Estimation of Breed Composition, Breed Heterosis and Epistatic Loss for Percent of Live Spermatozoa in Admixed Swiss Fleckvieh Bulls

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Summary

The objective of this study was to estimate non-additive genetic effects of heterosis and epistatic loss on percent of live spermatozoa in admixed Swiss Fleckvieh bulls, a composite of Simmental and Holstein Friesian cattle. Heterosis is the additional gain in productivity or fitness of crossbred progeny over the mid purebred parents mean which arises from intra-locus gene interaction. Epistatic effects generally reduce productivity or fitness due to lack of gene interactions of genes from different breeds, which is called epistatic loss. Bovine SNP chip data of were used to predict locus specific breed origin of alleles along the autosomes of 815 admixed bulls as well as 147 Holstein Friesian and 207 Simmental bulls representing the parental breeds. The breed proportions for admxied bulls based on 32,899 SNP were used to calculate breed heterozygosity and epistatic loss, considering additive by additive effects for 1,000,000 random pairs of loci. The average Holstein Friesian ancestry in admixed bulls was estimated to be 0.82. Results of fitting different linear mixed models showed that including breed heterozygosity and epistatic loss improved the model fitness (ΔAIC > 3). The heterosis effect and epistatic loss were estimated 2.5(±1.39) % and -0.65(±1.68) % of live spermatozoa, respectively. High correlation (0.97) between breed heterozygosity and epistatic loss values indicate strong confounding of these effects in the model, indicating that it is not possible to properly separate these effects.

Key words

Swiss Fleckvieh, admixture, breed composition, heterosis, epistatic loss, live spermatozoa

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Introduction

Systematic crossbreeding has been widely used in dairy cattle in order to optimize production and reproduction traits. Admixed animals can benefit from the difference in additive genetic levels of their purebred ancestral populations together with heterosis which is expressed only in crossbred populations.

Heterosis is defined as the superiority of a crossbred progeny compared with its mid-parents average for a particular trait (Falconer, 1989; Shull, 1948). The extent of heterosis depends on the difference in frequency of the alleles at every single locus contributing to heterosis, the number of involved breeds and the type of crossbreeding. Individual heterosis is a deviation from parental average, due to increased average heterozygosity of first generation (F1) or reciprocals, which includes any non-allelic interaction of alleles within locus. Heterosis is at maximum level at F1 and it drops to half in second generation (F2) and decreases after several generations due to recombination, which is called retained heterosis (Dickerson, 1969, 1973). Recombination loss is defined to measure deviations from linear associations of heterosis and productivity and was described as the average fraction of independently segregating gametes from both parents which are expected to be non-parental combinations (Dickerson, 1973). Epistatic loss is hypothesized to be caused by the breakdown of additive x additive interaction of alleles from different loci established by long term selection in purebred populations (Fries et al., 2002). Crossbred populations can provide excellent opportunity to study how interactions between alleles within locus and between loci can change the mean of particular traits at different generations after admixture.

For milk production traits, heterosis is reported from 2 to 8 %, while higher levels of heterosis are observed for functional and reproductive traits (Sorensen et al., 2008; VanRaden & Sanders, 2003). In this study we concentrated estimation of average breed effect, heterosis and epistatic loss on percent of live spermatozoa in Swiss Fleckvieh admixed bulls. For breed heterozygosity we used LAMP results on breed origin of each pair of alleles at SNP level (Sankararaman et al., 2008). For epistatic loss we considered the genetic effect of identical versus mixed breed ancestry of alleles of random pairs of loci along the genome. We fitted and compared models with effects of breed percentage, breed heterosis and epistatic loss for this trait.

Materials and methods

Phenotype and genotype

Phenotypic records (68,475) for percent of live spermatozoa for 1298 bulls were received from Swiss genetics in Switzerland. Available data were collected from 2000 to 2015 from one artificial insemination (AI) station. Bulls with less than 10 records were also not regarded in our analyses. Ejaculations which were recorded with less than three days interval were removed from data set. Records beyond the range mean ± 3 standard deviations were discarded. The total 1296 bulls with 43,782 records remained.

Imputed genotypes with FImpute (Sargolzaei et al., 2014) for all 1298 bulls with a subset of 44,999 SNP were received from Swissherdbook cooperative Zollikofen. Bulls were genotyped using Illumina Bovine SNP 8k, 50k, 150k and 777k BeadChip. Based on formal definition of Swissherdbook, animals with 0.125-0.875 pedigree ancestry level of HF are categorized as Swiss Fleckvieh. In this study, we assigned animals with 0.02-0.99 HF ancestry level as admixed animals.

The genotype data was checked, using the standard quality control with PLINK 1.90 (Chang et al., 2015; Purcell et al., 2007) and monomorphic SNP with call rate < 0.95, those SNP deviated from Hardy Weinberg equilibrium with P-value < 10^{-5} were removed from data set. Finally 38,299 SNP for 1169 bulls (147 HF, 207 SI and 815admixed animal) remained for the analyses.

To estimate breed composition at each single loci, we used LAMP 2.5. The locus specific ancestry proportion was estimated for each chromosome at each SNP position separately.

Statistical models

The fixed effects considered were age of bull (linear and quadratic), assistant, contemporary group (year-season of collection) and interval days between two consecutive ejaculations. The elapse between two consecutive ejaculations was also categorized into three different levels (3-6 days, 7-9 and >9 days interval). Season effect was defined as categorical variable (February to May, June to September and October to January).

$$y_{ijklmn} = \mu + \alpha_i + age_j + contempgroup_k + elapse_l + assitant_m + breedpercent_{ijklmn} + \varepsilon_{ijklmn}$$

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Where y_{ijklmn} is observation for each bull, μ is overall mean, α_i is random permanent effect of each bull age_j, $contempgroup_k$, $elapse_l$, $assistant_m$, are the fixed effects related to age of bulls, year season (contemporary groups), ejaculate intervals and assistant. $breedpercent_{ijklmn}$, $breedhet_{ijklmn}$, $epstloos_{ijklmn}$, are the regression coefficient for breed percent (proportion of HF), breed heterosis and epistatic loss effects and ε_{ijklmn} is the random error associated with each observation (CRAN package, lme4).

To fit the appropriate model considering breed composition, breed heterosis effect and recombination loss we set different models. Breed composition for pure HF bulls was coded as 1 and for pure SI bulls was coded as 0. Breed composition for admixed bulls was computed by taking the average HF proportions for all SNPs across the 29 autosomes based on the LAMP results. Breed heterosis was also calculated based on LAMP results, and was set to 1 where both alleles at each single SNP derived from different ancestral populations and 0 where both alleles came from the same breed origin. Values were averaged across the autosomes for admixed bulls while this quantity was set to 0 for purebred bulls. To include epistatic loss in the model, we randomly sampled 100,000 times one allele each from two different SNP for each admixed bull. Epistatic loss was set to zero

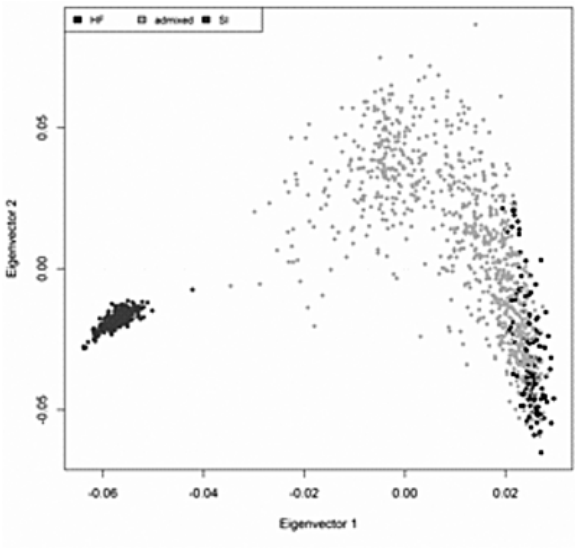

Figure 1. PCA results for HF and SI pure ancestral population and admixed bulls

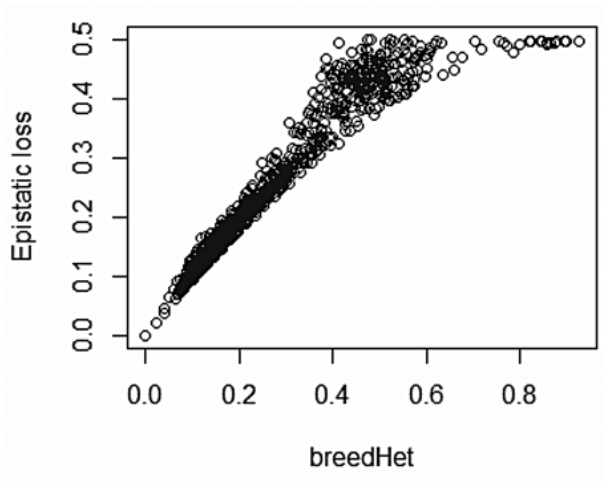

Figure 2. Scatter plot of breed heterozygosity and epistatic loss for percent of live spermatozoa (Pearson's correlation=0.97)

when the two alleles derived from the same ancestral origin and were set to one where they came from different ancestral populations, equivalent following the Kinghorn (1982) definition. ε

Results and discussion

The Illumina SNP genotyping data, containing 38,299 SNP for 1169 bulls (including 147HF, 207 SI and 815 admixed) were used. In the first step, we carried out PCA (Figure 1) to understand the population structure of purebred and admixed populations. The first two eigenvectors are shown, representing the overall genetic structure and distance of pure HF (black), SI (dark grey) and the admixed (light grey) bulls. To identify the breed fractions of the admixed bulls, we used unsupervised clustering analysis, which is performed by ADMIXTURE (Alexander et al., 2009). The average ancestry proportions were estimated 0.82 HF and 0.18 SI (0.16 SD) which were highly correlated (0.97) with estimated ancestry proportions from pedigree with 0.85 HF and 0.15 SI.

Estimates of heterosis and epistatic loss parameters

The total 42,121 phenotypic observations of the percent live spermatozoa as one of the semen quality traits for 1169 genotyped bulls were used to estimate the global levels of heterosis and epistatic loss for this trait in admixed Swiss Fleckvieh bulls. The overall statistics on percent of live spermatozoa is shown in Table 1.

Different models were used and model fits were compared. This was done by adding genetic effects in steps. Estimated regression coefficient of breed percentage, breed heterosis and epistatic loss effects relative to HF and SI purebred population are summarized in Table 2.

Other fixed effects showed significant difference between categories in all four models, but no difference for assistant (semen collector) was detected in all models.

Table 1. Statistics on percent of live spermatozoa in pure and admixed populations

	HF	SI	SF
No of bulls	147	207	815
No of records	4632	7330	30159
Mean (%)	85.66	86.11	86.42
Standard deviation (%)	3.10	3.88	3.28

Table 2. Regression coefficients (±standard error) for percent of live spermatozoa with different models

Models	Breed composition	Breed heterozygosity	Epistatic loss
Model 1	0.65 (0.19)	–	–
Model 2	0.41(0.19)	2.00(0.34)	–
Model 3	0.37(0.20)	–	2.03(0.41)
Model 4	0.43(0.20)	2.5(1.39)	–0.65(1.68)

Considering only breed percent in model 1 showed that pure HF bulls have 0.65 percent more live sperm in their ejaculates compared to pure SI bulls. In model 2, considering breed heterozygosity, differences were detected between admixed and purebred animals. Breed heterosis effect was estimated 2.00 (±0.34) percent. Considering epistatic loss (model 3) gives us 2.03(±0.41) above mean which is confounded with breed heterozygosity due to high correlation between these two effects (Figure 2). Considering all three genetic effects simultaneously in model 4, the estimates for heterosis and epistatic loss were 2.5 (±1.39) % and -0.65(±1.68) %, respectively. Separating these two effects is hard, since they are highly correlated (0.97).

Table 3. Model Adequacy comparing the sub model with full model

Models	ΔAIC	P-value
Model 1 and 2	33	3.62e-09 ***
Model 1 and 3	30	1.834e-08 ***
Model 1 and 4	31	2.546e-08 ***
Model 2 and 3	3	2.2e-16 ***
Model 2 and 4	2	0.695
Model 3 and 4	1	0.0689

We calculated ΔAIC (Table 3), to compare the different models. Model with AIC less than 2 indicated no significant difference between models. ΔAIC which are between 3 and 7 are considerably less support and the ones greater than 7 are not likely (Burnham & Anderson, 2002). ΔAIC of full model 4 compared to models 3 and 2 did not indicate better model fit of any of these 3 models. Comparing AIC values of model and 3 with 2 showed that model 2 is more likely than model 3. Comparing models 2, 3 and 4 with model 1 showed that model 1 with breed percent as the only genetic effect is not likely. The classical model with additive breed effect and heterosis shows a very clear positive heterosis effect. Separation of the effects of heterosis and epistatic loss was very difficult with the structure of levels of admixture found in the population studied because of very high correlation of the two effects. Confounding of these effects was also reported by (Fries et al., 2002).

Conclusion

Crossbred populations provide unique opportunity to study the effect of heterosis and epistatic loss on percent of live spermatozoa. Traits with relatively low heritability such as reproductive traits have shown high heterosis. In percent of live spermatozoa in admixed Swiss Fleckvieh bulls, the effect of heterosis was estimated 2.00 (±0.34) % and we expect 2 % more live spermatozoa in compare with the mean of purebred HF (85.66%) and SI (86.11%) ancestral populations. Including epistatic loss showed 0.65 % decrease in live spermatozoa. Due to high correlation between these two effects, the estimates of heterosis and epistatic loss were confounded.

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