BREEDING VALUES (BV) OF NORMAND SIRES IN FRANCE
FOR DAIRY, FUNCTIONNAL AND TYPE TRAITS

25/15 RELEASE (APRIL 2025)

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Breeding values (BV) are computed by GenEval.

Warning: The French evaluation model has changed in the beginning of the year 2022. We now use the Single Step approach to calculate GEBVs. The method part and formulas will be described later.

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Breeding values developed by the eBIS UMT (INRAe, IDELE and ELIANCE partnership).
Indexes calculated by GenEval and published by the French Livestock Institute under the responsibility of Breeding Organisms.

IDELE UMT eBIS GenEval

1. – CONVENTIONNAL SELECTION

1.1 – BREEDING VALUES FOR DAIRY TRAITS

BV for dairy traits are computed according to a BLUP - Animal Model procedure

1.1.1 - THE BLUP ANIMAL MODEL

All pedigree relationships are taken into account. Males and females are simultaneously evaluated. Permanent environment, environmental and genetic effects are simultaneously estimated. Selection of cows and mates are considered.

1.1.2 - TRAITS

BV is computed for:

- MP = True protein yield (kg; instead of crude protein yield)
- MG = Fat yield (kg)
- Lait = Milk (kg)
- TP = True protein content (‰)
- TB = Fat content (‰)
- INEL = Selection criterion aiming at maximizing the net margin of a dairy herd (no milk quotas, reduced E.U. prices, constant variable plus fixed costs, no substitution activities).

INEL (points) = 0.98 [MP + 0.2 MG + 1 TP + 0.5 TB] (standard deviation =20 points)

DEFINITION OF BASES

Rolling base

The average BV of cows born between years (n-8) and (n-6) included, having two known parents, at least one milk recorded lactation and a minimum reliability of 30%, is set to zero. That reference group is updated with the release in February.

Fixed base

The average BV of milk recorded cows with known sires and born between 1977 and 1980 included is set to zero.
Since 2014, the average BV of calving and stillbirth traits was fixed and includes sires born between 2002 and 2005 for Holstein, Normande and Montbeliarde breeds, and born between 2000 and 2005 for regional breeds.

1.1.3 - MODEL AND DATA

Data and genetic parameters

First to third parity daughters are included if their date of calving is 90 days or more before the computing date and, when in progress, more than 59 days long. The weights of lactations in progress more than 179 days long or completed lactations are 1 (first parity) and 0.8 (second and third parity) respectively. Second and third parities have smaller heritabilities and do not refer exactly to the same trait as first parities.
All cows with first calving date posterior to September 1st 1979 are considered.
Heritability and repeatability are 30 % and 50 % for yields, 50 % and 70 % for contents respectively.

Model

Completed lactations are precorrected for lactation length and partly for parity to mature equivalents. Lactations in progress are extended. The correction for lactation length aims at reducing the genetic decrease of fertility level when considering long high yield lactations.

Pre-corrected performances are explained by four groups of factors:

- BV,
- permanent environment,
- environmental identified factors,
- residual,

Environmental effects are computed within breed :

- herd * year,
- parity * region * year,

- calving month * parity * region * year - (first vs 2nd and 3rd parities),
- age at calving * parity * region * year,
- preceding dry period length * parity * region * year.

A heterogeneous variance model assuming heterogeneous residual variances and known constant ratios (heritability, repeatability) is applied. The linear model for the log residual variance at the herd-year level includes a region-year fixed effect and a herd-year random effect with a within herd autocorrelation. BVs are the expression of the genetic values according to the breed average residual standard deviation in 1996.

1.1.4 - RELIABILITY OF BV

Only the sum of weights (number of daughters - number of lactations) and the distribution of daughters between herds are taken into account. No ancestry information is included. According to reliability levels for yield traits, standard deviation of BV's are approximately the following:

Rel.	MP True protein yield (kg)	MG Fat yield (kg)	Lait Milk yield	TP True protein content (‰)	TB Fat content (‰)
0.50	±25	±32	±770	±1.6	±2.8
0.60	±22	±28	±689	±1.5	±2.5
0.70	±19	±24	±596	±1.3	±2.2
0.80	±15	±20	±487	±1.0	±1.8
0.90	±11	±14	±344	±0.7	±1.3
0.95	±8	±10	±244	±0.5	±0.9

BV's with 70 % reliability or above are official. If the reliability is between 60 % and 69 % high INEL levels are required for officializing BV.

1.2 - BREEDING VALUES FOR UDDER HEALTH TRAITS

Evaluations for five functional traits are available in France: Somatic cell score, functional longevity, female fertility, ease of birth and ease of calving.

1.2.1 - BREEDING VALUES FOR SOMATIC CELL SCORE = CEL

Data

All monthly Somatic Cell Counts (SCC) after 1/09/89 for parities 1 to 3, between 5 and 450 days in milk are used. Data before 1994 were not exhaustive.

① Somatic cell scores (SCS) are defined through a logarithmic transformation

$$\text{SCS} = \log_2\left(\frac{\text{CCS}}{100000}\right) + 3$$

② SCS are adjusted for days in milk and parity

③ A weighted average of adjusted SCS is computed as $\text{SCSL} = \dfrac{\sum \frac{R}{\sigma}[SCS\ adjusted]}{\sum \frac{R}{\sigma}}$

where R is the correlation between the test-day SCS and the average of other SCS and σ is the SCS standard deviation for a given number of days in milk.

④ SCSL are standardized for parity using a multiplicative factor: 1.15 for first parity, 1.08 for second parity, 1 for third parity.

Model and heritability

A BLUP animal model is applied and the statistic model is the same as for dairy traits, except for heterogeneous variances. Heritability and repetability of SCSL trait are 15 % and 35 % respectively.

Expression of breeding values and conditions for publication

Breeding values (CEL) are expressed in genetic standard deviation units and the publication is allowed with a reliability of at least 50 %. The rolling base is the same as for dairy traits with a minimum reliability of 50 %.
The scale is reversed and bulls with positive CEL are more desirable than others (see table at the end of § 2.1 in the french version).

1.2.2 BREEDING VALUE FOR CLINICAL MASTITIS (MACL)

The objective is to evaluate the occurrence of clinical mastitis (MACL), selected indirectly since 1997 through cell counts. Indeed, only a part of the resistance to mastitis was taken into account till now.

Definition of the trait and data selection

The information is 0 / 1 and can be recorded during milk recording. It applies to the first three lactations and is defined as follows: "At least one event of clinical mastitis recorded during the first 150 days in lactation.

One must be sure that a cow noted "0 = no clinical mastitis", is a healthy cow instead of a non recorded animal. To ensure this, a selection of data is required. The data taken into account begin in 1997. A selection of lactations per herd * year is done: a herd must declare a minimum of 5% lactations with at least one mastitis event (all lactations, with adjustments for herd size). +

Direct clinical mastitis (MACL)

An animal model including a permanent environmental effect (to account for the repeatability of the trait between lactations) is used. The following environmental effects are considered:

- Calving month*year
- Herd * year
- Calving age class*Lactation number*year

The model includes heterogeneous variances for the following effects:
- Lactation number*year
-Area*year

Thus, a difference in genetic values between animals will result in a difference in performances which varies according to lactation number, area and year. The heritability of the trait is in the range of 2-3% and the repeatability is around 5-6%.

	h² %	Repeatability %	Genetic standard deviation %
Prim'Holstein, Brune	1.8	5.5	4.12
Montbéliarde, Tarentaise	2.3	5.5	4.35
Normande	2.1	6.2	4.69
Simmental	2.3	5.5	3.57
Abondance	2.3	5.5	2.64

Combined clinical mastitis (MACLC)

Each elementary genetic evaluation is summarized into one corrected data per cow and trait. Functional (SCC, cow fertility FER, heifer fertility FERg, true functional longevity LGF, clinical mastitis MACL), milk and type traits (up to seven traits including milking speed, feet and legs, udder and body traits) are combined in an approximate Multi-trait BLUP Animal Model which produces three combined functional traits used in ISU calculations. So the reliability of combined MACL is increased especially thanks to cell counts and it replaces direct MACL as the official B.V.

Expression of breeding values and conditions for publication

Breeding values are expressed in genetic standard deviation units (one genetic S.D.=4 to 5 %) and the publication is allowed with a minimum reliability of 50 %. The rolling base is the same as for the dairy traits.

A positive BV for MACL is desirable and a 1 point difference in BV is equivalent to additional 2-2.5 percentage points in MC events of the daughters of a sire.

1.2.3 BREEDING VALUE FOR UDDER HEALTH SYNTHESIS (STMA)

Breeding Value for Udder Health Synthesis is a combination of Somatic Cell Score and Clinical Mastisis:

$$\mathbf{STMA = (0.6 * CELc + 0.4 * MACLc) / 0.90}$$

1.3 - BREEDING VALUES FOR REPRODUCTION

1.3.1 - BREEDING VALUES FOR FEMALE FERTILITY = FER

The purpose is to evaluate the fertility of adult daughters and not to describe the male fertility of the service sire.

Data

The analyzed trait is defined as the result (success/failure) of A.I. that have been made in milk recorded herds since September 1995. Those which happened at least 6 months before the run are assessed according to the following rules:

- when there is a subsequent calving, the successful A.I. is the most in accordance with the gestation length of the breed, in the interval between 45 days after IA and 15 days above the reference gestation length.
- when there is no subsequent calving, IA status is assessed according to the first of the following rules:
  - unsuccessful, if the female is known as dead or sold for slaughter;
  - successful, if the female is known as moved to a non milk recorded herd;
  - successful, if IA has occurred less than 340 days before; a probability of gestation is applied according to the time from IA, heifer or cow status, breed and IA rank;
  - successful, if IA has occurred more than 340 days before, when the lactation stage was less or equal to 260 days;
  - unsuccessful, if IA has occurred more than 340 days before, when the lactation stage was more than 260 days;

Subsequent A.I. within the same parity are discarded and preceding ones are considered as failed. Heifers, 1^{st}, 2^{nd} and 3^{rd} parity cows are included in the genetic evaluation, with at most 3 IA in the same parity.

Direct fertility (FER, FERG)

The fertility of heifers and the fertility of cows are considered as two correlated traits with a common heritability at 2%. Moreover, the corresponding two non-return rates between 18 and 56 days are evaluated but not published and used as predictors in step (c) below.

The traits are separately evaluated with a Blup Animal Model procedure. The model of analysis includes the following effects: herd and IA technician, within year ; parity; month and day in the week, within year and region ; calving-insemination interval for cows or age at insemination for heifers, within year; the inbreeding coefficients of the dam and its calf; the breed of the service bull; the service bull within year (random effect); the permanent environment of the cow (random effect).

Combined fertility (FERC)

Each elementary genetic evaluation is summarized into one corrected data per cow and trait. Functional (SCC, cow fertility FER, heifer fertility FERG, true functional longevity LGF, clinical mastitis MACL), milk and type traits (up to seven traits including milking speed, feet and legs, udder and body traits) are combined in an approximate Multi-trait BLUP Animal Model which produces three combined functional traits used in ISU calculations. So, the reliability of combined fertilities, FERC and FERGC is increased especially for young bulls. Combined BVs replace direct BVs as official figures.

Expression of breeding values and conditions for publication

Breeding values (FER) are expressed in genetic standard deviation units (one genetic S.D.= 7 %) and the publication is allowed with a minimum reliability of 50 %. The rolling base is the same as for the dairy traits without any minimum for reliability.

A positive BV for FER is desirable and a 1 point difference in BV is equivalent to additional 3.5 points in the conception rate of the adult daughters of a sire.

1.3.2 –INTERVAL BETWEEN CALVING AND FIRST AI (IVIA1)

IVIA1 reflects the genetic ability to initiate postpartum cyclicity even if, associated with AI, it depends partly on breeder decision
The evaluated trait is the interval in days between calving and first AI up to the third lactation. A positive value corresponds to a short interval after calving.

The evaluation model is a single-trait blup animal model with permanenet environment effect including the following fixed effects:

- Herd-year
- Calving month-year-region,
- Calving age,
- Parity preceding AI.

The heritability of the trait is between 3% and 6% and the repeatability is around 10%; genetic parameters by breed are listed below. After this step, direct results are included into the general procedure for combined functional traits presented above (see § 2-2-3-c and d).

	IVIA1		
	h² %	Repeatability %	Genetic standard deviation
Montbéliarde	3.7	8.8	5 d
Normande	3.4	8.1	5 d
Prim'holstein	6.1	12.2	7.75 d

1.3.2 –BREEDING VALUE FOR REPRODUCTION SYNTHESIS (REPRO)

This synthesis includes breeding values for Fertility of cows, Fertility of heifers and Interval between calving and first AI:

REPRO = 1.36986 (0.52 * FERc + 0.30 * FERGc + 0.18 * IVIA1c)

1.4 - BREEDING VALUES FOR OTHERS FUNCTIONNAL TRAITS

1.4.1- BREEDING VALUES FOR FUNCTIONAL LONGEVITY

- True longevity is defined as actual longevity, i.e., mainly dependent on production,
- Functional longevity is the ability to delay involuntary culling due to, e.g. sterility, lameness, mastitis, or other diseases.

The aim of the evaluation is to improve functional longevity. Functional longevity is approximated by correcting true longevity for the main source of voluntary culling, i.e., culling for low production.

Direct functional longevity (LGF)

Longevity is measured as Length of Productive Life (LPL), defined as the number of days from first calving to last test date known for lactations 1 to 5 starting after 01/01/1988. LPL is measured at time t_o, 5 months before the beginning of the computations.
Then two kinds of records are used:

- Uncensored records when LPL is known exactly (the cow is dead or culled). It is assumed to be the case when no milk record has been collected for the last 5 months,

- Censored records when animals are still alive at the time of the evaluation. It is the case for any cow:

- with a milk record collected during the last 5 months,
- sold to other herds,
- in a herd in which at least 50% of the animals has been culled or sold,

The joint analysis of censored and uncensored records is based on the concept of hazard rate defined as the probability of being culled at time t, given that the animal is alive immediately prior to t.

The hazard at time t of a particular cow is described as the product of:

- a baseline hazard function, depending on year, parity (1 to 5) and stage of lactation (0-270d, 270-380d, >=380d, dry period) describing how the hazard increases with parity and stage of lactation,
- a positive term (the exponential of a sum of time-dependent effects) describing how the baseline hazard rate is modified due to the own characteristics of the cow or of her herd. These effects include:

- a herd effect per year effect,
- a region per year effect,
- an age at first calving effect,
- an effect of the variation of herd size per year,
- an effect of within herd level of production (within-herd class of milk production per year-season + - within herd class of protein content per year + within herd class of fat content per year).
- sire and maternal grand-sire (genetic) effects corrected for the dam's year of birth

Heritability (assuming no censoring) is 12.6 % for Holstein, 14.5 % for Montbéliarde, 11.7 % for Normande and 14% for the other breeds.

Combined functional longevity (LGFC)

The published combined functional longevity merges direct information on functional longevity with information from traits genetically correlated with it (indicator traits). Whatever the trait considered, each record of a cow is summarized into one corrected record per cow and trait. Direct functional longevity, functional traits (SCC, cow fertility, heifer fertility, milking speed), milk yield and relevant type traits (up to seven traits including feet and legs, udder, body condition and other body traits) are all included into an approximate Multi-trait BLUP Animal Model. This global analysis produces three combined functional traits used in Total Merit Index (ISU) calculations, including combined longevity (LGFC). So, the LGFC reliability is increased compared to the LGF one, especially for young bulls. LGFC replaces LGF as the official B.V. for functional longevity.

Expression of breeding values and conditions for publication

Breeding values (LGF) are expressed in genetic standard deviation units and the publication is allowed with a reliability of at least 50 %. The rolling base is the same as for dairy traits without any minimum threshold for reliability. Bulls with positive LGF are more desirable

1.4.2- BREEDING VALUES FOR EASE OF BIRTH (NAI) AND EASE OF CALVING (VEL)

The aim is to evaluate birth conditions (direct effect) and calving conditions (direct and maternal effects) to avoid risky matings (e.g. with heifers).

Data

Calving ease scores are expressed on a scale from 1 to 5: 1 = no assistance, 2 = easy pulling, 3 = difficult calving, 4 = caesarean and 5 = embryotomy. Given the very low incidence of the last two categories, they were analysed together with code 3.
Records collected since 1990 are included if, for the corresponding region year combination, there are:

- fewer than 95 % records of code 1
- at least 33 % records of male calves in 1999
- at least 25 % records of male calves in 1997-1998
- at least 20 % records of male calves before 1997

If the data from a particular region are excluded in year n, the data from this region from 1990 to n-1 are also discarded.

Model and genetic parameters:

Data are analysed using a heteroskedastic threshold model.
Accounting for the heterogeneity of the residual variance adds robustness and flexibility to the model.
Records, expressed on the underlying scale are modeled including the following effects:
For the Prim'Holstein, Normande and Montbeliarde breeds:

As fixed effects:

- sex of calf by parity-age class (5 age classes in parity 1, 2 in parity 2, and 1 for each subsequent parity) interaction
- month by year interaction
- region by year interaction

As random effects:

- herd-year-season interaction (2 seasons: November to April and May to October)
- sire of calf
- sire of dam
- dam (within sire of dam)

Residual variances are described on the logarithmic scale with the effects of month year of calving, sex of calf, region and parity-age class.

For the other dairy breeds, the model includes:

As fixed effects:

- sex of the calf
- parity (4 classes: 1, 2, 3 to 5, 6 and more)
- month by year interaction

As random effects:

- herd by year interaction
- sire of calf
- sire of dam
- dam (within sire of dam)

For these breeds, a unit residual variance is assumed. Direct heritabilities were 5.6%, 7.8 % and 7.4 % in Holstein, Montbeliarde and Normande, while maternal heritabilities were 3.2%, 3.7 % and 4.3 % respectively. Genetic parameters of the Normande breed are used for other breeds.

Expression of breeding values and conditions for publication

Breeding values (NAI and VEL) are expressed in % of easy calvings (code 1 and 2) expected from first parity dams, assuming a sex ratio of 50 %. These expected % of easy calvings are centered to 89 % for the bulls belonging to the rolling base.
Publication of EBVs is allowed when reliability is at least 50 %.

1.4.3- BREEDING VALUES FOR DIRECT AND MATERNAL STILLBIRTH

The aim is to evaluate calf mortality at birth (direct effect) and mortality at calving (direct and maternal effects) within 48 hours after birth. But EBVs are expressed relative to the complementary traits: vitality at birth (VIN) and vitality at calving (VIV).

Data

Breeders involved in parentage registration must also declare causes and dates of transfer for all animals according to the EU obligatory registration. A calf is considered as stillborn if its cause of transfer is “dead” and if the difference between its transfer date and its birth date is at most 2 days.
Records collected since January 1st 1999 are included for a given area, beginning with the first year when there are at least 2.5% or 3% stillborn calves, depending on the breed. In such an area, a herd is included beginning with the first year when at least one stillbirth is recorded.

Model and genetic parameters

Data are analysed using a threshold model. The model is very similar to the one used for birth and calving conditions, except that accounting for heterogeneity of the residual variance is neither feasible nor necessary for all-or-none traits.
Records, expressed on the underlying scale are modeled including the following effects:

As fixed effects:

- sex of calf by parity-age class (5 age classes in parity 1, 2 in parity 2, and 1 for each subsequent parity) interaction
- area by year interaction
- month of calving by year interaction

as random effects:

- herd year interaction
- sire of calf
- sire of dam
- dam within sire

Direct heritabilities were 3% in Holstein, 5.9% in Montbéliarde and 4% in Normande breed, while maternal heritabilities were 6.6% in Holstein, 5.8% in Montbéliarde and 4.1% in Normande breed. Genetic parameters of the Montbéliarde breed are used for other less important breeds.

Expression of breeding values and conditions for publication

Estimated breeding values (VIN and VIV) are expressed in % of calves still alive 48 hours after birth, expected from first parity dams, assuming a sex ratio of 50 %. These expected % of calves are centered to 92 % for the bulls belonging to the rolling base.
Publication of EBVs is allowed when their reliability is 50 % or above.

1.5 - BREEDING VALUES FOR CARCASS TRAITS

Since 2015, evaluations for veal calves and young bulls have been set up.

1.5.1 – VEAL CALVES

Veal calves are defined as the calves slaughtered between 70 and 250 days. As long as they have a Montbéliarde mother, they are used for the evaluation, whether they are mixed race or not.

Four traits are evaluated: age at slaughter, carcass weight, carcass conformation and meat color. Data are analyzed according to a BLUP multi trait animal model, with a mother's permanent effect on the age at slaughter, correcting the following environment factors:

- father's breed;
- calf's sex;
- mother's delivering age (by year, from 2 to 11 years old or more than 12 years old);
- Fattening herd, year of birth of the calf, and the slaughter's season (October to February or March to September).

Veal calves genetic parameters (standard deviation in the first column, heritability on the diagonal, genetic correlations beyond diagonal)

	Standard deviation	Carcass weight	Age at slaughter	Carcass conformation	Meat color
Carcass weight	7.92 kg	*0.24*	-0.03	0.68	0.05
Age at slaughter	2.81 d		*0.09*	0.16	0.51
Carcass conformation	0.80 1/3 class			*0.34*	-0.42
Meat color	0.13 class				*0.11*

The breeding values are given according to the rolling base of each evaluation, set to 0 by convention, gathering the calves of Montbéliarde mother born during the last 5 years and having performances for the 4 traits. The unity for these breeding values are the genetic standard deviation for each elementary traits and the standard deviation of the reference population for the breeding values for the synthesis traits.

The breeding values are official when the bulls CD have reached 0.50 and when they have at least 25 calves with full information.

1.5.2 – YOUNG BULLS

Young bulls are defined as the animals slaughtered between 350 and 730 days. Only the purebred animals are considered in this evaluation.

3 traits are evaluated: age at slaughter, carcass weight and carcass conformation. Data are analyzed according to a BLUP multi trait animal model, with a mother's permanent effect on the age at slaughter, correcting the following environment factors:

- Birth's month;
- Mother's delivering rank (first calf or not) * mother's class age (in months);
- Fattening herd, year of birth of the calf, and the slaughter's season and year

Young bulls genetic parameters (standard deviation in the first column, heritability on the diagonal, genetic correlations beyond diagonal)

	Standard deviation	Carcass weight	Age at slaughter	Carcass conformation
Carcass weight	12.4 kg	*0.12*	-0.54	0.47
Age at slaughter	11.6 d		*0.14*	-0.02
Carcass conformation	0.48 1/3 class			*0.26*

The breeding values are given according to the rolling base of each evaluation, set to 0 by convention, gathering Normande young bulls born during the last 7 years and having performances for the 3 traits. The unity for these breeding values are the genetic standard deviation for each elementary traits and the standard deviation of the reference population for the breeding values for the synthesis traits.

The breeding values are official when the bulls CD have reached 0.50 and when they have at least 25 young bulls considered for the evaluation.

1.6 - BREEDING VALUES FOR TYPE TRAITS

Since 1988, classifiers approved by the Breed Association have been using linear scoring for type traits.

1.6.1 - DATA

First (or second) parity daughters are scored in the same time as all other contemporaries (Breed Association members) or a computer selected sample of cows in the herd (commercial breeders; 5 scored cows generally).

1.6.2 - BLUP MULTITRAIT ANIMAL MODEL

The first scoring only is considered in genetic evaluations. For a given trait data are corrected for:

- Stage of lactation * parity (1 or 2) * status * year
- age at calving * parity * status * year
- Herd - round - classifier (same herd, same classifier, same day of scoring).

« Status » is related to the way of scoring elementary body traits (measured with a stick vs eye-evaluated).
A heterogeneous variance model assuming constant heritability is applied. The Log residual variance depends on age at calving and stage of lactation (fixed effects within parity and status) and classifier (random effect within year and status, without autocorrelation) In a second step the multitrait approach is applied to corrected data.

1.6.3 - BV AND RELIABILITY

For type traits, BV's are units of genetic standard deviation (Genetic standard deviation = 12 points). The average BV rolling basis (same definition as for dairy traits) is 100. As a consequence, most of BV's are between 76 and 124. The reliability for type depends on the accuracy of ancestry evaluation and the number of test daughters and grand daughters with 0.25 heritability. Proofs are considered as official if the reliability for type is (70 % or above with at least 28 daughters).

1.6.4 - TRAITS

24 elementary traits, 3 general characteristics (Teats h2=0.39; Rump h2=0.34; Feet and Legs h2=0.09) and 4 composite indexes are evaluated.

BV for linear descriptive traits	H2		< 0	> 0	Composites
Milking speed	0.25	TR	Slow	Fast	Udder (MA)
Fore udder attachment	0.28	AA	Short	Long	
Rear udder	0.18	AR	Low	High	1.20 * (0.10 AA + 0.05 AR + 0.20 EQ + 0.05 OR + 0.15 EA + 0.20 LI + 0.25 PJ)
Udder depth	0.31	PJ	Deep	Shallow	
Udder balance	0.27	EQ	Low rear quarters	High rear quarters	
Udder cleft	0.33	LI	Absent	Deep	
Teat placement front	0.38	EA	Apart	Close	
Teat direction	0.35	OR	External	Internal	
Height at sacrum	0.66	HS	Short	Tall	Size (FT)
Chest width	0.26	LP	Narrow	Wide	1,195 * [0,10 HS + 0,30 LP + 0,30 PP + 0,30 IS]
Chest depth	0.55	PP	Shallow	Deep	
Rump length	0.44	LB	Short	Long	
Width at pins	0.47	IS	Narrow	Wide	
Rump angle	0.36	IB	High pins	Sloped	
Rear legs set	0.20	AJ	Sickled	Straight	
Feet and Legs	0.20	AP	Bad	Good	
Joint quality	0.22	QA	Rough	Good	Feet and Legs (APc)
Foot's angle	0.14	PI	Open	Close	1.259 * [0.23 AJ + 0.16 QA + 0.11 PI + 0.30 PA + 0.20 LO]
Parallelism	0.15	PA	Splayfooted	Parallel	
Locomotion	0.11	LO	Difficult	Easy	
Fattening state	0.15	ET	Thin	Rounded	
					Muscularity (Mu) 1,164 * [0,25 withers + 0,25 loin + 0,50 thighs]
			Type (MO)		1,65 * [0,45 MA + 0,15 FT + 0.15 MU + 0.25 AP]

1.7 - BREEDING VALUES FOR TOTAL MERIT (I.S.U.)

Studies dealing with INEL have also produced economic values for SCC, clinical mastisis, daughter fertility, interval between calving and first AI and functional longevity relative to milk production (INEL). A direct economic value was put on overall type (MO) by the Breed Association in order to get satisfactory responses to selection for the main type traits. The selection criterion ISU (on a rolling basis, average =100, standard deviation=20 points) gathers traits expressed in genetic standard deviation units. Notice that the three functional traits are combined traits, simultaneously evaluated by an approximate multitrait BLUP animal model (see § 2-2-b).

For meat production, the Breed Association has defined a carcass synthesis given below:

Carcass synthesis (SYBO) = 1.973 * [0.1125 ICRCjbf + 0.275 CONFjbf + 0.1125 ICRCvbf + 0.10 CONFvbf + 0.025 COULvbf + 0.225 MU + 0.15 FT]

At least, breeding value for ISU is defined:

ISU = 73 * [0.0225 ICRCjbf + 0.055 CONFjbf + 0.0225 ICRCvbf + 0.02 CONFvbf + 0.005 COULvbf + 0.045 MU + 0.03 FT + 0.0725 MA + 0.065 APc + 0.00444 MG + 0.007 MP + 0.095 CELc + 0.06 LGFc + 0.07 FERc + 0.04 FERGc + 0.065 MACLc + 0.025 IVIA1c + 0.0475 TR] + 100

1.8 - RESULTS

BVs are published if the bull has at least 40 daughters in 30 herds and its CD has reached the value of 70.

2. - GENOMIC SELECTION

2.1 – DEVELOPMENT OF GENOMIC EVALUATIONS

The French program of Marker assisted Selection (MAS) was set up in 2001 for the Montbéliarde, Normande and Holstein breeds in order to optimize the choice of young bulls without performance in the early steps of selection. It paved the way to a first genomic evaluation in fall 2008, followed by official genomic evaluations in June 2009, according to a model which was substantially updated in 2010 and 2015. The reference populations, initially consisting of French genotyped and progeny-tested bull of the Holstein, Montbéliarde and Normande breeds, were later increased including foreign progeny tested bulls in the Holstein (in 2010) and Brune (in 2014) breeds, through the Eurogenomics (Holstein) and Intergenomics (Brune) international consortia.

Since 2015, for the Montbéliarde and Normande breeds for which the number of progeny-tested bulls does not grow very quickly, the reference populations also include genotyped females with performances, for traits sufficiently heritable (milk production, type traits, somatic cell score).

The genomic evaluation is currently relying on prediction equations based on 43 080 Holstein bulls, 7 748 Brown Swiss bulls, 3 874 Montbéliarde bulls and 184 993 Montbéliarde cows, 3 104 Normande bulls and 69 209 Normande cows.

The phenotypes used are:

- For French bulls and traits described by linear models: DYD (« daughter yield deviations »), equal to the weighted average of yield deviations (YD = performances corrected for all non genetic effects in conventional evaluations) also corrected for the breeding value of their dams. In the particular case of the Montbéliarde and Normande breeds, this average does not include the YD of genotyped daughters;
- Since 2015, YD of genotyped cows;
- For foreign bulls or French bulls when traits are not described by a linear model (functional longevity, calving ease, ...): deregressed proofs, considered as equivalent to DYD fo foreign bulls or for French bulls when traits are not described by linear models (e.g., functional longevity or calving ease)

The genomic evaluation model developed in 2015 considers genomic information from the 54k chip or imputed from the low density (EuroG10k) chip: the 54k genotype of all animals is imputed using the FImpute software which currently appears to be the most precise and the fastest imputation tool.

Performances are decomposed into:

- a contribution of individual QTL (Quantitative Trait Loci) with moderate to large effects, detected using a Bayesian approach (Bayes Cpi).. For most traits, 3000 QTL are retained, instead of a maximum 700 with the previous model. The transmission of these QTL is traced through of 4-SNP (Single Nucleotide Polymorphism) haplotypes. The construction of these haplotypes has been optimized. These QTL explain 70 to 80% of the total genetic variance, against 45-50% or 55-60% previously for national and international breeds respectively;

- a contribution of many undetected QTL with tiny individual effects. Only the sum of their effect is considered, which is equivalent to consider a residual polygenic effect with an associated genomic relationship rather than the pedigree relationship matrix previously used. This sum of effects explains 20 to 30% of the total genetic variance. The genomic relationship matrix is constructed using the SNP of the EuroG10K chip, which are available for all animals, without any imputation step;

- an unexplained residual effect.

This model keeps the particularity of precisely tracing large QTL with a relatively large associated fraction of the total genetic variance. These QTL are breed and trait specific. But the model also resembles a standard GBLUP model with trait-independent SNP distributed all over the genome to estimate a residual « polygenic » effect. Hence the genomic breeding value of a particular animal can be written as:

$$\mathbf{G}_i = \sum_{j=1}^{J}\left(H_{ij1} + H_{ij2}\right) + \sum_{k=1}^{K}\left(SNP_{ik1} + SNP_{ik2}\right)$$

where $\mathbf{G}_i$ is the genomic breeding value of animal i, $\mathbf{H}_{ij1}$ is the paternal allele effect of the haplotype tracing QTL j, $\mathbf{H}_{ij2}$ is the maternal allele effect of the haplotype tracing QTL j, $\mathbf{SNP}_{ik1}$ is the effect of the paternal allele of SNP k, SNP_{ik2} is the maternal effect of SNP k. The effects of all QTL and alleles carried by animal i are summed up to generate $\mathbf{G}_i$

2.2 - GENOMIC EVALUATIONS OF BULLS AND COWS

The genomic breeding values are fully comparable to polygenic breeding values: they are expressed in the same unit and with respect to the same genetic base. When they exist, they replace the polygenic effects as the official ones.

Breeding companies involved in the implementation of the initial reference populations list the bulls they want to market on the basis of their genomic breeding values. Publication of genomic indexes is allowed when their quality of their genotype is considered acceptable and when their reliability (CD) is 0.50 or higher. This threshold is lowered to 0.35 for low heritability functional traits of regional breeds (Brune and Pie Rouge).

Bulls with authorized publication in Eurogenomics (Holstein) and Intergenomics (Brune) countries are also evaluated in France and follow the same publication rules as French bulls marketed on the basis of genomic breeding values
Other foreign bulls must have daughters with performances in at least 10 herds (in France or abroad) to have their genomic breeding values published in place of their MACE Interbull vales.

A joint evaluation of Holstein and Pie Rouge (Red) breeds is planned in the near future. Meanwhile, genomic breeding values of Pie Rouge animals come from the Holstein evaluation converted to the Pie Rouge scale using the Interbull conversion formula.

3. - FRENCH BREED SOCIETIES

ES: old code for the French Breed Societies in France
OS: code of the French Breed Societies with agreement following the European Zootechnical Regulation (UE 2016/1012)

Society	Bulls code	Name	Adress	Contact details
OS		Organisme de sélection en Race Normande	Zone d'Activités Le Gué Thibout 61 700 DOMFRONT EN POIRAIE FRANCE	Phone : 02.33.66.66.56 @ : contact@osnormande.fr web : www.lanormande.com
ES	C013	CIA CRESPELLE	Domaine de la Crespelle 35133 LA CHAPELLE JANSON FRANCE	Phone : 02 99 95 22 61 @ : contact@cia-crespelle.com web : www.cia-crespelle.com
ES	S916 S917 S918 S950	EVOLUTION X-Y	Rue Eric Tabarly CS 10040 35 530 NOYAL SUR VILAINE CEDEX FRANCE	Phone : 02.99.87.90.90 @ : contact@evolution-xy.fr web : www.evolution-xy.fr
ES	S956 S959 S112	ORIGEN NORMANDE	Domaine de Glatigny 50 rue Joseph Guillonneau – 14100 LISIEUX FRANCE	Phone : 06 85 20 49 56 @ : m.chambrial@origenplus.com web : www.origen-normande.com

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