

419. Estimation of breed admixture levels in Sri Lanka cattle and its relation to performance traits

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Abstract

Measuring ancestry levels of local admixed cattle in Sri Lanka provides insight on the most suitable dairy (cross)breeds for the local environment. Performance data of dairy cows (n=197) as well as blood samples for genotyping were collected from two governmental farms in the Kurunegala District in Sri Lanka. Admixture levels were calculated as proportional abundance of the Jersey, Holstein Friesian, and Sahiwal ancestry. The dominance component of heterosis was determined by calculating the abundance of non-homozygous genetic blocks. A mixed linear model was applied to find how performance and admixture levels were associated. For 305-day milk yield, significant predictors were found for Jersey ancestral breed proportion and the dominance component of heterosis for $P < 0.05$. Although the feasibility of a crossbreeding program needs to be considered, performance of local Indicine cattle can be improved substantially through crossbreeding with Taurine cattle, mainly through the dominance effects of heterosis.

Introduction

Crossbreeding is a widely used implementation in (sub)tropical countries to increase performance while pertaining favourable characteristics of the indigenous cattle, such as heat tolerance, tick resistance and the ability to perform on low-quality feedstuffs (Galukande *et al.*, 2013). Breeding policies in Sri Lanka have, to large extent, stimulated a continuous grading up of existing cattle using purebred exotic animals (Ministry of Livestock and Rural Community Development, 2010). Continuous upgrading has been reported to decrease performance (Syrstad, 1989) due to a decrease in heterosis as well as the loss of beneficial and necessary key traits, mainly relating to the adaptation of indicine cattle breeds to the local environmental conditions. So far, little research has been performed on breed composition of dairy cattle in Sri Lanka, although identifying admixture levels that correlate with high performance under the local climate(s) of Sri Lanka could substantially improve dairy production.

Materials & methods

Data collection. Phenotypes and blood samples from 197 dairy cows were collected from two governmental farms in Sri Lanka, which were used to estimate the link between performance and admixture level. Phenotypes were collected from 2008 to 2018 and included reproduction data and production data related to milk yield. Ancestry of Sri Lanka cattle were explored in global context and therefore included genotypes of purebred Holstein Friesian, purebred Jersey, local Sri Lankan cattle, purebred Sahiwal as well as several indigenous cattle breeds including Batu Haraka, Thawalam and White cattle. The bulk of genotyping was performed at the laboratories of International Atomic Energy Agency (IAEA) in Seibersdorf (Austria) using an Affymetrix Axiom Bovine chip with a density of 52,518 SNPs. Genotypes of Holstein Friesian and Jersey originated from the International Bovine HapMap Project, genotyped using the Illumina BovineHD chip with a density of 777,962 SNPs (Bovine HapMap Consortium *et al.*, 2009).

Data editing, selection and admixture analysis. Genotypes were merged and manipulated in PLINK1.9 (Chang *et al.*, 2015), resulting in a total of 35,284 overlapping SNPs. The merged data was explored using multidimensional scaling in the form of a PCA plot and ADMIXTURE analysis (Alexander *et al.*, 2009). To estimate the locus-specific ancestry in the autosomal chromosomes (n=29), data was phased with SHAPEIT v2 (Delaneau *et al.*, 2012) using a cattle recombination map from the Dryad (Ma *et al.*, 2016). Subsequently, locus-specific ancestry was calculated using the Ghap package (Utsunomiya *et al.*, 2020) where the reference populations (k=3) consisted of Holstein-Friesian (n=30), Jersey (n=30) and Sahiwal cattle (n=29). Admixture levels were calculated as proportional abundance of the Jersey, Holstein-Friesian and Sahiwal ancestry for all the generated genetic blocks per animal. Based on the ancestral haplotypes, the dominance component of heterosis was determined by calculating the abundance of genetic blocks of mixed ancestry, following Khayatzaheh *et al.*, 2018).

Mixed linear model. Admixture levels for locus-specific ancestry and the dominance component of heterosis were included in a mixed linear model to estimate how performance and admixture levels were associated. The model was run for milk yield and number of services per conception, using the lme4 package (Bates *et al.*, 2015) in R (R Core Team, 2020) to investigate the breed effect:

$$y_{ijklmnop} = \mu + \beta_1 HF_i + \beta_2 JR_j + \beta_3 Dominance_k + Parity_l + Farm_m + Cow_n + Year_o + e_{ijklmnop} \quad (1)$$

Where: $Y_{ijklmnop}$ is the dependent variable (305-day milk production, number of inseminations), μ is the overall intercept of the model, $\beta_1 HF_i$ is the fixed effect of the proportion Holstein-Friesian admixture level ($i=0$ to 1), $\beta_2 JR_j$ is the fixed effect proportion Jersey admixture level ($j=0$ to 1), $\beta_3 Dominance_k$ is the fixed effect of the dominance component of heterosis defined as the percentage homozygous blocks ($k=0$ to 1). $Parity_l$ is the fixed effect of the k^{th} number of parity ($l=1$ to 6, where 6 encompasses the parities 6-10), $Farm_m$ is the fixed effect of the m^{th} farm ($m=$ Andigama or Maradawila), Cow_n is the random effect of the n^{th} cow ($n=1$ to 168), $Year_o$ is the random effect of the birth year of the cow ($o=2005$ to 2019), $e_{ijklmnop}$ is the random residual effect with mean 0 and variance σ^2 . The model was tested for significant predictors using the lme4 summary statistics and a type III ANOVA test (Wald chi-square test).

Results

Locus-specific ancestry analysis. The supervised locus-specific ancestry analysis used to infer ancestral populations on haplotype level of the admixed cattle on Andigama and Maradawila farm was visualized using Ghap (Utsunomiya *et al.*, 2020, Figure 1). Main breed components consisted of Pakistan Sahiwal (red) and Jersey (green).

Mixed linear model for 305-day milk yield & number of services per conception. The model for 305-day milk yield indicated significant predictors for parity ($P=0.0199$), Jersey ancestral breed proportion ($P=0.0131$) and the dominance component of heterosis ($P=8.045e-06$) for $P<0.05$ (Table 1). The Holstein-Friesian breed component was showing a high standard error and was indicated as insignificant ($P=0.1425$) for $P<0.05$. Both breed components had a negative effect on milk yield, whereas the dominance component of heterosis increased milk yield substantially. The combination of these two components gives us the estimated milk yield response for full heterosis based on dominance effects at haplotype level.

Based on the results of this analysis, a pure Sahiwal would produce 1,076 kg milk at first parity. A first cross Sahiwal \times Jersey would result in an estimated milk yield of 1,839 kg for the first parity on Andigama farm (1,076.47 - (789.22 \times 0.5) + 1,156.85) and 2,076 kg for Maradawila farm (1,076.47 - (789.22 \times 0.5) + 1,156.85 + 237.63). A crossbred Sahiwal \times Holstein Friesian (not-significant) would result in an estimated milk yield of 1,871 kg for the first parity on Andigama farm (1,076.47 - (724.61 \times 0.5) + 1,156.85) and 2,109 kg

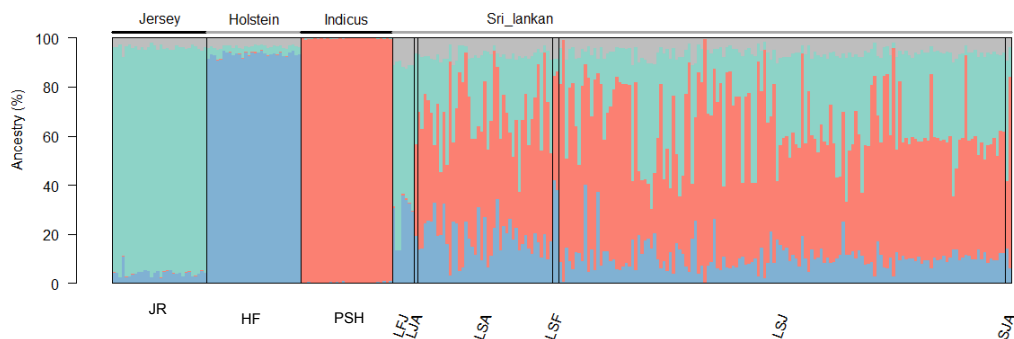


Figure 1. Locus specific ancestry predicted for admixed cattle population based on a reference panel including Jersey (JR: green), Holstein Friesian (HF: blue), and Pakistan Sahiwal (PSH: red). Admixed cattle include crossbred Sahiwal × Jersey × Australian Friesian Sahiwal (SJA); crossbred Sri Lankan Holstein Friesian × Jersey (LFJ); crossbred Sri Lankan Jersey × Australian Friesian Sahiwal (LJA); crossbred Sri Lankan Sahiwal × Australian Friesian Sahiwal (LSA); crossbred Sri Lankan Sahiwal × Holstein Friesian (LSF); crossbred Sri Lankan Sahiwal × Jersey (LSJ).

Table 1. Summary of linear mixed effects model for 305-day milk yield based including the fixed effects: Holstein Friesian proportion; Jersey proportion; parity; farm; and the dominance effect of heterosis.

a. Fixed effects		
	Estimate	Std. error
(Intercept)	1,076.47	143.15
Holstein Friesian	-724.61	494.04
Jersey	-789.22	317.93
Parity 2	131.35	62.01
Parity 3	95.04	69.86
Parity 4	10.01	87.27
Parity 5	-106.10	107.54
Parity 6+	-178.19	102.00
Dominance	1,156.85	259.15
Maradawila farm	237.63	91.15

for Maradawila farm $(1,076.47 - (724.61 \times 0.5) + 1,156.85 + 237.63)$. For the model estimating number of services per conception, no significant predictors were found for $P < 0.05$.

Discussion

Our findings suggest that an increased response in performance was mainly caused by the dominance effects of heterosis at haplotype level, indicated by the high correlation between the dominance effect of heterosis and 305-day milk yield. Heterosis effects are generally higher in functional traits with low heritability, such as those accounting for reproduction, survival, and fitness, whereas production traits with moderate heritability (e.g. milk yield and growth) are less affected by heterosis. Interestingly, our results showed a higher influence of heterosis on milk yield than on reproduction (number of services per conception). Since the (timing of) insemination of cows is nevertheless under the influence of the farm management, there might be additional influences that we did not account for. Heterosis effects are generally much larger in

crosses between temperate and tropical breeds (Wakchaure *et al.*, 2015. The large genetic distance between the breeds possibly explains the high influence of heterosis on milk yield in our study.

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