



Phylogenetic analysis of six duck populations

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ABSTRACT

Indigenous ducks play a vital role in sustainable livelihood of the poor duck farmers. In Tamil Nadu, two popular indigenous duck varieties viz., *Sanyasi* and *Keeri* are being reared traditionally by the duck farmers under nomadic system. In the same way, *Kuttanad* ducks are popular in Kerala and Assam ducks are popular in Assam. The present research work was undertaken to study the genetic distance between and within the indigenous ducks and exotic duck breeds by using duck specific microsatellite markers. From the blood samples the genomic DNA was isolated and characterized genetically. With the molecular data, dendrogram was constructed. This revealed that, *Keeri*, *Sanyasi*, *Kuttanad* and Assam ducks formed the first group with White Pekin in the second group and Muscovy in the third cluster. Among the Indian duck varieties, *Keeri* and *Sanyasi* ducks of Tamil Nadu were found to be closer to each other as indicated by the genetic distance value of 0.11. However, within this group, 26.33 and 29.87 per cent of differentiation were noticed between Assam and *Sanyasi* and Assam and *Keeri* ducks respectively. Higher genetic distance value of 0.92 (92 per cent) was observed between two exotic ducks. Based on the genetic distance and genetic diversity between the indigenous ducks, the duck varieties of Tamil Nadu, Kerala and Assam may be classified as distinct breeds.

Key words: Duck, Phylogenetic.

Asia is considered as the homeland for ducks holding 90 per cent of the world duck population. In India, out of the country's total egg production, 5.3 per cent comes from ducks and indigenous ducks contribute 92 per cent of the same. On the other hand, 30 per cent of the total meat production in the country is of poultry origin. The contribution of ducks in meat production also cannot be neglected. The distribution and demographic dynamics of duck population revealed that they are mainly concentrated in eastern, north eastern and southern states of the country. The leading states in duck population are West Bengal, Assam, Kerala, Andhra Pradesh, Tamil Nadu, Bihar and Orissa. The common Indian breeds/genetic groups of ducks are Indian Runner, *Nageswari*, *Syhetmete*, *Kuttanad*, *Arni* etc. Besides, non-descript ducks are also available in large numbers in many states of the country, contributing significantly to the total duck population. These indigenous ducks have innate potential to produce eggs and meat at considerable quantity with lesser input and they are a good dietary source of proteins. However, information on these duck populations, their physical and production characteristics are very scanty and there have been very few systematic studies of ducks in India.

In order to conserve this genetic resource, study on genetic diversity within and between duck populations using microsatellite markers would provide information for taking

priority decisions towards preservation. Microsatellite markers are frequently used in genotype identification, pedigree analysis and estimation of genetic diversity and genetic distance (Chen *et al.*, 2003; Yan *et al.*, 2005) and may be useful in resolving the phylogenetic relationships between closely related populations (Takezaki and Nei, 1996). The characterization of genetic diversity by employing molecular tools is a prerequisite in developing strategies for conservation, utilization of duck genetic resources and to the establishment of a sensible genetic preservation strategy for these populations. Hence, the present research was conducted to evaluate genetic diversity and relationships within and between Indian breeds of ducks based on microsatellite markers.

A total of 190 blood samples were collected from unrelated birds of both sexes of *Sanyasi*, *Keeri* in the study area, *Kuttanad* ducks from Kerala, Assam ducks, White Pekin and Muscovy ducks for molecular characterisation and phylogenetic analysis of the duck populations. From the blood samples, the genomic DNA was isolated by standard protocol. The FAO recommended 23 microsatellite markers with labelled forward primers were used for molecular characterization. These microsatellite primers were standardised for their annealing temperatures. Molecular characterization of various duck varieties was carried out using standard PCR protocol and the PCR amplicons were

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Table 1: Genetic distance among six duck populations

Duck Variety	<i>Keeri</i>	<i>Sanyasi</i>	Assam	<i>Kuttanad</i>	Muscovy	White Pekin
<i>Keeri</i>	-	-	-	-	-	-
<i>Sanyasi</i>	0.1113	-	-	-	-	-
Assam	0.2987	0.2633	-	-	-	-
<i>Kuttanad</i>	0.1864	0.1240	0.1672	-	-	-
Muscovy	0.8694	0.7358	0.8056	0.6975	-	-
White Pekin	0.7521	0.6534	0.6229	0.5326	0.9270	-

genotyped by capillary electrophoresis using automatic sequencer.

Using the simple allele sharing statistic (Bowcock *et al.*, 1994) and treating each animal as a taxonomic entity, the genetic similarity matrix was constructed using the POPGENE version 3.2 (Saitou and Nei, 1987) and a phylogeny tree was constructed using PHYLIP software programme (Felsenstein, 1993). The Nei's genetic distances (Nei, 1978) between populations were calculated and used to construct a phylogeny tree using the neighbour joining method. To interpret this tree, first a threshold was imposed to produce clusters and secondly, means and standard errors of genetic similarities within and between populations were calculated following the analysis of variance.

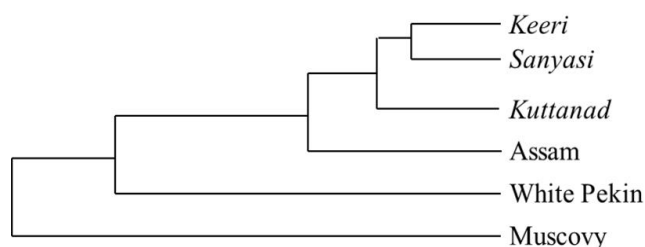
The dendrogram constructed using the neighbour joining procedure of PHYLIP version 3.5 (Fig. 1) revealed that the six duck populations were clustered into three groups. The first group included *Keeri*, *Sanyasi*, *Kuttanad* and Assam ducks; the second group included White Pekin ducks; and the third group had Muscovy ducks. Among the Indian duck varieties clustered together in the first group, *Keeri* and *Sanyasi* ducks of Tamil Nadu were found to be closer to each other as indicated by the genetic distance value (Table- 1) of 0.11 (11 per cent). However, within this group, 26.33 and 29.87 per cent of differentiation were noticed between Assam and *Sanyasi* and Assam and *Keeri* ducks respectively (Table 1). Similarly, longer genetic distance of 0.22 and 0.26 was reported between Tamil Nadu ducks and Jharkhand and Khaki Campbell ducks by Gaur *et al.* (2010). Higher genetic distance of 0.64 was observed between Assam and Uttarakhand ducks and lesser genetic distance (0.06) between Assam and West Bengal ducks by Mukesh *et al.* (2011). The

result of the cluster was consistent with the breeding history and region / environment of the six populations, since, the genetic distance goes in the ascending order from Tamil Nadu, Kerala, Assam and exotic breeds.

The result of Nei's genetic distance between six duck populations revealed the longest genetic distance of Muscovy and White Pekin ducks with other Indian duck varieties studied (Table- 1). As suggested by the dendrogram (Fig. 1), these two duck breeds were separated out from the ducks of Indian origin. Similarly, the longest genetic distance of 0.598 and 0.4558 between Muscovy and Pekin duck of Iran and China was reported by Ahmadi *et al.* (2007) and Wu *et al.* (2008) respectively. The reason that could be attributed for separation of White Pekin and Muscovy from the rest of the populations was the differences in the form and biological characters that is, the White Pekin ducks are morphologically different (white plumage) and meant for meat; while Muscovy ducks belong to different genera (*Cairina moschata*) with biological distinctiveness (higher incubation period and broodiness). The separation of Muscovy ducks from the rest of the population was consistent with the reports of Yan *et al.* (2005) and Wu *et al.* (2008). The genetic distance of more than 20 per cent was observed between the cluster of Indian ducks and it was consistent with the breeding history and region. It may be concluded that, due to higher the genetic distance and more genetic diversity between these duck population, the Indigenous ducks of Tamil Nadu, Kerala and Assam may be recognised as distinct breeds of ducks.

CONCLUSIONS

The microsatellite markers used in this study were duck specific markers and they were highly polymorphic indicating that they can be used effectively for genetic diversity and phylogenetic analyses of ducks. The genetic diversity is high among the duck populations studied which could be exploited for improving productivity. The genetic distance between Indian and exotic ducks was longest indicating the difference in nature and utility of the exotic breeds. Based on the genetic distances between the Indian duck populations, the Tamil Nadu, Kerala and Assam duck varieties may be classified as distinct breeds.

**Fig 1:** Phylogenetic tree of six duck populations

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