

Supplementary methods 1:

In the following, we provide further details on the cohort datasets and parameters used to estimate effective population size (N_e) for the three estimators.

1. Sibship assignment method

The sibship assignment method (Wang, 2009) is implemented in Colony 2.0.6.6 (Jones & Wang, 2010) and estimates N_e by determining the frequency of full-sib, half-sib and unrelated relationships when two individuals from the same cohort are randomly selected. Since our samples span four years, the dataset contains multiple cohorts. Therefore, age and sampling dates were used to obtain a single-cohort dataset: Individuals aged between 17.5 weeks and one year old sampled in year 2 were selected and represented a single cohort ($n = 30$). All 30 samples were born within approximately eight months of each other and were thus unlikely to be parents of other individuals in the cohort. Parent-offspring relationships would bias the N_e estimation, as it is difficult to distinguish parent-offspring from full-sib relationships (Wang, 2009). The output from the family reconstruction done in Colony under Dispersal was also used to ensure none of the individuals were potential parents of others in the cohort. N_e was estimated in Colony with a medium length run assuming monogamous mating for both sexes (Mills & Bester, 2005), with no inbreeding and no clones, using the full-likelihood method, optimal prior for N_e (with default values), sibship scaling and no updating of allele frequencies. Colony can take genotyping error into account, thus null allele frequency was calculated in MICRO-CHECKER and used as input in Colony, while the rate of other errors set to an assumed value of 0.0001, as few microsatellite datasets are truly error-free. This analysis was also performed assuming polygamy for both sexes. The effect on the mating system of culling one individual of a breeding pair is unknown, but the remaining individual may pair with a new mate, leading to a breakdown of the monogamous mating system.

2. Linkage disequilibrium method

This method estimated N_e in NeEstimator 2.01 (Do et al., 2014), using the same dataset used in Colony (as described above).

3. Estimator by parentage assignments

This method was implemented in AgeStructure 1.1 (Wang et al., 2010) and can estimate N_e with overlapping generations, as is the case with jackal, and requires sex, age and multilocus genotypes of a single sample of individuals taken at random. Thus, samples collected in year 2 and year 3 ($n = 145$) were selected to represent a single sample taken at random and classified into the following six age classes: Class 0 (too young to reproduce): 0-1 year old, Class 1: 1-2 years, Class 2: 2-3 years, Class 3: 3-4 years, Class 4: 4-5 years, Class 5: 5-7 years (comprising two years, to increase sample size in this last age class). Where individuals were aged as a range, e.g. 2-4 years, the midpoint, 3 years, was taken as the age. Where ages were equal to the boundary of two age classes, e.g. 2 years, the sample was classified into the upper age class, in this example Class 2. AgeStructure provides estimates of N_e , and generation length (mean and per sex). For the AgeStructure analysis, a minimum age for reproduction of one year for both sexes was chosen. Sexual maturity is reached at ~11 months (Mills & Bester, 2005), thus it was assumed that individuals do not mate before one year of age. Unequal fertility within age classes was selected as, often, sexually mature individuals temporarily forego breeding to remain with their parents as “helpers” to raise subsequent litters of pups, leading to unequal reproductive output between individuals (Mills & Bester, 2005). The sampling proportion within each age class was unknown. Genotyping error was accounted for by using the same information as in the Colony analysis. Analysis was run with 1000 bootstrap replicates and a 95% confidence level for parentage assignments.

In the following, we provide further details on the cohort datasets and parameters used to estimate genetic structure, relatedness and dispersal.

Genetic structure

STRUCTURE was run with the admixture model “allele frequency correlated” and without prior population information for 20 replicates each of $K = 1 - 27$, and a run length of 700,000 Markov Chain Monte Carlo iterations, following a burn-in period of 200,000 iterations. The optimum number of subpopulations was estimated by identifying the K with greatest increase in posterior probability (ΔK , Evanno, Regnaut & Goudet, 2005) and by evaluating the log likelihood of K ($\ln \Pr(X|K)$) curve, using

STRUCTURE HARVESTER (Earl & von Holdt, 2012). CLUMPAK (Cluster Markov Packager Across K; Kopelman et al., 2015) employs DISTRUCT (Rosenberg, 2004) and was used to graphically represent STRUCTURE runs. CLUMPAK obtains the membership coefficient matrices of replicate runs using CLUMPP (Jakobsson & Rosenberg, 2007), employing as a default, the LargeKGreedy algorithm with 2000 random input sequences. STRUCTURE analysis was repeated, with the above parameters with close relatives removed, using a relatedness cut-off of 0.25 in the software Friends and Family 21 (de Jager *et al.*, 2017). The R package Adegenet 2.1.1 (Jombart, 2008) was used to construct a PCA of the complete dataset.

Relatedness

To determine the appropriate estimator, we used the R package related (Pew et al., 2015) to simulate, from the allele frequencies, 100 pairs of each of the following relatedness categories: parent-offspring (PO), full-siblings (FS), half-siblings (HS) and unrelated (UR). The performance of six estimators was tested by estimating relatedness of these simulated pairs and determining which estimator correlated best with the simulated values by calculating Spearman's correlation coefficient (`cor.test` function in R). The estimators tested included: dyadic maximum likelihood "DyadML" (Milligan, 2003), Lynch-Li (Li, Weeks & Chakravarti, 1993), Lynch and Ritland (Lynch & Ritland, 1999), Queller and Goodnight (Queller & Goodnight, 1989), triadic maximum likelihood "TrioML" (Wang, 2007) and Wang (Wang, 2002).

Spatial analyses: To investigate genetic substructure at finer scales, we compared relatedness within (six farms where $n=1$ were excluded) and between farms by testing for a difference in means using the non-parametric two-sample Wilcoxon test in R (`wilcox.test` function), where H_0 = no difference in means. A 95% confidence level was applied for all tests. We conducted a spatial autocorrelation analysis (H_0 = random distribution of genotypes in space, i.e. $r_{\text{auto}} = 0$) in GenAlEx using 50 even distance classes of 1 km each (the largest distance between two samples was ~49 km), with 1000 bootstrap replicates of pairwise comparisons within each distance class (with replacement) used to generate 95% confidence intervals to determine significance of correlation within each distance class.

To determine if either sex dispersed significantly more than the other, we compared mean relatedness between sexes (mean relatedness is lower in the dispersing sex), using the Wilcoxon test. We also conducted spatial autocorrelation tests in GenAlEx for each sex separately, using the same parameters as before.

Temporal analyses: To investigate whether culling influenced the levels of relatedness or inbreeding over time, we tested for a difference in mean relatedness and individual inbreeding between years, using the Wilcoxon test.

Dispersal

Samples were classified as potential fathers, mothers and/or offspring based on the following age categories: (i) ≤ 1 year were classified as offspring only (jackals do not breed until 1-2 years of age) (Mills & Bester, 2005); (ii) 1-3 years were classified as potential fathers/mothers and potential offspring and (iii) ≥ 3 years were classified as potential fathers/mothers only. While animals older than three years could be offspring of even older individuals (e.g. five or six-year-old animals), the age classifications in this category become broader (e.g. >4 years, or 3-5 years), making discrete subdivision of these older individuals increasingly uncertain, with few samples per category, which in turn would increase the uncertainty of parent-offspring designations. Thus, we decided on a conservative approach to classify all individuals older than or equal to three years as potential parents only, likely leading to an underestimation of number of parent offspring pairs, but increased confidence in those pairs that were identified. Two samples had unknown ages and were classified as potential fathers/mothers and potential offspring. This resulted in 152 potential offspring, 33 potential fathers and 29 potential mothers.

Relationships were reconstructed in Colony with a medium length run assuming monogamous mating for both sexes (Mills & Bester, 2005), with no inbreeding and no clones, using the full-likelihood method, a weak sibship prior of 1.0 for both paternal and maternal sibship sizes, sibship scaling, no updating of allele frequencies and accounting for potential genotyping errors as before. To investigate dispersal, full-sibs sampled on different farms were identified (using the *.BestFSfamily output file from Colony) and distance between these individuals was measured using the GPS location of where they were culled. Distance was

measured between parent-offspring pairs regardless of whether they were sampled on different farms (using the *.ParentPair output file).