

Genetic diversity of insectivorous bats in Uttar Pradesh

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Summary

Presently, more than 1300 species of bats are known. Among the two sub orders of Chiroptera, the microchiropterans are the once that are mostly studied and most diverse group of bats. India is enshrined with almost 119 species of bats constituting into nine families. These include pteropodidae, Rhinopomatidae. Megadermatidae, Rhinolophidae, Hipposideridae, Molossidae, Emballonruidae and Vespertilionidae. About 75% species of bats are insectivorous with true powered flight and echolocation which has made them to seek shelters in many different types of structure. It has been complicated to determine the exact identity of species that occupy a similar ecological niche and have very close morphological characters.

Despite a large portion of species level taxonomy is based on a narrow array of data types like patterns of variability in morphology, ecology and genetic elements, still much of the complexity and evolutionary biology is yet to be revealed. Due to scarcity of appropriate genetic information. It becomes extremely difficult to study them in the wild. Thereby the proposed work of my research was to assess the genetic diversity of insectivorous bats in Uttar Pradesh.

Assessment of genetic diversity among the populations of Mouse tailed bats (Rhinopomatidae) was carried out in the district of Uttar Pradesh. The purpose of the work was to find the genetic diversity from the five populations of different geographical regions using RAPD-PCR technique. A total of 51 bands were detected by the five amplified primer (OPA-02, OPA-03, OPB-08, OPB-18 and OPD-02). They produced 10.2 bands per primer with an average and the molecular weight ranged from 912 to 158

base pair. The polymorphic loci among the populations of *R. hardwickii* varied considerably with (56.86%). Among all the primer used, OPB-08 produced the maximum amplified fragments.

The similarity coefficient values among the populations ranged from 0.60 to 1.00. The polymorphic information content values also ranged from 0.303 (OPB-18) to 0.557 (OPB-080), with a mean PIC value of 0.43. The PIC value suggests that enormous heterozygosity was associated with a high degree of polymorphism among the population, despite the increasing fragmentation of its habitat. So the high genetic diversity was observed in the study which further suggests that there is less threat to the population of *R. hardwickii*.

The genetic variation in the populations of the Indian false Vampire bat, *Megaderma lyra* by using the same molecular marker was carried out. *Megaderma lyra* belong to a heterogeneous group of echolocating bat and is scattered in patches in different regions of Uttar Pradesh. This species of bat is a non-migratory carnivorous and maintains high level of roost fidelity and its dispersal ability is still obscure. The bat population was collected from the neighboring colonies of Barabanki, Uttar Pradesh. All the neighboring colonies were located at a distance of 7-9 Km without any physical barrier. The data expressed quite low level of diversity within the five populations studied. A total of 59 bands were generated with the six primers used, (OPAA-09, OPW-02, OPB-18, OPR-08 and OPA-13) with an average of 9.8 bands per primer. Among the primers used OPA-11, produce the maximum number of bands. The molecular weight ranged from 100 – 900 base pair. The Polymorphic information content varied over 46.5%. The similarity coefficient values ranged from 0.432 to 1.00 while the

polymorphic information content (PIC) ranged from 0.651 (OPAA-09) to 0.720 (OPA-11). Thus the alleviated level of heterozygosity reveals that the populations will be less resilient to threats and less adaptive.

The genetic diversity among the colonies of *Scotophilus heathii* from ten different locations of Uttar Pradesh were carried out. The aim of this study was to check the level of heterozygosity (Polymorphism) among the populations studied. This vesper bat is ubiquitous and known to occupy the highest number of bat species in the chiropteran family. This insectivorous bat chooses to reside in the temperate areas of Europe and Asia resting during the day, feeding at night hours and often hibernating during the winter season. Although *S. heathii* have high potential for dispersion, yet they can display unexpected levels of genetic differentiation and strong geographic structure. RAPD markers were used to analyze the genetic relatedness among the ten populations of *S. heathii* in different geographical regions of Uttar Pradesh. The specimens were sampled from They are Balrampur BLR [1], Mirzapur MZR [2], Allahabad ALD [3], Sultanpur STR [4], Maharajganj MRJ [5], Gorakhpur GKP [6], Raebareli REB [7], Azamgarh AZH [8], Unnao UNO [9], and Fatepur FTP [10].

RAPD-PCR reaction was designed using a set of six primers OPR-08, OPA-11, OPAA-09, OPB-08, OPC-07 and OPA-17. All the ten samples of *S. heathii* collected showed noticeable level of genetic variation. All the primers expressed polymorphism and a total of 115 bands were detected. Out of the total bands observed 63% were found to be monomorphic while 36% of them gave polymorphic bands. The highest polymorphic information content were obtained with primer 0.0893 (OPR-03) and lowest with the primer 0.498 (OPA-17) with a mean of 0.70. The amplification product size

ranged from 150 – 950 base pair. The discrimination power of each locus was evaluated with the help of PIC value. The amount of genetic relatedness among the population of *S. heathii* spread over different regions was deduced by Jaccard coefficient analysis.

Among the results obtained from all the populations studied the maximum similarity 72% was observed between the population of Raebareli REB [7] and Maharajganj MRJ [5]. Minimum similarity value 39% was obtained between the populations of Balrampur BLR [1] and Unnao UNO [9]. From the above result it can be concluded that even if the species of *S. heathii* are far or close by, the geographical distance did not play a major role in separating them at a genetic level. Further these species changes the habitat according to their suitable niche and space, and of course the evolutionary potential of any species help them to cope with the changing environment. The contribution of genetic diversity to population viability is basically an interaction with physiological, behavioral and ecological processes. For more productive management, options should involve actions to restore genetic variability by reestablishing gene flow by selective translocation.