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3 **Performance of a novel breeding value in context of breed conservation**

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16 **Summary**

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18 For the maintenance of genetic diversity the improvement of approaches for breed
19 conservation is important. Many breeds have low native genetic contribution (NC) due to
20 introgression with high-yielding breeds. The aim of this work was to examine the
21 performance of a breeding value for NC in local breeds. Hence, the NC was considered as a
22 trait. Information on NC for two breeds was available. Genetic parameters were estimated by
23 applying different linear mixed models. Additionally, correlations with estimated breeding
24 values (EBV) of other traits were analysed. Estimated heritability for NC varies between 0.74
25 and 0.97. Furthermore, correlations between EBV for NC and reproduction traits were
26 positive, whereas the correlation between EBV for NC and milk yield was negative.

27
28 *Keywords: optiSel, ASReml, EBV, linear mixed model, genetic conservation*

29
30 **Introduction**

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32 To achieve conservation of local breeds different approaches have been proposed. Forming a
33 synthetic breed by combining a non-endangered breed with one or two highly endangered
34 local breeds as proposed by Bennewitz *et al.* (2008), may in fact result in continued
35 introgression from the high-yielding breed, which reduces the genetic contribution from
36 endangered local breeds. Optimum Contribution Selection (OCS) as proposed by Meuwissen
37 (1997) may further threaten the genetic material from the endangered local breeds if the
38 native genetic contribution (NC) and total merit are negatively correlated. The OCS approach
39 was extended to account for historical introgression by Wellmann *et al.* (2012) and Wang *et*
40 *al.* (2017).

41 The aim of this work was the investigation of an approach for conservation by
42 computing estimated breeding values (EBV) for the phenotype NC for endangered local
43 breeds with linear mixed models (LMM). Heritability (h^2) and correlations (r_G) with EBV of
44 other traits were calculated.

45
46 **Material and methods**

48 **Material**

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 50 The data consisted of phenotypes and breeding values of 58,999 German Angler, 19,682 Red
 51 dual purpose cattle (RDP), and their pedigrees. Phenotype information included animal ID,
 52 sire, dam, sex, farm, breeding values for several traits, and the NC estimated from pedigree.
 53 The NC were computed with function ‘pedBreedComp’ from R-package ‘optiSel’ from
 54 Wellmann (2017a) in R-statistic software (2017). For every individual the genetic
 55 contributions from native founders and from other breeds were computed according to the
 56 pedigree. It was the fraction of genes that originate from the respective breed. Pedigree data
 57 was provided from VIT (Vereinigte Informationssysteme Tierhaltung e.V., Verden, Germany)
 58 for the single breeds. The data quality was checked with function ‘completeness’ from R-
 59 package ‘optiSel’, and individuals with an equivalent number of complete generations smaller
 60 than 3 were removed from the analysis. All founders born after 1970 were considered non-
 61 native, whereas founders from the respective breed born before 1970 were considered native.

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 63 **Statistical model**

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 65 The linear mixed models A and B were fitted with R-package ‘asreml’ from Butler *et al.*
 66 (2009). The LMM can be written as

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 68
$$(1)$$

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 70 where \mathbf{y} denotes the n -vector of NC, \mathbf{b} is the vector of fixed effects, \mathbf{a} is the vector of random
 71 additive genetic effects of the animal distributed as $\mathbf{a} \sim N(\mathbf{0}, \mathbf{Z}_A \mathbf{A} \mathbf{Z}_A')$, where \mathbf{A} is the additive genetic variance,
 72 and \mathbf{Z}_A is the additive relationship matrix. Vector of independent random effects has distribution
 73 \mathbf{I} , and \mathbf{e} is the n -vector of independent residual errors with \mathbf{I} . Matrices \mathbf{X} , \mathbf{Z}_A , and \mathbf{Z} are
 74 design matrices associating observations with the appropriate combination of effects.

75 Fixed effects of birth, sex, sire, dam, and random effects of farm, sire, and dam were
 76 tested for significance with R-package ‘asremlPlus’ from Brien (2016). Date of birth and sex
 77 were significant ($p \leq 0.001$), thus they were included as fixed effects in all models. However,
 78 the random effects of farm, sire, and dam were not significant ($p \geq 0.01$). The heritability was
 79 calculated as

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 81
$$(2)$$

82
 83 **Results**

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 85 In order to avoid overestimations of h^2 two final model designs (Model A and B) with
 86 different random effects were compared for the two breeds. The trait was heritable in both
 87 models ($p < 0.005$).

88
 89 *Table 1. Heritability (h^2) with standard error (SE), additive genetic variance (σ^2), variance of*
 90 *herd effect (σ^2), and residual variance (σ^2) for NC.*

N ¹	Model A ²					Model B ³				
	h^2	SE	σ^2	σ^2	σ^2	h^2	SE	σ^2	σ^2	σ^2
N _α	0.89	0.0093	0.0043	0.0005	0.0000	0.93	0.0000	0.0031	-	0.0002

N_{β} 0.74 0.0036 0.0037 0.0013 0.0000 0.97 0.0000 0.0048 - 0.0001

91 ¹ N_{α} = 58,999 German Angler, N_{β} = 19,682 Red dual purpose cattle (RDP)

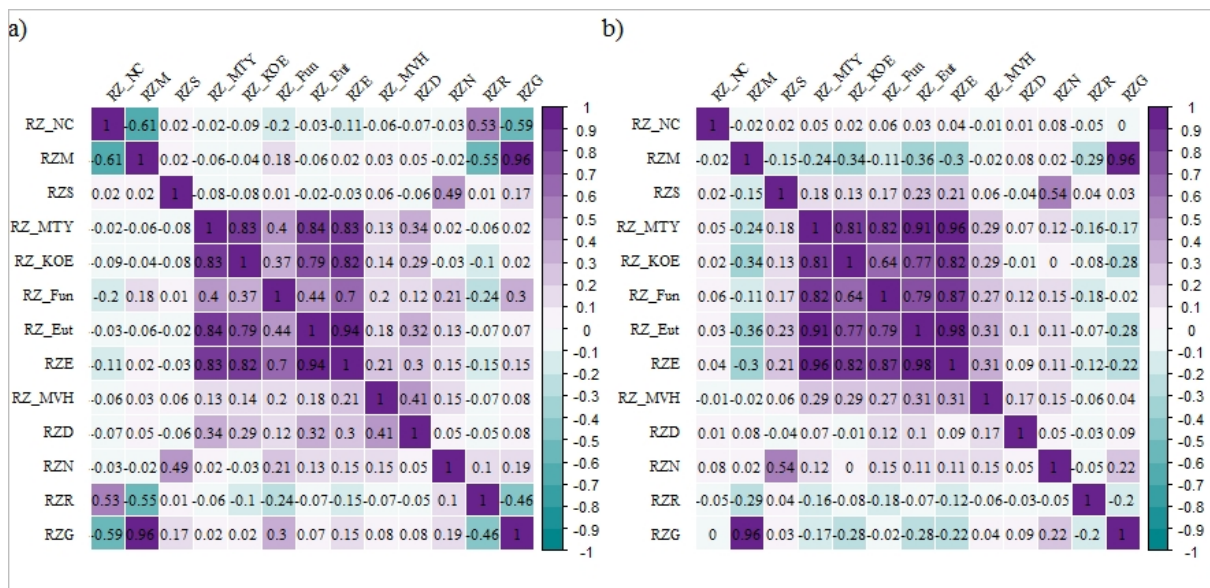
92 ² Model A: (fixed effects = born, sex / random effects = farm)

93 ³ Model B: (fixed effects = born, sex / random effects = none)

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95 The results are given in Table 1. The h^2 ranged from 0.74 to 0.97 with standard errors
 96 between 0.0000 to 0.0093 for the different sample sizes in all models and breeds. Hence, all
 97 models performed similarly, but the likelihood ratio test was not significant, thus the model B
 98 without farm effect provides a better fit for the data than the model A with farm effect.

99 Figure 1 shows correlations with reliabilities over 90% between the EBV of NC
 100 (RZ_NC) and conventional EBVs. For German Angler the RZ_NC is positively correlated
 101 with RZR ($r_G = 0.53$), which is a reproduction trait, and negatively correlated with RZM ($r_G =$
 102 -0.61), which is a milk yield trait, and RZG ($r_G = -0.59$), which is the total merit index. For
 103 RDP the RZ_NC is slightly positive correlated with RZN ($r_G = 0.08$), which is a longevity
 104 trait, and negatively correlated with RZR ($r_G = -0.05$) and RZM ($r_G = -0.02$). Surprisingly, the
 105 RZ_NC is also positively correlated with some fitness and conformation traits (RZS,
 106 RZ_MTY, RZ_KOE, RZ_Fun, RZ_Eut, and RZE), which could be due to different breeding
 107 goals in the RDP and in the introgressed breeds.
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109
 110 Figure 1. Correlations between RZ_NC and conventional EBVs for a): German Angler and
 111 b): Red dual purpose cattle (RDP).
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113 Discussion

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115 Breeding values for NC were negatively correlated with milk yield and total merit index
 116 (RZG), which shows that truncation selection or traditional OCS on RZG reduces the NC and
 117 thus threatens the native genetic background of local breeds. Hence, advanced OCS methods
 118 (Wellmann, 2017b) are needed for these breeds. The moderate correlations between RZ_NC
 119 and conventional functional traits show the connections between fitness traits and the native
 120 genetic background of these breeds. This indicates that the German Angler and the RDP carry
 121 valuable alleles that should be maintained.

122 Both, the h^2 of the trait NC and the variance of the additive effects are high, which
 123 enables response to selection for high RZ_NC. However, if the RZ_NC estimated from

124 pedigree is considered as a phenotype for the true NC, the model makes the wrong
125 assumption that the residuals are uncorrelated, which results in an overestimation of the
126 heritability. Moreover, the NC estimated from the pedigree does not account for Mendelian
127 segregation, which would cause the variance of the estimated NC to decrease considerably
128 after few generations. This can be avoided by replacing the RZ_NC estimated from pedigree
129 with a RZ_NC estimated from genotypes after few generations of selection to achieve
130 sustainable breeding progress.

131 **Conclusion**

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133 Favorable correlations between the RZ_NC and fertility traits were observed. The h^2
134 of the RZ_NC and the variance of their effects are high, which enables response to selection
135 for high RZ_NC. The negative correlation between RZ_NC and total merit shows the need to
136 select for RZ_NC if the native genetic background should be preserved. This should be
137 combined with advanced OCS to recover the genetic background and to maintain the
138 diversity at native alleles. Investigations should be expanded to implement selection for high
139 RZ_NC in breeding programs for endangered local breeds with historic introgression.
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