Status as of: 2021-06-08

**Form GENO**

**DESCRIPTION OF NATIONAL GENOMIC EVALUATION SYSTEMS**

|  |  |
| --- | --- |
| Country (or countries)  | Norway |
| Main trait groupa. NOTE. Only one trait group per form!  | Production traits: Milk, Fat, Protein |
| Breed(s)  | RDC (Norwegian Red) |
| Trait definition(s) and unit(s) of measurementAttach an appendix if needed  | 305-day milk (kg), fat (kg) and protein yield (kg) |
| Source of genotypes (chips used)  | Illumina 54k, Illumina 777k, Affymetrix 25, customized Affymetrix 55k and customized Illumina50K |
| Imputation method for missing genotypes  | Fimpute |
| Propagation of genomic information to non-genotyped descendants and ancestors  | Single step genomic evaluation (Christensen & Lund, 2010 and Legarra et al., 2009)  |
| Animals included in reference population (males, females, countries included, total number)  | Norwegian animals only: 4488 bulls, 47736 cows. 52224 in total. |
| Source of phenotypic data (DYD, de-regressed proofs, national EBVs and/or MACE evaluations)  | Ordinary phenotypes |
| Other criteria (data edits) for inclusion of records  | No |
| Criteria for extension of records (if applicable)  | No |
| Sire categories  | Genotyped bulls |
| Genomic model (linear, Bayesian, polygenic effect, genotypes or haplotypes)  | Single step genomic evaluation, where pedigree relationships have 10% weight into genomic relationship matrix (Aguilar et al., 2010)  |
| Blending of direct genomic value (DGV) with traditional EBV  | No |
| Environmental effects in the genetic evaluation model  | Year of calving\*month of calving\*parity, age at calving\*parity, days open\*parity, herd\*year of calving.Year of calving is defined “dynamic”. Most recent year =calvings after (today-465 days). Years before that is 365\*n days |
| Adjustment for heterogeneous variance in evaluation model  | Precorrection for heterogenous variance due to Age at calving \* Parity |
| Computation of genomic reliability  | As described in Misztal et al. (2013) implemented in Apax99 (MiX99 Development Team (2017)) |
| Blending of foreign/Interbull information in evaluation  | No |
| Genetic parameters in the evaluation  | Same as traditional genetic evaluation |
| Expression of genetic evaluationsIf standardized (e.g. RBV), give standardization formula in the appendix  | This is based on raw breeding values, without any scaling or standardization |
| Definition of genetic reference base  | Same as conventional genetic evaluation |
| Labeling of genomic evaluations  | G used as a label for all breeding values including genomic information |
| Criteria for official publication of evaluations  | When the bull is selected for AI and has got a herd book number |
| Number of evaluations / publications per year  | This number varies. In 2020: 30 evaluations |
| Use in total merit index  | Same as for traditional genetic evaluation |
| Anticipated changes in the near future  | No |
| Key reference on methodology applied  | Christensen OF, Lund MS. Genomic prediction when some animals are not genotyped. Genet Sel Evol. 2010 Jan 27;42:2. Legarra A, Aguilar I, Misztal I. A relationship matrix including full pedigree and genomic information. J Dairy Sci. 2009 Sep 1;92(9):4656–63Aguilar I, Misztal I, Johnson DL, Legarra A, Tsuruta S, Lawlor TJ. Hot topic: a unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score. J Dairy Sci. 2010 Feb;93(2):743–52. Misztal, I., et al. "Methods to approximate reliabilities in single-step genomic evaluation." *Journal of Dairy Science* 96.1 (2013): 647-654.MiX99: A software package for solving large mixed model equations. Release XI/2017, Natural Resources Institute Finland (Luke). Jokioinen, Finland. http://www.luke.fi/mix99 |
| Key organization: name, address, phone, fax, e-mail, web site  | Geno SA, Storhamargata 44, 2317 Hamar, Norway, +4791344102, oyvind.nordbo@geno.no, www.geno.no |

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

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| Approximate number of test bulls for this trait group: | ~343 |
| 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. | No foreign bulls others than those with large daughter groups in Norway |
| If using a truncation ≠ 4 years, provide the reason. | Truncation=5 years. This is to keep enough bulls in validation set, even after number of bulls pr year has reduced after implementing genomic selection |
| If applying an age cutoff for test bulls ≠ (YYYY-8), provide the reason | Cutoff=YYYY-10. This is to utilize all the bulls with their daughter information masked, when using truncation of 5 years of data. This would more reliable estimates of both regression coefficients and R^2 |

# Appendix GENO

## Parameters used in genetic/genomic evaluation

|  |  |
| --- | --- |
| Country (or countries):  | Norway |
| Main trait group:  | Production |
| Breed (repeat as necessary):  | RDC (Norwegian Red) |
| Trait  | Definition  | ITBa  | h2b  | Genetic varianceb  | Official proof standardisation formulac  |
| Milk yield: |  | X | 0.277 | 249532 | c=12; d=100 |
| Fat yield |  | X | 0.213 | 367 | c=12; d=100 |
| Protein yield: |  | X | 0.235 | 183 | c=12; d=100 |

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.