

Characterization of full-length MHC class II sequences in Indonesian and Vietnamese cynomolgus macaques

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Supplemental Table 1 Previously described full-length *Mafa* alleles

<i>Mafa</i> allele	Animals	Animal origin	Previously documented origin(s)	Accession #
<i>DPA1*02:03</i>	IN11	Indonesia	Ma (M5)	EF208807 (1)
<i>DPA1*04:01</i>	DR010, DR013, DR016, DR020	Vietnam	Ma (M4)	EF208808 (1)
<i>DPA1*07:02</i>	CE12	Indonesia	Ma (M1)	EF208810 (1)
<i>DPB1*21</i>	DR015, DR019, CE23	Both	In, Ma (M5, M6), Vi	AB235876 (2), AM086068 (3), EF208811 (1)
<i>DPB1*29</i>	IN01	Indonesia	In, Ma (M3)	AB235884 (2), EF208813 (1)
<i>DPB1*42</i>	CE12	Indonesia	Ma (M1)	EF208814 (1)
<i>DQA1*01:06</i>	CE28	Indonesia	Ma (M5)	EF208817 (1)
<i>DQA1*01:07</i>	DR014, DR015, IN04	Both	Ma (M4)	EF208818 (1)
<i>DRA*01:01:06</i>	CE16, IN04, WF05	Indonesia	In, Ph	AB306633 (4), EU877210 (5)
<i>DRA*01:02:01</i> group ^a	DR009, DR010, DR011, DR012, DR017, CE03, CE06, CE12, CE23 IN11, WF01, WF05	Both	Unk	AB306633 (4), EF208827 (1), EU877210 (5)
<i>DRA*01:03:01</i>	DR016, CE28, IN01, IN04, IN10, IN11	Both	In	AM943638 (4), EU877212 (5)
<i>DRA*02:01:01</i> group ^a	CE28	Indonesia	Ma (M1)	AB306631 (4), EF208828 (1), EU877220 (5)
<i>DRB*W1:03</i>	WF05	Indonesia	Ma (Unk haplotype)	AF492281 (7), AF492310 (7), AY362361 (6)
<i>DRB*W1:07</i>	IN04, WF01	Indonesia	Ch, Ph	AF492309 (7), AY340677 (6), DQ381754 (7)
<i>DRB*W4:01</i>	CE03, IN11	Indonesia	Ma (M6), Ph	AF492318 (7), AY340693 (6), EF442015 (1), DQ381744 (7)
<i>DRB*W21:01</i>	CE28	Indonesia	Ma (M1)	AF492295 (7), AF492301 (7), AY340688 (6), EF208831 (1)
<i>DRB1*04:02</i>	IN11	Indonesia	Ma (M2), Ph	AF492337 (7), AY340694 (6), DQ381741 (7), EF442018 (1), L76650 (8)
<i>DRB5*03:01:01</i>	DR016	Vietnam	Ma (M4)	AF492288 (7), AF492325 (7), AY340698 (6), EF208835 (1)

^aMultiple alleles which differ from one another only outside the coding region make up these groups. Due to space constraints, accession numbers are listed for one variant only.

All *Mafa* MHC class II alleles identified in this study were compared with those available in GenBank. Those which perfectly matched previously identified alleles for which the entire coding sequence was known are listed here. “Animal origin” indicates the origin of all animals in which the allele was detected in this study. “Both” denotes alleles found in the Indonesian and Vietnamese cohorts. Previously documented origin information was taken from the corresponding publication(s) and/or Genbank record(s). The abbreviations used were In=Indonesia, Ch=China, Ma=Mauritius, Ph=Philippines, Vi=Vietnam, Unk=Unknown. Mauritian haplotypes are indicated in parentheses. References for accession numbers are (1) O'Connor et al. 2007, (2) Sano et al. 2006, (3) Doxiadis et al. 2006, (4) unpublished, various sources, (5) Aarnink et al. 2010, (6) Leuchte et al. 2004, (7) Blancher et al. 2006, (8) Gaur and Nepom 1996.

Supplemental Table 2 Nucleotide sequences from other macaque species identical to novel *Mafa* alleles

<i>Mafa</i> allele name	<i>Mafa</i> accession #	Animals	Animal origin (<i>Mafa</i>)	Identical sequence from other macaque species	Accession # of identical sequence
<i>DPAI*02:07</i>	HM580026	DR012	Vietnam	<i>Maar-DPA*02:01</i> ^a <i>Mamu-DPAI*02</i> lineage ^{a,b}	AF026703 (1) AB548932 (3)
<i>DPAI*02:08:01</i>	HM580029	DR017	Vietnam	<i>Mamu-DPAI*02:02:01</i>	EF204948 (2)
<i>DPAI*02:13</i>	HM579967	IN10	Indonesia	<i>Maar-DPA*02:01</i> ^a <i>Mamu-DPAI*02</i> lineage ^{a,b}	AF026703 (1) AB548932 (3)
<i>DPAI*04:02</i>	HM579969	CE23, IN01, WF01	Indonesia	<i>Mamu-DPAI*04:03</i>	GQ471885 (3)
<i>DPAI*06:01</i>	HM580027	DR012	Vietnam	<i>Mamu-DPAI*06:01</i>	EF204949 (2), AB250753 (3)
<i>DPAI*07:04</i>	HM579964	CE12, CE28	Indonesia	<i>Mamu-DPAI*07</i> lineage ^b	AB250757 (3)
<i>DQAI*01:10</i>	HM579993	CE23	Indonesia	<i>Mamu-DQAI*01:08</i> ^a	AF091334 (4), FN395348 (3)
<i>DQAI*01:12</i>	HM580050	DR016	Vietnam	<i>Maar-DQAI*01:01</i> ^a <i>Mamu-DQAI*01:02</i>	M76204 (5) EF362440 (2), M76200 (5)
<i>DQAI*05:03:02</i>	HM579988	DR012, DR020, IN10, CE23	Both	<i>Mamu-DQAI*05:02</i> ^a	S76215 (6)
<i>DQAI*24:05</i>	HM579991	DR009, DR018, CE12	Both	<i>Mamu-DQAI*24</i> lineage ^b	AB551651 (3)
<i>DQAI*26:04</i>	HM580048	DR014, DR019	Vietnam	<i>Mamu-DQAI*26:01</i>	M76228 (5), EU934780 (3)
<i>DQBI*18:21</i>	HM580002	CE03	Indonesia	<i>Mamu-DQBI*18:18</i> ^a	EU580130 (7)

^aAvailable sequence limited to exon 2

^bAllele not officially named. Lineage inferred based on alignment with available sequences.

Novel *Mafa* alleles were compared to MHC class II sequences from other macaque species available in GenBank. Nucleotide-identical sequences are listed here. “Animal origin” indicates the origin of all animals in which the allele was detected in this study. “Both” denotes alleles found in both the Indonesian and Vietnamese cohorts. References for accession numbers are (1) Otting and Bontrop 1995, (2) Giraldo-Vela et al. 2008, (3) unpublished, various sources, (4) Sauermann 1998, (5) Kenter et al. 1992, (6) Christ et al. 1994, (7) Qiu et al. 2008.

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