GENOMIC EVALUATION OF THE HOLSTEIN BREED IN SPAIN

1. Estimation of Direct Breeding Values (VGD)

The direct breeding values are calculated using the method called GBLUP or Genomic BLUP. This method is a BLUP using a genomic relationship matrix as a matrix of relationships between genotypes. GBLUP assumes that all SNPs have the same variance and it follows a normal distribution. The genomic matrix called G, is a matrix of similarity between genotypes.

The use of G implies that individuals with very similar genotypes have similar genomic predictions.

The genomic evaluation is a single trait assessment, where the linear model used to estimate the direct genomic values (VGD) of each character is written as follows:

$$y=1\mu+Zg+e$$

where:

y: Deregresed proofs (PDR) of the Reference Population animals for a given trait, calculated from the current MACE proofs published by Interbull (Jairath *et ál.*, 1998).

μ: Population average.

g: Genetic effects vector.

Z: Design matrix relating the genetic values of animals with phenotypic data (in this case, PDR).

Normal distributions for genetic (g) and environmental (e) effects are assumed.

$$g \sim N\left(0, G\sigma_g^2\right) \quad \text{y} \quad e \sim N\left(0, D\sigma_e^2\right)$$

where:

G: Genetic relationship matrix as it defined by the method 2 of VanRaden (VanRaden, 2008), where the markers are weighted by their expected variance.

$$G = \frac{MM'}{\sum 2p_j\,(1 - p_j)}$$

where:

M: SNP matrix (n animal x m SNP).
p_j: Allelic frequency of SNP_j.

σg^2: Additive genetic variance.

D: Diagonal matrix with elements $d_{jj} = 1/\omega$, where ω is a weight for the PDR_j:

$$\omega = \frac{r^2_{PDR}}{(1-r^2_{PDR})} \quad \text{and} \quad r^2_{PDR} \quad \text{reliability of deregressed proofs}$$

σe^2: Residual Variance.

ω is used to take into account differences in reliability between deregressed proofs.

2. Polygenic effect

Part of the genetic variability is supposed to be captured by the SNPs; therefore we incorporate a polygenic effect that helps to explain the variability shown by the deregressed proofs through the genealogy, improving predictions of GBLUP. The percentage of variability expressed by the polygenic effect depends on each trait.

Previous validation studies were needed to define the percentage of genetic variability expressed by the polygenic effect for each trait:

Trait	% of polygenic effect (optimum)
Milk yield (kg)	15
Fat yield (kg)	15
Protein yield (kg)	30
Fat percentage	5
Protein percentage	5
Stature	5
Chest width	30
Body depth	5
Angularity	40
Rump angle	5
Thurl width	25
Rear legs side view	25
Rear legs rear view	40
Foot angle	40
Fore attachment	25
Rear attachment height	25
Median suspensory	40
Udder Depth	5
Front teat placement	25
Teat length	5
Rear teat placement	5
Feet and legs	50
Mobility	50
Somatic cell score	25
Longevity	1
Days open	5

3. Reference Population

Bulls genotyped at 50K or HD and progeny proven in the last National Evaluation or in the International (MACE of Interbull) are the group of animals that form the reference population. Since animals are not progeny tested for all traits at the same time, the reference population for each trait, is not integrated by the same number of bulls.

4. Expected Reliability of VGD

The genetic values are usually published together with the accuracy of the predictions, which is defined as the correlation between the predicted value and the true value or it´s the squared correlation. It is called the expected reliability of the value.

The expected Reliability is calculated by inverting the coefficient matrix of the mixed model equations to obtain the prediction error variance (VEP).

$$r_u^2 = 1 - \frac{VEP_u}{\sigma_u^2}$$

where:

r_u^2 : Expected reliability.

σ_u^2 : Additive genetic variance.

Since the expected reliability is over-estimated when compared to the cross validation studies for some characters, GBLUP reliability is multiplied by a scale factor S obtained from a previous validation study. The VGD are multiplied by √S in order to reduce this over-estimation, to obtain the corrected VGD:

$$VGD^* = \sqrt{S} * VGD$$

And therefore, the reliability of the corrected VGD is:

$$Fiab^*_{VGD} = S * r_u^2$$

5. Proofs combination (GEBV)

There are two sources of information to be combined, which are the VGD, and the progeny test proof (EBV), which in the case of candidates would be a pedigree index (IP). These two sources of information are combined as follows depending on the expected reliability of each type of proof.

$$GEBV = b_1 * VGD + b_2 * EBV$$

where:

$$b_1 = \frac{\frac{fiab_{VGD}}{(1- fiab_{VGD})}}{\frac{fiab_{VGD}}{(1- fiab_{VGD})} + \frac{fiab_{EBV}}{(1- fiab_{EBV})}} \qquad b_2 = \frac{\frac{fiab_{EBV}}{(1- fiab_{EBV})}}{\frac{fiab_{VGD}}{(1- fiab_{VGD})} + \frac{fiab_{EBV}}{(1- fiab_{EBV})}}$$

6. Reliability of GEBV (FGEBV)

To calculate the reliability of the combined value, the gain in reliability over the traditional genetic index is calculated. This gain is calculated through the validation study.

The reliability of the combined value is:

$$Fiab_{GEBV} = Fiab_{EBV} + Fiab_{GAIN}$$

Genetic reliability gain is calculated as follows:

$$Fiab_{GAIN} = \frac{R^2_{GEBV,\ PDR} - R^2_{IP,\ PDR}}{fiab_{PDR}}$$

$$Fiab_{GEBV} = \chi + (1 - \chi)\ Fiab_{EBV}$$

where:

χ $= Fiab_{GAIN}/(1 - Fiab_{EBV})$

7. Cross Validation study

All genomic evaluation should be verified through a cross-validation study. Here, recommendations of Mäntysaari *et ál.* (2010) are followed to validate genomic evaluations. These recommendations follow the same logic used by Interbull Method 3 to validate traditional genetic evaluations. This method, compare the genetic evaluation of bulls obtained after their first crop of daughters with their final evaluations, including all available information.

Regarding genomic evaluations, the animal population is divided into 2 groups: one, called the reference population for the study; knowing their phenotypes with the information available four years ago, this animals are used to estimate the effects of SNPs. Another, a group of younger animals (Testing Population) whose phenotype is not incorporated into the evaluation. Subsequently, the direct genomic values (VGD) and the combined genomic breeding values (GEBV) of this population are compared to their known deregressed proofs (PDR) currently.

This testing population, is formed by at least 150 animals tested with a number of effective daughters larger than 20 (effective daughters is a measure of the amount of information that exist in the progeny test proof).

To validate the proofs three parameters are taken into account:

- The accuracy of the test, calculated as the Pearson correlation between estimated VGD and known PDRs.
- The prediction bias calculated as the regression coefficient of the VGDs on the PDRs.
- The Mean Squared Error (MSE).

Reliability of the model is estimated by calculating the correlation between the PDRs and the VGDs taking into account the reliability of the PDRs.

$$Fiabl_{VGD} = R^2_{(VGD,PDR)} * \left(1 + \frac{k}{EDC} \right)$$

$$k = \frac{4 - h^2}{h^2}$$

where:

R^2: Squared correlation between VGDs and PDRs.

EDC: Effective Daughters contribution.

h^2: Heritability.

Reliability observed allows us to estimate the gain in reliability over traditional valuation provided by genomics as exposed previously.

8. GICO

GICO is the official index for total genetic merit. It combines the different traits according to their economic importance and their genetic correlations. It is used to rank the animals in the official lists of the best bulls and cows genotyped, with the breeding objective to improve future profitability of farms. The GICO formula is equivalent to the ICO.

The ICO was last updated in November 2015. The current formula is as follows:

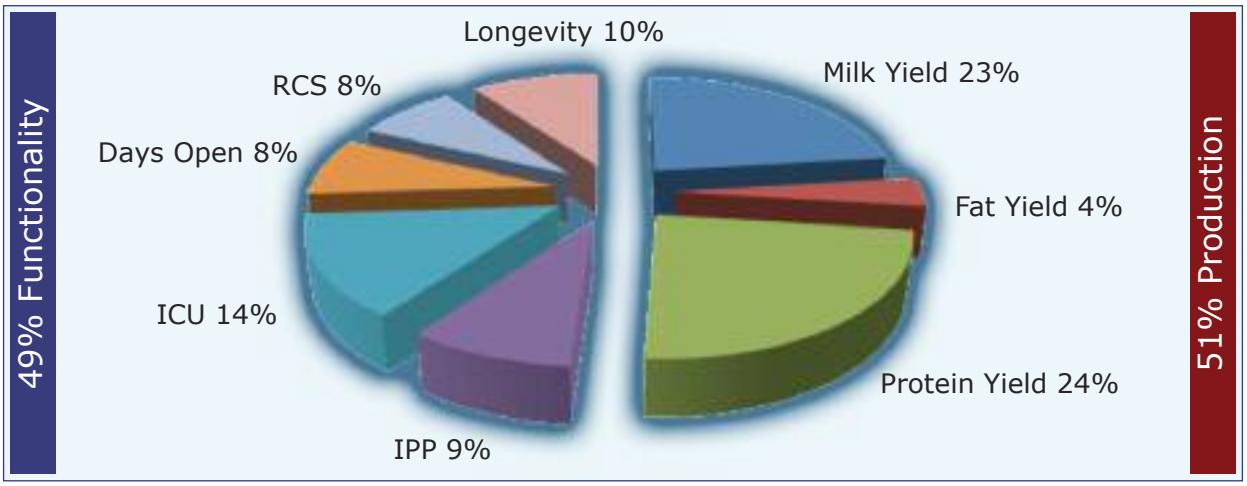
$$\textbf{ICO} = 1605 + 13{,}7 * \left(23*\frac{KL}{DT_{KL}} + 4*\frac{KG}{DT_{KG}} + 24*\frac{KP}{DT_{KP}} + 14*\frac{ICU}{DT_{ICU}} + 9*\frac{IPP}{DT_{IPP}} + 10*\frac{(Longevity-100)}{DT_{Long}} + 8*\frac{(RCS-100)}{DT_{RCS}} + 8*\frac{(DA-100)}{DT_{DA}} \right)$$

where, the standard deviations of each trait have the following values:

DT_{KL} = 765, for Milk Yield (KL)
DT_{KG} = 29, for Fat Yield (KG)
DT_{KP} = 22, for Protein Yield (KP)
DT_{ICU} = 1
DT_{IPP} = 1
DT_{Long} = 10
DT_{RCS} = 10
DT_{DA} = 10

ICU: Mammary system composite index
IPP: Feet and Legs composite index
RCS: Somatic Cell Score
DA: Days Open

Figure: Relative weights of traits included in the ICO



To compare the level of an individual animal in respect to the entire population, the ICO of each animal is accompanied by its percentile, which indicates the percentage of evaluated animals with a lower value. Percentile for cows and bulls are calculated separately. The percentile of the bulls is calculated taking into account only the bulls with daughters.

9. Requisites for publishing official genomic proofs

To have an official genomic proof, genomic bulls should be:

- Owned by one of the Spanish Breeding Programs.
- Over 10 months old at the time of publication.
- Registered in CONAFE.
- Labeled with an insemination code.
- Semen available.
- Genotyped at the density required by CONAFE for the official test.

Regarding females the requirements for official test are:

- Genomic evaluation available.
- Registered in CONAFE.

Also are evaluated and officially published those bulls whose genotypes has been received in EuroGenomics Young Bull Exchanges and nominated as publishable by the owner, and those AI bulls which official genomic proof has been request through the " EuroGenomics coop Fee System".

Evaluated animals that do not meet these requirements will have an unofficial and not publishable genomic breeding value only accessible to the sender owner of the sample.

10. Monthly genomic evaluations

In a monthly basis, CONAFE calculates GEBVs of animals genotyped in the period. Those breeding values are delivered to the farmers and breeding programs, and posted on the website of CONAFE when the animals get an official evaluation.

11. General Genomic Evaluation

Three times a year (March, June and November) the deregressed proofs from the last MACE evaluation are calculated and the Reference Population is updated, in order to calculate the GEBVs of all genotyped animals recorded in the CONAFE data base.

VGDs are combined with EBVs (offspring, females own value or pedigree index of young bulls and heifers).

A catalog is generated with the official tests:

- GEBVs in the case of animals genotyped.
- EBVs in the case of males not genotyped with enough information to obtain daughters.

Animals that have been evaluated taking into account their genomic information are marked with a test type "G".

12. Additional information to genomic proofs

SNP genotyping allows getting additional information to GEBVs, which are parentage verification and discovery, haplotype information, recessive traits and other genes of interest.

Parentage verification by SNPs:

When the animals and parents are genotyped. All those positions in which the sample and its parents are homozygous are compared, determining the correct affiliation if the percentage of incompatibilities is less than 1.1%, following the guidelines of ISAG for parentage verification using SNPs.

CONAFE check the parentage by SNPs of all animals that are evaluated genomically and issues parentage certificates.

Other characters:

Depending on the SNP chip version used to genotype each animal different additional information is obtained. Recessive traits such as BLAD, CVM, haplotypes related to fertility, genes of interest as the "Polled" or "Red Factor", the type of milk protein or presence of the Y chromosome in females that causes infertility.