Statistical Indicators
E-26
Publication Rules Sire Indexes

▪ Introduction

The breeding value estimation for sires is subjected to rules of the authorities. The Cooperation CRV is responsible for the publication of breeding values for sires.
Breeding values of sires are estimated based on information of their parents, observations on the animal itself and on their offspring. Some traits, such as milk production, cannot be measured in bulls. Then, only information of parents and offspring is used. Breeding values based on pedigree, performance and offspring are referred to as conventional breeding values. Breeding values can also be converted from international figures: Interbull carries out this conversion.

The introduction of genomics makes it possible to predict the genetic value of an individual animal based on DNA information. Breeding values based on genomic information are called genomic breeding values and are based on ancestor information and DNA information.

Genomic breeding values and conventional breeding values are estimated in two separate genetic evaluation systems. Breeding values from both systems are combined in a post-processing step after these two genetic evaluations, generating a combined breeding value. Starting December 2014, genomic information will be added to the breeding value estimation to obtain combined breeding values directly. The genomic information (DGV: Direct Genomic Value) will be treated as a pseudorecord/observation in the breeding value estimation. The new combined breeding value estimation provides a direct breeding value for bulls who have been genotyped or whose offspring have been genotyped. For bulls who have no offspring with performance, the genomic breeding value is based on ancestry, using only male ancestors and genomic information.

To publish a breeding value, this breeding value needs to comply with some publication criteria. Publication criteria are defined for conventional and for combined breeding values.
Only one breeding value is published for a certain trait of a bull. When genomic information is available for a bull, only the combined breeding value is published.

This chapter describes the publication rules for all traits of all sires, whose breeding values are published at the moment.

▪ Publication rules for conventional breeding values

The publication of conventional breeding values for sires depends on four criteria:
- The reliability of the breeding value;
- The use of information of offspring in the breeding value estimation;
- The genomic information (DGV) of the animal;
- The category to which the sire belongs.

Reliability

The breeding value estimation also calculates the reliability. This value, between 0,01 and 0,99 is a measure of the amount of information on which the breeding value is based and is presented as a percentage (1% and 99%). It is also a measure of the possible change of the breeding value when new information is added. To be published, breeding values have to meet a minimum value for reliability.

The EU-regulation 2016-1012 describe the minimum values for reliability as follows (appendix 3, part 3, article 7):

"For purebred breeding bulls of which the semen is meant to be used for artificial insemination, the minimum reliability should be at least:

a. for bulls belonging to the milk breeds (including dual purpose breeds) 0,50 for the most important traits of milk production …

b. for bulls belonging to the beef breeds (including dual purpose breeds) 0,30 for the most important traits of meat production …"

Genomic information

The genomic information will be made available by the bull owner (for his own bulls) in the form of Direct Genomic Values (DGVs). The DGVs will be added to the breeding value estimation as an estimation method of the DGVs when it is validated by Interbull.

Information on progeny

To receive a breeding value for a trait, a sire often depends on information of performances by his offspring. Besides the requirement regarding reliability, another requirement for publishing breeding values of sires is that every published breeding value has to contain information on the offspring of the sire. This means that the breeding value of a sire is published if at least one descendant has an observation for the concerning trait or for a correlated trait (predictor). The breeding value is also published if a sire has at least one descendant who contributes to the breeding value of the sire in the breeding value estimation. For example, a sire with one or more sons who has/have daughters in the breeding value estimation.

Category of the sires

The category of a sire (table 1) depends on

- whether a sire has been used as an AI sire;
- whether a sire has been tested nationally and/or internationally;
- the moment at which offspring of the sire has been born. This is determined by the available pedigree information in the Cooperation CRV breeding value estimation.

The categorization of sires is redone before every breeding value estimation. Therefore, the category of a sire is fixed during one and the same publication run and will not differ per trait. However, a sire can change categories over the course of time. Table 1 shows the requirements per category.

Table 1. Overview of requirements for categorization of sires

Category	Name and requirements
A	**Nationally tested AI sire** - The sire has an AI code in the Netherlands and/or Flanders - The number of days between the birth date of the sire and the 15th daughter in the pedigree file (1) of the breeding value estimation is 1800 days at the most - For privately-owned AI sires (AI code series 43000-44999 and 80000-83999) the number of days between the birth date of the sire and the 50th daughter in the pedigree file (1) of the breeding value estimation is 1800 days at the most
B	**Internationally tested AI sire** - The sire has been AI tested abroad and is present in the Interbull breeding value estimation for milk production with foreign daughters - The sire is not a category A sire: sire has less than 15 daughters in the pedigree file of the breeding value estimation or the number of days between the birth date of the sire and the 15th daughter in the pedigree file of the breeding value estimation is more than 1800 days, or does not have an AI code.
C	**Not AI tested sires** - The sire does not meet the requirements for a national or international AI sire
D	**International genomic AI sire** - The sire is used as an AI sire abroad and is present in the Interbull genomic conversion.

(1) The pedigree file is the complete pedigree file compiled from the pedigree files delivered by the studbook organizations

Publication rules

For all bull categories (see below) the reliability of the milk production breeding values need to be at least 50% to be published. For the meat breeding values, the reliability needs to be at least 30% to be published. For all other traits, the minimum reliability of a breeding value is 25% to be published.

Taking into account reliability, information on offspring, genomic information (DGV) of the bull himself and the above categories of sires, the following general publication rules apply:

A-category bulls:

- The national breeding value of AI sires that have been tested nationally (category A) will be published if the breeding value has a reliability of at least 50% for milk production traits, 30% for meat production traits and 25% for all other traits and if the information of at least one descendant or the bull's own genomic information was incorporated in the breeding value. For production traits an extra requirement is added, which demands the breeding value to be based on at least 15 daughters with observations, in at least 10 different herds.
- Bulls with their own genotype get a breeding value that is always from the national breeding value system
- When a bull has no own genotype and the Interbull breeding value has at least a 10% higher reliability, the Interbull breeding value is published. For conformation, for a bull without its own genotype, the national breeding value must be based on at least 15 inspected daughters in at least 10 different herds. For small local breeds, bulls must have at least 1 daughter regardless of the number of herds. Once the national breeding value for a bull is published, the national breeding value is retained. When a new Interbull trait is introduced, the 10% rule for that trait is again applied.

B-category bulls:

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- Bulls with their own genotype get a breeding value that is always from the national breeding value system
- When a bull has no own genotype and the Interbull breeding value has at least a 10% higher reliability, the Interbull breeding value is published
- As long as no Interbull breeding value is available, the national breeding value of AI sires that have been tested internationally (category B) will be published if it has a reliability of at least 50% for milk production traits, 30% for meat production traits and 25% for all other traits and if the information of at least one descendant or the bull's own genomic information has been incorporated in the breeding value or the bull has its own genomic information (DGV). This may be the case when a country, breed or trait is not participating in the Interbull evaluation.
- As soon as an Interbull breeding value is available, this will be published provided that the reliability is higher than 50% for milk production traits, 30% for meat production traits and 25% for all other traits. The Interbull breeding value will be overruled again by the national breeding value as soon as the national breeding value has a reliability of 90% or higher.

C-category bulls:

- The national breeding values of sires that have not been AI tested (category C) will be published if the reliability is more than 50% for milk production traits, 30% for meat production traits and 25% for all other traits and the breeding value is based on at least 10 descendants. Sires that have not been AI tested will not appear in the international indexation and will therefore never receive an Interbull breeding value.

D-category bulls:

- AI bulls who receive a converted genomic breeding value through Interbull, will have their breeding values published provided the reliability is 50% for milk production traits, 30% for meat production traits and 25% for all other traits. When no national genomic breeding value is available, the converted Interbull value is published.

These rules are applied per group of traits, considering the main trait as leading, e.g. percentage of reliability for final score is defining for all conformation traits. Table 2 indicates which trait is the main trait within a trait group. For AMS traits publication rules are adapted for each trait specifically. It is possible for one group of traits of a sire to be published as national breeding values and another group of traits of the same animal to be published as Interbull breeding values.

Table 2. Overview of the main traits per trait group

Trait group	Main trait
Milk production	Overall INET
Conformation	Final Score
Longevity	Longevity
Fertility	Overall Fertility
Somatic Cell Count	Overall Somatic Cell Count
Udder Health	Udder Health
Claw Health	Claw Health
Calf Survival	Calf Survival
Birthing Traits (direct effect)	Calving Ease
Maternal Calving Process	Maternal Calving Process
Vitality	Vitality
Maternal Vitality	Maternal Vitality
NVI(1)	NVI
Milking speed	Milking speed
Temperament	Temperament
Beef Merit Index traits	Beef Merit Index

Trait group	Main trait
Urea	Overall Urea
Reproduction disorders	Reproduction disorders
Metabolic disorder traits	Metabolic disorder – index
Ketose	Ketose
Feed intake	Feed intake
Resilience	Resilience
Methane	Methane

(1)NVI traits which do not have an official breeding value will not be used in the calculation of NVI.

▪ Publication rules for combined breeding values

If a bull has a genomic breeding value (DGV) for a trait, but he does not have offspring with performances for this trait, this breeding value is combined with the bull's pedigree-index. The pedigree index contains the breeding values of all known male ancestors of the bull.
If a bull has a genomic breeding value (DGV) for a trait and he has offspring with performances for this trait, the combined breeding values will be published. In this case, the genomic information will be added to the conventional breeding value as a pseudorecord.

A combined breeding value is published if
- the bull has an AI-code,
- the bull is at least 10 months of age,
- the reliability of the combined breeding value of the main trait (table 2) has a reliability of at least 50% for milk production traits, 30% for meat production traits and 25% for all other traits.

▪ Availability of breeding values

A breeding value is publishable if certain requirements are met. Table 3 shows a summary of the individual publication requirements per trait, in case the breeding values contain daughters with performance. This table shows the requirements needed for animals belonging to the A, B or C category.
For category D bulls, the genomic breeding values based on the Dutch/Flemish reference population will be published when available. Otherwise, the converted genomic breeding value from Interbull will be published.

For category D bulls, no NVI will be calculated when the production breeding values are based on the genomic Interbull conversion. Body weight breeding values will not be calculated when the conformation breeding values are based on the genomic Interbull conversion. Lifetime production indexes will not be calculated when the production breeding values are based on the genomic Interbull conversion. Breeding values or indexes that are a linear combination of traits will be calculated for category D bulls.

The breeding values for feed intake of a bull is determined be parental information, feed intake data of the daughters of the bull, genomic information of the bull and breeding values that serve as an indicator for feed intake. The indicators are production traits en bodyweight. For category D bulls, a feed intake breeding value will be published when a genomic breeding value is available. Breeding values based on the Interbull conversion or based on parental information will not be published.

The sires of categories A, B, C, and D are made available by Cooperation CRV. All publishable breeding values of the sires of categories A, B, C and D are available in the 031-file of the breeding value estimation. Parent averages may also meet the publication requirements, but they are never published in the publications or files.

Table 3. Publication requirements per trait group and category of the sire for the press publication and the sire files (ITB = Interbull, BV = breeding value)

	Category of the sire		
	A	**B**	**C**
Trait group	**nationally tested AI sire**	**internationally tested AI sire**	**Not AI tested sires**
NVI	- Production is official	- Production is official	- Production is official

Production	- A. For bulls **with** genomic information (based on own genotype) BV is taken from national system, if INET has a reliability of 50% or higher.
	- B. For bulls **without** genomic information (based on own genotype) National BV is taken, if INET has a reliability of 50% or higher and is based on at least 15 daughters in at least 10 herds. Those 15 daughters need to have a milk recording after day 120 of the first lactation. For small local breeds(1) bulls need to have at least 10 daughters with observations and no minimum for number of herds.
	- C. If bull also has ITB BV, then ITB BV is taken if ITB BV has at least a 10% higher reliability than the national BV and national BV has never been published before.
		- A. For bulls **with** genomic information (based on own genotype) BV is taken from national system, if INET has a reliability of 50% or higher.
		- B. For bulls **without** genomic information (based on own genotype) National BV is taken, if INET has a reliability of 50% or higher and is based on at least 15 daughters in at least 10 herds. Those 15 daughters need to have a milk recording after day 120 of the first lactation. For small local breeds(1) bulls need to have at least 10 daughters with observations and no minimum for number of herds.
		- C. If bull also has ITB BV, then ITB BV is taken if ITB BV has at least a 10% higher reliability than the national BV and national BV has never been published before.
		  - ITB BV with at least 50% reliability for INET.
		  - National BV if INET has a reliability of 90% or more.
			- National BV with a reliability of 50% or higher for INET and is based on at least 10 daughters.

Conformation[2]	- A. For bulls **with** genomic information (based on own genotype) in national system, FW is taken if it has a reliability of at least 25% for the main trait.
	- B. For bulls **without** genomic information (based on own genotype), national FW is published.
	  - If bull has at least 1 classified daughter and at least 25% reliability for the main trait.
	  - When bull also has ITB BV, then the
		- A. For bulls **with** genomic information (based on own genotype) in national system, FW is taken if it has a reliability of at least 25% for the main trait.
		- B. For bulls **without** genomic information (based on own genotype), national FW is published.
		  - If bull has at least 1 classified daughter and at least 25% reliability for the main trait.
		- When bull also has ITB BV, then the
			- National BV with a reliability of 25% or higher for the main trait and based on at least 10 daughters.

Trait group	Category of the sire		
	A	B	C
	nationally tested AI sire	internationally tested AI sire	Not AI tested sires
	National BV is taken if it is based on at least 15 classified daughters on at least 10 farms. - For small local breeds, bulls must have at least 1 classified daughter regardless of the number of farms. - C. If a breeding value cannot be published based on rules A and B, but there is an ITB BV, this ITB BV is published if it has at least 25% reliability for the main trait.	National BV is taken if it is based on at least 15 classified daughters on at least 10 farms. - C. If a breeding value cannot be published based on rules A and B, but there is an ITB BV, this ITB BV is published if it has at least 25% reliability for the main trait.	

	Category of the sire		
	A	B	C
Trait group	**nationally tested AI sire**	**internationally tested AI sire**	**Not AI tested sires**

Other traits
Longevity[3]
Birth Traits
Maternal Calving Process
Vitality
Maternal Vitality
Udder Health
Temperament
Milking Speed
Urea
Somatic cell count
Claw health
Calf survival
Automatic milking traits
Reproduction disorders
Milk fever
Clinical ketosis
Subclinical ketosis
Resilience
Methane
	- A. For bulls **with** genomic information (based on own genotype) BV is taken from national system.
	  - BV for main trait has a reliability of 25% or more.
	- B. For bulls **without** genomic information (based on own genotype) BV is taken from national system.
	  - BV for main trait has a reliability of 25% or more and a minimum of 1 offspring with phenotypic data.
	- C. ITB BV if ITB BV has at least a 10% higher reliability than the national BV and national BV has never been published before.
		- A. For bulls **with** genomic information (based on own genotype) BV is taken from national system.
		  - BV for main trait has a reliability of 25% or more.
		- B. For bulls **without** genomic information (based on own genotype) BV is taken from national system.
		  - BV for main trait has a reliability of 25% or more and a minimum of 1 offspring with phenotypic data.
		- C. ITB BV if ITB BV has at least a 10% higher reliability than the national BV and national BV has never been published before.
		  - National BV if main trait has a reliability of 90% or higher .
			- National BV with a reliability of 25% or higher for the main trait and based on at least 10 daughters.

Fertility	- A. For bulls **with** genomic information (based on own genotype) BV is taken from national system.
	  - National BV with a reliability of 25% or higher for fertility index.
	- B. For bulls **without** genomic information (based on own genotype) BV is taken from national system.
	  - National BV with a reliability of 25% or higher for fertility index and a minimum of 1 offspring with phenotypic data.
	- C. ITB BV if ITB BV for calving interval has at least a 10% higher reliability than the national BV for the main trait and national BV has never been published.
		- A. For bulls **with** genomic information (based on own genotype) BV is taken from national system.
		  - National BV with a reliability of 25% or higher for fertility index.
		- B. For bulls **without** genomic information (based on own genotype) BV is taken from national system.
		  - As long as ITB BV is not available: National BV with a reliability of 25% or higher for the main trait and a minimum of 1 offspring with phenotypic data.
		  - As soon as ITB BV is available: ITB BV with a reliability of 25% or more for calving interval.
			- National BV with a reliability of 25% or higher for fertility index and is based on at least 10 daughters.

Trait group	Category of the sire		
	A	B	C
	nationally tested AI sire	internationally tested AI sire	Not AI tested sires
	before.	- National BV if main trait has a reliability of 90% or higher	
Body Weight	- Underlying conformation traits meet the conformation requirements and body weight has a reliability of 25% or higher.	- Underlying conformation traits meet the conformation requirements and body weight has a reliability of 25% or higher.	- Underlying conformation traits meet the conformation requirements and body weight has a reliability of 25% or higher.
Calving index **Metabolic disorders - index**	- One of the breeding values for the underlying traits is official and the index has a reliability of at least 25% and a minimum of 1 offspring with phenotypic data.	- One of the breeding values of the underlying traits is official and the index has a reliability of at least 25% and a minimum of 1 offspring with phenotypic data.	- One of the breeding values of the underlying traits is official and the index has a reliability of at least 25%.
Beef Merit Index	- National BV with a reliability of 30% or higher for beef merit index and a minimum of 1 offspring with phenotypic data.	- National BV with a reliability of 30% or higher for beef merit index and a minimum of 1 offspring with phenotypic data.	- National BV with a reliability of 30% or higher for beef merit index and is based on at least 10 daughters. -

[1] Small local breeds are: Blaarkop, Fries Hollands, Fries Roodbont, Lakenvelder, Witrik, Brandrood, West-vlaams Rood, Oost Vlaams Wit-Rood, Belgisch Rood, Belgisch Blauw Mixte

[2] For conformation the calculation of the composites is only done when all linear traits, except front feet orientation and udder balance, are available.

[3] There is an additional demand for longevity for publication from national evaluation. The demand is that there must be at least 15 daughters in at least 10 herds with a minimum lactation length of 120 days.