Supplementary Information

Genetic structure of wild and domesticated grasscutters (*Thryonomys swinderianus*) from south-western Nigeria

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Material S1:

Power analysis to determine the utility of the multi-locus microsatellite data to detect heterogeneity at observed levels of differentiation (F_{ST}) was evaluated using POWSIM software (http://www.zoologi.su.se/~ryman/).

This software simulates multiple populations that have drifted apart (no gene flow) for *N* generations and tests the hypothesis of genetic homogeneity using Fisher's exact tests. We used the empirical allele frequencies from all 11 loci for simulations.

Sampling from the simulated populations was done using empirical samples sizes from wild grasscutter samples. We explored a variety of n_e and *t* (generation) values to explore the expected differentiation based on drift alone.

Results indicate that the power to detect significant differentiation is low if true N_e is small and the number of generations since divergence is very small. Neither of which is likely in rodents. F_{ST} approaching observed levels would require very large n_e (> 5 000) and greater than 100 generations of divergence.

Table of results for power analyses across generation times and n_e

F_{st}	Power	n_e	Generations
0	0.049	1000	0
0.005	0.759	1000	10
0.01	0.996	1000	20
0.0124	1	1000	25
0	0.068	2000	0
0.0025	0.345	2000	10
0.0012	0.739	2000	20
0.0063	0.852	2000	25
0.0087	0.987	2000	35
0.0124	0.999	2000	50
0	0.052	4000	0
0.0012	0.151	4000	10
0.0025	0.307	4000	20
0.0031	0.432	4000	25
0.0044	0.654	4000	35
0.0062	0.89	4000	50
0.0124	1	4000	100
0	0.058	5000	0
0.001	0.139	5000	10
0.002	0.259	5000	20
0.0025	0.318	5000	25
0.0035	0.491	5000	35
0.005	0.743	5000	50
0.01	0.995	5000	100