Status as of: 2021-12-13

**DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS**

|  |  |  |
| --- | --- | --- |
| **Country (or countries)** | Canada | |
| **Main trait group1 NOTE!** Only one trait group per form! | Conformation | |
| **Breed(s)** | Holstein, Jersey, Ayrshire, Brown Swiss, Guernsey, Canadienne and Milking Shorthorn | |
| **Trait definition(s) and unit(s) of measurement2** Attach an appendix if needed | see Appendix SM |
| **Method of measuring and collecting data** | Data are collected by classifiers. |
| **Time period for data inclusion** | Since 1993 (Holstein) Since 1982 (all other breeds) |
| **Age groups (e.g. parities) included** | Only scores from first lactation cows are included. |
| **Other criteria (data edits) for inclusion of records** |  |
| **Criteria for extension of records** (if applicable) | Records are not extended, but are weighted such that classifications closest to 30 months receive the maximum weight. |
| **Sire categories** | All bulls with progeny information including domestic and foreign AI bulls plus natural service herd sires |
| **Environmental effects3, pre-adjustments** | Data for many, but not all traits (as detailed in Appendix SM) are normalized using Snell scores. |
| **Method (model) of genetic evaluation3** | MT BLUP AM |
| **Environmental effects3 in the genetic evaluation model** | HOL: Fixed: Herd-Round-Classifier (HRC), interaction among: age at calving, stage of lactation when classified, time period when classified and the effect of re-classification within 1st parity.  Colored breeds: As for HOL but without time period of classification. |
| **Adjustment for heterogeneous variance in evaluation model** | Holstein only |
| **Use of genetic groups and relationships** | Phantom parent groups are defined separately for Canadian versus foreign ancestry according to birth year and path of selection. |
| **Blending of foreign/Interbull information in evaluation** | None |
| **Genetic parameters in the evaluation** | See appendix |
| **System validation** | Interbull genetic trend validation methods 1 and 3 |
| **Expression of genetic evaluations** If standardised (e.g. RBV), give standardisation formula in the appendix | Standardized scale with mean = 0 and SD = 5 |
| **Definition of genetic reference base**  **Next base change** | Proven bulls born in the most recent complete 10-year period (ex: for 2007, bulls born from 1992 to 2001 inclusive)  Base is updated every February |
| **Calculation of reliability** | MT approximation described by Tier and Meyer (2004) J. Anim. Br. Gen. 121:77. |
| **Criteria for official publication of evaluations** | HOL: Reliability ≥ 60% and 20 daughters in ≥10 herds AYS, and JER: Reliability ≥ 55% and 15 daughters in ≥10 herds BSW, GUE, Canadienne and Milking Shorthorn: Reliability ≥ 40% and 10 daughters in ≥5 herds |
| **Number of evaluations / publications per year** | Three evaluations (April, August and December) |
| **Use in total merit index4** | Mammary system, Feet & Legs, Dairy Strength and Rump are used in the LPI for at least some of the breeds. The LPI formula is updated annually for details see: <http://www.cdn.ca/articles.php> |
| **Anticipated changes in the near future** |  |
| **Key reference on methodology applied** |  |
| **Key organization: name, address, phone, fax, e-mail, web site** | Canadian Dairy Network, 660 Speedvale Avenue West  Suite 102  N1K 1E5, Guelph, Ontario, Canada  Tel:-    1-519 767 9660  Fax:-   1 519 767 6768  Web:-  [www.cdn.ca](http://www.cdn.ca/)  E-mail: [vandoorm@cdn.ca](mailto:vandoorm@cdn.ca) |

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).

**Parameters used in genetic evaluation**

|  |  |
| --- | --- |
| **Country (or countries):** | Canada |
| **Main trait group:** | Conformation |
| **Breed (repeat as necessary):** | Holstein |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Trait | Definition | ITBa | h2b | genetic  varianceb | official proof  standardisation formulac |
| Stature | Height at hips | X | .461 |  |  |
| \*Chest width |  | X | .203 |  |  |
| \*Body depth |  | X | .313 |  |  |
| \*Angularity  \*BCS |  | X | .177 |  |  |
| Rump angle |  | X | .406 |  |  |
| Rump width | Width at pins | X | .318 |  |  |
| \*Rear leg set | Rear legs side view | X | .201 |  |  |
| \*Rear leg rear view  \*Locomotion |  | X | .109 |  |  |
| \*Foot angle |  | X | .072 |  |  |
| \*Fore udder | attachment | X | .269 |  |  |
| Rear udder height |  | X | .249 |  |  |
| \*Udder support | Median Suspensory | X | .167 |  |  |
| Udder depth |  | X | .443 |  |  |
| \*Teat placement | (fore) | X | .273 |  |  |
| \*Teat length |  | X | .320 |  |  |
| \*Teat placement | (rear) | X | .291 |  |  |
| \*Overall conformation  score | Calculated from Scorecard traits | X |  |  |  |
| \*Overall udder score | Calculated from linears | X |  |  |  |
| \*Overall feet&leg score | Calculated from linears | X |  |  |  |

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.

\* Traits normalized using Snell scores

**Parameters used in genetic evaluation**

|  |  |
| --- | --- |
| **Country (or countries):** | Canada |
| **Main trait group:** | Conformation |
| **Breed (repeat as necessary):** | Jersey |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Trait | Definition | ITBa | h2b | genetic  varianceb | official proof  standardisation formulac |
| Stature | Height at withers | X | .299 |  |  |
| \*Chest width |  | X | .135 |  |  |
| \*Body depth |  | X | .252 |  |  |
| \*Angularity  \*BCS |  | X | .135 |  |  |
| Rump angle |  | X | .305 |  |  |
| Rump width | Width at pins | X | .189 |  |  |
| \*Rear leg set | Rear legs side view | X | .140 |  |  |
| \*Rear leg rear view  \*Locomotion |  | X | .087 |  |  |
| \*Foot angle |  | X | .084 |  |  |
| \*Fore udder | Attachment | X | .247 |  |  |
| Rear udder height |  | X | .244 |  |  |
| \*Udder support | Median Suspensory | X | .166 |  |  |
| Udder depth |  | X | .417 |  |  |
| \*Teat placement | (fore) | X | .237 |  |  |
| \*Teat length |  | X | .253 |  |  |
| \*Teat placement | (rear) | X | .278 |  |  |
| \*Overall conformation  score | Calculated from Scorecard traits | X |  |  |  |
| \*Overall udder score | Calculated from linears | X |  |  |  |
| \*Overall feet&leg score | Calculated from linears | X |  |  |  |

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.

\* Traits normalized using Snell scores

**Parameters used in genetic evaluation**

|  |  |
| --- | --- |
| **Country (or countries):** | Canada |
| **Main trait group:** | Conformation |
| **Breed (repeat as necessary):** | Ayrshire |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Trait | Definition | ITBa | h2b | genetic  varianceb | official proof  standardisation formulac |
| Stature | Height at withers | X | .471 |  |  |
| \*Chest width |  | X | .161 |  |  |
| \*Body depth |  | X | .302 |  |  |
| \*Angularity  \*BCS |  | X | .183 |  |  |
| Rump angle |  | X | .334 |  |  |
| Rump width | Width at pins | X | .333 |  |  |
| \*Rear leg set | Rear legs side view | X | .193 |  |  |
| \*Rear leg rear view  \*Locomotion |  | X | .162 |  |  |
| \*Foot angle |  | X | .073 |  |  |
| \*Fore udder | Attachment | X | .242 |  |  |
| Rear udder height |  | X | .246 |  |  |
| \*Udder support | Median Suspensory | X | .188 |  |  |
| Udder depth |  | X | .357 |  |  |
| \*Teat placement | (fore) | X | .236 |  |  |
| \*Teat length |  | X | .307 |  |  |
| \*Teat placement | (rear) | X | .267 |  |  |
| \*Overall conformation  score | Calculated from Scorecard traits | X |  |  |  |
| \*Overall udder score | Calculated from linears | X |  |  |  |
| \*Overall feet&leg score | Calculated from linears | X |  |  |  |

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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.

\* Traits normalized using Snell scores

**Parameters used in genetic evaluation**

|  |  |
| --- | --- |
| **Country (or countries):** | Canada |
| **Main trait group:** | Conformation |
| **Breed (repeat as necessary):** | Guernsey |

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Trait | Definition | ITBa | h2b | genetic  varianceb | official proof  standardisation formulac |
| Stature | Height at withers | X | .385 |  |  |
| \*Chest width |  | X | .148 |  |  |
| \*Body depth |  | X | .277 |  |  |
| \*Angularity  \*BCS |  | X | .159 |  |  |
| Rump angle |  | X | .320 |  |  |
| Rump width | Width at pins | X | .261 |  |  |
| \*Rear leg set | Rear legs side view | X | .167 |  |  |
| \*Rear leg rear view  \*Locomotion |  | X | .125 |  |  |
| \*Foot angle |  | X | .078 |  |  |
| \*Fore udder | Attachment | X | . 245 |  |  |
| Rear udder height |  | X | .245 |  |  |
| \*Udder support | Median Suspensory | X | .177 |  |  |
| Udder depth |  | X | .387 |  |  |
| \*Teat placement | (fore) | X | . 236 |  |  |
| \*Teat length |  | X | .280 |  |  |
| \*Teat placement | (rear) | X | .272 |  |  |
| \*Overall conformation  score | Calculated from Scorecard traits | X |  |  |  |
| \*Overall udder score | Calculated from linears | X |  |  |  |
| \*Overall feet&leg score | Calculated from linears | X |  |  |  |

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.

\* Traits normalized using Snell scores

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

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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Trait | Definition | h2a | genetic  variancea | official proof  standardisation formulab |
| Stature | Height at withers | .385 |  |  |
| \*Chest width |  | .148 |  |  |
| \*Body depth |  | .277 |  |  |
| \*Angularity |  | .159 |  |  |
| Rump angle |  | .320 |  |  |
| Rump Width | Width at pins | .261 |  |  |
| \*Rear Leg Side View |  | .167 |  |  |
| \*Pasterns/Foot Angle | Foot Angle | .078 |  |  |
| \*Deep Heel (Hoof Height) |  | .078 |  |  |
| \*Fore Udder Attachment | Attachment | .245 |  |  |
| Rear Udder Attachment Height |  | .245 |  |  |
| Rear Udder Attachment Width |  | .194 |  |  |
| \*Udder Support | Median Suspensory | .177 |  |  |
| Udder Depth |  | .387 |  |  |
| \*Front Teat Placement | (fore) | .236 |  |  |
| \*Teat Length |  | .280 |  |  |
| \*Rear Teat Placement | (rear) | .272 |  |  |
| \*Overall Conformation Score | Calculated from Scorecard traits |  |  |  |
| \*Overall Udder Score | Calculated from linears |  |  |  |
| \*Overall Feet & Leg Score | Calculated from linears |  |  |  |
| \*Overall Frame | Calculated from linears |  |  |  |
| \*Top Line | Loin Strength | .171 |  |  |
| \*Overall Rump | Calculated from linears |  |  |  |
| \*Thurl Position | Thurl Placement | .163 |  |  |
| \*Hock Quality | Bone Quality | .262 |  |  |

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.

\* Traits normalized using Snell scores