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Symposium review: Possibilities in an age of genomics: The future of selection indices¹

J. B. Cole² and P. M. VanRaden

Animal Genomics and Improvement Laboratory, Agricultural Research Service, USDA, Beltsville, MD 20705-2350

ABSTRACT

Selective breeding has been practiced since domestication, but early breeders commonly selected on appearance (e.g., coat color) rather than performance traits (e.g., milk yield). A breeding index converts information about several traits into a single number used for selection and to predict an animal's own performance. Calculation of selection indices is straightforward when phenotype and pedigree data are available. Prediction of economic values 3 to 10 yr in the future, when the offspring of matings planned using the index will be lactating, is more challenging. The first USDA selection index included only milk and fat yield, whereas the latest version of the lifetime net merit index includes 13 traits and composites (weighted averages of other additional traits). Selection indices are revised to reflect improved knowledge of biology, new sources of data, and changing economic conditions. Single-trait selection often suffers from antagonistic correlations with traits not in the selection objective. Multiple-trait selection avoids those problems at the cost of less-than-maximal progress for individual traits. How many and which traits to include is not simple to determine because traits are not independent. Many countries use indices that reflect the needs of different producers in different environments. Although the emphasis placed on trait groups differs, most indices include yield, fertility, health, and type traits. Addition of milk composition, feed intake, and other traits is possible, but they are more costly to collect and many are not yet directly rewarded in the marketplace, such as with incentives from milk processing plants. As the number of traits grows, custom selection indices can more closely match genotypes to the environments in which they will perform. Traditional selection required recording lots of cows across many farms, but genomic selection favors collecting more detailed information from cooperating farms. A similar strategy may be useful in less developed countries. Recording important new traits on a fraction of cows can quickly benefit the whole population through genomics.

Key words: breeding program, genetic improvement, selection index

INTRODUCTION

Breeding indices are important tools in modern dairy cattle breeding. They provide a way to combine information about many traits into a single number that can be used to rank animals and make breeding decisions. The need for such a tool was recognized very early in the history of modern animal breeding, when Hazel and Lush (1942) applied the method of Smith (1934) to the improvement of economically important traits of livestock. The ideal breeding objective for dairy cattle remains a popular topic and has been reviewed periodically (e.g., Hazel et al., 1994; Philipsson et al., 1994; VanRaden, 2004; Miglior et al., 2005; Shook, 2006), but there is no single selection objective that is best for all populations or all herds within a population.

Historically, selection indices in the United States were developed by the USDA and purebred dairy cattle associations, frequently with input from scientists at land-grant universities, using data available through the national milk recording system and breed type appraisal programs. Proposed indices were typically reviewed by groups of experts and information about the derivation of the indices was published in technical and trade publications, ensuring confidence in the values because of that review process. Recently, genetic evaluations for novel traits and new selection indices have been computed and distributed by companies such as CRV (Arnhem, the Netherlands), Genex (Shawano, WI), and Zoetis (Parsippany-Troy Hills, NJ). This provides farmers with new tools and may drive demand for new phenotypes, but transparent review processes may be lacking. The purpose of this paper is to present a brief overview of how selection indices are constructed. describe traits included in current indices, review desirable properties of new traits, discuss traits that may be included in selection indices in the future, and dem-

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²Corresponding author: john.cole@ars.usda.gov



Figure 1. Changes in fat yield for US Holsteins, 1957 to 2015. The black (red) area represents average production in 1957, the light gray (blue) area shows changes due to improved feeding and management, and the dark gray (green) area shows gains from increased genetic merit. Color version available online.

onstrate that selection indices are robust to incorrect assumptions about model parameters.

SELECTION INDICES

Improving Animal Performance

Animal performance is a function of both genetic and environmental factors and interactions among the two. Predictions of genetic merit are based on a quantitative model that assumes that traits are controlled by many genes, each of which has a small effect on the phenotype (Falconer and MacKay, 1996). This model has been found to accurately describe many traits of economic importance in dairy cattle (Cole et al., 2009). Environmental influences include all sources of phenotypic variation that cannot be attributed to genetics, such as nutrition, climate, disease exposure, error in measurement, and other unknown factors. These factors vary from farm to farm and between individual animals on the same farm and may change over time (e.g., Windig et al., 2005).

Figure 1 shows the change in fat yield for US Holsteins between 1957 and 2015. Production in 1957 is used as a baseline, and gains over time were found to be evenly divided between increased genetic potential and improvements in feeding and management. Gains in genetics and management each represent 28% of 2015 production, whereas the 1957 base represents 44% of current yield. The proportion of gains from improved genetics versus improved environment differs from trait to trait and is a function of the heritability of a trait. Fat yield has a heritability of 20% (VanRaden, 2017), whereas daughter pregnancy rate has a heritability of only 4% (VanRaden et al., 2004). When the proportion of variance in a trait due to genetics is low, it is often easier to make gains by improving the environment in which the cow is performing, and gains from genetic improvement may not be visible to producers for a long time.

Construction of Selection Indices

The following discussion focuses on the simplest formulation of a selection index; greater detail, including derivations, may be found in the literature (e.g., Lin, 1978; Cameron, 1997). When using a selection index, the goal is to improve one or more traits, referred to as the selection objective, by ranking and choosing mates using a combination of one or more traits, known as the selection criterion. In modern breeding programs, the selection objective is typically a measure of lifetime profitability, whereas the selection criterion usually comprises traits that are included in national milk recording programs. In the mathematical terms of Hazel and Lush (1942), an index including m terms in the selection criterion for an animal takes the form

$$\mathbf{I} = \mathbf{b}_1 \mathbf{X}_1 + \mathbf{b}_2 \mathbf{X}_2 + \ldots + \mathbf{b}_m \mathbf{X}_m,$$

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where I is the selection criterion, b_i is the emphasis placed on the ith trait, and X_i is the animal's phenotype for the ith trait in the index. Index weights are calculated as a function of (co)variances among the traits in the objective and the criterion and the economic weights of the individual traits:

$$\mathbf{b} = \mathbf{P}^{-1}\mathbf{G}\mathbf{a},$$

where **b** is a vector of index weights, **P** is the phenotypic (co)variance matrix for the traits in the selection criterion, **G** is a matrix of genetic (co)variances among the traits in the criterion and the objective, and **a** is a vector of economic weights associated with the traits in the criterion. If all of the parameters used to compute the index are correct, then it is the most efficient way of improving all of the traits in the selection objective. However, in modern breeding programs, mixed model equations include **P** and **G** to first obtain multitrait evaluations ($\hat{\mathbf{u}}$), and those are combined directly by their economic values as $\mathbf{a}^*\hat{\mathbf{u}}$.

When the traits in the selection criterion and selection objective differ, as is often the case, an additional calculation is necessary to determine the correlated response to selection of the traits in the objective in response to selection on the traits in the criterion. This is a straightforward extension of the well-known breeder's equation (Cameron, 1997)

$$\Delta g_j = \frac{b'G_j}{\sqrt{b'Pb}}$$

where Δg_j is the correlated response of trait j in the selection objective in response to selection on the selection criterion, and G_j is the correlation between trait j and the traits in the selection criterion. This equation shows that the correlated response is a function of the genetic correlations among the traits in the objective and the criterion and the index weights.

The literature on selection index methodology is quite extensive, and many special cases can be accommodated. For example, one trait can be held at a constant level while others are changed (Kempthorne and Nordskog, 1959), economic value can have nonlinear relationships with the traits in the index (Goddard, 1983), selection can proceed in stages where objectives change over time (Cunningham, 1975), and quota systems can drive the economic value of yield traits (Gibson, 1989). Selection index methodology also has been used to determine rates of genetic and economic gain under genomic selection programs in a deterministic fashion (Dekkers, 2007; König et al., 2009). Readers are

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directed to more comprehensive works on selection index methodology for additional details (e.g., Van Vleck, 1993; Weller, 1994; Cameron, 1997).

Contribution of Genomic Information

Genomic selection allows breeders to make decisions more quickly by using dense DNA marker information to compute high-reliability predictions of genetic merit early in an animal's life (Nejati-Javaremi et al., 1997; Meuwissen et al., 2001). From the perspective of the breeding objective, the principal effect of genomic selection is on the reliabilities of the breeding values used in the index (VanRaden et al., 2009), but the technology provides several other advantages, including lower costs of proving bulls (Schaeffer, 2006), greater rates of genetic gain from shorter generation intervals (García-Ruiz et al., 2016), detection of previously unknown genetic disorders (VanRaden et al., 2011), and identification of genes that influence economically important traits (Cole et al., 2011). A trait with a low heritability, such as daughter pregnancy rate $(h^2 =$ (0.04), requires more daughter phenotypes to produce a breeding value with the same reliability as a trait with higher heritability, such as fat yield $(h^2 = 0.30)$, and genotypes provide more information for low-heritability traits. Pedigree information alone is equivalent to approximately 7 daughter records, whereas a genotype is worth 34 daughter records for fat or 131 daughter records for daughter pregnancy rate. Genomics allows us to publish useable evaluations much sooner than in the past and make more profitable management decisions on the farm (e.g., Pryce and Hayes, 2012; Van Eenennaam et al., 2014).

Selection for Many Traits

The number of traits included in a typical selection criterion has grown over time, from 1 or 2 yield traits to many nonvield traits, including fertility, health, and fitness traits. This allows farmers to make use of more information than in the past and takes advantage of correlations among traits (important traits rarely have correlations of 0 with other important traits). Many traits may have direct economic value; for example, milk plants often pay premiums for low SCS in addition to payments for high protein and fat components. Traits can also have indirect value; for example, SCS can predict mastitis losses if mastitis is not recorded directly. Substantial losses can occur when indirect values are ignored—for example, the well-documented negative correlation of fertility with milk yield (Figure 2; Lucy, 2001). Balanced selection improves traits according to



Figure 2. Changes in daughter pregnancy rate (DPR) for US Holsteins, 1957 to 2015. The black (red) area represents average production in 1957, the light gray (blue) area shows changes due to improved feeding and management, and the dark gray (green) area shows gains from increased genetic merit. Color version available online.

their economic values, and selection indices should be periodically updated to include new traits and reflect changing economic conditions as well as changing genetic parameters between and among traits. However, as traits are added to an index it becomes increasingly difficult to predict a priori whether the new index will have greater or reduced response compared with the index with fewer traits (Sivanadian and Smith, 1997).

Derivation of Economic Values

The vector of economic values (\mathbf{a}) included in the calculation of index weights is used to assign values to traits based on their importance to the selection objective. Two general approaches may be used to derive those weights. The first, which might be called the empirical approach, uses data from scientific studies and field reports to quantify incomes and expenses associated with the traits in the selection objective and criterion. The goal of this approach is to allow the best available economic information to drive the formulation of the index, and it is used in the calculation of the USDA's Lifetime Net Merit Index (NM\$) and some breed-specific indices, such as the American Jersey Cattle Association's (2017) Jersey Performance Index. The second, which might be called the subjective approach, has been used to construct indices such as Holstein Association USA Inc.'s (2017) Total Performance Index (TPI), assigns values to traits based on the cow that breeders would like to see in the future. Those targets for breed improvement are developed by groups of breeders and experts and are driven by both quantitative and qualitative factors. Quantitative factors include incomes and expenses associated with costs of raising animals and the value of products sold, whereas qualitative factors include such things as the desirable conformation for cows of a particular breed. Direct economic values for some traits, most notably conformation traits, often are difficult to calculate but may be very important to farmers who breed and own registered cattle. Both approaches to placing values on individual traits produce broadly similar results (2010) NM\$ and TPI had a correlation of 0.88), but the differences between the indices reflect important economic factors affecting the users. Customized indices at the farm level were first delivered by McGilliard and Clay (1983) and proposed in Australia (Bowman et al., 1996) but were not widely used in the United States. As herds continue to grow larger, managers may have an incentive to customize their own indices (Dickrell, 2017).

Subindices

One way to make indices easier to understand is to construct them from a series of subindices. For example, NM\$ includes 3 type composites that combine information from several traits, and the calving ability dollars (CA\$) subindex combines sire and daughter 3690

NM\$ 2017	=	PROD\$ (43) Milk (1) Fat yield (24) Protein yield (18)	LONG\$ (27) Productive life (13) Cow livability (7) Somatic cell score (7)	FERT\$ (10) Daughter pregnancy — rate (7) Heifer conception — rate (1) Cow conception — rate (2)	TYPE\$ (16) Feet & legs (4) Udder (7) Body size (5)	CA\$ (5) Calving ease (2) Stillbirth (2)
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b)

REVISED NM\$	=	PROD\$ (41) Milk (1) Fat yield (23) Protein yield (17)	LONG\$ (25) Productive — life (12) Cow livability — (7) Somatic cell — score (6)	FERT\$ (10) Daughter — pregnancy — rate (6) Heifer conception — rate (1) Cow conception — rate (2) Age at first — calf (1)	TYPE\$ (12) Feet & legs — (2) Udder (6) Body size — (4)	CA\$ (6) Calving — ease (2) Stillbirth (2) Gestation — length (2)	HEALTH\$ (6) Mastitis (1) Metritis (1) Retained — placenta (1) Ketosis (1) Displaced — abomasum (1) Milk fever (1)

Figure 3. An example of lifetime net merit (NM\$) constructed from production (PROD\$), longevity (LONG\$), fertility (FERT\$), conformation (TYPE\$), and calving ability (CA\$) subindices. Panel (a) shows April 2017 NM\$, whereas panel (b) shows a hypothetical revision to NM\$ that includes a new health subindex (HEALTH\$) and additional traits in some subindices. Color version available online.

calving ease and sire and daughter stillbirth into a single quantity. All the breeder will see when the index is revised are the changes in emphasis on each of the subindices rather than changes to each of the individual traits (Figure 3). Farmers need to understand only the function of each subindex instead of dozens of traits. The Ideal Commercial Cow Index (**ICC\$**; Genex, 2006) is constructed in this way: ICC\$ is the sum of the production efficiency (PREF\$), health (HLTH\$), fertility and fitness (FYFT\$), milking ability (MABL\$), and calving ability (CABL\$) subindices. The advantages of this approach are small when indices contain only a few traits but increase rapidly as the number of traits included grows. Composite traits have a similar purpose but often are unitless instead of having monetary value.

The Irish EBI Index (ICBF, 2017) comprises 7 subindices: milk production, fertility, calving performance, beef carcass, cow maintenance, cow management, and health. The calving performance subindex receives 10% of the total emphasis and includes PTA for direct and maternal dystocia, gestation length, and stillbirth. The health subindex, with 4% of the emphasis, includes direct (clinical mastitis) and indirect (SCC) measures of udder health as well as lameness. These examples demonstrate the use of direct (e.g., dystocia, clinical mastitis) traits in combination with indirect (e.g., gestation length, SCC) indirect (indicator) traits.

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PHENOTYPES IN SELECTION INDICES

What Traits Are Included in Current Selection Indices?

The traits included in USDA selection indices over time, and weights placed on each, are shown in Table 1. The first USDA index, Predicted Difference Dollars (PD\$), included only milk and fat yield in the selection criterion, whereas the 2017 revision of NM\$ (Van-Raden, 2017) includes information about 33 different traits when subindices are considered. Selection indices differ within and across countries because economic conditions, traits recorded, and breeds used are not the same everywhere. Figure 4 shows traits included in total merit indices from 15 different countries. Trait definitions may differ slightly from one country to another, but common trait groups include yield (e.g., milk volume, fat and protein yield), longevity (e.g., productive life), fertility (e.g., nonreturn rate, days open), udder health (e.g., SCS, clinical mastitis), calving traits (e.g., dystocia, stillbirth), milking traits (e.g., milking speed), and conformation (e.g., udder conformation, feet and leg score). Although some broad similarities exist among indices-most include direct emphasis on protein yield—no two are the same, even within a country. For example, NM\$ includes more emphasis

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