

SEQUENCE REGISTER

S.C. Alberts

Thirteen *Mhc-DQA1* alleles from two populations of baboons

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Several recent studies have identified alleles at the baboon *Mhc-DQA* and *Mhc-DQB* loci (Gyllensten and Erlich 1989; Kenter et al 1992; Mwenda et al 1997). These loci show the high levels of polymorphism that typify the class II loci in many taxa (Bontrop 1994; Kenter et al 1992). However, all of the baboon major histocompatibility complex (MHC) class II alleles reported to date have been isolated from laboratory animals or cell lines. This has left unresolved the question of whether levels of polymorphism at these loci are high within any single wild or captive baboon population.

The current study reports 13 *DQA1* alleles found in two study populations of baboons, one wild and outbred and the other captive and inbred. The wild population consists of 11 social groups of yellow baboons (*Papio cynocephalus*) in Amboseli National Park, Kenya (Samuels and Altmann 1991). The captive population consists of a single social group of guinea baboons (*P. papio*), at Brookfield Zoo in Brookfield, Illinois, USA. The Amboseli and Brookfield populations represent geographically distinct species (although taxonomic status is in dispute; Jolly 1993; Kingdon 1997; Rowe 1996), with indigenous ranges in eastern/central and in far western Africa, respectively.

The Amboseli baboon population is part of a large baboon metapopulation in southern Kenya. Males (the dispersing sex in baboons as in many mammals) move freely between social groups within Amboseli as well as between Amboseli and neighboring areas, particularly

to the south and east of Amboseli (Alberts and Altmann 1995; Samuels and Altmann 1991). The Amboseli population itself is at the edge of a hybrid zone between *Papio cynocephalus* and *P. anubis* (Samuels and Altmann 1986, 1991); the majority of individuals in the population exhibit a cynocephalus phenotype but anubis males sometimes immigrate into the cynocephalus groups. Anubis and cynocephalus individuals readily mate in Amboseli (Samuels and Altmann 1986) and viable offspring with hybrid phenotypes result (Samuels and Altmann 1986; S. Alberts and J. Altmann, unpublished data).

The Brookfield population of *P. papio* originated in western Africa and was established at the Brookfield Zoo in 1938. A small number of *P. anubis* or *P. hamadryas* may have been added early in the population's history (Lacy and Foster 1988). The Brookfield population is inbred, and exhibits a 75% loss of genetic variability relative to wild populations for 32 blood proteins (Lacy and Foster 1988), as well as unusually low levels of variability in multilocus DNA fingerprints (Bruford and Altmann 1993).

Genomic DNA from 24 baboons (15 individuals from Brookfield and 9 from Amboseli) was extracted from whole blood using a standard proteinase K digestion and phenol/chloroform extraction (Sambrook et al 1989). The second exon of the *DQA1* locus was amplified by means of the polymerase chain reaction (PCR), using human primers GH26 and GH27 (Scharf et al 1986). A standard PCR protocol was followed, with an annealing temperature of 52 °C (3 °C lower than the optimal annealing temperature when amplifying human DNA; Gyllensten and Erlich 1988). The resulting product was cloned into the Invitrogen pCR2.1 vector (Invitrogen, San Diego, Calif.). Positive clones were sequenced and visualized on an ABI 370 A automated sequencer using a fluorescein-labeled sequencing method and standard M13 primers (Applied Biosystems, Norwalk, Conn.). Sequences were analyzed by comparison with published sequences, using the program BLAST 2.0 available on the NCBI website

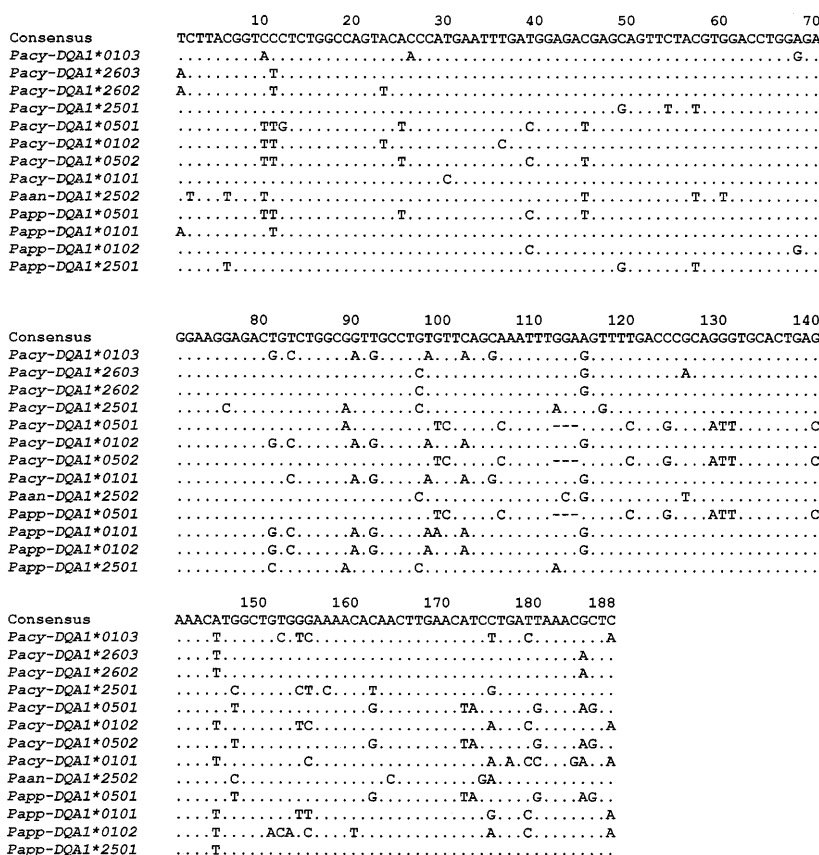
S.C. Alberts¹
MCZ Laboratories, Harvard University, Boston, MA, USA

Present address:

¹S.C. Alberts (✉)
Department of Zoology, Duke University, Box 90325,
Durham, NC 27708, USA
e-mail: alberts@duke.edu,
Tel.: +1-919-6607272,
Fax: +1-919-6846168

Table 1 Baboon *Mhc-DQA1* alleles

Allele designation	Population	Species	Common name	Percent identity with consensus	Accession number
<i>Pacy-DQA1*0103</i>	Amboseli	<i>P. c. cynocephalus</i>	Yellow baboon	94	AF110834
<i>Pacy-DQA1*2603</i>	Amboseli	<i>P. c. cynocephalus</i>	Yellow baboon	97	AF110835
<i>Pacy-DQA1*2602</i>	Amboseli	<i>P. c. cynocephalus</i>	Yellow baboon	97	AF110836
<i>Pacy-DQA1*2502</i>	Amboseli	<i>P. c. cynocephalus</i>	Yellow baboon	95	AF110838
<i>Pacy-DQA1*0501</i>	Amboseli	<i>P. c. cynocephalus</i>	Yellow baboon	89	AF110839
<i>Pacy-DQA1*0102</i>	Amboseli	<i>P. c. cynocephalus</i>	Yellow baboon	94	AF110840
<i>Pacy-DQA1*0502</i>	Amboseli	<i>P. c. cynocephalus</i>	Yellow baboon	90	AF1131888
<i>Pacy-DQA1*0101</i>	Amboseli	<i>P. c. cynocephalus</i>	Yellow baboon	95	AF110841
<i>Paan-DQA1*2502</i>	Amboseli	<i>P. c. anubis</i>	Olive baboon	94	AF110837
<i>Papp-DQA1*0501</i>	Brookfield	<i>P. c. papio</i>	Guinea baboon	90	AF110842
<i>Papp-DQA1*0101</i>	Brookfield	<i>P. c. papio</i>	Guinea baboon	94	AF110843
<i>Papp-DQA1*0102</i>	Brookfield	<i>P. c. papio</i>	Guinea baboon	95	AF110844
<i>Papp-DQA1*2501</i>	Brookfield	<i>P. c. papio</i>	Guinea baboon	96	AF110845

Fig. 1 Alignment of *Mhc-DQA1* sequences of baboon, relative to the primate *Mhc-DQA1* consensus sequence (Bontrop 1994). Identities are shown by dots and deletions are shown by dashes

(www.ncbi.nlm.nih.gov). Sequence designations were assigned according to a proposal by Klein and co-workers (1990).

Thirteen alleles were identified among the 24 animals (Fig. 1, Table 1). Eight of these represented sequences unique to Amboseli and three represented sequences unique to Brookfield. One Brookfield allele (*Papp-DQA1*0501*) was identical in nucleotide sequence to an Amboseli allele (*Pacy-DQA1*0502*). All but one of the thirteen alleles were cloned and sequenced in at least two individuals from either Amboseli or Brookfield. The exception was *Paan-*

*DQA1*2502*, which has thus far been identified in only one animal, an anubis male living in a cynocephalus group in the Amboseli population.

Twelve of the thirteen alleles have not been described before, and one (*Pacy-DQA1*0501*) was previously identified in a laboratory animal by Mwenda and co-workers (1997). Two of the thirteen alleles were identical in nucleotide sequence to alleles reported in other species: *Pacy-DQA1*0101* was identical to *Paan-DQA1*0102* reported by Mwenda and co-workers (1997), and *Papp-DQA1*0102* was identical to *Popy-DQA2*01*, an allele at an untranscribed locus described

