The use of genetic parameters for the standardisation of linear type classification in Italy

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Abstract

In Italy around 260000 first parity Holstein cows are yearly scored by a group of about 25 classifiers. The linear classification data are subsequently used in the genetic evaluation for type traits. It is very important that all classifiers rank animals consistently and use a consistent data definition at all times. It is important to develop tools that allow to evaluate the repeatability of scores for all traits within and between classifiers. The use of genetic parameters to assess the quality of work of classifiers within a country was first documented by Veerkamp et al. 2002. One year of routine classification data were used to determine genetic parameters within and between classifiers in a series of bivariate analysis for all conformation traits that are currently used in the Italian selection index. The objective was to verify if the methodology could be applied in Italy where classifiers work within an assigned geographical area. In turn, observations from one classifiers were compared with data from the whole group of classifiers and estimated heritability and genetic correlation were used to assess repeatability and consistency of classifiers respectively. Results for genetic correlations ranged from 0.73 to 0.99. More subjective and complex traits like angularity did show a higher number of cases of genetic correlations lower than 0.80 compared to traits like stature that are easy to standardize. The procedure will soon become part of the official routine genetic evaluation; it will be used to assess the work quality of the classifiers. It will be used once a year by the responsible of the classification service in Italy to discuss with each classifiers specific issues related to specific traits. The final objective is to improve the overall quality of data provided for genetic evaluation of Holstein cows and bulls in Italy..

Introduction

Type classification in Italy is part of the standard service provided to herds registered for milk recording and it is a direct responsibility of breed organisations like ANAFI.

A group of around 25 classifiers are trained for scoring all first parity cows visiting all herds twice per year. These data are then used for official genetic evaluation.

Type traits are a very important source of information for genetic evaluation purposes because they are score early in the life of the animal and they are genetically correlated to many economically important traits.

It is very important that all classifiers score animal in a consistent manner and are consistent over time.

In order to achieve this consistency all classifiers meet 8 times per year scoring the same cows together and re-aligning themselves to a common scale.

Data of those commonly scored cows are then used to verify how consistent classifiers are with themselves and with the other classifiers.

Over time it was felt that those commonly scored cows were not enough to measure the overall quality of data collected for type classification.

The use of genetic parameters to assess the quality of work of classifiers within a country was first documented by Veerkamp et al. 2002. The advantage of this methodology is that it makes use of all the cows scored by each classifier during his normal daily work.

The heritability estimated for each classifier is used as a criteria for the repeatability of scores within classifiers and the genetic correlations between scores by different classifiers can be used as a measure of the repeatability between classifiers.

The objective of this study was therefore:

- to develop a procedure that would allow to monitor the quality of data collected by classifiers using all data collected each year;
- evaluate if the approach was applicable also in Italy where classifiers work in a specific and constant area.

Material and Methods

All the around 260000 cows scored each year by the classifiers are the data used for the analysis. Cows are scored for 19 linear traits with a scale from 1 to 50.

For this study all classification data from January 1, 2007 to December 31st, 2007 were used.

Herds with less than 10 records or with daughters of less than 3 sires were discarded. It was also required that in the final dataset sires had at least 15 daughters.

A total of 168110 observations related to 25 classifiers were used in the analysis, related to around 9000 sires and more than 24000 herd-year-round of classification.

Genetic parameters were estimated using VCE-5 (Kovac and Groeneveld, 2003) and a sire model, including the additive genetic relationship between sires in the relationship matrix. Each individual classifier was compared as trait 1 to all other classifiers as trait2. Variance components were estimated in s series of bivariate analyses in which scores from each classifiers were analyzed as the first traits and the combined scores for all others classifiers as the second trait. Therefore for all 19 traits and 25 classifiers, the following variances were estimated for the random sires and residual effects.

$$Sire = \begin{bmatrix} \sigma^2_{S1} & \sigma^2_{S12} \\ \sigma^2_{S12} & \sigma^2_{S2} \end{bmatrix}; \mathrm{Re}\,sidual = \begin{bmatrix} \sigma^2_{e1} & 0 \\ 0 & \sigma^2_{e2} \end{bmatrix}$$

Where σ^2_{S1} and σ^2_{S2} = sire variance for trait 1 and 2 respectively and σ^2_{S12} = covariance between trait 1 and 2; σ^2_{e1} and σ^2_{e2} = residual variance for trait 1 and 2 respectively. Residual covariance was zero as each animal was scored only once.

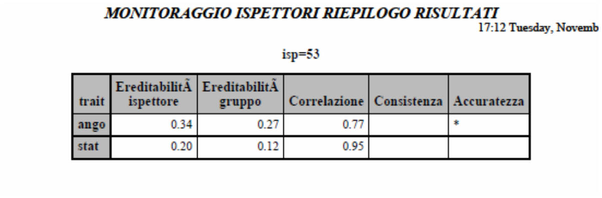
The heritability for each classifier was calculates as 4* σ^2_{S1} / ($\sigma^2_{S1} + \sigma^2_{e1}$), and the genetic correlation between each classifier and the combined scores of all other classifiers was calculated as $r_g = \sigma^2_{S12} / (\sigma^2_{S1}\ \sigma^2_{S2})$.

Fixed effects were fitted across the two traits and included herd-year-round of classification and the interaction between age, stage of lactation and biennium.

Results and discussion

Only results related to angularity and stature will be presented in this paper.

Figure 1 reports an example of output of the procedure referred to each classifiers that will flag values that are below 0.80 for the correlations and when the heritability for the classifiers is lower compared to the heritability of the whole group. This output is what the classifier manager will use to discuss with each person in order to identify potential problems and strategies to solve them in order to improve the quality of the data.



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trait	EreditabilitÃ ispettore	EreditabilitÃ gruppo	Correlazione	Consistenza	Accuratezza
ango	0.34	0.27	0.77		*
stat	0.20	0.12	0.95		

Figure 1 – Example of summary output from the procedure.

Genetic correlations for those two traits which are the most easy to score (stature) and the most difficult to standardize (angularity) varies from 0.73 to 0.99.

The trait with more inconsistencies across classifiers was angularity as expected with 30% of classifiers showing a genetic correlation less than 0.80.

Only 2 classifiers out of 25 did show problems on both traits on repeatability within and between classifiers at the same time.

There were few cases in which the heritability of the classifier was significantly lower than the group but given the specific areas in which classifiers work it needs to be assessed if other factors may be the cause of the inconsistency. Pedigree errors in some area may be higher than in others and may affect the results.

Conclusions

The new procedure is now in place. It works for all traits and it is an useful tool to monitor the quality of type classification. This will affect at the end the quality and the stability of genetic evaluation for type traits. It is going to be tested first on all traits that are included in the selection index like feet & legs and linear traits of the udder which are the main components. The final setting will envision to run the analysis at least once per year to give the responsible of the type classification service indication of where potential problem may be and give him an objective indication of how to address them with the appropriate people.

Acknowledgements

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References

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