

NEW ALLELE Alerts

Fifty-one full-length major histocompatibility complex class II alleles in the olive baboon (*Papio anubis*)

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Here we report 51 novel major histocompatibility complex (MHC) class II alleles in a group of related olive baboons.

Olive baboons (*Papio anubis*), named after their greenish grey fur, are widespread in equatorial Africa, and are found in countries from the east to the west coast of the continent. They live in a variety of habitats across this broad range, mostly in grasslands, but they are also seen in evergreen forests and near areas of human habitation (pin.primare.wisc.edu/factsheets/entry/olive_baboon). Although not as frequent as the Asian macaque species, baboons are used as animal models in studies on human infectious diseases such as acquired immune deficiency syndrome (AIDS) and malaria (1, 2). The application of these animals in immune-related diseases dictates the investigation of genes and gene products composing their immune systems.

In this study, the transcripts of MHC genes in a group of 25-related olive baboons was explored. The cDNAs of the orthologs of human class II genes, named Paan-DRA, -DQA1, -DQB1, -DPA1 and -DPB1, were amplified with primers that had proven their effectiveness in macaques species (3). After

cloning and Sanger sequencing on a capillary system, the results were analysed using MacVector version 14.5.3 (MacVector, Inc., Cambridge, UK).

In total 51 full-length alleles were submitted to the EMBL-EBI database, and for official designations to the non-human primate section of the IPD-MHC database (Figure 1) (4). In the designations of MHC class II sequences the first two digits following the asterisk reflect the allelic lineage, which is defined as a group of alleles that originate from one ancestral structure (5). The majority of the lineages found in the olive baboon are also present in the macaques, indicating shared ancestry with these monkeys that are widespread in Asia.

On the basis of the parent/offspring affiliations in the group it was possible to determine the combinations of alleles that segregate on each chromosome. A total of 11 haplotypes were found that combine the alleles of the five investigated class II genes (Figure 1). In other cases, only the DQ and DP pairs were determined, which are listed at the base of Figure 1. Some alleles are present in combination with two alternative alleles. For example, *Paan-DQA1*25:02:01* is observed with *-DQB1*18:01* or *-DQB1*18:04*. Alleles of the *DQA1*01* lineage are exclusively paired with those of the *DQB1*06* lineage, which is also the case in the macaques and in humans (6).

Paan-	Acc. Nr.	Paan-	Acc. Nr.	Paan-	Acc. Nr.	Paan-	Acc. Nr.	Paan-	Acc. Nr.	N	
1	<i>DRA*01:01:01</i>	LT546100	<i>DQA1*26:01</i>	LT607042	<i>DQB1*15:01</i>	LT559126	<i>DPA1*14:02</i>	LT607043	<i>DPB1*21:01</i>	LT595040	3
2	<i>DRA*01:01:02</i>	LT546101	<i>DQA1*01:02</i>	LT607033	<i>DQB1*06:05</i>	LT559125	<i>DPA1*16:01</i>	LT546116	<i>DPB1*19:01</i>	LT595038	4
3	<i>DRA*01:01:02</i>		<i>DQA1*01:04</i>	LT607035	<i>DQB1*06:01</i>	LT546106	<i>DPA1*16:01</i>		<i>DPB1*19:01</i>		5
4	<i>DRA*01:01:02</i>		<i>DQA1*05:02</i>	LT607038	<i>DQB1*18:02</i>	LT559129	<i>DPA1*02:03</i>	LT595042	<i>DPB1*14:01</i>	LT546123	6
5	<i>DRA*01:01:02</i>		<i>DQA1*25:02:01</i>	LT607040	<i>DQB1*18:01</i>	LT546107	<i>DPA1*04:03</i>	LT546111	<i>DPB1*03:01:02</i>	LT546118	2
6	<i>DRA*01:01:03</i>	LT546102	<i>DQA1*01:01</i>	LT607032	<i>DQB1*06:04</i>	LT559124	<i>DPA1*04:01</i>	LT546109	<i>DPB1*03:02</i>	LT546119	3
7	<i>DRA*01:01:03</i>		<i>DQA1*25:02:01</i>		<i>DQB1*18:04</i>	LT559131	<i>DPA1*04:01</i>		<i>DPB1*03:02</i>		2
8	<i>DRA*01:01:03</i>		<i>DQA1*25:02:02</i>	LT607041	<i>DQB1*18:01</i>		<i>DPA1*16:01</i>		<i>DPB1*19:01</i>		4
9	<i>DRA*01:02:02</i>	LT546104	<i>DQA1*01:03</i>	LT607034	<i>DQB1*06:02</i>	LT559122	<i>DPA1*14:01:02</i>	LT546114	<i>DPB1*19:02</i>	LT595039	3
10	<i>DRA*01:02:02</i>		<i>DQA1*05:01</i>	LT607037	<i>DQB1*16:01</i>	LT559128	<i>DPA1*14:01:01</i>	LT546113	<i>DPB1*21:01</i>		2
11	<i>DRA*01:03</i>	LT546105	<i>DQA1*26:01</i>		<i>DQB1*15:01</i>		<i>DPA1*16:01</i>		<i>DPB1*19:01</i>		4
			<i>DQA1*01:05</i>	LT607036	<i>DQB1*06:03</i>	LT559123					1
			<i>DQA1*24:01</i>	LT607042	<i>DQB1*18:03</i>	LT559130					1
			nd		<i>DQB1*15:02</i>	LT559127					1
							<i>DPA1*02:01</i>	LT546108	<i>DPB1*26:01</i>	LT546122	1
							<i>DPA1*02:02</i>	LT595041	<i>DPB1*06:01</i>	LT546121	1
							<i>DPA1*04:02</i>	LT546110	<i>DPB1*03:01:01</i>	LT546117	1
							<i>DPA1*09:01</i>	LT546112	<i>DPB1*21:01</i>		1
							<i>DPA1*15:01</i>	LT546115	<i>DPB1*03:03</i>	LT546120	1
	<i>DRA*01:02:01</i>	LT546103									

Figure 1 The novel alleles observed in this study combined with the accession numbers. Each row in the table represents a combination of alleles of different genes on a chromosome, or haplotype. nd, not detected.

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Conflict of interests

The authors have declared no conflicting interests.

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