INTRODUCTION

Sumatran elephant (*Elephas maximus sumatranus* Temminck, 1847) is one of the Asian elephant subspecies distributed across the Sumatran mainland. The Sumatran elephant has been classified as critically endangered under the International Union for Conservation of Nature and Natural Resources (IUCN) Red List (Gopala et al., 2011). World Wide Fund for Nature (WWF) Indonesia estimated that the Sumatran elephant population was about 2,400-2,800, and the population continuously reduced due to the lack of habitat and hunting activity (WWF 2008). Fragmentation and habitat loss are primary factors of a globally declined population (Gopala et al., 2011; Hermes et al., 2013). Fragmentation and isolation of populations lead to demographic problems and shrinking genetic diversity due to limited gene flow between elephant populations. Limited gene flow may cause genetic drift, inbreeding, loss of allelic expression, and decrease disease resistance (Allendorf et al., 2012). Thus, it is necessary to preserve Sumatran elephants and maintain their genetic diversity as part of conservation genetic strategies. With genetic analysis, it is possible to study status, distribution, kinship, ancestry, and genetic inheritance. Genetic analysis can be done using different techniques, one of which is based on mitochondrial cytochrome b gene (*Cyt b*). Blood samples were collected from 11 elephants in Seblat Natural Ecotourism Park. Based on mt-DNA Cytochrome b gene analysis, low genetic diversity was found in the Sumatran elephant population, indicated by 99-100% sequence similarity among elephant samples. Phylogenetic analysis showed that all elephants were in the same clade and has a close relationship with Borneo elephants. Additionally, the Median-joining network illustrated only two haplotypes in the Sumatran elephant population. The low genetic diversity of the Sumatran elephant indicates that a strategic breeding program should be seriously taken into account to prevent the Sumatran elephant from extinction.

Key words: Cytochrome b, genetic diversity, mitochondrial DNA, Sumatran elephant

ABSTRACT

Sumatran elephant (*Elephas maximus sumatranus* Temminck, 1847) is one of the Asian elephant subspecies distributed in Sumatera Island and classified as endangered species due to hunting and high habitat fragmentation. This study aimed to analyze the genetic relationship of Sumatran elephants based on the mitochondrial cytochrome b gene (*Cyt b*). Blood samples were collected from 11 elephants in Seblat Natural Ecotourism Park. Based on mt-DNA Cytochrome b gene analysis, low genetic diversity was found in the Sumatran elephant population, indicated by 99-100% sequence similarity among elephant samples. Phylogenetic analysis showed that all elephants were in the same clade and has a close relationship with Borneo elephants. Additionally, the Median-joining network illustrated only two haplotypes in the Sumatran elephant population. The low genetic diversity of the Sumatran elephant indicates that a strategic breeding program should be seriously taken into account to prevent the Sumatran elephant from extinction.

Key words: Cytochrome b, genetic diversity, mitochondrial DNA, Sumatran elephant
DNA (mtDNA) and microsatellite diversity for Asian elephant populations and found a single mitochondrial haplotype in Bornean elephant samples analyzed from Sabah.

Another Sumatran elephant habitat in Indonesia is Natural Ecotourism Park (TWA), Seblat, North Bengkulu, and currently, there are 11 domesticated Sumatran elephants there. Meanwhile, genetic analysis using mtDNA Cytochrome b (Cyt b) of those captive elephants has never been conducted and reported in Indonesia. Therefore, we conducted a genetic analysis of Sumatran elephants in Natural Ecotourism Park (TWA), Seblat, North Bengkulu for determining their genetic diversity based on the mtDNA Cyt b gene.

MATERIALS AND METHODS

Samples collection and preparation
Blood samples were collected for a month on August 2018 from a total of 11 individuals of Sumatran elephants in Natural Ecotourism Park (TWA), Seblat, North Bengkulu (Table 1). Blood samples were put into a 5 mL tube containing EDTA using 21G 2 mL syringes from the elephant’s ears. They were kept at -21 °C until further analysis.

Extraction of genomic DNA
A total of 100 µL of blood was used for DNA extraction following Geneaid Blood and Tissue Mini Kit (GS100, GS300) protocol. The DNA purity was checked using a UV-Vis spectrophotometer (Thermo Scientific Evolution 200 series, United State) at a wavelength of 260 nm and 280 nm.

DNA amplification and visualization
A total length of 630 bp mtDNA Cyt b gene fragment was amplified using MDL 3 [5'-CCCACAATTAATGGGCGGAGCG-3’] and MDL 5 [5'-TTACATGAATTGTGCGACCAACCAG-3’] primers (Fernando et al., 2000). The PCR reaction started with pre-denaturation at 94 °C for 4 min, and it was followed by 40 cycles of denaturation at 94 °C for 30 s, annealing at 55ºC for 45 s, extension at 72 °C for a min, and final extension at 72 °C for 7 min. The PCR product was pipetted into 1% agarose gel and run for 30 min at 100 Volt. Then, the gel was stained with ethidium bromide for 15 min, followed by washing with ddH2O for 1 min. Visualization of DNA was performed under UV light using the Gel Documentation System (Axygen). The PCR product was sent to PT. Genetika Sains Indonesia and forwarded to first Best Malaysia for sequencing.

Table 1. Profile and DNA purity of 11 captive Sumatran elephants (Elephas maximus sumatranus Temminck, 1847) in Natural Ecotourism Park (TWA) in Seblat, North Bengkulu

<table>
<thead>
<tr>
<th>Elephant Identity</th>
<th>Gender</th>
<th>Origin</th>
<th>Wavelength (nm)</th>
<th>Concentration (ng/µL)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mega (MG)</td>
<td>Female</td>
<td>Ipuh, Muko-Muko</td>
<td>0.074</td>
<td>0.058</td>
</tr>
<tr>
<td>Anggarini (AG)</td>
<td>Female</td>
<td>Ipuh, Muko-Muko</td>
<td>0.065</td>
<td>0.054</td>
</tr>
<tr>
<td>Desi (DS)</td>
<td>Female</td>
<td>Seblat, North Bengkulu</td>
<td>0.066</td>
<td>0.053</td>
</tr>
<tr>
<td>Sari (SR)</td>
<td>Female</td>
<td>Ipuh, Muko-Muko</td>
<td>0.056</td>
<td>0.049</td>
</tr>
<tr>
<td>Devi (DV)</td>
<td>Female</td>
<td>Ipuh, Muko-Muko</td>
<td>0.056</td>
<td>0.049</td>
</tr>
<tr>
<td>FT</td>
<td>Female</td>
<td>Ipuh, Muko-Muko</td>
<td>0.064</td>
<td>0.052</td>
</tr>
<tr>
<td>Darmi (DR)</td>
<td>Female</td>
<td>PT, Alno Group, Air Rami, North Bengkulu</td>
<td>0.072</td>
<td>0.057</td>
</tr>
<tr>
<td>Bona (BN)</td>
<td>Female</td>
<td>Ipuh, Muko-Muko</td>
<td>0.077</td>
<td>0.062</td>
</tr>
<tr>
<td>Robi (RB)</td>
<td>Male</td>
<td>Ipuh, Muko-Muko</td>
<td>0.070</td>
<td>0.056</td>
</tr>
<tr>
<td>Nelson (NL)</td>
<td>Male</td>
<td>Seblat, North Bengkulu</td>
<td>0.071</td>
<td>0.058</td>
</tr>
<tr>
<td>Ucok (UC)</td>
<td>Male</td>
<td>Seblat, North Bengkulu</td>
<td>0.069</td>
<td>0.056</td>
</tr>
</tbody>
</table>
RESULTS

The DNA quantification

The DNA quantification results showed that extracted genomic DNA of 11 captive elephants was in high concentration. It ranged from 491.7 to 596 ng/μL (Table 1). Devi (DV) was the highest DNA concentration (596 ng/μL), while FT was the lowest DNA concentration (417 ng/μL). The total concentration of genomic DNA to amplify more than 500 base pairs of DNA fragments was recommended as 40 ng/μL (First Base DNA Sequencing Service 2000). Therefore, the DNA concentration extracted from elephants can be used for sequencing analysis. The result of DNA amplification showed that the amplicon size was 630 base pairs (Figure 1).

Analysis of Cyt b gene sequence in Sumatran elephant

Sequences of the Sumatran elephant have been registered and can be accessed at National Center for Biotechnology Information (NCBI) website. Basic local alignment search tool (BLAST) analysis showed that all elephants were closely related to *Elephas maximus*. The similarity value between the elephant Cyt b gene sequence with a published sequence on the NCBI website ranged from 98.49 to 100% (Table 3). A high similarity percentage (99 to 100%) indicated that elephants were identified as the same species as *Elephas maximus*. Based on the alignment of samples with two Asian elephant subspecies, *E. maximus maximus*, and *E. maximus indicus*, all samples are closely related to *E. maximus borneensis*.

All sequences obtained in this study were then aligned to find out polymorphisms within the Cyt b gene fragment. A total of 25 polymorphism sites were found in the Sumatran elephant population compared to published sequences. All Sumatran elephants were genetically similar due to only one polymorphism found within this population at the position of 001, which has the same Timine between Darmi (DR) and Robi (RB) (Table 3).

Phylogenetic tree and network analysis of Sumatran elephant

The phylogenetic tree was constructed for 11 captive Sumatran elephants from TWA, Seblat, and North Bengkulu with comparative elephant genes from the gene bank (Figure 2). In this figure, there were two main clusters. Cluster 1 grouped 34 elephants that segregated two individuals, HQ113851.1 for species with LaoPDR-E haplotype and AJ303056.1 for having

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**Table 2.** The accession number of mtDNA Cyt b sequences obtained in this study and out-group sequences based on NCBI

<table>
<thead>
<tr>
<th>mtDNA Cyt-b sequences obtained in this study</th>
<th>Accession Number (NCBI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>AY245825.2</td>
<td></td>
</tr>
<tr>
<td>AY245812.2</td>
<td></td>
</tr>
<tr>
<td>AY245825.2</td>
<td></td>
</tr>
<tr>
<td>FJ979436.1</td>
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<td>AY245803.2</td>
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<td>AY245825.2</td>
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<td>AY245810.2</td>
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<td>AY245806.2</td>
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<tr>
<td>mtDNA Cyt-b sequences of outgroup</td>
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<tr>
<td>AF132520.1</td>
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<td>EU116015.1</td>
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<td>AF132526.1</td>
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<td>MN14748.1</td>
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<td>FJ753556.1</td>
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</table>
mitochondrial partial Cyt b gene-Israel, while Cluster II was formed based on 495th nucleotide (counted from the first base of PCR product) consisting of Adenine (A) with bootstrap value was 54 (Table 4). Figure 2 also showed that 11 captive Sumatran elephants have a close relationship with Asian elephants as shown by the 100% of similarity value. A high similarity value (100%) indicates a close relationship among 11 Sumatran elephants in TWA, Seblat.

Median Joining Network (MJ-Network) analysis was conducted to get haplotype distribution and haplogroup of Sumatran elephants and published sequences on the NCBI website. A total of 18 haplotypes with 16 parsimony variable sites and 10 singleton variable sites have been identified in this study (Table 4). Sumatran elephants were grouped into two haplotypes, i.e. haplotypes 1 and 2. Nine Sumatran elephant samples were grouped into haplotype 1 which is not shared with other elephants. Moreover, two Sumatran elephants were grouped into haplotype 2 which is shared with the Borneo elephant (AY245825.2) (Figure 3). These findings indicated that Sumatran elephants have a close relationship with the Borneo elephant.

![Image](image_url)

**Fig. 1.** The PCR product of mtDNA Cyt b gene in Sumatran elephant population. 1kb is a 1 kb marker ladder; 1 to 11 are Sumatran elephant samples.

**Table 3.** Alignment of partial Cyt b gene of Sumatran elephants (*Elephas maximus sumatranus* Temminck, 1847) compared with Asian elephants (*Elephas maximus*) at Genebank

<table>
<thead>
<tr>
<th>Sample name</th>
<th>Species affiliation</th>
<th>Similarity (%)</th>
<th>Origin species</th>
<th>Accession Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mega (MG)</td>
<td><em>Elephas maximus</em> haplotype BT</td>
<td>100.00</td>
<td>Borneo</td>
<td>AY245825.2</td>
</tr>
<tr>
<td></td>
<td><em>Elephas maximus</em> haplotype BU</td>
<td>99.83</td>
<td>Borneo</td>
<td>AY245812.2</td>
</tr>
<tr>
<td>Anggraini (AG)</td>
<td><em>Elephas maximus</em> haplotype BT</td>
<td>100.00</td>
<td>Borneo</td>
<td>AY245825.2</td>
</tr>
<tr>
<td></td>
<td><em>Elephas maximus</em> isolate 24</td>
<td>99.15</td>
<td>North America</td>
<td>FJ979436.1</td>
</tr>
<tr>
<td>Desi (DS)</td>
<td><em>Elephas maximus</em> haplotype BT</td>
<td>100.00</td>
<td>Borneo</td>
<td>AY245825.2</td>
</tr>
<tr>
<td></td>
<td><em>Elephas maximus</em> isolate 26</td>
<td>99.15</td>
<td>North America</td>
<td>FJ979437.1</td>
</tr>
<tr>
<td>Sari (SR)</td>
<td><em>Elephas maximus</em> haplotype BT</td>
<td>100.00</td>
<td>Borneo</td>
<td>AY245825.2</td>
</tr>
<tr>
<td></td>
<td><em>Elephas maximus</em> haplotype BH</td>
<td>99.15</td>
<td>Borneo</td>
<td>AY245803.2</td>
</tr>
<tr>
<td>Devi (DV)</td>
<td><em>Elephas maximus</em> haplotype BT</td>
<td>100.00</td>
<td>Borneo</td>
<td>AY245825.2</td>
</tr>
<tr>
<td></td>
<td><em>Elephas maximus</em> haplotype BR</td>
<td>99.15</td>
<td>Borneo</td>
<td>AY245811.2</td>
</tr>
<tr>
<td>Fatma (FT)</td>
<td><em>Elephas maximus</em> haplotype BT</td>
<td>100.00</td>
<td>Borneo</td>
<td>AY245825.2</td>
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<tr>
<td></td>
<td><em>Elephas maximus</em> isolate EmTHb13</td>
<td>99.15</td>
<td>Thailand</td>
<td>KJ187801.1</td>
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<tr>
<td>Darmi (DR)</td>
<td><em>Elephas maximus</em> isolate EmTHb01</td>
<td>99.15</td>
<td>Thailand</td>
<td>KJ187789.1</td>
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<tr>
<td></td>
<td><em>Elephas maximus</em> haplotype BU</td>
<td>99.83</td>
<td>Borneo</td>
<td>AY245812.2</td>
</tr>
<tr>
<td>Bona (BN)</td>
<td><em>Elephas maximus</em> haplotype BQ</td>
<td>99.15</td>
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<td>Borneo</td>
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</tr>
<tr>
<td>Robi (RB)</td>
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<td><em>Elephas maximus</em> haplotype BM</td>
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<td>AY245814.2</td>
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<tr>
<td>Nelson (NL)</td>
<td><em>Elephas maximus</em> isolate 199</td>
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<td><em>Elephas maximus</em> haplotype LaoPDR-E</td>
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<td>Nakai Plateau, Laos</td>
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</tr>
<tr>
<td>Ucok (UC)</td>
<td><em>Elephas maximus</em> haplotype BK</td>
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<td>Borneo</td>
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</tr>
<tr>
<td></td>
<td><em>Elephas maximus</em> haplotype BM</td>
<td>98.98</td>
<td>Borneo</td>
<td>AY245806.2</td>
</tr>
</tbody>
</table>
Fig. 2. Phylogenetic tree of 11 captive Sumatran elephants (Elephas maximus sumatranus Temminck, 1847) and outgroup. Construction is based on the neighbor-joining tree method with a 1000x bootstrap replication value.
Table 4. Nucleotide site of partial Cyt b gene Sumatran elephants (*Elephas maximus sumatranus* Temminck, 1847) compared with Asian elephants (*Elephas maximus*) at Genbank

<table>
<thead>
<tr>
<th>Position</th>
<th>0 0 0 1 1 2 2 3 3 3 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 5 5 5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Elephant</td>
<td>0 0 4 2 4 0 5 7 8 8 9 9 0 0 1 2 3 4 4 4 4 4 4 4 4 4 5 5 5</td>
</tr>
<tr>
<td>1 5 8 8 1 4 0 3 0 2 2 3 3 4 8 0 0 2 5 2 0 5 6 3 7</td>
<td></td>
</tr>
</tbody>
</table>

| Female 1 (MG) | A | C | T | A | G | G | C | T | A | T | A | C | T | G | T | T | A | T | A | A | A | G | T | C | A |
| Female 2 (AG) |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Female 3 (DS) |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Female 4 (SR) |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Female 5 (DV) |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Female 6 (FT) |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Female 7 (DR) |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Female 8 (BN) |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Male 1 (RB)   | T |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Male 2 (NL)   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Male 3 (UC)   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| AY245825.2    | T |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| AY245807.2    | T |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| AY245812.2    | T |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FJ979436.1    | T | T | G |   |   | G |   | C |   | C |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FJ979458.1    | T | G |   |   | C |   | C |   | G |   | C |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| AY245813.2    | T | C | G |   | T |   | C |   | C |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| AY245816.2    | T | G |   |   | C |   | C |   | G |   | C |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| KJ187789.1    | T | G |   |   | C |   | C |   | G |   | C |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| FJ979501.1    | T | G |   |   | G |   | C |   | C |   | G |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| AJ303036.1    | T | G | A |   | G |   | G |   | C |   | C |   | A | T |   |   |   |   |   |   |   |   |   |   |   |   |
| FJ979437.1    | T | C | G |   | T |   | C |   | C |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| AY245809.2    | T | T | G |   | T |   | G |   | C |   | C |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| AY245811.2    | T | G |   |   | C |   | C |   | C |   | G |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| KJ187801.1    | T | T | G | A |   | G |   | C |   | C |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| KJ187791.1    | T | C | G |   | T |   | C |   | C |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| HQ113851.1    | T | C | G |   | C |   | C |   | C |   | G | A | C | T |   |   |   |   |   |   |   |   |   |   |   |   |
| FJ979514.1    | T | T | G |   | G |   | C |   | C |   | T |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| AY245824.2    | T | T | G |   | G |   | C |   | C |   | G |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| AY245814.2    | T | G |   |   | C |   | C |   | G |   | C |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| AY245803.2    | T | G |   |   | C |   | C |   | C |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| AY245806.2    | T | T | G |   | G |   | C |   | C |   | A |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| AY245810.2    | T | T | G |   | G |   | A |   | C |   | C |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| KJ187790.1    | T | G |   |   | C |   | T |   | G |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| AY245804.2    | T | T | G |   | G |   | C |   | C |   | T |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| KJ187803.1    | T | T | G |   | G |   | C |   | C |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
DISCUSSION

High similarity sequences among Sumatran elephants were found in this population which indicated their genetic variation was low. It might be due to founder events, bottlenecks, genetic drift, inbreeding, and small population size for a long time (Frankham et al. 2010). A previous study reported by Sulandari & Zein (2012) stated that there were 21 Sumatran elephants in Seblat captivity. Currently, we found only 11 Sumatran elephants there. This result indicated that Sumatran elephants in Seblat National Park were critically endangered. A sustainable breeding program is extremely needed to improve their population in Seblat. This high similarity also suggested that mtDNA diversity, especially in the Cytochrome b gene region, is very low in the Seblat. This result is in agreement with previous studies using other mtDNA fragments, such as D-loop, COXII, and COI (Sulandari & Zein, 2012; Wibowo et al., 2021; Virnarenata et al., 2021).

The low genetic diversity of Sumatran Island may also increase higher reproductive failure because removal of heterozygous alleles. Habel and Zachos (2013) stated that low genetic diversity might be due to inbreeding, which causes the existence of homozygous individuals, mutation damage of recessive alleles, bottlenecks effect, and gene flow imbalance. Previous studies that showed the Sumatran elephant experienced a decline in terms of low genetic diversity by using other mtDNA targets have been reported by some researchers (Hedges et al., 2005; Sulandari & Zien 2012; Nur et al., 2019). Conservation efforts can be conducted to prevent the extinction of the Sumatran elephant (Elephas maximus sumatranus Temminck, 1847). The number of Sumatran elephants in Seblat is decreased by year. It can be a serious problem to maintain the elephant population. Strategic action should be designed to increase Sumatran elephant diversity and their number by introducing foreign elephants from other regions or by artificial insemination, especially in Natural Park (TWA), Seblat. The elephant breeding program should also be deeply studied to create a sustainable program. According to Heber et al. (2012), high heterogeneity in a population likely rise the potency of breeding, so allele diversity will increase in the population.

This study found two haplotypes of the Sumatran elephant (haplotype 1 & 2). These two haplotypes were also previously reported by Sulandari and Zein (2012) which also have low genetic diversity as in this study. This study showed that most elephant samples were grouped into haplotype 1, and only two samples were grouped into haplotype 2 which deviated from haplotype 1. Sumatran elephant has haplotypes that are different from the elephant in India (Ahlering et al., 2011; Elliza et al., 2015). However, introduction from Borneo elephant was found based on haplotype analysis in this study. This probability may be happening because animals can easily migrate during the Pleistocene glaciations period, much of the Sunda
shelf was exposed and the western Indo-Malayan archipelago formed a single landmass designated as Sundaland (MacKinnon et al., 1996). Borneo elephant has six haplotypes that share with other elephants from Thailand, Malaysia, and South Asia (Vidya et al., 2011). Because the haplotype has low genetic diversity, further studies are needed to increase or even maintain the Sumatran elephant population such as in breeding strategies between elephants.

CONCLUSION

In conclusion, the genetic diversity of Sumatran elephants in Seblat was very low based on a partial fragment of the mtDNA Cytochrome b gene. Sustainable breeding programs and conservation should be taken into account to improve the genetic diversity of Sumatran elephants in Seblat, therefore they can be saved from extinction. One of the recommended breeding strategies is a genetic exchange between captive populations and wild groups. To reach successful output in a breeding program, it should observe several alterations, such as reducing overwork, increasing social interaction, feeding them effectively, etc.

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CONFLICT OF INTEREST

The authors declare no conflict of interest.

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