

## DESCRIPTION OF NATIONAL GENETIC EVALUATION SYSTEMS

|                                                                          |                                                                                                                                                                                    |
|--------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Country (or countries)</b>                                            | Mexico                                                                                                                                                                             |
| <b>Main trait group<sup>1</sup></b>                                      | Production                                                                                                                                                                         |
| <b>Breed(s)</b>                                                          | Holstein                                                                                                                                                                           |
| <b>Trait definition(s) and unit(s) of measurement<sup>2</sup></b>        | Milk (Kg), fat (Kg) and protein (Kg)                                                                                                                                               |
| <b>Method of measuring and collecting data</b>                           | Milk recording by the Mexican Holstein Association (MHA). For fat and protein yields, milk samples are sent to the MHA lab at least every two months for analysis by mid-infrared. |
| <b>Time period for data inclusion</b>                                    | Cows born since 1990.                                                                                                                                                              |
| <b>Age groups (e.g. parities) included</b>                               | First 3 lactations.                                                                                                                                                                |
| <b>Other criteria (data edits) for inclusion of records</b>              | Records for fat and protein test out of range ( <1.5% and> 8% ) were removed. Standardized Milk lactations out of range (<3500 kg and> 22000 kg) were removed                      |
| <b>Criteria for extension of records (if applicable)</b>                 | Records with <305 days extended to 305 days                                                                                                                                        |
| <b>Sire categories</b>                                                   | All bulls with born progeny information by AI                                                                                                                                      |
| <b>Environmental effects<sup>3</sup>, pre-adjustments</b>                | None                                                                                                                                                                               |
| <b>Method (model) of genetic evaluation<sup>3</sup></b>                  | ST – BLUP – AM                                                                                                                                                                     |
| <b>Environmental effects<sup>3</sup> in the genetic evaluation model</b> | F: Herd-Year-Season and age of parity.<br>R: Permanent environmental effect, sire-herd interaction, animal and residual effects.                                                   |
| <b>Adjustment for heterogeneous variance in evaluation model</b>         | Heterogeneous variances within herd-year are adjusted to a common variability simultaneously with the genetic evaluation and assuming constant heritabilities across environments. |
| <b>Use of genetic groups and relationships</b>                           | Relationship matrix is not modified. Individuals with unknown parents are grouped by heard-birth year in five year intervals.                                                      |
| <b>Blending of foreign/Interbull information in evaluation</b>           | None                                                                                                                                                                               |
| <b>Genetic parameters in the evaluation</b>                              | See Appendix PR for $h^2$ and genetic variance estimates.                                                                                                                          |
| <b>System validation</b>                                                 | Data quality control and genetic trend validation method 1                                                                                                                         |
| <b>Expression of genetic evaluations</b>                                 | HTP Kg                                                                                                                                                                             |
| <b>Definition of genetic reference base</b>                              | 2015 genetic reference base are cows born in 2010                                                                                                                                  |
| <b>Next base change</b>                                                  | In 2020 (cows born in 2015)                                                                                                                                                        |

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| <b>Calculation of reliability</b>                                    | <p>Reliability was estimated as follows (Rincent et al 2012):</p> $\text{Reliability} = \sqrt{1 - \text{PEV}/\sigma_g^2}$ <p>where <math>\sigma_g^2</math> is the additive genetic variance and PEV represents the portion of the genetic variance unexplained by the model. PEV is the square of the standard error.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| <b>Criteria for official publication of evaluations</b>              | Sires born from year 2000, minimum reliability of 65% and minimum 10 daughters in 3 herds.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| <b>Number of evaluations / publications per year</b>                 | 2 per year: February and August                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| <b>Use in total merit index<sup>4</sup></b>                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| <b>Anticipated changes in the near future</b>                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| <b>Key reference on methodology applied</b>                          | <p>Ruiz-López FJ; García-Ruiz A; Moreno-Rodríguez E. ¿Qué Toro? Evaluación genética semestral de toros y vacas Holstein para producción de leche, conformación y longevidad. Estudio No 52. 2016. INIFAP CENID FyMA. p188.</p> <p>Powell RL; Wiggans GR. Animal model evaluations for mexican Holstein. 1991. J. Dairy Sci. 74:1420-1227.</p> <p>Rincent R; Laloë D; Nicolas S; Altmann T; Brunel D; Revilla P; Moreau L. Maximizing the reliability of genomic selection by optimizing the calibration set of reference individuals: comparison of methods in two diverse groups of maize inbreds (Zea mays L.). 2012. Genetics, 192(2).</p> <p>Moro-Méndez J; Ruiz-López FJ. Estimación de parámetros genéticos para características de conformación en bovinos Holstein de México. 1999. Técnica Pecuaria en México. 37(1):41-53.</p> |
| <b>Key organization: name, address, phone, fax, e-mail, web site</b> | <p>Centro de Investigación Disciplinaria en Fisiología y Mejoramiento Animal INIFAP-SAGARPA.</p> <p>Km. 1. Carretera a Colón, Ajuchitlán, Querétaro; México.</p> <p>+52 (419) 2920036</p> <p>+52 (442) 2243933</p> <p><a href="mailto:ruiz.felipe@inifap.gob.mx">ruiz.felipe@inifap.gob.mx</a></p> <p><a href="mailto:garcia.adriana@inifap.gob.mx">garcia.adriana@inifap.gob.mx</a></p> <p><a href="http://www.inifap.gob.mx">www.inifap.gob.mx</a></p>                                                                                                                                                                                                                                                                                                                                                                                 |

1) Either: Production (e.g. milk, fat, protein), Conformation, Health (e.g. mastitis resistance, milk somatic cell, resistance to diseases other than mastitis), Longevity (e.g. direct longevity, combined 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](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 for national genetic evaluations for production traits as provided to Interbull

|                                |            |
|--------------------------------|------------|
| <b>Country (or countries):</b> | Mexico     |
| <b>Main trait group:</b>       | Production |
| <b>Breed(s):</b>               | HOL        |

| Trait          | $h^2$ <sup>a</sup> | genetic variance <sup>a</sup> | official proof standardisation formula <sup>b</sup> |
|----------------|--------------------|-------------------------------|-----------------------------------------------------|
| Milk yield:    | 0.20               | 1125400                       |                                                     |
| Fat yield:     | 0.23               | 1557                          |                                                     |
| Protein yield: | 0.23               | 1077                          |                                                     |

<sup>a</sup> If lactations, or part of lactations, are treated as separate traits, provide heritability estimates and genetic variances separately for each lactation, as well as for all lactations pooled, i.e. for the trait submitted to Interbull.

<sup>b</sup> Expressed as follows:  
 $\text{StandEval} = ((\text{eval} - a) / b) * c + d$  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.