

**GENETIC STRUCTURE OF A BROWN LEMUR INTERSPECIFIC HYBRID POPULATION IN BERENTY, MADAGASCAR**

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The purpose of the study is to clarify the genetic structure of the hybrid population between two brown lemur species with different number of chromosomes (*Eulemur rufus*:  $2n=60$  and *E. collaris*:  $2n=52$ ). This population has rapidly grown since a small number of founders were introduced to Berenty Private Reserve in the 1970s and 1980s. We collected tissue and blood samples from Berenty lemurs ( $n=81$ ) and the parental species, *E. rufus* ( $n=11$ ) at Kirindy Forest Reserve and *E. collaris* ( $n=7$ ) at Nahampoana Private Reserve in accordance with the guide for the care and use of laboratory primates (KUPRI 1986, 2002). We analyzed karyotypes, the mitochondrial D-loop sequence and 12 loci of microsatellite DNA. The Berenty lemurs showed the variety of number of chromosomes ( $2n=56$  to  $60$ ), indicating that the population contains hybrid and backcross individuals. MtDNA analysis revealed that females of both species participated in the formation of Berenty population. The results of microsatellite analysis showed that genetic diversity of Berenty population was relatively high with a mean heterozygosity of 0.73, and no genetic differentiation was observed within the population. Genetic constitution of Berenty population was close to that of *E. rufus* of Kirindy. Relatedness among Berenty lemurs indicated that free-ranging groups contained related members, such as a parent and its offspring, siblings, and an aunt and a niece. This seems to reflect the characteristics of female philopatry and male dispersal. The Berenty population has maintained nearly random mating, and the population continues to grow without the negative effects of hybridization.

Keywords: brown lemur, interspecific hybrid, genetic structure, Berenty