**Supplementary Materials for**

**Atypically high reproductive skew in a small wild chimpanzee community in a human-dominated landscape**

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**Supplementary Methods**

*Reproductively Mature Males at Bulindi*

**Table S1.** Estimated age ranges for each of the male chimpanzees present and reproductively mature for at least a portion of the main study period (2012-2016). Ages were estimated, based on physical and behavioral characteristics [Boesch and Boesch-Achermann, 2000; Goodall, 1986], since all reproductively mature males were born prior to habituation of the study community.

Estimated Age In:

Male ID 2012 - 2016

SLa 25-28 - 29-32

KTa 29-32 - NAc

MRa 21-22 - 25-26

TMb 10-11 - NAc

MOb 7 - 11

aIdentified in 2007 [McLennan, 2010].

bIdentified in 2012.

cKT and TM disappeared in 2014 and 2015, respectively, and were not present,

nor candidate fathers at Bulindi, in 2016.

*DNA Extraction and Amplification*

We extracted DNA from samples using the GeneMATRIX Stool DNA Purification Kit (Roboklon) according to the manufacturer’s instructions. We then genotyped the extracts at 15 microsatellite loci, including amelogenin, used for sex determination [Bradley et al., 2001] in a modification of the two-step PCR procedure described in Arandjelovic et al. [2009]. To minimize the risk of obtaining erroneous genotypes due to allelic dropout, we used a multiple tubes approach [Taberlet et al., 1996], amplifying each DNA extract in triplicate and confirming homozygous alleles with a minimum of three unambiguous occurrences in independent replicates [Arandjelovic et al., 2009].

*Parentage Analysis*

We conducted parentage analyses using a likelihood-based method in CERVUS 3.0.7 [Kalinowski et al., 2007]. Allele frequencies used for all analyses were derived from population-level data across the habitat [McCarthy et al., 2015], which was possible due to recent gene flow in this region [McCarthy et al., 2018]. We first conducted a maternity analysis to confirm pedigree-assigned maternities. We did so by conducting a simulation of parentage analysis that included eight candidate mothers (all adult females present during the study period) and eight candidate offspring (all offspring born during the study period, except one who died before the sampling period). We simulated 10,000 offspring, using a minimum of 10 loci typed and an estimated genotyping error rate of 0.01. Next we used these assigned maternities to conduct a paternity analysis that included a total of 6 candidate fathers, of which 4 were sampled. We again simulated 10,000 offspring with a minimum of 10 loci typed and an estimated genotyping error rate of 0.01.

We also conducted parentage analyses for seven offspring born between 2005 and 2011, which included all surviving offspring born around and following the time initial study of the Bulindi chimpanzees began, but prior to SL achieving alpha status [unpublished data]. Due to differences in the availability of demographic data and genetic samples between this time period and the main study period (2012-2016), we conducted parentage simulations and analyses separately to optimize the log-likelihood scores we obtained for parentage assignments. For the seven sampled offspring born from 2005-2011, we conducted a maternity analysis that included six candidate mothers (est. proportion sampled = 0.6) and confirmed the maternities for all seven offspring with >99% confidence. The subsequent paternity analysis included a conservative estimate of 10 total candidate fathers, of which 3 were sampled. Unsampled fathers included 4 additional mature males who were individually identified during 2007-2008 but had disappeared by 2012, as well as the potential for several additional males who 1) sired offspring born early during this period before any males were identifiable to researchers, but subsequently died soon after, 2) matured between 2008 and 2011 and sired offspring, but subsequently died before 2012, or 3) resided outside the community and sired offspring via extra-group copulation (EGC). As with the main study period, we simulated 10,000 offspring in both the maternity and paternity analyses, using a minimum of 10 loci typed and an estimated genotyping error rate of 0.01. The resulting paternity was assigned with >99% confidence.

**Supplementary Results**

Of seven offspring sampled who were born between 2005 and 2011, paternity could only be assigned for one offspring: young, low-ranking MR was assigned as father to offspring JN (Table S1). In the other six offspring, across individuals there were up to four paternal alleles observed at a given microsatellite locus, which indicated that at least two additional unsampled fathers sired these offspring. Given the low proportion of paternities that could be assigned, alpha male reproductive skew during this period could not be determined with precision. Of the six unassigned paternities distributed among at least two additional males, a single male could have sired between one and five offspring. This would lead to a single male (of unconfirmed rank) siring between 14 and 71% of offspring between 2005 and 2011.

**Table S2.** Paternity analysis results for offspring born between 2005 and 2011

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Offspring | | | Mother | Assigned father | | |
| ID | Sex | Y.o.B.a | ID | IDb | Rank | N comp.c |
| MO | M | ~2005-6 | OL | NA |  |  |
| JM | F | ~2005-6 | MD | NA |  |  |
| JN | F | ~2006-7 | JY | MR | Low | ≥6 (2006) |
| JK | M | ~2008-9 | MN | NA |  |  |
| TB | F | ~2009 | TD | NA |  |  |
| AR | M | ~2009 | OL | NA |  |  |
| GD | M | ~2009 | MD | NA |  |  |

aBirth years are estimates +/- 1 year.

bNA indicates that paternity analysis did not yield a paternity assignment with >95% confidence.

cEstimated number of male competitors present in the Bulindi community at the approximate date of conception.

**Supplementary References**

Arandjelovic M, Guschanski K, Schubert G, Harris TR, Thalmann O, Siedel H, et al. (2009). Two-step multiplex polymerase chain reaction improves the speed and accuracy of genotyping using DNA from noninvasive and museum samples. *Molecular Ecology Resources* 9: 28–36.

Boesch C, Boesch-Achermann H (2000). The Chimpanzees of the Taï Forest. New York, Oxford University Press.

Bradley BJ, Chambers KE, Vigilant L (2001). Accurate DNA-based sex identification of apes using non-invasive samples. *Conservation Biology* 2: 179–181.

Goodall J (1986). *The Chimpanzees of Gombe: Patterns of Behaviour*. Cambridge, MA, Harvard University Press.

Kalinowski ST, Taper ML, Marshall TC (2007). Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. *Molecular Ecology* 16: 1099–1106.

McCarthy MS, Lester JD, Howe EJ, Arandjelovic M, Stanford CB, Vigilant L (2015). Genetic censusing identifies an unexpectedly sizeable population of an endangered large mammal in a fragmented forest landscape. *BMC Ecology* 15: 21.

McCarthy MS, Lester JD, Langergraber KE, Stanford CB, Vigilant L (2018). Genetic analysis suggests dispersal among chimpanzees in a fragmented forest landscape in Uganda. *American Journal of Primatology* 80: e22902.

McLennan MR (2010). *Chimpanzee ecology and interactions with people in an unprotected human-dominated landscape at Bulindi, western Uganda*. Doctoral dissertation, Oxford Brookes University, UK.

Taberlet P, Griffin S, Goossens B, Questiau S, Manceau V, Escaravage N, et al. (1996). Reliable genotyping of samples with very low DNA quantities using PCR. *Nucleic Acids Research* 24: 3189–3194.