

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

Country (or countries)	France
Main trait group¹	Production
NOTE! Only one trait group per form!	
Breed(s)	[I] Prim' Holstein and Pie Rouge (HOL), Montbéliarde (SIM FRM), Normande (NMD) [II] Simmental Française (SIM FRA), Brune (BSW), Abondance, Tarentaise, Bleue du Nord, Rouge des prés (ex Maine Anjou), Flamande, Bretonne Pie Noire, Salers Each breed evaluated separately
Trait definition(s) and unit(s) of measurement² Attach an appendix if needed	Milk, fat and true protein Yields (kg), fat and true protein ‰
Method of measuring and collecting data	Data from Milk Recording.(91% A4, 9% AT). Validations according to National Technical Rules of Milk recording (updated in 2002)
Time period for data inclusion	All lactations started after September 1 st 1980, no limit for pedigree information
Age groups (e.g. parities) included	Parities 1 to 3, with weights for completed lactations : 1, 0.8, and 0.8, respectively
Other criteria (data edits) for inclusion of records	Lactations from HOL cows without pedigree excluded. First lactation required, Lactation in progress (=less than 305 days in milk) with at least 60 days in milk Extension of records: <ul style="list-style-type: none"> First lactation : lactation in progress: extended if DIM > 60; terminated lactations: no extension, but adjusted for DIM Later lactations : lactations in progress and terminated lactations: extended if DIM > 60
Criteria for extension of records (if applicable)	
Sire categories	All bulls (a total of 160000 bulls, of which 12000 are AI bulls, 7000 ET produced + 1000 imported bulls)
Environmental effects³, pre-adjustments	Multiplicative pre-adjustment for parity (1.3 ; 1.17 ; 1.105 for parities 1 to 3 respectively) Multiplicative Pre-adjustment for lactation length, if the lactation is not extended with the factor : 385/(80+DIM) HOL: Pre-adjustment for Holstein * Friesian heterosis and recombination loss (see Boichard et al, 1993)
Method (model) of genetic evaluation³	ST – RP – BLUP – AM

Environmental effects³ in the genetic evaluation model	<p>PE (R);Herd * Year (F); parity * region * year (F); Calving month * parity * region * year (1st vs 2nd and 3rd parities) (F); Age at calving * parity * region * year (F); Preceding dry period length * parity * region * year (for 2nd and 3rd parities)(F)</p> <p>Number of levels : Regions : HOL : 39. Normande : 7; Montbéliarde : 3</p> <p>Age, all breeds : 27; Calving month, all breeds : 12 ; Dry period, all breeds : 6</p>
Adjustment for heterogeneous variance in evaluation model	Performances adjusted for within HY residual variance, assuming known constant ratios (heritability, repeatability). The linear model for the log residual HY variance includes a region-year fixed effect and a HY random effect with a within herd autocorrelation.
Use of genetic groups and relationships	Groups of unknown parents defined according to birth year (2 years interval) and region or country origin of the progeny (a total of 8 countries and 260 groups in HOL)
Blending of foreign/Interbull information in evaluation	
Genetic parameters in the evaluation	<p>$h^2 = 0.30$ for Yields, 0.50 for contents</p> <p>$t = 0.50$ for Yields, 0.70 for contents</p>
System validation	Checks on Data quality; Planned connection between regions (= young bulls with 1 st crop daughters in several regions) during progeny test. EBV correlations; analysis of proofs variation according to number of daughters and status of bull (Progeny tested or not, 1 st or 2 nd crop) and % of completed lactations. Validation of genetic trend (Interbull Methods I, II & III). Analysis of residuals within classes (ex: within department, region, 1 st or 2 nd crop)
Expression of genetic evaluations If standardised (e.g. RBV), give standardisation formula in the appendix	EBV ; Fixed base for variability : EBVs are published according to the breed average residual standard deviation in 1996 (1995 for HOL)
Definition of genetic reference base	Yearly rolling base, updated in February: average cows EBV born from (n-8) to (n-6) years.
Next base change	March 2017 (These bases are updated each year in the 1 st evaluation of the year).
Calculation of reliability	Reliability computed with Harris and Johnson method (1998)
Criteria for official publication of evaluations	<p>HOL : $REL \geq 0.50$ in at least 10 herds</p> <p>Montbéliarde and Normande : $REL \geq 0.70$, at least 40 daughters in 30 herds</p> <p>Brune, Abondance, Tarentaise, Simmental Française: $REL \geq 0.60$, at least 20 daughters</p> <p>Salers, Bretonne Pie noire, Bleue du Nord, Flamande Rouge des prés: $REL \geq 0.50$ and at least 10 daughters</p>
Number of evaluations / publications per year	3: February, June, October

Use in total merit index⁴

1. INEL = Index Economique Laitier (one for all the breeds)

$INEL = 0.98 * (Prot\ Y + 0.2 * Fat\ Y + 1 * Prot\ content + 0.5 * Fat\ content)$

($\sigma_g = 20$)

Weights expressed in σ_g : 71% Protein Yield, 19% Fat Yield, 5% Fat Content, 5% Protein content

2. ISU = Index de Synthèse UPRA = Total Merit Index

- Prim'Holstein (HOL): $ISU = 19.62 / 0.35 (0.35\ SYNT / 25.2 + 0.108\ SCC + 0.072\ MACL + 0.11\ cow\ fertility + 0.055\ heifer\ fertility + 0.055\ Interval\ from\ calving\ to\ first\ service + 0.05\ longevity + 0.05\ Milking\ speed + 0.15\ Overall\ conformation) + 100$

With $SYNT = 1.079 (Protein\ Y + 0.1\ Fat\ Y + 0.5\ Fat\ content + Protein\ Content)$

(35% Production, 15% Conformation, 22% Female Fertility, 18% Udder Health, 5% Longevity, 5% Milking Speed)

- Normande: $ISU = 22.11 / 0.40 (0.40\ SYNT / 22.45 + 0.0925\ SCC + 0.0925\ MACL + 0.0775\ cow\ fertility + 0.03875\ heifer\ fertility + 0.03875\ Interval\ from\ calving\ to\ first\ service + 0.05\ longevity + 0.03\ Milking\ speed + 0.18\ Overall\ conformation) + 100$

With $SYNT = 1.098 (Protein\ Y + 0.1\ Fat\ Y)$

(40% Production, 18% Conformation, 15.5% Female Fertility, 18.5% Udder Health, 5% Longevity, 3% Milking Speed)

- Montbéliarde (SIM FRM): $ISU = 23.39 / 0.45 (0.45\ SYNT / 25.2 + 0.087\ SCC + 0.058\ MACL + 0.09\ cow\ fertility + 0.045\ Heifer\ fertility + 0.045\ Interval\ from\ calving\ to\ first\ service + 0.05\ heifer\ fertility + 0.05\ [TR/Teat-100]/12 + 0.125\ [Overall\ conformation-100]/12) + 100$

With $SYNT = 1.055\ Protein\ Y + 0.1\ Fat\ Y + 3\ Protein\ Content + 0.5\ Fat\ content$

(45% Production, 12.5% Conformation, 18% Female Fertility, 14.5% Udder Health, 5% Longevity, 5% Milking Speed)

- Brune (BSW): $ISU = 100 + 18.11 * (INEL / 20 + 0.50\ cmb\ SCC + 0.50\ cmb\ Fertility + 0.125\ cmb\ longevity + 0.325\ overall\ type)$

(40% Production, 20% SCC, 20% Female Fertility, 15% Conformation, 5% Longevity)

- Pie Rouge : $ISU = 100 + 18.09 [SYNT / 20 + 0.20\ SCC + 0.25\ Cow\ Fertility + 0.20\ LGFC + 0.25\ (Overall\ Conformation - 100) / 12]$

with $SYNT = 0.99 [Prot\ Y + 0.2 * Fat\ Y + 2 * Prot\ content + Fat\ content]$

For more details: see Ducrocq et al, 2001

Anticipated changes in the near future

Key reference on methodology applied

Bonaïti B., Boichard D., Verrier E., Ducrocq V., Barbat A., Briend M., 1990. La méthode française d'évaluation génétique des reproducteurs laitiers. INRA Prod. Anim. 3, 83-92
Boichard D., Bonaïti B., Barbat A., 1993. Effect of Holstein crossbreeding in the French black and white cattle population. J Dairy Sci., 76, 1157-1162.
Boichard D et al, 1995. Three methods to validate the estimation of genetic trend in dairy cattle. J Dairy Sci., 78, 431-437
Robert-Granié C., Bonaïti B., Boichard D., Barbat A., 1999: Accounting for variance heterogeneity in French dairy cattle genetic evaluation. Livest. Prod. Sci., 62, 343-357
Harris, B. & Johnson, D. 1998. Approximate reliabilities of genetic evaluations under an animal model. J Dairy Sci., 81, 2723-2728

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- 1) Either: Production (e.g. milk, fat, protein), Conformation, Health (e.g. mastitis resistance, milk somatic cell, resistance to diseases other than mastitis), Longevity, Calving (e.g. stillbirth, calving ease), Female fertility (e.g. non-return rate, interval between reproductive events, number of AI's, heat strength), Workability (e.g. milking speed, temperament), Beef production, Efficiency (e.g. body weight, energy balance, body conditioning score), or Other traits.
- 2) Indicate frequencies per category if the trait is categorical and specify transformation of data if practiced.
- 3) Use abbreviations for most common effects (see document with list of abbreviations at http://www-interbull.slu.se/service_documentation/General/list_of_abbreviations.rtf) and indicate random (R) or fixed (F).
- 4) Please give economic weights and indicate how they are expressed (preferably in genetic standard deviation units).

Parameters used in genetic evaluation

Country (or countries): France
Main trait group: Production
Breed (repeat as necessary): HOL, BSW, SIM FRAM, SIM FRA, NMD

Trait	Definition	ITB ^a	h ^{2b}	genetic variance ^b	official proof standardisation formula ^c
Milk Yield, HOL	3 first parities, HOL		0.30	575440.69	758.58
Fat Yield, HOL	3 first parities, HOL		0.30	973.81	31.21
Protein Yield, HOL	3 first parities, HOL		0.30	518.29	22.77
Fat content, HOL	3 first parities, HOL		0.50	8.84	2.97
Protein content, HOL	3 first parities, HOL		0.50	2.18	1.48
Milk Yield, NMD	3 first parities, NMD		0.30	349748.78	591.40
Fat Yield, NMD	3 first parities, NMD		0.30	744.60	27.29
Protein Yield, NMD	3 first parities, NMD		0.30	389.38	19.73
Fat content, NMD	3 first parities, NMD		0.50	7.48	2.73
Protein content, NMD	3 first parities, NMD		0.50	2.21	1.49
Milk Yield, SIM FRM	3 first parities, SIM FRM		0.30	436736.89	660.86
Fat Yield, SIM FRM	3 first parities, SIM FRM		0.30	733.04	27.07
Protein Yield, SIM FRM	3 first parities, SIM FRM		0.30	457.71	21.39
Fat content, SIM FRM	3 first parities, SIM FRM		0.50	5.88	2.43
Protein content, SIM FRM	3 first parities, SIM FRM		0.50	1.92	1.39
Milk Yield, SIM FRA	3 first parities, SIM FRA		0.30	415220.68	644.38
Fat Yield, SIM FRA	3 first parities, SIM FRA		0.30	744.87	27.29
Protein Yield, SIM FRA	3 first parities, SIM FRA		0.30	442.25	21.03
Fat content, SIM FRA	3 first parities, SIM FRA		0.50	8.47	2.91
Protein content, SIM FRA	3 first parities, SIM FRA		0.50	1.91	1.38
Milk Yield, BSW	3 first parities, BSW		0.30	503066.85	709.27
Fat Yield, BSW	3 first parities, BSW		0.30	917.35	30.29
Protein Yield, BSW	3 first parities, BSW		0.30	550.93	23.47
Fat content, BSW	3 first parities, BSW		0.50	7.65	2.77
Protein content, BSW	3 first parities, BSW		0.50	2.26	1.50

^a Indicate, with X, traits that are submitted to Interbull for international genetic evaluations.

^b If repeated records are treated as separate traits, provide heritability estimates and genetic variances separately for each trait, as well as for all traits pooled, i.e. for the trait submitted to Interbull.

^c Expressed as follows:

StandEval=((eval-a)/b)*c+d where a=mean of the base adjustment, b=standard deviation of the base, c=standard deviation of expression (include sign if scale is reversed), and d=base of expression.