CHAPTER 6
SUMMARY AND CONCLUSION

6.1. Summary

In the present study a comprehensive comparative evaluation of genetic status of the greater one-horned rhinoceros was done based on microsatellite marker following a noninvasive genetic monitoring approach. The study encompassed five wild populations of greater one-horned rhinoceros in India. The results obtained in the study are summarized briefly below,

a. The present study showed that the greater one-horned rhinoceros populations of India carry moderate to high level of genetic diversity.

b. Among all the five populations studied, KNP population showed the highest level of heterozygosity (He = 0.590 ± 0.13; Ho = 0.670 ± 0.15), while Gorumara population showed the lowest level of heterozygosity (He = 0.352 ± 0.20; Ho = 0.409 ± 0.27).

c. Although signatures of past bottlenecking were observed in two populations from Assam, viz., KNP and ONP, its effect on overall genetic diversity was not very prominent in both the populations.

d. The within population genetic variation was observed to be high (83.1%) in comparison to among population variation (16.9%) as was indicated by the AMOVA results.

e. The pair wise F_{ST} estimates showed considerable amount of genetic differentiation among the greater one-horned rhinoceros populations of India. Especially, the GNP population was found to be significantly different from the other rhino populations sampled.

f. Bayesian clustering showed the GNP and JNP population carry unique genetic signatures. The populations of Assam i.e., KNP, ONP and PWLS were observed to be admixed populations.

g. Among the 238 individual rhinos genotyped in the present study, seven individuals were found to be first generation migrants (F_0). Of these seven individuals, one individual sampled in ONP migrated from PWLS while rest of the six individuals sampled in KNP migrated from ONP. No first generation migrants were detected in the populations of West Bengal.

h. The results obtained in the present study showed an asymmetric pattern of migration among the rhinoceros populations of Assam with observed mean migration rate (m) $\geq$ 0.056. The mean migration rates between 'STRUCTURE' defined populations were observed to be insignificant.

6.2. Conclusion

With the development of human civilization, the use of natural resources to meet the human needs has increased by leaps and bounds. Unrestricted extraction of natural resources has led to unparallel destruction of natural habitats of wild animals, as a consequence of which many species have gone extinct from the earth while many others are facing the risk of extinction. Degradation of habitats and fragmentation has been shown to have negative effect on genetic variability of species thus affecting its long term viability. Genetic monitoring offers the scope to evaluate the genetic status of populations of wild animals. For the development of effective conservation and management plan, the knowledge of genetic status is imperative as genetic factors could lead to species extinction. Furthermore, genetic diversity at species level is also vital for sustaining ecosystem diversity and its survival.

The results of the present study will be crucial in determining the conservation needs of the greater one-horned rhinoceros, thus enabling the design of effective conservation and management plan for the species to ensure its long term survival. The results clearly show that the rhinoceros populations still maintain moderate to high level of genetic diversity and unlike, previously thought, the impact of rapid reduction in population size during the beginning of the 20th century did not have any prominent effect. The observed levels of genetic differentiation among the rhinoceros populations, especially, in case of the populations of West Bengal need immediate attention. Fragmentation of suitable habitats of greater one-horned rhinoceros has been a major concern for conservation biologists over the years. Looking at the present scenario, these populations may continue to remain in isolation which along with limited migration may have serious implications. Therefore, efforts should be given to restore the natural connectivity between these populations which will facilitate movement of individual rhinos. Furthermore, priority should be given for genetic restocking of JNP and GNP which showed unique genetic signatures in the present study. The present study showed admixture among the rhino populations of Assam, viz., KNP, ONP and PWLS. Nonetheless, habitat fragmentation still remains a threat to these populations which might affect the migration pattern of individual rhinos which is still existent among these populations which is evident from the present study. Efforts to preserve the connectivity between these populations therefore need appreciation.

In the present study, the effect of landscape features on the gene flow among the rhinoceros populations could not be assessed precisely due to lack of information on the human settlement data along with data on population demography, behavioural changes in rhinoceros in response to human activity and changes in the habitat configuration induced by fragmentation at a landscape level. Therefore, future studies should be undertaken to evaluate such information in the entire landscape which will help in determining the effect of habitat fragmentation of the on gene flow. Also, studies should be undertaken to better understand the migration patterns of greater one horned rhinoceros populations of India in the future. While conducting such studies, emphasis should be given to generate data for multiple years as single session sampling may not be adequate to arrive to a fruitful conclusion. Furthermore, generating data on the adaptive genetic variations should also be considered which will help to better understand the evolutionary process acting on the populations.

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APPENDIX I

Plate 1: Greater one-horned rhinoceros *Rhinoceros unicornis* in its Natural Habitat

APPENDIX II

(a)

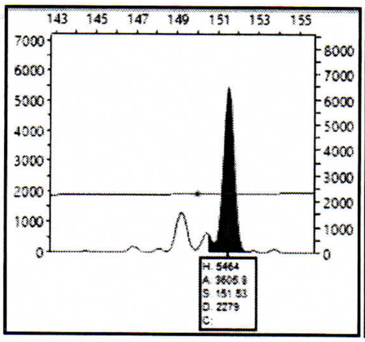
(b)

(c)

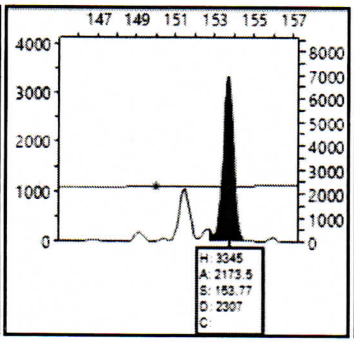
Plate 2: Rhino dung heaps (a) and (b); Collection of dung samples in field (c)

APPENDIX III

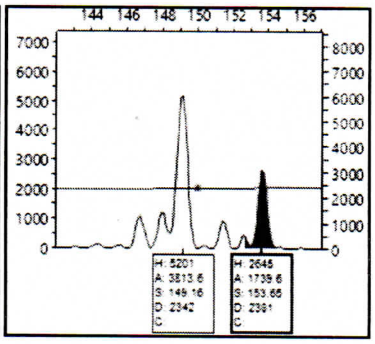
Marker: Rh1



Genotype: 152,152

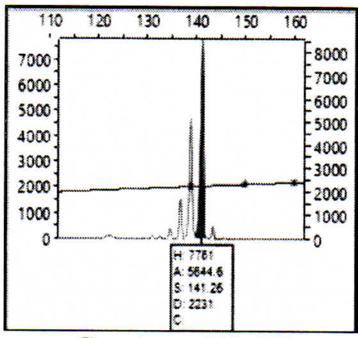


Genotype: 154,154

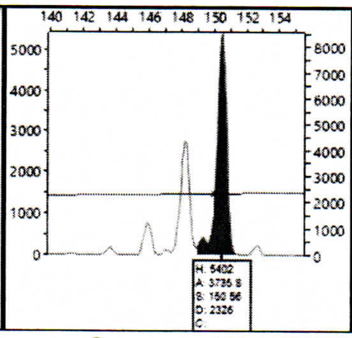


Genotype: 148,154

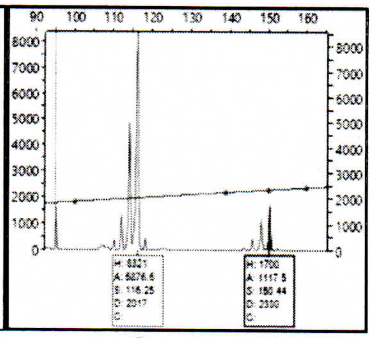
Marker: Rh3



Genotype: 140, 140

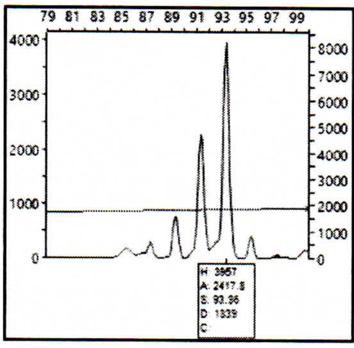


Genotype: 150,150

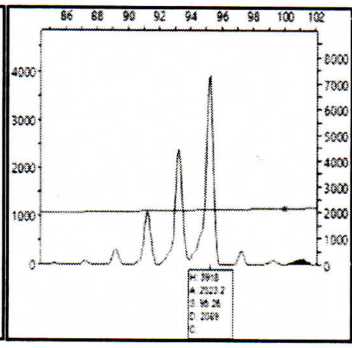


Genotype: 116,150

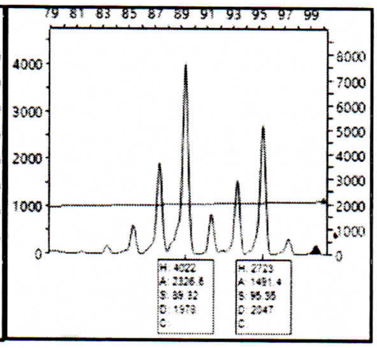
Marker: Rh4



Genotype: 093,093



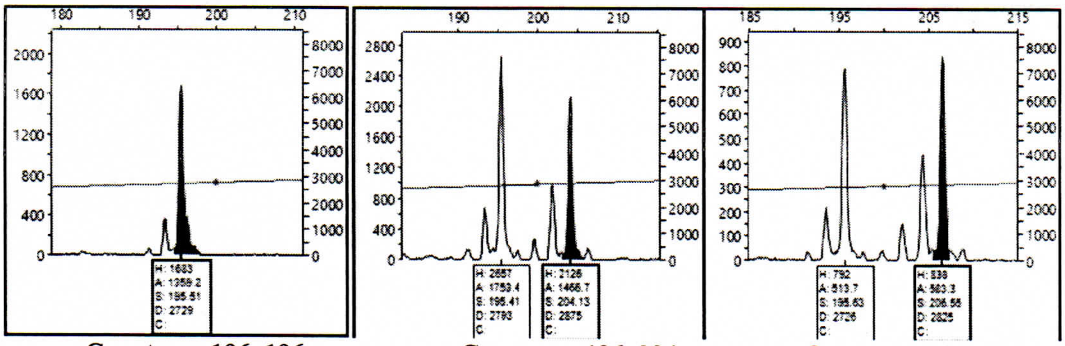
Genotype: 095,095



Genotype: 089,095

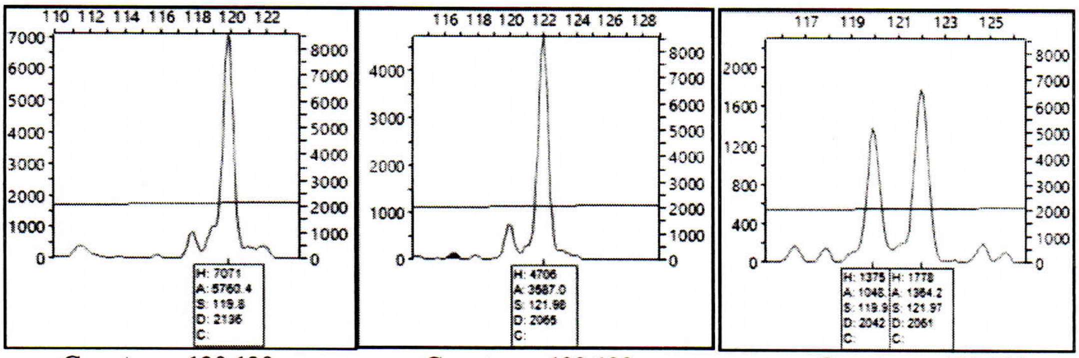
Plate 3: Representative electropherograms of microsatellite markers Rh1, Rh3 and Rh4

Marker: Rh5



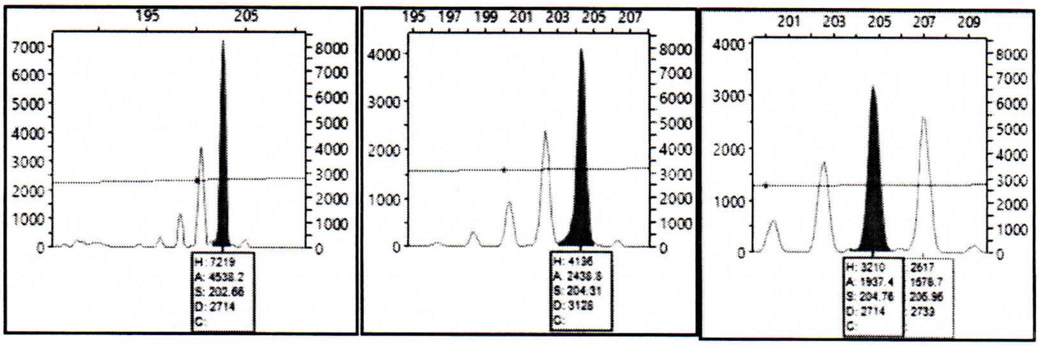
Genotype: 196, 196 | Genotype: 196, 204 | Genotype: 196, 206

Marker: Rh6



Genotype: 120,120 | Genotype: 122,122 | Genotype: 120,122

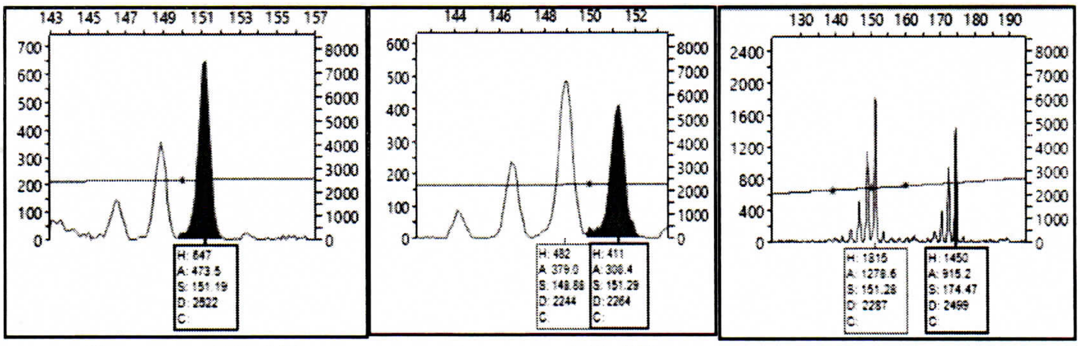
Marker: Rh7



Genotype: 202,202 | Genotype: 204, 204 | Genotype: 204, 206

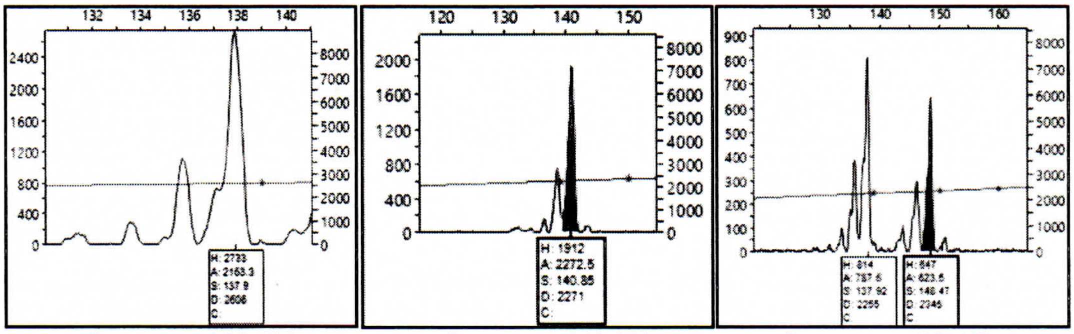
Plate 4: Representative electropherograms of microsatellite marker Rh5, Rh6 and Rh7

Marker: Rh9



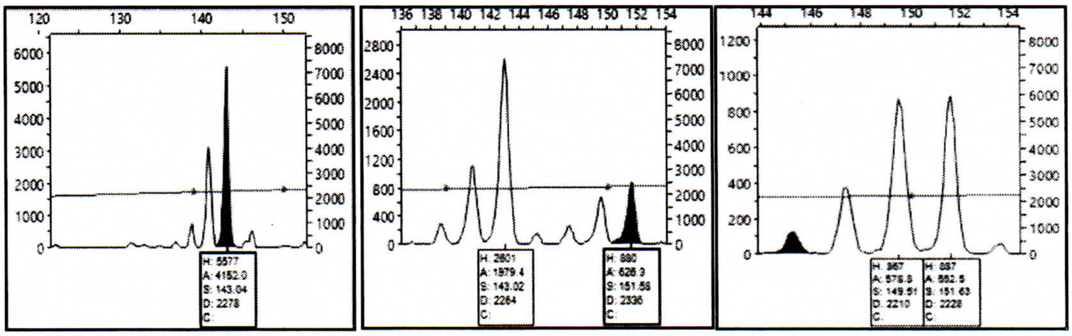
Genotype: 150, 150 | **Genotype: 148, 150** | **Genotype: 150, 174**

Marker: Rh10



Genotype: 138,138 | **Genotype: 140,140** | **Genotype: 138,148**

Marker: Rh11



Genotype: 143,143 | **Genotype: 143,151** | **Genotype: 149,151**

Plate 5: Representative electropherograms of microsatellite marker Rh9, Rh10 and Rh11