Sölkner, J., Khayatzadeh, N., Gebreselama, T., Meseret, S., Mrode, R., Gebreyohanes, G., Lamont, S., Van Goor, A., Curik, I., Gebre, K. (2026) Genomic prediction of components of heterosis for crosses of cattle breeds and advanced intercross lines of chicken, *Proceedings 13th World Congress on Genetics Applied to Livestock Production* 23899: https://doi.org/10.31274/wcgalp.23899
©2026 Sölkner, et al. CC BY-NC-ND

Genomic prediction of components of heterosis for crosses of cattle breeds and advanced intercross lines of chicken

J. Sölkner[1*], N. Khayatzadeh[2], T. Gebreselama.[1,6], S. Meseret[3], R. Mrode[3], G. Gebreyohanes[3], S.J. Lamont[4], A. Van Goor[5], I. Curik[6], and K.T. Gebre[7]

[1]BOKU University, Vienna, Austria, [2]SUISAG, Sempach, Switzerland, [3]International Livestock Research Institute, Nairobi, Kenya & Addis Ababa, Ethiopia, [4]Iowa State University, Ames, Iowa, U.S.A., [5]USDA-NIFA, Kansas City, Missouri, U.S.A., [6]University of Zagreb, Zagreb, Croatia, [7]Mekelle University, Tigray, Ethiopia,
**Corresponding author: johann.soelkner@boku.ac.at*

Introduction

Heterosis, or hybrid vigor, is an extremely important part of genetic systems in livestock, as evidenced by commercial (terminal) crosses in chicken and pig, as well as the establishment of composite lines/breeds in many species. Key components of heterosis are dominance and epistatic effects. Dominance effects are typically positive, due to an increased portfolio of solutions to environmental disturbances, caused by a higher number of different alleles resulting in increased heterozygosity across the genome. Epistatic effects are expected to be negative, due to break-up of established positive interactions of genes within populations. This has been evidenced when crossing high yielding cattle breeds from regions with a history of genetic improvement with local breeds in developing countries. F1 crosses tend to outperform compared to averages of parental breeds, while F2, expected to express half the heterosis based on dominance effects, tend to underperform compared to expected. Traditionally, levels of dominance and epistasis have been derived from pedigrees, using various formulae. Genomics provides options for estimating such effects even without pedigrees available. Local ancestry calculation along the chromosomes provides evidence as to whether the two alleles of a locus of an individual are derived from either breed (i.e. are "breed homozygous" for one breed) or are derived from two breeds ("breed heterozygous"). Calculation of levels of breed difference, dominance and epistatic loss can be derived from these ancestry states. Here, we are presenting key results from three studies, one already published, one submitted, and one with preliminary results, all implementing genomic prediction of heterosis effects based on ancestry states of SNP along chromosomes. The first study investigates sperm quality of bulls of Swiss Fleckvieh, an advanced cross of Simmental and Holstein Friesian cattle, the second analyzed data of generations 18 and 19 of an advanced intercross line (AIL) of Fayoumi inbred line x Broiler chicken, and the third study was about recent crosses of local (Fogera and Boran) and "exotic" (Holstein Friesian and Jersey) cattle in Ethiopia.

Materials & Methods

Study 1 (Swiss Fleckvieh). Sperm quality phenotypes of 1,179 Swiss bulls genotyped with a 50K SNP chip were included in this study (Khayatzadeh *et al*., 2018). Data on 38,205 SNP of 818 admixed Swiss Fleckvieh (SWF), as well as 148 Red Holstein Friesian (RHF) and 213 Simmental (SI) bulls were used to predict breed origin of alleles. Sperm quality traits were volume in ml, concentration (billions per ml) and percentage of live sperm, collected in a total of 42,442 ejaculates on a single Artificial Insemination (AI) Station. The transformed number of spermatozoa for each ejaculate was calculated by multiplying volume with concentration and then applying Box-Cox transformation. The statistical model of analysis included the random permanent environmental effect of each bull as well as fixed effects of age of bull, year-season

(contemporary groups), ejaculate intervals and assistant, as well as regression coefficients for breed ancestry proportion (proportion of Red Holstein Friesian (RHF) and Swiss Simmental (SI)), dominance component of heterosis, epistatic loss. The regressor variables were derived from local ancestry calculation applying LAMP 2.5 (Sankararaman *et al*., 2008), counting the proportion of RHF alleles across all SNP, the proportion of SNP with mixed ancestry and the proportion of 100,000 randomly pairs of SNP with alternative purebred ancestry. The analyses were performed following methodology applied by (Ferenčaković *et al*., 2017).

Study 2 (Advanced intercross line of chicken). The aim of this study was to estimate breed differences as well as dominance and epistatic components of heterosis, using genome-wide local genetic ancestry for body weight, body temperature and blood parameters of heat stressed of 18th and 19th generations of advanced intercross line (AIL) chickens derived from two highly divergent chicken lines, i.e Fayoumi and commercial broiler (Van Goor *et al*., 2015). A total of 839 chickens with phenotypes and 431,399 SNP genotypic data (Affymetrix 600K) from 462 chickens were analyzed. Local ancestry for the AIL population was inferred using Efficient Local Ancestry Inference (ELAI) software (Yang *et al*., 2013), with genotypic data from the AIL founders (six inbred Fayoumi females and one broiler male). Genome-wide locus-specific breed ancestry was then used to estimate breed difference, dominance, and epistatic loss components of heterosis. A linear model was applied, incorporating sex and hatching period as fixed effects, and additive, dominance, and epistatic loss as covariates for prediction of heterosis.

Study 3 (Cattle in Ethiopia). The data for this study were collected in the framework of the Ethiopia component of the African Dairy Genetics Gains project, developed and implemented under the leadership of the International Livestock Research Institute (Meseret *et al*., 2022). The dataset analyzed in this study comprises genotypic information from 4,906 cattle representing four distinct breeds: Fogera, Boran, Jersey, and Holstein Friesian. Genotyping was performed using a panel of 38,344 SNP markers, retained following standard quality control procedures. For analytical purposes, these breeds were grouped into two broad categories: exotic, comprising the breeds Jersey and Holstein Friesian, and local, encompassing the indigenous Ethiopian breeds Fogera and Boran. Among the total sample, 66 individuals were assigned to the exotic group, 81 to the local group, and 4,759 were classified as admixed. Phenotypes were 69,915 daily milk records and 5,300 calving interval records of 4,759 genotyped animals. The linear model of analysis incorporated the random permanent environmental effect of each cow, fixed effects of parity, stage of lactation and calving season, and additive, dominance, and epistatic loss as covariates.

Results & Discussion

Study 1 (Swiss Fleckvieh). The average ancestry proportions of admixed bulls were estimated 0.82 RHF and 0.18 SI (0.16 SD) which were highly correlated (0.97) with pedigree ancestry proportions with average 0.85 RHF and 0.15 SI, respectively. Estimated breed differences were significant for all traits, apart from concentration. Volume and transformed number of sperm were higher for SI, while percentage of live sperm was better for RHF. Including the dominance component of heterosis in the model was highly significant for volume, number of spermatozoa and percentage of live sperm. It increased volume by 1.24 ml, transformed number of sperm by 0.28 and percentage of live sperm by 1.40%. Epistatic loss was estimated significant for volume and transformed number of sperm, indicating 7.6 ml less volume and 1.57 less transformed number of spermatozoa are expected in admixed population, due to epistatic loss. All significant results were in accordance with theory of heterosis, predicting a positive dominance component of heterosis and a negative epistatic loss. Yet, it was difficult to properly separate these two

components, due to positive correlation of indicators of breed heterozygosity and epistasis. The new definition of epistasis in this study, counting the proportion of pairs of loci with alternative pure ancestries, was more effective than the definition of Kinghorn (Kinghorn, 1983);where epistatic loss was set to 0 when the two non-allelic genes had the same ancestral origin and was set to 1 when they came from different ancestral populations.

Study 2 (Advanced intercross line of chicken). The parental lines of this advanced intercross, Fayoumi and broiler, were phenotypically very different in body size and growth. For instance, body weight at day 28 was 620g for Broiler and 190g for Fayoumi. Phenotypes of a total of 15 traits were grouped into body weight, body temperature, hematological, electrolyte, and blood gas traits. Estimated breed differences were significant for most traits, except for one electrolyte (sodium) and three blood gas traits. The dominance effect of heterosis was non-significant for most traits, except for one electrolyte and two blood gas traits. The effect of epistasis was significant in many instances, including body weight and body temperature, where the effect was unfavorable, as expected by theory. Yet, the indicators for dominance and epistatic effects were highly correlated, r=0.87. Inference on dominance vs epistatic loss should be therefore interpreted cautiously. The combined non-additive signal is more robust than its decomposition. When dropping the epistatic effect from the model, dominance was significant for most of the traits, yet with unexpected direction for body weight and body temperature. While not expected based on heterosis theory, results are consistent with an old study of crosses of layer chicken (Cahaner *et al*., 1996), where the effect of heterozygosity, expressed as composite band frequency from DNA fingerprinting, was also negative for body weight and egg production. Using SNP heterozygosity instead of mixed ancestry as dominance indicator in our study gave quite similar results, also negative trends for body weight with increased heterozygosity.

Study 3 (Cattle in Ethiopia). The data set different from the ones of studies 1 and 2 in the sense of including mostly recent crosses of the two types of cattle. As expected, daily milk production of pure local animal was much lower than that of pure exotic, with least squares means of 7.35kg versus 14.25kg. For calving interval, corresponding values were 754 versus 679 days, indicating a shorter calving interval of exotic cows. Dominance and epistatic effects were both not significant for either of the two traits. In a model excluding epistatic effects, dominance was still not significant. Note that the correlation with indicators of dominance and epistasis was lower than in study 2, r=0.23. When replacing the dominance indicator based on mixed ancestry by SNP heterozygosity, results changed dramatically. Estimates of breed means for daily milk yield were 5.26kg and 11.76kg, the estimator for the dominance effect was 5.63. Based on this result, the mean of F1 animals showing full heterosis is expected to be 11.89kg, very close to purebred exotic. For calving intervals, corresponding local, exotic and F1 predictions were 761, 719 and 708 days. Such results, showing similar performance of pure exotic and F1 animals, are quite frequently observed in low input systems (Galukande *et al*., 2013).

Conclusions

Crossbreeding of any kind, it being terminal or continuous, is an extremely important component of agricultural systems. Therefore, understanding the genetic basis of heterosis is crucial, be it in plant breeding (Labroo *et al*., 2021) or livestock production (Amuzu-Aweh *et al*., 2013, Akanno *et al*., 2018, Bunning *et al*., 2019). Here we show results of three studies, applying genomic indicators of breed difference, dominance component of heterosis and epistatic loss, based on allelic ancestry of high throughput SNP data. The results of these studies are not very consistent. In the study on sperm quality of bulls in a high input system, results were very much according to expectations, positive of dominance and negative for epistasis. In

the second study on advance intercross lines of chicken, dominance and epistasis were either non-significant or partly according to and partly contrary to expectation. In the third study, analysing data of local and "exotic" cattle in low input systems, a big difference was found when interpreting dominance effects based on mixed ancestry versus SNP heterozygosity. One reason for that could be the small number of reference "exotic" animals and that estimates may be sensitive to reference definition. More studies are needed for better understanding of heterosis effects, particularly in livestock.

References

Akanno, E. C., M. K. Abo-Ismail, L. Chen, *et al*. 2018. Journal of Animal Science 96(3):830-845.

Amuzu-Aweh, E. N., P. Bijma, B. Kinghorn, *et al*. 2013. Heredity 111(6):530-538.

Bunning, H., E. Wall, M. G. Chagunda, *et al*. Journal of Animal Science 97(1):29-34.

Cahaner, A., E. Smith, S. Swenson, *et al*. 1996. Poultry science 75(12):1463-1467.

Ferenčaković, M., J. Sölkner, M. Kapš, *et al*. 2017. Journal of Dairy Science 100(6):4721-4730.

Galukande, E., H. Mulindwa, M. Wurzinger, *et al*. 2013. Animal Genetic Resources/Resources génétiques animales/Recursos genéticos animales 52:111-125.

Khayatzadeh, N., G. Mészáros, Y. T. Utsunomiya, F. *et al*. 2018. Journal of Animal Breeding and Genetics 135(1):45-53.

Kinghorn, B. 1983. Genetic effects in crossbreeding. 3. Epistatic loss in crossbred mice.

Labroo, M. R., A. J. Studer, and J. E. Rutkoski. 2021. Frontiers in genetics 12:643761.

Meseret, S., G. Gebreyohanes, R. A. Mrode, *et al*. 2022. The pathway to genetic gains in Ethiopian dairy Cattle: Lessons learned from African Dairy Genetic Gains Program and tips to ensure sustainability.

Sankararaman, S., S. Sridhar, G. Kimmel, *et al*. 2008.The American Journal of Human Genetics 82(2):290-303.

Van Goor, A., K. J. Bolek, C. M. Ashwell, *et al*. 2015. Genetics Selection Evolution 47(1):96.

Yang, J. J., J. Li, A. Buu, *et al*. 2013. Bioinformatics 29(21):2750-2756.