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Selection index in pig breeding

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Abstract. This article describes the principles of selection index construction. Mathematical formulas are presented for calculating selection index weights using the economic weights of the breeding objective and breeder-specified target genetic gains. Methods are presented for assessing index accuracy, selection response for the index, and genetic gain for each individual trait.

Keywords: selection index; breeding objective; breeding value; genomic selection; BLUP.

Introduction

Pig breeding aims to improve multiple traits. Three methods can be used to select parents when several traits are selected simultaneously: independent culling levels, tandem selection, and selection index selection [14].

Independent culling levels are a strategy in which a minimum acceptable level (threshold) is specified for each trait, and a candidate is rejected if it fails to meet even one of these thresholds.

Under tandem selection, only one trait is improved in each generation. Once that trait reaches its target value, selection proceeds to the next trait.

A selection index is a numerical assessment of an animal's merit, expressed as a linear combination of its traits or genetic components, taking account of their economic importance and genetic relationships.

In 1942, it was demonstrated that, for independent traits with equal variance, heritability, and economic importance, the response to selection using a selection index exceeds the response obtained with tandem selection. The efficiency advantage of the selection index is proportional to $\sqrt{n}$, where n is the number of traits in the breeding objective [14, 15]. It was also demonstrated that the efficiency of independent culling levels lies between that of tandem selection and selection index selection.

In 1992, it was proposed that a combination of estimated breeding values (EBVs), obtained by best linear unbiased prediction (BLUP), should be used instead of a combination of traits [29]. An EBV is a more reliable indicator of an animal's true genetic merit than a trait that includes a substantial environmental component. This produces rankings that correspond more closely to true genetic merit and, consequently, a greater response to selection.

A restricted selection index is a version of the classical selection index in which constraints are imposed on the expected genetic response in one or more traits. Three main methods are used to construct restricted selection indices [28]: the Kempthorne index [23], the Harville index [22], and the Yamada index [35]. Restricted selection indices are used for traits such as litter size. Unrestricted selection for this trait reduces mean birth weight and increases the proportion of low-birth-weight piglets, resulting in greater losses [24].

This paper describes the principles of selection index construction. Mathematical formulas are presented for calculating index weights, index accuracy, the response to selection for the index, and the response for each individual trait. The paper shows how to account for four pathways of inheritance (dam to dam, dam to sire, sire to dam, and sire to sire) to estimate selection response more accurately.

The theory is presented for the general case in which the set of traits in the breeding objective differs from the set in the index. Multistage selection indices, optimum contribution selection to minimize the increase in inbreeding while maximizing genetic gain, and bioeconomic models for assessing the economic importance of traits are also briefly discussed.

Objective of the study

The objective is to systematize and briefly summarize the theoretical and methodological foundations of selection index construction in pig breeding. These include approaches to calculating index weights from the economic weights of the breeding objective and specified genetic gains, as well as methods for assessing index accuracy, expected selection response, and genetic gain in individual traits. The study also considers multistage selection indices, optimum contribution selection as a tool for limiting the increase in inbreeding, and bioeconomic models as a basis for establishing the importance of traits in a breeding program.

Materials and methods

This study is a narrative review of publications on the theory of selection index construction in pig breeding, including approaches based on economic weights and desired genetic gains.

The literature was searched in PubMed, Scopus, Web of Science, and Google Scholar for the period 1936-2026, with a search cutoff of February 24, 2026. Publications used in the review were identified through targeted keyword searches and examination of reference lists in scientific papers. The search focused mainly on English-language publications. Key search terms included combinations of breeding objective, aggregate genotype, economic weights, bioeconomic model, selection index, restricted selection index, desired gains, multistage selection, EBV, genomic selection, single-step, pig/swine, and related terms.

Results

Breeding objective

The first step in developing a selection index is to choose the breeding objective. The breeding objective H (also termed the aggregate genotype, economic genotype, or aggregate breeding value) is expressed as a linear combination of an animal's true breeding values for all economically important traits, weighted by their economic values [16]. Mathematically, the breeding objective is expressed as:

$$H = \sum_{i=1}^n a_i g_i, \quad (1)$$

where a_i is the economic weight of trait i , g_i is the animal's true breeding value for trait i , and n is the number of traits in the breeding objective.

Usually, only the additive component of breeding value is considered because it is easier to estimate, for example using BLUP. Economic weights have units of rubles per unit of a trait. Because each weight is multiplied by the corresponding trait in Equation (1), the breeding objective is expressed in rubles. Thus, animals can be ranked according to their value in rubles, and the most valuable animals can be selected for the next generation.

Economic weights depend on the set of traits included in the breeding objective. This means that the economic weights of traits change when the set of traits in H changes. The ratios among economic weights, rather than their absolute values, are decisive: multiplying all weights by the same constant changes only the scale of the index and preserves the ranking of animals.

Because achieving a breeding objective takes time, the set of traits and their economic weights should be determined with anticipated market conditions in mind. Economic weights are estimated using a bioeconomic model of the enterprise. Economically important traits that cannot be measured directly should also be included in the breeding objective [9].

The breeding objective provides the basis for constructing a selection index that includes traits that can be measured, are cost-effective to measure, and are genetically correlated with the traits in the breeding objective [12]. The set of traits in the breeding objective may therefore differ from that in the selection index [29].

In commercial pig breeding, a selection index is generally supplemented by thresholds for defects and conformation [10, 25]. In a three-breed cross, for example Landrace x Yorkshire to produce an F1 sow, followed by F1 sow x Duroc to produce a commercial crossbred, two selection indices may be used: (1) one for the two maternal breeds, Landrace and Yorkshire, and (2) one for the paternal breed, Duroc [8]. A separate selection index has also been proposed for selecting sows to produce F1 crossbred replacement gilts [1].

Selection index based on economic weights

The breeding objective is defined by true breeding values for economically important traits, but measuring all of these traits is often impossible in practice. A selection index is therefore used for selection. In 1936 for plants and in 1943 for animals, a linear combination of traits, termed a selection index, was proposed as an alternative to the breeding objective [16, 31]:

$$I = \sum_{i=1}^m b_i X_i, \quad (2)$$

where I is the selection index, m is the number of traits in the selection index, b_i is the weight of the breeding value of trait i in the index, and X_i is the measured value of trait i .

The number of traits m in the selection index may differ from the number of true breeding values for traits in the breeding objective H .

Traits that are difficult or uneconomical to measure are replaced by indicator traits. Indicator traits are genetically correlated with one or more traits in the breeding objective. For example, lean meat percentage is difficult to measure in a live animal. However, it is known to be represented by a combination of two traits, backfat thickness and loin eye depth, which explain 78% of its variance [2]. Selection index weights are estimated by maximizing the correlation between the selection index and the breeding objective [33]:

$$b = P^{-1}Ga, \quad (3)$$

where P is the $m \times m$ variance-covariance matrix of the traits, with trait variances on the diagonal and covariances between traits off the diagonal; G is the $m \times n$ variance-covariance matrix between the measured traits in I and the breeding values in H ; and a is the vector of economic weights in H . The length of a is n .

If the selection index contains the same traits whose true breeding values are used in the breeding objective, G has dimensions $n \times n$. In this case, the diagonal elements of G are the genetic variances of the traits, and the off-diagonal elements are genetic covariances between traits in the breeding objective.

To increase selection accuracy, estimated genetic components, EBVs, are used in the selection index instead of traits. In this case, the index is written as [29]:

$$I^{EBV} = \sum_{i=1}^m b_i^{EBV} EBV_i, \quad (4)$$

where I^{EBV} is the EBV-based selection index, m is the number of genetic components (estimated breeding values) in the genomic selection index, b_i^{EBV} is the weight of the breeding value of trait i in the selection index, and EBV_i is the estimated breeding value for trait i .

The weight vector b^{EBV} is estimated using:

$$b^{EBV} = G_{EBV,EBV}^{-1} G_{EBV,g} a, \quad (5)$$

where b^{EBV} is the vector of genomic selection index weights; $G_{EBV,EBV}$ is the $m \times m$ variance-covariance matrix of estimated breeding values (EBV_i) in the selection index I^{EBV} ; and $G_{EBV,g}$ is the $m \times n$ genetic variance-covariance matrix between EBV_i in the selection index I^{EBV} and g_i in the breeding objective H .

The elements of $G_{EBV,EBV}$ depend on the accuracy of the EBV estimates. If the set of traits in the selection index is the same as that in the breeding objective, then $G_{EBV,EBV} = G_{EBV,g}$, and the weights in the genomic selection index equal the economic weights in the breeding objective [29]:

$$b^{EBV} = G_{EBV,EBV}^{-1} G_{EBV,g} a = a. \quad (6)$$

The covariance between I^{EBV} and H is:

$$\begin{aligned} \text{cov}(I^{EBV}, H) &= \text{cov}(b^{EBVT} EBV, a^T g) \\ &= b^{EBVT} \text{cov}(EBV, g) a = b^{EBVT} G_{EBV,g} a, \end{aligned} \quad (7)$$

where g is the animal's true breeding value from Equation (1), and b^{EBVT} and a^T are the transposed vectors of selection index weights and economic weights of the breeding objective, respectively.

Substituting Equation (5) into Equation (7) gives an expression for the covariance between I^{EBV} and H without the weights b^{EBV} , following the chapter "Properties of the selection index" [33]:

$$\begin{aligned} \text{cov}(I^{EBV}, H) &= b^{EBVT} G_{EBV,g} a \\ &= a^T G_{EBV,g}^T G_{EBV,EBV}^{-1} G_{EBV,g} a. \end{aligned} \quad (8)$$

The variance of the selection index, $\sigma_{I^{EBV}}^2$, is calculated as follows, in accordance with the chapter "Properties of the selection index" [33]:

$$\begin{aligned} \sigma_{I^{EBV}}^2 &= b^{EBVT} G_{EBV,EBV} b^{EBV} \\ &= a^T G_{EBV,g}^T G_{EBV,EBV}^{-1} G_{EBV,g} a. \end{aligned} \quad (9)$$

Combining Equations (9) and (8) shows that the covariance between the selection index and the breeding objective equals the variance of the selection index:

$$\text{cov}(I^{EBV}, H) = \sigma_{I^{EBV}}^2. \quad (10)$$

Selection index accuracy is measured as the correlation between I^{EBV} and H :

$$r_{I^{EBV},H} = \text{cor}(I^{EBV}, H) = \frac{\text{cov}(I^{EBV}, H)}{\sigma_{I^{EBV}} \sigma_H} = \frac{\sigma_{I^{EBV}}^2}{\sigma_{I^{EBV}} \sigma_H} = \frac{\sigma_{I^{EBV}}}{\sigma_H}, \quad (11)$$

where $\sigma_H = \sqrt{a^T G_{g,g} a}$ is the standard deviation (the square root of the variance) of the breeding objective H , and $G_{g,g}$ is the variance-covariance matrix of true breeding values in H [6].

Equation (11) shows that index accuracy depends on the standard deviations of I^{EBV} and H . These, in turn, depend on the economic weights a , covariances among EBVs (represented by $G_{EBV,EBV}$), and covariances between EBVs and g (represented by $G_{EBV,g}$). Thus, with fixed economic weights, increasing selection index accuracy requires improving the reliability of EBV estimation (the accuracy of $G_{EBV,EBV}$ and $G_{EBV,g}$).

It is known that, when EBVs are obtained using BLUP, the equality $\text{cov}(EBV, g) = \text{var}(EBV)$ holds [6]. The reliability of the estimate is therefore:

$$\begin{aligned} \text{Reliability}_i &= \text{cor}(EBV_i, g_i)^2 = \frac{\text{cov}(EBV_i, g_i)^2}{\text{var}(EBV_i)\text{var}(g_i)} \\ &= \frac{\text{var}(EBV_i)^2}{\text{var}(EBV_i)\text{var}(g_i)} = \frac{\text{var}(EBV_i)}{\text{var}(g_i)}. \end{aligned} \quad (12)$$

The quantity $\text{var}(EBV_i)$ decreases as the accuracy of breeding value estimation decreases, and reaches zero when accuracy is zero. In a selection index, EBV_i therefore has a greater influence when its index weight is larger and its estimation accuracy is higher. In the simplest case, in which the breeding objective and selection index contain only one trait ($m = n = i = 1$), Equations (11) and (12) show that selection index accuracy equals the square root of the reliability of the breeding value estimate:

$$r_{I^{EBV}, H} = \text{cor}(EBV_i, g_i) = \sqrt{\text{Reliability}_i}.$$

The selection response for the index, that is, the expected change in the mean selection index of the offspring, is [5, 33]:

$$R_{I^{EBV}} = k \sigma_H r_{I^{EBV}, H} = k \sigma_H \frac{\sigma_{I^{EBV}}}{\sigma_H} = k \sigma_{I^{EBV}}, \quad (13)$$

where $k = \varphi(\Phi^{-1}(1 - p)) / p$ is selection intensity (p is the selection cutoff, φ is the probability density function of the normal distribution, and z is the truncation threshold in standard units). In the R programming language, k is calculated as `k <- dnorm(qnorm(1 - p)) / p`. Selected values of k are given in the table below [11].

Table. Selection intensity as a function of the selection cutoff in a normal distribution

Selection cutoff p , %	Selection intensity k
50.00	0.798
25.00	1.271
10.00	1.755
5.00	2.063
1.00	2.665
0.01	3.958

It is more convenient to express selection response per unit of time:

$$\Delta G_{I^{EBV}} = R_{I^{EBV}} / L = k \sigma_{I^{EBV}} / L, \quad (14)$$

where $\Delta G_{I^{EBV}}$ is the selection response for the index per unit of time, and L is the generation interval: the time from the birth of an animal selected to become a parent to the birth of its offspring. In other words, L is the mean age of a selected parent when its offspring is born.

Selection index accuracies calculated using Equation (11), as well as selection intensities, differ between sows and boars because fewer boars are required for breeding. In this case, the selection response for the index per unit of time is written as:

$$\Delta G_{I^{EBV}} = \frac{k^d \sigma_{I^{EBV}}^d + k^s \sigma_{I^{EBV}}^s}{L^d + L^s}, \quad (15)$$

where k^d and k^s are selection intensities, σ^d and σ^s for I^{EBV} are the standard deviations of the selection indices, and L^d and L^s are generation intervals for sows (superscript d , dam) and boars (superscript s , sire), respectively.

In the general case, four pathways of inheritance must be considered:

1. From a boar in one generation to a boar in the next generation (SS, sire to sire).
2. From a sow in one generation to a sow in the next generation (DD, dam to dam).
3. From a sow in one generation to a boar in the next generation (DS, dam to sire).
4. From a boar in one generation to a sow in the next generation (SD, sire to dam).

For each pathway, $G_{EBV,EBV}$ and, consequently, the selection index accuracy calculated using Equation (11) also differ because the accuracy of the animals' EBV estimates differs. The selection response for the index per unit of time is then:

$$\Delta G_{I^{EBV}} = \frac{R_{I^{EBV}}^{SS} + R_{I^{EBV}}^{DD} + R_{I^{EBV}}^{DS} + R_{I^{EBV}}^{SD}}{L^{SS} + L^{DD} + L^{DS} + L^{SD}}, \quad (16)$$

where R^{SS} , R^{DD} , R^{DS} , and R^{SD} for I^{EBV} are selection responses for the index along the four inheritance pathways, and L^{SS} , L^{DD} , L^{DS} , and L^{SD} are the generation intervals for these pathways.

Genetic gain for each trait in the breeding objective is [5, 33]:

$$R = k G_{EBV,g}^T b^{EBV} / \sigma_{I^{EBV}}, \quad (17)$$

where R is a vector of length m containing the genetic gains for each trait in the breeding objective H .

To estimate genetic gains more accurately, mean genetic gain per unit of time should be estimated across the four inheritance pathways, by analogy with Equation (16).

Selection index based on genetic gain

Selection index weights can be estimated using breeder-specified target (proportional) genetic changes in traits. This is useful, for example, when economic weights have not been estimated with sufficient accuracy or when a specialist needs to maintain a particular level of genetic gain.

A restricted selection index is used in this case. This index was developed to constrain genetic gain in specified traits, and its theory was subsequently extended to maintain a prescribed rate of genetic gain.

There are three main methods for constructing a restricted selection index: the Kempthorne index [23], the Harville index [22], and the Yamada index [35].

The Kempthorne index maximizes the breeding objective H while fixing the change in certain traits at zero.

The Harville index maximizes the breeding objective H subject to desired changes in certain traits.

The Yamada index is used to achieve specified genetic gains in all traits. An extended Yamada index also exists, allowing lower and upper thresholds for genetic gain to be specified for each trait, so that the response to selection remains within these limits [20].

The Yamada approach for breeder-specified genetic gains R is described below [35]. The vector of genomic selection index weights is [21, 28, 33, 35]:

$$b^{EBV} = G_{EBV,EBV}^{-1} G_{EBV,g} (G_{EBV,g}^T G_{EBV,EBV}^{-1} G_{EBV,g})^{-1} R. \quad (18)$$

If the set of traits in the selection index is the same as that in the breeding objective, $G_{EBV,EBV} = G_{EBV,g}$, Equation (18) simplifies to [28]:

$$b^{EBV} = G_{EBV,EBV}^{-1} R. \quad (19)$$

According to Equation (6), the selection index weights b^{EBV} coincide with the economic weights a in the breeding objective when the same traits are included in the selection index and the breeding objective. In this case, only the specified genetic gains R are needed to calculate the standard deviation of the breeding objective, $\sigma_H = a^T G_{g,g} a$.

The theoretical accuracy of the selection index can then be estimated using Equation (11). It should be remembered that, because the weights a are estimated from specified genetic gains rather than a bioeconomic model, they are pseudo-economic (non-market) weights. Comparing these weights with market-based weights may indicate a need to adjust the specified genetic gains. It should also be noted that R here represents desired genetic gain and is only a target value. The actual value may differ.

Multistage selection index

A multistage selection index extends classical selection index theory to situations in which selection decisions are made sequentially in several stages as information of differing cost and accuracy becomes available. Early stages use readily available, large-scale, relatively inexpensive data sources (for example, early phenotypes, pedigree information, and initial EBVs) to screen animals and reduce the number of candidates. Later stages use more informative but expensive measurements (for example, genotyping, station testing, and progeny testing), constructing a new index from an expanded data set and making the final selection within the already conditionally selected (truncated) subset. A fundamental feature of a multistage scheme is the maximization of expected genetic gain per unit of expenditure on data collection [4, 7].

Optimal selection with an inbreeding constraint

Optimum contribution selection (OCS) is a method of selecting breeding animals that simultaneously maximizes genetic gain and limits the rate of inbreeding by optimizing the contribution of genetic material from each selected candidate to the gene pool of the next generation. The method was developed to address the problem that selection based on an index maximizes genetic gain but may lead to excessive use of a small number of outstanding breeding animals, increasing inbreeding and reducing genetic diversity [13, 27].

Bioeconomic model

A bioeconomic model in breeding is a formalized model of a production system in which profit or gross margin (revenue minus costs) is expressed as a function of the mean levels of key biological traits and management decisions (feeding, culling, and reproduction). It enables quantitative assessment of how genetic improvement in each trait changes economic performance.

The first detailed descriptions of methods for deriving economic weights in pig breeding were provided in several studies [9, 32], and these methods were implemented in bioeconomic models in a number of papers [19, 30].

A simple approach to deriving economic weights in pig breeding, using a separate model for each trait, was described in several studies [3, 17, 18]. A flexible bioeconomic model for different production systems and associated software were developed by M. Wolfová [26, 34]. This software is available free of charge on request from the author.

Conclusion

Practical implementation of a selection index at an enterprise begins by formalizing the breeding objective H : the set of target traits and their economic weights, or the specified directions of genetic change [16]. The weights of the selection index, which is a linear combination of EBVs, are then calculated [29]. Two approaches can be used: one based on economic weights [29], and the other on target genetic gains [21, 28, 33, 35].

Using economic weights is the preferred method because it directly incorporates information on the future profit generated by an animal. However, it requires the development of a bioeconomic model to derive economic weights [3, 9, 17-19, 30, 32].

The target genetic change approach is convenient when reliable economic weights are unavailable. Before calculating selection index weights, the quality of the input EBVs must be ensured, and genetic variances and covariances between traits must be estimated. Introducing an index into breeding practice should be accompanied by validation using farm data: assessment of index accuracy [6], the predicted response for the index, and expected correlated responses for each trait, followed by monitoring of genetic trends [5, 33].

To control inbreeding, a constraint on the rate of inbreeding must be incorporated, for example through OCS contribution optimization [13, 27]. The breeding objective and selection index should be updated regularly as target values are achieved and economic conditions change [36].

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