**Form GE**

Status as of: 2019-04-16

**DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS**

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| **Country (or countries)** | France | |
| **Main trait group** | Longevity | |
| **Breed(s)** | Prim’ Holstein and Pie Rouge (HOL), Montbéliarde (SIM FRM), Normande, Simmental Française (SIM FRA), Brown Swiss (BSW), 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 evaluations:   * Functional Longevity (LGF) is computed first but is not published, except for some very old bulls. * Combined Functional Longevity (LGFc is computed in a second step combining direct longevity information and early predictors (SCC, Mastitis occurrence, fertility traits, some type traits)   Unit of measurement: Length of Productive life (LPL) of cow. LPL is  measured up to time t0= 4 months before the beginning of the evaluation run. |
| **Method of measuring and collecting data** | Length of productive life, calculated based on milk recording data = number of days between first calving and last known test date |
| **Time period for data inclusion** | All parities (up to 6th calving) from official milk recording with calving after January 1st, 1988 |
| **Age groups (e.g. parities) included** | Parities 1 to 5. Cows reaching their 6th calving are considered as censored on that day. |
| **Other criteria (data edits) for inclusion of records** | Cows born from an 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 a year before evaluation time. If herd size decreases by >50% on a particular year, records are censored |
| **Criteria for extension of records** (if applicable) | Not applicable |
| **Sire categories** | AI sires |
| **Environmental effects3, pre-adjustments** | No pre-adjustment |
| **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.  The baseline λ0(t | i,j) after t days of LPL for a cow in lactation number j (j=1 to 5) with her jth calving at time τj is λ0(t | i,j) = Weibull k (t-τj) where index k depends on lactation number j and on stage of lactation with 4 classes (where (t-τj) is between 0 and 270, between 270 and 380, above 380, dry period).    Combined longevity is computed using an approximate MT BLUP AM based on precorrected records for Functionnal (SCC, Fertility, Longevity), dairy (Milk Yield and Protein content), Milking Speed and 5 type traits. LGFc is published and used in the total merit index. |
| **Environmental effects3 in the genetic evaluation model** | * Herd-Year (Random, log gamma) time-dependent * Class of variation in herd size within herd size group (F): time-dependent effect, classes are defined as follows:   • Herd size ≤ 5: 1 class  • 5<Herd size≤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%)   * Age at first calving (Fixed): Time independent classes of 1 month (with one class for age <20 months and one for age>40 months). * Year-region (Fixed): time dependent, with 8, 7, 3 and 2 regions for Holstein, Normande, Montbéliarde and 1 for the other breeds. * Production classes (Fixed): milk production (10 classes of 10% each); Protein content (5 classes of 20% each) ;   Fat content (5 classes of 20% each)  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. The effect of milk production class is defined in interaction with year of calving-season (4 calendar seasons) for Holstein, Montbéliarde and Normande. For theses breeds, classes of fat and protein contents, the interaction is with year of calving only. For the other breeds, because of their limited size, the only interaction is between milk production class and year of calving (no interaction for classes of fat and protein content)  A second interaction for milk production class is also computed with lactation number (with 2 levels: lactation 1, and 2 and more).   * Year of birth of the dam of the cow (estimated if unknown) (Fixed)   For the minor breeds: there is no interaction between production classes and year (-season). Instead, a year-season (4 seasons) effect is included as well as a lactation number effect (to distinguish between parities 2, 3 , 4 and 5, which are considered together in the baseline) |
| **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** | (Sire) Genetic variance: Holstein: 0.040; Montbéliarde: 0.047; Normande: 0.040; Abondance: 0.049 ; BSW :0.040 ; Tarentaise : 0.040 ; French Simmental : 0.040 |
| **System validation** | Method 3 |
| **Expression of genetic evaluations** If standardised (e.g. RBV), give standardisation formula in the appendix | RBV (m= 0, σs=1, positive = better longevity)  RBV = Sire effect on risk of culling / (-genetic standard deviation)  – Rolling basis |
| **Definition of genetic reference base**  **Next base change** | 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  February 2014 (These bases are updated each year in February). |
| **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** | 3 for LGF and LGFc |
| **Use in total merit index4** | 1. Use in ISU= Index de Synthèse UPRA = total merit index  Defined by each breed:  For ISU, Combined functionnal proofs are computed by an approximate MT BLUP AM based on precorrected records for Functionnal (SCC, Fertility, Longevity), dairy (Milk Yield and Protein content), Milking Speed and 5 type traits. (cmb= combined in the following formulae):  • 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% UdderHealth, 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 Overal 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 Longevity + 0.05  [Milking speed-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 + 21.81 / 0.40\* [0.40 INEL/25.2 + 0.12 SCC + 0.08 MACL + 0.10 Cow fertility + 0.05 Heifer fertility+ 0.05 Interval from calving to first service + 0.05 Longevity + 0.15 Overall conformation]  (40% Production, 20% UdderHealth, 20% Female Fertility, 15% Conformation, 5% Longevity)  • Pie Rouge : ISU = 100 + 19.06 / 0.35\* [0.35 SYNT/25.2 + 0.108 SCC + 0.072 MACL + 0.13 Cow fertility + 0.065 Heifer fertility + 0.065 Interval from calving to first service + 0.05 Longevity + 0.03 (Milking speed -100/12)+ 0.13 (Overall conformation-100/12)]  with SYNT = 1.003 [Prot Y + 0.1 Fat Y + 3 Prot content + Fat content]  • Simmental française (SIM FRA) : ISU = 100 + 23.32 / 0.45\* [0.45 SYNT/25.2 + 0.087 SCC + 0.058 MACL + 0.0725 Cow fertility + 0.03625 Heifer fertility + 0.03625 Interval from calving to first service + 0.05 Longevity + 0.03 (Milking speed -100/12) + 0.18 (Overall conformation -100/12)]  Avec SYNT = 1.055 [Prot Y + 0.1 Fat Y + 2 Prot content+ 0.5 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., Sölkner, J., Mészáros, G. (2010): Survival Kit v6 - A software package for survival analysis. In: 9th World Congress on Genetics to Livestock Production, August 1-6, 2010, Leipzig, Germany.  Ducrocq, V., Sölkner, J., Mészáros, G. The Survival Kit. available at http://www.nas.boku.ac.at/nuwi/the-survival-kit/ |
| **Key organisation: name, address, phone, fax, e-mail, web site** | Computing:  GenEval Evaluation génétique des animaux d’élevage  3 rue du Petit Robinson F78350 Jouy-en-Josas  Mail: [contact.international@geneval.fr](mailto:contact.international@geneval.fr)  Phone : +33 (0) 1 85 36 05 05 Web site : <https://www.geneval.fr/>  Publishing:  Institut de l’Elevage  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 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).

**Form GE Appendix LO**

**Parameters for national genetic evaluations for longevity traits as provided to Interbull**

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| **Country (or countries):** |  |
| **Main trait group:** | Longevity |
| **Breed(s):** | HOL, SIM FRM, BSW |

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| Trait | Breed | h2 | Sire genetic  variance | official proof  standardisation formulaa |
| Direct longevity: | HOL | 0.154 | 0.040 | a=0  b=1, c=1 and d=rolling base (computed at each release) |
|  | SIM FRM | 0.179 | 0.047 | a=0  b=1, c=1 and d=rolling base (computed at each release) |
|  | BSW | 0.154 | 0.040 | a=0  b=1, c=1 and 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.