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Wildlife Research

Supplementary Material

Origins and population genetics of sambar deer (*Cervus unicolor*) introduced to Australia and New Zealand

Lee A. Rollins[A,B,*], *Daniel Lees*[B], *Andrew P. Woolnough*[C,D], *Andrea J. West*[B], *Michael Perry*[E], *and David M. Forsyth*[A,F]

[A]Evolution & Ecology Research Centre, School of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney, NSW 2052, Australia.

[B]Centre for Integrative Ecology, School of Life and Environmental Sciences, Deakin University, Locked Bag 20000, Geelong, Vic. 3216, Australia.

[C]Department of Jobs, Precincts and Regions, 121 Exhibition Street, Melbourne, Vic. 3000, Australia.

[D]Research, Innovation and Commercialisation, The University of Melbourne, Parkville, Vic. 3010, Australia.

[E]Department of Conservation, 59 Marine Parade, Napier 4110, New Zealand.

[F]Vertebrate Pest Research Unit, New South Wales Department of Primary Industries, 1447 Forest Road, Orange, NSW 2800, Australia.

[*]Correspondence to: Lee A. Rollins Evolution & Ecology Research Centre, School of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney, NSW 2052, Australia Email: l.rollins@unsw.edu.au

Table S1 DNA sequences of sambar deer included in network analysis (trimmed to 144 bp). GenBank Accession Numbers beginning with "MF" are described in Martins et al. 2018 and those beginning with "KF" are described in Gupta et al. 2015. The 'Eastern Clade' represents individuals sampled from Bengal, India, to the eastern extent of the native range (grey haplotypes in Fig. 5). The 'Western Clade' represents individuals sampled in India to the west of Bengal and also in Sri Lanka (black haplotypes in Fig. 5).

Haplotype Name In Figure 5	Sample Name in Original Study	GenBank Accession Number	Sampling Locality
Eastern Clade			
RUN12	RUN12	MF176995	Sarawak, Borneo
RUN20	RUN20	MF176996	Mentawai
RUN44	RUN44	MF177006	South Thailand
RUN47	RUN47	MF177025	South Thailand
RUN51	RUN51	MF177026	South Thailand
RUN55	RUN55	MF177007	Bhutan Dooars, India
RUN58	RUN58	MF177008	South Myanmar
RUN62	RUN62	MF177010	Bengal, India
SE1	RUN28 / RUN42 / RUN61	MF176997 / MF177004 / MF177009	Thailand / Sumatra / Central Java
SE2	RUN2 / RUN38	MF176993 / MF177002	Sumatra
SE3	RUN5 / RUN6 / RUN19	MF177019 / MF177020 / MF177021	North Borneo
SE4	RUN26 / RUN45	MF177023 / MF177024	Borneo / East Sumatra
SE5	RUN65 / RUN66	MF177029 / MF177030	South Sumatra / West Sumatra
Western Clade			
IND1	RUC3 / RUC20	KF133983 / KF648589	South India
IND2	RUC16 / RUC26	KF133996 / KF648595	India Central Highlands
IND3	RUC 6 / RUC7 / RUC8 / RUC9 / RUC17 / RUC19 / RUC22 / RUC25	KF133986 / KF133987 / KF133988 / KF133989 / KF133997 / KF133999 / KF648591 / KF648594	South India India Central Highlands
IND4	AF291884 / RUN33	AF291884 / MF176999	India
IND5	RUC10 / RUC12 / RUC13 / RUC14 / RUC15 / RUC21 / RUC23 / RUC24	KF133990 / KF133992 / KF133993 / KF133994 / KF133995 / KF648590 / KF648592 / KF648593	South India India Central Highlands
RUC1	RUC1	KF133981	South India
RUC2	RUC2	KF133982	South India
RUC4	RUC4	KF133984	South India

RUC5	RUC5	KF133985	South India
RUC11	RUC11	KF133991	South India
RUC18	RUC18	KF133998	India Centra Highlands
SRIL	RUN3 / RUN10 / RUN35 / RUN56	MF176993 / MF176994 / MF177001 / MF177028	Sri Lanka

Table S2 Primers screened with sequence, original reference (R1), reference where primers were amplified in cervids (R2), whether the locus amplified (Amp), and whether the locus was polymorphic (Poly).

Primer Name	Primer Sequence	R1	R2	Amp	Poly
BM203	F-GGGTGTGACATTTTGTTCCC R-CTGCTCGCCACTAGTCCTTC	(Bishop *et al.* 1994)	(Sanchez-Fernandez *et al.* 2008)	yes	yes*
BM757	F-TGGAAACAATGTAAACCTGGG R-TTGAGCCACCAAGGAACC	(Bishop *et al.* 1994)	(Senn and Pemberton 2009)	yes	yes
BM888	F-ACTAGGAGGCCATATAGGAGGC R-AGCTCAAAACGAGGGACAGGG	(Bishop *et al.* 1994)	(Pérez-Espona *et al.* 2008)	yes	no
BMC1222	F-CCAATTTTGCAGATAAGAAAA R-CCTGAGTGTTCCTCCTGAGT	(Bishop *et al.* 1994)	(Pérez-Espona *et al.* 2008)	no	--
BOVIRBP	F-TGTATGATCACCTTCTATGCTTC R-GCTTTAGGTAATCATCAGATAGC	(Moore *et al.* 1992)	(Senn and Pemberton 2009)	yes	no
Ca13	F-CAGAAAGTTGTGAGGCACAG R-GTGGCCTCTGTTTCAGTGTA	(Gaur *et al.* 2003)	(Gaur *et al.* 2003)	yes	yes
Ca18	F-TTCCGTCTCTCCCCTTAATA R-TGGATCTGAGATTTCTGCTG	(Gaur *et al.* 2003)	(Gaur *et al.* 2003)	yes	yes
Ca30	F-CTATCCCATAGCCCAGTGAT R-TTTCCTCTTCCCTCTTCCTT	(Gaur *et al.* 2003)	(Gaur *et al.* 2003)	yes	no
Ca38	F-CAACTTGTCCAAAGTTGTGC R-TAGGTGGCTTTGTCTCTGCT	(Gaur *et al.* 2003)	(Gaur *et al.* 2003)	yes	yes*
Ca43	F-GAATTCCATGGACAGAGGAG R-AAGGGTTGTCTGTGATGCTT	(Gaur *et al.* 2003)	(Gaur *et al.* 2003)	yes	yes
Ca60	F-GCCCTTCGTACGTACTTGTT R-AAAGTCAGACAGAGGGAGGG	(Gaur *et al.* 2003)	(Gaur *et al.* 2003)	yes	no
Ca67	F-TAATCCTAACTCCTGGACCC R-CAAGAATTTTGGAGGGAAGC	(Gaur *et al.* 2003)	(Gaur *et al.* 2003)	yes	no

Ca71	F-TGCACACCCCCAGTCTGGT R-GTCTCACCTTTCCCATCAGC	(Gaur *et al.* 2003)	(Gaur *et al.* 2003)	yes	No
Ca75	F-ATGGCTCTCTTCCCCAAGT R-ACAGGTGGAAAGGAGGTTGT	(Gaur *et al.* 2003)	(Gaur *et al.* 2003)	no	--
CEH-2	F-TTCCCTTCTGGCGGTTGA R-AAGAGGATATGCGCGTGTGTA	(Zhang *et al.* 2008)	(Zhang *et al.* 2008)	yes*	--
CEH-5	F-GAGCTGGTCCTCTGCGTGAT R-CAGGCAGATTCTTTACCGTTG	(Zhang *et al.* 2008)	(Zhang *et al.* 2008)	yes	yes
CelJP27	F-GCAAATCAGAAATAGACCCACAGAC R-GATCCCCTCCTTGTGCCAC	(Marshall *et al.* 1998)	(Pérez-Espona *et al.* 2008)	yes	yes
CelJP38	F-GCTCCAGATTATTCCAGTGTATTGCC R-CTGCACAGAGTCGGACACAAC	(Marshall *et al.* 1998)	(Pérez-Espona *et al.* 2008)	yes	yes
CSSM003	F-GTACCTTAAGGTCAAGGGCTTTCT R-TGGGTCCAATTGAGAATCTTCATG	(Moore *et al.* 1991)	(Pérez-Espona *et al.* 2008)	yes	yes
CSSM43	F-AAAACTCTGGGAACTTGAAAACTA R-GTTACAAATTTAAGAGACAGAGTT	(Barendse *et al.* 1994)	(Sanchez-Fernandez *et al.* 2008)	no	--
FSHB	F-CAGTTTCTAAGGCTACATGGT R-TGGGATATAGACTTAGTGGC	(Moore *et al.* 1992)	(Senn and Pemberton 2009)	no	--
IDVGA55	F-GTGACTGTATTTGTGAACACCTA R-TCTAAAACGGAGGCAGAGATG	(Moore *et al.* 1992)	(Senn and Pemberton 2009)	no	--
NVHRT173	F-CTTGCCCATTTAGTGTTTTCT R-TGCGTGTCATTGAATAGGAG	(Røed and Midthjell 1998)	(Sanchez-Fernandez *et al.* 2008)	yes	yes
NVHRT48	F-CGTGAATCTTAACCAGGTCT R-GGTCAGCTTCATTTAGAAAC	(Røed and Midthjell 1998)	(Sanchez-Fernandez *et al.* 2008)	yes	no
OarCP26	F-GGCCTAACAGAATTCAGATGATGTTGC R-CCATACTGACGGCTGGTTCC	(Buchanan and Crawford 1993)	(Pérez-Espona *et al.* 2008)	no	--

OarFCB193	F-GCTTGGAAATAACCCTCCTGCATCCC R-TTCATCTCAGACTGGGATTCAGAAAGGC	(Buchanan and Crawford 1993)	(Pérez-Espona *et al.* 2008)	yes	yes
OarFCB304	F-CGCTGCTGTCAACTGGGTCAGGG R-CCCTAGGAGCTTTCAATAAAGAATCGG	(Buchanan and Crawford 1993)	(Pérez-Espona *et al.* 2008)	yes	no
OarFCB5	F-AAGTTAATTTTCTGGCTGGAAAACCCCAG R-ACCTGACCCTTACTCTCTTCACTC	(Buchanan *et al.* 1994)	(Pérez-Espona *et al.* 2008)	yes	yes
RM095	F-TCCATGGGGTCGCAAACAGTGG R-ATCCCTCCATTTGTTGTGGAGTT	(Bishop *et al.* 1994)	(Senn and Pemberton 2009)	yes	yes
RM12	F-CTGAGCTCAGGGGTTTTTGCT R-ACTGGGAACCAAGGACTGTCA	(Barendse *et al.* 1994)	(Senn and Pemberton 2009)	yes	yes
RM188	F-GGGTTCACAAAGAGCTGGAC R-GCACTATTGGGCTGGTGATT	(Barendse *et al.* 1994)	(Senn and Pemberton 2009)	yes	yes
RME25	F-AGTGGGTAAAGGAGCCTGGT R-TTATTGATCCCAGCCTGTGC	(Grosse *et al.* 1995)	(Kuehn *et al.* 2003)	yes	yes
RT1	F-CATATGGCTAACTACCTAGCTTGCC R-GAGTCCCAAAGATTTCAGCCCTAC	(Wilson *et al.* 1997)	(Pérez-Espona *et al.* 2008)	yes	no
RT13	F-GCCCAGTGTTAGGAAAGAAG R-CATCCCAGAACAGGAGTGAG	(Wilson *et al.* 1997)	(Pérez-Espona *et al.* 2008)	no	--
RT25	F-TGCCAAGGAACCAAGATGTC R-CCATTCCAGTATTATTGCCTG	(Wilson *et al.* 1997)	(Pérez-Espona *et al.* 2008)	yes	no
RT7	F-CTTTGCCCTGTTCTACTCTTCTTCTC R-GCACTGGTTTAGGCCCTTGG	(Wilson *et al.* 1997)	(Pérez-Espona *et al.* 2008)	yes	yes
T108	F-CATGTGGAGATAGGTAGACAGA R-CCATTCTGAGTAGCTGATTCA	(Jones *et al.* 2002)	(Jones *et al.* 2002)	yes	yes
T156	F-TCTTCCTGACCTGTGTCTTG R-GATGAATACCCAGTCTTGTCTG	(Jones *et al.* 2002)	(Jones *et al.* 2002)	yes	yes

T172	F-AGCATCTCCCCTTTCAACA R-CTTCCCAACCCAAGTATCG	(Jones *et al.* 2002)	(Jones *et al.* 2002)	no	--
T193	F-AGTCCAAGCCTGCTAAATAA R-CTGCTGTTGTCATCATTACC	(Jones *et al.* 2002)	(Jones *et al.* 2002)	yes	yes
T26	F-GTTCCAATAGACACGCTCAT R-TGCCATAGTTTTTCCTACCTT	(Jones *et al.* 2002)	(Jones *et al.* 2002)	yes	no
T268	F-GATGATAACAGCTCAACAGAT R-ATTCCCTTCTCCAGTGTATG	(Jones *et al.* 2002)	(Jones *et al.* 2002)	yes	no
T501	F-CTCCTCATTATTACCCTGTGAA R-ACATGCTTTGACCAAGACC	(Jones *et al.* 2002)	(Jones *et al.* 2002)	yes	yes
T507	F-AGGCAGATGCTTCACCATC R-TGTGGAGCACCTCACACAT	(Jones *et al.* 2002)	(Jones *et al.* 2002)	yes	yes
TGLA127	F-CAATTGTGTGGTAGTTTGGACATTC R-ACACTATTGCAAAAGGACCTCCAATT	(Georges and Massey 1992)	(Senn and Pemberton 2009)	no	--
TGLA337	F-TTTGTTAAGGATAGTAGGCTACT R-GCTCTTCCCTTGGTTTCCTTG	(Georges and Massey 1992)	(Senn and Pemberton 2009)	no	--
TGLA94	F-CATCAAAACAGTGAAGGATGATTGCCAG R-CGAATCTCTTCTAGGGATTGAGACTG	(Georges and Massey 1992)	(Pérez-Espona *et al.* 2008)	yes	yes
Haut14	F-CCAGGGAAGATGAAGTGACC R-TGACCTTCACTCATGTTATTAA	(Steffen *et al.* 1993)	(Kuehn *et al.* 2003)	no	--

[*] Poor amplification.

Table S3 Cross-specific microsatellite primer names, absolute amount of primer per 5 µl reaction (picomoles), multiplex, number of alleles (N_A) and size range found in the 87 individuals included in this study.

Primer	Amount	Multiplex	N_A	Size range (bp)
BM757	4.0	1	8	186-205
Ca18	6.0	1	9	125-149
CEH-5	0.7	1	4	187-196
CELJP38	1.0	1	5	206-220
OarFCB193	1.0	1	7	108-132
T507	1.0	1	5	139-181
Ca43	1.0	2	5	251-261
CSSM003	2.0	2	5	206-223
NVHRT173	4.0	2	3	226-234
T156	1.5	2	6	135-183
Ca13	0.5	3	3	205-209
CelJP27	4.0	3	2	186-188
OarFCB5	4.0	3	5	90-101
RM12	2.0	3	9	127-157
RT7	2.0	3	9	217-248
T193	2.0	3	4	172-201
T501	3.0	3	4	228-242
TGLA94	1.0	3	5	120-147

Table S4 Sequence of the 143bp segment of the mitochondrial control region in Australian and New Zealand sambar deer used to draw the haplotype network shown in Fig. 5. Polymorphic positions between the Australian and New Zealand haplotypes are shown in red.

Australian Haplotype
AACATGCGTATCCCGTCCACTAGATCACGAGCTTGGTCACCATGCCGCGTGAAACCAGCAACCCGCTGGGCAGGGAT CCCTCTTCTCGCTCCGGGCCCATGACTCGTGGGGGTAGCTATTTAATGAACTTTATCAGACATCTG
New Zealand Haplotype
AACATGCGTATCCCGTCCACTAGATCACGAGCTTGATCACCATGCCGCGTGAAATCAGCAACCCGCTGGGCAGGGAT CCCTCTTCTCGCTCCGGGCCCATAAACCGTGGGGGTAGCTATTTAATGAACTTTATCAGACATCTG

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