We assigned parentage to offspring using the R-package MasterBayes vs. 2.57 [Ref]. The pedigree was estimated with the function *MLEped*, which calculates a Maximum likelihood estimate of the pedigree. The probability of an allele being miss scored was set to the default value of 0.005 (Check sensitivity to this). Because of the experimental design, only adults present in group where the egg was recorded should be potential parents. Misassignments in the process of egg marking, transfer of egg id from egg to the hatched chick, and during blood sampling for genotyping are however possible. We therefore refrained from defining any prior requirements of the group of offspring and adults. As blood samples were not obtained for two adult males and two adult females, we also included the presence of these unsampled adults in the population when estimating parentage.

With this analysis we could assign full parentage with 95% confidence for 1341 offspring (97.4 %). Only 16 offspring (1.2%) were assigned to parents from a different group than the offspring. The assigned sire and dam always belonged to the same group in the year where the offspring was recorded. This supports that these are indeed the parents of offspring whose group of origin was misassigned during recording.

Given the low rate of misassignments and the confidence by which we could assign them, we reran the analyses with several adjustments to assign parentage to the remaining 31 unassigned offspring. We omitted all groups with unsampled adults and limited the possible parents to adults from the same group as the offspring. This provided full parentage with 95% confidence for additional 15 offspring.

Of the remaining unassigned 21 offspring, 11 were from groups that housed one of the four unsampled adults. We therefore ran separate models for each of these eight groups. This was done with MCMC in the function *MCMCped*, as this allowed us to inspect the posterior distribution of parentage for each offspring. All 11 offspring were assigned full parentage with 95% confidence, and all with one of the parents being the unsampled adult in the group. The assignment of this parent was therefore done by exclusion. We emphasize that this was done with high certainty as all 11 offspring had at least 90 called genotypes.

The 10 offspring that was unassigned, 4 had less than 25 called genotypes.

**References**

Hadfield J.D., Richardson D.S. & Burke T. (2009) Towards unbiased parentage assignment: combining genetic, behavioural and spatial data in a Bayesian framework