

Supporting Information

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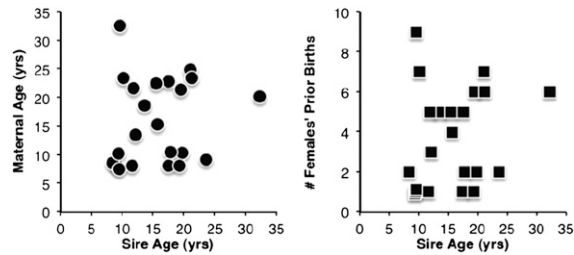


Fig. S1. Sire age vs. maternal age and reproductive history. Data are depicted at the time the offspring in this study were conceived. There was no relationship between sire age and either maternal age (Spearman's rank correlation $\rho = 0.265$, $n = 22$, $P = 0.234$) or maternal fecundity (Spearman's rank correlation $\rho = 0.310$, $n = 22$, $P = 0.161$).

A. Overview of the marker loci, primer concentrations, and thermal cycling profile used in each multiplex reaction.

Primer Set	Loci	Primer Concentrations (μM)	Cycling Conditions
Multiplex 1	LL1118, D5S111, D8S260	0.10 - 0.10 - 0.10	PCR 1
Multiplex 2	SB38, LL1115, LL157	0.08 - 0.14 - 0.08	PCR 1
Multiplex 3	D8S165, LL113, LL1110	0.04 - 0.04 - 0.22	PCR 1
Multiplex 4	SB30, D17S804, LEON15	0.13 - 0.11 - 0.06	PCR 1
Multiplex 5	Lr.P2BH6, APM1, AB06	0.14 - 0.08 - 0.08	PCR 2
Multiplex 6	D13S160, LEON21	0.10 - 0.10	PCR 2

B. Detailed thermal cycling profiles used for multiplex PCR.

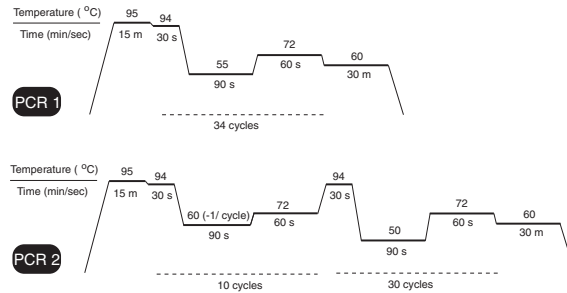


Fig. S2. Multiplex PCR combinations and PCR conditions used for genotyping. (A) Overview of the marker loci, primer concentrations, and thermal cycling profile used in each multiplex reaction. (B) Detailed thermal cycling profiles used for multiplex PCR.

Table S1. Reproductive and residency histories of offsprings' mothers

Adult female ID	No. of offspring in sample	Reproductive history	Residency history	No. of sons among the set of potential sires
BR	1	Multiparous	Natal	0
DB	1	Nulliparous	Natal	0
FE	2	Multiparous	Immigrant	0
GA	1	Multiparous	Immigrant	1
HE	1	Multiparous	Immigrant	2
IZ	1	Multiparous	Immigrant	2
JU	1	Multiparous	Immigrant	1
KA	1	Multiparous	Immigrant	0
KI-M2	1	Nulliparous	Immigrant	0
MD-J	1	Nulliparous	Immigrant	0
MY-M2	1	Nulliparous	Immigrant	0
NY	1	Multiparous	Present as adult since 1982	4
PL	1	Multiparous	Immigrant	2
SA	1	Primiparous	Immigrant	0
TN-M2	1	Nulliparous	Immigrant	0
TZ	1	Multiparous	Immigrant	3
UR	1	Primiparous	Immigrant	0
VD	1	Multiparous	Immigrant	0
XI	1	Nulliparous	Immigrant	0
YA	1	Primiparous	Immigrant	0
ZU	1	Nulliparous	Immigrant	0

Table S2. Potential sires' histories

Adult male ID	No. of offspring sired	Maximum no. of fertilizations	Maximum no. of fertilizations, excluding maternally related partners	Age (y) at first fertilization in this sample	Age (y) at last fertilization in this sample	No. of adult maternal brothers living	Male's mother living?	No. of adult maternal sisters resident
AG	0	22	22	12.90	15.36	1	Yes	0
AM	1	22	22	19.57	22.04	1	Yes	0
BE	4	22	21	15.37	17.84	0	Yes	2
BLK	0	22	22	15.34	17.81	0	No	0
CO	2	22	22	13.14	15.61	0	No	0
DA	3	22	21	18.79	21.25	1	Yes	1
DI	1	22	21	22.53	25.00	1	Yes	1
GU	0	22	21	7.14	9.61	0	Yes	0
HO	1	22	21	9.16	11.62	1	Yes	0
HR	0	10	10	6.25*	8.72	1	Yes	0
IJ	0	3	3	4.09*	6.56	1	Yes	0
IN	0	22	21	10.03	12.50	1	Yes	0
IV	1	11	?	32.23 [†]	Deceased	?	?	?
JR	0	22	21	12.96	15.43	0	Yes	0
NE	1	22	21	17.12	19.59	3	Yes	0
NI	0	22	21	22.54	25.00	3	Yes	0
NO	1	22	21	11.25	13.72	3	Yes	0
NR	2	22	21	8.18	10.64	3	Yes	0
PB	0	11	10	5.19*	7.65	1	Yes	0
PE	1	22	21	8.28	10.74	1	Yes	0
RB	0	22	22	16.25	18.72	0	No	0
TH	3	22	21	9.18	11.65	2	Yes	0
TL	1	22	21	11.87	14.34	2	Yes	0
TU	0	12	11	6.31*	8.78	2	Yes	0

*Had not yet completed a copulation (see text) and were not included as possible sires in the paternity analysis until they were observed to do so.

[†]Present as an adult since 1982, thus age is estimated and maternal kin are unknown.

Table S3. Genotypes and DNA template concentrations for each individual

ID LOCI	LL113	LL1110	LL1115	LL1118	LL157	SB30	SB38	LEON15	LEON21	APM01	AB06	Lr-P2BH6	D5S111	D8S165	D8S260	D13S160	D17S804	DNA (ng/ μ L)	
Mothers																			
NY	183/183	220/223	200/200	138/160	224/232	97/103	126/128	263/263	367/379	200/204	271/273	102/112	164/168	137/137	205/205	243/243	154/160	0.96	
BR	179/180	212/221	200/200	142/145	224/224	97/97	128/132	263/265	367/379	204/210	267/271	98/112	174/174	141/141	201/211	239/245	154/162	0.36	
ZU	180/185	212/212	196/200	147/147	226/226	103/103	132/138	265/267	379/379	200/210	267/271	112/114	164/170	139/141	205/211	239/243	152/154	1.40	
YA	180/183	212/220	194/194	138/147	224/230	83/87	132/138	259/267	379/379	202/202	261/271	108/112	164/168	143/146	211/211	243/243	156/160	2.16	
KI	180/185	212/220	194/206	140/160	224/224	87/103	138/140	267/267	379/379	204/206	261/261	92/92	164/164	137/146	201/211	239/243	152/160	4.95	
MD	180/183	220/220	200/200	142/147	224/232	87/97	126/132	265/265	379/379	200/204	271/273	98/114	168/174	137/141	211/211	239/243	160/160	2.25	
MY	180/183	212/220	200/206	142/147	224/230	101/103	132/144	265/267	367/379	202/206	271/273	98/108	164/168	137/137	205/205	243/243	152/154	2.43	
SA	179/185	212/212	200/200	142/147	226/226	87/87	126/132	259/267	379/379	200/210	271/273	112/112	162/170	139/141	205/211	243/243	160/160	1.92	
TN	183/185	220/221	200/200	140/142	224/230	83/103	132/136	263/269	379/379	200/210	267/271	106/112	164/164	137/143	205/211	243/243	160/160	2.25	
UR	180/185	212/212	194/200	142/147	226/226	97/103	126/132	265/265	379/379	200/200	271/273	112/112	162/174	141/141	211/211	239/243	154/156	1.37	
VD	179/183	218/221	194/200	138/147	226/232	87/103	126/132	259/263	379/379	206/210	271/273	110/112	164/170	141/143	211/211	239/243	154/160	2.21	
XI	179/185	220/221	206/206	158/160	224/224	83/103	132/144	263/269	379/379	200/202	271/273	112/114	162/170	139/143	205/205	243/243	156/160	2.14	
FE	180/183	220/221	194/200	138/142	224/230	103/103	132/132	259/265	375/379	200/204	261/271	102/112	164/168	137/139	211/211	243/247	154/154	1.56	
IZ	183/185	212/218	200/200	142/158	226/232	87/97	138/144	263/265	379/379	200/204	267/273	98/112	162/162	137/141	201/211	243/245	154/162	1.17	
JU	180/183	212/220	194/200	142/147	226/230	83/97	132/132	259/263	375/379	200/210	271/271	112/112	162/170	137/139	205/211	247/247	154/160	0.74	
HE	183/185	218/220	200/200	142/142	224/226	97/101	132/144	263/265	367/379	200/200	271/273	112/112	162/174	137/139	205/211	239/243	154/160	0.93	
TZ	183/183	212/218	196/200	142/147	224/226	97/103	126/136	259/265	375/379	200/210	267/273	92/112	162/170	141/146	211/211	239/243	154/160	0.85	
KA	180/180	212/212	194/200	142/142	226/226	87/87	132/144	265/267	379/379	200/200	271/273	108/112	164/170	137/137	211/211	243/243	154/160	1.30	
PL	180/185	218/220	194/200	142/147	224/226	103/103	132/132	259/265	367/379	200/202	271/271	112/112	162/170	137/137	205/211	239/247	154/156	0.46	
Infants																			
BM	179/180	218/221	200/200	142/142	224/224	87/97	132/138	263/267	367/379	204/210	267/271	112/112	162/174	137/141	211/211	239/245	152/162	2.53	
HG	183/183	218/220	200/200	142/158	226/232	97/101	128/132	263/265	379/379	200/200	271/271	92/112	168/174	137/139	205/211	243/243	154/160	2.76	
JB	180/183	212/221	200/200	142/147	226/230	83/103	132/132	259/265	375/375	200/210	271/271	112/112	162/164	137/141	211/211	247/247	156/160	1.40	
KPA	180/180	212/220	194/194	142/142	224/226	87/97	132/132	265/267	379/379	200/210	271/271	112/112	164/164	137/141	211/211	229/243	156/160	1.62	
NV	183/183	212/220	200/200	142/160	224/232	103/103	126/126	259/263	379/379	200/200	273/273	106/112	164/170	137/137	205/205	243/243	154/160	2.33	
PTN	183/185	218/220	194/200	142/142	226/230	97/103	132/136	259/267	379/379	200/202	267/271	112/112	162/164	137/139	211/211	239/243	154/156	2.85	
TCA	180/183	218/221	196/200	142/147	224/224	103/103	132/136	265/265	379/379	204/210	267/271	112/112	170/170	141/146	211/211	229/239	154/160	1.77	
FRD	179/180	212/220	194/200	138/142	224/226	87/103	132/144	259/267	367/375	200/204	271/273	102/112	168/168	139/146	211/211	243/247	154/160	1.15	
IC	183/185	218/221	200/200	142/142	226/232	87/87	128/144	265/267	367/379	204/204	267/273	112/112	162/164	137/141	211/211	245/245	154/160	3.99	
KNA	183/185	220/221	194/200	140/142	224/224	87/103	132/138	263/267	379/379	206/206	261/271	92/106	164/170	141/146	211/211	239/243	152/154	2.84	
MEL	180/183	212/220	200/200	138/147	232/232	97/101	132/136	265/265	375/379	200/204	267/271	98/112	168/174	137/141	205/211	243/243	154/160	2.83	
MTR	180/183	220/221	200/200	138/142	224/224	97/101	144/144	259/267	379/379	200/202	273/273	98/112	164/164	131/137	205/205	243/247	152/160	3.02	
XHI	180/185	212/220	194/206	158/160	224/226	83/103	132/132	259/263	379/379	200/202	267/273	98/112	164/170	137/146	211/211	239/243	152/160	4.12	
YY	180/183	220/220	194/206	138/142	224/230	83/97	138/140	259/259	379/379	202/210	261/261	108/112	164/168	143/143	211/211	243/243	156/160	1.71	
DN	183/183	220/221	200/200	142/160	224/224	101/103	126/136	263/263	379/379	206/210	267/273	106/112	164/170	141/143	211/211	243/243	154/160	3.03	
FELC	179/180	212/221	194/200	138/142	224/230	87/103	132/144	259/265	375/379	200/204	271/273	102/112	164/164	137/141	205/211	243/243	154/154	1.31	
GH	183/183	212/220	200/200	142/147	230/232	103/103	136/144	263/267	375/379	202/202	271/273	112/114	164/170	139/139	205/211	243/243	154/160	2.85	
SF	179/183	212/223	200/200	147/160	226/230	87/101	132/136	263/267	367/379	204/210	267/271	112/112	168/170	137/139	205/205	243/243	154/160	4.12	
US	180/180	212/212	200/200	142/158	226/232	97/103	132/132	265/265	379/379	200/210	271/271	102/112	162/164	139/141	205/211	243/247	156/160	3.96	
VG	179/180	212/221	200/200	147/160	226/226	97/103	126/132	263/265	367/375	202/210	271/273	110/112	162/164	137/141	211/211	243/243	154/154	1.84	
TRN	183/185	220/221	200/200	140/142	230/230	97/103	132/136	263/267	379/379	202/210	267/271	112/112	164/164	131/137	205/211	243/243	154/160	3.90	
ZMA	183/185	212/220	196/200	142/147	226/226	103/103	132/136	259/267	379/379	200/200	267/271	112/112	164/164	139/141	205/211	243/243	152/160	0.36	

Table S4. Summary statistics for the 17 microsatellite marker loci used in this study

Locus	Alleles	HObs	HExp	PIC	F(Null)	H-W	Reference
<i>LL113</i>	4	0.76	0.72	0.66	-0.03	NS	(1)
<i>LL1110</i>	6	0.79	0.74	0.69	-0.04	NS	(1)
<i>LL1115</i>	4	0.39	0.43	0.40	0.05*	ND	(1)
<i>LL1118</i>	7	0.72	0.69	0.66	-0.01	NS	(1)
<i>LL157</i>	4	0.66	0.70	0.64	0.03*	NS	(1)
<i>SB30</i>	5	0.76	0.73	0.68	-0.02	NS	(2)
<i>SB38</i>	7	0.79	0.78	0.75	-0.02	NS	(2)
<i>LEON15</i>	5	0.76	0.75	0.70	-0.01	NS	(3)
<i>LEON21</i>	3	0.43	0.46	0.41	0.04*	NS	(3)
<i>APM01</i>	5	0.79	0.77	0.72	-0.02	NS	(4)
<i>AB06</i>	4	0.76	0.70	0.63	-0.06	NS	(5)
<i>Lr.P2BH6</i>	8	0.58	0.55	0.53	-0.04	NS	(6)
<i>D5S111</i>	5	0.69	0.73	0.69	0.04*	NS	(7)
<i>D8S165</i>	7	0.79	0.78	0.74	-0.01	NS	(8)
<i>D8S260</i>	3	0.46	0.51	0.42	0.05*	NS	(9)
<i>D13S160</i>	5	0.60	0.59	0.55	-0.01	NS	(9)
<i>D17S804</i>	5	0.79	0.69	0.63	-0.08	NS	(9)
Mean	5	0.68	0.67	0.62	-0.01	—	—

HExp, expected heterozygosity; HObs, observed heterozygosity; H-W, Hardy-Weinberg equilibrium test (ND, not done; NS, not significant; some genotype frequencies are lower than 5%); F(Null): estimated frequency of null alleles (*indicates a positive and significant estimated frequency of null alleles); PIC, polymorphic information content.

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- Bohle UR, Zischler H (2002) Polymorphic microsatellite loci for the mustached tamarin (*Saguinus mystax*) and their cross-species amplification in other New World monkeys. *Mol Ecol Notes* 2:1–3.
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- Cortés-Ortiz L, Mondragón E, Cabotage J (2010) Isolation and characterization of microsatellite loci for the study of Mexican howler monkeys, their natural hybrids, and other Neotropical primates. *Conserv Genetics Resources* 2:21–26.
- Goncalves EC, Silva A, Barbosa MSR, Schneider MPC (2004) Isolation and characterization of microsatellite loci in Amazonian red-handed howlers *Alouatta belzebul* (Primates, Platyrrhini). *Mol Ecol Notes* 4:406–408.
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- Weber JL, May PE (1989) Abundant class of human DNA polymorphisms which can be typed using the polymerase chain reaction. *Am J Hum Genet* 44:388–396.
- Weissenbach J, et al. (1992) A second-generation linkage map of the human genome. *Nature* 359:794–801.

Table S5. Paternities assigned at $\geq 99\%$ confidence based on 17- and 12-locus genotype datasets

Offspring ID (from oldest to youngest)	Most likely sire	17 loci	12 loci*
		No. of mismatches with next most likely sire	No. of mismatches with next most likely sire
DN	TH	3	1
FELC	IV	2	1 [†]
GH	BE	2	1
HG	NO	5	3
IC	CO	4	3
NV	TH	4	3
SF	NR	4	2
US	AM	5	3
VG	TL	4	2
BM	HO	4	4
JB	DA	2	1
MEL	NR	5	3
XHI	PE	3	2 [‡]
YY	DI	3	1
FRD	CO	5	2
KNA	TH	4	3
KPA	DA	2	1
MTR	NE	2	2
PTN	BE	3	2
TCA	DA	3	1
TRN	BE	4	2
ZMA	BE	2	2

*Excludes the five loci with a positive estimated frequency of null alleles (Table S4): *LL1115*, *LL157*, *LEON21*, *D5S111*, and *D8S260*.

[†]In the analysis excluding two additional loci, *LL1110* and *1113*, a different male (IJ) was assigned paternity at the $\geq 95\%$ confidence level, with male IV identified as the second most-likely sire. The genotypes of both IV and IJ were perfectly compatible with that of FELC, and the change in assignment in the 10-locus analysis is almost certainly because of discarding valuable information from seven variable loci. In all of the larger datasets, male IJ mismatches from that of FELC at ≥ 1 locus. Additionally, the young age of male IJ at the time of FELC's conception (which occurred before the onset of IJ's sexual activity) also argues strongly against the possibility that he could have been the sire.

[‡]In the analysis excluding two additional loci, *LL1110* and *LL113*, confidence in this assignment dropped to the $\geq 95\%$ level.

Table S6. Results of the DADSHARE analysis examining which potential sires could have shared a father

Male IDs*	Possible paternal sibling set [†]	Maternal genotype included? [‡]	Age difference from closest younger potential male paternal sibling [§]
IJ	A	Yes	NA
PB	B	Yes	NA
HR	A	Yes	2.16
TU	C	Yes	NA
GU	D	Yes	NA
NR	E	Yes	NA
PE	F	Yes	NA
HO	G	Yes	NA
TH	C	Yes	2.87
IN	A	Yes	3.78
NO	G	Yes	2.09
TL	E	Yes	3.69
AG	E	No	<u>1.03</u>
JR	D	Yes	<u>5.82</u>
CO	A	No	3.11
BLK	H	No	NA
BE	H	No	<u>0.03</u>
RB	C	No	<u>7.07</u>
NE	A	Yes	3.98
DA	A	No	<u>1.67</u>
AM	I	No	NA
DI	D	No	9.57
NI	B	Yes	17.35
IV	A	No	13.44

*Adult males, listed from youngest to oldest, taken from the list of potential sires for the present study (Table S2).

[†]The potential paternal sibling set indicates those groups of males, indicated by the same letters, that DADSHARE identified as having the possibility of having been sired by the same father, given the potential sires' genotypes and the genotype of their mothers.

[‡]Maternal genotypes were included only if the males' mothers were among the set of females whose genotypes were known from the paternity study (i.e., those females who contributed offspring to the 2005–2007 infant cohorts).

[§]Closest difference in age (older minus younger) between adult males that DADSHARE identified as possibly sharing a father. NA indicates that no younger male with the same potential father exists in the dataset. There were only three cases (boldfaced and underlined) where the age difference between males who could have had the same father is <2 y, as described in the text. Male relative ages are as shown in Table S2.