**Form GE Status as of: 2015-01-20**

**DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS**

|  |  |  |
| --- | --- | --- |
| **Country (or countries)** | France | |
| **Main trait group1** | Conformation | |
| **Breed(s)** | RED (*Pie Rouge des Plaines*) | |
| **Trait definition(s) and unit(s) of measurement2** Attach an appendix if needed | See appendix TD (trait definition) |
| **Method of measuring and collecting data** | Linear or scoring measurements by technicians |
| **Time period for data inclusion** | Records from 1995 for group 1 traits (cf. appendix TD) and from 2001 for group 2 traits (cf. appendix TD). |
| **Age groups (e.g. parities) included** | Parity 1 (if missing then parity 2) |
| **Other criteria (data edits) for inclusion of records** | 1st scoring |
| **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** | According to Origin \* BY \* Sex |
| **Blending of foreign/Interbull information in evaluation** | No |
| **Genetic parameters in the evaluation** | Cf appendix GE, CO and MTP |
| **System validation** | Checks on Data quality; Planned connection between regions (= young bulls with 1st crop daughters) 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 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 definition: bulls (with known father) born between years (n-12) and (n-7) with a genetic evaluation REL ≥ 50%.  February 2012. |
| **Calculation of reliability** | REL are estimated for each trait using Harris & Johnson approach but edited REL are FTP REL for traits of group 1 (cf. appendix TD) and TD REL for traits of group 2 (cf. appendix TD). |
| **Criteria for official publication of evaluations** | REL (as defined before) ≥ 50% and no of daughters ≥ 15. |
| **Number of evaluations / publications per year** | 2: in January and in June |
| **Use in total merit index4** | Overall composites are used in Total Merit Index (ISU) defined for each breed as follows (for RED):  50% Production + 11% Combined SCC + 14% Combined Fertility + 11% Combined Functional Longevity + 14% Overall type score1 |
| **Anticipated changes in the near future** | New traits will be investigated and if possible included in the genetic evaluation process. |
| **Key reference on methodology applied** |  |
| **Key organisation: name, address, phone, fax, e-mail, web site** | Computing:  INRA  Station de Génétique Quantitative et Appliquée  Domaine de Vilvert  F78352 Jouy en Josas cedex  Mail: helene.larroque@jouy.inra.fr  Phone: +33 1 34 6 5 22 04, Fax : +33 1 34 65 22 10  Web site: http://www-sgqa.jouy.inra.fr  Publishing:  Institut de l’Elevage  149 Rue de Bercy  F75595 Paris cedex 12  Mail: sophie.mattalia@inst-elevage.asso.fr  Web site: www.inst-elevage.asso.fr |

1) Overall type score: TY\_o = 1/2 ( UD\_o + DT)

**Form GE Appendix TD**

**Parameters used in genetic evaluation**

|  |  |
| --- | --- |
| **Country (or countries):** | France |
| **Main trait group:** | Conformation |
| **Breed (repeat as necessary):** | RED (*Pie Rouge des Plaines*) |

|  |  |  |  |
| --- | --- | --- | --- |
| Trait abb. | Name | Trait group | Scored since |
| **Capacity** | | | |
| HS | Height at sacrum | 1 | 1995 |
| CW | Chest width | 2 | 2001 |
| CD | Chest depth | 1 | 1995 |
| BL | Back line | 2 | 2001 |
| MU | Muscularity | 1 | 1995 (updating in 2005) |
| DT | Dairy type | 1 | 1995 |
|  |  |  |  |
| TY\_o | Overall conformation = 1/2 ( UD\_o + DT) | 1 |  |
|  |  |  |  |
| **Rump** | | | |
| RA | Rump angle | 1 | 1995 |
| RW | Rump width | 1 | 1995 |
|  | | | |
| **Feet and legs** | | | |
| RLS | Angle of the hock | 1 | 1995 |
| RLR | Rear leg rear view | 2 | 2001 |
| HD | Heel depth | 1 | 1995 |
|  |  |  |  |
| **Udder** |  |  |  |
| FU | Fore udder | 1 | 1995 |
| RUH | Rear udder height | 1 | 1995 |
| CL | Central ligament | 1 | 1995 |
| UD | Udder depth | 1 | 1995 |
| TL | Teat length | 1 | 1995 |
| FTP | Front teat placement | 1 | 1995 |
| TD | Teat direction | 2 | 2001 |
| UB | Udder balance | 2 | 2001 |
| UD\_o | Overall udder score | 1 | 1995 (updating in 2005) |
|  |  |  |  |
|  | | | |
|  |  |  |  |
|  |  |  |  |
|  |  |  |  |

**Form GE Appendix GE**

**Parameters used in genetic evaluation**

|  |  |
| --- | --- |
| **Country (or countries):** | France |
| **Main trait group:** | Conformation |
| **Breed (repeat as necessary):** | RED (*Pie Rouge des Plaines*) |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Trait | Definition  ( *if unclear correspondence with ITB trait*) | ITBa | h2b | genetic  varianceb  (²G) | official proof  standardisation formulac |
| HS | Height at sacrum | X | 0.55 | 4.96 | a=0, b=G, c=12 and d=100 |
| CW | Chest width | X | 0.25 | 0.25 | a=0, b=G, c=12 and d=100 |
| CD | Chest depth 🡪 *Body depth* | X | 0.27 | 0.22 | a=0, b=G, c=12 and d=100 |
| BL | Back line |  | 0.15 | 0.15 | a=0, b=G, c=12 and d=100 |
| MU**d** | Muscularity 🡪 *Opposite of angularity***d** | X | 0.36 | 0.42 | a=0, b=G, c=12 and d=100 |
| DT | Dairy type |  | 0.49 | 1.06 | a=0, b=G, c=12 and d=100 |
| RA | Rump angle | X | 0.40 | 0.50 | a=0, b=G, c=12 and d=100 |
| RW | Rump width | X | 0.14 | 0.06 | a=0, b=G, c=12 and d=100 |
| RLS | Angle of the hock 🡪 *Rear leg set* | X | 0.10 | 0.05 | a=0, b=G, c=12 and d=100 |
| RLR | Rear leg rear view | X | 0.15 | 0.15 | a=0, b=G, c=12 and d=100 |
| HD | Heel depth 🡪 *Foot angle* | X | 0.14 | 0.08 | a=0, b=G, c=12 and d=100 |
| FU | Fore udder | X | 0.27 | 0.37 | a=0, b=G, c=12 and d=100 |
| RUH | Rear udder height | X | 0.31 | 0.28 | a=0, b=G, c=12 and d=100 |
| CL | Central ligament 🡪 *Udder support* | X | 0.21 | 0.30 | a=0, b=G, c=12 and d=100 |
| UD | Udder depth | X | 0.39 | 0.44 | a=0, b=G, c=12 and d=100 |
| TL | Teat length | X | 0.34 | 0.49 | a=0, b=G, c=12 and d=100 |
| FTP | Front teat placement | X | 0.31 | 0.46 | a=0, b=G, c=12 and d=100 |
| TD | Teat direction | X | 0.30 | 0.30 | a=0, b=G, c=12 and d=100 |
| UB | Udder balance |  | 0.25 | 0.25 | a=0, b=G, c=12 and d=100 |
| UD\_o | Overall udder score | X | 0.41 | 1.25 | a=0, b=G, c=12 and d=100 |
| TY\_o | Overall conformation = 1/2 ( UD\_o + DT) | X | 0.31 | 1 | a=0, b=G, c=12 and d=100 |
| LO | Locomotion |  |  |  |  |
| BCS | Body Condition Score |  |  |  |  |

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

b 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.

c 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.

**d In 015 data file muscularity RBVs are expressed**

**on a reversed scale compared to French publishing scale for Angularity prediction and**

**as published in France for BCS prediction.**

**Form GE Appendix CO**

**Parameters for national genetic evaluations for conformation traits as provided to Interbull  
(all breeds except Brown Swiss)**

|  |  |
| --- | --- |
| **Country (or countries):** | France |
| **Main trait group:** | Conformation |
| **Breed(s):** | RED (*Pie Rouge des Plaines*) |

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| trait | Definition | h² | genetic variance | official proof standardisation formula\*\*: a=100, c=12, d: computed at each evaluation (rolling basis) b factor given in this column: | | |
| Stature | Height at Sacrum | 0.55 | 4.96 | b= |  | 2.2260 |
| Chest width | Chest Width | 0.25 | 0.25 | b= |  | 0.5000 |
| Body depth | Body Depth | 0.27 | 0.22 | b= |  | 0.4690 |
| Angularity | Angularity | 0.36 | 0.42 | b= |  | 0.6470 |
| Rump angle | Rump Angle | 0.40 | 0.50 | b= |  | 0.7060 |
| Rump width | Rump Width | 0.14 | 0.06 | b= |  | 0.2490 |
| Rear leg set | Rear Leg Set | 0.10 | 0.05 | b= |  | 0.2280 |
| Rear Leg Rear View | Rear Leg Rear View | 0.15 | 0.15 | b= |  | 0.3870 |
| Foot angle | Foot Angle | 0.14 | 0.08 | b= |  | 0.2830 |
| Fore udder | Fore Udder Attachment | 0.27 | 0.37 | b= |  | 0.6120 |
| Rear udder height | Rear Udder Height | 0.31 | 0.28 | b= |  | 0.5330 |
| Udder support | Udder Cleft | 0.21 | 0.31 | b= |  | 0.5520 |
| Udder depth | Udder Depth (Udder- Hocks distance) | 0.39 | 0.44 | b= |  | 0.6630 |
| Teat placement | Teat Placement Front | 0.31 | 0.46 | b= |  | 0.6750 |
| Teat length | Teat Length | 0.34 | 0.49 | b= |  | 0.6990 |
| Teat Direction Rear | Teat Direction Rear | 0.30 | 0.30 | b= |  | 0.5480 |
| Overall Conformation score | Linear combination of linear traits (see formula in the general description) | 0.31 | 1.00 |  |  |  |
| Overal Udder score | Linear combination of linear traits (see formula in the general description) | 0.41 | 1.00 |  |  |  |
| Overal Feet & Leg score | Linear combination of linear traits (see formula in the general description) |  |  |  |  |  |
| Locomotion | Locomotion |  |  |  |  |  |
| Body Condition Score | Body Condition Score | 0.36 | 0.42 | b= |  | 0.6470 |

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**

|  |  |
| --- | --- |
| **Country (or countries):** | France |
| **Main trait group:** | Conformation |
| **Breed(s):** | RED (*Pie Rouge des Plaines*) |

***Heritability (on the diagonal), genetic correlations (above the diagonal) and residual correlations (below the diagonal) between traits.***

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | sta | bde | rwi | ran | rls | fan | fua | ruh | ude | usu | ftp | ftl | ang | cwi | tem | rlr | msp | rtp |
| sta | **0.55** | 0.53 | 0.49 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| bde | 0.15 | **0.27** | 0.36 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| rwi | 0.13 | 0.05 | **0.14** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| ran | 0.00 | 0.00 | 0.00 | **0.40** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| rls | 0.00 | 0.00 | 0.00 | 0.00 | **0.10** | -0.65 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| fan | 0.00 | 0.00 | 0.00 | 0.00 | -0.27 | **0.14** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| fua | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.27** | 0.68 | 0.78 | 0.46 | 0.63 | -0.19 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| ruh | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.16 | **0.31** | 0.69 | 0.55 | 0.47 | -0.14 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| ude | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.21 | 0.21 | **0.39** | 0.46 | 0.58 | -0.13 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| usu | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.11 | 0.24 | 0.17 | **0.21** | 0.45 | -0.12 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| ftp | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.18 | 0.16 | 0.19 | 0.30 | **0.31** | -0.38 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| ftl | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.04 | 0.04 | 0.00 | 0.00 | 0.08 | **0.34** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| ang | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.36** | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 |
| cwi | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.25** | 0.00 | 0.00 | 0.00 | 0.00 |
| tem | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.15** | 0.00 | 0.00 | 0.00 |
| rlr | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.15** | 0.00 | 0.00 |
| msp | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.25** | 0.00 |
| rtp | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | **0.30** |