

Future Animal Improvement Programs Applied to Global Populations

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Abstract

In the future, breeders may apply reproductive, computational, and genomic methods to global populations nearly as easily as with national populations now. Dairy cattle breeders exchange traditional breeding values worldwide via Interbull, and new methods are outlined for exchanging either genomic evaluations or genotypes. Goals are to adapt multi-trait across country evaluation (MACE) in the short term and to merge genotypes in the long term. Genotyped young animals are rapidly replacing progeny tested bulls and phenotyped cows as sources of breeding stock. Advanced reproductive techniques to shorten generation intervals could be more profitable as the accuracy of female and young animal selection increases.

Keywords: genomic selection, international evaluation, reproductive technology, phenotypes

Introduction

The global population of animal breeders will develop new statistical, genetic, reproductive, and other technologies to improve the global population of animals. A quick review of past programs and trends may be helpful before forecasting future changes.

Organizations

Breeding programs evolved gradually from within-herd phenotypic selection to local and regional cooperatives to national evaluations and now international evaluations. Many natural-service bull associations were organized in the United States before 1945 but were then replaced by new organizations that provided artificial insemination (Figure 1). Breeding companies today have global marketing networks. For example, 21 million units of semen were sold domestically and 14 million units exported from U.S. dairy bulls (NAAB, 2009).

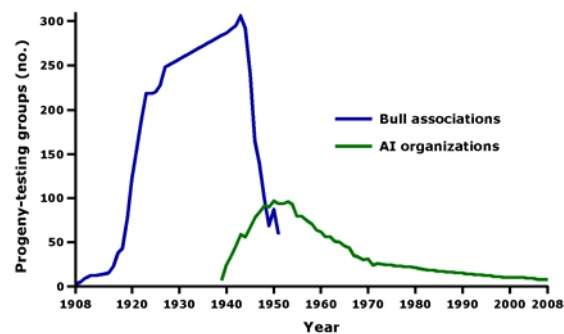


Figure 1. Numbers of progeny testing groups.

Genomic technology could lead to new organizations or international mergers, but individual breeders will continue to play a major role if the technology is open rather than restricted. Swine and poultry breeding companies may find that more open exchange such as in dairy cattle leads to more rapid progress in the genomic era. Separate breeding companies can each pay to test their own animals, but shared investment in genotyping of reference populations can reduce costs and increase returns.

Phenotypes

Selection programs require measuring traits. Numbers and percentages of cows in official milk recording programs grew steadily over the last century as evidenced by Figure 2, and many new traits have been added. Larger farms collect much automatic data but might not provide it for use in evaluations unless paid to do so.

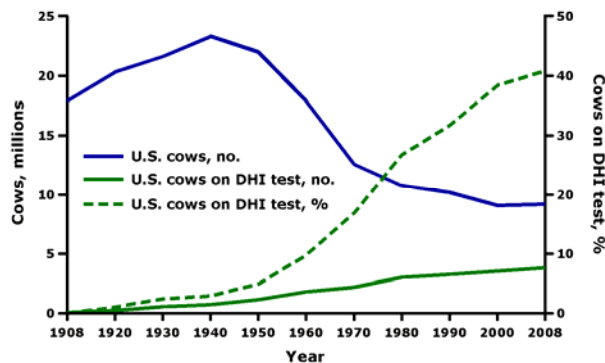


Figure 2. A century of U.S. milk recording.

Countries could merge phenotypes for standard traits such as production, somatic cell score, and longevity across borders to reduce evaluation efforts within each country and to simplify across border marketing. As the prices for genotyping decrease and the supplies of genotypes rapidly expand, phenotypes for new or less heritable traits will become a limiting factor. Individual country data sets for traits recorded only recently such as heifer fertility may be too small for reliable genomic predictions, whereas a combined international file could give better results. Organizations should share costs of both genotyping and phenotyping and may provide access only to competitors that also invest. Incentives are needed to continue collecting phenotypes.

Genotypes

Livestock and poultry breeders can now trace genetic inheritance and predict merit at birth using chips costing about \$200 per animal and containing 50,000 genetic markers (De Roos *et al.*, 2009; Matukumalli *et al.*, 2009). Accuracy of predictions depends primarily on the number of animals that have phenotypes matched to genotypes (VanRaden *et al.*, 2009). Large data sets are easier to obtain and to evaluate if all breeders use the same set of

markers. Competing companies may share investment costs for chip development and genotyping of reference populations.

Lower density and higher density marker sets will become available in the near future. Marker subsets may be selected to provide, for example, 40% of the benefit of the full set for only 10% of the cost. Whole herds could be screened and parentage tested using low density chips. A test for 384 SNPs is expected to be available in late 2009, containing a standard set of 96 SNPs for international parentage testing and the other 288 chosen to maximize net merit reliability. Different marker sets could be combined using haplotyping, and computer methods to infer missing genotypes are a rapidly growing area of research (Habier *et al.*, 2009; Burdick *et al.*, 2006).

A chip containing >500,000 markers could be available in 2010 and is expected to contain all SNPs from both previous 50K chips to allow simpler imputation of missing SNPs for previously genotyped animals. Selection of SNPs could be either equally spaced as in Matukumalli *et al.* (2009) or more dense in regions identified as important by 50K results. Holstein bull ToMar Blackstar (USA1929410) has been fully sequenced for all 2.8 billion DNA base pairs by USDA's Bovine Functional Genomics Laboratory.

Evaluation

International evaluations express foreign and domestic data on a common scale for easier comparison and combine information from different sources to increase accuracy. Dairy breeders have relied on multi-trait across country evaluation (MACE) since 1995 to exchange estimated breeding values (EBVs) within Interbull. Genomic MACE equations are being developed to exchange genomic EBVs. Details are provided by Sullivan and VanRaden (2009), and the main difference is accounting for residual correlations among genomic EBVs provided by different countries.

Combined genotype files from multiple countries can be evaluated with two different approaches. The first is to apply single-trait

genomic evaluation methods to input data that includes traditional MACE EBVs for foreign bulls. The second is to apply multi-trait methods to national input data on all scales simultaneously. The first option is currently used by the United States and Canada, whereas the second option could be used for a proposed evaluation of Brown Swiss genotypes from several countries.

Multi-country genomic evaluation was compared to separate single-country evaluations using simulated genotypes for 8193 Brown Swiss bulls from 9 countries, including all bulls with daughters and also 120 young bulls sampled in the United States. Reliabilities for selecting foreign young bulls were low from either parent average (PA) or MACE because sires and maternal grandsires were simulated but dams were not. Gains were much larger from both within-country and across-country genomic evaluation. Table 1 shows reliability from just one replicate used to demonstrate the multi-country method. The order of countries listed is from most to fewest proven Brown Swiss bulls.

Computing times were reasonable for both the simulated 9-country example and for a 2-country evaluation of 21,944 U.S. and Canadian genotyped Holsteins. More processors would be needed to evaluate many traits on all scales in a short time window at either a central location or at distributed sites. Remaining issues are if central processing or distributed processing will provide better service and if research groups will have access to the genomic data.

Table 1. Reliability for young U.S. Brown Swiss bulls.

Country	Reliability			
	Traditional		Genomic	
	PA	MACE	Within	Across
DEU	4	11	64	69
CHE	14	17	65	73
ITA	1	12	34	64
USA	20	20	55	70
SLO	0	11	6	55
FRA	2	15	21	66
CAN	1	14	9	61
NLD	2	13	6	58
NZL	1	1	1	26

Countries with fairly small populations compute evaluations of phenotypic data, but much larger populations are needed for successful genomic evaluation. Duties of national evaluation centers may need to be reorganized so that each contributes specialized research to a larger project instead of duplicating the same calculations with each nation's genomic data as they do now with phenotypic data.

Interaction

Genetic by environment interactions reduce the advantages of global selection. Low genetic correlations among neighboring countries may not be biological and instead are artifacts of national or international estimation systems. Evaluations that model interaction of genes with environmental variables rather than countries should be more precise but require central processing of phenotypes (Zwald *et al.*, 2003). Regressions on environmental variables such as temperature could be fit within or across countries and then used to extrapolate to more extreme environments. More reranking and larger benefits may occur for exports to the tropics than for the domestic market with a mixture of warm and cool seasons.

A global scale instead of separate country scales could be useful to breeding companies that select and market breeding stock across many environments (Powell and VanRaden, 2002). Economic values differ with production systems. If similar traits are evaluated in each environment, a global selection index can also be constructed as a weighted average of within-country or within-environment indexes to determine a world ranking. A world index could be useful to breeders in countries without an index or that measure fewer traits instead of selecting on a single country ranking.

Reproduction

Embryo transfer could replace artificial insemination as the primary reproductive tool on many farms, especially in warm climates (Hansen and Block, 2004). The direction of transfer will be reversed, with heifers as donors and cows as recipients. Simulations

indicate that as genomic reliabilities and rates of progress increase, advantages of young females increase (Schaeffer, 2006). A new market could develop for genotyped frozen embryos. Average merit of the animals born could be much higher by selecting before rather than after gestation.

Crossbreeding is widely used in most livestock and could also be profitable in dairy cattle. For example, transfer of Holstein × Jersey cross embryos into Holstein by Jersey cross cows can give a perpetual F1 herd with both maximum heterosis and maximum uniformity, similar to hybrid corn. However, more long term progress could occur with a composite population because the best alleles in any breed could be combined and selected jointly while still retaining some heterosis.

Transgenic animals offer much potential in the long term. The technology has already produced very useful livestock that could be profitable if marketing restrictions are lifted (Wall *et al.*, 2005). In some cases, additional copies of an important gene are inserted back into the same species (Brophy *et al.*, 2003). Animals produced by this approach might not be labeled transgenic and might need little regulation because similar insertions, deletions, and mutations happen constantly in nature within species during meiosis. Eventually, laboratory selection and assembly of the best chromosomes from different animals into one embryo might be preferred instead of the trial and error from meiosis and mating. Scientific methods might replace traditional reproduction.

Summary

Genetic gains increased over the last century as breeders collected more data and formed larger organizations. Future gains from genomics, advanced reproductive tools, and statistical methods will accelerate these trends. Global genomic evaluations are possible but must account for genotype by environment interaction and adapt quickly to available data and customer needs. Future breeding programs may increase use of designed crossbreeding programs, embryo transfer, embryo selection, and transgenics. Research in any country is quickly transferred to others, leading to future

global improvements. Open exchange of ideas to improve animals should continue, while at the same time allowing breeders and companies to compete and to profit from investing in new technologies.

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