A high quality pedigree and genetic markers both reveal inbreeding depression for quality but not survival in a cooperative mammal

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Supporting information

Evaluating potential biases in parentage assignment

We performed three analyses to evaluate whether our parentage assignments could have been biased towards heterozygous individuals.

Analysis of the empirical dataset

First, we tested for an association between parental heterozygosity and the confidence with which parents were assigned in our empirical pedigree. Confidence was modelled as a binomial response variable in a generalised linear model (GLM). A binomial error structure was used because MasterBayes defines confidence as the proportion of times a particular parent is assigned to an offspring in the MCMC chain. The two predictor variables were paternal and maternal sMLH respectively. This model was significantly better than an intercept-only model as indicated by a likelihood ratio test ($-2LL_2 = 3030.2$, $p < 0.0001$). Furthermore, a slight bias was found against heterozygotes (Table S1) such that parents with sMLH values two standard deviations below the mean were predicted to have an assignment probability 0.02 greater than parents with sMLH two standard deviations above the mean.

Table S1. Results of a binomial GLM of the confidence with which parents were assigned in our empirical pedigree. Statistical significance was determined using likelihood ratio tests.

Term	Estimate	Standard Error	$-2LL_1$	*p*-value
(Intercept)	0.9435	0.0091		
sMLH sire	-0.1274	0.0078	265.91	<0.0001
sMLH dam	-0.3100	0.0066	2232.5	<0.0001

Analysis of a simple simulated pedigree

Second, we simulated random mating between 15 males and 15 females to produce 15 offspring. All genotypes were simulated based on the empirical allele frequencies. The offspring were then assigned parents from among the 30 candidate parents using the R package MasterBayes as described in the Materials and methods section of the manuscript. The above steps were repeated 1000 times. We found that 94% of all simulated offspring were assigned parents with a probability of 1.0 and hence no bias could be detected.

Analysis of a simulated pedigree with close inbreeding

Finally, we simulated a pedigree with close inbreeding, in which parentage assignment is technically more challenging because candidate parents are related and have reduced allelic diversity compared to the total population. We simulated the genotypes of 30 full siblings with a 50:50 sex ratio and then simulated random mating among these individuals to produce 15 inbred offspring. An example pedigree is shown below in Figure S1. We then used MasterBayes to assign parentage to these offspring using the simulated parental generation as candidate parents. This procedure was repeated 1000 times.

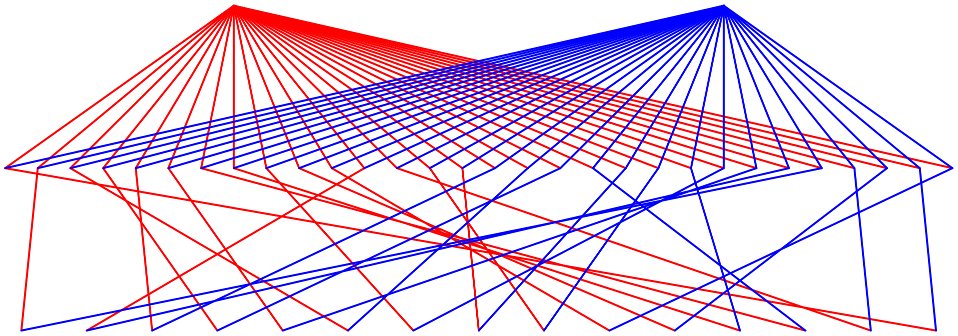

Figure S1. An example of a simulated pedigree with close inbreeding. Dam lines are shown in red and sire lines are shown in blue.

As above, we modelled the confidence of parentage assignment using a GLM with a binomial error structure and paternal and maternal sMLH fitted as predictor variables. To assess the significance of this model, we used a likelihood ratio test to compare it with an intercept-only model. As found in our previous analysis of the empirical pedigree, the more complex model explained significantly more variation ($-2LL_2 = 37646$, $p < 0.001$) and a small bias was found against heterozygotes. Specifically, parents with sMLH values two standard deviations below the mean were predicted to be assigned parentage with a probability of 0.038 greater than equivalent individuals with sMLH values two standard deviations above the mean.

Table S2. Results of a binomial GLM of the confidence with which parents were assigned in a simulated pedigree with close inbreeding. Statistical significance was determined using likelihood ratio tests.

Term	Estimate	Standard Error	$-2LL_1$	*p*-value
(Intercept)	5.1400	0.0129		
Paternal sMLH	-1.0576	0.0081	16866	<0.0001
Maternal sMLH	-1.1893	0.0081	21584	<0.0001

Changes in inbreeding with age

Table S3. Table reporting the mean and variance in f_{ped} and sMLH of individuals split into cohorts based on their survival to at least a given age.

Cohort	Mean f_{ped}	Variance f_{ped}	Mean sMLH	Variance sMLH
0	0.056	0.005	0.984	0.032
1	0.051	0.004	0.992	0.033
2	0.057	0.006	0.954	0.038
3	0.083	0.008	0.967	0.042
4	0.086	0.008	0.996	0.026
5	0.059	0.006	0.986	0.045

Correlation between inbreeding and fitness

To help comparison between studies, the correlation coefficients of f_{ped} and sMLH with each measure of fitness directly are presented in table S4.

Table S4. Table reporting the correlation coefficient between each of the two measures of inbreeding and all five fitness measures.

Fitness trait	**Correlation coefficient of fitness trait with f_{ped}**	**Correlation coefficient of fitness trait with sMLH**
Juvenile survival	-0.00	-0.01
Adult survival	0.09	0.03
Yearling weight	-0.24	0.10
Annual reproductive success ♀	-0.15	0.03
Annual reproductive success♂	-0.18	0.27

Allele numbers for microsatellites

Table S5. Numbers of alleles found at 43 banded mongoose microsatellites.

Marker	**Number of alleles**
Mon16	6
Mon17	4
Mon25	8
Mon41	4
Mon69	8
Mon19	7

Mon32	4
Mon38	5
Mon65	3
Mon66	2
Mon67	4
Mon68	5
Mon70	5
Mon29	3
Mon31	6
Mon35	5
Mon36	5
Mon42	6
Mon49	5
Mon9	6
A226	4
A248	5
Ag6	6
Hj35	8
M53	4
Mm10.7	4
Mm5.1	4
Ss10.4	5
Ss13.8	6
TGN	5
fs15	3
fs44	5
fs46	3
fs48	3
fs50	4
hic.2.52	8
hic.4.30	9
Ss11.12	10
AHT130	4
Ag8	4
Ss7.1	6
fs41	8
hic.1.95	5