

# Mate choice for neutral and MHC genetic characteristics in Alpine marmots: different targets in different contexts?

**Appendix S2** Estimation of relatedness with pedigree and correlations between (1) the relatedness estimated with the pedigree and the relatedness estimated with the Queller & Goodnight (1989) and (2) the relatedness estimated with the pedigree and the MHC proteic dissimilarity

## *Methods*

To test whether neutral genetic compatibility estimated with the genetic characteristics at 16 microsatellites represent genome-wide patterns, relatedness was estimated based on pedigree information obtained with parentage analysis. The pedigree-based relatedness was calculated using the function `kin` implemented in the R package “synbreed” (Wimmer *et al.*, 2012). Spearman's rank correlation coefficients were calculated between the pedigree-based relatedness and the Queller & Goodnight's relatedness. Also, to discard whether pedigree-based relatedness and MHC compatibility convey similar information, Spearman's rank correlation coefficients were calculated between the pedigree-based relatedness and MHC proteic dissimilarity.

## *Results*

As expected, pedigree-based relatedness was correlated with Queller & Goodnight's relatedness ( $\rho = 0.45$ ; CI 95% = [0.31, 0.56];  $n = 158$ ,  $P = <0.0001$ ), suggesting that Queller & Goodnight's relatedness calculated at 16 microsatellite are representative of genome-wide patterns.

Pedigree-based relatedness and MHC compatibility estimators were not correlated regardless of the MHC loci considered (MHC class I proteic dissimilarity:  $\rho = -0.11$ ; CI 95% = [-0.27, 0.05];  $n = 148$ ,  $P = 0.17$ ; MHC class II proteic dissimilarity:  $\rho = 0.16$ ; CI 95% = [-0.31, 0.01];  $n = 152$ ,  $P = 0.05$ ), suggesting that MHC loci and pedigree-based relatedness convey rather different information.

## **References**

- Queller, D. C., & Goodnight, K. F. (1989). Estimating relatedness using genetic-markers. *Evolution*, 43, 258-275.
- Wimmer, V., Albrecht, T., Auinger, H. J., & Schön, C. C. (2012). synbreed: a framework for the analysis of genomic prediction data using R. *Bioinformatics*, 28, 2086-2087.