

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEM

June 2012

Country (or countries)	France
Main trait group¹	Longevity
Breed(s)	[I] HOL, Montbéliarde, Normande [II] Simmental Française (SIM), BSW, Pie Rouge des Plaines (RED), Abondance, Tarentaise Each breed evaluated separately
Trait definition(s) and unit(s) of measurement² Attach an appendix if needed	Productive life and Combined Longevity: Two different Proofs: <ul style="list-style-type: none"> ▪ The Functional Longevity (LGF) is computed in a first step but is not published, except for some very old bulls. ▪ The Combined Functional Longevity (LGFc): estimated in a second step Unit of measurement: Length of Productive life (LPL) of cow. LPL is measured at time t_0 , 4 months before the beginning of the evaluation run.
Method of measuring and collecting data	Length of productive life, calculated with the data from the milk recording system = number of days between first calving and last known test date.
Time period for data inclusion	All Parities from the official milk recording scheme with calving after January 1 st , 1988
Age groups (e.g. parities) included	Parities 1 to 5. Cows are considered as censored when they reached their 6 th calving.
Other criteria (data edits) for inclusion of records	Cows born from a AI bull and with official pedigree registration. Cows raised in herds having at least 5 cows from the same breed. First parities excluded if first calving occurred less than 120 days before evaluation time If herd size decreases by >50%: records are censored
Sire categories	AI sires
Environmental effects³, pre-adjustments	None
Method (model) of genetic evaluation³	Direct longevity : ST S-MGS survival analysis model, applying a proportional hazard model with a stratified, piecewise Weibull, baseline hazard distribution. For the Holstein, Normande and Montbéliarde breeds, the stratification is within year and lactation number (1 to 5). In other words, the baseline $\lambda_0(t i, j)$ after t days of LPL for a cow in year i and lactation number j with her j th calving at time τ_j is $\lambda_0(t i, j) = \text{Weibull}_k(t - \tau_j)$ where k depends on i, j and a stage of lactation with 4 classes ($(t - \tau_j)$ between 0 and 270, between 270 and 380, above 380, dry period). For the minor breeds, the stratification is just within stage of lactation and lactation number (with 2 levels: lactation 1, and 2 and more) . Combined longevity computed using an approximate MT BLUP AM based on precorrected records for Fonctionnal (SCC, Fertility, Longevity), dairy (Milk Yield and Protein content), Milking Speed and 5 type traits. LGF _c is published and used in the total merit index.
Environmental effects³ in the genetic evaluation model	<i>Herd-Year</i> (Random, log gamma) time-dependent <i>Class of variation in herd size within herd size group</i> (F): time-dependent effect, classes are defined as follows: <ul style="list-style-type: none"> • Herd size ≤ 5: 1 class • $5 < \text{Herd size} \leq 20$: 3 classes (variation of $< -10\%$; -10 to $+10\%$; $> +10\%$) • Herd size > 20: 5 classes (variation of $< -15\%$; -15 to -5%; -5 to $+5\%$; $+5$ to $+15\%$ and $> +15\%$) <i>Age at first calving</i> (Fixed): Time independent classes of 1 month (with one class for age < 20 months and one for age > 40 months). <i>Year-region</i> (Fixed): time dependent, with 8,7 and 3 regions for Holstein, Normande and Montbéliarde.

	<p><i>Production classes:</i> milk production (10 classes of 10% each); Protein content (5 classes of 20% each); Fat content (5 classes of 20% each)</p> <p>The production classes are defined by comparing the 305d production of the cow with the average production of the herd. First and later parities are considered separately. For milk production, two types of interactions are accounted for: interaction with <i>year-season</i> (4 calendar seasons) and interaction with <i>stage of lactation x lactation number</i> (with 2 levels: lactation 1, and 2 and more). For fat and protein content, the interaction considered is with <i>year</i>.</p> <p>For the minor breeds: there is no interaction between production classes and year(-season). Instead, a <i>year-season</i> (4 seasons) effect is included as well as a <i>lactation number effect</i> (to distinguish between parities 2, 3, 4 and 5, which are considered together in the baseline)</p>
Adjustment for heterogeneous variance in evaluation model	None
Use of genetic groups and relationships	Yes
Blending of foreign/Interbull information in evaluation	None
Genetic parameters in the evaluation	$\sigma^2_s = 0.0288$ (Normande); 0.0347 (Holstein); 0.0411 (Montbéliarde); 0.0444 (minor breeds) h^2 on original scale (see definition in Yazdi et al, 2002) = 8.9 % (Normande); 10.8% (Holstein); 13.0% (Montbéliarde), 14.0% (minor breeds) rg used for Combined longevity: see attached table
System validation	Method 2 adapted to the longevity case (see Ducrocq, 2004)
Expression of genetic evaluations If standardised (e.g. RBV), give standardisation formula on PART 2	RBV ($m=0$, $\sigma_s=1$, positive = better longevity) RBV = Sire effect on risk of culling / ($-\sigma_s$) – Rolling basis
Definition of genetic reference base	Male Rolling basis = AI bulls with a reliability on LGFc of at least 0.50 and : HOL, Montbéliarde, Normande : born between years N-10 and N-7, Other breeds : born between years N-12 and N-7
Next base change	June 2013 (These bases are updated each year in June).
Calculation of reliability	For direct Longevity: see Yazdi et al, 2002 Reliability of combined Longevity: MT BLUP AM REL using Harris and Johnson approach
Criteria for official publication of evaluations	Bulls born since 1986: combined longevity (LGFc) published if reliability ≥ 0.50 for LGFc; older bulls: direct longevity (LGF) published if reliability ≥ 0.50
Number of evaluations / publications per year	2 for LGF (June/October), 3 for LGFc (June / October / January).
Use in total merit index⁴(updated at February 2012)	<p>1. Use in ISU= Index de Synthèse UPRA = total merit index</p> <p>Defined by each breed:</p> <p>For ISU, Combined functional proofs are computed by an approximate MT BLUP AM based on precorrected records for Functional (SCC, Fertility, Longevity), dairy (Milk Yield and Protein content), Milking Speed and 5 type traits. (cmb= combined in the following formulae):</p> <ul style="list-style-type: none"> 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 <p>With SYNT = 1.079 (Protein Y + 0.1 Fat Y + 0.5 Fat content + Protein Content)</p> <p>(35% Production, 15% Conformation, 22% Female Fertility, 18% Udder</p>

Health, 5% Longevity, 5% Milking Speed)

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

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

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): $ISU = 100 + 18.11 * (INEL/20 + 0.50 \text{ cmb SCC} + 0.50 \text{ cmb Fertility} + 0.125 \text{ cmb longevity} + 0.325 \text{ overall type})$
(40% Production, 20% SCC, 20% Female Fertility, 15% Conformation, 5% Longevity)
- Pie Rouge (RED) : $ISU = 100 + 18.09 [SYNT/20 + 0.20 SCC + 0.25 \text{ Cow Fertility} + 0.20 LGFC + 0.25 (Overall Conformation - 100)/12]$
with SYNT = 0.99 [Prot Y + 0.2 * Fat Y + 2 * Prot content + Fat content]

For more details: see Ducrocq et al (b), 2001

Anticipated changes in the near future

Key reference on methodology applied

- V. Ducrocq, 1997: Survival Analysis, a statistical tool for longevity data – EAAP Meeting, August 25-28, Wien
- V. Ducrocq, 1999: Two years of experience with the French genetic evaluation of dairy bulls on production adjusted longevity of their daughters. Gift Workshop May 9-11, Jouy en Josas, France. *Interbull Bulletin 21*, 60-67
- V. Ducrocq, 2001 (a): A two step procedure to get animal model solutions in Weibull survival models used for genetic evaluations on length of productive life. Interbull meeting, August 30-31, Budapest, Hungary. *Interbull Bulletin 27*, 147-152
- Ducrocq V., Boichard D., Barbat A., and Larroque H, 2001 (b) : Multitrait evaluation and total merit Index. EAAP Meeting, Budapest, August 26-28, 2001
- Yazdi MH, Visscher PM, Ducrocq V., Thompson R., 2002 : Heritability, reliability of genetic evaluations and response to selection in proportional hazard models. *J. Dairy Sci.*, 85, 1563-1577
- Ducrocq V, 2004. Illustration of a trend validation test for longevity evaluations. *Interbull Meeting*, May 29-31. *Sousse, Tunisia*.

Key organization: name, address, phone, fax, e-mail, web site

Computing:
INRA
Génétique Animale et Biologie Intégrative (GABI)
Domaine de Vilvert
F78352 Jouy en Josas cedex
Mail: didier.boichard@dga.jouy.inra.fr
Phone : +33 1 34 6 5 22 04, Fax : +33 1 34 65 22 10
<http://www.jouy.inra.fr/gabi>

Publishing:
Institut de l'Élevage
149 Rue de Bercy
F75595 Paris cedex 12
Mail: sophie.mattalia@idele.fr
Web site : www.idele.fr

- 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 extension or 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/framesida-general.htm) and indicate random (R) or fixed (F).
- 4) Please give economic weights and indicate how they are expressed (preferably in genetic standard deviation units).

DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEM

Country (or countries)	France
Main trait group	Longevity
Breed (repeat as necessary)	HOL, Normande, Montbéliarde

Genetic correlations between Fonctionnal (SCC, Fertility, Longevity), dairy (Milk Yield and Protein content), Milking Speed and type traits used to compute combined Functional traits (updated June, 2012)
(Warning: in these tables: Longevity: positive = higher risk of culling; SCC positive = more SCC; RUH on the reverse scale)

Holstein

	Milk	SCC	Long	Fer heif	Fer cow	Milk Speed	Udder Depth	Fore Ud Att	Rump angle	Body depth	Ang	Loco
Milk	1	0,03	-0,17	-0,12	-0,22	+	-0,22	-0,13	0,09	0,16	0,33	0,12
SCC	0,03	1	0,5	-0,12	-0,25	0,37	-0,27	-0,07	-	0,13	0,18	-
Long	-0,17	0,5	1	-0,31	-0,47	-0,17	-0,41	-0,21	-0,1	0,2	0,02	-0,12
Fer heif	-0,12	-0,12	-0,31	1	0,6	0,09	-0,02	0,01	0,17	0,02	0,21	-0,05
Fer cow	-0,22	-0,25	-0,47	0,6	1	0,03	0,13	0,02	0,23	-0,3	-0,2	-0,1
Milk Speed	0,01	0,37	-0,17	0,09	0,03	1	0,28	0,23	+	+	0,17	+
Udder Depth	-0,22	-0,27	-0,41	-0,02	0,13	0,28	1	0,52	-0,05	-	-0,09	0,14
Fore Ud Att	-0,13	-0,07	-0,21	0,01	0,02	0,23	0,52	1	-0,12	0,09	-	0,14
Rump angle	0,09	-	-0,1	0,17	0,23	+	-0,05	-0,12	1	0,05	+	+
Body depth	0,16	0,13	0,2	0,02	-0,3	+	-0,04	0,09	0,05	1	0,7	0,05
Ang	0,33	0,18	0,02	0,21	-0,2	0,17	-0,09	-0,03	0	0,7	1	-0,06
Loco	0,12	-	-0,12	-0,05	-0,1	+	0,14	0,14	0,03	0,05	-0,06	1

Montbéliarde

	Milk	SCC	Long	Fer heif	Fer cow	Chest Depth	Fore Ud. Att	Udder Depth	Udder Bal	Teat Form	Milk Speed	Feet&Legs
Milk	1,00	-0,16	+	0,05	-0,22	0,07	0,12	-0,33	-0,09	0,07	-0,16	+
SCC	-0,16	1	0,40	0,20	0,32	-0,12	0,06	0,46	0,14	-0,25	-0,08	+
Long	0,05	0,40	1	0,32	0,43	-0,08	0,31	0,55	0,32	-0,24	0,42	0,26
Fer heif	0,05	0,20	0,32	1	0,68	-0,08	0,09	+	0,14	0,07	0,03	0,09
Fer cow	-0,22	0,32	0,43	0,68	1	-0,16	0,10	0,20	0,11	+	+	0,07
Chest Depth	0,07	-0,12	-0,08	-0,08	-0,16	1	-0,10	-0,08	0,09	0,09	+	-
Fore Ud. Att	0,12	0,06	0,31	0,09	0,10	-0,10	1	0,23	-0,44	0,17	0,31	0,08
Udder Depth	-0,33	0,46	0,55	0,01	0,20	-0,08	0,23	1	0,39	-0,21	0,31	0,15
Udder Bal	-0,09	0,14	0,32	0,14	0,11	0,09	0,44	0,39	1	-0,12	-0,24	-0,15
Teat Form	0,07	-0,25	-0,24	0,07	0,00	0,09	-0,17	-0,21	-0,12	1	-0,19	-0,09
Milk Speed	0,16	-0,08	0,42	0,03	0,00	0,01	0,31	0,31	0,24	-0,19	1	0,08
Feet&Legs	0,02	0,05	0,26	0,09	0,07	-0,04	0,08	0,15	0,15	-0,09	0,08	1

Normande

	Milk	SCC	Long	Fer heif	Fer cow	Stat	Feet&Legs	Fillet	Fore Ud Att.	Udder Bal	Udder Depth	Milk Speed
Milk	1	0,05	0,21	+	-0,28	0,15	-	-0,39	+	-0,12	-0,30	0,07
SCC	0,05	1	0,46	0,22	0,27	-0,10	+	0,10	0,11	0,18	0,21	0,32
Long	0,21	0,46	1	0,32	0,37	+	0,21	+	0,33	0,39	0,43	0,21
Fer heif	+	0,22	0,32	1	0,65	-0,20	-0,08	-0,14	0,07	-0,07	0,05	-
Fer cow	-0,28	0,27	0,37	0,65	1	-0,21	-0,06	0,15	+	-	0,23	-0,13
Stat	0,15	-0,10	+	-0,20	-0,21	1	+	0,05	-0,11	-0,08	0,29	0,10
Feet&Legs	-0,03	+	0,21	-0,08	-0,06	+	1	0,24	0,14	0,20	0,18	0,13
Fillet	-0,39	0,10	+	-0,14	0,15	0,05	0,24	1	0,06	0,15	0,16	-0,05
Fore Ud Att.	+	0,11	0,33	0,07	+	-0,11	0,14	0,06	1	0,59	0,29	0,26
Udder Bal	-0,12	0,18	0,39	-0,07	-0,01	-0,08	0,20	0,15	0,59	1	0,38	0,25
Udder Depth	-0,30	0,21	0,43	0,05	0,23	0,29	0,18	0,16	0,29	0,38	1	0,29
Milk Speed	0,07	-0,32	0,21	-	-0,13	0,10	0,13	-0,05	0,26	0,25	0,29	1

+/-: more or less than 0.05

Trait name	Breed	h^2	genetic variance	official proof standardisation formula ^a
Direct Longevity	HOL	0.108	0.00120409	a= 0 b=1 et c= 1 , d= rolling base (computed at each release)
	BSW	0.14	0.00197136	a= 0 b=1 et c= 1 , d= rolling base (computed at each release)
	MON	0.13	0.00168921	a= 0 b=1 et c= 1 , d= rolling base (computed at each release)

a 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.