

GENOMIC SELECTION IN LIVESTOCK IMPROVEMENT – A BRIEF OVERVIEW OF DAIRY CATTLE

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Abstract

Many countries use molecular tools and genomic selection in breeding programmes to reach rapid rates of genetic gains, especially in dairy cattle in developed countries. This paper provides a brief overview on genomic selection in dairy cattle. Some aspects related the status of genomic selection application in livestock improvement are showed. Following the examples provided by other countries, genomic selection should be considered for animal breeding improvement strategies in Romania too.

Key words: dairy cattle, genomic selection, genomic prediction, selection indices.

INTRODUCTION

The increasing number of the world's population result in a higher food demand, especially meat and dairy products, so that animal production had to face a significantly increment. Advances in genetics and the use of modern genetic tools in breeding programmes led to a rapid genetic progress towards the development and highly specialized breeds related to the production traits (Woelders et. al., 2006). The breeding programmes need to be adapted to the actual status of progress registered in the genetic area. The objectives of livestock production should consider a better characterization of population and various breeds, for implementing of suitable livestock breeding and improvement programmes (Hoffmann et. al., 2010). Breeds characterization at phenotypes level and their interaction with production systems and at genetic level is essential. Anyway, the available information related to the genetic traits of each breed still need to be approached. Characterization of the population and individual genetics, next to the further development of livestock breeding and improvement programmes is a critical element (FAO, 2011). Traditional selection stands

for recording lots of cows across many farms, opposite to genomic selection, targeting more detailed information from cooperating farms, so that such similar strategies could be useful in less developed countries (Cole, VanRaden, 2017).

Genomic technologies use DNA information on a large scale to predict the performance potential of cattle and also concur to efficient herd management to increase productivity, genetic improvement, health and welfare, shortening the generation interval (Hart, 2017). Breeding indices are important tools in modern dairy cattle breeding, providing a way to combine information related many traits into a single value, for ranking animals and making breeding decisions (Cole, VanRaden, 2017). Genomic selection help farmers to select animals for the next generation of replacements within the herd rather than relying on phenotypic assessment alone, facilitating an earlier identification of the elite animals within the herd (Hart, 2017).

The information from animal pedigree next to genetic markers increase the reliability of genomic estimated breeding values (GEBV) (Hart, 2017). The reasonable cost of genomic evaluation compared to those of embryo transfer, multiple ovulation, or sexed semen technologies, stands for applying both methods to enhance both profit and genetic gains (Hart, 2017). The ideal breeding objective for dairy cattle is still a popular topic, and also there is no single selection objective to be considered best for all populations or all herds within a population (Cole, VanRaden, 2017). Overall, genomic selection facilitate a better selection of animals for herd and also a better accuracy in breeding pair selection (Hart, 2017).

Thus, the present paper provides an overview on genomic selection use in dairy cattle, highlighting at the same time the perspectives and the priorities for considering such methods for breeding and improvement programmes in Romania.

SELECTION INDICES AND TRAITS

The use of a selection index is to improve one or more traits, by ranking and choosing mates based on a combination of one or more traits, the selection objective in modern breeding programs aiming typically a measure of lifetime profitability and the selection criterion usually comprises traits included in national milk recording programs (Cole, VanRaden, 2017). Genomic technology enables to breed cattle according to specific goals, such as for higher milk yield or higher fertility in young bulls (Hart, 2017). Farmers need to understand only the function of each subindex instead of dozens of traits (Cole, VanRaden, 2017).

Indices are constructed based on a series of subindices. Indices revision can be directed to include new or additional traits in some

subindices. The lifetime net merit (NM\$) indice was constructed from production (PROD\$), longevity (LONG\$), fertility (FERT\$), conformation (TYPE\$), calving ability (CA\$) and lately, new health subindex (HEALTH\$) (Cole, VanRaden, 2017). The Ideal Commercial Cow Index (ICCS; Genex, 2006) was constructed based on the production efficiency (PREF\$), health (HLTH\$), fertility and fitness (FYFT\$), milking ability (MABL\$), and calving ability (CABL\$) subindices. The Irish EBI Index (ICBF, 2017) comprises 7 subindices like milk production, fertility, calving performance, beef carcass, cow maintenance, cow management, and health. In the past, the proposed indices were typically reviewed by groups of experts, and information related to the derivation of the indices was provided to ensure confidence in the values. Recently, genetic evaluations for novel traits and new selection indices are computed and distributed by companies (i.e. CRV (Arnhem, the Netherlands), Genex (Shawano, WI), Zoetis (Parsippany-Troy Hills, NJ)), but transparent review processes may be lacking (Cole, VanRaden, 2017).

Selection indices vary within and across countries due to different economic conditions, traits recorded and specific breeds (table 1).

Table 1

Selection indices used in various countries

Index abbreviations	Index specification	Country
GDM	genes diffusion merit	France
RZG	total merit index	Germany
£PLI	profitable lifetime index	Great Britain
PFT	production, functionality and type index	Italy
ICO	total genetic merit index	Spain
BW	breeding worth	New Zealand
ISEL	total selection index	Switzerland
NVI	Netherlands cattle improvement index	The Netherlands
EBI	economic breeding index	Ireland
NTM	Nordic total merit	Denmark, Finland, Sweden
TPI	total performance index	U.S.A.
GM\$	grazing merit	
CM\$	cheese merit	
NM\$	net merit	
LPI	lifetime profit index	Canada
NTP	Nippon total profit	Japan
PD11	Israeli 2011 breeding index	Israel
HWI	health weighted index	Australia
TWI	type weighted index	
BPI	balanced performance index	

Prior to genomic testing use on a farm, it is important to ascertain the traits that will be selected to achieve on farm goals (Hart, 2017). Recording important new traits on a fraction of cows can quickly benefit the whole population through genomics. The number of traits included in a typical selection criterion has grown over time, from 1 or 2 yield traits to many non-yield traits, including fertility, health, and fitness traits (Cole, VanRaden, 2017). Usually, selected traits differ slightly in various countries, but there are common trait groups defined (table 2).

Table 2

Common group traits and selected traits in various countries

Common trait group	Example of traits included in the common trait group
yield	milk volume
	fat yield
	protein yield
longevity	productive life
fertility	nonreturn rate
	days open
udder health	SCS
	clinical mastitis
calving traits	dystocia
	stillbirth
milking traits	milking speed
conformation	udder conformation
	feet score
	leg score

For example, the genomic profile of a heifer use the key indexes: the profitable lifetime index (£PLI) and type merit, harboring production traits such as: milk kg, fat kg, protein kg, fat %, protein %, as well as health and fitness traits as follows: mammary composite, feet and legs composite, temperament, ease of milking, locomotion, condition score, TB advantage, lifespan, SCC, fertility. The profitable lifetime index (£PLI) provides an economic breeding index for UK herds (Hart, 2017).

The first USDA index, predicted difference dollars (PD\$), included only milk and fat yield in the traits, whereas the 2017 revision of the lifetime net merit (NM\$) rely on 33 different traits included in various subindices.

The traits that should be included in future selection indices is still a concern, some traits showing a growing interest to dairy farmers. Some countries are showing interest to include specific traits in their selection indices, but some do not. Traits as health and fitness, feed intake, fertility, genetic diversity, milk composition, omics data, or other traits maybe adopted for individual breeding programs, could be considered for future

selection indices in various countries (Cole, VanRaden, 2017). New traits and strategies are still demanding for livestock improvement.

GENOMIC SELECTION APPLICATION IN DAIRY CATTLE

Genomic selection is a form of marker-assisted selection (MAS), in which genetic markers covering the whole genome are used so that all QTL are in linkage disequilibrium with at least one marker (Yadav et al., 2018).

In developed countries, genomic selection (GS) lead to rapid rates of genetic gains especially in dairy cattle, resulting in a higher proportion of genomically proven young bulls for breeding (Mrode et. al., 2019).

Developing countries are facing issues related small holder systems with small herd sizes or the existence of breed associations, resulting in some degree of data and pedigree recording and genetic evaluation or even the lack of performance and pedigree recording; also, some countries still had to face the lack of breeding structures such as artificial insemination companies, to drive breed improvement programs. Therefore presently, in developing countries most genotyping activities are undertaken by breed organizations or associations, or are a result of several development projects (Kosgey, Okeyo, 2007, Carvalheiro, 2014, Brown et al., 2016, Silva et al., 2016, Mrode et. al., 2019).

Genomic selection in dairy cattle has been used to discover the markers and improvement of the traits associated with milk production, cow health, udder health, and cow conformation, Australia being the leader on genomic selection in dairy cows, along with other countries like US, Canada, China, etc. (Yadav et al., 2018). In practice, genomic selection refers to selection decisions based on genomic estimated breeding values (GEBV) (Yadav et al., 2018). The accuracy of genomic prediction in dairy cattle shows values exceeding 0.8 for production traits and 0.7 for fertility, longevity, somatic cell count and other traits (Wiggans et al. 2011). Using SNP effects from one breed to calculate GEBV in another breed vice versa was not satisfactory. SNP estimates calculated from a Holstein-Friesian reference population did not produce accurate GEBV in Jersey bulls, and the correlations ranged from -0.1 to 0.3 (Yadav et al., 2018).

Implementing genomic selection in dairy cattle has resulted in increased genetic gain in many countries, so that related dairy genomic predictions, many countries collaborate to assemble large reference sets, being three consortiums established (Eurogenomics, including the Netherlands, Germany, France, the Nordic countries, Spain, and Poland; The North American Consortium including USA, Canada, Italy, and Great Britain; and a “rest of the world” consortium consisting of a number of remaining countries) (Yadav et al., 2018). Worldwide, approximately 2 million dairy cattle have been genotyped for purposes of genomic

prediction, from which 934,780 Holstein, 120,439 Jersey, 19,588 and 4,767 Ayrshire in USA (Wiggans, personal communication referred in Meuwissen et. al., 2019).

Lately, the genetic selection of dairy heifers can be a better option than selection for young bulls alone, as a part of selection for breeding (Hart, 2017). In many countries, most of the genotyped animals are now heifer calves and even if genotyping young bull calves results in the greatest genetic gain, genotyping is now sufficiently cheap to be applied to heifer calves for the choosing which heifers to retain in the herd or the bulls to which to mate, to minimize inbreeding (Pryce, Hayes 2012).

Next-generation sequencing and associated technologies facilitated breed composition, parent verification, genome diversity and genome-wide selection sweeps assessment, such data being used in breeding programs aiming genomic selection. (Mrode et. al., 2019). In 2007, the first draft of bovine genome enabled the Illumina Company, in collaboration with an international consortium to develop a chip for genotyping over 54,000 single nucleotide polymorphisms (SNP) simultaneously, that was used to genotype existing progeny-tested bulls (Boichard et. al, 2016). Such technology showed genomic breeding values enough accurate to replace progeny testing and allowing young bulls semen with genomic evaluation only the dissemination (Boichard et. al, 2016). Cross validation approaches implemented in most studies show accuracies of 0.20–0.60, meanwhile genotyping based on a mixture of HD and LD chips, followed by imputation to the HD lead to accuracies of 0.74–0.99 (Mrode et. al., 2019).

The genomic best linear unbiased prediction (GBLUP), single-step GBLUP (ssGBLUP) and SNP-BLUP methods are very similar to traditional BLUP, the pedigree relationships being replaced by genomic relationships. (Habier et al., 2007, Goddard et al., 2011, Vitezica et al., 2011, Legarra et al., 2014, Yadav et al., 2018, Meuwissen et. al., 2019,).

Genomic prediction studies in developing countries are mostly target dairy and beef cattle, usually with small reference populations (500–3000 animals) and are mostly cows, the input variables tending to be pre-corrected phenotypic records and the various Bayesian methods use are feasible in addition to GBLUP (Mrode et. al., 2019). Various commercial chips vary related the efficacy of imputation in dairy cattle breeds in terms of the impact on the accuracy of imputation and genomic prediction, based on different reference populations and different imputation algorithms (Browning, Browning, 2016, Das et al., 2016, Aliloo et al., 2018).

The number of genotyped animals tend to be limited, are mostly females, therefore having a major impact on both the size and structure of the reference and validation populations (Mrode et. al., 2019). Nowadays, genomic selection is used on a large scale in dairy cattle industry and with

the advancement it may be used for the improvement of all the livestock population (Yadav et al., 2018).

CONCLUSIONS

In developing countries genomic selection could use the advantages of various dairy sires already genotyped and phenotyped, from developed countries, but also need to find solutions for efficient and satisfactory performance and pedigree recording next to genetic evaluation, for breeding and improvement programs.

A strength collaboration between developing and developed countries, next to the ability of Governments to enable policies, statutory and regulatory frameworks, by putting in place farmers, institutions, breed organizations and associations, artificial insemination companies could stand for breeding and improvement programmes in dairy cattle.

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