

GENETIC EVALUATION NOTES

HOLSTEIN AND JERSEY

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HOLSTEIN

1. SELECTION INDEXES

1.1. PFT (Productivity, Functionality and Type)

PFT is the selection index of the Italian Holstein breed, which combines milk production, functionality and type. The official ranking is based on PFT and ranges from 0 to 99 dividing the population in percentiles. The ranking is calculated separately for bulls and cows. The rank 99 identifies the best 1% of bulls and cows. Since December 2011, rank 98 (best 2% of the population) is the official limit for a bull to be used in A.I. The following table shows the relative weight of each trait included in PFT. Last PFT adjustment is from December 2019.

The formula for PFT is as follows:

$$\begin{aligned}
 \text{PFT} = & 9.1 * \{ [33 * ((\text{protein kg} - \text{avg protein kg}) / \text{std protein kg})] + \\
 & [8 * ((\text{fat kg} - \text{avg fat kg}) / \text{std fat kg})] + \\
 & [3 * ((\text{protein\%} - \text{avg protein\%}) / \text{std protein\%})] + \\
 & [3 * ((\text{fat\%} - \text{avg fat\%}) / \text{std fat\%})] + \\
 & [5 * (((\text{longevity} - 100) / 5) / \text{std longevity})] + \\
 & [20 * (((\text{fertility} - 100) / 5) / \text{std fertility})] + \\
 & [5 * (((\text{somatic cell score} - 100) / 5) / \text{std scs})] + \\
 & [9 * (\text{icm} / \text{std icm})] + \\
 & [4 * (\text{type} / \text{std type})] + \\
 & [4 * (\text{iap} / \text{std iap})] + \\
 & [6 * (((\text{mst} - 100) / 5) / \text{std mst})] \}
 \end{aligned}$$

which determines a 47:36:17 ratio between production, functionality and conformation.

Table 1A. Weights considered in PFT

PRODUCTION	WEIGHTS	FUNCTIONALITY	WEIGHTS	CONFORMATION	WEIGHTS
Milk kg	0	Longevity	5	Type	4
Fat kg	8	Somatic Cells	5	Udder (ICM)	9
Protein kg	33	Fertility	20	Feet & Legs (IAP)	4
Fat %	3	MST (Mastitis)	6		
Protein %	3				

1.2. IES (Economic and Functional)

IES is a selection index which has the aim to maximize genetic progress, both in the economic sense as well as for health and welfare traits. The index is based on an estimate of average costs and revenues in the entire cow's productive life. Revenues considered are the average milk cost and quality parameters payments. Costs are quantified by considering costs for rearing heifers, the dry matter intake needed for growth, maintenance and production, but also the information about animal health and welfare, estimable from genetic and genomic indexes (fertility, mastitis resistance and calving ease).

This index is expressed as the expected economic difference (€) between any single individual (or bulls' daughters) and the reference genetic base. The index will be updated periodically, either for the economic value estimation, (in order to use updated market prices), either for the introduction of new genetic indexes that will be set up, such as animal welfare, mastitis resistance, feed efficiency or reduction of environmental impact.

This index, estimated over the life of a single cow (€), is expressed as a net income (revenues – costs) compared to the average of the population. The index is published for artificial insemination bulls and genotyped females. The table shows the relative weight of each trait included in IES index. The IES index formula is as follows:

$$\begin{aligned} \text{IES} = & 0.32 * \text{fat kg} + 1.37 * \text{protein kg} + 0.043 * \text{fat\%} * 100 + \\ & 0.0188 * \text{protein} * 100 - 5 * \text{stature} + 4 * \text{locomotion} + \\ & 1 * \text{udder depth} + 20.51 * (\text{longevity} - 100)/5 + \\ & 6 * ((\text{scs}-100)/5.7) + 18 * (\text{fertility}-100)/5 + 3.35 * ((\text{bcs}-100)/5) + \\ & 3.51 * ((\text{maternal calving ease}-100)/5) \end{aligned}$$

which determines a 39:51:10 ratio between production, functionality and conformation.

Table 1B. Weights considered in IES

PRODUCTION	WEIGHT	FUNCTIONALITY	WEIGHT	CONFORMATION	WEIGHT
Milk kg	0	Longevity	20,51	Stature	-5
Fat kg	8	Somatic Cells	6	Locomotion	4
Protein kg	27,62	Maternal Calving Ease	3,51	Udder Depth	1
Fat %	1	Fertility	18		
Protein %	2	Body Condition Score	3,35		

1.3. ICS-PR (Cheesemaking and Sustainability Index – Parmigiano Reggiano)

ICS-PR is a selection index which has the aim to select those animals whose daughters maximize the profit for farms by producing milk which is provided to for long-ripening cheese production. This index has to consider the new breeding regulations and it has to be profitable for farmers, furthermore it has to be sustainable in the ethic, economic-social and environmental contexts.

It is based on the estimation of average costs and revenues per lactation over the entire productive career of the cow, by including in one hand the expenses necessary for the rearing of the cow (mostly food, but also health), the cheese-making and transport of

milk, on the other hand the estimated revenues of the entire productive career of the cow and the value of the animal at the end of career.

Indices For cheese yield prediction, expressed as kg of cheese, fat and protein percentage, somatic cells count (SCC) and k-casein genotype are considered. The index is expressed as net income (revenue – cost), estimated on the entire cow’s productive life (€), with respect to the average cow population. Bulls used to derive index weights had a reliability of at least 50% and rank greater than 59. The following table depicts the relative weight of each trait included in ICS-PR. The formula for ICS-PR is as follows:

$$\begin{aligned} \text{ICS-PR} = & 0.05 * \text{fat kg} + 0.30 * \text{protein kg} - 0.02 * \text{stature} + 0.03 * \text{locomotion} + \\ & 0.02 * \text{udder depth} + 0.14 * ((\text{scs}-100)/5.70) + \\ & 0.09 * ((\text{maternal calving ease}-100)/5) + \\ & 0.10 * ((\text{longevity}-100)/5) + 0.05 * ((\text{mastitis}-100)/5) + 0.20 * ((\text{fertility}-100)/5) \end{aligned}$$

To this formula needs to be added a premium:

- 0.10 € / day of life for k-casein BB bull’s daughters
- 0.05 € / day of life for k-casein AB bull’s daughters

which determines a 35:58:7 ratio between production, functionality and conformation.

Table 1C. Weights considered in ICS-PR

Production	Weight	Functionality	Weight	Conformation	Weight
Milk kg	0	Longevity	10	Stature	-2
Fat kg	5	Somatic Cells	14	Locomotion	3
Protein kg	30	Maternal Calving Ease	9	Udder Depth	2
		Fertility	20		
		Mastitis	5		

2. MORPHOLOGICAL AND FUNCTIONAL COMPOSITE INDEXES

2.1. ICM (Udder Composite Index)

The goal of the ICM index is to breed for a functional udder. Its formula is based on percentages of weights for the breeding values based on the linear scores of the udder, defined according to their relation with the functional longevity of the animals and is as follows:

$$\begin{aligned} \text{ICM} = & 0.20 * \text{fore attachment strength} + \\ & 0.20 * \text{rear attachment height} + \\ & 0.15 * \text{udder support} + \\ & 0.20 * \text{udder depth} + \\ & 0.10 * \text{front teat placement} + \\ & 0.05 * \text{teat length} + \\ & 0.10 * \text{rear teat placement} \end{aligned}$$

With the December 2021 release, the rear teat placement and teat length traits were added to the formula. In addition, a 'neutral range' has been introduced for the penalties of the three traits of the teats: in this way we want to reward bulls that have an ideal or almost ideal index. These neutral range are:

Table 2A. Neutral ranges in ICM

Trait	Phenotypic SD -	Phenotypic SD +
Front teat placement	0	1
Teat length	0.5	1.5
Rear teat placement	-1.5	-0.5

2.2. IAP (Feet & Legs Composite Index)

The IAP index, used for the first time in May 2000, combines three indices based on linear traits relative to feet and legs and locomotion evaluated by the classifier. The weights express (as a percentage) the relative importance of each trait (due to correlations) in relation with the trait 'feet & legs functionality', and are the following:

$$\begin{aligned} \text{IAP} = & 0.160 * \text{foot angle} + \\ & 0.244 * \text{rear leg rear view} + \\ & 0.408 * \text{locomotion} + \\ & -0.208 * \text{abs}(\text{rear legs side view} + 1) \end{aligned}$$

2.3. TYPE

Following the review of December 2014, the index for TYPE is derived from 17 indices based on linear traits to ensure the same definition across all Italian and foreign bulls. The formula has been derived from genetic correlations among the 17 different traits and the genetic correlations with the actual definition of Final Score officially used by classifiers. Rear legs side view and rear teat placement have an intermediate optimum. Type is calculated as follows:

$$\begin{aligned} \text{TYPE} = & 0.000 * \text{stature} + 0.128 * \text{strength} + 0.031 * \text{body depth} + \\ & 0.158 * \text{angularity} + 0.044 * \text{rump angle} + \\ & 0.013 * \text{rump width} - 0.025 * \text{abs}(\text{rear legs side view} + 1) + \\ & 0.038 * \text{rear legs rear view} + 0.050 * \text{foot angle} + \\ & 0.175 * \text{udder front} + 0.072 * \text{rear height} + \\ & 0.030 * \text{udder support} + 0.014 * \text{udder depth} + \\ & 0.050 * \text{front teat placement} + 0.023 * \text{teat size} - \\ & 0.032 * \text{abs}(\text{rear teat placement} + 1) + 0.016 * \text{locomotion} \end{aligned}$$

2.4. IMA (Automated Milking Index)

In December 2021 IMA - Automated Milking Index was released. It is a compound index which aims to identify the bulls that give their daughters greater ease in milking operations (attachment, milk ejection, udder health...). It is an index that has mean of 100 and standard deviation of 5, like all functional indices. IMA is calculated as:

$$\begin{aligned} \text{IMA} = & 0.25 * \text{rear teats position} + \\ & 0.20 * \text{front teats length} + \\ & 0.20 * \text{milkability} + \\ & 0.15 * \text{SCS} + \\ & 0.15 * \text{locomotion} + \\ & 0.05 * \text{ICM} \end{aligned}$$

For 4 traits out of 6, very strong penalties are applied: the reason is to avoid bulls from having an overall average index, due to 5 good traits and an extremely negative one (for example a score of -3 on the size of the teats). Therefore, the penalties are:

Rear teats position: penalty with index > +2 std and major penalty with index > +3 std

Front teats length: penalty with index < -2 std and greater penalty with index < -3 std

Locomotion: penalty with index < 0 std

Milking: penalty with an index < 95 and a greater penalty with an index < 90

2.5. Wellbeing index

With the CTC of 2022, a compound index for welfare was also approved. This is an index that aims to identify sires that generate daughters with better morphological/functional characteristics from an animal welfare point of view. In addition, the genetic aspect is also included, rewarding polled sires and penalizing carriers of unfavorable haplotypes/genes.

It is an index that is expressed with mean 100 and standard deviation 5, like all functional indexes. The following characters are included:

$$\begin{aligned} \text{Wellbeing} = & 0.30 * \text{udder health} + \\ & 0.25 * \text{fertility} + \\ & 0.15 * \text{longevity} + \\ & 0.15 * \text{BCS} + \\ & 0.05 * \text{heat tolerance} + \\ & 0.05 * \text{cow calving ease} + \\ & 0.05 * \text{locomotion} \end{aligned}$$

Once the index has been calculated on a scale of 100, the following bonus/penalty points will be given:

- + 1.25 for heterozygous polled subjects
- + 2.5 for homozygous polled subjects
- - 5 for subjects carrying one or more deleterious genes/haplotypes

What does this index consist of? Analyzing the phenotypic averages of the daughters of bulls having high and low indexes, it can be seen that, on average, high index daughters live longer and perform better in their careers.

Table 2B. Differences between the average phenotypes of the daughters.

	Longevity, d	Milk, kg	Fat, kg	Protein, kg
Daughter phenotypic difference	133.3 gg	4,560 kg	174 kg	132

3. BREEDING VALUES FOR PRODUCTION TRAITS AND SOMATIC CELL SCORE (SCS)

3.1. Data recording

ANAFIBJ receives every week from the Italian Breeders Association (AIA) all the milk records collected by the personnel of the Regional Breeders Associations (ARAs). Alternate recording data (AT) are projected to 24 hours records complying with ICAR standards. All available records are used. Every lactation has a weighting factor expressing its accuracy: AT records are worth 98% of monthly complete records (A records).

All the records collected between day 5 and day 305 of a lactation are used, up to at most three lactations. Besides ordinary data editing, records abnormally deviating from each cow's estimated lactation curve are discarded.

3.2. Environmental effects

A random regression test day model is adopted, estimating every effect using a function that explains their variability from day 5 to day 305 of lactation. Breeding values for milk, fat, protein and somatic cells are estimated simultaneously, thus making use of genetic correlations among traits that improve total reliability of estimates. Estimated fixed effects are age at calving, calving season (spring or autumn), area of production (Northern, Central or Southern Italy and "Parmesan cheese area") and the five-years period in which production occurred (from 1990).

Average variability of milk, fat and protein for each herd is calculated every year, using all available test-day records; this parameter measures variability of herd productions around total average and helps in identifying higher and lower than average variability herds, then in adjusting them to match the "correct" scale.

The "correct" scale consists of variability within each herd due to primiparous cows born between 2015 and 2017 (the genetic base cows). This correction for heterogeneity of variance allows differences among animals to be measured in a common scale for all herds. Animals are compared according to herd-year-test day and parity. Cows are divided into a first and a multiple parity class; this last effect allows to account for every management effect within herd and time.

3.3. Random effects

The animal effect, after which the Animal Model statistical method is named, allows for the estimation of breeding values of all individuals within the population. In the random regression test day model, the hypothesis is that animals express a different genetic value each day of lactation in response to environmental stimulation. A function is therefore estimated for each animal based on five parameters. Besides, all animals with (cows) or without (bulls) production records are considered simultaneously, together with all their relationships, allowing for the deviation from contemporaries to be resolved into its dam and sire components and taking into account, for instance, the fact that on the best cows usually the best available bulls are used.

A second random effect is the permanent environmental effect: each cow can have more than one lactation. Therefore, it is necessary to estimate occasional management effects that may have a negative (a mastitis which severely damages one of the quarters), or a positive (a very positive interaction with a healthy environment) influence on her lifetime production. Also in this case, a five-parameter function is estimated.

3.4. How the breeding value is expressed

The traits for which breeding values are calculated are milk, fat and protein yields and somatic cell score (SCS).

3.4.1. Production traits

Heritability varies according to day of lactation and parity and usually is around 0.30, thus establishing a 30:70 ratio between genetic and environmental variability.

The three resulting breeding values, for first, second and third lactation, are then combined in an index of total three-lactation production:

$$EBV_{305_{tot}} = 0.333 * EBV_{305_1} + 0.333 * EBV_{305_2} + 0.333 * EBV_{305_3}$$

This index is expressed in kilograms as a deviation from a reference base (the genetic base), that sets the zero-point of breeding values. The genetic base is variable and is updated every year in April; its purpose is to express the breeding values relative to the value of the reference cows. Current genetic base reflects the genetic value of the cows born between 2015 and 2017. Every year the triennium will be moved forward one year.

Percentages are computed with reference to the 305 days phenotypic productions of cows of the genetic base. The base values are published on the web page in the section related to genetic proofs (<http://www.anafibj.it/>). The base values are then used in the following formula to calculate the breeding values for percentages:

$$\begin{aligned} Fat\% &= 100 * (fat\ BASE + fat) / (milk\ BASE + milk) - fat\% \ BASE \\ Protein\% &= 100 * (protein\ BASE + protein) / (milk + BASE) - protein\% \ BASE \end{aligned}$$

A bull is officially proven when he reaches a minimum reliability of 80% and has at least 30 daughters with 120 DIM. For all foreign bulls the results provided by INTERBULL are used (decision n° 256 of the Central Technical Committee 25/10/2013).

3.4.2. Somatic cell score

Heritability varies according to parity and day of lactation and usually ranges from 0.17 in first lactation to 0.25 in third lactation. The resulting three breeding values for first, second and third lactation are combined in a total index for SCS, that express the mean somatic cell score in the three lactations, using the following formula:

$$EBV_{tot} = 0.333 * EBV_{305_1} + 0.333 * EBV_{305_2} + 0.333 * EBV_{305_3}$$

This index is expressed on a scale with mean equal to 100 and standard deviation equal to 5. Current genetic base represents the genetic value of cows born between 2015 and 2017 as for the production traits. Also, for SCS indexes, for all foreign bulls the results provided by INTERBULL are used.

3.4.3. Persistency index and maturity rate

The individual lactation curves that the random regression test-day model provides for each cow, allow us to quantify the genetic component for persistency of production. The percent ratio between 280 days and 60 days production is calculated, in order to express persistency with an indicator. The index is on a scale with mean 100 and SD equal to 5. There are three indexes for persistency, one for each lactation, and a combined indicator, computed using the following formula:

$$\text{PERS}_{\text{tot}} = 0.50 * \text{PERS}_1 + 0.25 * \text{PERS}_2 + 0.25 * \text{PERS}_3$$

Maturity rate measures, on the other hand, the difference between the sum of fat and protein kilograms in third and first lactation. The result is then expressed on a scale with mean 100 and SD equal to 5. It allows us to distinguish which bulls produce daughters with performances improving through lactations (values above 100), from those whose daughters perform the best in first lactation (values below 100).

4. MST (Udder Health Index)

4.1. Data recording

Data for all cows collected every month by the personnel of the Breeder's Regional Associations (ARAs) are available. Single test-day Somatic Cells Count (SCC) data of each animal are log-transformed to somatic cell score (SCS) as $SCS = \log_2 (SCC/100,000)$.

An index was created using all the available information in the data-set. Novel traits were validated on a sample data-set with the objective of selection (i.e., clinical mastitis) and, thanks to an available data-set and to effective measurements on cow's mastitis presence (or absence) within lactation, four novel traits have shown the strongest genetic correlation. These traits are:

- Mean SCS between 5 and 150 DIM;
- Standard deviation of SCS within lactation;
- Severity, defined as the ratio between the number of test-days with SCC greater than 400,000 cells/mL;
- Total number of test-days within lactation and peak defined as the number of peaks during lactation (number of times when SCC shows a change from <100,000 to 400,000 cells/ml on three consecutive test-days).

Genetic correlations of the four traits to clinical mastitis and their heritability are depicted in the following table. These traits are combined together in an aggregate selection index to exhibit individuals which are more susceptible to clinical mastitis.

Trait	Heritability	Genetic correlation with clinical mastitis
Clinical mastitis	3%	
SCS ₅₋₁₅₀	17%	39%
SD_SCS	5%	44%
Severity of infection (%)	11%	41%
Peak	4%	51%

4.2. Environmental effects

The environmental factors considered in the model are: herd-year-season, age at first calving and number of test-day records within lactation.

4.3. Random effects

The only random effect is the animal effect, considering bulls and cows at the same time, accounting for genetic level of mating and using all available pedigree information.

4.4. How the breeding value is expressed

Currently breeding values are available only for first parity cows. Heritability of the aggregate udder health index is 15%. The index is expressed on a scale with mean 100 and SD of 5. Animals with indexes greater than 100 are those animals whose offspring will be more genetically resistant to mastitis.

5. BREEDING VALUES FOR TYPE TRAITS

5.1. Data recording

Information of type evaluations carried out on all first-calf heifers classified one to three times a year by the classifiers is used for the calculation of the breeding values. Unlike what happens with the production proofs, in this case age variation is not so strong and there is no repeated data. For each cow only one classification is used.

5.2. Environmental effects

Among the animals classified in a herd there are differences by age and stages of lactation which undoubtedly influence their body condition and appearance. All traits are evaluated together in a multiple trait analysis. The classifier scores what he/she sees, therefore the statistical model must take into consideration this different condition by using an interaction effect between age, stage of lactation and a two-year period of evaluation. The indexes are calculated simultaneously for all linear traits.

Cows are compared among them on an equal herd-year-round of classification: this allows to simultaneously take into account all managerial effects of each single herd and also the year and the classifier who evaluated the animal.

5.3. Random effects

The only random effect taken into consideration is that of the animal. All parental relationships existing among the population are taken into consideration, and this allows to estimate the genetic value of all animals, taking into account possible preferential or corrective mating.

5.4. How the breeding value is expressed

The breeding values of all linear type traits evaluated since 1984 and final score are calculated. Table illustrates the heritability data utilized for the calculation. A zero-breeding value refers to the genetic level of animals born between 2015 and 2017, i.e. the genetic are those animals whose offspring will be more genetically resistant to mastitis, for which the same rules of the production traits apply.

All breeding values are standardized for the variability of the cows in the genetic base. In this way, all traits can be measured on the same scale (see figure), which goes from -3 to $+3$ both for cows and bulls.

Actually, bulls and cows do not vary in the same way: in particular, bulls have high breeding values due to a higher selection, especially for production traits, and well above the cows' average. For this reason, bulls' traits tend to vary towards extremes which are higher than 3.

On the table the heritability values of all traits, the phenotypic average of the animals in the genetic base, and the equivalent in points (linear scale) of one standard deviation of that breeding value can be seen. The table values vary at every base change and they are updated on the web page, where genetic proofs are.

The breeding value is published when a bull has at least 10 daughters in 5 herds, in case of bulls with daughters in Italy. Conversion of breeding values to the Italian scale is used for bulls imported from abroad with daughters still not classified in Italy. For foreign bulls the official proof is the Italian one of INTERBULL.

Table 5A. Genetic base 2015-2017

Linear Trait	Heritability	Average Base	DS in linear points
Stature	0.40	31.68	2.50
Dairy strength	0.25	27.72	1.37
Body depth	0.30	30.90	1.54
Angularity	0.23	28.74	1.20
Rump angle	0.23	24.87	1.61
Rump width	0.22	27.42	1.52
Rear leg set	0.16	25.56	0.98
Heel depth	0.10	26.07	0.78
Fore udder attachment strength	0.20	24.99	1.54
Rear udder attachment height	0.21	27.90	1.35
Rear udder attachment width	0.24	29.64	1.08
Udder support	0.16	29.01	1.15
Udder depth	0.30	29.67	2.27
Front teat placement	0.19	25.29	1.10
Teat size	0.19	22.89	1.22
Rear leg rear view	0.06	26.67	0.66
Feet and legs functionality	0.10	23.64	0.75
Rear teat placement	0.18	30.75	1.69
Conformation	0.14	25.65	1.30
Locomotion	0.14	21.66	0.48

6. BODY CONDITION SCORE (BCS)

6.1. Data recording

Body condition score is a visual score by the classifiers of fat covering the pelvic and lumbar regions; its scoring is based on a 1 (very thin) to 5 (very fat) scale with 0.25-point increments. In particular, the fat reserves of the tail region, the angularity of hips and pins, and the prominence of spinous parts are evaluated by classifiers, in such a way as to be able to define the appreciation of the animal's energy reserves. The index is considered in the official national evaluation since December 2013.

6.2. Environmental effects

There are differences in age, interval since birth and production levels among the animals present in the farm which undoubtedly influence the morphological-metabolic status of the animal. The classifier scores what he sees, which is why the statistical model used takes into account these differences through the interaction effect between age and the lactations stage. Animals are compared according to herd-year-classification day: this allows to take into account simultaneously all the internal management effects for each farm and year and the classifier who carried out the evaluation.

6.3. Random effects

The only random effect taken into consideration is the animal. All parental relationships existing among the population are taken into consideration, and this allows to estimate the genetic value of all animals, taking into account possible preferential or corrective matings.

6.4. How the breeding value is expressed

The genetic index for BCS is expressed on a scale with mean 100 and SD equal to 5, like for other functional traits. It tells us which are the bulls, whose daughters (values above 100) have a better body condition. Each standard deviation (which is equal to a 5 on the scale of the index) is worth about 0.08 points BCS: bulls with a genetic level of less than 90 have daughters with BCS equal to 2.78, bulls with EBV between 95 and 105 have daughters with BCS of between 2.94 and 3.01 and bulls with indexes above 110 have daughters with BCS equal to 3.16 points.

Table 6A. Daughter Phenotypic average based on genetic bull level

Genetic bulls level	Phenotypic average of daughter
Below to 90	2.78
From 90 to 94	2.85
From 95 to 99	2.94
From 100 to 104	3.02
From 105 to 109	3.09
Above to 110	3.16

7. IPA (Composite Calving Breeding Value)

The composite calving breeding value (IPA) summarizes all the information held by the Association relating to the calving event: calving ease, stillbirth and gestation length. All the breeding values that are part of it have a direct component, relating to the effect that the bull has on the calving of the cow it is mated with, and a maternal component, relating to the effect of the bull on the calvings of the daughters. The direct composite calving breeding value weights the direct calving ease at 70%, the direct stillbirth at 20% and the direct gestation length at 10%: the same distribution of weights is applied in the maternal composite calving breeding value, which is composed of the three maternal components. The published breeding value relates to the first calving.

7.1. Calving breeding values

7.1.1. The data

The calving data includes an assessment by the breeder of the degree of difficulty on a five-point scale:

- A = easy calving
- B = assisted calving
- C = cesarean calving
- D = difficult calving
- E = embryotomy

The data used for the evaluation start from 1987 and are filtered on the basis of the quality of the registration by the herds, eliminating all those that:

- > 92% records coded as A;
- > 92% records coded as B;
- > 15% records coded as C and over.

A filter is also applied on the number of contemporaries in each group to ensure an effective comparison.

Being numerically smaller, births in categories C, D and E are merged into a single category.

In order to analyze the trait with a linear model, and to make it evaluable through the single-step procedure in the future, the Snell-transformation based on classes of parity order/sex/province/5-year period is applied. The published breeding values relate to the first calving.

7.1.2. Fixed effects

The applied model is a *multiple-trait repeatability linear animal model*. The fixed effects considered for the first calving are the contemporaries, i.e. the interaction between herd and year of birth (5-year period), the interaction between province, month and year of birth (5-year period) and the interaction between the mother's age, the sex of the calf and the year of birth (2-year period).

7.1.3. Random effects

As far as the first parity is concerned, the random effects are the additive genetic of the animal born (direct effect) and the mother one (maternal effect).

7.1.4. How the breeding value is expressed

The resulting breeding values are two: one for the direct and one for the maternal. Both are reported on a scale with mean 100 and standard deviation equal to 5. Bulls with values greater than 100 are improvers for these traits.

7.2. STILLBIRTH BREEDING VALUE

7.2.1. The data

The phenotype is binary: calf alive or dead within the first 48 hours of birth. In order to analyze the trait with a linear model, and to make it evaluable through the single-step procedure in the future, the Snell-transformation based on classes of parity order/sex/province/5-year period is applied. The published breeding values relate to the first calving.

7.2.1. Fixed effects

The applied model is a *multiple-trait repeatability linear animal model*. The fixed effects considered for the first calving are the contemporaries, i.e. the interaction between herd and year of birth (5-year period), the interaction between province, month and year of birth (5-year period) and the interaction between the mother's age, the sex of the calf and the year of birth (2-year period).

7.2.1. Random effects

As far as the first parity is concerned, the random effects are the additive genetic of the animal born (direct effect) and of the mother (maternal effect).

7.2.1. How the breeding value is expressed

The resulting breeding values are two: one for the direct stillbirth and one for the maternal stillbirth. Both are reported on a scale with mean 100 and standard deviation equal to 5. Bulls with values greater than 100 are improvers for these traits.

7.3. GESTATION LENGTH BREEDING VALUE

7.3.1. The data

The phenotype is the length of gestation measured in days. The published breeding value relates to the first calving.

7.3.2. Fixed effects

The applied model is a multiple-trait repeatability linear animal model. The fixed effects considered for the first calving are the interaction between farm, year and season of conception, the interaction between year and month of calving and age at calving in months.

7.3.3. Random effects

As far as the first parity is concerned, the random effects are the additive genetic of the animal born (direct effect) and of the mother (maternal effect).

7.3.4. How the breeding value is expressed

The resulting breeding values are two: one for the direct gestation length (relative to the genetic effect that the bull has on the time spent by the offspring in the uterus) and one for the maternal gestation length (relative to the genetic effect that the bull has on the length of gestation of the daughters). Both are reported on a scale with mean 100 and standard deviation equal to 5. Bulls with values higher than 100 transmit a greater length of gestation. The optimum for this trait, in both its components, is intermediate: the top bulls will be those with an index close to 100.

8. MLK (Workability index)

8.1. Data recording

Workability is recorded twice a year by the milk recording system: all animals that are slower than the average of the herd is identified. The phenotype is binary; it can have just two possible values: 'slow' or 'not slow'.

8.2. Fixed effects

The applied model is a threshold model: it creates a continuous variable of liability and places a threshold on the scale of this variable. As soon as the threshold is reached, the phenotype (slow milking) appears. First, we accounted for **calving season**, identified as hot or cold, **parity order** and **days in milk** (divided into 7 classes). **Fat + protein production** is fitted as a linear regression, i.e. the risk of a cow being recorded as slow increases by a constant value (regression coefficient) for each more gram she produces than the mean. However, since production depends on the lactation stage, this effect has been inserted so as to have **a regression coefficient for each class of days in milk**.

8.3. Random effects

First of all, the effect of the **contemporaries** is considered, i.e. the herd-year-semester variable. This variable is fitted as a random effect, since there are categories of contemporaries with all the same values (called extreme categories: for example, to consider all cows marked as not slow as a fixed effect would lead to biased estimates). Moreover, the fact of having more measurements recorded over time on the same cow leads to the inclusion of the permanent environmental effect of the animal. Finally, the additive genetic effect of the animal determines the value of the sire.

8.4. How the breeding value is expressed

The heritability of the trait on the liability scale is 27.5%. The breeding values (BV) are expressed on a scale with a mean of 100 and a standard deviation equal to 5: animals with a BV greater than 100 will have fewer slow daughters than the genetic base. Both extremes, positive (higher BV bulls) and negative (lower BV bulls) should be handled carefully. Sires with a low Milkability BV should be protected for this trait in the mating plan, those with a very high BV for the Udder Health BV.

9. FHL (Functional Longevity breeding value)

9.1. Data recording

The general lactations records give a precious information: the productive career of all the Holsteins in milk recording. It's known for how many lactations an animal has produced before leaving the farm, at what productive levels her productions were located compared to the farm average, how often she gave birth etc.

It's possible to notice, over time, the trend of the farms: some of them are stable, some are closing and others are enlarging themselves. All these data, if properly analyzed, tell us the dynamic of the elimination of animals from the farm. Next to those animals which have already closed their career, there are those who have just started it.

9.2. Environmental effects

The production changes over time and so does the animal situation in the farm. There are some permanent factors which do not change, such as the first calving age of an animal, that, by the way, determines her survival capacity over time. Then there are time dependent factors such as the age effects on the lactation stage, the milk yield productive level within the year (which is divided into nine classes: four under the average, average, four above the average), the fat percentage productive level within the year (5 classes), the protein percentage productive level within the year (5 classes), the yearly changes in the herd size, and at the end the year-season effect, on which external factors have an influence, among those the recoveries, the market dynamics (quota) or the pathologies that lead to extraordinary elimination patterns of the animals.

9.3. Random effects

The bull, maternal grandsire and herd-year-season effects are considered. The applied model, based on the survival functions, derives from medical studies and is called survival analysis; it is a sire-maternal grandsire model.

9.4. The combined index

The reliability of the survival index of the bulls, in particular for the young animals (those who have all the daughters still in production) is definitely low, a little bit higher than a pedigree index. Such an index doesn't give enough information about the real survival of daughters. Despite this, from the type evaluation of the daughters it is possible to get a partial information about their longevity. From this the composed index for the longevity originates: survival index, feet & legs and udder index are combined together, by taking into consideration the genetic correlation existing between the several traits. In particular, the correlation between udder and functional longevity is 0.48 and the one between feet & legs and longevity is 0.14.

9.5. How the breeding value is expressed

Only the index of bulls which have at least a reliability of 50% or higher is published. The heritability of this trait is around 10%. The longevity index is expressed like a genetic value on a scale with mean 100 and SD of 5 just like for the other functional traits. Minimum and maximum value are approximately 80 and 120. The bulls that give longer-lived daughters have values above 100.

9.6. What does it really mean

The functional longevity concept is not easy to explain: it is not the rough longevity the one which is possible to observe in the farm, because this one is correlated with the productive level of the animals. The concept of longevity itself is related to fertility, to health of the animal, etc.

Besides this, between functional longevity (the number of lactations that the animal is able to carry on during her career) and real longevity, there is a precise relation.

In order to try to quantify the real difference between animals carriers of very positive longevity genes and those carriers of genes with very negative effects on the longevity of their daughters, a simple statistic of the data for the bulls having more than 200 daughters born between 1980 and 1988 has been computed. The differences found are listed in the table below:

Table 9A. Relationship between FHL Index and phenotype

Genetic Level	Average number of daughter's lactations	Average number of eliminated daughter's lactations
Lower than 90	2.30	2.10
Around 100	2.58	2.30
Higher than 110	3.20	2.90

The expected difference is one lactation.

10. IAF (Female Fertility Index)

10.1. Data recording

The data bases with inseminations, calving and pregnancy checks are the information used for genetic evaluation for fertility. On this data several checks guarantee that only good quality records will be used for genetic evaluation (about 20% of the total records are discarded). The majority of records discarded are questionable first insemination data. Together with these data bases also linear trait and lactation databases are used. Indeed, for a complex trait as fertility, direct and indirect traits are used all together. The direct traits considered are: heifer's age at first insemination, cow's and heifer's non-return rate at 56 days, cow's interval from calving to first insemination and cow's and heifer's interval from first to last insemination. Indirect traits are: cow's BCS and cow's mature equivalent 305 first parity lactation. All traits are measured on first parity cows and heifers in order to evaluate daughter fertility of all bulls. The five traits measured on cows are considered simultaneously in order to fully exploit the genetic correlations that exist across these traits and to maximize the estimation precision. The same happens for the three traits measured on heifers. The two estimated values are then combined together and the aggregate breeding value for fertility is the combination of the 90% of the cow's fertility breeding value and the 10% of the breeding value estimated on heifers.

10.2. Environmental effects

Every trait is affected by different environmental effects. Thus, every trait has its own statistical model. Effects associated with cow's interval from calving to first insemination and for cow's interval from first to last insemination are::

- a) herd-year-season of calving,
- b) calving month,
- c) age at calving by year of calving;

for cow's non-return rate at 56 days effects are:

- a) herd-year-season of calving,
- b) insemination month,
- c) age at calving by year of calving;

environmental effects considered for BCS are the same used for genetic evaluation for type traits:

- a) herd-year-round of classification,
- b) age at calving by stage of lactation,
- c) year of calving;

for heifer's age at first insemination effects are:

- a) herd-year of birth,
- b) month of birth;

for heifer's interval from first to last insemination and for heifer's non-return rate at 56 days factors considered are:

- a) herd-year-season of birth,
- b) year-month of insemination.

Finally, environmental effect considered for 305 mature equivalent milk yield is simply the herd-year-season of calving effect.

10.3. Random effects

The animal effect is evaluated thus considering bulls and cows at the same time, accounting for genetic level of mating and using all available pedigree information. It is a multiple trait animal model.

10.4 The combined index

At the end of the computation step eight genetic proofs are available. The objective of selection is to improve fertility in general terms. In order to achieve this in an easy and simple way the chosen objective trait is conception rate at first service. This trait is genetically correlated with each of the eight evaluated traits and the final proofs combine all of them to maximize the improvement on conception rate at first service by placing the following emphases:

Table 10A. IAF Index for cows

Trait	Genetic correlation with conception rate	Relative importance in the combined proof %
Days calving-first insemination	-0.30	16
Non-Return Rate 56	+0.77	13
Days first-last insemination	-0.89	55
BCS	+0.28	7
305 mature equivalent milk	-0.29	9

Table 10B. IAF Index for heifers

Trait	Genetic correlation with conception rate	Relative importance in the combined proof
Age at first insemination	-0.06	10
Non-Return Rate 56	+0.67	43
Days first-last insemination	-0.73	47

10.5. How the breeding value is expressed

Only the index of those bulls which have at least a reliability of 50% or higher is published. The heritability of the traits varies from 2 to 26%. The fertility index (IAF) is expressed on a scale with mean 100 and SD of 5 just like for the other functional traits, minimum and maximum values are between 80 and approximately 120. Bulls with higher fertility have values greater than 100.

10.6. What does it really mean

In spite of the low heritability values, especially for direct traits, the genetic variability among animals is very high. In the top 5% bull population group for PFT there are individuals that have an 85 proof and others that reach 110. For cows, each standard deviation (that corresponds to a value of 5 on the proof scale) above 100 corresponds to: +5% conception rate, -11 days first to last insemination interval, -3 days calving to first insemination interval and +3% on non-return rate at 56 days; whereas for heifers it corresponds to: +2% conception rate, -1.45 days first to last insemination interval, +0.1 month age at first calving and +2% on non-return rate at 56 days.

Table 10C. Differences found among the best and the worst bulls for the cows:

Cows	Daughter phenotypic average					
	Bull genetic level	First-last INS	BCS	Calving-1 st INS	Non return rate 56 days	Conception rate
Below 95		86.81	2.96	89.24	54%	28%
95 to 105		73.14	2.99	87.27	57%	33%
Above 105		62.05	3.03	84.72	60%	38%

Differences found among the best and the worst bulls for the heifers:

Heifers	Daughter phenotypic average				
	Bull genetic level	First-last INS	Age at 1 st INS	Non return rate 56 days	Conception rate
Below 95		29.80	17.1	75%	58%
95 to 105		27.32	17.2	77%	60%
Above 105		25.87	17.3	79%	62%

11. BFE (Bull Fertility index)

11.1. Data recording

Data used for male fertility indicator are information available in the ANAFIBJ database, on non-return rate on 56 days (NRR56). This information is available since 2006 for all lactating cows. On the basis of this information, it was possible to calculate the percentage of the non-return rate for all service bulls. The data used take into account the inseminations of the last five years and the bulls older than 15 months. In this way we use the most useful and current information, in order to avoid alterations in the final results.

11.2. Environmental effects

The model used to calculate bulls' fertility takes into account the age of the bull and its origin including bull state (genomic, in progeny test, progeny tested) and AI center that produces the semen, and also, the cows' fertility such as, the interval between calving and conception, expressed as classes of days open, the energy used in the production of milk (ECM) and parity. The animals are compared with each other for the same herd-year-season of insemination, allowing to take into account simultaneously all the internal reporting effects at each herd.

11.3. Random effects

The bull and the permanent environmental effect of the cow are considered as random effects.

11.4. How it is expressed

The bull fertility indicator is expressed on scale 100 and standard deviation of 5 just like for the other functional traits. The bulls with index greater than 100, will become more fertile, with this indicator it is possible to identify the more and less fertile bulls in comparison with the average population. This indicator will be available for all Italian and foreign bulls used in Italy and with at least 80% of reliability.

12. AFC (Age at First Calving Index)

12.1. Data recording

Data stored in the national database of the ANAFIBJ including age at first calving (AFC) of heifers born since 1993 were used and AFC outside the range 18 to 35 months were discarded from the dataset. Only one evaluation per animal was used.

12.2. Environmental effects

The environmental effects (fixed effects) considered are the interaction between herd-year-season of birth. Seasons considered were two, in order to keep the same group size of contemporaries. The other effect of the model were classes of gestation length.

12.3. Random effects

The animal effect is evaluated thus considering bulls and cows at the same time, accounting for genetic level of mating and using all available pedigree information.

12.4. How the breeding value is expressed

The age at first calving index is expressed as a genetic value on a scale with mean 100 and SD of 5 just like for the other functional traits. The value 100 corresponds to the average breeding value of the 2022 genetic base. Bulls higher than 100 will transmit an earlier age at first calving than bulls lower than 100. Only the index of bulls which have at least a reliability of 50% or higher, and at least 30 daughters in at least 30 herds is published.

Table 12A. Age at First Calving index (AFC) Parameters

Trait	Heritability	Mean Phenotypic	SD Phenotypic
Age at first calving	0.038	26.88	0.92

13. NITROGEN EFFICIENCY INDEX

13.1. Data

It is an index consisting of two characters, urea % that weights 0.56 and protein % that weights 0.44. Test days from 2017 are used to calculate this index. The objective is to obtain maximum nitrogen efficiency, expressed as maximum protein output in milk and minimum urea output at the same time.

13.2. Environmental effects

The following fixed effects are included: DIM, that is lactation days (between 5 and 305 days), parity of the animal (1 to 3), the group of contemporaries identified as herd-test day, age in months within parity and the interaction between DIM and parity.

13.3. Random effects

The animal and the permanent environmental effect of the cow are considered as random effects. It is a repeatability animal model.

13.4. The expression of the index

The index for nitrogen efficiency is expressed on a scale of 100 and standard deviation 5, as for the other functional traits. Bulls above 100 will give their daughters on average 2 mg/dL less urea in milk. The index is published when the bull has a minimum reliability of 50% and at least 20 daughters in 20 herds. It has a heritability of 0.177.

14. IHT (Heat Tolerance Index)

14.1. Data

The aim is to estimate the animal heat tolerance genetic effect. Therefore, by identifying the environment with the bio-climate indicator THI (Temperature Humidity Index), the procedure makes it possible to estimate the genetic merit of individuals from the phenotypes detected.

To estimate this component accurately, a large amount of data is needed, as in any genetic evaluation process.

THI is calculated from weather stations distributed in the Italian territory. ANAFIBJ has georeferenced **147 weather stations** and all farms, using their specific latitudes and longitudes. This allows to determine the distance between each weather station and each farm, and to assign the closest weather stations to each farm. Weather information is added to all functional control data. The maximum daily temperature and humidity are used to estimate THI. The average of the 7 days before the functional control (1-7d) represents the period with the greatest impact on milk production.

14.2. Environmental effects

The model reports the following fixed effects: interaction year of birth * calving season, lactation stage interaction (DIM 5 - 305 days in 10-day classes) * order of calving (1 - 3) * year of calving, and the group of contemporaneous parameters identified as "herd, year and season control" (4 seasons).

14.3. Random effects

The general additive genetic effect of the animal and the additive genetic effect in presence of heat stress are considered as random effects. The latter is determined by the interaction between the animal and (*) the THI and represents the additive genetic effect of heat tolerance (HT) for the cow.

14.4. How the breeding value is expressed

The zero of the index is the genetic level of the animals born in 2015 - 2017, the same genetic base as the one applied for productive traits. The IHT hot tolerance index is expressed on a scale 100 and on a standard deviation 5, as for the other functional traits. Above-average values refer to individuals who transmit a greater heat tolerance to the offspring. Table 14A shows two key elements:

- 1) The heat tolerance trait is heritable: the latter shows a heritability value of 16%, indicating the possibility of selecting animals that are more resistant to high temperatures.
- 2) The antagonism between the animal genotype and the environment can also be noted.

Table 14A. Heat tolerance (HT) genetic parameters

Milk (kg/d)	Genetic Parameters
Heritability (h^2)	0.16
Correlation genotype; THI (genotype * environment)	-0.45

Example

Two groups of bulls with over a thousand daughters have been identified:

- With an average HT index of 105 or more
- those with an average HT index not exceeding 95.

In these two groups two production seasons have been identified: “summer” and “winter”.

- in the TOP group (HT 105) there was a production difference of -2.7 kg/day between summer and winter;
- in the LOW group (HT 95) the difference in production between summer and winter is -3.6 kg/day.

There is a difference of about 1 kg of milk between the two groups, indicating the possibility of correctly distinguishing, through the HT index, the most resistant animals from the most sensitive ones, which show a greater drop in production.

15. GENOMIC EVALUATION

Since December 2011 genomics (the branch of molecular biology that studies the genome) has become a new selection tool in the hands of breeders of the Italian Holstein. Previously the methods used to estimate the genetic value of commercial animals were based (and still are for those that are not using genomics) on two types of information:

- a. phenotype data (observable performance of daughters)
- b. pedigree (sire, dam and progeny)

With the invention of new DNA analysis technologies it is now possible to “know” a part of an individual’s genes (genotype), estimate its value and calculate a genomic index.

This new methodology can be used to:

1. estimate the genetic value of a young animal with greater reliability than a pedigree index;
2. reduce the generation interval;
3. maximize the choice of animals to be sent to progeny tests and/or to be used as sires of bulls/cows;
4. increase the reliability of bulls undergoing testing when the number of daughters is limited.

In short, a genomic index is calculated as follows:

1. genotyping individual animals;
2. collecting phenotypes (traditional genetic indexes - EBV);
3. estimating the value of the individual markers (SNP) which determines the genotype;
4. calculating the direct (DGV) and overall (GEBV) genomic index.

On an international level, ANAFIBJ is now officially accredited with ICAR, for relative’s assessment. Moreover, ANAFIBJ joins with Interbull GenoEX-PSE project to share bulls and cows’ markers in order to assess international bulls’ offspring.

15.1. Data

The data used, refer both to the genotypes of the bulls and to their traditional genetic indexes and is used as the input phenotype for estimating the effects of individual markers. The genotypes were collected thanks to ANAFIBJ’s collaboration on two research projects (SelMol and Prozoo), a cooperative agreement with four AI centers in Italy, exchanging material with certain European countries (Ireland and Switzerland), and an international agreement with North America (USA and Canada), United Kingdom and Switzerland. Several others have provided genotypes as well. Over 360,000 approved genotypes are now available. Genomic data available (March 2021) is shown in the following table:

Table 15A. Number of individuals in preliminar genomic evaluation 7/2023

Genomic Data	Number
Total genotyped bulls	312,258
Total genotyped heifers/cows	224,785
Training population	40,858

It must be noted that the number of genotyped animals is continuously increasing, since AI centers and breeders are continuing to collect samples from calves so that they can preselect the best animals.

15.2. Statistical model

In order to calculate a genomic index, one must estimate the value of the individual markers (currently more than 68,000) which make up the genotype of the individual. This estimate assumes that a mathematical model is used, which starts from the traditional indexes of a group of highly reliable (proven) sires and provides estimating equations based on individual markers. These equations can be used to calculate the genomic value of animals that are young or without progeny. The estimation process can be summed up as follows:

1. the input data is cleaned (control of sex, call rate and parents);
2. the reference population is identified (proven sires);
3. the effects of markers are estimated using the traditional EBV values of the proven sires;
4. the genomic index of all the animals is calculated.

The model used at ANAFIBJ to estimate these effects includes not only the 68,000 markers obtained after initial editing (cleaning) procedures, but also a so-called “polygenic” effect, which is entered in the model through the kinship information of the animals. The part of the variability not explained by the genetic markers can be “recovered” by incorporating kinships between the animals into the model:

$$\text{DGV} = \text{Markers} + \text{Classic kinship} + \text{error}$$

15.3. Genomic index for bulls

Once the value of individual markers is obtained, it is possible to calculate a direct genomic index for both bulls with daughters and those without daughters (young bulls). In the case of bulls with daughters, the direct genomic information is combined with the traditional index to increase its reliability. The final result is the GEBV. The weight of the two pieces of information (direct genomic and traditional EBV) depends on the number of available daughters; as the number of daughters increases, the weight of the direct genomic index decreases.

In the case of young bulls (a young bull has no daughters, so a traditional index is not available), the direct genomic index (DGV) obtained directly from the model without combining it with other information is used.

15.4. Genomic index for cows

The same approach as for male genomics can also be applied to female selection. Direct genomic breeding values (DGV) are estimated on the basis of the markers and pedigree (polygenic effect).

For cows (animals with information on their performance), are combined the traditional index (IGV) and those calculated using DNA analysis (DGV). Their traditional index (IGV) is not based only on pedigree but also on their performance (lactations, score, etc.). The weight of the two indexes (direct genomic and traditional EBV) depends on the number of lactations: as the number increases, the weight of the direct genomic index decreases. This is still lower than what happens with the proven bulls. In fact,

the conventional indexes of the cows have less information than the proven bulls, for which the reliability, and therefore the weight is much lower. In practice, while for proven bulls their genomic index is similar to that calculated with the daughters, in cows major differences between IGV and genomic index are found. For young animals, of which there is no available information on their performance or their offspring, the direct genomic index (DGV) is used.

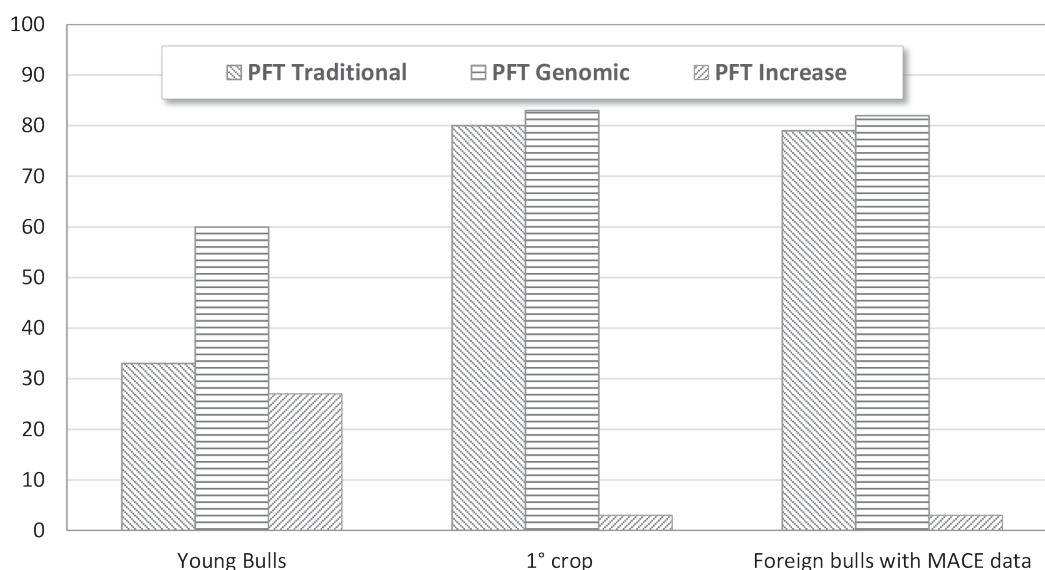
Table 15B. Summary of information in the indices

Indexes	Proven bulls	Heifers/Calves	Cows
Traditional Index (IGT/IGV)	Pedigree + daughters phenotype	Pedigree	Pedigree + phenotype
Direct Genomic Index (DGV)	DNA + Pedigree	DNA + Pedigree	DNA + Pedigree
Genomic Index (GEBV)	DGV & IGT	DGV	DGV & IGV

15.5. Reliability

One of the greatest advantages of genomic evaluation is the superior reliability of the indexes obtained especially when bulls without daughters are considered. At present, a young bull is evaluated only using a pedigree index, whose reliability rarely exceeds 35%. Using genomics, indexes can be obtained with a reliability of approx. 65-70%, which is approximately double the value obtained with the classic method. For cows it is the same, genomic index have a reliability around 60-70%. A newborn heifer with DNA analysis has about the same reliability as a cow with three lactations. This sharp increase of reliability, compared with the traditional pedigree that has about 30% of reliability, should push to use more the number of heifers used as potential bull dams. Observing the national selection index (PFT) in figure 2, one can see the difference in reliability between traditional evaluation and genomic evaluation, both for proven sires (Italian or foreign) and for young bulls.

Figure 15C. Reliability between traditional and genomic evaluation. National selection index (PFT) for proven sires and for young bulls

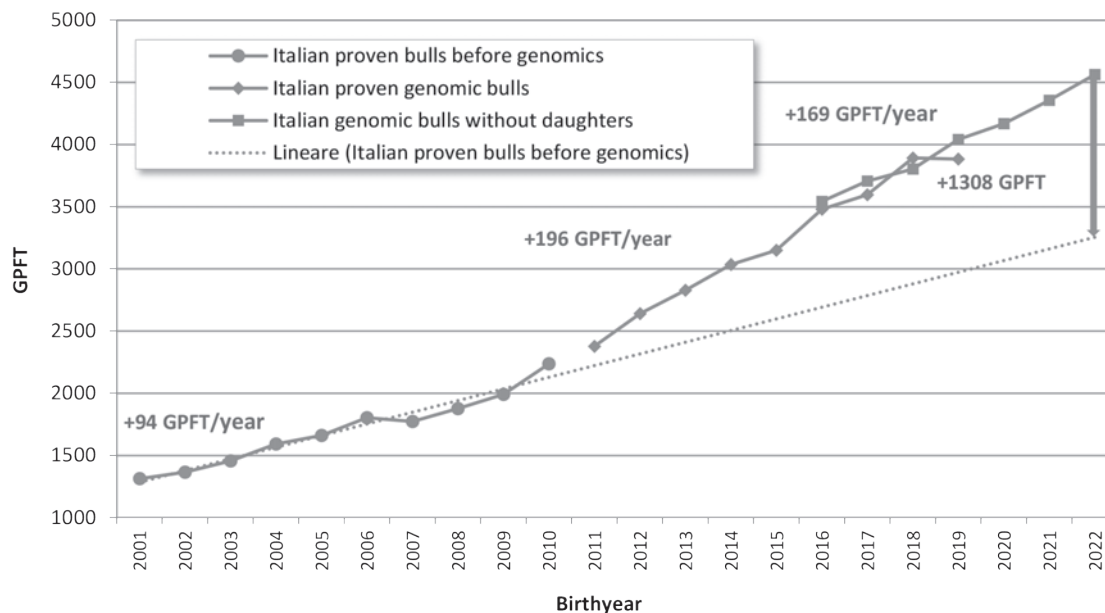


In young bulls the average increase in reliability for PFT is approx. 25%, but is lower for proven sires. This result is to be expected because it shows that genomics adds little for sires with daughters, since the data for estimating them is provided by their daughters.

15.6. Genetic trend

Trend of GPFT in recent years has had a considerable increase; in the graph of GPFT it is easily seen that the increase of GPFT 2009-2018 is significantly higher than that of the pre-genomic era.

Figure 15D. Genetic trend GPFT. The impact of genomics on the selection program can be seen clearly in the change in genetic trend.



Proven bulls born before 2009 were selected without the use of genomics, while in 2010 the genomics started to have an impact on the system. A trend line dashed (red) is shown to highlight what would be the genetic trend without the introduction of genomics. Looking at the period 2009-2018, it can be noted that:

- The trend line shows a red dashed genetic progress of 142 points per years;
- Blue line depicts Italian bulls with daughters. It proves the great results achieved by genomics;
- Since genomic analyses have started, a genetic progress of +347 points / year is depicted. The difference between the green line and the dashed trend line shows that the use of genomics has led to an extra increase of GPFT of 205 points. It means that genomics has added 144% extra genetic progress.

15.7. Haplotype and genetic factors

Genomics is continuously evolving and very often new DNA chips are added. New genetic disorders and important economic traits have been discovered in this way. Thanks to DNA analysis and genealogy it is possible to see which animals are carriers of these traits. In recent years, a particular attention to the haplotypes (DNA segments) and to genetic factors has been given. When the causative gene is unknown, a DNA segment is used, while when the causal gene is known, a direct test on the

genetic factor is applied. In the case of genetic factors, only one or two markers with a functional impact are used and not a group of markers, such as for the identification of haplotypes.

The availability of these on DNA tests enables:

- Monitoring the presence of traits (desired or undesired);
- Exploit desired traits;
- Diminish the presence of undesired traits or prevent them from being disseminated;
- Avoiding risky matings;
- Avoiding investments in young bulls with undesirable traits or with genetic defects. In this way, AI centers can reduce risks in making investments of bulls which later may manifest some of these genetic defects. On the other hand, the advantage for farmers is to reduce and / or avoid the health problems in their herd. In this way genomics is providing added value to farmers.

Table shows all the genetic traits currently under control. Since November 2015 the direct tests were added to markers that determine genetic factors, such as K-casein.

Table 15E. Genetic traits now monitored

Trait	Lethal	Effect
Reproduction	Y	Brachyspina, HH1, HH2, HH3, HH4, HH5, HH6, HH7, BLAD, Citrullinemia, CVM, DUMPS, Spinal muscular atrophy, Spinal demyelination, Congenital muscular dystonia 2, Maple syrup urine disease, Osteopetrosiss
Feet	Y	Mulefoot
Horns	N	Polled
Survival	Y	Deficiency of cholesterol, Dilated-Cardiomyopathy, Factor XI, Ehlers-Danlos syndrome
Hair	N	Red recessive, Red dominant, Telstar, Silver color dilutor
Milk	N	Alfa S2-casein, Beta-casein AB, Beta-Lactoglobulin, Kappa-casein AB, Kappa-casein ABE, Kappa-casein ABCE

Since February 2016, ANAFIBJ has added an imputation process (an estimation of missing genotype segments using information from animals with the same DNA strands) also for genetic deficiencies in order to obtain information about genotyped animals whose DNA panels do not include these factors. Thanks to this process, the genetic factor information is revealed for genotyped animals with different DNA panels (i.e., panels without information about these factors). It is important to emphasize that for DNA panels containing genetic factor information any tests are available to directly identify them; however, thanks to the imputation process it is possible to trace DNA segment transmissions which reveal these genetic factors. Nowadays, information about these deficiencies is available for at least 300,000 animals. For each tested animal, the result specifies if it comes from a direct test or from the imputation process. Results from imputation are unofficial, so they are not published. Despite this, they are available for AI centers and for mating programs.

JERSEY

16. THE SELECTION INDEX

1.1 IQJ (Jersey Quality Index)

IQJ is the selection index of the Italian Jersey breed. Used for the first time in 2001, this index combined only milk quality traits (milk and protein), then in 2005 three linear traits relative to functional udder have been added, fore attachment strength, ligament and udder depth.

The formula for IQJ is as follows:

$$\text{IQJ} = 1.33 \times (-0.03 \times \text{milk kg} + 2.94 \times \text{protein kg} + 1.55 \times \text{fore attachment strength} + 1.51 \times \text{ligament} + 13.06 \times \text{udder depth})$$

which determines a 84:16 ratio between production and functionality.

The table below shows the relative weight of each trait included in IQJ:

PRODUCTION	WEIGHTS	FUNCTIONALITY	WEIGHTS
Milk Kg	19	Fore attachment strength	2
Fat Kg	0	Ligament	2
Protein Kg	65	Udder depth	12

17. BREEDING VALUES FOR PRODUCTION TRAITS

17.1. Data recording

The production data from the monthly milk controls done by ARA arrive from the Italian Farmers Association (AIA). All the records collected between day 5 and day 305 of lactation are used, up to third lactation.

17.2. Environmental effects

A random regression test day model is adopted, estimating every effect using a function that explains their variability from day 5 to day 305 of lactation. Breeding values for milk, fat and protein are estimated simultaneously, thus making use of genetic correlations among traits that improve total accuracy of estimates. Estimated fixed effects are parity, calving season, year and month of calving and age at calving.

Average variability of milk, fat and protein within herds are calculated every year, using all available test-day records; this parameter measures variability of herd productions around total average and helps in identifying higher and lower than average variability herds before adjusting them to match the “correct” scale.

The “correct” scale is within herd variability of primiparous cows born between 2010 and 2015 (the genetic base cows). This correction for heterogeneity of variance allows differences among animals to be measured in a unique scale for every herd. Animals are compared according to herd-year-test day and parity. Cows are divided into first and multiple parity class, this last effect allows to account for every management effect within herd and time.

17.3. Random effects

The animal effect, after which the Animal Model statistical method is named, allows for the estimation of breeding values of all animals within the population, both male and female, with all their relationships.

17.4. How the breeding values is expressed

The traits for which breeding values are calculated are milk, fat and protein yields. This index is expressed in kilograms as a deviation from a reference base (the genetic base), that sets the zero of breeding values. The genetic base is variable and it is updated in April every five years; its purpose is to express the breeding values relative to the value of the cows in the herds at the present time. Current genetic base reflects genetic value of the cows born between 2010 and 2015 and has been updated in April 2020. Percentages are computed with reference to the 305 days phenotypic productions of cows of the genetic base. The base values are then used in the following formula to calculate the breeding values for percentages:

$$\begin{aligned} \text{Fat\%} &= 100 \times (\text{fat BASE} + \text{fat}) / (\text{milk BASE} + \text{milk}) - \text{fat\% BASE} \\ \text{Protein\%} &= 100 \times (\text{protein BASE} + \text{protein}) / (\text{milk} + \text{BASE}) - \text{protein\% BASE} \end{aligned}$$

17.5. What is published

For all bulls, including foreign bulls, are used the results provided by INTERBULL (decision n° 256 of the Central Technical Committee 25/10/2013).

Table 17A. Genetic Base 2010-2015 Jersey

Trait	Average Base	Genetic gain
Milk	7,309.40	-103,32
Fat	365.27	-7.54
Protein	283.11	-3.90
Fat %	5.04	-0.40
Protein %	3.88	0.00

18. BREEDING VALUES FOR TYPE TRAITS

18.1. Data recording

Information of type evaluations carried out on all first-calf heifers classified two or four times a year by the breed inspectors (over the last ten years) is used for the calculation of the breeding values. Unlike to what happens with the production proofs, in this case age variation is not so strong and there is no repeated data. For each cow only one evaluation is used.

18.2. Environmental effects

An animal model is used. The fixed effects are the interaction between month of calving and stage of lactation at the time of calving, calving age and the herd-year-season of scoring.

18.3. Random effects

The only random effect taken into consideration is the one of the animal. All parental relationships existing among the population are taken into consideration. This allows to estimate the genetic value of all animals, taking into account possible preferential or corrective mating.

18.4. How the breeding values is expressed

The breeding values of all linear type traits evaluated since 2004 and final score are calculated. Table illustrates the heritability data utilized for the calculation.

A zero-breeding value refers to the genetic level of animals born between 2010 and 2015, i.e. the genetic base, for which the same rules of the production traits apply. All breeding values are standardized for the variability of the cows in the genetic base; in this way, all traits can be measured on the same scale.

On the Table you can see the heritability values of all traits, the phenotypic average of the animals in the genetic base, and the equivalent in points (linear scale) of one standard deviation of that breeding value. The table values will vary at every change of the base and will be updated on the web page, where genetic proofs are.

Table 18A. Genetic Base 2010-2015 Jersey

Linear Trait	Heritability	Average Base	DS in linear points
Final score	0.22	80.73	1.00
Stature	0.36	26.85	2.19
Strength	0.26	26.40	1.08
Body depth	0.25	29.58	1.02
Angularity	0.24	29.91	1.02
Rump angle	0.28	24.69	1.44
Rump width	0.15	25.23	0.99
Rear leg set	0.11	27.06	0.75
Rear leg rear view	0.07	28.20	1.00
Heel depth	0.08	24.93	0.69
Feet and legs functionality	0.09	25.20	1.00
Fore udder attachment	0.22	24.78	1.38
Rear udder height	0.17	28.08	1.02
Rear attachment width	0.28	30.39	1.29
Ligament	0.11	27.78	0.78
Udder depth	0.36	29.58	0.11
Front teat placement	0.11	24.12	0.78
Teat size	0.18	23.13	1.14

18.5 What is published

For all bulls, including foreign bulls, are used the results provided by INTERBULL (decision n° 256 of the Central Technical Committee 25/10/2013).

19. MORPHOLOGICAL COMPOSITE INDEXES - JERSEY

19.1. ICM (Udder Composite Index)

ICM is a composite index focused on udder health. The breeding goal is the reduction of SCC in milk. Linear type traits are considered as follows:

$$\begin{aligned} \text{ICM} = & 0.03 * \text{rear udder height} + \\ & 0.30 * \text{udder depth} + \\ & 0.18 * \text{ligament} + \\ & 0.25 * \text{fore udder attachment} + \\ & 0.06 * \text{teat size} + \\ & 0.18 * \text{front teat placement} \end{aligned}$$

In order to avoid the rewarding of animals having too close and long teats, an intermediate optimum has been introduced for the following traits:

Table 19A. Optimum intervals in Jersey breed, ICM

Trait	Phenotypic SD -	Phenotypic SD +
Posizione capezzoli anteriori	-0.5	1.0
Dimensione dei capezzoli	-0.5	0.5

The animals with scores outside the optimum range will be penalized.

19.2. IAP (Feet & Legs Composite Index)

Composite IAP Index is aimed at improving locomotion, longevity and career milk production of the breed. It is derived from the combination of three indices, based on linear characters for limbs, feet and locomotion, evaluated by inspectors.

Linear type traits are considered as follows:

$$\begin{aligned} \text{IAP} = & 0.12 * \text{foot angle} + \\ & 0.40 * \text{feet and legs functionality} + \\ & 0.36 * \text{legs side view} + \\ & - 0.12 * \text{legs rear view}. \end{aligned}$$

An intermediate optimum for the trait “legs side view” is considered, in order to reward animals that do not have defects.

Table 19B. Optimum interval in Jersey breed, IAP

Trait	Phenotypic SD -	Phenotypic SD +
Legs side view	-0.5	0.5

20. BREEDING VALUES FOR SOMATIC CELL SCORE (SCS)

20.1. Data recording

The somatic cells count is collected by the Italian Breeders Association (AIA) every month.

All the records collected between day 5 and day 305 of lactation are used, up to third lactation. Besides ordinary data editing, records abnormally deviating from each cow's estimated lactation curve are discarded. A repeatability animal model is used.

20.2. Environmental effects

The fixed effects are parity, season of calving, days in milk (gathered in groups of 30 days) and the herd-year-day of control.

20.3. Random effects

The random effects are the genetic effect of the animal and the permanent environment.

20.4. How the breeding values is expressed

It is expressed as deviation from the Genetic base, which changes every 5 years in April evaluation): the mean is 100 and the standard deviation (SD) is 5 (phenotypic values can be found in the table below). The phenotypic values of the positive and negative standard deviations are different, as the distribution is distorted.

Table 20A. SCC parameters-Jersey

Trait	Heritability	PhenotypicSD	Mean Phenotypic	PhenotypicSD
		-		+
Somatic cells count (thousands cells/ml)	0.09	+50	278	-30

THE INTERNATIONAL PROOFS

21.1. Data

Input data for International genetic evaluation are the Official Breeding Values computed in each country participating in the service. The service of international evaluation is run by International Bull Evaluation Service (INTERBULL) in Sweden. All countries, including Italy, are sending their official proofs to this center at a given date determined by a calendar of publications approved each year. All breeding values for bulls with at least 10 daughters in 10 herds, are sent to INTERBULL while, for calving ease, the limits are bulls with at least 50 daughters in 10 herds. For test day model data, since April 2023, the traits for which the international genetic evaluation is available are: milk, fat, protein, standard morphological traits, calving ease (direct and maternal); stillbirth (direct and maternal), somatic cells, fertility and body condition (BCS).

21.2. MACE MODEL

Each trait is evaluated by INTERBULL with a *Multiple Across Country Evaluation* (MACE in brief): in practice the proof in each country contributing to the evaluation is considered as a separate trait. In this way it is possible to compare bull rankings across countries. The difference across countries is measured through genetic correlation among the various countries. The effects accounted for in the model are the country average and the genetic groups for the maternal grand dam and for the material grand sire in case they are born before 1986. Table shows the genetic correlations (April 2023) between Italy and some of the participating countries for all the traits for which the international evaluation is provided.

Table 21A. Correlations among Italy and other countries

Country	HOLSTEIN						
	Protein	Type	Cells	Mastitis	Longevity	Fertility	Calving ease
USA	0.87	0.84	0.89	0.68	0.76	0.91	0.45
CAN	0.85	0.70	0.90	0.79	0.76	0.86	0.44
FRA	0.84	0.87	0.93	0.80	0.64	0.86	0.48
DFS	0.85	0.82	0.93	0.77	0.68	0.84	0.45
NLD	0.82	0.80	0.89	0.89	0.53	0.84	0.44
DEU	0.86	0.79	0.95	0.72	0.74	0.91	0.40
AUS	0.60	0.51	0.78	0.65	0.52	0.69	0.37
NZL	0.57	0.50	0.74	0.66	0.48	0.63	0.29

JERSEY			
Country	Protein	Type	Somatic cells
USA	0.86	0.78	0.85
CAN	0.86	0.70	0.87
DFS	0.84	0.72	0.91
NLD	0.81	0.80	0.87
DEU	0.85	-	-
AUS	0.67	0.48	0.71
NZL	0.61	0.54	0.65

21.3. How it works

When a bull presents index in a single country, the genetic value of the latter (as deviation of the daughters from the average for a given character) is estimated by subtracting the contribution of the pedigree and transferring the index to the scale of all other countries. In doing so, account shall be taken of information relating to genetic correlation and to the difference in scale between the two indexes. To this deviation is added the value of the pedigree, by adapting the index on the scale of the country of interest.

When a bull has daughters in more than one country the deviations are weighted by the number of daughters and then summed together before re-adding the pedigree in the country of interest.

21.4. GMACE model – Young bulls (Holstein)

With the arrival of genomic evaluations in various countries, there has been a growing interest and demand for the international marketing of semen of young genomic bulls. The fact that indexes for progeny-tested bulls are not comparable between countries also extends to young genomic bulls. For this reason, as of August 2015, INTERBULL has made a genomic MACE official for young bulls. This process is called GMACE (Genomic Multiple Across Country Evaluation) and includes international genomic assessments for sires without daughters. The GMACE evaluation uses the official national GEBV indexes estimated in each country by returning a genomic evaluation on the scale of all acceding states, even those where genomics is not yet applied or is not official.

This service will help Italian breeders to evaluate the genetic merit of young bulls belonging to countries which are not part of the Intercontinental consortium (USA, Canada, Great Britain, Italy and Switzerland), evaluated directly at national level.

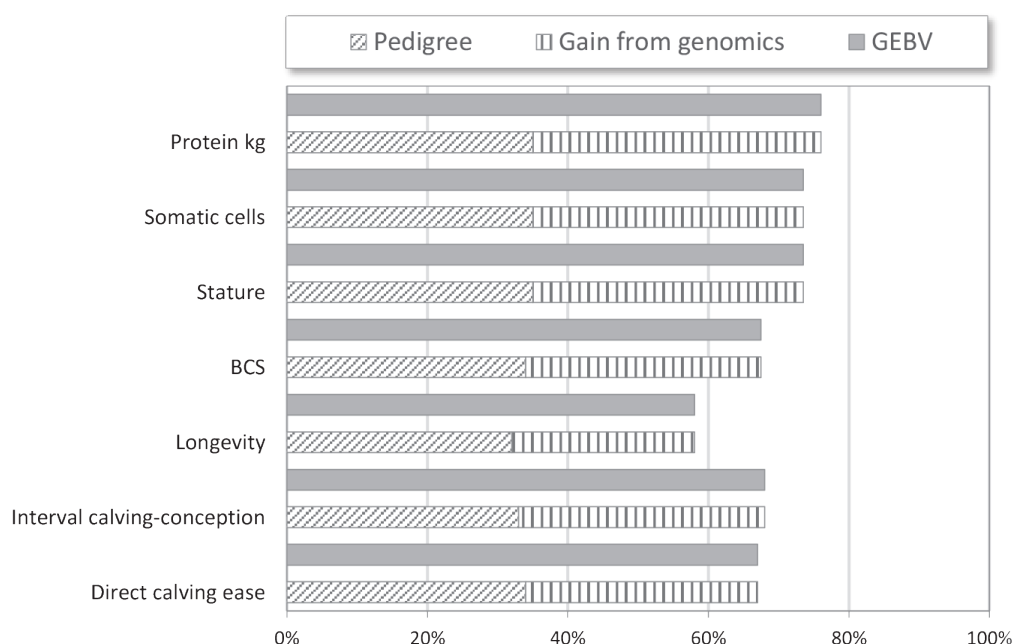
21.5. How it works

Each country that wants to participate in the GMACE evaluation sends to INTERBULL the national genomic indexes for all the traits for which genomic validation has pas-

sed. Currently in Italy all the traits for which the national genomic index is official (production, morphology and functionality) have been validated. Clearly, the ideal scenario would be to witness a direct exchange of genotypes between all countries, as well as within the states belonging to the Intercontinental consortium (United States, Canada, Great Britain, Italy and Switzerland) or EuroGenomics (France, Scandinavian countries, Germany, Spain, Holland/Flanders and Poland).

By starting directly from the genotype of each individual animal, the estimation of genomic indices is much more reliable than the one of a pedigree index, especially for young bulls that, either do not have observations on daughters yet, or have a limited number of offspring. Figure 4 shows the reliability level of pedigree and genomic indices for the different character groups.

Figure 4. **Reliability of pedigree index and genomic index.** Different traits estimated from genomic data-base of ANAFIBJ



What is published

INTERBULL computations give back to each country the breeding value of all bulls evaluated in the world (around 70,000 bulls) on the country scale. Each country has approved rules of publications of those proofs. These rules are subject to changes and the up-to-date rules are always published on the website, in the area related to breeding values. In August 2007 in Italy, the rules of publications were as follows:

Holstein

PRODUCTION (3 traits) – CONFORMATION (21) – LONGEVITY – UDDER HEALTH (2 traits) - FERTILITY (5 traits) – CALVING (2 traits) - WORKABILITY

Jersey

PRODUCTION (3 traits) – CONFORMATION (18) – UDDER HEALTH (somatic cells)

GLOSSARY

Allele: A particular DNA variant that may be responsible for alternative expressions of a trait. Every individual has a paternal allele and a maternal allele, which may be the same (homozygote) or different (heterozygote).

DGV: Direct genomic index (the simple sum of the effects of markers).

DNA: (deoxyribonucleic acid). The substance that makes up the gene pool. It is formed by a sequence of 4 core bases.

EBV: Traditional index.

Genetic factor: Genetic variant where the gene is known.

GEBV: The combination of a traditional index (EBV) and a direct genomic index (DGV).

Gene: The basic physical unit of heredity. A segment of DNA that codes for a function or several correlated functions.

Genome: The set of chromosomes contained in the DNA in an organism.

Genomics: The field of molecular biology that deals with the study of the genome.

Genotyping: The process of determining a genotype by analyzing DNA. A specified sequence is compared with another. SNP genotyping measures genetic variations (alleles) in the polymorphism of a single nucleotide (SNP).

Genotype: The set of genes that make up the DNA of an organism or population.

Haplotype: DNA segment strictly linked. It can pass from parent to offspring

Imputation: Methodology used to estimate missing parts of a genotype using information from related individuals.

Molecular markers: Pieces of DNA whose alleles can be easily identified in the laboratory. They are used to identify neighboring genes.

Nucleotide: The building block of DNA.

SNP molecular marker panel: A laboratory kit used to determine the genotype of a certain individual (genotyping). These kits may contain different quantities of information. Moreover in these panels are also included markers which can identify known genes (i.e.: milk proteins).

Polymorphism: The simultaneous presence of two or more alleles or nucleotides in the same population.

Proven genomic bull: bull with daughters whose final index (GEBV) results from the combination of the traditional index (EBV) and the direct genomic index (DGV).

SNP: Single Nucleotide Polymorphism. Polymorphism in a specific base or nucleotide in the DNA sequence.

Young genomic bull: bull without daughters whose index (DGV) is obtained directly from the markers and from the pedigree.

RED COLOR

- Red factor

CARRIER	RED
RF	R

Trait linked to a recessive gene (MC1R), therefore only the recessive homozygous subjects for this character will have the red coat. If the two ascendants have the black coat but are heterozygous for the MC1R gene, therefore

subjects carrying the red factor, the probability that a red homozygous subject is born is 25%. Whereas if the ascendants are respectively heterozygous and homozygous, there is a 50% probability that the calves can be born with the red mantle.

Direct genomic testing is available for this character.

- Variant Red

Trait linked to a dominant gene (COPA), therefore also the heterozygous subjects are born with red coat.

All dominant and heterozygous homozygous subjects will be red, only recessive homozygous subjects will be black.

Direct genomic testing is available for this character.

BLAD

POSITIVE	NEGATIVE
BL	TL

Bovine Leukocyte Adhesion Deficiency

It is an autosomal recessive lethal genetic abnormality in cattle. It affects the immune system of the animal by making it free of antibodies and causing its death, even after infec-

tions easily treatable. From a strictly biological point of view, this anomaly is linked to the decrease of a membrane receptor that regulates the passage of antibodies through the membranes and prevent the fight against infection.

All F.A. enabled bulls in Italy must be tested for this genetic anomaly. Bulls carrying this anomaly cannot be authorized to the F.A. in Italy.

Direct genomic testing is available for this trait.

MULEFOOT/SYNDACTYLISM

POSITIVE	NEGATIVE
MF	TM

It's a congenital malformation of the distal parts of one or more limbs, linked to an autosomal recessive gene.

It consists of the complete or partial fusion or not division of the nail. Generally, it is a bone problem that affects the

phalanges, but can also extend and affect the metacarpal and/or metatarsal.

The disease can manifest itself in a variable way: usually the most affected foot is the right front, followed by the left front, right back and left back.

In the first months of life, the animal can live almost normally but, with the increase of weight, it incurs difficulties in walking, up to the impossibility of remaining in a quadrupedal position.

The positive individuals for Mulefoot cannot be qualified to the F.A. in Italy.

Direct genomic testing is available for this trait.

CVM

POSITIVE	NEGATIVE
CV	TV

Complex Vertebral Malformation.

This genetic anomaly involves the abnormal development of the spine and the cervical and/or thoracic vertebrae, as well as the distal portions of the limbs in fetuses homozygous for

the trait. In such cases, the spine and the cervical and/or thoracic vertebrae are shortened and the distal portions of the limbs are retroverse.

It is an inherited genetic disorder linked to an autosomal recessive gene. Generally homozygous animals die during pregnancy or a few days after childbirth.

Bulls carrying this anomaly cannot be authorized to the F.A. in Italy.

Direct genomic testing is available for this trait.

BRACHYSPINA

POSITIVE	NEGATIVE
BY	TY

Brachyspina is a genetic defect linked to an autosomal recessive gene that causes physical deformities in the fetus and induces embryonic death. Affected calves have a reduced body weight as well as a shortening of the spine with

long and thin limbs. There is also frequently a hypoplasia of the jaw, that is only outlined and on which the incisors are inserted in a disorderly way.

Bulls carrying this anomaly cannot be authorized to the F.A. in Italy.

Direct genomic testing is available for this trait.

CHOLESTEROL DEFICIENCY

POSITIVE	NEGATIVE
CD	CF

It is a genetic disease linked to a recessive gene that involves a reduced or non-existent ability to synthesis of cholesterol, a fundamental molecule in preserving cell membranes. The calves homozygous for this genetic defect, have strong

diarrheal episodes, loss of appetite, slimming and incompatibility with life.

Bulls carrying this anomaly cannot be authorized to the F.A. in Italy.

Direct genomic testing is available for this trait.

FREE MARTINISM

Infertility condition that may occur in females born from twin births in co-presence of male individuals. It consists of the presence, in the same individual, of two different cell lines: one male (XY) and one female (XX). It comes from a placental anastomosis that involves the passage of male cells to the female fetus.

The molecular test is performed on female phenotypically subjects on a non-clotted blood sample.

POLLED

HOMOZYGOUS	HETEROZYGOUS	NOT CARRIER
PS	PC	PF

Genetic condition in cattle that determines the absence of horns.

This condition is linked to a dominant gene, therefore it will be sufficient to have

only one copy of the polled gene, so that the subject does not manifest phenotypically horns.

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