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CHAPTER VI

DISCUSSION

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6. DISCUSSION

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). This study evaluated the population genetic structure of the six species of Estrildidae found in the subcontinent.

The present study reveals that PCR based fingerprinting technique, RAPD is an informative methodology for estimating the extent of genetic diversity as well as to determine the pattern of genetic relationships between different species of Estrildidae, with polymorphism levels sufficient to establish informative fingerprints with relatively fewer primer sets. The RAPD procedures proved to be a useful tool for assessing genetic variability because band profiles with the selected primers were reproducible. Despite the high proportion of excluded bands a substantial number of polymorphic markers was detected. The information obtained from the present study could be of practical use for mapping the Estrildidae genome.

6.1: GENETIC VARIATION AND DIFFERENTIATION OF ESTRILIDAE

This study of the Estrildidae found that the observed values of the proportion of polymorphic markers were very similar to, although slightly lower than the overall values for the Passeriformes (Kakizawa and watada, 1985) . Although the species studied are popularly caged, most of the material came from wild populations, thus the lower value cannot be
considered to be attributable to random genetic drift due to artificial breeding, but rather to a peculiarity of the Estrildidae.

Within Estrildidae, the mean genetic distance at the species level was calculated as 0.243 which are slightly higher than the avian mean of 0.123 (Avise et al, 1982). This difference can be attributed to the high values exhibited by the two species of Amandava 0.396 and 0.297 by A. formosa and A. amandava respectively.

In the study the two species of Estrilda, *Amandava amandava* and *Amandava formosa* recognized by Kakizawa and Watada (1985) as belonging to the subgroup Estrildi of the group Estrildinae have been analyzed for their population genetic structure to identify their relationships and variations. The genus Estrilda represent a group that has separated relatively early. Owing to the plumage coloration they are distinct from the mannikins and are commonly called the waxbills. Inspite of their relationships within the genus, their genetic distance values (0.396 and 0.297) reveal that they are distantly related. Wolters (1975–85) had placed these two species in different genera owing to the aberrations in their characters. But the mean within species genetic distance values of the two species indicate that *A. formosa* is less genetically diverse than *A. amandava*. *A. formosa* is an endemic species of central India. But the within population genetic variation measured by percentage band sharing and percentage polymorphism reveal that variations in *A. formosa* are not significantly low compared to the other munia species. Inspite of that they are categorized as vulnerable, owing to their deteriorating habitat and endemism.

The group Lonchurinae, commonly called mannikins show no sexual dimorphism. They form a uniform group in a single genus the Lonchura. They are widely distributed in Africa, South-East Asia, India and Australia. The four species considered; *L. malabarica*, *L. malacca*, *L. punctulata* and *L. striata* are the common species in India.(Manakadan and
They show low levels of genetic distances within them indicating a relatively recent genetic differentiation of the group.

By the analysis of genetic distances between individuals of each species the amount of within species genetic diversity was estimated. The mean genetic distance values indicated that all the four species exhibit considerable diversity with them. Among the species; *L.punctulata* and *L.striata* with the shortest mean genetic distances (0.104 and 0.113) can be considered the closest relatives and the most recently diverged species. *L. malacca* with a mean genetic distance value of 0.124, shows a greater diversity. *L. malabarica* commonly called the Indian silver bill or the White-rumped munia shows a significantly high genetic diversity (0.256). It is a well established species of the subcontinent (Harrison, 1964). The values clearly indicate that the *L. malabarica* is the true representative of the Lonchura population of the subcontinent and that populations of *L. punctulata, L.striata, and L.malacca* may have emerged later from it.

6.2: PHYLOGENETIC RELATIONSHIPS WITHIN THE ESTRILDIDAE

The results showed that the mean genetic distance between the species of Estrildidae was 0.346 between the genus Estrilda or Amandava while in the genus Lonchura the value of mean genetic distance was only 0.153. As the mean genetic distances between species in the Estrildinae was higher than that of those in the Lonchurinae, and from the values obtained it is observed that the rate of genetic differentiation decreased from the species Estrildinae to the species Lonchurinae, reflecting a progressively more recent speciation in which the older species are found in the Estrildinae. However, with further studies on more species and more number of loci changes of the interspecific relationships within the Lonchurinae and Estrildinae can be expected.
The Estrildidae are divided into two main groups with a genetic difference of 0.44 (Kakizawa and Watada, 1985). Both of these groups; the Estrildinae and the Lonchurinae each consist of sub groups, named: (1) Amadini (2) Estrildi (3) Erythmi (4) Poephili (5) Lonchuri and (6) Heteromunii (Kakizawa et al 1985).

Of the six species considered for the study, the two Amandava species; *A. amandava* and *A. Formosa* belonged to the sub group Estrildi of the group Estrildinae. Estrildi comprise of many genera which separated relatively early. The species of Estrildi are known to show much variation even within the same genus. They may be closely or sometimes very distantly related.

In this study from the dendrogram it is clear that the group Estrildinae consisting of the two species had separated relatively early. Kakizawa had observed a further division of this group into subgroups of which *A. amandava* is an older species belonging to the older subgroup. From the present study also it can be considered that the species *A. Amandava* had branched off first from an ancestral group common to the Estrildinae group and had remained undifferentiated. Enjoying a wide spread distribution the Red munia can be considered as the representative species which has undergone the least evolutionary pressure.

*A. formosa*, the Green Munia on the other hand is a species that has separated out later and became endemic to the parts of north India. With a red bill on a green body its attraction as cage bird has made it vulnerable. Present study indicated that the Green Munias had considerable within population variation. Therefore translocations between population to promote gene flow is likely to have little or no influence on maintaining the population levels beyond vulnerability. Thus management interventions to acquire and maintain quality habitat that promote population increases and migration are likely to be the most beneficial measures. The green munia population being genetically unique compared to other species of Estrildidae
in the subcontinent, may be considered as an important evolutionary unit of conservation.

The four species of Lonchura obtained for the study belonged to the subgroup Lonchuri of the group Lonchurinae. They form a uniform group represented by a single genus Lonchura with no sexual dimorphism bright plumage coloration. They are all somber coloured. The Lonchuri consists of three groups (Delacour, 1943, Mayer et al. 1968) based on their distribution, the African, Indian and the Australasian. The species of Lonchura are very closely related to each other with a genetic distance of less than 0.219. The low levels of genetic distance within Lonchuri indicates the relatively recent genetic differentiation of this group. The four species of Lonchura has shown considerable within species genetic variability. They reflect a continuous and abundant distribution. They are all common pests of agriculture and may therefore be considered for control and management programmes in agriculture.

A fifth species of Lonchura, *L. kelaarti*, the Black throated munia endemic to the Western Ghats though chosen for the study, was not obtained during the course of the work. The search for the bird during the course of the study has bought up many questions, which has triggered the need for future research on the endemic species of Estrildidae, both *A. Formosa* and *L. kelaarti* in India (Gaston, 1983). In 1983 Gaston has observed that species characteristic of the heavily disturbed lowland ecosystems of the Indogangetic plain and the peninsular India show signs of increased rate of extinction or vulnerability to extinction. With its preferred habitat of the high range forest vegetation, the species *L. kelaarti* has become highly localized and uncommon. (Satish et al, 2001). The species is distributed in the high rainfall, moist deciduous and evergreen forests of southwest India and the Western Ghats. This forest has been much reduced by commercial timber extraction and the construction of hydropower dams, but areas of seminatural forests remain except in the narrow strip of coastal plains where natural forest has
been practically eliminated. With further reduction of their preferred habitat, *L. kelaarti* could easily become vulnerable to extinction.

6.3: MOLECULAR GENETICS AND CONSERVATION

Conservation biology seeks to maintain both unique species and the genetic diversity within those species. Without the help of molecular genetics, however, it’s not necessarily easy to quantify either quality. Using mitochondrial DNA, polymerase chain reactions techniques, and microsatellite DNA, molecular genetists help biologists determine which species are genetically distinct and whether their DNA are adequately diverse, allowing wise management of endangered species.

Effective conservation and restoration plans for species at risk of extinction or extirpation require clearly definable units of management. Currently, most management units are arbitrarily defined as meta populations, which inhabit contiguous and adequate habitat. Classically, the principle processes in meta-population dynamics are extinction, migration, and colonization to establish new local populations. The key questions are how these processes jointly affect the dynamics and the evolution of local populations within which the conspecifics are more likely to interact with other than with conspecifics from other populations. However, isolation is usually not complete and since most organisms have some power of dispersal, members of a local population have a low but positive probability of interaction with individuals from other localities. Depending on the rate of emigration, demographic and genetic dynamics will be influenced by this migration, as well as by local birth and death rates. Genetic information is rarely available on population structures, levels of gene flow, or relatedness of geographic populations of many species of conservation concern. To develop management strategies for maintaining evolutionarily significant lineages that will ensure long-term population stability and reduce the need for protection through the regulatory process, a thorough understanding of the evolutionary
relationships (e.g., levels of gene exchange) among geographically proximate and distal populations are essential. Molecular genetics has recently achieved an important place in contemporary conservation biology as it has proven to be a robust tool for identifying reproductive isolation among populations, permitting the delineation of management units, and allowing assessment of conservation procedures for an evolutionary perceptive.

The recognition of recent accelerated depletion of species as a consequence of human industrial development has spawned a wide interest in identifying threats to endangered species (Gaston, 1980, 1984). In addition to ecological and demographic perils it has become clear that small populations that narrowly survive demographic contraction may undergo close inbreeding genetic drift, and loss of overall genomic variation due to a allelic loss of reduction to homozygosity.

6.4: CONCLUSION

The genetic similarity of Amandava with Lonchura species is low as indicated by the separation of these two groups in the RAPD analyses. The informative primers identified in the studies will be useful in genetic analysis of Estrildidae species. The putative species-specific bands can be used as probes to ascertain whether they are in low or high copy numbers in the Estrildid genome, and such specific bands may be used for genotype characterization. Further, putative species-specific RAPD markers could be converted to sequence characterized amplification regions (SCARs) after sequencing and designing primer pairs to develop robust species specific markers (Fritsch, 1996). The study also provides a basis for conservationists to make informed choices on selection of parental material based on genetic diversity to help overcome some of the problems usually associated to develop management strategies for maintaining evolutionarily significant lineages that will ensure long – term population stability.