DNA Fingerprinting and the Problems of Paternity Determination in an Inbred Captive Population of Guinea Baboons (*Papio hamadryas papio*)

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**Abstract.** Multilocus DNA fingerprinting was carried out on 65 individuals from a captive colony of guinea baboons (*Papio hamadryas papio*) at Brookfield Zoo, in order to determine the allocation of reproductive success among 7 active males. DNA fingerprinting was found to reveal very low levels of genetic variability in the study population, rendering discrimination of different levels of relatedness, and hence paternity, impossible. A method was therefore developed for emphasizing the region of the fingerprint pattern which revealed the greatest level of band variability, and the effect of this experimental modification on band sharing statistics was tested. Band sharing coefficients among unrelated individuals were significantly lower using the modified system, which was then applied to paternity testing in the whole population. However even when using the modified system, of the 33 offspring analyzed only 4 could be assigned solely to 1 male, 14 offspring were assigned to 1 of 2 males, 7 offspring had 3 potential fathers, and the remainder had 4 or more possible fathers. The implications of the limitations of these data for behavioural studies and genetic management of captive populations are discussed.

**Key Words:** DNA fingerprinting; Baboons; Inbreeding; Paternity.

**Introduction**

Between 1985 and 1988, detailed observations of behavioural affinities and matings were carried out on a captive population of guinea baboons (*Papio hamadryas papio*) housed on 'Baboon Island' at Brookfield Zoo (*Samuels & Altmann, unpubl.*). The colony was founded in 1938 with 58 individuals, which were supplemented in 1939 and 1940 with additional females, most of which were guinea baboons, but some were possibly olive baboons (*P. h. anubis*) and hamadryas baboons (*P. h. hamadryas*). Animals have been periodically removed throughout the colony’s history, particularly in the 1960’s when many males and all individuals which were atypical of the guinea baboon phenotype were removed. Since that time 40 – 60 baboons have been continuously kept on the island, with about half being adult, and at no time since 1940 have any unrelated individuals been introduced into the colony. It has been presumed, therefore that there is considerable inbreeding in this population (*Lacy & Foster, 1988*). Since 1970, maternity records have been kept, but the presence of multiple reproductively active males in the colony has prevented the assignment of paternity to specific individuals (*Lacy & Foster, 1988; Turner et al., 1992*). During the period of this study seven males were actually or potentially reproductively active.
Lacy and Foster (1988) have attempted to determine paternities in this colony using protein electrophoresis, however this proved impossible as of the 32 loci examined, 31 were invariant. Mean heterozygosity was 1.0%, compared with values from wild baboon populations of 3.9% for *P. h. papio* (Lucotte, 1979), 1.8% (Lucotte, 1979), 1.7%, and 2.9% (Shotake, 1981) for *P. h. anubis*, 2.8% for *P. h. cynocephalus* (Lucotte, 1979), 3.6% and 4.5% (Shotake, 1981), and 5.0% (Lucotte, 1979) for *P. h. hamadryas*. These data would indicate that the Baboon Island population suffers depressed levels of genetic variability due probably both to inbreeding and genetic bottlenecks caused by aspects of colony management.

One possible means of uncovering genetic variability in the Baboon Island population, not detected by protein electrophoresis, is to utilize DNA sequences known to be highly variable. To date the most polymorphic DNA loci known comprise a class of hypervariable tandem-repetitive sequences known variously as VNTRs (Variable Number of Tandem Repeats) or minisatellites (Wyman & White, 1980; Jeffreys et al., 1985a; Nakamura et al., 1987) which mutate rapidly by the gain or loss of different numbers of repeat units. Related sequences of this type are most commonly revealed simultaneously in a multilocus DNA fingerprint (Jeffreys et al., 1985a, b; see Wickers, 1993). Recently, Turner et al. (1992) carried out multilocus DNA fingerprinting on four randomly chosen individuals from the Baboon Island population, using probes 33.6 and 33.15 (Jeffreys et al., 1985a, b). Very little variation was apparent in the 33.15 fingerprint pattern, which was not thought to be specific to the individuals analyzed.

In this paper we describe a further study in this population using DNA fingerprinting, designed both to quantify any residual genetic variation occurring among the colony members, and to test whether a combination of different multilocus minisatellite probes could be used to unequivocally identify fathers in this inbred population.

**MATERIALS AND METHODS**

DNA fingerprinting was carried out using the general protocols described in Bruford et al. (1992), with the following modifications specific for guinea baboon fingerprints. DNA was extracted from 3 ml of frozen baboon blood with: (1) an equal volume of phenol; (2) an equal volume of phenol/chloroform; and (3) a similar volume of chloroform:isoamyl alcohol (Jeffreys & Morton, 1987). The DNA was subsequently precipitated in two volumes of 100% ethanol, and dissolved in TE (10 mM Tris, 1 mM EDTA pH 8.0).

**Probe/enzyme test gel**

Five μg samples of high molecular weight DNA were taken from four individuals belonging to different family groups (based on matrilines traced back 15 years) and were digested separately with *Hinf I, Hae III, Alu I*, and *Mbo I*. The digested DNA was electrophoresed at 1.5 v/cm through a 25 cm, 1% agarose gel until 2 kb fragments had migrated 200 mm, and was blotted onto a nylon membrane under vacuum. The membrane was probed with 33.6 and 33.15 (Jeffreys et al., 1985a) in phosphate hybridization buffer (Westneat et al., 1988; Bruford et al., 1992) and washed at low stringency (0.26 M Na2HPO4, 1% SDS for 15 min., 2×SSC, 0.1% SDS for 15 min., both at 60°C). Autoradiographic film was exposed for between two and five days before being developed.