Description of the genetic evaluation systems used in the Walloon Region of Belgium

APRIL 2022

Sylvie VANDERICK, Rodrigo Reis Mota, Katrien WIJNROCX
& Nicolas GENGLER

Terra Research and Teaching Centre, Université de Liège, Gembloux Agro-Bio Tech

Introduction

For almost 20 years, following the regionalization of agriculture in Belgium, the Walloon Region has fully developed and continues to develop its own genetic and genomic evaluation systems. in order to provide Walloon breeders with tools adapted and useful to their needs.

Since 2002, genetic evaluation systems for production and conformation traits have been routinely used. Likewise, genetic evaluation system for udder health (using somatic cell scores) has been routinely used since 2003, as well as for longevity since 2005, for female fertility since 2007, and for body condition score since 2010. Finally, calving ease has been evaluated by genetic evaluation system in routine since 2013. Therefore, these genetic evaluation systems allow the Walloon Region of Belgium to participate to the international MACE evaluations performed by INTERBULL for all traits nationally evaluated.

Moreover, since July 2013, genomic evaluation systems have been used in routine for most of these traits, thus enabling the Walloon Region of Belgium to participate to the international genomic evaluations (GMACE) performed by INTERBULL.

The purpose of this document is to give a synthesis of the systems developed and used to evaluate the Walloon dairy cattle.

Production traits

Introduction

The genetic evaluations for production traits (milk, fat and protein yields) in the Walloon Region are based on a test-day model. The most important feature of this approach is that it allows the use of all individual or elementary results obtained at the time of milk recording. The results ("breeding values") which come directly from this computation are expressed in equivalent 305 days of lactation and as average of the first three lactations and will be indicated later by "D" (for domestic). Domestic results of the bulls which have sufficient daughters in the Walloon Region are sent to INTERBULL. In return, INTERBULL sends back international breeding values for these bulls and many others, expressed on a base specific for the Walloon Region.

Regional Walloon evaluations: Test-Day model

Basic principles of the computation

Just like the old lactation models, a test-day model is also a BLUP animal model approach; therefore, it allows the unbiased comparison of similar animals which are in the same environment at the same time. This comparison corrects for possible genetic differences between individuals to compare. In a test-day model, a cow is compared with the other animals in an equal lactation, milked at the same moment (test-day) in the same herd. Other differences like lactation stage, age, gestation in progress are also taken into account by the model.

Particularities

The method used in the Walloon Region has certain specific characteristics compared to those of other evaluations, in order to fit within the specific needs of the Walloon breeders:

1. Multi-breed modelling, which corresponds better to the structure of our herds.
2. Multi-lactation (first to third) and multi-trait (milk, fat, protein) modelling: allowing the model to adapt well to missing lactations and/or traits, which makes it already compatible with possible future systems of differentiated testing.
3. Modelling intra-herd and year of calving lactation curves with regression of the result towards the lactation curve of the population, which is an optimal approach to hold account of the differences between herds for example due to different feeding systems (automatic feeding stations, total mixed rations).
4. Modelling and pre-correction for differences in lactation curves and for intra-lactation evolution due to the age and the breed, weighted according to the racial composition.

Further details are available in Auvray and Gengler (2002) and in Croquet et al. (2006).

Results

Computations with test-day models allow to evaluate the phenotypic potential ("producing ability") corrected for the not-specific effects of the environment, the genetic potential of each cow having known records and the genetic potential of the relatives. This can be done trait by trait, lactation by lactation and for each day in production during these lactations. Obviously this mass of results is not publishable just as it is for the moment and one recapitulates this information's over a standard period of 305 days in milk and expresses it as the average on three lactations. The genetic potential thus estimated is called domestic breeding value ("D"). These breeding values, for a selected group of sires, also contribute to the international evaluation at INTERBULL.

In the near future, other information will be extracted from Walloon computations, in particular persistency (to be able to maintain the production through lactation) and the rate of maturity (evolution of production from lactation to lactation).

INTERBULL international evaluation

INTERBULL computations are based on sire information provided by various populations and are carried out by regrouping those results in order to allow a single list by population of all the bulls. The method of evaluation is a multi-population analysis called MACE (Multiple Across Country Evaluation) and that can be schematized like this:

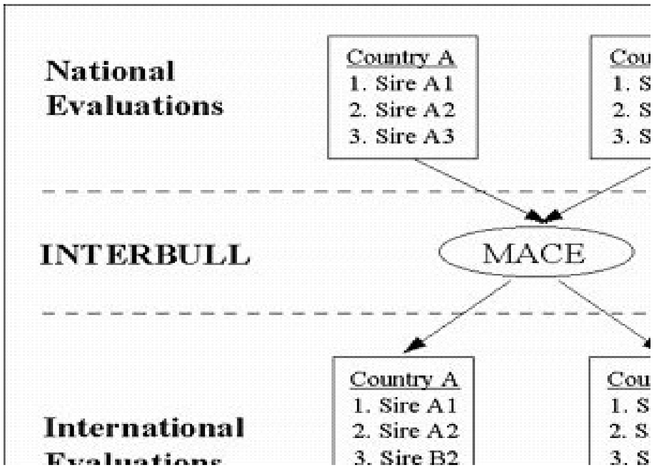

Figure 1: Schematic representation of INTERBULL evaluations (Source INTERBULL)

The different populations or evaluations send the breeding values of the bulls used in their population. INTERBULL regroups this multinational information and computes a genetic value for all the bulls in each population. Thus the various bulls A1, A2 and A3 coming from A population or country, and the bulls B1, B2 and B3 coming from B population or country, find themselves in only one single list per population. Notice that the order in each population is more similar with another if the correlation (thus the similarity of the results of these various populations) is high. For example, if A is Walloon Region and B is a population which is on the other side of the Earth, one expects great differences, but if B is a population near geographically, one expects relatively few differences. Notice that other factors play and create differences. For example, since some populations use various types of models, test-day or still lactation. The results provided by INTERBULL to the Walloon Region are thus always different from those provided to the Netherlands (regrouping Flanders). Moreover, INTERBULL provides the results on the Walloon scale, different from the others. «I» indicate the breeding values provided by INTERBULL, but they are completely comparable with the domestic ones. All domestic or INTERBULL results are comparable and are associated with a reliability which varies between 0 and 99% (or expressed as for one from 0.01 to 0.99), the accuracy of the evaluations increasing with this value.

Publication bases

Two bases of publication are used which are detailed in the document addressing this point. The first base is the INTERBULL 2020HC base and the second one is 2020BC base corresponding to the cows of Dual-Purpose Belgian-Blue breed born in 2015. A specific basis for Eastern Belgian Red and White breed animals is under consideration.

The sire file available here uses only the 2020HC base and contains only the results of the bulls with a minimum of 75% Holstein gene. The decision to keep for practically all the animals a single base also answers a wish to allow an equitable comparison between animals and facilitate a use of the results for management tools.

With the perspective of an increased future use of cross animals such an approach has the merit to allow to an easier comparison individuals of different breeds.

Publication rules

According to the origin of the evaluation:

- **Code “IP1”**: Bulls with an **I**NTERBULL evaluation coming from MACE evaluation (**P**olygenic), considered publishable in their country and having at least 50% INTERBULL reliability;
- **Code "IG1"**: Bulls with an INTERBULL evaluation from GMACE evaluation (**G**enomic), considered publishable in their country and having at least 50% INTERBULL reliability;
- **Code "DP1"**: Bulls without an INTERBULL evaluation for the trait, but with a Walloon (**D**omestic) **P**olygenic proof, i.e. estimated based only on Walloon phenotypic data, and having at least 50% domestic reliability;
- **Code "DG1"**: Bulls without an INTERBULL evaluation, but with a Walloon (**D**omestic) **G**enomic proof, i.e. estimated based only on Walloon genomic data and for which the animal's own genotype has been used, and having at least 50% domestic reliability;
- **Code "DG0"**: Bulls without an INTERBULL evaluation, but with a Walloon (**D**omestic) **G**enomic proof, i.e. estimated based only on Walloon genomic data but for which the animal's own genotype has not been used, and having at least 50% domestic reliability.

Only proofs for sires born after January 1, 1985 are published!

With the number of Walloon daughters, it is also possible to appreciate the Walloon contribution to the INTERBULL breeding value.

Udder Health

Introduction

Since May 2003, the Walloon Region has a routine genetic evaluation for somatic cells and participates in INTERBULL international evaluations for this trait.

This genetic evaluation system is based on a test-day model similar to that used in production and on the use of somatic cell counts (SCC) transformed on a cellular logarithmic scale called cell score (SCS):

$$\mathrm{SCS} = [\log_2(\mathrm{SCC}/100000)] + 3$$

Values of SCS are therefore around 3, with lower SCC associated to lower SCS.

Walloon computation: modified test-day model

The genetic evaluation model is very similar to the test-day model used for production traits with two modifications:

1. No intra-herds random regressions are used, because preliminary studies had not shown their interest;
2. Introduction of an iterative weighting of SCS records by a function expressing the suspicion of a mastitis event at that test-day.

This last modification is significant because it allows passing from a purely descriptive evaluation of somatic cells to an evaluation which allows a better appreciation of the relationship between mastitis incidence and SCS, so an evaluation of udder health. The weighting method is based on the comparison of the observed SCS and the expected SCS at a given test-day. The SCS records that are above the level of expected SCS based on standardized residuals of the test-day model have a higher weight than those below the expected level. Weights vary between two asymptotic values: 0 ($-\infty$) and 2.65 ($+\infty$) and follow a sigmoid distribution. The average of the weights is 1. Further details are in Gengler and Mayeres (2003) and in Croquet et al. (2006).

INTERBULL international evaluation

International evaluation done by INTERBULL follows the same procedures as for production traits, except that INTERBULL does two evaluations:

1. The first one with the somatic cell results of all the populations (including the Walloon Region),
2. The second one replaces the somatic cell results by those for mastitis if available.

The evaluation method is the same one as for the production, therefore a multi-country (population) analysis called MACE (Multiple Across Country Evaluation). Two lists of sires are available in return: one for each computation.

Publication bases

As the domestic method of evaluation used is optimized to improve correlation with mastitis events via a system of weightings, the values of the second evaluation – the one that groups together the "somatic cell" (SCS) evaluations with the mastitis evaluations - was selected for the publication of the breeding values of the sires. It automatically combines somatic cell results and mastitis results from various countries. For this reason, in isolated cases, a bull may get significantly lower reliability than in another given country.

A single base of publication is used for all animals; it is the 2020HC INTERBULL base.

Since April 2015, the functional trait udder health and other functional traits are expressed on a standardized scale with a mean of 100 and a standard deviation of 10. The standard deviation is calculated on the estimated breeding values for animals of the genetic base, i.e. all cows with records born in 2015 (2020HC base). Moreover, in the same time, the scale of udder health was inverted to express it on a positive scale as the other functional traits: higher breeding values are desirable.

Publication rules

According to the origin of the evaluation:

- **Code "IP1"**: Bulls with an **I**NTERBULL evaluation coming from MACE evaluation (**P**olygenic), considered publishable in their country and having at least 45% INTERBULL reliability;
- **Code "IG1"**: Bulls with an **I**NTERBULL evaluation from GMACE evaluation (**G**enomic), considered publishable in their country and having at least 45% INTERBULL reliability;
- **Code "DP1"**: Bulls without an INTERBULL evaluation for the trait, but with a Walloon (**D**omestic) **P**olygenic proof, i.e. estimated based only on Walloon phenotypic data, and having at least 45% domestic reliability;
- **Code "DG1"**: Bulls without an INTERBULL evaluation, but with a Walloon (**D**omestic) **G**enomic proof, i.e. estimated based only on Walloon genomic data and for which the animal’s own genotype has been used, and having at least 45% domestic reliability;
- **Code "DG0"**: Bulls without an INTERBULL evaluation, but with a Walloon (**D**omestic) **G**enomic proof, i.e. estimated based only on Walloon genomic data but for which the animal's own genotype has not been used, and having at least 45% domestic reliability.

Only proofs for sires born after January 1, 1985 are published!

With the number of Walloon daughters, it is possible to appreciate the Walloon contribution to the INTERBULL breeding value.

Conformation traits (type)

Introduction

The Walloon genetic evaluations for the conformation traits follow very closely the classification work made in the field. Indeed, the breeding values for 25 classified linear traits and for 8 synthetic traits, therefore more than the 19 INTERBULL traits are available to breeders and more than the traits currently recorder in the field. The method of computation is extremely advanced, associating multi-trait approach for several lactations, presence of missing values and adjustment for the differences in variances between classifier, herds and time. Results obtained come from 4 sources: from the "D" origin computation, from the "I" INTERBULL computation, from the prediction "P" of the 15 other traits by using those of INTERBULL, possibly combined with those obtained in the Walloon Region "B".

Table 1: Denomination and use of the evaluated traits.

Walloon number	*Trait*	*INTERBULL number*
1	Stature	1
2	Chest width	2
3	Body depth	3
4	Chest depth	
5	Loin strength	
6	Rump length	
7	Rump angle	5
8	Hips width	
9	Rump width	6
10	Foot angle	9
11	Rear leg set	7
12	Bone quality	
13	Rear leg rear view	8
14	Udder balance	
15	Udder depth	13
16	Teat placement side	
17	Udder support	12
18	Udder texture	
19	Fore udder	10
20	Front teat placement	14
21	Teat length	15
22	Rear udder height	11
23	Rear udder width	
24	Rear teat placement	16
25	Angularity	4
Syn1	Overall development	
Syn2	Overall rump	
Syn3	Overall feet and leg score	19
Syn4	Overall udder score	18
Syn5	Overall fore udder	
Syn6	Overall rear udder	
Syn7	Overall dairy trait	
Syn8	Overall conformation score	17

Walloon evaluation: repeatability multi-trait model

Basic principles of the computation

This multi-trait multi-lactation model is also a BLUP approach, therefore an equitable comparison of similar animals which are in the same environment at the same time. This comparison corrects for possible genetic differences between individuals to compare.

Particularities

The method used in Walloon Region has certain characteristics compared to those of other populations:

1. Modelling allows the presence of missing values, e.g. missing values due to a classification system changes over time. These system changes explain why we use more traits than are currently routinely classified.
2. Multi-trait modelling in order to take account of links between morphological traits. If a trait is missing, what is known about the morphology of the animal for another trait is used.
3. Modelling with correction for the heterogeneous variance, therefore differences in dispersion of the results, and this for the system, the classifier and the herd.
4. Modelling of more than one classification: if the cow is classified at least once before the third lactation (included), all classifications are taken into account by the model.

The method is extremely similar with that used in the USA until recently for the non-Holstein breeds. Other details are in Gengler et al. (2000) and in Croquet et al. (2006).

Results

The genetic potential is expressed, after INTERBULL computation, on a relative scale with 0 for the mean of **all the cows with classification records born in 2015** and their standard deviation put to 1. The standard deviations used to standardise to 1 are available in Table 2.

All results are comparable and are associated with a reliability which varies between 0 and 99%, the accuracy of the evaluations increasing with this value.

Table 2: Phenotypic and genetic means and standard deviations calculated on HC2020 animals (cows born in 2015 with a linear classification N=9054)

Trait		Genetic SD	Phenotypic mean**	Phenotypic SD**
Stature	1	0.62	7.66	1.35
Chest width	2	0.15	5.79	0.91
Body depth	3	0.24	6.18	0.89
Chest depth	4	0.22	N/A	N/A
Loin strength	5	0.16	6.47	0.79
Rump length	6	0.16	N/A	N/A
Rump angle	7	0.30	4.74	0.93
Hips width	8	0.20	N/A	N/A
Rump width	9	0.29	5.40	0.90
Foot angle	10	0.08	5.48	0.90
Rear leg set	11	0.14	5.57	0.80
Bone quality	12	0.23	6.40	0.96
Rear leg rear view	13	0.14	5.00	1.00
Udder balance	14	0.20	5.67	0.86
Udder depth	15	0.25	4.78	0.76
Teat placement side	16	0.15	N/A	N/A
Udder support	17	0.26	6.34	1.06
Udder texture	18	0.15	6.40	0.86
Fore udder	19	0.25	6.03	1.06
Front teat placement	20	0.30	5.09	0.83
Teat length	21	0.32	4.90	0.89
Rear udder height	22	0.25	6.61	1.03
Rear udder width	23	0.21	5.54	1.05
Rear teat placement*	24	0.24	6.83	0.78
Angularity	25	0.23	6.09	0.67
Overall development	syn1	1.09	83.62	3.36
Overall rump	syn2	0.77	83.12	3.32
Overall feet and leg score	syn3	0.45	81.77	2.95
Overall udder score	syn4	0.58	83.84	2.25
Overall fore udder	syn5	0.63	83.92	2.60
Overall rear udder	syn6	0.59	83.62	2.53
Overall dairy trait	syn7	0.76	82.41	2.07
Overall conformation score	syn8	0.56	82.59	1.78

* This trait has a different sense from the scale used by the classifiers.

** N/A indicates that for this trait there were no observations in the reference group of animals.

The interpretation of Table 2 allows a better understanding of the current position of the animals on the reference scales from 1 to 9. By respecting the meanings of the phenotypic scales, it is thus known that for an animal whose parents' average relative estimated breeding value is 2 for the overall conformation score, a corrected score expected from the descendant is 82.59 + (2 x 0.56) = 83.71. It should also be pointed out that some traits with an intermediate optimum have migrated to extremes, such as stature (7.66 very large) and rear teat placement (6.83, in observed scale 3.17 therefore very narrow).

INTERBULL international evaluation

Basic principles

INTERBULL carries out international evaluations regrouping results from different populations in order to create a single list by population of all the bulls. This is made trait by trait for 19 basic traits. The method of computation is the same as for production, therefore a multi-population analysis called MACE (Multiple Across Country Evaluation).

Breeding values provided by INTERBULL for the 19 INTERBULL traits are indicated by "I", but they are completely comparable with the domestic results.

Prediction and combinations of information for the 14 not processed by INTERBULL traits

The 14 not processed by INTERBULL traits are predicted (“P“ code) starting from information with “I” code transmitted by INTERBULL by using a standard procedure of selection index (Weigel et al., 1998) which takes account of links between traits as estimated in the Walloon Region. Whenever Walloon results ("D") exist for these same traits combination of the results ("B" code) is carried out by a weighted average (Weigel et al., 1998). This method allows carrying out pseudo-MACE for the not processed by INTERBULL traits by integrating the results of Walloon classifications.

Publication bases

A publication base is used for morphological traits. It is the INTERBULL 2020HC base because there is not official classification for other breeds. For Belgian Blue breed, an evaluation of the official cross-border classification is on the way.

Publication rules

According to the origin of the evaluation:

- **Code "P1"**: Bulls with an **I**NTERBULL evaluation coming from MACE evaluation (**P**olygenic), considered publishable in their country and having at least 50% INTERBULL reliability for stature;
- **Code "IG1"**: Bulls with an **I**NTERBULL evaluation from GMACE evaluation (**G**enomic), considered publishable in their country and having at least 50% INTERBULL reliability for stature;
- **Code "DP1"**: Bulls without an INTERBULL evaluation for the trait, but with a Walloon (**D**omestic) **P**olygenic proof, i.e. estimated based only on Walloon phenotypic data, and having at least 50% domestic reliability for stature;
- **Code "DG1"**: Bulls without an INTERBULL evaluation, but with a Walloon (**D**omestic) **G**enomic proof, i.e. estimated based only on Walloon genomic information and for which the animal's own genotype has been used, and having at least 50% domestic reliability for stature;
- **Code "DG0"**: Bulls without an INTERBULL evaluation, but with a Walloon (**D**omestic) **G**enomic proof, i.e. estimated based only on Walloon genomic data but for which the animal's own genotype has not been used, and having at least 50% domestic reliability;
- **Code "PP1"**: proof for this trait is **P**redicted from Interbull **P**olygenic (MACE) results for other traits;
- **Code "PG1"**: proof for this trait is **P**redicted from Interbull Genomic (**G**MACE) results for other trait;
- **Code "BM1"**: proof for this trait is a **B**lended proof combining predicted information (from "PP1" or "PG1") with information from "DP1" or "DG1" ➔ **M**ixed information.

With the percentage of Walloon daughters, it is possible to appreciate the Walloon contribution to the INTERBULL breeding value.

Longevity

Introduction

Since May 2005, the Walloon Region has been routinely using a genetic evaluation for direct longevity in Holsteins and participates in INTERBULL international evaluations for this trait. This genetic evaluation system is based on an improved approach that has similar bases as the currently used in Canada. Other countries such as the Netherlands and Germany have implemented new systems that are variations of the approach. In Wallonia, the survival of lactating animals in lactation is modelled across all lactations.

Walloon computation

Basic principles of the computation

This multi-lactation model is also a BLUP animal model approach, therefore an equitable comparison of similar animals which are in the same environment at the same time. This comparison corrects for possible genetic differences between individuals to compare.

Particularities

The method used in Walloon Region has certain characteristics compared to those of other populations:

1. Multi-lactation modelling: first five lactations and the next, regrouped with the fifth lactations for the fixed and random effects
2. Lactation survival modelling using a lactation random regression model which allows including records from previous lactation of cows that are still alive.

Further details are available in Gengler et al. (2005).

INTERBULL international evaluation

INTERBULL carries out international evaluations regrouping results from different populations in order to create a single list by population of all the bulls. The evaluation method is the same one as for the production, therefore a multi-country (population) analysis called MACE (Multiple Across Country Evaluation). Only results of direct longevity, coming from different populations, are used by INTERBULL.

« Combined » longevity index

For young bulls, the reliabilities associated at their breeding values for direct longevity are pretty low since longevity of daughters is proved after several years. In order to improve the reliabilities, but also to take correlations (Vanderick et al., 2006) between traits considered as being good predictors of longevity, i.e. type traits and udder health, the single trait longevity is transformed into multi-trait longevity according to selection index theory. This multi-trait longevity is called “combined” longevity combining three sources of information (direct and predicted from other traits). This allows to predict a longevity breeding value even if there are missing traits, such as direct longevity for example (in this case, code “P” for predicted). This combined longevity is computed after the INTERBULL computations.

Since April 2015, a procedure based on the theory of selection index has been used to compute simultaneously combined longevity with the combined female fertility (CFF) and the functional economic index (V€F). This procedure allows avoiding sharp shifts between two successive computations even if traits in the information vector change!

Publication base

A single base of publication is used; it is the 2020HC INTERBULL base.

Since April 2015, the functional trait combined longevity and other functional traits are expressed on a standardized scale with a mean of 100 and a standard deviation of 10. The standard deviation is calculated on the animals of the genetic base, i.e. all cows with records born in 2015 (2020HC base).

Publication rules

According to the origin of the evaluation:

- **Code "IP1"**: Bulls with an **I**NTERBULL evaluation coming from MACE evaluation (**P**olygenic), considered publishable in their country and having at least 30% INTERBULL reliability;
- **Code "IG1"**: Bulls with an **I**NTERBULL evaluation from GMACE evaluation (**G**enomic), considered publishable in their country and having at least 30% INTERBULL reliability;
- **Code "DP1"**: Bulls without an INTERBULL evaluation for the trait, but with a Walloon (**D**omestic) **P**olygenic proof, i.e. estimated based only on Walloon phenotypic data, and having at least 30% domestic reliability;
- **Code "DG1"**: Bulls without an INTERBULL evaluation, but with a Walloon (**D**omestic) **G**enomic proof, i.e. estimated based only on Walloon genomic and for which the animal’s own genotype has been used, data and having at least 30% domestic reliability;
- **Code "DG0"**: Bulls without an INTERBULL evaluation, but with a Walloon (**D**omestic) **G**enomic proof, i.e. estimated based only on Walloon genomic data but for which the animal's own genotype has not been used, and having at least 30% domestic reliability;
- **Code "PM1"**: Bulls without an INTERBULL evaluation for longevity trait and whose proof for this trait is **P**redicted from INTERBULL MACE (polygenic) or GMACE (genomic) results for other traits (➔ **M**ixed information), and having at least 30% mixed reliability.

With the number of Walloon daughters, it is possible to appreciate the Walloon contribution to the INTERBULL breeding value.

Female Fertility

Introduction

Since 2007, the Walloon Region used a genetic evaluation system for pregnancy rate (PR) in Holsteins and participates in INTERBULL international evaluations of female fertility with this trait. The international breeding values on Walloon basis were provided to breeders starting in September 2008. In 2010, some changes were realised in order to express as well as possible female fertility of Walloon dairy cattle.

Walloon computation

Evaluated trait

Pregnancy rate is defined as the percentage of no pregnant cows that become pregnant during each 21-d period (normal oestrous cycle). This measure is derived from days open (DO) that are the number of days where the cow is no pregnant and it takes voluntary waiting period into account:

$$PR = \frac{21}{DO - voluntary\ waiting\ \ period + k}$$

where k is half of a reproductive cycle so equal to 11 and voluntary waiting period is estimated to 45 days in our production circumstances. This notion of DO is also closely related to the notion of calving interval. As the pregnancy rate better expresses the selection objective, we prefer PR to DO.

Basic principles of the computation

The genetic evaluation system is an animal model adapted for repeated records. It is solved using BLUP; therefore, it provides a fair comparison of similar animals that are in the same environment at the same time. This comparison corrects for possible genetic differences between individuals to compare. The model is adapted for repeated data so one record by lactation. Some studies showed a low heritability for this trait, around 4%.

INTERBULL international evaluation and INTERBULL post-processing

Evaluated traits

To evaluate the trait group “Female Fertility”, the various populations participating to INTERBULL work with different traits such as the non-return rate, the interval calving-first insemination, the calving intervals or derived traits (DO, pregnancy rate), age at first insemination, etc. In order to facilitate the evaluations, INTERBULL groups the traits in five groups and therefore does five evaluations (one per group):

1. Maiden heifer's ability to conceive (e.g. conception rate, non-return rate, number of inseminations, interval first insemination-conception)
2. Lactating cow's ability to recycle after calving. (e.g. the interval calving-first insemination)
3. Lactating cow's ability to conceive (1) (e.g. conception rate or non-return rate)
4. Lactating cow's ability to conceive (2), (e.g. interval first insemination-conception or interval first-last insemination)
5. Lactating cow's measurements of interval traits calving-conception (e.g. days open or calving interval)

Basic principles

INTERBULL carries out international evaluations regrouping results from different populations in order to create a single list by population of all the bulls. The method of evaluation is the same as for production, therefore a multi-population analysis called MACE (Multiple Across Country Evaluation).

However, not all populations participate in all of the five groups and so all the bulls are not internationally evaluated. Moreover, traits used in an evaluation could be different, providing low genetic correlations between populations for this evaluation.

Since our trait is the pregnancy rate (calving interval), we participate at evaluations 2, 4 and 5. In return, INTERBULL provides from 0 to 3 international breeding values for bulls on the Walloon scale only for the groups 2, 4 and 5. It should be noticed that these values are not, in a strict sense, equivalent to those sent to INTERBULL.

The Walloon Region is an importing area of foreign genetic materials. Moreover, at the international level, there are numerous ways to express female fertility and these expressions have a priori small convergence between them. In order to find a common variation of these expressions, we carried out a study of the female fertility indexes published[1] in the six major import countries of genetic materials for the Walloon Region (Germany, Canada, Italy, France, Netherlands and USA). We found that only one value can express 80% of the common variation of these six indices. So, this value has been assumed as our sub breeding goal for female fertility.

In order to predict this goal, by using information from the national and international female fertility breeding values and from other traits breeding values, an approach of calculation was developed and is presented here.

Combined Female Fertility index

For young bulls, the reliabilities associated at their breeding values for direct[2] female fertility are pretty low since only information of daughter fertility through the first lactation is available. Furthermore, there are also bulls without international breeding values for each of the three groups in which Walloon Region participates but having international breeding values in the two others. Consequently, we developed a combined female fertility index combining two sources of information: direct female fertility and indirect[2] female fertility.

The international breeding values are combined, in function of their availability, in one value of direct female fertility according to a linear combination whose coefficients were estimated during the study described above.

Several studies showed that female fertility can be predicted by correlated traits. This allows predicting a female fertility breeding value even if there are missing traits (in this case, code “P” for predicted from INTERBULL traits). Based on nine traits evaluated in the Walloon Region, a breeding value of indirect female fertility can be predicted. These traits are: milk yield, protein, udder health, stature, body depth, overall udder score, overall feet and legs score, final conformation and Body Condition Score (BCS) or angularity when BCS is missing since recorded in Walloon Region for a few years.

Finally, a “combined” female fertility index is computed (breeding value of combined female fertility) after the INTERBULL computations thanks to the combination of direct and indirect information. More details are available in Vanderick et al. (2009).

Since April 2015, a procedure based on the theory of selection index has been used to compute simultaneously “combined” female fertility (CFF) with the “combined” longevity and the functional economic index (V€F). This procedure allows avoiding sharp shifts between two successive computations even if traits in the information vector change!

---

[1] Index published is the value used in each country to select the animals. This index is often composed by extra information not provided by INTERBULL.

[2] Direct means coming from data describing the female fertility, in opposition with indirect that means predicting by correlated traits.

Publication base

A single base of publication is used; it is the 2020HC INTERBULL base.

Since April 2015, the functional trait combined female fertility and other functional traits are expressed on a standardized scale with a mean of 100 and a standard deviation of 10. The standard deviation is calculated on the animals of the genetic base, i.e. all cows with records born in 2015 (2020HC base).

Publication rules

According to the origin of the evaluation:

- **Code "IP1"**: Bulls with an **I**NTERBULL evaluation coming from MACE evaluation (**P**olygenic), considered publishable in their country and having at least 30% INTERBULL reliability;
- **Code "IG1"**: Bulls with an **I**NTERBULL evaluation from GMACE evaluation (**G**enomic), considered publishable in their country and having at least 30% INTERBULL reliability;
- **Code "DP1"**: Bulls without an INTERBULL evaluation for the trait, but with a Walloon (**D**omestic) **P**olygenic proof, i.e. estimated based only on Walloon phenotypic data, and having at least 30% domestic reliability;
- **Code "DG1"**: Bulls without an INTERBULL evaluation, but with a Walloon (**D**omestic) **G**enomic proof, i.e. estimated based only on Walloon genomic data and for which the animal’s own genotype has been used, and having at least 30% domestic reliability;
- **Code "DG0"**: Bulls without an INTERBULL evaluation, but with a Walloon (**D**omestic) **G**enomic proof, i.e. estimated based only on Walloon genomic data but for which the animal's own genotype has not been used, and having at least 30% domestic reliability;
- **Code "PM1"**: Bulls without an INTERBULL evaluation for female fertility trait and whose proof for this trait is **P**redicted from INTERBULL MACE (polygenic) or GMACE (genomic) results for other traits (➔ **M**ixed information), and having at least 30% mixed reliability.

With the number of Walloon daughters, it is possible to appreciate the Walloon contribution to the INTERBULL breeding value.

Body Condition Score

Introduction

Body condition score (**BCS**) is a subjective measure of stored energy reserves of dairy cows. Currently, in the Walloon Region of Belgium, BCS is collected by milk recording agents or classifiers on a scale from 1 (=emaciated cow) to 9 (=obese cow). The BCS profile changes throughout the lactation: fresh cows in peak lactation tend to be in a negative energy balance and therefore lose condition; dry cows and low producers are in positive energy balance and gain condition. BCS is therefore related to milk production and it is an indicator of health and fertility.

Walloon computation

A genetic evaluation for BCS has been carried out routinely in the Walloon Region of Belgium since September 2010. Currently this calculation does not use the BCS taken during the linear classification, but only the angularity data. The features of the model are:

1. random regression test-day model,
2. multi-lactation (first to third) modelling,
3. multi-trait modelling: BCS is jointly modelled with angularity (or dairy character); the two-trait model allow increasing the reliabilities of BCS breeding values because angularity information provides additional correlated information and data depth in time.

Breeding value of BCS is expressed as the minimum daily estimated breeding value before 200 days in milk. Higher values are desirable in order to select cows with limited condition loss in early lactation. More details are provided in Bastin et al. (2010).

BCS has been included in the “combined” female fertility index. Because it is an indirect indicator of female fertility, it was integrated in the indirect female fertility index.

INTERBULL international evaluation

INTERBULL carries out international evaluations regrouping results from different populations in order to create a single list by population of all the bulls. The method of computation is the same as for production, therefore a multi-population analysis called MACE (Multiple Across Country Evaluation). Breeding values provided by INTERBULL for BCS are indicated by "I", but they are completely comparable with the domestic results.

Publication bases

A publication database is used; it is the INTERBULL designated database 2010HC is based on animals with actual BCS data.

Publication rules

According to the origin of the evaluation:

- **Code "IP1"**: Bulls with an **I**NTERBULL evaluation coming from MACE evaluation (**P**olygenic), considered publishable in their country and having at least 30% INTERBULL reliability;
- **Code "IG1"**: Bulls with an **I**NTERBULL evaluation from GMACE evaluation (**G**enomic), considered publishable in their country and having at least 30% INTERBULL reliability;
- **Code "DP1"**: Bulls without an INTERBULL evaluation for the trait, but with a Walloon (**D**omestic) **P**olygenic proof, i.e. estimated based only on Walloon phenotypic data, and having at least 30% domestic reliability;
- **Code "DG1"**: Bulls without an INTERBULL evaluation, but with a Walloon (**D**omestic) **G**enomic proof, i.e. estimated based only on Walloon genomic data and for which the animal's own genotype has been used, and having at least 30% INTERBULL reliability;
- **Code "DG0"**: Bulls without an INTERBULL evaluation, but with a Walloon (**D**omestic) **G**enomic proof, i.e. estimated based only on Walloon genomic data but for which the animal's own genotype has not been used, and having at least 30% domestic reliability.

With the number of Walloon daughters, it is possible to appreciate the Walloon contribution to the INTERBULL breeding value.

Calving ease

Introduction

Calving ease measures the presence or absence of dystocia and its intensity. Dystocia may be defined as calving difficulty resulting from prolonged spontaneous calving or prolonged or severe assisted extraction.

In the Walloon Region of Belgium, calving ease is scored by dairy breeders on a voluntary basis. Calving ease scores range from 1 to 5:

Score	Interpretation
1	Easy pull
2	Hard pull
3	Caesarean
4	Normal (without assistance)
5	Embryotomy

Walloon computation

Since April 2013, a genetic evaluation of calving ease has been routinely run for Walloon Holstein dairy cattle. For purposes of the evaluation, calving ease scores were reordered as described below:

Score	Interprétation
1	Caesarean and Embryotomy
2	Hard pull
3	Easy pull
4	Normal (without assistance)

The genetic evaluation model is a univariate linear animal model and it is solved using a BLUP animal model approach; therefore, it provides a fair comparison of similar animals that are in the same environment at the same time. Calving ease is affected by two additive genetic components:

1. the calf's contribution i.e. the ability of the calf to be easily born (direct effect).
2. the dam's contribution i.e. the ability of the dam to easily give birth (maternal effect).

The direct additive effect is expressed only once, when the calf is born, whereas the maternal additive effect is expressed several times, each time a cow calves. Moreover, both these effects can be negatively or positively correlated, or uncorrelated according to studies.

According to a study (Vanderick et al., 2014) carried out for the development of the current genetic evaluation system of calving ease, no relevant genetic correlation between direct and maternal effects on ease of calving was found.

From this genetic evaluation system, two breeding values are estimated for each animal: a breeding value for direct calving ease (DCE) and one for maternal calving ease (MCE).

More details are provided in Vanderick et al. (2013) and in Vanderick et al. (2014).

INTERBULL international evaluation

INTERBULL carries out international evaluations regrouping results from different populations in order to create a single list by population of all the bulls. The method of computation is the same as for production, therefore a multi-population analysis called MACE (Multiple Across Country Evaluation). Breeding values provided by INTERBULL for BCS are indicated by "I", but they are completely comparable with the domestic results.

Publication base

A single base of publication is used; it is the 2020HC INTERBULL base.

Since April 2015, the functional traits direct and maternal calving ease and other functional traits are expressed on a standardized scale with a mean of 100 and a standard deviation of 10. The standard deviation is calculated on the animals of the genetic base, i.e. all cows with records born in 2015 (2020HC base).

Publication rules

According to the origin of the evaluation:

- **Code “IP1”**: Bulls with an **I**NTERBULL evaluation coming from MACE evaluation (**P**olygenic), considered publishable in their country and having at least 30% INTERBULL reliability;
- **Code "IG1"**: Bulls with an **I**NTERBULL evaluation from GMACE evaluation (**G**enomic), considered publishable in their country and having at least 30% INTERBULL reliability;
- **Code "DP1"**: Bulls without an INTERBULL evaluation for the trait, but with a Walloon (**D**omestic) **P**olygenic proof, i.e. estimated based only on Walloon phenotypic data, and having at least 30% domestic reliability;
- **Code "DG1"**: Bulls without an INTERBULL evaluation, but with a Walloon (**D**omestic) **G**enomic proof, i.e. estimated based only on Walloon genomic data and for which the animal’s own genotype has been used, and having at least 30% domestic reliability;
- **Code "DG0"**: Bulls without an INTERBULL evaluation, but with a Walloon (**D**omestic) **G**enomic proof, i.e. estimated based only on Walloon genomic data but for which the animal's own genotype has not been used, and having at least 30% domestic reliability.

With the number of Walloon daughters, it is possible to appreciate the Walloon contribution to the INTERBULL breeding value.

Holstein genomic computations

Introduction

Details of the procedures currently used in genomic evaluation are detailed by Colinet et al (2018). Here is a summary.

Principles of genomic calculations

For Holstein animals, for which we have SNP genotypes and for their ancestors, the latest breeding values with the associated reliability are extracted from 3 sources of information:

1. Domestic breeding values
2. MACE breeding values
3. Breeding values sent for these MACE calculations

The single-step calculations are repeated for all evaluated traits and generate the domestic GEBVs (Genomically Enhanced Estimated Breeding Values) mentioned above.

INTERBULL genomic breeding values of bulls

The results of this calculation are provided to INTERBULL who combine them across the participating populations in the context of the GMACE. They will also directly provide the breeding values of foreign bulls on a Walloon basis.

Generation and use of SNP values for interim calculations

By using adapted strategies, the GEBVs are reduced by the polygenic contribution in order to represent DGVs (direct genomic values). These DGVs undergo an inverse transformation generating SNP solutions. These solutions are made available to elevéo in order to offer an interim calculation service to breeders while awaiting evaluations.

Integration of foreign information into breeding values for cows

Introduction

All breeding values reported in the Walloon Region for cows contain foreign information if available and this is carried over for one additional generation.

INTERBULL breeding values of sires

INTERBULL provides directly breeding values for foreign bulls on the Walloon scale.

Breeding values of foreign dams

Dams from Germany and Luxembourg, the Netherlands, France, Italy, Canada and USA of Walloon cows are identifying. Through collaboration with the respective genetic evaluation centres, breeding values for production traits for those cows are obtained (if available) and converted to the Walloon scale.

Integration of foreign breeding values

All foreign information is introduced through modification of parent averages and their integration using a procedure presented by VanRaden (2001). Two iterations are run allowing grand-parents to influence their grand-children. This is a compromise between feasibility and completeness of updating.

Global Index V€G and partial indexes V€L, V€T (V€C, V€P and V€M) and V€F

Introduction

In order to allow to the Walloon breeders to choose parents in spite of the existence of almost 40 evaluated traits, an overall index (which is composed of several partial indices) was developed. These indices, global and partial, reflect a selection target of economic profitability to life, as well as the components of this one.

The global index (**V€G**) contains partial indexes for:

- milk production traits (« Valeur économique Lait » – **V€L**),
- morphology traits (« Valeur économique type fonctionnel » - **V€P**)
- functional traits (« Valeur économique fonctionnelle » -**V€F**)

Development and definition of V€G, V€L, V€T, and V€F.

In a first stage, an economic function of profitability to life was established using a similar approach with that of VanRaden used in the United States of America (VanRaden and Cole, 2014). This method has the characteristic to be multiplicative in respect to longevity, i.e. to regard successive lactations as repetition of profitability by lactation. The use of this approach was made possible through the adjustment of economic coefficients to our situation and the simplification the equations. Lifetime economic profitability has therefore been defined as the prediction of the economic result per lactation multiplied by the expected longevity of the females, thus updating the expected overall economic result. This lifetime economic profitability function is therefore a representation of our current selection target (V€G).

In a second stage, relations between quantities of milk, fat and protein were established by taking account of the situation of payment of milk in Walloon Region in order to develop a synthetic milk index (V€L). In these computations considerations of the relation of the paid prices were included, of the costs, the losses due to the production of not paid components (especially lactose), of quota and of current evolution of the genetic percentage trends). This allowed releasing a relation between standardized quantities thus taking account the fact that for example the fat content is more variable than the protein one.

Then in a third stage, after having established groups of traits for udder and feet and legs using literature, coefficients of linear prediction of economic function of lifetime profitability were obtained from multiple regression coefficients. Two second order partial indices were developed: feet and leg economic value (V€M) and udder economic index (V€P). Traits of morphology related to the body were grouped into a third second order partial index: capacity economic index (V€C). The sum of these three indices is called functional type economic index (V€T).

In a fourth stage, carried out in February 2004, a new partial synthetic index called Functional Economic Value (V€F) was developed to take into account functional traits (udder health, longevity, female fertility...).

These different economic (partial) indexes have obviously evolved over time since the routine implementation of the first genetic evaluation systems in 2002. The evolution of these indexes, in terms of the relative importance of the different partial indexes and traits, is summarised in Table 3.

Table 3: Evolution of partial synthetic indexes and characters (in terms of relative importance)

Partial index / trait		2002 November	2004 February	2006 August	2015 April	2020 December
V€G	V€L	/	55%	48%	48%	48%
	V€F		9%	28%	28%	28%
	V€T		36%	24%	24%	24%
V€L	Milk	20% (-)	20% (-)	21% (-)	21% (-)	**20% (-)**
	Fat	30%	30%	19%	19%	**40%**
	Protein	50%	50%	60%	60%	**40%**
V€F	Udder health	/	100%	18%	12%	**25%**
	Longevity	/	/	82%	74%	**25%**
	Female fertility	/	/	/	7%	**25%**
	Direct calving ease	/	/	/	3%	**12,5%**
	Maternal calving ease	/	/	/	4%	**12,5%**
V€T	V€C	17%	17%	6%	6%	6%
	V€M	35%	35%	36%	36%	36%
	V€P	48%	48%	58%	58%	58%
V€C	Stature	45%	45%	/	/	/
	Chest width	15%	15%	/	/	/
	Body depth	15%	15%	/	/	/
	Angularity	20% (-)	20% (-)	/	/	/
	Rump width	5%	5%	/	/	/
	Overall development (syn1)	/	/	28% (-)	28% (-)	28% (-)
	Overall udder score (syn4)	/	/	51%	51%	51%
	Overall conformation score (syn8)	/	/	21% (-)	21% (-)	21% (-)
V€M	Rear leg set	8%	8%	16% (-)	16% (-)	16% (-)
	Rear leg rear view	18%	18%	8%	8%	8%
	Foot angle	74%	74%	/	/	/
	Bone quality	/	/	41%	41%	41%
	Overall feet and leg score (syn3)	/	/	35%	35%	35%
V€P	Fore udder	14%	14%	14%	14%	14%
	Rear udder height	23%	23%	23%	23%	23%
	Udder support	9%	9%	9%	9%	9%
	Udder depth	23%	23%	23%	23%	23%
	Front teat placement	4%	4%	4%	4%	4%
	Rear teat placement	18% (-)	18% (-)	18% (-)	18% (-)	18% (-)
	Teat length	9% (-)	9% (-)	9% (-)	9% (-)	9% (-)

The latest changes date from December 2020 and concern V€L and V€F. Indeed, following the outlook for the milk market and its valuation, as well as comments from players in the field (producers, breeders, sellers, etc.), a new V€L and a new V€F have been refined.

The synthetic milk index (V€L) has therefore evolved to take into account the evolution of the remuneration and production costs of milk closer to 50/50 of the fat/protein ratio (in standardised terms). Consequently, the relationship between standardised quantities has become 20%, 40% and 40% for milk, fat and protein redefining the V€L. It is important to underline that we continue to prefer a negative weight for the quantity of milk instead of directly considering the rates, unlike other populations who use the latter approach. The major reason is that in the Walloon milk payment system, prices are affected by the quantities and not the rates. However, producing other non-valuable components also has a cost, especially but not exclusively, lactose. The contribution of the V€L to the overall selection objective (V€G) remains at 48% as before.

The functional synthetic index (V€F) still contains the following 5 functional traits: udder health, longevity, female fertility, direct and maternal calving ease. Nevertheless, the relative contributions have been refined to take into account the demands of the field and the genetic progress observed. The relative contribution of longevity has thus been reduced to 25% while the relative contributions of udder health, female fertility and calving ease have increased to 25% (the 25% relative contribution of calving ease being divided in two between direct and maternal calving ease). The calculation of the V€F continues (as has been the case since April 2015) to be carried out at the same time as the calculation of the "combined" longevity index and the "combined" female fertility index through a selection index type procedure, thus allowing for gradual transitions between successive calculations even if the traits composing the information vector change. The contribution of the V€F to the overall selection objective (V€G) remains at 28% as before.

Table 4 gives a synthetic view of the relative importance of the various partial indices (all expressed in Euro), and traits, as well as the coefficients. The V€G is the sum of the V€L, the V€T and the V€F indexes. The V€T itself formed by adding the three morphological partial indexes V€M, V€C and V€P.

The correlations between V€G and the various partial indexes and traits making it up are also presented in Table 4. These correlations give an idea of the responses to the expected selection in relative terms. Take longevity as an example, its correlation with the V€G is 0.62. Therefore, selecting 1 standard deviation of V€G is expected to move by 1 * 0.62 standard deviation.

As a reminder, all the indexes (global and partial) are associated with a reliability which is still called "repeatability" in Wallonia and "coefficient of determination" in France. The reliability of the different indexes is calculated using the genetic correlations between traits and the reliability associated with each trait of the index.

Table 4: Relative importance of the different partial indexes and traits and their correlations with V€G

				Relative importance in		Correlation with[1]
Index	Partial index / trait	Coefficient	Standard deviation	Partial index	V€G	V€G
V€G	V€L	1	96.21	48%	48%	0.73
	V€F	1	55.71	28%	28%	0.63
	V€T	1	48,30	24%	24%	0.;40
V€L	Milk (kg)	-0.060	532	20%	10%	0.31
	Fat (kg)	3.62	17.70	40%	19%	0.72
	Protein (kg)	4.00	16.04	40%	19%	0.55
V€F	Udder health[2]	1.79	10	25%	7%	0.44
	Longevity[2]	1.79	10	25%	7%	0.62
	Female fertility[2]	1.79	10	25%	7%	0.15
	Direct calving ease[2]	0.89	10	12.5%	3.5%	0.48
	Maternal calving ease[2]	0.89	10	12.5%	3.5%	0.43
V€T	V€M	1	21.19	36%	9%	0.36
	V€C	1	3.62	6%	1%	0.18
	V€P	1	33.84	58%	14%	0.32
V€M	Rear leg set	-4.11	1	16%	1.4%	-0.09
	Rear leg rear view	2.06	1	8%	0.7%	0.28
	Bone quality	10.54	1	41%	3.7%	0.20
	Feet and legs (syn3)	9.00	1	35%	3.2%	0.33
V€C	Overall development (syn1)	-4.32	1	28%	0.3%	-0.01
	Final conformation (syn8)	7.88	1	51%	0.5%	0.19
	Overall udder (syn4)	-3.24	1	21%	0.2%	0.27
V€P	Fore udder	8.64	1	14%	2.0%	0.28
	Rear udder height	14.19	1	23%	3.2%	0.25
	Udder support	5.55	1	9%	1.3%	-0.11
	Udder depth	14.19	1	23%	3.2%	0.25
	Front teat placement	2.47	1	4%	0.5%	0.22
	Rear teat placement	-11.11	1	18%	2.5%	0.03
	Teat length	-5.55	1	9%	1.3%	-0.14

[1] Correlations computed on the latest generation of bulls used in the Walloon region of Belgium (born between 2008 and 2012) which are therefore sires of calves currently being born in 2020 (N=582).

[2] Index from which the mean of 100 is subtracted.

Literature cited

Auvray, B., and N. Gengler. 2002. Feasibility of a Walloon test-day model and study of its potential as tool for selection and management. In Proceedings of the 2002 Interbull meeting. Interlaaken, Switzerland. 123–127.

Bastin, C., A. Gillon, X. Massart, H. Soyeurt, S. Vanderick, C. Bertozzi, and N. Gengler. 2010. Genetic evaluation for body condition score in the Walloon Region of Belgium. Interbull Bull. 85.

Colinet, F.G., J. Vandenplas, S. Vanderick, H. Hammami, R.R. Mota, A. Gillon, X. Hubin, C Bertozzi, and N. Gengler. 2018. Bayesian single-step genomic evaluations combining local and foreign information in Walloon Holsteins. Animal 12: 98-905.

Croquet, C., P. Mayeres, A. Gillon, S. Vanderick, and N. Gengler. 2006. Inbreeding depression for global and partial economic indexes, production, type, and functional traits. J. Dairy Sci. 89:2257–2267.

Gengler, N., and P. Mayeres. 2003. Use of a weighted random regression test-day model to better relate observed somatic cell score to mastitis infection likelihood. Interbull Bull. 92.

Gengler, N., S. Vanderick, P. Mayeres, A. Gillon, and C. Croquet. 2005. Genetic evaluation of cow survival using a lactation random regression model. Interbull Bull. 176.

Gengler, N., G. Wiggans, J. Wright, and T. Druet. 2000. Multitrait genetic evaluation of Jersey type with integrated accounting for heterogeneous (co) variances. Interbull Bull. 108.

Vanderick, S., C. Bastin, and N. Gengler. 2009. Expressing female fertility in the Walloon Region of Belgium: How to do? Interbull Bull. 10.

Vanderick, S., C. Croquet, H. Soyeurt, H. Hammami, P. Mayeres, and N. Gengler. 2006. Integration of longevity into the Walloon genetic evaluation system. Interbull Bull. 22.

Vanderick, S., T. Troch, A. Gillon, G. Glorieux, P. Faux, and N. Gengler. 2013. Genetic evaluation of calving ease for Walloon Holstein dairy cattle. Interbull Bull. 32–37.

Vanderick, S., T. Troch, A. Gillon, G. Glorieux, and N. Gengler. 2014. Genetic parameters for direct and maternal calving ease in Walloon dairy cattle based on linear and threshold models. J. Anim. Breed. Genet. 131:513–521. doi:10.1111/jbg.12105.

VanRaden, P. 2001. Methods to combine estimated breeding values obtained from separate sources. J. Dairy Sci. 84:E47–E55.

VanRaden, P., and J. Cole. 2014. Net merit as a measure of lifetime profit: 2014 revision. Anim. Improv. Programs Lab. ARS-USDA Beltsville MD.

Weigel, K., T. Lawlor, P. VanRaden, and G. Wiggans. 1998. Use of linear type and production data to supplement early predicted transmitting abilities for productive life. J. Dairy Sci. 81:2040–2044.