ABSTRACT: This communication is the first report on mitochondrial lineage of Andaman wild boar based on mitochondrial D-loop sequence information. Andaman wild boar is an endangered endemic species of Andaman & Nicobar archipelago. D-loop sequence information of Andaman wild boar (MT024628-29) was compared with endemic Sus species of Southeast Asia, Eurasian clades of wild boar and Indian wild boar characterized from mainland of India. Phylogenetic analysis, median joining (MJ) network and genetic distance analysis revealed that Andaman wild boar belonged to S. scrofa. Earlier literature suggested that Eurasian wild boars are clustered into five clades. Our analysis revealed that Andaman wild boar had the least genetic distance with Asiatic clade and had the highest genetic distance with the Italian clade. This data was further supported by pairwise Fst. Phylogenetic analysis, MJ network and PCA plot could identify genetic affinity of Andaman wild boar with Asiatic clade of wild boar. Interestingly, Andaman wild boar clustered with wild boars found in two specified geographical regions of India. This may be justified as leftover of cultural diffusion during c. 500/400 BCE.

Key words: Andaman wild boar, Sus, Island Southeast Asia (ISEA), Molecular characterization, D-loop.

INTRODUCTION

Andaman and Nicobar Islands (ANI), a part of Island South East Asia (ISEA), is known globally for its rich floral and faunal diversity. ANI is comprised of 572 islands, among which 37 are inhabited by human population. Geographically, these islands are situated at the juncture of Bay of Bengal and the Andaman Sea. This part of ISEA is known for endemism of faunal species. Records suggest that out of 6697 faunal species present in these islands, 13.5% has been assigned as endemic species (Rao et al. 2013). As per notification of International Union for Conservation of Nature (IUCN), five endemic animal species of these islands are threatened. Andaman wild boar, popularly known as Maupin pig, falls under this threatened category and at present the total population is less than one hundred (www.cpreec.org/123htm). These pigs are inhabitant of Jarawa reserve forest area of Andaman archipelago (De et al. 2013) and fall under the category of schedule III of the Indian Wildlife (Protection) Act, 1972.

Southeast Asia (SEA) is considered a hotspot of wild boar diversity. The uniqueness has occurred due to continuous formation and reformation of islands and islets since early Pliocene as a result of sea level fluctuation (c. 5.2 million years ago, Mya) (Lucchini et al. 2005). The statement on wild boar diversity was further supported by the existence of three informal groups of Sus in SEA; S. verrucosus, S. philippensis (Philippines warty pig) and S. scrofa. The former group consists of S. verrucosus (Javan warty pig), S. barbatus (Bornean warty pig), S. celebensis (Celebes warty pig) and S. cebifrons (Visayan warty pig) (Groves 1997). However, another literature suggests the co-existence of another Sus species in SEA, S. salvanius (pygmy hog) (www.jspui/bitstream/...
which was later characterized as *Porcula salvania* (Funk et al. 2007). Further, global scenario suggests that, Eurasian wild boars consist of five clades present in Asian and European countries. They are known as Asiatic, Near Eastern 1 (NE1), Near Eastern 2 (NE2), European and Italian (Larson et al. 2007, Ottoni et al. 2013).

Indian wild boar (*Sus scrofa cristatusus*), distributed in mainland of India, has been characterized on phenotypic and molecular signature (Srivastava et al. 2015, Jadav et al. 2019). But to date, Andaman wild boar has not been characterized except one solitary preliminary report on phenotypic characterization (De et al. 2013). Moreover, the molecular identity of these pigs is still unknown.

Considering the lack of information on maternal inheritance of Andaman wild boar, we for the first time report the maternal lineage of Andaman wild boar based on D-loop sequence of mitochondrial DNA (mtDNA). In addition, the present report seems to be the pioneer comparative assessment on phylogenetic position of Andaman wild boar reported from SEA with clades reported from vast area of Eurasia as well as Indian subcontinent.

**MATERIALS AND METHODS**

**Ethical approval**

For conducting the present study, all relevant institutional and national guidelines were followed. Andaman wild boar is protected under Wildlife Act 1972 and for that reason, official permission from the Department of Environment and Forest, Andaman and Nicobar Administration was obtained for conducting the present study.

**Study area and sampling**

These pigs were kept at ‘Mini Zoo’ of Andaman and Nicobar Islands. For collection of blood sample, the pig was restrained properly using a snout rope and the neck was stretched upwards. Then the neck region was cleaned with 70 % alcohol and betadine. A 21-gauge needle was inserted caudo-dorsally into the vena cava approximately 1” cranial to the sternum and to the right of the midline. Approximately 3-5 ml blood sample was collected into a vacutainer containing clot activator. The samples were transported to the laboratory maintaining cold chain.

**DNA isolation, PCR amplification and sequencing of mtDNA control region (D-loop)**

Genomic DNA from blood sample was isolated using a commercial kit (GSure Blood DNA Mini Kit, GCC Biotech India Pvt. Ltd, Kolkata, India, Cat. No. G4626) following protocol recommended by the manufacturer. The quality and concentration of isolated DNA samples were checked spectrophotometrically (Eppendorf, Hamburg, Germany). Extracted DNA samples were stored at -20°C till further use.

Partial fragment of the D-loop sequence (678 bp) was amplified using sense and antisense primers described earlier (Giuffra et al. 2000). In brief, PCR was done in a 25 µl volume which contained 2.5 µl of 10 X Taq buffer with 1.5 mM MgCl₂, 0.2 mM dNTPs, 1 µM each forward and reverse primer, 1 IU Taq DNA polymerase (GCC Biotech India Pvt. Ltd, Kolkata, India) and approximately 30 ng genomic DNA with cycling condition mentioned earlier (Georgescu et al. 2012). Amplicon was purified and sequenced in both directions by Sanger dideoxy fingerprinting. The generated sequences were edited using Sequencher v 5.4.6 (Gene Codes Corporation, USA).

**Bioinformatics analysis**

Mitochondrial D-loop sequences of Andaman wild boar were submitted to GenBank with accession numbers MT024628 and MT024629. The sequences were aligned by Clustal W using MEGA X (Thompson et al. 1994, Kumar et al. 2018). To analyze and compare the D-loop sequence information of Andaman wild boar, D-loop

| Parameter | Asiatic | NE1 | NE2 | Italian | European |
|-----------|---------|-----|-----|---------|----------|
| k         | 9.300   | 14.667 | 15.444 | 17.000 | 10.800 |
| PiT       | 0.00800 | 0.01605 | 0.01185 | 0.01624 | 0.00948 |
| Neutrality tests | | | | | |
| Tajima’s D | -.25538 | 0.01780 | -.21249 | -1.09380 | |
| Fu and Li’s D* | 0.46770 | -.35386 | -.21249 | -1.09380 | |
| Fu and Li’s F* | 0.31799 | -.29245 | -.20080 | -1.11335 | |

k= Average number of nucleotide differences between populations; PiT= Nucleotide Diversity (p>0.10).
Table 1 (Supplementary). Retrieved GenBank accession numbers and geographical distribution of wild boars used for analysis.

| Sl No. | Species of Sus | Accession number | Geographical distribution |
|--------|----------------|------------------|--------------------------|
| 1.     | S. scrofa      | NC_000845        | South East Asia and Europe |
| 2.     | S. scrofa      | MK248682         | Andaman & Nicobar Islands |
| 3.     | S. scrofa      | KP126954         | China                    |
| 4.     | S. verrucosus  | NC_023536, KP926379 | Indonesian islands, Java, Bawean |
| 5.     | S. barbatus    | NC_026992, KP789021 | Sumatra, Borneo, Malay Peninsula |
| 6.     | S. celebensis  | NC_024860, KM203891 | Indonesia              |
| 7.     | S. philippensis| DQ779367, DQ779400 | Philippines           |
| 8.     | S. cebifrons   | NC_023541, KP952600 | Philippines           |
| 9.     | S. salvanius   | NC_043879        | India                   |
| 10.    | S. salvanius   | NC_000845        | South East Asia and Europe |
| 11.    | S. scrofa      | FJ601392, FJ601401, DQ496829, AY884683 | China (Asiatic clade) |
| 12.    | S. scrofa      | EF545584         | Vietnam (Asiatic clade) |
| 13.    | S. scrofa      | DQ872957, DQ872953, DQ872951, DQ872938, DQ872958, DQ872947 | Iran (Asiatic clade, NE1, NE2) |
| 14.    | S. scrofa      | HM010482         | Russia (Asiatic clade) |
| 15.    | S. scrofa      | DQ872980         | Turkmenistan (Asiatic clade) |
| 16.    | S. scrofa      | JX894186, AY884619, JX894161, DQ872940, DQ872966 | Turkey (Asiatic clade, NE2) |
| 17.    | S. scrofa      | AY884694, AY884727 | Armenia (NE2) |
| 18.    | S. scrofa      | DQ872969         | Georgia (NE1) |
| 19.    | S. scrofa      | AY884690, AY884721, AY884720, AY884723 | Italy (Italian clade) |
| 20.    | S. scrofa      | AY463069, AY463065 | Germany (European clade) |
| 21.    | S. scrofa      | JQ273209         | The Netherlands (European clade) |
| 22.    | S. scrofa      | JQ668032         | Chile (European clade) |
| 23.    | S. scrofa      | KJ427774, KJ427773, KJ427765, KJ427764, KJ427763 | Eastern and Southern India |
| 24.    | S. scrofa      | KJ427764         | Eastern and Southern India |
| 25.    | S. scrofa      | KJ427761, KJ427759, KJ427753 | Central India |
| 26.    | S. scrofa      | KJ427760         | Central and Northern India |
| 27.    | S. scrofa      | KJ427758         | Western India |
| 28.    | S. scrofa      | KJ427757, KJ427755 | Central and Southern India |
| 29.    | S. scrofa      | KJ427756, KJ427754 | Northern India |
| 30.    | S. scrofa cristatus | KM016430-KM016443, NC_039090 | India |
| 31.    | S. scrofa cristatus | AY884701, AY884671 | India (Oxford Univ. Museum specimen) |
Table 2. Pair-wise Fst values (below diagonal) between Andaman wild boar (AWB) and clades of Eurasian wild boar.

| Pig clades | AWB     | Asiatic  | European | Italian | NE1     | NE2     |
|------------|---------|----------|----------|---------|---------|---------|
| AWB        | 0.00000 |          |          |         |         |         |
| Asiatic    | 0.71873*| 0.00000  |          |         |         |         |
| European   | 0.88355*| 0.81673* | 0.00000  |         |         |         |
| Italian    | 0.88406 | 0.79248* | 0.83871* | 0.00000 |         |         |
| NE1        | 0.80866 | 0.74599* | 0.80126* | 0.77730*| 0.00000 |         |
| NE2        | 0.77132*| 0.71445* | 0.72566* | 0.70649*| 0.60555*| 0.00000 |

NE= Near East, * indicates significant difference (p<0.05)

Table 2 (Supplementary). Pair-wise genetic distance of Andaman wild pig with endemic Sus species of South East Asia (SEA).

| Informal group of Genus: Sus | S. scrofa (n=3) | S. verrucosus group | S. philippensis (n=2) | Porcula salvania (n=1) |
|-----------------------------|-----------------|----------------------|------------------------|------------------------|
|                             |                 | S. verrucosus (n=2) | S. barbatus (n=2)     | S. celebensis (n=2)    | S. cebifrons (n=2)    | S. philippensis (n=2) | Porcula salvania (n=1) |
|                             |                 | 0.0138620297        |                       | 0.0360340309           | 0.0376868106          | 0.0502791527          | 0.0497668944           |
|                             |                 | 0.0376868106        | 0.0502791527          | 0.0497668944           | 0.0293016892          | 0.0834889305          |

Table 3. Genetic diversity estimates of Andaman wild boar with other Indian wild pigs.

| Parameter | Clade A (n=5) | Clade B (n=2) | Clade C (n=11) | Clade D (n=12) |
|-----------|---------------|---------------|----------------|----------------|
| k         | 12.000        | 14.000        | 17.818         | 16.583         |
| PiT       | 0.02074       | 0.02441       | 0.01964        | 0.01758        |
| Neutrality test |                |               |                |                |
| Tajima D  | 0.64126       | -             | -1.53026       | -1.76606       |
| Fu and Li’s D* | 0.86160       | -             | -1.64779       | -1.77155       |
| Fu and Li’s F* | 0.89471       | -             | -1.83283       | -2.01429       |

k= Average number of nucleotide differences between populations; PiT= Nucleotide diversity (p>0.10).

Table 3 (Supplementary). Analysis of molecular variance (AMOVA) among Asian, European, Near East (NE) and Italian boar.

| Source of variation | d.f. | Sum of squares | Variance components | Percentage of variation | Fst value | p value |
|---------------------|------|----------------|---------------------|------------------------|-----------|---------|
| Among populations   | 3    | 110.103        | 4.44001 (Va)        | 62.92                  | 0.62924   | 0.00    |
| Within populations  | 29   | 75.867         | 2.61609 (Vb)        | 37.08                  |           |         |
| Total               | 32   | 185.970        | 7.05610             | 100.00                 |           |         |

(Significance level=0.0500).
Fig. 1 (a-b). Phylogenetic relationship of seven *Sus* species of Southeast Asia.

[(a) Phylogenetic tree, (b) Median-joining (MJ) network. Phylogenetic tree was constructed by Neighbour-joining method using 638 bp fragment of mitochondrial DNA control region in MEGAX using 1000 bootstrap replicates. MJ network was drawn in POPART using 638 bp fragment of mitochondrial DNA control region. AWB indicates Andaman wild boar].
sequence information of endemic species of Sus of SEA, Eurasian wild boar, Sus spp. reported from mainland of India and pygmy hog (Porcula salvania) were retrieved from GenBank (Supplementary Table 1). Phylogenetic analysis was done by Neighbor-Joining method with Tamura-Nei model as implemented in MEGAX following 1,000 bootstrap replications (Saitou and Nei 1987, Tamura and Nei 1993). Evolutionary relationship among the sequences was inferred by a median-joining (MJ) network constructed in POPART with default settings (Bandelt et al. 1999, Leigh and Bryant 2015). Pairwise distance of sequence information between Andaman wild boar and endemic species of Sus of SEA was calculated using the Maximum Composite Likelihood model in MEGAX (Tamura et al. 2004). Polymorphic sites of Andaman wild boar and Eurasian clades of wild boar were deduced after aligning the sequences with reference sequence of S. scrofa cristatus (NC_039090) by Clustal W using MEGA X. Genetic diversity parameters, mismatch distribution and neutrality tests (Tajima’s D test, Fu and Li’s D test and Fu and Li’s F test) were calculated by DnaSp software (Rozas et al. 2017). Analysis of molecular variance (AMOVA) was performed in Arlequin ver 3.5.2.3 (Excoffier et al. 1992, Slatkin 1995, Excoffier and Lischer 2010). Principal component analysis based on genetic distance was done in GenLEX6.5 (Peakall and Smouse 2006, Peakall and Smouse 2012).

Table 4. Pair wise Fst values (below diagonal) between Andaman wild boar (AWB) and clades of Indian wild boar.

| Indian wild boar clades | Clade A | Clade B | Clade C | Clade D |
|-------------------------|---------|---------|---------|---------|
| Clade A                 | 0.00000 |         |         |         |
| Clade B                 | 0.44612 | 0.00000 |         |         |
| Clade C                 | 0.60623*| 0.45616*| 0.00000 |         |
| Clade D                 | 0.60585*| 0.17927 | 0.49213*| 0.00000 |

*Indicates significant difference (p<0.05).

RESULTS AND DISCUSSION
Genetic relationship of Andaman wild boar with endemic Sus species of SEA
To characterize Andaman wild boar, analysis of its D-loop sequence information has been done using three different datasets. Initially, Andaman wild boar has been compared with endemic Sus species of ISEA because of existence of two main evolutionary clades of endemic species of wild boar in this part of Asia since early Pliocene period (Larson et al. 2007, Shapiro et al. 2004). One clade includes pig population present in Philippines (S. cebifrons) and Sulawesi (S. celebensis). The second one includes pigs of S. verrucosus group and Eurasian wild boar species, S. scrofa (Lucchini et al. 2005, Larson et al. 2007). Besides existence of two major groups of endemic species in SEA, existence of S. salvanius (www.jspui/bitstream/10603/140490/5/05) alias P. salvania (NC_043879) has been confirmed (Funk et al. 2007). S. scrofa is one of the most adaptable species distributed in Palearctic region (Demirbas et al. 2016).

In the present study, genetic distance of Andaman wild boar was found lowest with S. scrofa (0.0138620297) and highest with P. salvania (0.834889305) (Supplementary Table 2). Neighbor-Joining phylogenetic tree and median-joining network based on 638 bp fragment of D-loop sequence revealed that endemic species of Sus of SEA is clustered into seven distinct clades. Andaman wild boar (MT024628-29) shared clade with S. scrofa (Fig. 1) indicating that they belong to S. scrofa. Earlier study suggested that S. scrofa originated in ISEA and later dispersed to different parts of Indian subcontinent. Subsequently, the species spread into East Asia and finally to Eurasia (Larson et al. 2005).

Our analysis on genetic distance revealed that, pair-wise distance of S. cebifrons and S. celebensis were more compared to S. philippensis, S. verrucosus and S. barbatus (Supplementary Table 2). Our observation agrees to earlier findings of Lucchini et al. 2005 in which it was mentioned that S. cebifrons and S. celebensis were...
distantly related as compared to *S. philippensis*, *S. verrucosus* and *S. barbatus*.

**Genetic relationship of Andaman wild boar with Eurasian wild boar clades**

Further, we have compared the sequence information of Andaman wild boar with Eurasian wild boar which was diversified during glacial Pleistocene period (Larson *et al.* 2005). Three Eurasian wild boar clades are present; one is confined to Cradle of Civilization (clade NE), one in continental Europe (clade European) (Giuffra *et al.* 2000, Larson *et al.* 2005) and third one in Italian Peninsula (clade Italian) (Okumura *et al.* 2001, Alves *et al.* 2003,

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*Fig. 1. (Supplementary) (a-e). Genetic diversity estimates of Andaman wild boar with Eurasian wild boar clades.*

[Dxy indicates average number of nucleotide substitution per site between populations with Jukes and Cantor correction, Da indicates Number of net nucleotide substitution per site between populations with Jukes and Cantor correction, NE indicates Near East].

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Fig. 2 (a-b). Phylogenetic relationship of Andaman wild boar with Eurasian wild boar clades. [(a) Phylogenetic tree, (b) Median-joining (MJ) network. Phylogenetic tree was constructed by Neighbour-joining method using 626 bp fragment of mitochondrial DNA control region in MEGAX using 1000 bootstrap replicates. MJ network was drawn in POPART using 626 bp fragment of mitochondrial DNA control region. AWB indicates Andaman wild boar].

First account on maternal lineage of andaman wild boar (moupin pig), an endangered endemic...
Based on mitochondrial marker, NE clade has been further bifurcated into NE1 and NE2 (Larson et al. 2005, Ottoni et al. 2013). The result of genetic diversity estimates of Andaman wild boar with globally recognized Eurasian wild boar clades (Asiatic, NE1, NE2, Italian and European) has been depicted in Table 1 and Supplementary Fig. 1. Average number of pair-wise differences (k), nucleotide diversity \( \Pi(t) \), average number of nucleotide substitution per site with Jukes and Cantor \( D_{xy} \) and number of net nucleotide substitution per site with Jukes and Cantor \( D_{a} \) values were the least with Asiatic clade of wild boar (9.3, 0.008, 0.01493 and 0.01238, respectively). The highest k, \( \Pi(t) \), \( D_{xy} \) and \( D_{a} \) values were observed with Italian clade of Eurasian wild boar (17, 0.01624, 0.02724 and 0.01238, respectively). Neutrality test was found statistically non-significant (\( p>0.10 \)). Tajima’s D test showed negative values for Asiatic, Italian and European wild boar. Further, Fu and Li’s test had negative values for NE, Italian and European clades (Table 1). Pair-wise data of Fst values for Eurasian wild boar has been depicted in Table 2. Pair-wise Fst values ranged from 0.71873 to 0.88406. Fst values were statistically significant (\( p<0.05 \)) for Asiatic, European and NE2 clades on the comparative score with Andaman wild boar. AMOVA results showed more genetic variation among population than within population (Supplementary Table 3). When D-loop sequence was compared to referral sequence of \( S. scrofa \) (NC_039090), a total of 19, 14, 19, 18, 19 and 23 variable sites were detected in Andaman wild boar, Asiatic, NE2, NE1, Italian and European clades respectively (Supplementary Fig. 2). A PCA of Eurasian clades was done by clubbing the data of Andaman wild boar with Asiatic clade. PCA results showed that, percentage of variation explained by axis1, axis2 and axis3 were 29.93, 18.85 and 14.35 respectively. NE1 and NE2 were closer to each other, and same observation was recorded between European and Italian clades (Supplementary Fig. 3). Phylogenetic and MJ network analysis based on D-loop 626 nucleotide sequence revealed that Andaman wild boar shared the cluster with Asiatic clade of Eurasian wild boar (Fig. 2). This is further to mention that Italian peninsula is known as hotspot of diversity for unique presence of European flora and fauna. Additionally, mountain Alps acted as a geographical barrier. These factors promoted genetic isolation of peninsular populations which led to differentiation of Italian flora and fauna by genetic drift (Scandura et al. 2008). This explains the unique genetic diversity of Italian wild boar and maybe the reason behind higher genetic diversity with Andaman wild boar and Asiatic clade compared to NE and European clades of Eurasian wild boar (Supplementary Fig. 1, Table 1). Further, in this study we have calculated pair-wise Fst to know the genetic differentiation. Fst values among Andaman wild boar and Eurasian clades of pigs showed the least and highest values for Asiatic and Italian clades, respectively (Table 2). By PCA analysis, we observed similar result in terms of genetic distance and relatedness between Andaman wild boar and Eurasian clades. Andaman wild boar clustered closely with Asiatic clade and maintained distance with rest of the clades of Eurasian wild boar (Supplementary Fig. 3).
First account on maternal lineage of Andaman wild boar (moupin pig), an endangered endemic...

Fig. 3 (a-b). Phylogenetic relationship of Andaman wild boar with wild boars of mainland of India. [(a) Phylogenetic tree, (b) Median-joining (MJ) network. Phylogenetic tree was constructed by Neighbour-joining method using 397 bp fragment of mitochondrial DNA control region in MEGAX using 1000 bootstrap replicates. MJ network was drawn in POPART using 397 bp fragment of mitochondrial DNA control region. AWB indicates Andaman wild boar].
Genetic relationship of Andaman wild boar with wild boars of mainland of India

Lastly, we made comparison of Andaman wild boar with wild boars characterized from different parts of India. Phylogenetic and MJ network analysis using 32 nucleotide sequence information from Indian wild boars revealed that Indian wild boars could be clustered into four groups. Andaman wild boar belonged to cluster A. The wild boars of clade A had the geographical provenance restricted to Eastern and Southern India (Fig. 3). k, PiT, Dxy (JC) and Da (JC) of Andaman wild boar was found the lowest with clade A of Indian wild boar (12, 0.02074, 0.3038, 0.02380, respectively) and the highest with clade C of Indian wild boar for values of k (17), Dxy (JC) (0.04511) and Da (JC) (0.04021) (Table 3, Fig. 4). Tajima’s D test and Fu and Li’s test had negative values for clade C and D (Table 3). PCA analysis showed that percentage of variation explained by axis1, axis2 and axis3 were 32.98, 17.75 and 11.65, respectively. Clade A and Andaman wild boar formed a separate cluster, clade B and D formed a single cluster and clade C formed a separate cluster (Supplementary Fig. 4). Pair-wise Fst values ranged from 0.17927 to 0.60623. Fst values were statistically significant for clade C and clade D while comparing Andaman wild boar with these two clades (Table 4). AMOVA result showed significant genetic variations within and among populations (Supplementary Table 4). Mismatch distribution for Indian wild pigs, clades A, C and D showed multimodal distribution. Four major peaks were observed in clade A. Two major peaks were observed in clade C and D (Fig. 5). Hypotheses on dispersal of animals suggested demic or cultural diffusion
which happened either due to human migration or through trade (Larson *et al.* 2007). Archaeological evidence suggested maritime trade links between India and both coastal and inland SEA from c. 500/400 BCE onwards (Singh 2009) and there might be transportation of Andaman wild boar to coastal Southern and Eastern of India. Therefore, Andaman wild boar might be a leftover of cultural diffusion in these two geographical regions of India.

Earlier report on matrilineage study on Indian wild...
boar (*S. scrofa cristatus*) indicated that Indian wild boar exhibited a clear phylogenetic bifurcation from European-American and Asiatic pig clades (Jadav et al. 2019). Separate matrilineage of Indian wild boar may be due to differentiation of wild boar which was dispersed from ISEA to Indian subcontinent followed by subsequent movement to East Asia before final progressive spread across Eurasia (Larson et al. 2005). Therefore, Andaman wild boar had genetic affinity towards Asiatic clade and genetically different from wild boar characterized earlier from mainland of India (Jadav et al. 2019). This is interesting to note that, this is a common phenomenon in temperate mammal species, and we justify the genetic variation between Andaman wild boar and Indian wild boar as the quaternary contraction or expansion events due to impending climate change scenario (Hewitt 2004). Our data on molecular characterization of Andaman wild boar and its difference from wild boar of mainland of India is further strengthened by the observations on phenotypic characterization on previous reports (www.jspui/bitstream/10603/140490/5/05). In earlier literature this has been described that, Indian wild boar (*S. scrofa cristatus*) is large and heavily built. The pig is 36” at shoulder height and weighs 65-90 kg (www.jspui/bitstream/10603/140490/5/05). On the contrary, Andaman wild boar characterized earlier was short textured (20” at shoulder level) and weight was also less (16 kg) (De et al. 2013). Therefore, on records we conclude that Andaman wild boar and Indian wild boar are genetically and phenotypically different.

Statistical analyses of data (Tajima’s D test and Fu and Li’s tests) were suggestive of population expansion of Eurasian clades (Table 1). Again, negative values by Fu and Li’s tests were also indicative of population expansion for clades C and D (Table 3) (Tajima 1989, Fu and Li 1993). Likewise, two major peaks in the maximum

Fig. 5. Mismatch distribution (pairwise number of differences) for Indian wild pig.  
[Mismatch distribution shows the expected and observed pairwise differences between the sequences with the respective frequency].
frequency by mismatch analysis in clades C and D were also indicative of population expansion events (Lwin et al. 2018).

CONCLUSION
The new information on genetic characterization of Andaman wild boar is an addition to the existing knowledge pool on wild boar diversity. Matrilineage analysis could differentiate Andaman wild boar and wild boars available in mainland of India.

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