WEITZMAN APPROACH AND COMPONENTS OF DIVERSITY IN NORTHERN EUROPEAN SHEEP BREEDS


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INTRODUCTION

Recently, the Weitzman (1992) approach has been used for quantifying the importance of breeds in conservation of domestic animals diversity (Thaon d’Arnoldi et al. 1998, Barker 2001, Canon et al. 2001). In this approach, pairwise genetic distances calculated from molecular data are transformed to a diversity value. Another way of diversity evaluation was proposed by Petit et al. (1998). He measured diversity as mean expected heterozygosity or as allelic richness and considered the effect of one population to total diversity. This effect is decomposed into two components, one resulting from within population diversity and second resulting from divergence of a population from the remaining pool of populations. Both methods were applied to a set of 32 sheep breeds, genotyped for 22 unlinked microsatellite markers. The aim of this study was to compare conservation values these two methods give for individual populations or breeds and investigate the relationship between Weitzman marginal losses of diversity and the two components of Petit et al. (1998).

MATERIAL AND METHODS

Sheep breeds. In the study, 32 sheep breeds from Northern Europe with 13–55 individuals per breed were included. These breeds were: Finnsheep (30 individuals analysed), Finnsheep Kainuu (30), Åland Sheep (25), Russian North Karelian (31), Russian Romanov (31), Swedish Finewool (32), Swedish Rya (31), Swedish Pelt Sheep (30), Swedish Dala Fur sheep (29), Swedish Gute (20), Swedish Woodsheep (38), Swedish Roslag (30), Danish Heath (21), Danish Marsh (28), Texel (24), Greenland Sheep (17), Faroe Island Sheep (21), Norwegian Steigar (29), Norwegian Dala Sheep (55), Norwegian Rygja Sheep (28), Cheviot (28), Norwegian Spæl Sheep (30), Norwegian Old Spæl Sheep (29), Old Norwegian Wild (37), Norwegian Troender Sheep (25), Fuglestad Sheep (13), Icelandic Sheep (30), Icelandic Leader Sheep (35), Lithuanian Coarsewooled (30), Lithuanian Blackfaced (30), Latvian Darkheaded (32) and Estonian Ruhnu (24).

Genetic loci studied. Altogether 923 unrelated animals were genotyped for 22 microsatellite markers: OarFCB128, OarFCB304, OarFCB48, OarHH47, McM527, MAF65, MAF48,
MAF36, MAF214, INRA023, BM8125, BM0757, BM1818, BM6526, BM1314, BM4621, BM6506, OarCP38, OarCP20, OarCP34, CSSM31 and OarVH72.

**Statistical analyses.** The Weitzman approach was applied with implementation of Canon *et al.* (2001) using $D_A$ distances to calculate marginal losses of diversity for each population. The contribution of different populations to total diversity and allelic richness was calculated according Petit *et al.* (1998), using CONTRIB, software available at http://www.pierroton.inra.fr/genetics/labo/Software/. In their method, contribution of each population to the total diversity (CT) and to the total allelic richness (CTR) are divided into two components, one related to the within population diversity (CS and CSR), the other related to the divergence from the remaining populations (CD and CDR).

**RESULTS AND DISCUSSION**
Marginal loss of diversity due to extinction of a breed according to the Weitzman approach and the divergence component of Petit *et al.* (1998) both quantify the diversity that results from uniqueness of the population. The two approaches give values that have highly significant positive correlation (Figure 1a and 1d). Anyway, the comparison of Weitzman marginal loss of diversity and the contribution to total diversity as defined by Petit *et al.* (1998) have only a weak positive correlation (Figure 1c and 1f). This is due to the effect of the within population diversity component that has a highly significant negative correlation with Weitzman marginal loss of diversity (Figure 1b and 1e). For example the Weitzman approach gives the highest value (0.076) for the population that is mostly divergent (CD = 0.013, CDR = 0.013) from the remaining populations. At the same time, within population diversity of this population is lower than the mean of the pool, which leads to negative values of within population components (CS = -0.011, CSR = -0.012). Weitzman’s marginal loss of diversity is lowest (0.011) for a population that is not strongly diverged from remaining pool (CD = -0.003, CDR = -0.006), but has one of the largest within population components (CS = 0.002, CSR = 0.005). Because of this relation of the two components, the task of setting conservation priorities does not seem straightforward.

Relative importance of heterozygosity compared to allelic diversity depends on scope of time considered. Heterozygosity is related to ability of immediate response to selection and allelic diversity to limits of long-term response to selection (e.g. James 1971). In the current study the comparison of Weitzman and Petit *et al.* (1998) approaches related to heterozygosity and allelic divergence showed similar results.

**CONCLUSIONS**
The Weitzman approach and the divergence component of Petit *et al.* (1998) agree on the conservation value caused by uniqueness of the populations. Contribution of a population to diversity is a sum of divergence and within population characteristics. Contribution to total diversity of Petit *et al.* (1998) showed a positive, but non significant correlation with Weitzman’s marginal losses of diversity. Our study indicates that setting conservation priorities according to the Weitzman approach only might therefore be misleading.
Figure 1. Comparison of Weitzman (1992) marginal loss of diversity with Petit et al. (1998) divergence (a and d) and within population diversity (b and c) components and contribution of population to total diversity (a, b and c) and total allelic richness (d, e and f).
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