Status as of: 2019-04-16

**Form GENO**

**DESCRIPTION OF NATIONAL GENOMIC EVALUATION SYSTEMS**

|  |  |
| --- | --- |
| Country (or countries)  | France |
| Main trait groupa. NOTE. Only one trait group per form!  | Longevity |
| Breed(s)  | [I] Holstein, Montbéliarde, Normande and Brown SwissEach breed evaluated separately |
| Trait definition(s) and unit(s) of measurementAttach an appendix if needed  | Productive life = Functional Longevity (LGF)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. |
| Source of genotypes (chips used)  | Genotypes from Illumina50K SNP Chip or from lower density imputed on the 50K chip |
| Imputation method for missing genotypes  | Based on Fimpute (Szargolzei et al, 2014) |
| Propagation of genomic information to non-genotyped descendants and ancestors  | None |
| Animals included in reference population (males, females, countries included, total number)  | Holstein : 30700 bulls from the Eurogenomics consortiumMontbéliarde : 2650 bulls (France)Normande : 2330 bulls (France)Brown Swiss - 6015 bulls from the Intergenomics consortium |
| Source of phenotypic data (DYD, de-regressed proofs, national EBVs and/or MACE evaluations)  | For bulls: DYD of sires obtained from conventional national genetic evaluation (or de-regressed MACE EBVs if DYD are not available(e.g., for foreign bulls)) of sires obtained from conventional national genetic evaluation |
| Other criteria (data edits) for inclusion of records  | Based on genotypes, individuals that are incompatible with their declared parents are removed |
| Criteria for extension of records (if applicable)  |  |
| Sire categories  | All genotyped bulls + genotyped females in Montbéliarde and Normande |
| Genomic model (linear, Bayesian, polygenic effect, genotypes or haplotypes)  | Single trait Mixed Linear model including a regression on identical-by-statehaplotypes associated with up to 3000 QTL and a residual polygenic effect Applied after a QTL detection with Bayes Cpi |
| Blending of direct genomic value (DGV) with traditional EBV  | For Holstein and Brown Swiss genotyped females only |
| Environmental effects in the genetic evaluation model  | Overall mean (possibly different when both DYD and de-regressed EBV are used) |
| Adjustment for heterogeneous variance in evaluation model  | Using corresponding EDC |
| Computation of genomic reliability  | Approximated from the BLUP coefficient matrix |
| Blending of foreign/Interbull information in evaluation  | Use of de-regressed Interbull EBVI when DYD are not available |
| Genetic parameters in the evaluation  | Same global heritability as the conventional genetic evaluation On average 20% of genetic variance attributed to the residual polygenic effect, the rest equally distributed across haplotypes |
| Expression of genetic evaluationsIf standardized (e.g. RBV), give standardization formula in the appendix  | See GE Form conventional genetic evaluation |
| Definition of genetic reference base  | See GE Form conventional genetic evaluation |
| Labeling of genomic evaluations  |  |
| Criteria for official publication of evaluations  | Only for bulls officially declared as “bulls known from GEBV information”, genotype reliable, the parents and four grand-parents are known andReliability of GEBV >= 0.50 |
| Number of evaluations / publications per year  | 6 genomic evaluations among which 3 are official (April, August, December) |
| Use in total merit index  | INEL and ISU (see GE Form for conventional genetic evaluation) |
| Anticipated changes in the near future  | Extension to regional dairy breeds |
| Key reference on methodology applied  | Sargolzei, M., J. P. Chesnais, and F. S. Schenkel. 2014. A new approach for efficient genotype imputation using information from relatives. BMC Genomics, [15:478](http://www.biomedcentral.com/1471-2164/15/478) Idele, La nouvelle méthode française d’évaluation génomique IBL n° 2015-5, Référence n°0015202010(<http://idele.fr/no_cache/recherche/publication/idelesolr/recommends/ibl2015-5-la-nouvelle-methode-francaise-devaluation-genomique.html>)Croiseau P. et al. , 2015. Comparison of different Marker-Assisted BLUP models for a new French genomic evaluation. EAAP meeting. Warsaw, Poland. |
| Key organization: name, address, phone, fax, e-mail, web site  | Computing: GenEvalEvaluation génétique des animaux d’élevage3 rue du Petit RobinsonF78350 Jouy-en-Josas Mail: contact.international@geneval.frPhone : +33 (0) 1 85 36 05 05Web site : <https://www.geneval.fr/>Publishing:Institut de l’Elevage149 Rue de BercyF75595 Paris cedex 12Mail: sophie.mattalia@idele.frWeb site : [www.idele.fr](http://www.idele.fr) |

aEither: 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.

## System Validation

|  |  |
| --- | --- |
| Approximate number of test bulls for this trait group: | Holstein: 870 |
| If including foreign reference bulls:4-yr old de-regressed MACE EBVs, ORCurrent de-regressed MACE EBVsIf including foreign test bulls (type of proof 21 or 22), provide the reason. |  |
| If using a truncation ≠ 4 years, provide the reason. |  - |
| If applying an age cutoff for test bulls ≠ (YYYY-8), provide the reason | - |

# Appendix GENO

## Parameters used in genetic/genomic evaluation

## *Same as conventional evaluations: see GE Form*

|  |  |
| --- | --- |
| Country (or countries):  |  |
| Main trait group:  |  |
| Breed (repeat as necessary):  |  |
| Trait  | Definition  | ITBa  | h2b  | Genetic varianceb  | Official proof standardisation formulac  |
|  |  |  |  |  |  |
|  |  |  |  |  |  |

aIndicate, with X, traits that are submitted to Interbull for international genetic evaluations.

bIf 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.

cExpressed 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.