Cluster analysis on across-country genetic correlations for overall type traits and body condition score of Holstein bulls

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ARTICLE INFO

ABSTRACT

The aim of the study is to examine the progress in trait harmonization among member countries participating in the International Bull Evaluation Service Organization (Interbull) for overall conformation score (OCS), overall udder score (OUS), overall feet and legs (OFL), and body condition score (BCS) of Holstein bulls. Input values for the cluster analysis were across-country genetic correlations estimated among 8 countries from 2001 to 2011 for overall type traits and among 12 countries from 2009 to 2011 for BCS. Changes in evaluation procedure and trait definition affected the clustering of countries. For OCS, the evolution was clear, particularly for Australia; the genetic correlations between this country and the majority of other members decreased during the years. Other changes in clustering were due to modifications in trait definitions introduced by France (2004), Germany (2007) and United Kingdom–Ireland (2005, 2008 and 2011). The genetic correlations for OUS were generally higher than those for OCS, and changes in clustering were less pronounced: the structure of clusters remained unchanged from 2004 to 2007. For OFL, Australia was even more distant than for the other two composite traits, probably due to the use of "side view foot diagonal" as best predictor of OFL. The changes in trait definition introduced by France Black and White Holstein (2001) and Italy (2003 and 2007) entailed modifications in the structure of dendrograms. The cluster analysis well depicts the difference among countries that sent information on BCS to Interbull and countries that sent angularity as predictor of BCS, as they were grouped in two distinct clusters and the correlations between them were negative. Major effort is needed to harmonize the traits among countries.

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1. Introduction

The International Bull Evaluation Service Organization (Interbull) provides international breeding values of dairy bulls to its member countries (Interbull, 2011a). The first genetic evaluation at Interbull took place in August 1994, and now three official evaluations per year are performed. F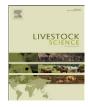orty traits, grouped in 7 major categories, 6 breeds, and 30 member countries are involved in the routine evaluation (Interbull, 2012).

The multiple-trait across-country evaluation (MACE) model was developed by Schaeffer (1994) 18 years ago and since then the methodology has undergone several changes. A time edit for the birth date of bulls was introduced (Weigel and Banos, 1997; De Jong, 2003). Then, the effective daughter contributions replaced the number of daughters as weighting factor (Fikse and Banos, 2001), and in 2004, the procedure to estimate genetic correlations was modified (Wilmink and Fikse, 2004). Furthermore, in 2012 the sire-dam pedigree replaced the sire-maternal grandsire pedigree to improve the quality of the estimations (Jakobsen and Dürr, 2012).

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Among the 7 major trait groups evaluated by Interbull, the one dealing with conformation is the biggest. For the Holstein breed, it includes 18 linear and 3 overall traits, namely overall conformation score (OCS), overall udder (OUS) and overall feet and legs (OFL). Linear traits should be similarly defined across countries (ICAR, 2011; Mark, 2004; WHFF, 2008) but, in practice, relevant differences still exist (Battagin et al., 2011). Overall traits are often heterogeneous across countries and depend on the specific national definition (Battagin et al., 2012; Canavesi et al., 2006; Shook, 2006). For this reason, there is much discussion on the efficiency of MACE to evaluate these characteristics, in particular the OCS (Canavesi et al., 2006; Miglior et al., 2004, 2007). Interbull Centre has evaluated BCS since January 2009 and international breeding values are now distributed to 11 member countries (Interbull, 2011b). When similar traits evaluated in 2 or more countries have different definitions, across-country genetic correlations are expected to be low and the ranking of bulls could be affected. Some countries changed the definition of the overall traits over the years and others started to send an "international predictor" instead of the official overall trait to Interbull. The international predictor is a composite trait for OCS that maximizes the correlation between a country and the USA, which is the major provider of bulls in the international evaluation (Canavesi et al., 2006).

The aim of the study is to document the progress in traits harmonization over time for overall type traits (OCS, OUS and OFL) and BCS using the across-country genetic correlations of Holstein bulls as starting values for the cluster analysis.

2. Materials and methods

The genetic correlations among 8 reference member countries [Australia (AUS), Canada (CAN), France Black and White Holstein (FRA), Germany (DEU), Italy (ITA), The Netherlands (NLD), the United Kingdom and Ireland (GBR), and the United States (USA)], estimated by Interbull from 2001 to 2011, were the input values in the hierarchical cluster analysis for OCS, OUS and OFL. For BCS, the correlation among the 12 countries participating in the MACE evaluation for this trait, from 2009 to 2011, were used. The countries were Belgium (BEL), CAN, Switzerland Black and White Holstein (CHE), Czech Republic (CZE), DEU, Denmark–Finland–Sweden (DFS), FRA, France Red Holstein (FRR), GBR, ITA, NLD and USA.

Hierarchical cluster analysis was performed using the CLUSTER procedure (SAS Institute Inc., 2008). The distance (d_{ij}) between countries i and j was calculated as $d_{ij} = 1 - rG_{ij}^2$, where rG_{ij} is the genetic correlation between countries i and j. Dendrograms were plotted using the TREE procedure (SAS Institute Inc., 2008). Information regarding any changes in national procedure made by countries during the routine evaluation, as well as the across-country genetic correlations, was available in the public area of Interbull's website (Interbull, 2011b).

3. Results and discussion

3.1. Overall conformation score

The 8 reference countries used the following definitions for OCS in May 2001: final score as individual trait (CAN and ITA), overall score as composite trait (FRA, GBR and NLD), overall score as individual trait (USA), general appearance (AUS), and relative total breeding value for type (DEU). The dendrogram of 2001 (Fig. 1) shows the presence of 4 clusters: (1) AUS, (2) DEU, GBR and ITA, (3) NLD and USA, and (4) CAN and FRA. From 2001 to 2002, the correlations between countries increased, probably as a consequence of changes introduced by Interbull. In particular: (1) in November 2001, the modification of the structure of sub-settings to estimate correlations (Jorjani, 2001); (2) in May 2002, the use of the number of common bulls as a weighting factor in the weighted bending procedure to obtain positive definite correlation matrices; and (3) in November 2002, the requirement for inclusion of second country proof (based on imported semen of bulls proven outside the country of first registration) in the evaluations (Interbull, 2011b).

From 2001 to 2011, AUS became the most distant country, probably due to an increase in genotype by environment differences with other countries included in the analysis (Zwald et al., 2001). Australia showed the highest genetic correlation with GBR (the maximum value was 0.86 in 2002) and the lowest genetic correlation with FRA (the minimum value was 0.53 in 2001). Overall, the genetic correlation of AUS decreased with the majority of countries, and this trend is well depicted in Fig. 1. Canada showed the highest correlation with USA (mean value of 0.87). The genetic correlations between CAN and other countries were stable in the whole period, except for AUS, which showed a decrease from 0.66 in 2001 to 0.59 in 2011. Germany exhibited the highest genetic correlation with ITA (mean value of 0.89), and the most important change was between 2006 and 2007: the country modified trait definition, and its genetic correlations increased with all other countries except CAN and ITA (Fig. 1). France Black and White Holstein showed the highest genetic correlation with NLD (mean value of 0.84) and the most relevant change in 2004, when the country modified the definition of OCS (Interbull, 2011b). In 2003, FRA was the most distant country, while from 2004, it grouped with CAN, NLD, USA (from 2004 to 2008) and ITA (from 2009 to 2011; Fig. 1). The GBR had the highest genetic correlations with DEU (mean value of 0.83). The GBR changed the trait definition 3 times: in 2005, 2008 and 2011. In 2005 and 2008 the genetic correlations with other countries decreased, whereas in 2011, there was a notable increment of genetic correlations (e.g., from 0.65 to 0.89 with FRA) because the new OCS was obtained from a linear combination of EBV, which best predicts USA PTA for type. The USA (0.83), ITA (0.83) and NLD (0.82) showed the highest average correlations across the analyzed countries. The changes made by ITA, NLD and USA did not influence the genetic correlations with the other countries. Rather, the increase or decrease of the correlations for OCS was due to the improvement made by the other members.