

Appendix B – STRUCTURE analysis

The software *STRUCTURE* (Pritchard et al. 2000) was used to determine the number of genetic clusters prior to reinforcement (i.e. based on the $n = 262$ individuals present at the time of release in March 2002, $n = 259$ successfully genotyped, see Table 1), and the probability of assignment of these individuals to each of the respective clusters. We used a burn-in of 200 000 and a MCMC length of 500 000 replications. The simulated number of clusters (K) ranged from 1 to 4, where the upper limit of 4 was chosen based on results in Jensen et al. (2013). For a plot with $K=3$ see Fig.B1. Twelve independent simulations were performed for each K to check for consistency across runs. Convergence was evaluated by visual inspection. The results were assessed using *STRUCTURE HARVESTER* (Earl and vonHoldt 2012) and the Evanno method, which determines the most likely K based on the distribution of ΔK (Evanno et al. 2005). The genetic difference between the two K populations (pairwise $F_{ST} = 0.0176$, 95 % CI: 0.0135-0.0219) were assessed with using *HIERFSTAT* (Goudet 2005).

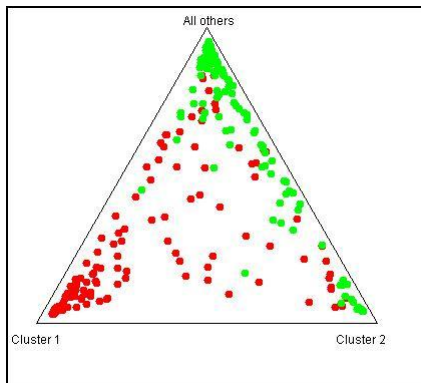


Fig. B1. Triangular plot, assuming $K=3$. Dots are mostly aligning according to two populations.

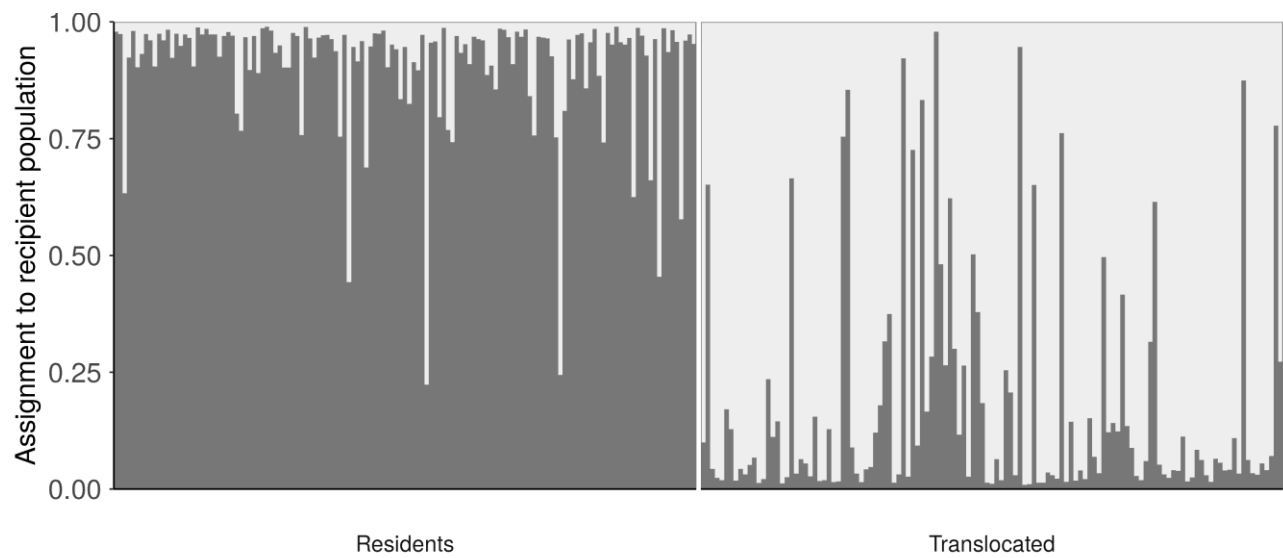


Figure B2. Population clusters from *STRUCTURE* (Pritchard et al. 2000) and *STRUCTURE HARVESTER* (Earl and vonHoldt 2012) of resident and translocated individuals in a reinforcement experiment of house sparrows. Each bar represents an individual, and the height of dark grey bars indicates the probability of assignment to the recipient population (Vikna). The left panel shows the resident individuals from Vikna (residents), and the right panel shows the translocated individuals from Vega (translocated).

References

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