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!  | Female Fertility |
| Breed(s)  | [I] Holstein, Montbéliarde, Normande and Brown SwissEach breed evaluated separately |
| Trait definition(s) and unit(s) of measurementAttach an appendix if needed  | Conception rate for maiden heifers (=HCO for all breeds) and lactating cows (=CC1 for all breeds and CC2 for BSW and RED). For both traits, results of each insemination (1= success/0=failure) of AI made in milk recorded herds. Results are defined using the following rules :1. when there was a subsequent calving, the successful insemination is defined as the closest service to the theoretical conception date. The theoretical gestation length was 282 days. Moreover, the interval from successful service to calving is restricted to the standard gestation length +/- 15 days. Subsequent inseminations within the same parity are discarded, whereas preceding inseminations are considered as failed. A insemination, which occurred within a 3-day period before the successful insemination, is discarded.
2. the last insemination was considered as successful if abortion or early calving may be assumed, ie when a calving was recorded between 45 and 267 days after the last insemination.
3. the last insemination, if recorded in the last 340 days, was given a probability of gestation (between 0 and 1, instead of 0 or 1) according to statut ( heifer or lactating cows), rank of insemination (1, 2, 3 and more), time elapsed since the insemination (1 to 340 days).
4. when there was no subsequent calving, all inseminations but the last are considered as failed. The last insemination is considered as successful, except when days in milk in current lactation are more than 260 days and the insemination was older than 340 days, ie when the cow was likely to have been culled for non pregnancy.
5. when several inseminations occurred within a 4-day period, only the first one is considered.

Interval between calving and first AI (=IVIA1=CRC for all breeds) reflect the genetic ability to initiate postpartum cycling even if, associated with AI, it depends partly on breeder decision. This interval is evaluated in day. A positive value corresponds to a short interval after calving.Interval between first and last AI (=IFL=CC2 for HOL breed only) : 1. when the last AI was considered as successful, the interval is calculated as day of last AI – day of first AI.
2. when the last AI was considered as failure, the interval is calculated as day of last AI – day of first AI + 68 days.
3. This interval is evaluated in days.

A positive value corresponds to a short interval between first and last AI. |
| 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: 1510 |
| 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.