Paleogene (ca. 60 Ma) in the Palaeartic region, and dispersed during the

climatic changes of the Eocene–Oligocene transition at ca. 43 Ma (Dlussky et al., 2008). Wetterer (2017) gave a glimpse of distribution of *O. smaragdina* in this continent with some interesting evidence of distribution. Due to widespread distribution and evolutionary history, *O. smaragdina* were considered to be a valuable materials for biogeographic study in tropical Asia.

Azuma et al. (2006) proposed an outline of the Phylogeography of *O. smaragdina* and she revealed the identity of *O. smaragdina* population of Bangladesh as South East Asian type that distinct from the Indian types by means of mitochondrial DNA analysis of COI and Cytb genes. Similar findings were observed from Asaka (2010) who found a large genetic gap of *O. smaragdina* populations from Bangladesh from India and Sri Lanka where Indian population originated from the Indian refuge and Bangladesh population originated from the Indochina refuge. However, Rahman et al (2017a) in their phylogeographic study based on

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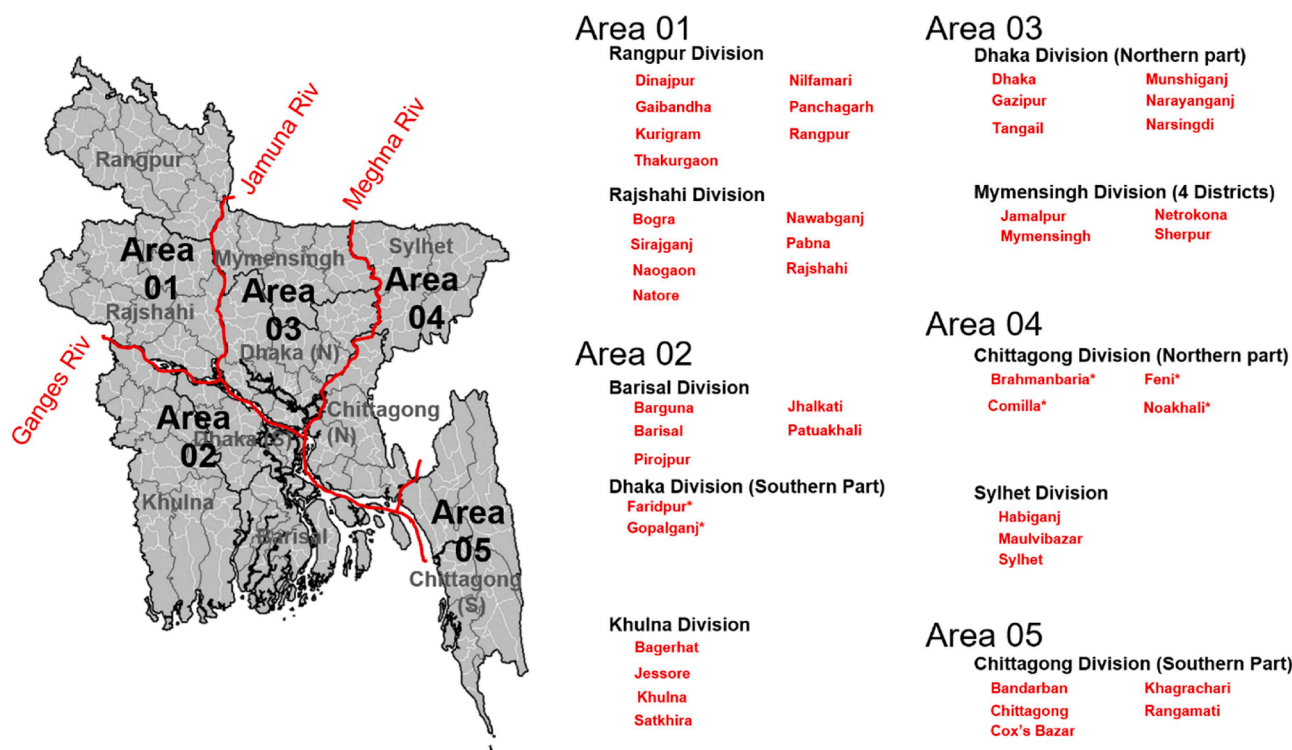
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Setting of the research areas



The red letters show the District names where the sampling has conducted during March 2013 to December 2017.

Fig. 1. Study sites of 5 broad areas based on three main rivers in Bangladesh. The red line across the map showing the river flow that separated 5 broad areas in Bangladesh. In the text, red color indicating the district name from where sampling were done in each area. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

mitochondrial Cytb and CO1 genes, identified the western Bangladeshi population of *O. smaragdina* as Indian type. Based on this interesting result, a details comprehensive phylogeographic study including eastern, northern and central part of Bangladesh were conducted by Rahman et al (2017b). They identified the western Bangladesh population are mainly Indian type whereas the Eastern part is dominating by South East Asian type, although the middle part of the country were occupied by overlapping populations of both Indian and South East Asian type.

Climatic oscillations during the Pleistocene period have a strong effect on the genetic diversity and distribution of extant species (Hewitt, 2004). Increased aridity and decreased temperatures during the glacial led to a fragmentation of tropical environments influenced the genetic diversity of *O. smaragdina* in these tropics as well. Phylogeographic study with diversified haplotype distribution network precisely congregate the genetic diversity phenomena in a particular geographical area. The purpose of this experiment was to identify the available haplotypes and analyze haplotype network for better understanding the phylogeographic results of *O. smaragdina* in Bangladesh. The goal was to

get insights into the genetic structure and geographical patterns of genetic variation of *O. smaragdina* across much of its distribution based on this haplotype distribution in Bangladesh.

Materials and methods

The setting of the study sites

Based on three main rivers, Ganges, Jamuna, and Meghna, the study area in Bangladesh was broadly categorized into five areas under 8 divisions. The detailed information of that 5 broad areas is presented in the following figure (Fig. 1) and the samplings sites were presented in Fig. 2.

Sampling and preparation of specimens

Adult *O. smaragdina* workers were collected from 71 colonies at 67 localities in 38 districts belonging to 7 divisions of Bangladesh (Fig. 2) during 2013 to 2018. The detailed locality information were provided in

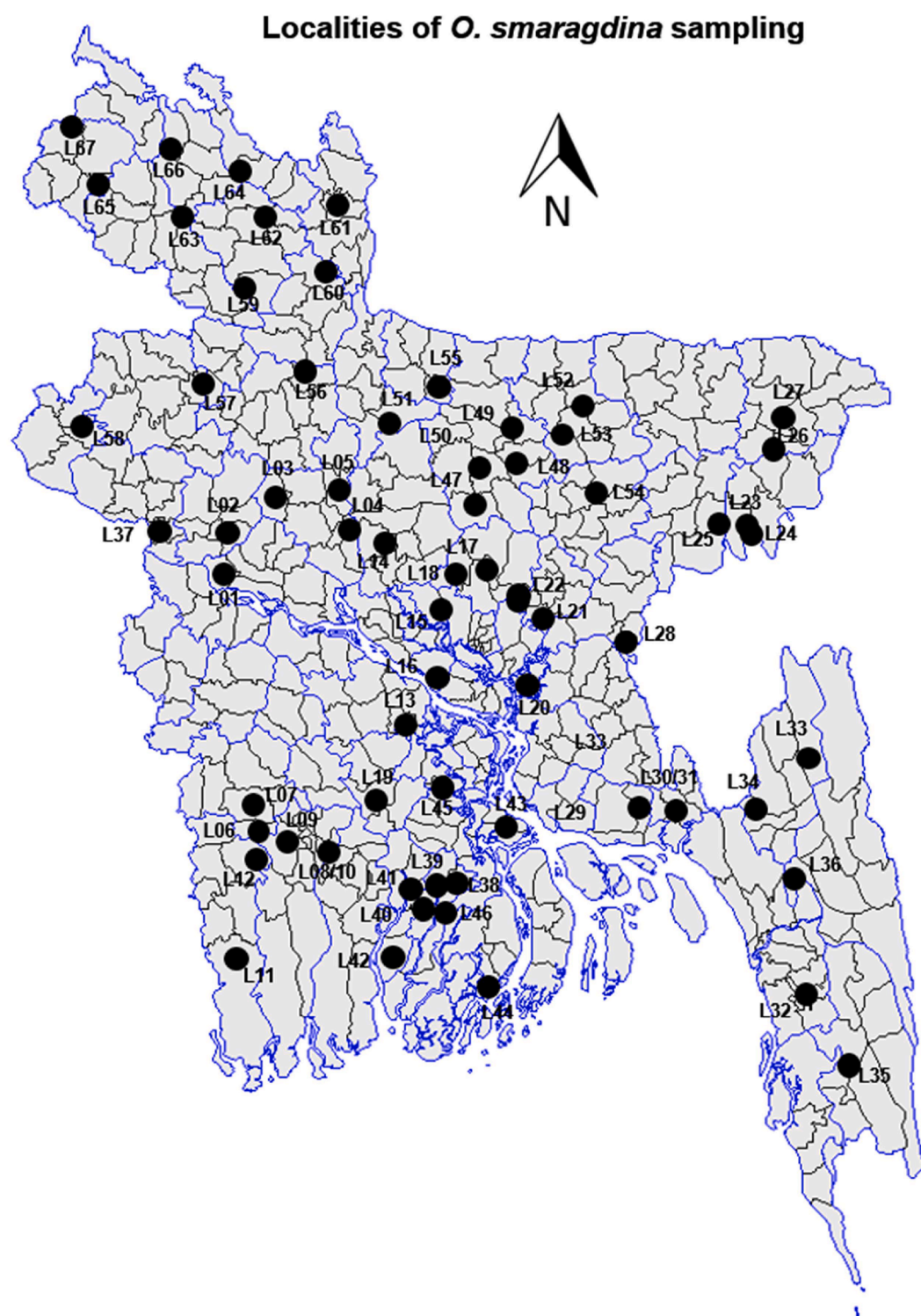


Fig. 2. The sampling sites of *O. smaragdina* in Bangladesh. Locality codes correspond to those in Table 1.

Table 1

Detailed locality information with GenBank accession number of sequencing data.

Locality code	Locality Name	No. of colonies	Upazila	District	Division	Collection Date	Accession number COI
L01	Ishwardi	1	Ishwardi	Pabna	Rajshahi	18 Mar. 2014	KX385842
L02	Bonpara	1	Baraigram	Natore	Rajshahi	19 Mar. 2014	KX385843
L03	Tarash	1	Tarash	Sirajganj	Rajshahi	18 Mar. 2014	KX385841
L04	Chauhali	1	Belkuchi	Sirajganj	Rajshahi	19 Mar. 2014	KX389168
L05	w side of Jamuna Bridge	1	Sirajganj sadar	Sirajganj	Rajshahi	18 Mar. 2014	KX385840
L06	Panjia	1	Keshabpur	Jessore	Khulna	04 Mar. 2014	KX371575
L07	Manirampur	1	Manirampur	Jessore	Khulna	14 Sep. 2013	KX355139
L08	Khulna Univ. Campus	1	Batiaghata	Khulna	Khulna	03 Mar. 2014	KX379493
L08	Khulna Univ. Campus	1	Batiaghata	Khulna	Khulna	03 Mar. 2014	KX379494
L09	Chuknagar	1	Dumuria	Khulna	Khulna	04 Mar. 2014	KX385837
L10	Batiaghata	1	Batiaghata	Khulna	Khulna	15 Sep. 2013	KX389167
L11	Atulia	1	Shyamnagar	Satkhira	Khulna	24 Mar. 2014	KX385844
L12	Modonpur	1	Tala	Satkhira	Khulna	25 Mar. 2014	KX385845
L13	Bhanga	1	Bhanga	Faridpur	Dhaka	09 Nov. 2014	KX389172
L14	Elenga	1	Kalihati	Tangail	Dhaka	18 Mar. 2014	KX385839
L15	Kumrail	1	Dharmrai	Dhaka	Dhaka	19 Oct. 2014	KX389169
L16	Thanamore	1	Dohar	Dhaka	Dhaka	21 Oct. 2014	KX389170
L17	Bhawal National park	1	Joydebpur	Gazipur	Dhaka	17 Mar. 2014	KX385838
L18	Nurbag	1	Kaliakoir	Gazipur	Dhaka	22 Oct. 2014	KX389171
L19	Pachuria	1	Gopalganj sadar	Gopalganj	Dhaka	29 Oct 2014	KY618816
L20	Nimtali	1	Shirajdikhan	Munshiganj	Dhaka	21 Oct 2014	KY628426
L21	Panchdona	1	Norsingi	Norsindi	Dhaka	20 Oct 2014	KY657490
L22	Charpara	1	Kaliganj	Gazipur	Dhaka	20 Oct 2014	KY628425
L23	Tea Resort Center	1	Sreemangal	Moulvibazar	Sylhet	14 Nov 2014	KY618809
L24	Lauchara National Park	1	Sreemangal	Moulvibazar	Sylhet	15 Nov 2014	KY618815
L25	Bahubal	1	Bahubal	Habiganj	Sylhet	14 Nov 2014	KY618818
L26	Tarau	1	Balaganj	Sylhet	Sylhet	15 Nov 2014	KY618817
L27	Doradarpur	1	Dakhin surma	Sylhet	Sylhet	15 Nov 2014	KY618810
L28	Mondabag	1	Kasba	Bramhanbaria	Chittagong	10 Aug 2015	KY608802
L29	Sebarhat	1	Senbag	Noakhali	Chittagong	13 Aug 2015	KY608803
L30	Mohipal	1	Feni Sadar	Feni	Chittagong	14 Aug. 2015	KY618811
L31	Mohipal Primary School	1	Feni Sadar	Feni	Chittagong	14 Aug. 2015	KY628427
L32	Satkania	1	Satkania	Chittagong	Chittagong	16 Aug 2015	KY657489
L33	Dighinala HRC	1	Dighinala	Khagrachari	Chittagong	12 Aug 2015	KY608804
L34	Matiranga Dhibi	1	Matiranga	Khagrachari	Chittagong	18 Aug 2015	KY608805
L35	Rumakarai	1	Ruma	Bandarban	Chittagong	20 Aug 2015	KY657488
L36	Kawkhali Bazar	1	Kawkhali	Rangamati	Chittagong	21 Aug 2015	KY583089
L37	Thanapara Sardah	1	Charghat	Rajshahi	Rajshahi	23 Nov 2015	KY628429
L38	Nalchiti primary sc. field	1	Nalchiti	Jhalokati	Barisal	15Feb 2016	KY618814
L39	BRAC More	1	Jhalokati Sadar	Jhalokati	Barisal	15 Feb. 2016	KY657491
L40	Bagharibazar	1	Rajapur	Jhalokati	Barisal	16 Feb. 2016	KY618813
L41	Kawkhali Upz P chottor	1	Kawkhali	Pirojpur	Barisal	16 Feb. 2016	KY583090
L42	Shakharikati	1	Mathbaria	Pirojpur	Barisal	16 Feb. 2016	KY583091
L43	Patarhat	1	Mehendiganj	Barisal	Barisal	18 Feb 2016	KY583092
L44	Panpatti	1	Golachipa	Patuakhali	Barisal	20 Feb 2016	KY583093
L45	Agailjhara uni P office	1	Agailjhara	Barisal	Barisal	10 Feb 2016	KY628430
L46	Mohespur	1	Bakerganj	Barisal	Barisal	10 Feb 2016	KY618812
L47	Bhaluka Bazar	1	Bhaluka	Mymensingh	Mymensingh	12 Nov 2016	KY657499
L48	Trishal primary school	1	Trishal	Mymensingh	Mymensingh	12 Nov 2016	KY657500
L49	BAU campus	2	BAU sadar	Mymensingh	Mymensingh	13 Nov 2016	KY657501
L49	BAU campus	2	BAU sadar	Mymensingh	Mymensingh	13 Nov 2016	KY657502
L50	Nandail	1	Muktagacha	Mymensingh	Mymensingh	30 Oct 2016	KY657503
L51	Sarishabari highschool	1	Sarishabari	Jamalpur	Mymensingh	02 Nov 2016	KY657504
L52	Sadar Hospital and pri sch	2	Netrokona sadar	Netrokona	Mymensingh	03 Nov 2016	KY657494
L52	Sadar Hospital and pri sch	2	Netrokona sadar	Netrokona	Mymensingh	03 Nov 2016	KY657495
L53	Gauripur Upz complex	1	Gauripur	Mymensingh	Mymensingh	10 Nov 2016	KY657496
L54	Dighir par	2	Hosenpur	Kishorganj	Mymensingh	01 Nov 2016	KY657497
L55	Sadar Thana more	1	Sherpur sadar	Sherpur	Mymensingh	03 Nov 2016	KY657498
L56	Dhunat Upz. Chatter	1	Dhunat	Bogra	Rajshahi	04 Jan. 2018	MG873538
L57	Municipality Orchard	1	Naoga Sadar	Naogaon	Rajshahi	04 Jan. 2018	MG873539
L58	Nijampur	1	Nachole	Chapainawabganj	Rajshahi	03 Jan. 2018	MG873540
L59	Hakimpur Nursery	1	Hakimpur	Dinajpur	Rangpur	29 Dec. 2017	MG873541
L60	Shibpur	1	Gabindaganj sadar	Gaibandha	Rangpur	02 Jan. 2018	MG873542
L61	Ghariaidanga	1	Rujarhat	Kurigram	Rangpur	30 Dec.2017	MG873543
L62	Rasulpur School ground	1	Pirganj	Rangpur	Rangpur	27 Dec. 2017	MG873544
L63	Saidpur airport surrounding	1	Saidpur	Nilfamari	Rangpur	01 Jan. 2018	MG873545
L64	Barobala	1	Mithapukur	Rangpur	Rangpur	28 Dec.2017	MG873546
L65	Pirganj fire station orchard	1	Pirganj	Thakurgaon	Rangpur	31 Dec. 2017	MG873547
L66	Debiganj bus stand	1	Debiganj	Panchagar	Rangpur	25 Dec. 2017	MG873548
L67	Atwari sadar thana more	1	Atwari	Panchagar	Rangpur	26 Dec. 2017	MG873549

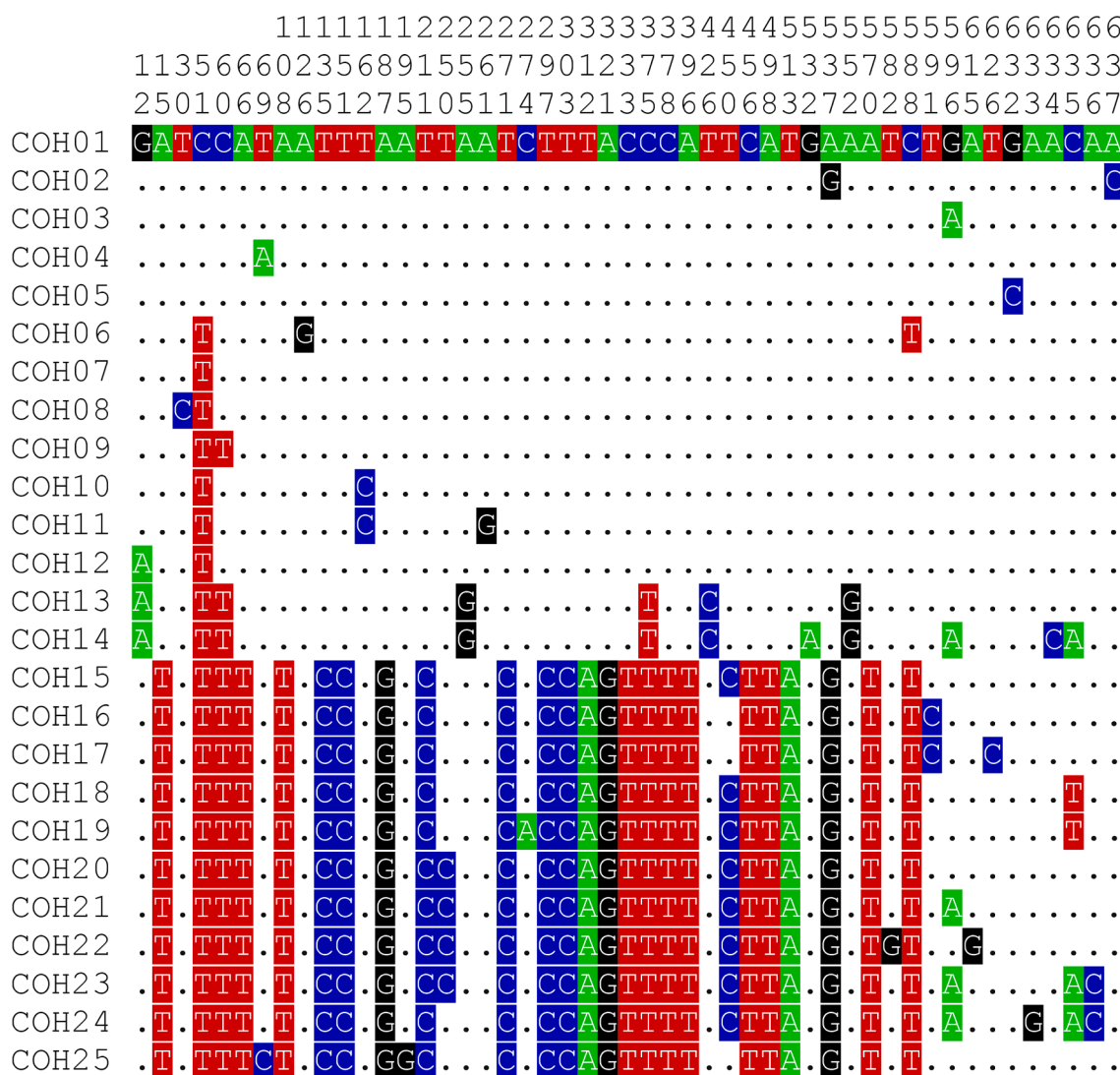


Fig. 3. Twenty five haplotypes in Bangladesh and their variable sites with changed position. The upper three numeric lines denotes the position on longitudinal basis of the each sequence. Each dot represent the identical sequence.

Table 1. The specimens were preserved in 99% ethanol prior to DNA extraction.

Molecular data collection

The molecular analyses were conducted in the Institute of Tropical Agriculture laboratory of Kyushu University, Japan. Genomic DNA was extracted from the legs of specimens that were preserved in alcohol by using QIAGEN DNeasy Blood and Tissue kit (Qiagen, Maryland, USA). Amplification of both mitochondrial and nuclear DNA was done by polymerase chain reaction (PCR). For, mitochondrial DNA analysis, primers for COI gene fragment, COI 1–3 (5'ATAATTTTATAGTTATACC'3) and COI 2–4 (5'TCCTAAAAATGTTGAGGAAA'3) were used as forward and reverse primers as cited by Crozier and Crozier (1993). The thermal cycling

parameters for COI basically followed the protocols established by Crozier and Crozier (1995) and Sameshima et al. (1999), including 95 °C for 5 min for initial denaturation, 35 cycles of dissociation (92 °C, 1 min), annealing (54 °C, 1 min), and extension (70 °C, 2 min). For Enzymatic PCR and sequencing clean-up, Illustra and ExoProStar were followed according to the instruction of the manufacturer GE Healthcare. Exonuclease (1 reaction μL^{-1} , Solution in 20 mM Tris-HCl (pH 7.5), 0.1 mM EDTA, 1 mM DTT, 50% (v/v) glycerol) and Alkaline phosphate (1 reaction μL^{-1} , Solution in 20 mM HEPES-NaOH (pH 7.4), 1 mM MgCl_2 , 0.1 mM ZnCl_2 , 0.1% (v/v) Triton X-100, 50% (v/v) glycerol) were added to the PCR product and incubate 37 °C for 15 min and 80 °C for 15 min to inactivate the enzymes.

For cycle sequencing, ABI PRISM Big Dye Terminator v3.1 cycle sequencing kits from Applied Biosystems were used in an automated sequencer. Sequencing reactions were performed using ABI 3100 Avant

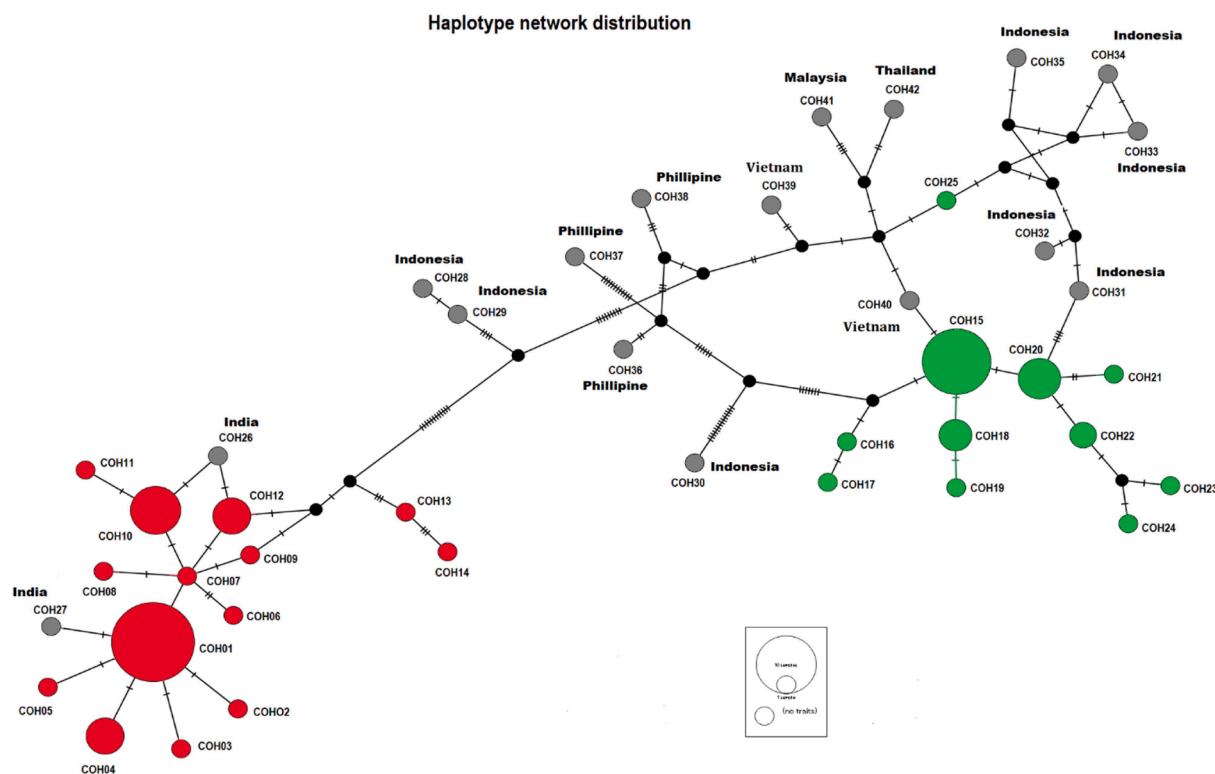


Fig. 4. Haplotype network of *O. smaragdina*. Solid colored circles indicate individual haplotype while inferred haplotypes are depicted by black circles. Single bar connecting two haplotypes corresponds to a single base pair mutation. Each hatch mark on the bar indicate single base pair mutations. Haplotypes belonging to Indian clades are separated from the SE Asian clades by one of the largest number of mutational steps (27) inferred in the network. The locality information corresponding to each haplotype are represented in Table 2.

DNA Sequencer (Applied Biosystems).

Haplotype network analysis

For haplotype network analysis of *O. smaragdina* populations, a total 93 sequences of 693 bp, have been analyzed including 71 sequences of COI genes from 67 localities of Bangladesh. The joining of all the haplotypes identified from Bangladesh with the referential sequence data of COI was used from Azuma et al. (2002), Azuma et al. (2006) and Asaka (2010) has been done for networking. The sequencing analysis was done by using Vector NTI Advance ver. 11.5 software. The sequences of COI were aligned by ClustalW using MEGA 6.0 software (Tamura et al., 2013). Haplotype network were determined by using TCS 1.21 software and the network figure has been generated based on TCS results by POP ART- 1.7 (Clement et al., 2000). The nucleotide sequences of COI were deposited in the GenBank with accession number were corresponding to Table 1.

Results and discussions

Oecophylla smaragdina haplotypes in Bangladesh

Forty-two haplotypes were recorded from 93 sequences of COI mitochondrial gene of 639 bp. The nucleotide diversity was 0.025 and a total 89 segregating sites were recorded. The total number of parsimony

informative sites was 50. Seventy two sequence of COI genes have been used from the samples of *O. smaragdina* in Bangladesh resulted 25 haplotypes. The 25 haplotypes identified from Bangladesh are presented in Fig. 3. In this figure, only the variable sites and its position were displayed.

Haplotype networking

Bangladeshi haplotypes were marked from COH01 to COH25. COH26 to COH27 are considered as Indian type, COH28 to COH35 are from Indonesia, COH36 to COH38 from Philippines, COH39 to COH40 from Vietnam, COH41 from Malaysia and COH42 from Thailand (Fig. 4). The detailed haplotype list were presented in Table 2. Bangladeshi haplotypes were clustered into two distinct zone on the network tree. Haplotype COH01 to COH13 were closely associated with the haplotypes from the Panjab state of India with COH26 and COH27. Moreover, COH10 and COH12 includes the haplotypes from Indian isolates along with the Bangladeshi haplotypes. On the other hand the Bangladeshi haplotypes from COH14 to COH25 are found to be clustered with the haplotypes associated from SE Asian clades. They were well connected with the haplotypes from Indonesia and Vietnam. Like other ant species, *O. smaragdina* were profoundly influenced by Pleistocene glaciation. This also happened in this South Asian continent.

The haplotype network showed a clear distribution of Indian and SE Asian haplotypes in Bangladesh. This shape of network seems

Table 2

List of haplotypes inferred from COI gene sequences corresponding to Fig. 4.

SI No.	Haplotype No.	Corresponding locality (Country)
1	COH01	L01, L02, L05, L07, L09, L10, L11, L13, L19, L38, L40, L56, L57, L58, L60, L61, L63, L66, L67 (Bangladesh)
2	COH02	L44 (Bangladesh)
3	COH03	L04 (Bangladesh)
4	COH04	L16, L20, L21, L32 (Bangladesh)
5	COH05	L62 (Bangladesh)
6	COH06	L17 (Bangladesh)
7	COH07	L14 (Bangladesh)
8	COH08	L22 (Bangladesh)
9	COH09	L12
10	COH10	L08, L08 (02), L03, L59, L64 (Bangladesh) ISOA2 (India)
11	COH11	L18
12	COH12	L06 (Bangladesh), ISOA3, ISOA4, ISOA5 (India)
13	COH13	L45 (Bangladesh)
14	COH14	L46 (Bangladesh)
15	COH15	Nurbag, L23, L24, L25, L27, L29, L30, L34, L35, L47, L49, L53, L54, L55 (Bangladesh)
16	COH16	L36 (Bangladesh)
17	COH17	L32 (Bangladesh)
18	COH18	L41, L42, L43 (Bangladesh)
19	COH19	L37 (Bangladesh)
20	COH20	L52 (2), L52, L28, L33, L26 (Bangladesh)
21	COH21	L49(2) (Bangladesh)
22	COH22	L39 (Bangladesh)
23	COH23	L51 (Bangladesh)
24	COH24	L48 (Bangladesh)
25	COH25	L31 (Bangladesh)
26	COH26	ISOA6 (India)
27	COH27	ISOA1 (India)
28	COH28	Larantuka (Indonesia)
29	COH29	Lewleba (Indonesia)
30	COH30	Sulawesi (Indonesia)
31	COH31	Bogor (Indonesia)
32	COH32	Bali (Indonesia)
33	COH33	Rakata (Indonesia)
34	COH34	Jakarta (Indonesia)
35	COH35	Lombok (Philippine)
36	COH36	Manilla (Philippine)
37	COH37	Diplog (Philippine)
38	COH38	Moalboal (Philippine)
39	COH39	Hunloc (Vietnam)
40	COH40	Hatlot (Vietnam)
41	COH41	Kualalumpur (Malaysia)
42	COH42	Bangkok (Thailand)

bottleneck-type. The two types (groups) are connected with many missing haplotypes (longer branch); it is suggesting survived populations remained in refugia. Star-like subnetworks suggest recent expansion of populations. In the geographical distribution suggested that the western haplotypes are relatively less diverse and is connected mainly with the Indian haplotypes while the haplotypes from eastern part showed more genetic diversification.

Distribution pattern of Indian and SE Asian type of *O. smaragdina*

The geographical distribution of Indian and SE Asian haplotypes corresponding to sampling locality are shown in Fig. 5. Haplotype network analysis clearly mentioned the presence of both Indian and SE Asian types in Bangladesh. However, their distribution is not equal. The western part mostly occupied by Indian type, eastern part is occupied by SE Asian type and the central part has the overlapping populations of

both the types. This result is identical to the results of phylogeographic study by Rahman et al. (2017b). According to those results, Bangladesh can be considered as a transitional zone of both the two clades. Divergence time of the ant genus *O. smaragdina* is thought to be a significant factor of such distribution. Diversification within groups in this continent was recorded from the Middle Pliocene to Early Pleistocene (Azuma et al. 2002). After this period, world has encountered a significant climatic change.

It might also affect the distribution of *O. smaragdina* in different parts of the world. Lokkers (1986) suggested two limiting factors, low temperature and humidity for distribution range of *O. smaragdina* in Australia. During Last Glacial Maximum (LGM), the tropic region shifted southward and it retained northward after glaciation. The present study suggested that the Indian and Southeast Asian clades of *O. smaragdina* expanded their distribution northward along suitable regions with high temperature and humidity, and then the two types supposedly encountered and overlapped in central Bangladesh.

Vidya et al. (2009) have found the similar results in their phylogeographic study of distribution of Asian elephants. This sorts of haplotype network distribution revealed that there was no effective barrier of separating Indian and SE Asian haplotypes in Bangladesh, hence Bangladesh is considered as a transitional zone of genetic diversification of *O. smaragdina* populations. In the previous phylogeographic study by Azuma et al. (2002, 2006), the diversification of *O. smaragdina* occurred during Pleistocene in this continent and the effects of last glacial maximum (LGM) might have an influential phenomenon of such distribution. Romalho et al. (2016), assessed the haplotype diversity and distribution patterns based on the correlation between genetic and geographic distance and revealed that *Camponotus textor* has deep population divergence resulted three distinct groups that featured the possible reduction of gene flow between colonies. This can be supported by the findings of Seal et al. (2015) who mentioned in their phylogeography of two *Trachymyrmex* species along the south eastern coastal plain of North America and characterized the both species by reduced haplotypic variation that may indicate recent expansion and / or bottleneck associated with changed climatic condition. The haplotype network includes several small clades (with 2–4 haplotypes in each) with geographically limited distribution, but one geographical region may have received haplotypes from two or more of such clades. This pattern could indicate mixing of different gene pools during postglacial colonization from an ancestral source with some spatial genetic differentiation that can support the findings of Goropashnaya et al (2007). The results of the study suggest a scenario of dispersal: 1) before Last Glacial Maximum (LGM), the haplotypes observed in Bangladesh would be already established; 2) during the LGM, the Bengal Delta supposed to be vacant for *O. smaragdina* distribution because the northern limit of the species would be located down to the south; 3) after the LGM, the isolated populations in southern refuge areas of India and SE Asia extended to south, and in Bengal Delta the Indian type populations came from west and the SE Asian type populations from east; 4) when the Indian type populations and the SE Asian type populations contacted in the Bengal Delta, each of the types already contained several haplotypes of mtDNA, and reproductive isolation is not established.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Distribution pattern of *O. smaragdina* in Bangladesh

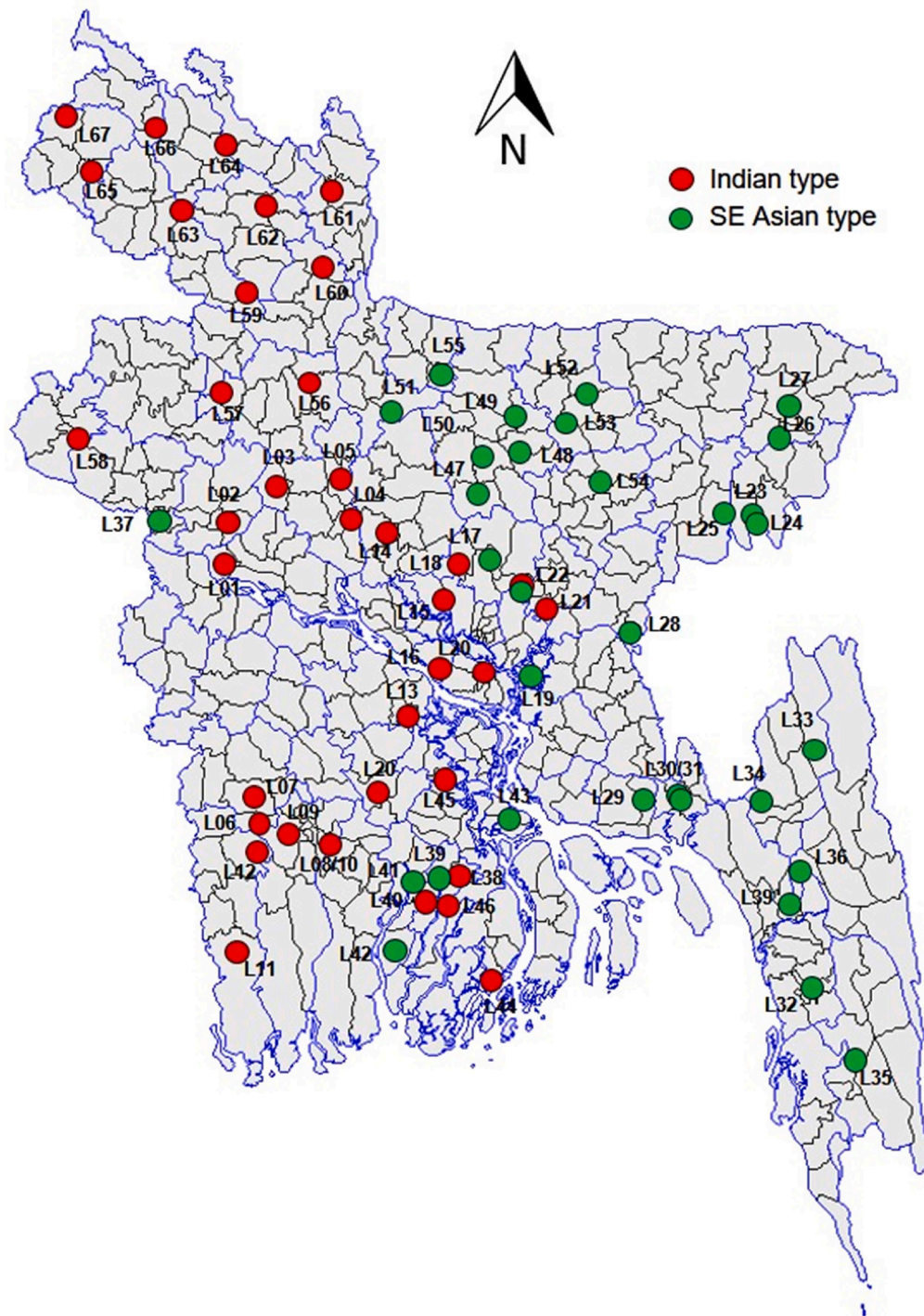


Fig. 5. Geographical distribution of Indian and SE Asian haplotypes in Bangladesh. The red and green circle denotes the Indian and SE Asian haplotypes respectively. The locality of the respective haplotypes are corresponding to [Tables 1 & 2](#). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

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