BREEDING AND GENETICS: APPLICATIONS AND METHODS IN ANIMAL BREEDING—LIVESTOCK II

0170 Genetic gain and economic weights in selection for boar fertility traits in a cross-breeding system. D. Gonzalez-Peña Fundora[*1], R. V. Knox[1], J. Pettigrew[1], M. D. MacNeil[2], and S. L. Rodriguez Zas[1], *[2]University of Illinois, Urbana, [2]Delta G, Miles City, MT.*

Four boar fertility traits: semen volume (VOL, mL), semen concentration (CON, x10^3/mm^3), progressive motion of spermatozoa (MOT, %), and abnormal spermatozoa (ABN, %) provide complementary information about boar fertility. It is now feasible to include these traits in genetic improvement programs. However, there is limited information on the genetic and economic parameters necessary to assess the impact of selection for these traits. Objectives of this study were to estimate economic weights for these traits and to evaluate genetic gain that results from including them in a three-tier, three-way crossbreeding scheme (maternal nucleus lines A and B and paternal nucleus line C). Three cases were simulated in ZPLAN. Case I (baseline case) encompassed genetic selection for number of pigs born alive (NBA), litter birth weight (LBW), adjusted 21-d litter weight (A21), number at 21 d (N21), days to 113.5 kg (D113), backfat (BF), average daily gain (ADG), feed efficiency (FE), and lean carcass % (LEAN). Case II included Case I and a novel fertility indicator called DOSES that combines the four boar fertility traits (VOL * CON/1000) * (MOT/100 * (1 − (ABN/100))/(number of spermatozoa per dose). Case III included Case I and the four boar fertility traits individually. Estimated economic weights represent the net economic gain per unit of genetic improvement in VOL, CON, MOT, ABN, and DOSES ranged from 0.21 to 1.44 $/ml, 0.12 to 0.83 $/x$10^3$/$mm^3$, 0.61 to 12.66 $/%, -0.53 to -10.88 $/%, and 2.01 to 41.43%/dose as number of semen collections per week was reduced from 7 to 1. Average genetic gains remained stable for the maternal traits (NBA, LBW, A21, N21) in Case II and III, relative to Case I. Genetic gains in Cases II and III relative to Case I dropped by 59.2% and 25.8% (BF), 50% and 50% (FE), and 84.4% and 59.4% (LEAN), respectively. The relative economic weights decreased in Case II and III relative to I by 21% and 15% (line A), 18% and 12% (line B) and 32% and 23% (line C), respectively. Selection including the four boar fertility traits separately (Case III) was preferable to using one combined indicator (Case II) by enabling genetic gains in these traits without compromising the genetic gains in the maternal traits.

Key Words: boar fertility traits, economic weights, three-way crossbreeding scheme

0171 A genome-wide association study for egg shell strength in the genome of brown-egg layers. R. A. Ghebrewold[*1,2], M. Heidaritabar[1], A. Vereijken[3], B. J. Ducro[4], and J. W. M. Bastiaansen[4], *[1]Wageningen University, Wageningen, Netherlands, [2]Norwegian University of Life Sciences, Ås, Norway, [3]Hendrix Genetics, Boxmeer, Netherlands, [4]Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands.*

Egg shell quality is important for commercial egg production. The objective of this study was to identify single nucleotide polymorphisms (SNPs) that are significantly associated with egg shell strength using either own phenotype or deregressed estimated breeding values (DEBV) in brown-egg laying chickens. In this study egg shell strength data were available for 8113 purebred line chickens, of which 2220 had 60k SNP genotype data. Genetic background of shell strength was confirmed by a heritability estimate of 0.29 (SE = 0.03) from this data. The number of chickens with both genotypes and phenotype was 650. Three genome wide association analyses (GWAS) were performed. Single SNP regression (SSR) was used to estimate the SNP effects. The first GWAS analysis was performed on 650 chickens and the model for SSR used own phenotype as the response variable and identified no significant associations (FDR $\leq$ 0.05). To increase the statistical power, DEBV, with their weights, were used as the response variable for two additional association analyses. Chickens with reliabilities of DEBV less than 0.05 were removed from the data set, resulting in 1429 chickens and 36,103 SNPs. In the second GWAS study, we found two significant SNP (FDR $\leq$ 0.05) associated with egg shell strength on GGA1 and GGA2. The third GWAS analysis was performed with a more stringent data filtering, only chickens with reliabilities of DEBV greater than 0.08 were kept (N = 1147). With the more stringent filtering, no significant SNP associations were found (FDR $\leq$ 0.05). Less stringent data filtering can lead to more significant results, probably due to higher power from including more animals, but could also indicate false positive results from including unreliable data points. In addition, GWAS analysis with DEBV as phenotypes may not be a simple solution that works well in any species. The utility of DEBV for GWAS in chickens may be smaller because more information comes from half and full sib families in comparison to for instance cattle.

Key Words: egg shell strength, GWAS, deregression

0172 The identification of a putative mutation for SLICK hair coat in Senepol cattle.

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The slick hair coat (SLICK) is a dominantly inherited trait typically associated with tropically adapted, Criollo-derived cattle breeds. The trait is of interest relative to climate change, due to its association with improved thermo-tolerance and subsequent increased productivity. The goal of this work was to identify the mutation underlying the *SLICK* locus, which was previously mapped to a 4 cM region on chromosome (Chr) 20. To refine this map position, BovineHD genotypes were generated from a sampling (N = 195 animals) of Senepol, Carora, Romosinuano, three additional slick-haired cross-bred lineages and a group of non-slick ancestral breeds. Genome-wide association analysis narrowed the SLICK locus to a 0.8Mb (37.7-38.5 Mbp UMD 3.1) consensus region, which contains *SKP2* and *SPEF2* as possible candidate genes. Three specific haplotype patterns were identified in slick individuals, all with zero frequency in non-slick individuals. In an attempt to identify candidate causative mutations in this region, whole genome re-sequencing was completed for one Romosinuano and five Senepol animals. SNP discovery and annotation analyses revealed a putative causative polymorphism within *prolactin receptor* (*PRLR*), which would truncate an encoded domain involved in JAK/STAT5 signaling. Validation testing of this SNP and 37 others was done across a DNA panel (N = 466) that included representation from five SLICK and seven non-SLICK breeds. The results strongly suggest the frameshift mutation in *PRLR* is the causative mutation underlying SLICK in Senepol and some Romosinuano cattle. However, no associations between this SNP and SLICK animals from Limonero and Carora breeds were found. This information along with accompanying population structure information supports potentially two independent SLICK mutations, one common to Senepol and Romosinuano and another in Limonero and Carora.

Key Words: slick hair coat, cattle, prolactin receptor

0173 Genomic selection of Nili-Ravi buffalo.

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Among three well-documented breeds of buffalo dairy breeds in Pakistan, Nili-Ravi is the best milk producer owing to its characteristic of disease and parasitic resistance, and a better convertor of roughages into useful products than cattle. A selection program to enhance the genetic potential for milk production of Nili-Ravi using progeny testing program is going on. Traditional progeny testing program has made a remarkable improvement in the genetic potential of dairy cattle in the developed world. However, this program faces severe implementation issues in buffalo improvement due to limitation of resources and basic infrastructure. Simulated studies have shown the potential of genomic selection in shortening generation interval and increasing the accuracy of selection (especially young bulls) that can bring a relatively rapid genetic improvement. The current study intends to explore the application of genomic selection in a typical buffalo breeding perspective using Nili-Ravi in Pakistan as an example. The assumed size of the training population for genomic selection was 15,860 present with BRI, Pattoki. Our calculations indicated that genomic selection can reduce the generation intervals in the male to male selection pathway from 9.5 yr down to 3.3 yr. It can result in almost 2 times increase in response to selection compared to that in a progeny testing program. Furthermore, it reduced the costs of proving bulls by 88%. The present study suggests the initiation of the program of genomic selection for Nili-Ravi in Pakistan and may serve as an example for other developing countries. The findings of the current study may encourage researchers and policymakers to use genomic selection for improvement in the productivity of dairy cattle of developing countries.

Key Words: developing country, genomic selection, Nili-Ravi buffalo