

Mitochondrial Sequence Variation, Haplotype Diversity, and Relationships Among Dromedary Camel-types

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Supplementary tables

Table S1: A brief description of the new samples generated for this study. The samples are unrelated and belong to six different camel-types. The Cdrom number mentioned in the table corresponds to the ID for each individual.

Camel-types	Gender	n	Cdrom number
Majaheem	Male	1	264
	Female	20	100-140-148-171-193-194-195-196-198-199-201-202-204-229-250-257-258-259-260-263
	Unknown	4	145-197-203-334
Sofor	Male	2	93-192
	Female	20	70-92-178-261-212-213-214-215-216-217-218-219-338-342-346-352-358-365-366-367
	Unknown	3	170-243-359
Shaele	Male	1	221
	Female	22	73-89-90-91-110-111-112-113-169-173-179-181-188-189-205-207-237-241-247-251-265-306
	Unknown	2	206-242
Shageh	Male	5	163-176-223-292-232
	Female	5	135-158-209-210-236
Homor	Male	2	160-222
	Female	7	137-155-180-187-190-121-208
Waddah	Male	1	161
	Female	24	86-96-102-107-108-109-114-126-128-131-132-133-142-149-152-151-156-157-159-162-165-167-168-175

Table S2: Description of mtDNA sequences (867bp) obtained from publicly available (published) sources as well as unpublished sources (from Saudi Arabia). Each camel-type was assigned to its country of origin.

Country	Camel-type	Sample size (published)	Sample size (unpublished)
Algeria	Sahraoui	17	---
	Targui	16	---
Australia	NA	38	3
Chad	Arabi	13	---
Egypt	Jebali	29	---
Ethiopia	Borena	27	---
Iran	NA	30	---
India	NA	19	---
Jordan	NA	26	---
	Rendille	9	5
	Turkana	7	2
Kenya	Gabbra	4	1
	NA	13	---
Kuwait	Shaele	18	---
Libya	NA	9	---
	Kala	16	---
	Ja	15	---
Niger	Kubule	2	---
	Kurri	13	---
	NA	7	---
Oman	Batinah	30	1
	Dhofar	22	3
	NA	---	4
Pakistan	Kohi	21	---
	Raidi	17	---
	NA	---	1
	Awarik	30	14
	Awadi	27	6
	Hadana	23	4
	Sahlia	17	6
Saudi Arabia	Hurra	15	11
	Maghateer	16	9
	Sofor	18	6
	Majaheem	14	4
	Shaele	12	6

Somalia	NA	14	4
	Hawari	6	---
	Hasani	3	---
	Kababish	6	---
Sudan	Baladia	17	---
	Kenana	2	---
	Arabi	2	---
	NA	34	5
Syria	Raka	13	---
Tunisia	NA	31	---
United Arab Emirates	Omani	5	8
	Khalfan	5	---
	NA	23	---
Yemen	NA	8	---

Table S3: Mitochondrial DNA polymorphisms in the sequenced 867bp among the 972 studied samples. Nucleotide positions are according to Genbank (NC009849).

		Coding		Noncoding		Total
		CYTB	tRNA ^{thr}	tRNA ^{pro}	D-loop	
Nucleotide position	Start	15112	15296	15364	15430	15112
	End	15295	15364	15429	~15979	~ 15979
Length (bp)		184	68	64	549	867
Number of haplotypes		11	6	7	58	82
Haplotype diversity		0.202	0.245	0.020	0.700	0.725
Variable sites		10	5	6	28	48
Transitions		9	5	6	26	45
Transversions		1	0	0	2	3

Table S4: The identified polymorphic sites within the 867bp sequenced mitochondrial region. Relative position is the variant position in relation to the sequenced region, while the mitochondrial genome position is the actual position of the variant according to the reference sequence used from Genbank (NC009849).

Polymorphic site	Relative position	Mito. ref. position	Type	Variant
1	12	15123	Transversion	G/T
2	37	15149	Transition	T/C
3	44	15155	Transition	A/G
4	49	15160	Transition	G/A
5	56	15167	Transition	A/G
6	60	15171	Transition	G/A
7	72	15183	Transition	T/C
8	82	15193	Transition	A/G
9	130	15241	Transition	C/T
10	146	15257	Transition	G/A
11	224	15335	Transition	T/C
12	225	15336	Transition	A/G
13	234	15345	Transition	G/A
14	236	15347	Transition	C/T
15	243	15354	Transition	T/C
16	256	15367	Transition	G/A
17	258	15369	Transition	G/A
18	263	15374	Transition	G/A
19	264	15375	Transition	G/A
20	267	15378	Transition	A/G
21	282	15393	Transition	G/A

22	322	15433	Transition	T/C
23	355	15466	Transition	T/C
24	367	15478	Transition	A/G
25	370	15490	Transition	C/T
26	373	15493	Transition	A/G
27	375	15495	Transition	G/A
28	381	15501	Transition	C/T
29	336	15446	Transition/ transversion	A/G/T
30	384	15504	Transition	G/A
31	385	15505	Transition	G/A
32	389	15506	Transition	G/A
33	393	15510	Transition	G/A
34	397	15514	Transition	C/T
35	414	15531	Transition	C/T
36	442	15559	Transition	A/G
37	452	15569	Transversion	A/C
38	489	15606	Transition	A/G
39	491	15608	Transition	T/C
40	508	15625	Transition	G/A
41	512	15629	Transition	T/C
42	535	15652	Transition	T/C
43	600	15717	Transition	T/C
44	601	15718	Transition	A/G
45	684	15801	Transition	T/C
46	744	15861	Transition	C/T
47	747	15864	Transition	A/G
48	810	15927	Transition	G/C

Table S5: The identified haplotype sequences of *Camelus dromedarius* along with the two naming systems, frequency in percentage, haplogroup clustering, and accession number. Shown sequences only included the variable sites and not invariable sites. Variable sites were mentioned in Table S4.

Old Name	New Name	Frequency%	Sequence	Haplogroup	Accession #
A16	A2	2.37	GTAGAGTACGTAACCTGGGGAGTGTACAACGGGGCCAAATATTTATTAC	A	JX946207
A17	A22	0.31	GTAGAGTACGTAACCTGGGGAGTGTACAACGGGGCCAAATATTTATCAC	A	JX946230
A18	A17	0.41	GTAGAGTACGTAACCTGGGGAGTGCACAACGGGGCCAAATATTTATTAC	A	JX946236
A19	A11	0.21	GTAAAGTACGTAACCTGGGGAGTGTACAACGGGGCCAAATATTTATTAC	A	JX946238
A20	A13	0.10	GTAGAGTACGTAACCTGGGGAGTGTACAACGGGGCCAAATATTTGTTAC	A	JX946253
A21	A1	5.56	GTAAAGTACGTAACCTGGGGAGTGTACAACGGGGCCAAATATTTATCAC	A	JX946214
A22	A3	1.75	GTAAAGTACGTAACCTGGGGAGTGTACAACGGGGCCAAATATTCATCAC	A	JX946227
A30	A9	0.10	GTAAAGTACGTAACCTGGGGAGTGTACAACGGGGCCAAATATTTATCAG	A	JX946263
A31	A5	0.10	GTAAAGTACGTAACCTGGGGAGTGTACAACGGGGCCAAATATTTGTCAC	A	JX946261
A32	A7	0.21	GTAAAGTATGTAACCTGGGGAGTGTACAACGGGGCCAAATATTTATCAC	A	JX946258
A42	A19	0.21	GTAAAGTACGTAACCTGGGGAGTGTACAACGGGGCCAAATATTCATTAC	A	JX946234
A43	A12	0.10	GTAGAGTACGTAACCTGGGGAGTGTACAACGAGGCCAAATATTTATTAC	A	JX946243
A55	A8	0.21	GTAAAGTACGTAACCTGGGGAGTGTACAACGGGGCCAAAGTATTTATCAC	A	JX946266
A56	A16	0.21	GTAGAGTACGTAACCTGGGGAGTGTACAACGGGGTCAAATATTTATTAC	A	JX946256
A57	A20	0.10	GTAAAGTACGTAACCTGGGGAGTGTACAACGGGGCCAAACATTCATCAC	A	JX946237
A58	A15	0.21	GTAGAGTACGTAACCTGGGGAGTGTACAACGGGGCCAAACATTTATTAC	A	JX946231
A64	A10	0.21	GTAAAGTACGTAACCTGGGGAGTGTACAACGGGGCCAAACATTTATCAC	A	JX946268
A65	A4	0.31	GTAAAGTACGTAATTGGGGAGTGTACAACGGGGCCAAATATTTATCAC	A	JX946240
A66	A6	0.21	GTAAAGTACGTAACCTGGGGAGCGTACAACGGGGCCAAATATTTATCAC	A	JX946216
A67	A18	0.31	GTAGAGTACGTAACCTGGGGAGTGTACAATGGGGCCAAATATCTATTAC	A	JX946217
A68	A21	0.21	GTAAAGTACGTAACCTGGGGAGTGTACAACGGGGCCAAATGTTTATCAG	A	JX946215
A70	A23	0.21	GTAGAGTACGTAGCTGGGGAGTGTACAACGGGGCCAAATATTTATCAC	A	KF719284
B1	B1	50.51	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATGTTTATCAG	B	JX946208
B2	B16	0.21	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATGTCTATCAG	B	JX946220
B3	B38	0.21	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATATTTGTCAG	B	JX946221

B4	B17	0.21	GTAGAGCACGTAGCTGGGGAGTATACAGCGGGGCCAAATGTTTATCAG	B	JX946250
B5	B4	6.79	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATATTTATCAG	B	JX946211
B6	B56	0.31	GTAGAGTACATAGCTGGGGAGTATACAGCGGGGCCAAATGTTTATCGG	B	JX946210
B7	B18	0.10	GTAGAGTACGTAGCTGGGGAATATACAGCGGGGCCAAATGTTTATCAG	B	JX946251
B8	B32	0.10	GTAGAGTACGTAGCTGGGGAGTATGCAGCGGGGCCAAATGTTTATCGG	B	JX946252
B9	B2	7.72	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATGTTTATCGG	B	JX946206
B10	B3	7.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATGTTTATTAG	B	JX946209
B11	B35	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATGTTTGTTAG	B	JX946254
B12	B7	1.13	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATGTTTGTCAG	B	JX946249
B13	B10	0.31	GTAGAGTACGTAACCTGGGGAGTGTACAACGGGGGCCAAACATTTATTAC	B	JX946226
B14	B19	0.10	GTAGAGTACGTGGCTGGGGAGTATACAGCGGGGCCAAATGTTTATCAG	B	JX946228
B15	B58	0.10	GTAGAGTACGTAGCCGGGGAGTATACAGCGGGGCCAAATATTTATTAG	B	JX946229
B23	B5	2.88	GTAGAGTACGTAGCTGGGGAGTATACAGCGGAGCCAAATGTTTATCAG	B	JX946218
B24	B30	0.21	GTAGAGTACGTAGCTGGGGAGTATACGGCGGGGCCAAATGTTTATCGG	B	JX946270
B25	B39	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGAGCCAAATGTTTATCGG	B	JX946262
B26	B50	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGAGCCAAATATTTATCAG	B	JX946259
B27	B36	0.10	GTAGGGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATATTTATCAG	B	JX946260
B28	B6	1.13	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCGAATGTTTATCAG	B	JX946233
B29	B31	0.21	GTAGAGTACGTAGCTAGGGAGTATACAGCGGGGCCAAATGTTTATCGG	B	JX946219
B33	B55	0.21	GTGGAGTACGTAGCTGGGGAGTGTACAGCGAGGCCAAATGTTTATCGG	B	JX946248
B34	B29	0.41	GTAGAGTACGTAGCTGGGGAGTATATAGCGGGGCCAAATGTTTATCAG	B	JX946272
B35	B45	0.21	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATGTTCATCAG	B	JX946222
B36	B8	0.62	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATGCTTATCAG	B	JX946223
B37	B37	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAACATTTATCAG	B	JX946224
B38	B23	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCACATGTTTATCAG	B	JX946246
B39	B22	0.10	GTAGAGTGCGTAGCTGGGGAGTATACAGCGGGGCCAAATGTTTATCAG	B	JX946235
B40	B20	0.10	GTAGAGTACGTAGCTGGGGGGTATACAGCGGGGCCAAATGTTTATCAG	B	JX946239
B41	B42	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGACCAAAATATTTATCAG	B	JX946247
B44	B13	0.21	GTAGAGTACGTAGCTGGGGAGTATACAGCAGGGCCAAATGTTTATCAG	B	JX946264
B45	B14	0.21	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGTCAAATGTTTATCAG	B	JX946273
B46	B33	0.41	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATATTTATTAG	B	JX946232
B47	B21	0.10	GTAGAGTACGCAGCTGGGGAGTATACAGCGGGGCCAAATGTTTATCAG	B	JX946245

B48	B44	0.21	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATGTTTGTCGG	B	JX946265
B49	B47	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATATTCATCAG	B	JX946244
B50	B15	0.21	GTAGAGTACGTAACCTGGGGAGTATACAGCGGGGCCAAATGTTTATCAG	B	JX946271
B51	B34	0.31	GCAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATATTTATCAG	B	JX946213
B52	B46	0.10	TTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATATTTATCAG	B	JX946255
B53	B24	0.10	GTAGAGTACGTAGCTGAGGAGTATACAGCGGGGCCAAATGTTTATCAG	B	JX946257
B54	B11	0.31	GTAGAGTACGTAGCTGGGGAGTATACAGCGAGGGCCAAATGTTTATCAG	B	JX946225
B59	B54	0.31	GTAGAGTACGTAGCTGGGGAGTTTACAGCGGGGCCAAATGTTTATCGG	B	JX946241
B60	B9	0.31	GTAGAGTACATAGCTGGGGAGTATACAGCGGGGCCAAATGTTTATCAG	B	JX946242
B61	B57	0.21	GTAGAGTACATAGCTGGAGAGTATACAGCGGGGCCAAATGTTTATCGG	B	JX946269
B62	B12	0.31	GTAGAGTACGTAGCCGGGGAGTATACAGCGGGGCCAAATGTTTATCAG	B	JX946267
B63	B40	0.21	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATATTTATCGG	B	JX946212
B69	A24	0.10	GTAGAGTACGTAGCTGGGGAGTATACAACGGGGGCCAAATATTTATTAC	A	KF719283
B71	B43	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGAGGGCCAAATGTTTATTAG	B	KF719285
B72	B48	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATATTCATCAC	B	KF719286
B76	A14	0.10	GTAGAGTACGTAACCTGGGGAGTGTACAACGGGGGCCAAATATTTATTAG	A	KF719287
H74	B49	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATATTTGTCAC	B	MT164347
H75	B53	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCTAAATGTTTACCAG	B	MT164355
H76	B25	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCTAAATGTTTATCAG	B	MT164357
H77	B26	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATGTTTACCAG	B	MT164364
H78	B51	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATATTTATCAC	B	MT164365
H79	B27	0.21	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGGCCAAATGTTTATCAC	B	MT164381/ MT164396
H80	B28	0.21	GTAGAATACGTAGCTGGGGAGTATACAGCGGGGCCAAATGTTTATCAG	B	MT164390/ MT164402
H81	B41	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGGACCAAATGTTTATCAG	B	MT164427
H82	B52	0.10	GTAGAGTACGTAGCTGGGGAGTATACAGCGGAGCCGAATGTTTATTAG	B	MT164458

Table S7: Significance of the pairwise differences in genetic distance values (F_{st}) for the Mezayen camel-types. Abr = camel-type name abbreviation. Green cells indicate the presence of statistically significant differences between the compared pair, and orange ones represent values slightly higher than 0.05. The significant level for all comparisons is $\alpha = 0.05$.

Camel-type	Abr	N	SFR	SHL	MJH	MGH	SHQ	HMR	WDH
Sofor	SFR	49							
Shaele	SHL	61	0.88						
Majaheem	MJH	43	0.36	0.03					
Maghateer	MGH	25	0.89	0.71	0.02				
Shageh	SHQ	10	0.37	0.39	0.04	<0.001			
Homor	HMR	9	0.04	0.17	<0.001	0.02	0.47		
Waddah	WDH	25	0.06	0.08	0.33	0.03	0.02	0.01	