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Recent developments in cattle, pig, sheep and horse breeding - a review

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Abstract

The aim of this review was to summarize new genetic approaches and techniques in the breeding of cattle, pigs, sheep and horses. Often production and reproductive traits are treated separately in genetic evaluations, but advantages may accrue to their joint evaluation. A good example is the system in pig breeding. Simplified breeding objectives are generally no longer appropriate and consequently becoming increasingly complex. The goal of selection for improved animal performance is to increase the profit of the production system; therefore, economic selection indices are now used in most livestock breeding programmes. Recent developments in dairy cattle breeding have focused on the incorporation of molecular information into genetic evaluations and on increasing the importance of longevity and health in breeding objectives to maximize the change in profit. For a genetic evaluation of meat yield (beef, pig, sheep), several types of information can be used, including data from performance test stations, records from progeny tests and measurements taken at slaughter. The standard genetic evaluation method of evaluation of growth or milk production has been the multi-trait animal model, but a test-day model with random regression is becoming the new standard, in sheep as well. Reviews of molecular genetics and pedigree analyses for performance traits in horses are described. Genome – wide selection is becoming a world standard for dairy cattle, and for other farm animals it is under development.

Genetic indices, farm animal, molecular genetics, genomic selection

Populations of farm animals are undergoing continuous selection in an attempt to improve economic efficiency of animal production. Established procedures are being refined as new techniques are developed and implemented. The aim of this review was to summarize new genetic approaches and techniques in the breeding of cattle, sheep, pigs, and horses.

Cattle

The most dramatic recent developments in dairy cattle breeding are the incorporation of molecular information into genetic evaluations for individual production traits and the revision of breeding objectives to increased emphasis placed on longevity and health.

Incorporation of genetic markers into genetic evaluation is beneficial especially in evaluations of young animals lacking individual or progeny performance information. Initially, several markers within, or in linkage disequilibrium, with QTLs (quantitative trait loci) identified by haplotype or single marker association mapping were utilized (Grapes et al. 2006; Liu et al. 2008; Boleckova et al. 2012a).

Investigations reporting QTLs for milk production traits include those of Khatkar et al. (2004), who found important QTLs for milk yield on chromosomes 6, 14 and 20, and Boichard et al. (2003) who found genome wide important QTLs affecting milk yield on chromosome 14. These associations were subsequently confirmed by Mai et al. (2010). Matejickova et al. (2013) confirmed the importance of QTLs on chromosome 6 and 14 (including aQTL at position 0 cM on chromosome 14 affecting milk protein percentage) and authors also found addition significant QTLs affecting milk production traits on chromosomes 7, 11, 23. Grisart et al. (2004) identified gene DGAT1 on chromosome 14,

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and Rychtarova et al. (2014) identified genes BTN1A1, ORL1 and STAT1, all of which influenced milk production traits while DGAT1 and BTN1A1 affected reproductive traits as well. Boleckova et al. (2012b) reported that the PRL gene influenced milk production traits, while Signorelli et al. (2009) identified the GHR gene on chromosome 20 as a QTL for milk production traits.

The most frequently used SNP (single nucleotide polymorphism) chip for bull genotyping is the Illumina BovineSNP50 v2 BeadChip which includes 54,609 SNPs. The Illumina Bovine3K BeadChip, including 2,900 SNPs, is usable especially for female genotyping. Wiggans et al. (2012) reported that GEBV prediction reliability for bulls genotyped by the 50K chip to be 0.04-0.06 higher than reliabilities for those same bulls genotyped by the 3Kchip. For combination of information from both chips, imputation can be used. Szyda et al. (2013) investigated the possibility of reducing the number of assessed markers on accuracy and found that using only those 3,000 SNPs with the highest relationship to estimated milk production allowed reasonably good prediction of GEBV.

Several methods have been developed to incorporate information from SNP chips into prediction of genomic breeding value (GEBV) (Meuwissen et al. 2001). Methods include multistep procedures LS, BayesA, BayesB, RR-BLUP (Meuwissen et al. 2001), B-LASSO (Park and Casella 2008) and GBLUP (VanRaden 2008), as well as the single-step procedure ssGBLUP (Misztal et al. 2009; Aguilar et al. 2010; Christensen and Lund 2010; Pribyl et al. 2012). The main advantage of incorporation of information from SNP chips into breeding value prediction is to increase reliability of prediction. Hayes et al. (2009) reported reliabilities of young bull GEBV prediction up to 0.67, depending *inter alia* on the heritability of the production trait. VanRaden et al. (2009) stated that reliabilities of GEBV predictions were on average 0.23 higher than reliabilities of pedigree based breeding value predictions. Thus, the use of genomic breeding values in comparison to conventional breeding values is expected to lead to a more rapid response to selection and more profitable breeding programmes (Schaeffer 2006; König et al. 2009; Pryce et al. 2010), thanks to higher reliability of GEBV prediction (Hayes et al. 2009) and shorter generation intervals. A disadvantage of multistep methods is the risk of bias in international evaluation, thanks to strong pre-selection in national breeding programs. Such bias could be transferred into international evaluation. Bias could be avoided in single step breeding value prediction in which genotyped and non-genotyped animals are included (Patry et al. 2013).

The best procedure appears to be ssGBLUP, because this method increases reliability of breeding value prediction for genotyped and non-genotyped animals as well (Christensen and Lund 2010). Dependent variables in ssGBLUP are phenotypic records. Pribyl et al. (2013) used, instead of phenotypic records, deregressed proofs (DRP) of bulls not having performance recorded daughters. They reported an increase of GEBV prediction reliabilities ranging from 0.53 vs. 0.63 for predictions without vs. with the incorporation of DRPs. Incorporation of bull DRPs is beneficial especially in small populations. National GEBV prediction procedures should undergo validation by comparing prediction of young bull GEBVs with EBVs of those same bulls after progeny testing and when DYD yields are used as the dependent variable. Validated reliability reflecting correlation of prediction to DYD in domestic conditions may then be calculated (Mäntysaari et al. 2010). For international evaluation, Sullivan and VanRaden (2009) developed the genomic multiple across country evaluation (GMACE) procedure.

Changes in the breeding objectives in recent years have focused especially on the incorporation of and increasing emphasis on functional traits such as reproductive and health traits, linear type traits, and longevity. These traits have an important impact on profitability of milk production and herd replacement. Wolfova et al. (2007) reported that longevity has a particularly strong economic impact. Zavadilova et al. (2009) reported heritabilities of 0.05 and 0.04 for actual and functional longevity in the Czech Fleckvieh. Tsuruta et al. (2005) reported heritabilities ranging from 0.08–0.1 in US Holsteins, similar to estimates of 0.08 and 0.11 reported by Meszaros et al. (2013) in the Pinzgau cattle. In the Czech Holsteins, heritability of functional longevity was 0.025 on a log scale and 0.041 on the trait as originally recorded (Pachova et al. 2005). Longevity is often reported to be associated with age at first calving (Ducrocq 2005; M'hamdi et al. 2010; Zavadilova and Stipkova 2013), udder linear traits (especially udder attachment, udder depth, teats) and angularity and body condition score (Sölkner and Petschina 1999; Strapak et al. 2005; Zavadilova et al. 2011a). Zavadilova and Stipkova (2012) reported higher correlations of longevity with functional rather than with actual longevity. It should be noted that linear scoring, especially in case of udder traits, can be influenced by the time of scoring (Kasap et al. 2014).

The most common reasons for cow culling are problems with reproduction and udder diseases. Days open and the interval from parturition to first service are the traits most often used as selection criteria, with heritabilities ranging from 0.02 to 0.1 (Wall et al. 2003; Andersen-Ranberg et al. 2005; Jamrozik et al. 2005; Sun et al. 2009; Zink et al. 2012; Zavadilova and Zink 2013).

Selection to improve udder health can be implemented through indirect selection for somatic cell count (SCC), somatic cell score (SCS) and linear scores for udder size and morphology. These traits have low to intermediate heritabilities (Nemcova et al. 2011). Direct selection on udder health is generally not possible because of the lack of recorded data (Zavadilova et al. 2011b). Nemcova et al. (2007) investigated the importance of linear udder traits and concluded that high SCS scores in cows were associated with deep udders, weak central ligaments and poor fore udder attachment.

For genetic evaluation of meat yield, several information sources can be used, including data from performance test stations, records from progeny tests (station or field) and measurements taken at slaughter. The most commonly used analytical method for evaluation is the multi-trait animal model, the traits being net gain (calculated as carcass weight divided by age), "SEUROP" carcass conformation score (grades S to P according to muscularity), fatness classes (1 - lean, 5 - very fat) and meat percentage (Schild et al. 2003).

Nesetrilova (2005) described the growth curve for the Czech Fleckvieh cattle up to 1,400 days of age using a multiphase growth model. Vesela et al. (2011) estimated the genetic indices of beef cattle production traits in the SEUROP system. Vostry et al. (2012a, 2014) described growth evaluation of beef bulls in performance testing stations. Svitakova et al. (2014) examined alternative measures of growth potential of bulls in testing stations, whether genetic index estimates of such traits changed over time and whether existing methods for performance testing were appropriate.

Bogdanovic et al. (2002) evaluated performance tests for Simmental bulls and found that selection based on an individual performance test was appropriate for traits of medium (e. g. growth) to higher heritability. In their study, daily gain during different time periods (before the test, during the test and over the lifetime) and weight (at the beginning of the test, monthly during the test and at the end of the test) was evaluated.

Duchacek et al. (2011) reported that the average breeding value of an Angus cattle population changed over the course of time, presumably reflecting a genetic change resulting from a cumulative response to selection.

The thoroughly researched multi-trait method of genetic analysis is common practice for evaluation of growth. The random regression test-day model (RR-TDM) method, however, has been more narrowly analysed (Albuquerque and Meyer 2001; Nobre et al. 2003a, b; Meyer 2005). Krejcova et al. (2007) compared these two models using data from performance test stations on breeding bulls and concluded that the more appropriate method of evaluation was RR-TDM. For using this method of calculation it is necessary to weigh bulls at regular and relatively frequent intervals (Pribyl et al. 2008). Genetic indices for beef production are often estimated only for beef cattle (Arango et al. 2002; Baldi et al. 2012).

Pigs

In genetic evaluation of pigs, production and reproductive traits are generally conducted separately. There are some arguments for simultaneous analysis of both groups of traits. Through additional information from genetic correlations between production and reproductive traits, the accuracy of genetic evaluation could be increased, even though heritabilities of reproductive traits are generally low. Furthermore, no single trait value, but the whole animal is selected and then joint evaluation of traits is natural way. Furthermore, breeding values for all traits would be predicted for all animals. The linear combination of these traits with economic weights would result in aggregate genotypic values that could be directly used for selection (Krupa and Wolf 2013). On the other hand, (Hermesch et al. 2000; Chen et al. 2003; Holm et al. 2004) have reported low (and antagonistic) genetic correlations between production and reproductive traits. This is in agreement with Arango et al. (2005) and Kapell et al. (2009), who reported relatively high antagonistic correlations. A general problem in comparing studies of growth traits of pigs is the substantial diversity in definition of growth traits. Estany et al. (2002a, b) reported that reproductive, production, and quality traits in pigs are probably not genetically independent.

The effect of service sire was analysed in some studies of reproductive traits. Wolf and Wolfova (2012a) examined the impact of including a service sire effect on litter size traits for Czech Large White and Czech Landrace sows. Three different animal models were evaluated for each litter size trait (total number of piglets born, born alive and weaned): (i) the service sire effect was included and the complete relationship matrix for all the animals (service sires and sows) was taken into account; (ii) the service sire effect was included as a random effect without inclusion of the relationship matrix; (iii) the service sire effect was omitted from the model. Using the residual variance as a criterion, both models including the service sire effect were slightly better than the model without this effect. Estimates of genetic indices were very similar for the two models including the service sire effect. The proportion of variance for service sire was in the range from 2 to 3% (standard error approx. 0.2%) in the Czech Large White and 2% (standard error approx. 0.3%) in the Czech Landrace for all three litter size traits and all models. In results of other authors, proportion of variance in the number of piglets born attributable to service sires varied from 0.00 to 0.05 for models including the relationship matrix and from 0.00 to 0.03 for models without the relationship matrix (Serenius et al. 2003; Su et al. 2007; Köck et al. 2009).

A different approach to genetic evaluation of reproductive traits of pigs is to analyse alternative traits such as piglet losses. Wolf and Wolfova (2012b) studied the effect of service sire on the number of stillborn piglets and the number of piglets that died till weaning. Animal models with versus without a service sire effect were compared. Estimates of genetic indices were very similar for the two models. The heritability for the number of stillborn piglets was 0.06 for both breeds and both models, and the heritability for the number of piglets that died till weaning was 0.07 in the Czech Large White and 0.05 to 0.06 in the Czech Landrace. The proportion of variance due to the service sire was very low (between 0.8 and 1.6%). Similar low heritabilities have been reported by other authors (Serenius et al. 2003; Su et al. 2007; Kapell et al. 2009; Chen et al. 2010). A general question is whether selection against piglet losses may be effective. Farrowing losses are probably caused mainly by biological factors, and the estimated heritability is very low. Furthermore, the number of stillborn piglets may be connected with the heterogeneity (within-litter standard deviation or variance) of individual piglet weight at birth. There are indications that a higher heterogeneity may be associated with a higher number of stillborn piglets (Huby et al. 2003; Wolf et al. 2008).

Nagyne-Kiszlinger et al. (2013) analysed the following reproductive traits: number of piglets born alive (NBA), gestation length (GL), farrowing interval (FI) and age at first insemination (AFI) for two purebred and two reciprocal crossbred populations using a two-trait model with repeatability, and with a two-trait model for age at first insemination. The heritabilities were 0.06 for all four populations, 0.06–0.09 and 0.22–0.3 for FI, NBA and GL, respectively. There were large differences between heritabilities of AFI in purebred (0.28, 0.26) and crossbred (0.41, 0.40) populations. Dube et al. (2012) reported a heritability of 0.07 for NBA from a repeatability animal model.

Comparisons of different genetic index estimation methods for litter size are described by Skorput et al. (2014). The objective of that study was to estimate genetic indices for litter size of the Black Slavonian pigs using the repeatability, multiple trait, and random regression models. Estimated heritabilities were in the range from 0.03 to 0.26. Kapell et al. (2011) used a Bayesian analysis for reproductive traits.

Wittenbourg et al. (2011) studied within litter variability of piglet birth weight and its relationship to piglet survival. The within sex sample variance of birth weights per litter was designated as a trait of the sow. Estimates of heritability for the different measures ranged from 11 to 12%. Douglas et al. (2013) confirmed that the effect of low piglet birth weight was associated with poor growth performance in pigs from birth to slaughter.

Dall'Olio et al. (2013) studied the association between single nucleotide polymorphisms in candidate genes and reproductive traits in the Italian Large White sows. Association analyses were performed with the following traits: number of piglets born alive (NBA), number of stillborn piglets (NSB1), total number born (TNB1), NBAI estimated breeding values (EBVs) and NBA random residuals (RRs). SNPs in BMPR1B, FUT1, GPX5, RBP4, and TGFBR1 genes were identified. Mucha et al. (2013) reported associations between mutations in the EGF, AREG and LIF genes and NBA, the number of piglets alive at 21 days of age, the age of sows at first farrowing, and the interval between successive litters.

Sheep

Growth performance can be recorded under farm conditions (Wolc et al. 2011; Zishiri et al. 2014) or in test stations (Gorjanc et al. 2009a; Gamasaee et al. 2010), on live animals (Mandal et al. 2012; Zishiri et al. 2014) or on carcasses (Mortimer et al. 2014). Modern technologies such as ultrasound, computer tomography scanning (Milerski 2001; Junkuszew and Ringdorfer 2005; Maxa et al. 2007; Maximini et al. 2012) and video image analysis (Rius-Vilarrasa et al. 2009) can be used to assess body composition and carcass merit.

Variance components and genetic indices for measurements of body weight or growth can be estimated using single or multi-trait animal models (Gorjanc et al. 2009a; Mandal et al. 2012) or random regression models, if consecutive measurements are available (Kariuki et al. 2010; Wolc et al. 2011). Wolc et al. (2011) reported that direct heritability of growth traits tended to increase with advancing age, whereas the maternal genetic effect was reduced at older ages. The proportion of variance for permanent environmental effects was relatively stable across time. Eye muscle depth (m. longissimus dorsi) and back fat depth are recorded primarily in meat sheep (Maxa et al. 2007; Maximini et al. 2012).

Meat quality traits (meat tenderness, meat colour, polyunsaturated fat content, mineral content and muscle oxidative capacity) were found to be generally of moderate heritability by Mortimer et al. (2014). Exceptions were intramuscular fat (0.48), ultimate pH (0.08) and fresh meat colour (0.08–0.10). Jandasek et al. (2014) observed differences in physico-chemical and sensory characteristics of lamb meat between sire breeds. Several measures of meat quality appear to have the potential for inclusion into breeding objectives for meat breeds of sheep.

Greasy fleece weight, clean fleece weight, staple length, staple strength and fibre diameter at first or later shearing are traits found to be moderately heritable in Merino (Ciappesoni et al. 2013; Di et al. 2014) and Romney (Wuliji et al. 2011; Scobie et al. 2012) sheep. As reported by Krupova et al. (2009), wool production and quality traits currently have very low economic importance in selection programs.

Heritabilities of reproductive traits generally are low. The most frequently recorded traits are the number of lambs born, number of lambs born alive, number of lambs weaned, litter weight, ewe fertility, ovulation rate, ewe rearing ability and lamb survival. Fixed effects for lambing year or season and age of the ewe at lambing (Rashidi et al. 2011; Mohammadi et al. 2012; Boujenane et al. 2013) or age at lambing within parity (Skorput et al. 2011) are usually included in repeatability models, linear models (Mohammadi et al. 2012; Boujenane et al. 2013; Schmidova et al. 2014) and threshold models (Mohammadi et al. 2012).

Heritabilities for litter size (number of lambs born) range from 0.04 to 0.14 (Maxa et al. 2007; Rashidi et al. 2011; Mohammadi et al. 2012), and similar heritabilities have been reported for other reproductive traits (Mohammadi et al. 2012; Boujenane et al. 2013). Schmidova et al. (2014) observed that genetic variance components differed among breeds.

The economics of lamb meat production is profoundly influenced by the number of weaned lambs, which is related to ewe fecundity, but also to lamb survival. Lamb survival can be treated as a trait of the dam or a trait of the individual (Vostry and Milerski 2013). Estimates of direct heritability are in the range from 0.01 to 0.13, while maternal heritability estimates range from 0.01 to 0.07 (Maxa et al. 2009; Vatankhah and Talebi 2009; Hatcher et al. 2010; Vostry and Milerski 2013).

Because a test-day model is more effective in accounting for the environmental variation within a lactation than a whole lactation model (Bauer et al. 2012), breeding values for milk yield of ewes have been predominantly estimated using this procedure (Oravcova et al. 2006; Bauer et al. 2012; Komprej et al. 2012, 2013). Lifetime production can also be analysed (Gorjanc et al. 2009b). In addition to random genetic and environmental effects, the effects of days-in-milk, test day (possibly including the effect of interactions with the flock), parity, age at lambing, litter size and the number of weaned lambs are usually included in models for genetic evaluation of milk production (Bauer et al. 2012). The month of lambing or the interval between lambing and the first test-day are other important sources of variation (Carta et al. 2009). The effect of the number of suckled lambs is evident only in breeds of low production level; whereas in high-producing breeds, a positive effect existed only on first test-day records of twin bearing ewes (Carta et al. 2009).

Heritabilities for dairy traits on a total lactation basis are low to moderate for milk, fat, and protein yields (Komprej et al. 2009; Bauer et al. 2012; Dimov 2013) and high for fat and protein percentages (Pelmus et al. 2014).

Duchemin et al. (2012) showed that utilization of molecular markers can improve current selection methods. For example, accuracies of GEBV for males at birth can be increased by18 to 25% according to traits.

Attention is also paid to breeding for morphological characteristics of the udders in dairy sheep (Milerski et al. 2006; Rovai et al. 2009; Sadeghi et al. 2014).

Selection to increase the profit of a sheep breeding enterprise requires calculation of economic values (increased profit per unit of selection response) for each trait in the breeding objective. Such values have been calculated under specific economic conditions in different countries, as reported by Conington et al. (2004); Jones et al.(2004); Fuerst-Waltl and Baumung (2009); Krupova et al.(2009); Wolfova et al.(2009) and Wolfova et al. (2011a,b). Many investigations have shown that economic values of traits can be sensitive to market prices of sheep products and to differences in input costs. The market prices of animal products (milk or meat) are of higher importance in determining marginal economic values than prices for inputs, especially for the marginal economic value of milk and meat production traits (Krupova et al. 2013). The price of lamb is the most important factor influencing marginal economic values in meat sheep (Kosgey et al. 2003; Conington et al. 2004; Lôbo et al. 2011).

Horses

Horse breeding was focused on sports performance but for smaller populations of local breeds, knowledge of the genetic variability and maintaining a certain degree of diversity is now important. Modern molecular tools such as parentage testing using microsatellite genotyping are powerful in guiding management and conservation of horses (Galov et al. 2005). These authors evaluated nine microsatellite loci (HTG4, HTG7, HTG10, HMS2, HMS3, HMS6, VHL20, ASB2; AHT5) in 53 Posavina, 37 Croatian Coldblood and 33 Lipizzaner in Croatia. Results showed that all tested loci were highly polymorphic. Allelic diversity in the Lipizzaner was 4.78 standard error across loci, while the Posavina and the Croatian Coldblood had higher allelic diversities (approximately 7.0 across loci).

Mahrous et al. (2011) also analysed genetic variation using five microsatellite markers (AHT4, HTG10, ABS2, ABS23, and CA245) in three horse breeds in Egypt (Arabian, Thoroughbred, and Egyptian Native). Three of the microsatellites were highly polymorphic, the highest being HTG10. The lowest mean heterozygosity was 0.754 in the Arabian breed, while the highest was for the Thoroughbred at 0.829. Mitochondrial D-loop sequence variation among the Hucul horses from the Czech Republic was described by Czernekova et al. (2013). A700-bp fragment of the mtDNA D-loop region (positions 15,430–16,129) was sequenced. From 165 samples representing 15 maternal lines, 14 haplotypes of this D-loop hypervariable region were identified.

Another study involving the Hucul horse was performed by Stachurska et al. (2012) in Poland. The Hucul breed was included in the Global Strategy for the Management of Farm Animal Genetic Resources, which aims at preserving the animal gene pool in an unaltered state. Huculs are bay, black, blue dun, yellow dun, tobiano, and chestnut. Grey and chestnut Huculs have always been undesirable. The aim of the study was to determine the frequency of alleles affecting coat colours in the population. The examined loci were ASIP, MC1R, DUN, KIT, and STX17. The ASIP and MC1R loci, on ECA22 and ECA3, respectively, control the so-called basic colours (Marklund et al. 1996; Rieder et al. 2001). Stachurska et al. (2012) concluded that the genetic structure of the Hucul population was not constant and does not comply strictly with the preservation aim. Breeders prefer bay, non-diluted, and tobiano horses and it may lead to undesired changes in the allele frequency.

Pedigree analyses allow assessment of the extent of inbreeding and family structures within a population (Gutierrez et al. 2005). Pjontek et al. (2012) applied the technique to four endangered horse breeds in Slovakia. The most complete pedigrees were found for the Lipizzan and Shagya Arabian breeds. The mean values of inbreeding ranged from 2.67% for the Slovak Sport Pony to 6.26% for the Hucul. The mean inbreeding coefficients in the Lipizzan and Shagya Arabian were 4.02% and 3.95%, respectively.

In Czech populations of cold-blooded Norik, Silesian Norik and Czech-Moravian Belgian horses, Vostry et al. (2011) found the mean inbreeding values of 1.51, 3.23 and 3.53%, respectively. Vincente et al. (2012) reported a much higher mean inbreeding coefficient, 9.92% for all registered animals, for the Lusitano horse. The effective number of founders and the number of ancestors contributing to the current genetic pool were 27.5 and 11.7, respectively. Much higher effective numbers of founders and ancestors, 94 and 32, respectively, were reported in the Lipizzan horse by Pjontek et al. (2012).

Galov et al. (2013) examined the genetic structure and admixture between Posavina and Croatian Coldblood in contrast to the Lipizzan horses from Croatia. The Posavina and Croatian Coldblood are Croatian autochthonous horse breeds with interwoven breeding histories. In contrast, the Lipizzan breed has the oldest formalized breeding program in Croatia and no record of recent genetic introgression from other breeds. Results showed that different breeding schemes and histories had a strong and measurable impact on the population's genetic structure within and between the three breeds. The Lipizzan showed genetic differentiation from the other two breeds.

The Old Kladruber horse is an autochthonous breed that is recognized as a genetic resource in the Czech Republic. Vostry et al. (2012b) studied the occurrence of dermal melanoma within the breed and reported that the white colour in greying white horses, one of the basic colour varieties in breed, is a result of progressive greying that is the loss of coat pigmentation with age. Increased susceptibility to dermal melanoma has been associated with greying of white horses by Fleury et al. (2000) and Heizerling et al. (2001).

Further studies of the Old Kladruber horse by Vostry et al. (2012c) were focused on selection for important conformation traits and reduction in the number of recorded characteristics from the present 36 to 24 traits with regard to a high number of described traits and a lower number of individuals. In order to reduce the number of the described traits, they advised omitting traits with less heritability than 0.10 and traits highly genetically correlated with other recorded traits.

Summary

More appropriate approaches for breeding value prediction for various species have been identified. Selection programs aim to increase the profit for breeders; therefore many authors focused on that topic. Genome-wide selection has become a world standard for dairy cattle breeding. This method takes proper account of information from relatives in assessing the genetic merit of individuals. For some classes of farm animals, molecular genetic approaches include seeking to identify new QTLs and developing genome-wide selection programmes. Primary impediments to further development include the high cost of high-density SNP arrays and difficulty in finding well-structured reference populations to estimate SNP effects for traits that are routinely measured or are costly to record. In the future, research is likely to be expanded to genetic improvement in health status of animals, e.g. mastitis in dairy cows. Longevity, robustness and fertility are also likely to increase in importance in livestock breeding programs.

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