SUMMARY

Thachappully Asokan Ligi “Reconstruction of phylogeny of birds of the group estrildidae by using DNA comparisons and DNA makers”, Department of Zoology, St.Joseph's College Devagiri, University of Calicut, 2004
SUMMARY

Population genetic theory predicts that small and isolated populations tend to lose genetic variations through genetic drift. (Lacy, 1987, Bouzat et al. 1998) As the human habitats continue to grow and rapidly encroach the wildlife habitats a better understanding of the population genetic structure of the wildlife is desirable for the development of management interventions that may circumvent their extinction possibilities. There are at least three biological reasons that make the preservation of genetic variation of wildlife populations one of the major goals of conservation biology. First, the loss of genetic variation may increase the probability of population extinction through a decline in fecundity and viability, i.e. inbreeding depression. (Lacy 1987; Ralls, 1988; Meffe and Carroll, 1994; Frankham; 1995). Second, populations with low levels of genetic variation, upon which natural selections can operate, may have reduced opportunities for future adaptation through evolutionary change (Lande and Barrowclough, 1987; Fahrig and Merriam, 1994; Meffe and Carroll, 1994). Third, the preservation of genetic variation may play a key role in identifying evolutionary significant units for conservation, i.e. genetically distinct populations of management concern (Meffe and Carroll, 1994).

During the past few years, there has been considerable debate concerning the possible effects of fragmentation, isolation and small population size on the genetic variability of bird populations. The high vagility of many bird species typically results in high levels of gene flow and thus little local genetic differentiation. (Barrowclough, 1980). Only a limited number of studies have demonstrated genetic effects as a result of fragmentation of continental bird populations. (Stangel et al. 1992; Haig et al 1993).
In this study firstly, the population genetic structure of the six munia (family Estrildidae) species of the subcontinent was evaluated and the levels of within species genetic variability assessed to determine the levels of genetic diversity within each species. Secondly the interspecific relationship between the six species was determined to estimate the levels of differentiation and relationships between the species to reconstruct the phylogeny of the family Estrildidae in the subcontinent. The studies of within and between populations provided insights on speciation and a better understanding of the evolutionary trends. It proved to be important for assessing prospective evolutionary potentials as well as for risk assessments and conservation strategies.

Advances in molecular techniques have led to an explosive increase in the studies of avian phylogeny. Polymerase chain reaction (PCR) amplifications of small amounts of DNA (nanogram), enable us to analyse genetic profiles without harming endangered birds. RAPD was chosen because it is expeditious and inexpensive and does not require a previous knowledge of the genome of species under study (Lynch and Milligan, 1994). Earlier comparisons showed that RAPD and isozyme results are very similar, with the RAPD technique revealing even higher amounts of variation (Baruffi et al., 1995).

Only six species of Estrildidae could be considered for the study. Two species belonged to the genus Estrilda or Amandava; the Red munia *A.amandava*, and the Green munia *A.Formosa*. And the other four species belonged the genus Lonchura; the White backed munia, *Lonchura striata*, the Black headed munia *Lonchura malacca*, the Spotted munia *Lonchura punctulata*, and the White throated munia *Lonchura malabarica*. Another species of Lonchura, *L.kelaarti* though chosen for the study was not obtained during the course of the work. With its preferred habitat of high range vegetation; the species has become highly localized and uncommon.
(Satish et al, 2003). *L.kelaarti* and *A.Formosa* are the two endemics of the family Estrildidae.

In the present study the two species of Estrilda, *A.amandava* and *A.Formosa* recognized by Kakizawa and Watada, 1985 as belonging to the subgroup Estrildi of the group Estrildinae were analyzed for their within species genetic diversities and the between population relationships and variations. Owing to their coloured plumage the two estrilids have been grouped together. But a considerably high between species genetic distance have been observed compared to the passerines. Wolters, (1975-82) had placed these species in two different genera owing to the aberration in their characters. *A. amandava* is a widely distributed and well established species. The within population genetic diversity estimated does not show any levels of deterioration. Whereas, *A. Formosa* is an endemic with restricted distribution in central India. The pattern of genetic diversity observed in the population of *A. Formosa* is consistent with the idea that recent fragmentation and isolation may have increased their local differentiation from other estrilids and decreased their within population genetic variability as a result of stochastic events associated with small population size and inbreeding. And inbreeding will consistently lead to a decrease in genetic variability over time. The study clearly indicates that the Green munia population is genetically unique and may be considered as an important evolutionary unit of conservation.

The four species of Lonchura belonged to the subgroup Lonchuri of the group Lonchurinae (Kakizawa and Watada, 1985; Mayr, 1968; Wolters, 1975-82; Delacour, 1943). Commonly known as the mannikins they form a uniform group with somber plumage coloration which show no sexual color dimorphism. Considerably good within species genetic variation has been noted among the Lonchura species reflecting a continuous and abundance in distribution. The less degree of genetic differentiation among the Lonchura species is possibly related to the short period that these
populations have been isolated. It also indicates the relatively recent genetic
differentiation of the group. Analysis of percentage polymorphism reveals
*L. Malacca* as the most genetically diverse species. Hence assuming that the
Malacca population is representative of “large” genetically diverse populations, then populations of the other three Lonchura species may be depauperate.
*L. malabarica* or the Indian silverbill also exhibit a considerably good genetic
diversity. The phylogenetic dendrogram reveals *L.punctulata* and *L. striata* as the direct descendants of the Indian silver bill, *L. malabarica*. The genetic
distances of *L.punctulata* and *L striata* reflect their extremely low genetic
differentiation and most recent speciation. A fifth species of Lonchura, *L. kelaarti* an endemic species of the Western Ghats could not be included in the present study owing to its sparse and restricted distribution. Yet the
distribution of the species has not so far been reported as deteriorating. The
species is distributed in the high rainfall moist deciduous and evergreen
forests of the southwest India and the western ghats. This forest has been
much reduced by commercial timber extraction and the construction of
hydropower dams. Only moderate areas of seminatural forests remain except in the narrow strips of coastal plains where natural forests has been practically eliminated. With further reduction of their preferred habitat *L. kelaarti* could easily become vulnerable to extinction.

The results show that of the two groups of Estrildidae considered, the genus Lonchura with lower rate of genetic differentiation reflect more recent speciation and that the older species belong to the Amandava or genus Estrilda. This result adds extra weight to the hypothetical African origin of the Estrildidae as recognized by Kakizawa and Watada. (1985). The population structure of the endemic species *A. Formosa* and *L. kelaarti* reported in this study is consistent with the idea that fragmentation, isolation and small population size may be affecting their genetic variability. Therefore present status of the two endemics warrants further investigations.