**Form GE Status as of: 2019-12-02**

**DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS**

|  |  |
| --- | --- |
| **Country (or countries)** | France |
| **Main trait group1** | Conformation |
| **Breed(s)** | Brown Swiss |
| **Trait definition(s) and unit(s) of measurement2**see appendix GE for details | 27 linear traits (5 new in June 2012); 5 general characteristics (body, rump, feet and legs, udder, dairy character) ; milking speed, body condition score, Overall conformation score = 1.4396 \* [0.40 UD\_o + 0.25 FL\_o + 0.25 BODY\_o + 0.10 RUMP\_o ] |
| **Method of measuring and collecting data** | Linear or scoring measurements by technicians (1-9, except for milking speed: 1-5) |
| **Time period for data inclusion** | Records from September 1996 |
| **Age groups (e.g. parities) included** | Parity 1 (if missing then parity 2) |
| **Other criteria (data edits) for inclusion of records** | One score by cow. If by mistake, a cow is scored twice, the score is chosen as close as possible to 30 months |
| **Criteria for extension of records** (if applicable) |  |
| **Sire categories** | All sires |
| **Environmental effects3, pre-adjustments**  | None |
| **Method (model) of genetic evaluation3** | MT-BLUB AM |
| **Environmental effects3 in the genetic evaluation model** | Stage of lactation \* parity \* year(F); Age at calving \* parity (1 or 2) \* year(F); Herd – round – classifier(F) |
| **Adjustment for heterogeneous variance in evaluation model** | No |
| **Use of genetic groups and relationships** | Groups of unknown parents defined according to sex, birth year and region or country origin of the progeny |
| **Blending of foreign/Interbull information in evaluation** | No |
| **Genetic parameters in the evaluation** | Cf appendix CO and MTP |
| **System validation** | Checks on Data quality; Planned connection between regions (= young bullswith 1st 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, 1st or 2nd crop). Validation of genetic trend (Interbull Methods II & III). Analysis of residuals within classes (ex: within department, region, 1st or 2nd crop) |
| **Expression of genetic evaluations**If standardised (e.g. RBV), give standardisation formula in the appendix | RBV |
| **Definition of genetic reference base****Next base change** | Male rolling base: the average BV of French AI bulls with at least 15 daughters is set to zero.April 2016 (These bases change each February) |
| **Calculation of reliability** |  |
| **Criteria for official publication of evaluations** | REL ≥ 0.50 for BSW |
| **Number of evaluations / publications per year** | 3 : April, August, December |
| **Use in total merit index4** | ISU = 100 + 21.81 / 0.40\* [0.40 INEL/25.2 + 0.12 SCScmb + 0.08 MAScmb + 0.10 CC1cmb + 0.05 HCOcmb + 0.05 CRCcmb + 0.05 LONGcmb + 0.15 Overall conformation] (40% Production, 20% UdderHealth, 20% Female Fertility, 15% Conformation, 5% Longevity) |
| **Anticipated changes in the near future** |  |
| **Key reference on methodology applied** |  |
| **Key organisation: name, address, phone, fax, e-mail, web site** | Computing: GENEVALEvaluations génétique des animaux d’élevage3 rue du Petit RobinsonF78350 Jouy en JosasMail: stephane.barbier@geneval.frPhone : +33 1 85 36 05 00, <http://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) |

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 unit

**Form GE Appendix CO**

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

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| --- | --- |
| **Country (or countries):** | France |
| **Main trait group:** | Conformation |
| **Breed(s):** | Brown Swiss |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| trait | Definition | h² | genetic variance | official proof standardisation formula\*\*: a=0, c=1, d: computed at each evaluation (rolling basis) b factor given in this column: |
| Stature | Height at sacrum (eye evaluated) | 0.59 | 1.45 | b= |   | 1.2033 |
| Chest Width  | chest depth | 0.22 | 0.28 | b= |   | 0.5257 |
| Body Depth | Maximum distance between top and bottom lines | 0.38 | 0.48 | b= |   | 0.6906 |
| Angularity | General characteristic Dairy Character (so-called “Type” in French) | 0.36 | 0.47 | b= |   | 0.6861 |
| Rump Angle | Hip to pins (level=4; optimum=5) | 0.34 | 0.28 | b= |   | 0.5259 |
| Rump Width | Width at hips (eye evaluated) | 0.37 | 0.63 | b= |   | 0.7906 |
| Rear Leg Side View | Straight to sickled (optimum=5) | 0.17 | 0.18 | b= |   | 0.5290 |
| Foot Angle | Low to step (optimum=5) | 0.13 | 0.14 | b= |   | 0.3726 |
| Heel Depth (Hoof Height) | Shallow to deep | 0.09 | 0.09 | b= |   | 0.3028 |
| Fore Udder Attachment  | Length; short to long (optimum=7) | 0.28 | 0.63 | b= |   | 0.7002 |
| Rear Udder Attachment Height | Distance between vulva and top of secreting tissue | 0.21 | 0.29 | b= |   | 0.5388 |
| Rear Udder Attachment Width | Rear Udder Attachment Width | 0.27 | 0.46 | b= |   | 0.6813 |
| Udder Support | Cleft between teats and above | 0.30 | 0.61 | b= |   | 0.7839 |
| Udder Depth | Distance between hocks and the bottom point of udder (level=4) | 0.39 | 0.35 | b= |   | 0.5931 |
| Front Teat Placement | Distance between fore teats (optimum=5) | 0.45 | 0.80 | b= |   | 0.8962 |
| Teat Length | Short to long (optimum=5) | 0.47 | 0.76 | b= |   | 0.8724 |
| Rear Teat Placement | Rear Teat Placement | 0.37 | 0.51 | b= |   | 0.7165 |
| Overall Conformation Score | Composite computed from 4 proofsc | 0.41 | 1.00 |   |   |   |
| Overall Udder Score | Global note | 0.37 | 1.00 |   |   |   |
| Overall Feet & Leg Score | Global note | 0.10 | 1.00 |   |   |   |
| Milking Speed | Milking Speed  |  0.25 |  0.19 | b= |   | 0.4368 |
| Fore Udder Length | Fore Udder Length |  0.28 |   0.49 | b= |   | 0.7002 |
| Udder Balance | Udder Balance |  0.27 |  0.23 | b= |   | 0.4835 |
| Teat Direction | Teat Direction |  0.37 |  0.44 | b= |   | 0.6617 |
| Rump Length  | Rump Length  |  0.28 |  0.31 | b= |   | 0.5547 |
| Top Line | Top Line | 0.17 |  0.10 | b= |   | 0.3151 |
| Hock Position | Hock Position | 0.29 |  0.30 | b= |   | 0.5453 |
| Overall Frame | Overall Frame | 0.49 |  6.14 | b= |   | 2.4778 |
| Overall Rump  | Overall Rump  | 0.19 |  1.67 | b= |   | 1.2910 |
| Thurl Position | Thurl Position | 0.14 |  0.15 | b= |   | 0.3879 |
| Teat Thickness | Teat Thickness | 0.37 |  0.43 | b= |   | 0.6524 |

a 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.

b 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.

**Form GE Appendix MTP**

**Parameters for national genetic evaluations for conformation traits: heritability and genetic correlation**

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| --- | --- |
| **Country (or countries):** | France |
| **Main trait group:** | Conformation |
| **Breed(s):** | Brown Swiss |

Heritability (on the diagonal) and genetic correlations (above the diagonal) between traits

