Session 1: Managing genetic diversity in cattle in the era of genomic selection (with Interbull)
Chair: Reinhard Reents
Date/Time: 08:30-12:30

Abstract number: 26496 / accepted / order: 1 / pres.means: Theatre / time: 30

Genomic tools to improve progress and preserve variation for future generations

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Use of genomic tools has greatly decreased generation intervals and increased genetic progress in dairy cattle, but faster selection cycles can also increase rates of inbreeding per unit of time. Average pedigree inbreeding of Holstein cows increased from 4.6% in 2000 to 5.6% in 2009 to 6.6% in 2015. The 0.17% per year recent rate of inbreeding is larger than in the previous decade but similar to the rate of 0.16% from 1985 to 2000. Recent rates from 2009 to 2015 were only 0.09% per year for Jersey and 0.13% for Brown Swiss cows. Breeders have reduced the effects of inbreeding depression in the short term by focusing on genomic rather than pedigree inbreeding in mating programs, avoiding carrier matings, selecting against lethal defects, or crossbreeding. Genomic relationships of > 1 million genotyped females with > 5,000 marketed males have been used in industry mating programs since 2014 and are updated monthly for new females. Haplotype or laboratory genotype tests for 22 recessive defects, red, and polled are provided for all genotyped animals. Pedigree breed composition has been provided since 2007 and genomic breed base representation since 2016, allowing breeders to examine ancestry of each animal even if pedigrees are incomplete or missing. Genomic evaluations on all-breed scale were computed but not released yet for 25 traits of 44,023 crossbreds including 20,367 with no official evaluation because of breed check edits. The new evaluations were for 1,822 Jersey x Holstein crossbreds with >40% of both breeds (F1 crosses), 7,237 Holstein backcrosses with >67% and <94% Holstein, 7,820 Jersey backcrosses, 388 Brown Swiss crosses, plus other mixtures. In the long term, selecting for rare favorable alleles within the same breed, introgressing new alleles from another breed, and gene editing or transgenic tools could help maintain or increase genetic variation. Many genomic tools are available to help breeders make progress and manage diversity in the current generation while preserving variation for future selection.

Abstract number: 27010 / accepted / order: 2 / pres.means: Theatre / time: 15

Genetic diversity of sires used in the Irish dairy industry

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Maintenance of genetic diversity in the Irish dairy industry is one of the driving motivations for having a nationally co-ordinated progeny test structure. This paper reports on analysis of co-ancestry and inbreeding trends between and among cohorts of bulls with progeny in Ireland over the past 15 years. The cohorts include bulls used widely and not included in the progeny test, bulls sourced from Ireland included in the progeny test, foreign sourced bulls included in the progeny test, and those foreign bulls not included in the progeny test. Average co-ancestry for these bulls with subsets of the cow population are also presented. The cow population is divided into those herds who have had a contract mating organised with an artificial insemination breeding company at least once in their history, versus those that have not.

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Pedigree inbreeding underestimate true inbreeding in genomic dairy cattle breeding schemes

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In this study, we compare the rate of true inbreeding (ΔF_{true}) and inbreeding calculated from pedigree (ΔF_{ped}) in different dairy cattle breeding schemes with different reference population structures. We hypothesize, that pedigree inbreeding underestimates the true inbreeding in a fully genomic breeding scheme. The reasoning is, that pedigree inbreeding assumes that all changes in allele frequencies is attributed to genetic drift, meaning all loci are expected to be neutral. This assumption is violated in all breeding schemes and in genomic breeding schemes in particular. To test our hypothesis, we evaluated true inbreeding across the genome using simulated populations and genome structures that mimic previously reported LD in dairy cattle. Two population-structures were considered; a high and a low LD (LDH and LDL). We simulated two daughter proven bull schemes (PB) mimicking

a small breeding program and a large breeding program with 5 and 20 yearly selected PB (PB-POPS and PB-POPL). For the LDH structure, a large and a small breeding program (LDH-POPL and LDH-POPS) were studied. For the POPL, a reference population was built, consisting of 10.000 PB. Each year, 2.000 genotyped cows and 100 genotyped PB were included in the reference population. For POPS, the reference population consisted of 1.000 PB and each year 2.000 genotyped cows and 50 genotyped PB were included. For the LDL structure, only POPL was analyzed. All breeding schemes were investigated over a timeframe of ten years. The average reliabilities of the genomic estimated breeding values for the three genomic schemes were 0.42 (LDH-POPL), 0.38 (LDL-POPL) and 0.34 (LDH-POPS). For the PB schemes (PB-POPS and PB-POPL), ΔF_{ped} was approximately 4% lower than ΔF_{true}. For the POPS-LDH scheme, ΔF_{ped} was 50% lower than ΔFtrue and for POPL-LDH, it was 56% lower. In POPL-LDL, which had more heterogeneity, ΔF_{ped} was estimated to be 37% lower. The result confirmed our hypothesis as we can conclude that ΔF_{ped} underestimates true inbreeding in a genomic breeding scheme where breeding candidates are selected on genomic estimated breeding values.

Abstract number: 26820 / accepted / order: 4 / pres.means: Theatre / time: 15

Genetic diversity measures of local European cattle breeds for conservation purposes

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The Slovak Pinzgau cattle faces the bottleneck effect and the loss of diversity due to unequal use of founders and significant population decline. Further population size reduction can lead to serious problems. High-throughput molecular information of 179 genotyped individuals was used to characterise genetic diversity and differentiation of Slovak Pinzgau, Austrian Pinzgau, Cika and Piedmontese cattle by Bayesian clustering algorithm. A gene flow network for the clusters estimated from admixture results was produced. The low estimate of genetic differentiation (F_{ST}) in Pinzgau cattle populations indicated that differentiation among these populations is low, particularly owing to a common historical origin and high gene flow. The changes in the log marginal likelihood indicated Austrian Pinzgau as the most similar breed to Slovak Pinzgau. All population except Piedmontese showed two ways of gene flow among populations which means that Piedmontese was involved in formation of analysed breeds while these breeds were not involved in creation of Piedmontese. Genetic evaluation represents an important tool in breeding and cattle selection. It is more strategically important than ever to preserve as much of the livestock diversity as possible, to ensure a prompt and proper response to the needs of future generations. The information provided by the fine-scale genetic characterization of this study clearly shows that there is a difference in genetic composition of Slovak and Austrian populations as well as Cika and Piedmontese. Despite economic pressures and intensive action of dairy breeds, due to Pinzgau population size, Slovakia has the potential to serve as a basic gene reserve with the European and World importance.

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Long-term impact of optimum contribution selection on breeds with historical introgression

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In the breeding schemes of small local breeds, two conflicts have to be addressed: the conflict between increasing genetic gain while managing the inbreeding level, and the conflict between maintaining genetic diversity while controlling the loss of genetic uniqueness. Advanced optimum contribution selection (OCS) approaches were compared for balancing these conflicting objectives via constraining migrant contributions (MCs) and kinships at native alleles in the offspring. The aim of the study was to evaluate the performance of different OCS strategies in subsequent simulated generations obtained from genomic data of Angler cattle, a local cattle breed in northern Germany. Genotypes were available for 131 bulls and 137 cows born between 1986 and 2014. A total of 23,448 SNPs were used in the analysis and were phased with Beagle. The R package optiSel was used to estimate foreign breed contributions and kinships from genotype data and to perform the optimization. A base population with a size of 1,000 animals (500 males and 500 females) was generated from the Angler genotypes. Pedigree and genotypes of each generation were simulated according to the optimum contributions of selection candidates in the previous generation. Three scenarios were compared with truncation selection. In all scenarios the aim was to maximize genetic gain, and segment based kinship was constrained to achieve an effective population size of 100. The first scenario was traditional OCS with only the constraint on segment based kinship. In the second scenario there was an additional constraint on segment based kinship at native alleles, and MCs were maintained at the current level. In the third scenario segment based kinship at native alleles was constrained as well, but MCs were reduced each generation. Results showed that traditional OCS procedure has slight advantages in increasing genetic gain whilst controlling relatedness compared to truncation selection. However, the introgression of foreign genetic material by traditional OCS is not desirable in the local breed conservation. In the long run, constraining MC and kinship at native alleles in the OCS procedure is a promising approach to increase genetic gain whilst maintaining genetic uniqueness and diversity.

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Using recombination to maintain genetic diversity

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The rate of genetic gain increased due to genomic selection. Consequently, inbreeding rate increased and a loss of genetic diversity might occur. Recombination breaks existing haplotypes and leads to new haplotypes, which is necessary to maintain genetic diversity. To investigate the nature of recombination, genotypes of over 200,000 German-Holstein were analyzed. The average global number of crossovers ranged from 23.3 in males to 24.3 in females. A univariate animal model was used to estimate variance components and breeding values for the number of global recombinations in males and females separately. The chiptype was modeled as a fixed effect. Heritability of the global number of recombinations was higher in females than in males. The 50k-based genome-wide association study showed previously reported additive QTL for genome-wide number of recombinations on chromosome 6 and 10 in males and on chromosome 1, 3, 6, 10 in females. We identified additional QTL on chromosome 3 for males and on chromosome 20 for females. Furthermore, we investigated dominance effects on the global number of recombinations and found significant effects for the mentioned QTL. Additionally, heritabilities and genetic correlations between chromosome-wise numbers of recombination were investigated, using a multivariate model for chromosomes 1 to 12. Different genetic correlation patterns between chromosomes were observed. For example, the number of recombinations on chromosomes 2 and 11 were genetically highly correlated with chromosomes 3 to 5. In contrast, chromosome 10 showed low genetic correlations to all other chromosomes except chromosome 8. The global number of recombinations dropped over the last decades in both sexes. This decrease accelerated with the implementation of genomic selection. To stop this loss of genetic variation, new approaches are needed, e.g., to the inclusion of the global number of recombinations in breeding schemes.

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Using genomics to manage progress and diversity: an industry perspective

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In the last decade, genomics has become the routine tool to breed AI-bulls. In most countries most dairy farmers now use genomic bulls ad no longer daughter proven bulls to breed the next generation. The advent of genomics coincides with a further professionalization of commercial breeding programs. Because we now have the better tools, it also pays off to make maximum use of it.Consequently, breeding programs not only make best use of genomic prediction, but also focus on reducing the generation interval and increasing the use of reproduction technology. In addition, one can see that breeding goals has become more alike across countries. The net effect of all these developments is a huge risk of inbreeding levels climbing faster and higher than ever before. The only way to mitigate this risk is by managing genetic diversity within breeding programs with the same rigour as we manage genetic progress. Genetic diversity management consists of the following elements: - Segmentation. Customers desire choice. Creating a segmented portfolio of bulls gives a geat opportunity to also create genetic diversity (when executed smartly) - Implementing genetic contribution theory - Limiting the use of individual animals - Sourcing of new animals for the breeding nucleus via extensive genomic screening - Strict monitoring Although both the genetic and inbreeding trend in the population are driven by what happens within the breeding programs of AI companies, the same companies can also help farmers to overcome the inbreeding challenge. First by offering a wide portfolio of bulls. Second by advocating mating programs that include (genomic) inbreeding management and account for inbreeding depression. Third by providing tools that allow farmers to assess the relatedness of potential bulls to the herd of a farmer during the semen purchasing process. Fourth by creating insights via monitoring tools.

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Biodiversity within and between European Red dairy breeds – conservation through utilization

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Red dairy breeds across Europe represent a unique source of genetic diversity and are partly organized in trans-national breeding programs but are also well adapted to local conditions. ReDiverse's objective is to develop and to set in place collaborative and integrated novel breeding and management concepts to achieve a resilient and competitive use of these resources and to strengthen best practices for small farm holders to improve product quality and to supply ecosystem services according to their specific circumstances. The challenge of establishing appropriate breeding and maintenance strategies for diverse farm systems and regional markets is met by multi-actor operations considering economic, structural and social diversity in participating countries to offer tailored solutions. The holistic approach relies on integrative research of scientists in the fields of animal genetics, proteomics, economy and social sciences. Cutting edge technology such as large scale genomic and proteomic tools will be implemented to enhance genetic progress and to characterize specific properties. Innovative survey approaches will assess the impact of the sector on social acceptance and the needs of farmers. The project will generate novel knowledge and concepts that will be timely disseminated to lead-users in the breeding and dairy industries, food sector, farmers' cooperatives and among farmers.

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The effect of using whole genome sequence instead of a lower density SNP chip on GWAS

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The interest in using whole genome sequence (WGS) data for genomic prediction is increasing with the increasing availability of WGS data. WGS data can be seen as the ultimate resolution for DNA genotyping, since it contains all variants, including the causal mutations underlying traits. Therefore, our assumption of using WGS data for Genome Wide Association Study (GWAS) was to find SNP closer to the QTLs, that explain a higher proportion of phenotypic variance and that will hold stronger across line. To investigate this assumption, GWAS was performed for the number of teats using 80K, and 660K SNP chip data, and imputed WGS data from 12184 Large White and 4993 Dutch Landrace pigs. A SNP was defined as significant if it had a –log10(P-value) > 5; and a QTL region was defined as a region of 1 MB around the most significant SNP. GWAS results were validated in an independent set of animals within and across line by estimating the phenotypic variance explained by the significant SNP. Results show that the number of QTL regions increased from low SNP density chips to WGS data. In addition to newly found QTL regions, some QTL regions were linked to known from previous studies QTL regions. Within line, we found that increasing the SNP density from 80K to 660K increased the proportion of phenotypic variance explained by the significant SNP. However, increasing the SNP density from 660K to WGS did not increase of the proportion of phenotypic variance explained. Across line, the proportion of phenotypic variance explained increased with increasing the SNP density, even from 660K to WGS. In conclusion, increasing the SNP density to WGS data increased the number of observed QTL and the proportion of phenotypic variance explained by the significant SNP across line, suggesting that the observed significant SNP were closer to the QTLs when using WGS.

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Genetic trends from single-step GBLUP and traditional BLUP for production traits in US Holstein

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The objective of this study was to compare genetic trends from a single-step genomic BLUP (ssGBLUP) and the traditional BLUP models for milk production traits in US Holstein. Phenotypes were 305-day milk, fat, and protein yield from 21,527,040 cows recorded between January, 1990 and August, 2015. The pedigree file included

29,651,623 animals limited to 3 generations back from recorded or genotyped animals. Genotypes for 764,029 animals were utilized, and analyzes were by a three-trait repeatability model as used in the US official genetic evaluation. Unknown parent groups were incorporated into the inverse of a relationship matrix (H^{-1} in ssGBLUP and A^{-1} in BLUP) with the QP-transformation. In ssGBLUP, 18,359 genotyped animals were randomly chosen as core animals to calculate the inverse of genomic relationship matrix with the APY algorithm. Computations with BLUP took 6.5 hours and 1.4 GB of memory, and computations with ssGBLUP took 13 hours and 115 GB of memory. For genotyped sires with at least 50 daughters, the trends for PTA and GPTA were similar up to 2008, with a higher trend for ssGBLUP later (approx. by 82 kg milk, 5 kg fat and 3 kg protein for bulls born in 2010). For genotyped cows, the trends were similar up to 2006, with a higher trend for ssGBLUP later (approx. by 245 kg milk, 10 kg fat and 7 kg protein for cows born in 2013). For all cows, the trends were slightly higher for ssGBLUP, with much smaller differences than for genotyped cows, and with a decline in 2013 for milk and protein. Trends for BLUP indicate bias due to genomic preselection for genotyped sires and cows. ssGBLUP seems to at least partially account for that bias and is computationally suitable for national evaluations.

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Development of genomic selection in dairy cattle in two emerging countries: South Africa and India

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In large developed countries, genomic selection has radically transformed dairy cattle breeding, with collateral impact on the international semen market. Emerging countries are often strong semen importers. Few of them are Interbull members. However, if they are a member, MACE evaluations of progeny tested bulls give them access to EBV on their own scale. At least in theory, this allows for a rational choice of semen to import. This is no longer the case with genomic evaluations, for which the constitution of a proper reference population is complex. As a consequence, the gap between countries with expertise in genomic selection and the others is widening fast. However, genomic selection also offers new opportunities in emerging countries, because it does not require sophisticated national performance recording systems and it more easily leads to selection adapted to local environments. The project “GENOSOUTH2” of the INRA SELGEN metaprogramme aims at promoting the local implementation of genomic selection of dairy cattle, with 2 countries as case study: in South Africa, the objective is to develop a prototype for national genomic evaluation in Holstein cattle, exploiting the participation of the country to Interbull MACE evaluations, in order to enlarge the reference population while accommodating two very contrasted feeding systems. In India, BAIF, the largest Indian NGO in agriculture, is developing a female reference population of crossbred Bos taurus x Bos Indicus animals, facing a number of challenges such as very small average herd sizes, scarce identification and limited performance recording. We will describe the motivations, the current constraints and the expected benefits of these two initiatives. Local genomic evaluations are fundamental for sustainable genetic progress of dairy cattle in harsh environments.

Abstract number: 26096 / accepted / order: 12 / pres.means: Poster

GENETIC DIVERSITY OF THE MEXICAN AND SPANISH LIDIA POPULATIONS BY USING A SUBSET OF NON-LINKED SNPs

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Retaining features of the auroch (Bos taurus primigenius), the Lidia bovine is a primitive breed that has its origin ~250 years ago in the Iberian Peninsula, where is still distributed along with France and several American countries. Selected upon a behavior that enhances their aggressiveness, these bovines were raised to take part in popular festivities that nowadays reinforce the identity of regional cultures. Different festivities demanded diverse behavior patterns, prompting a fragmentation of the breed into small lineages. In Mexico, mainly two families of breeders imported Lidia bovines from Spain in the early XXth century specializing their production either reproducing the new arrivals among them or realizing systematic crosses with local populations. Genetic diversity and structure of the Mexican and Spanish Lidia populations has been assessed with microsatellite data, but nowadays SNP molecular markers allows higher resolution level. Genetic diversity of the Mexican and Spanish Lidia populations and their relationship were assessed by using the 50K BeadChip on 468 individuals, who were genotyped, and after applying strict filtering criteria, 573 non-linked SNPs were selected. In both populations Similar gene diversity values were observed: remarkable for the Mexican population. Significant FIS values mean a strong subdivision within and higher F_{ST} genetic distances were observed in the Spanish than in the Mexican population. Genetic structure analysis showed similarity of three Spanish lineages with González family and some Llaguno breeders, but most Llaguno family clustered separated: genetic differentiation along with high gene diversity suggest an introgression of creole cattle in the constitution of the Mexican population.

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Inbreeding trend and pedigree evaluation in Polish Holstein-Friesian cattle

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The aim of this study was to evaluate observed and future inbreeding level in Polish Holstein-Friesian cattle population. In total over 9.8 mln animals were used in the analysis coming from the pedigree of Polish Federation of Cattle Breeders and Dairy Farmers. Inbreeding level, as an average per birth year, was estimated with the method accounting for missing parents information with the assumption of year 1950 as the base year. If an animal had no ancestral records, an average inbreeding level from its birth year was assigned. The future inbreeding was estimated as an average inbreeding of possible offspring of bulls and cows available for mating in a certain year. It was observed that 30-50% of animals born between 1985 and 2015 had no relevant ancestral information, which was caused by a high number of new farms entering the national milk recordings. For the last 20 years the observed inbreeding has been clearly higher than future inbreeding. In year 2015 the observed inbreeding level was 3.30%, while future inbreeding was 2.89%. The average increase of inbreeding in years 2001-2015 was 0.10%, which was similar to other countries monitored by World Holstein Friesian Federation. The estimates of future inbreeding suggested that observed inbreeding could be even lower than currently observed. This may be achieved with computerized assisted matings, however, still deep pedigrees are essential. Thus, the importance of keeping pedigree entries complete should be highlight. The obtained inbreeding levels indicated that population of Holstein-Friesian in Poland has one of the lowest values in the world and that its increase over the past decades remained on a safe level similar to other countries.

Abstract number: 26668 / accepted / order: 14 / pres.means: Poster

Genotyping females improves genomic breeding values for new traits

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Genotyping females is considered to provide gains in reliabilities of estimated breeding values of young selection candidates for new traits for which there is no reference set yet. By the use of a simulation we investigated two different strategies to establish a reference set for so called new traits where performance recording has begun only recently and phenotypes of daughters were available for one or two generations of bulls only. In design ‘NTsires’ cows are phenotyped but only their sires are genotyped and used in the reference set. In design ‘NTcows’ genotypes of phenotyped cows are available and cows are used directly as the reference set. Simulated heritability of the trait was 0.05. We studied the effects on validation reliabilities and unbiasedness of predicted values for selection candidates. We additionally illustrate and discuss the effects of a selected daughter sample and an unbalanced sampling of daughters. If the number of phenotypes is limited, as it is in the case of a new trait, it is always better to collect and use genotypes and phenotypes on the same animals instead of aggregating phenotypes of daughters and using them by relating them to their sires’ genotypes. We found that the benefits that can be achieved are also sensitive to the sampling strategy used when selecting females for genotyping.

Abstract number: 26716 / accepted / order: 15 / pres.means: Poster

Genetic patterns predicting fertility in Estonian dairy cattle

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Aim of the study was to assess the genetic variability in connection with fertility of Estonian Holstein cows. Firstly, 2619 cows with estimated production and fertility breeding values (EBV) were randomly selected from Estonian Livestock Performance Recording Ltd database and their genotypes in genes relevant to production and fertility (ABCG2, DGAT1, CSN gene cluster, CYP11B1, LEP, LGB and SPP1) were determined. Secondly, ~5% of cows with the most extreme fertility EBV were selected from the both sides of fertility EBV distribution, resulting in 141

cows with low fertility EBV (average 81.6 points) and 147 cows with high fertility EBV (average 122.4 points). These 288 cows were genotyped using the BovineLD SNP chip (Illumina, Inc.). The analysis of variance revealed strong statistically significant effects of DGAT1, CSN2, CSN3 and CSN1S2 on fertility. Also, DGAT1 and LGB were statistically significantly related to milk fat content EBV, and DGAT1 and CSN2 to milk protein content EBV (for all listed relationships $p<10^{-5}$). The Fisher exact test revealed more than 10% of the chip SNPs across the whole genome associating with fertility ($p<10^{-5}$) in Estonian Holstein. The genome regions with the highest proportion of significant SNPs were found at chromosomes X and 7. The strongest relationships between SNP and fertility ($p<10^{-15}$) were discovered in BTA 6, 8, 9, 10, 17, 24, 29 and in X chromosome. From the adjacent SNPs of the previously studied genes only one marker in casein gene region was highly significantly ($p<10^{-5}$) related with the fertility EBV groups. We also detected heterozygosity excess in the group of cows with low fertility that potentially could indicate the deleterious polymorphisms causing decreased fertility. Finally, the assignment test performed chromosome-wise indicated clear patterns in SNPs distinguishing the fertility groups. Estonian Ministry of Education and Research (grants IUT8-1, IUT8-2) and Bio-Competence Centre of Healthy Dairy Products LLC (project EU48686).

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Linkage disequilibrium and imputation power in Gyr beef cattle

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The aim of this study was to evaluate imputation accuracy and to estimate linkage disequilibrium (LD) at 25-50kb, 50-100kb and 100-500kb distances in a Gyr small closed population selected for post weaning weight. Genotypes of 155 and 18 animals were obtained through Illumina Bovine LDv4 (33K) and BovineHD BeadChip panels, respectively. Missing genotypes were imputed using FImpute software considering HD panel as reference. After imputation step, quality control was performed for minor allele frequency (MAF) less than 0.02 and call rate less than 0.10, remaining 173 animals and 418.086 SNPs for LD analyzes. Accuracy of imputation was evaluated by three methodology: a) concordance rate (CR), b) imputation quality score (IQS) and c) simple correlation (ρ). The LD correlation coefficient (r^2) was obtained by Plink and RStudio software. Values of 96%, 97% and 97% were obtained for CR, IQS and ρ, respectively, showing high imputation quality. FImpute was appropriated for low MAF SNPs imputation. The r^2 at 25-50kb, 50-100kb and 100-500kb distances were 0.35, 0.29 and 0.18, respectively. LD persistence was observed at distances up to 100kb, decreasing as the distance length increases. The r^2 values were higher than those described in the literature for zebu cattle, showing that the animals shared long segments of haplotypes in this closed herd.

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Optimum Genetic Contribution in the Swiss Original Braunvieh cattle population

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The Original Braunvieh (OB) cattle population is a local breed with about 10,000 cows in the herd-book. The breed is well-known for its dual-purpose characteristics and is characterized by a high proportion of matings through natural service (around 50%). Genomic breeding values are available since 2014. In a retrospective study we investigated the use of optimum genetic contributions (OGC) in OB using the conventional total merit index, milk index and pedigree-information for breeding animals having offspring born in 2014. We compared the realized genetic parameters (selection response and average inbreeding coefficients) with the results from optimized matings that would have resulted by following recommendations of EVA software. Computing capacity was a limiting factor if all cows were to be considered in the analysis. Based on our data a weight of 1 on merit combined with weights ranging from 200-400 on relationship lead to an improvement of the actual selection scheme. The results support, that selection response and average inbreeding coefficients could have been optimized by using EVA. For practical breeding programs the application of OGC on the two paths sires to breed bulls and dams to breed bulls seems promising.

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First genetic analysis of four Algerian cattle populations from dense SNP data

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This work is realized in the framework of biodiversity of animal genetic resources in general and cattle in particular. In Algeria, we were interested in the constitution of a first unrelated DNA library (121) of four (04) local cattle populations: Cheurfa, Guelmoise, "Chélifienne" and Biskra. We genotyped these individuals DNA using the Illumina Bovine SNP50. A statistical analysis of these four bovine populations was carried out using Principal Component Analysis (PCA) based on all molecular data of SNPs genotyped using software R. However, in order to better clarify the respective roles of geographic isolation, gene flow and the historical origin of the populations studied, a comparison with a larger set of 19 breeds corresponding to African, European taurines and zebu was needed. The results of the ACP show a clear distribution of the four Algerian bovine populations as a representation of triangular gradient with peaks corresponding to African taurines, European taurines and zebu breeds. We also detected the influence of zebu breeds in Cheurfa and Guelmoise populations. Moreover, our results were consistent with previous historical and archaeological reports on the gene flow that existed between North Africa and South European breeds. The aims of for this work would be, in the medium term, to safeguard biodiversity by setting up a strategy for the conservation and preservation of our bovine genetic resources and, in the long term, a possible selection for an improvement of this species for economic purposes. Keywords : ACP.- Algerian cattle - Biodiversity - DNA- SNP data.