Advances in Dairy Research
ISSN: 2329-888X

De Mello et al., Adv Dairy Res 2014, 2:1
DOI: 10.4172/2329-888X.1000110

Short Communication Open Access

Progress in Dairy Cattle Selection

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Abstract

Advances in animal selection have allowed greater genetic gains in milk production. These advances conducted to increase profitability due to higher productivity. In this short communication, different methods used in dairy cattle selection will be discussed. This brief history aims to report the first selection methods used; its progress and current perspectives of selection by genomic information.

Keywords: Marker-assisted selection; Breeding value; Molecular markers; Genomic selection

Introduction

The current level of genetic improvement in dairy herds is the result of advances in methodologies able to identify genetically superior animals with greater efficiency. However, the traditional selection depends strongly on the number of phenotypic records to increase the accuracy of estimates. Thus, traits difficult to measure, such as those later expressed, limited to sex or of low heritability are more difficult to be improved [1,2]. From the bovine genome sequencing in 2009, a new breakthrough was possible in selection methodologies, mainly for production traits like mentioned above. Historically, new selection criteria (measured traits) were introduced into genetic evaluations to increase the accuracy of the estimations by identifying the effects affecting production traits.

Dairy cattle breeding followed the progress of selection methodologies. Initially, the herds were selected from group deviations to predict the animal breeding value [3]. Based on the methodology developed by Henderson in the mid-40 a large advancement was possible. Henderson, modifying the normal equations of the least squares method, developed the basis for the methodology of mixed models (MMM) [4]. From the advances in computer science, it was possible to implement sire model methodologies and, finally, an animal model that allowed solving the complex equations of the mixed models. The genetic evaluation using the animal model for estimates breeding value (EBV) has been widely accepted, and the model is currently being worldwide used in its various applications.

The advent of molecular biology techniques enabled to access genomic information allowing distinguishing individuals by differences in the nucleotide sequences, so-called molecular markers. Molecular markers associated with production traits enabled the selection of individuals without influence of the environment by marker-assisted selection (MAS).

Despite the progress afforded by MAS using this methodology it is still timely in breeding programs of dairy cattle due to most traits of interest are governed by a large number of loci. The use of a limited number of loci by this methodology can result in capture only part of the proportion of genetic variance, conditioned on small genetic gains [5]. Moreover, the complexity of the calculations involved the estimation of breeding values with incorporating of information molecular markers hampers the use of MAS [6].

A major turning point came from the final sequencing of the bovine genome, following the genomic sequencing of other species [7]. The bovine genome project allowed the identification of ~35 million SNP (single nucleotide polymorphism) [8]. The SNP are scattered densely in the genome allowing the development of new methodologies based on dense panels of markers. Advances in genotyping technologies has enabled more effective implementation of the methodology proposed by Meuwissen in 2001 [9].

A new technology called genomic selection is revolutionizing dairy cattle breeding allows estimating breeding value (GEBV) based on the genotype of the hundreds of thousands of SNP densely distributed throughout the genome [10]. The genomic breeding values (GEBV) are predicted as the sum of effects of all markers [9]. Traditional selection methodologies are dependent on the phenotypic record of the animal and its offspring to estimate the breeding value accurately. In contrast, the genomic selection allows to estimate the genomic value of each individual without using phenotypic data, based only on the previously estimated SNP effect in a reference population [11]. The reference population is a herd with phenotype data, pedigree and genotypes known.

The efficiency of genomic selection versus traditional breeding programs has been reported in several studies, which suggests an increase of at least 50% in the annual genetic gain using genomic selection [12-14]. In addition, there is a decrease of around 92% in costs by not carrying of the progeny test [12].

The most common problem of genetic selection, particularly in dairy cattle is related to the intensive use of the best animals for a long period, leading to inbreeding. According to Daetwyler et al. [15], the genomic selection can reduce the inbreeding rates by generation compared to traditional BLU methodology, besides being used for identifying animals with lower degree of kinship, thus increasing the genetic diversity of certain populations with high inbreeding levels [16]. However, due to lower generation interval the use of genomic selection can increase inbreeding per year [17].

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Received December 12, 2013; **Accepted** January 27, 2014; **Published** January 29, 2014

Citation: De Mello F, Kern EL, Bertoli CD (2014) Progress in Dairy Cattle Selection. Adv Dairy Res 2: 110. doi: 10.4172/2329-888X.1000110

Many barriers are found for the implementation of this promising methodology, such as the high cost to genotype the reference populations, ideal racial composition [18,19], adaptation of genetic evaluations to include genomic information, managing long-term gain with genomic selection and computational challenges [20]. Nevertheless, this new methodology has showed great impact, especially on dairy cattle, because it allows obtaining estimates of genomic value more accurately mainly in young animals [19] therefore reducing the generation interval considerably. Moreover, the genomic selection will enable to reduce the production costs through precocious selection; before the productive/reproductive age due to prediction of breeding values of animals without phenotypic information database.

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