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National and international genetic evaluations for body condition score and related traits in Italian Holstein Friesian breed

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Abstract

Body condition score (BCS) has gained notable interest in the last decades as an important management tool in the dairy herd because it can be used as an indicator of overall energy status and of adipose stores mobilization during lactation. Moreover, BCS can be used as a predictor of fertility, health, and welfare status of cows. The Italian Holstein Breeder Association (ANAFI) started to collect data for BCS in 2007, but a national genetic evaluation for this trait is still not available. The increasing trade of dairy bull semen in the last thirty years has led to the increase of genetic links among countries. Nonetheless, using the genetic evaluations made by one country to evaluate bulls from another country without appropriate conversion is not a good way to compare animals. In 1983 the International Bull Evaluation Service (Interbull, Sweden) was established in response to the need for universal comparison criteria of dairy bulls across countries. The first international genetic evaluation for BCS was carried out in 2009 and involved 11 countries. Until now, Italian Holstein participated in the Interbull evaluation using angularity as the best predictor of BCS. 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. Based on these considerations, it is important for the Italian Holstein Breeder Association to have a national evaluation for BCS and to participate in the Interbull evaluation with BCS as a direct trait. The aims of the thesis were to study the status of international genetic evaluation of BCS and overall type traits, to estimate genetic variance of BCS, to estimate the genetic correlations of BCS with production and type traits (in particular angularity and locomotion), and finally to analyse the results of the first international genetic evaluation with BCS as a direct trait in Italian Holstein bulls. The investigation performed among countries that participated in the Interbull evaluation showed that differences for overall traits were mostly due to the heterogeneity in trait definitions. For BCS, the differences were due to the use of best predictors. Overall traits are important in selection indices to improve functional traits, and their definition depends on the specific breeding goals in each country. Across-country genetic correlations were useful in evaluating differences among countries. The cluster analysis over the years showed that changes in the Interbull evaluation procedure and trait definition influenced the genetic correlations across countries. National genomic evaluation for type traits has been adopted by some countries, while at the international level, Interbull is developing the methodology required to provide international comparisons of genomically enhanced breeding values to member organizations. The additive genetic variances of BCS estimated in the Italian Holstein population were low but in agreement with estimates reported in literature. The genetic relationships of BCS with milk yield were moderate and indicated that high producing cows tend to be thinner. The correlations of BCS with fat and protein content and fat to protein ratio were almost negligible. BCS seemed to be genetically independent with most of type traits, except for chest width, rear leg set side view and rear udder height. BCS showed a strong genetic correlation with its predictor (angularity), although this correlation decreased over the years, due to the change in angularity definition that occurred in 2009. Locomotion showed low genetic variance, and favourable genetic correlations with production and type traits. Using BCS as a direct trait improved the Italian Holstein across-country genetic correlations, increasing the number of Italian bulls in the top positions of other countries' ranks. At the same time, in the Italian rank, the number of bulls of countries using BCS increased as well. Clear unfavourable genetic trend was found in the Holstein Friesian breed from all countries that participated in the Interbull evaluation of BCS. The Italian bulls had an unfavourable genetic trend as well, which was negative for most of the years considered, even though it was in line with bulls from other countries.

Riassunto

Il punteggio di condizione corporea (BCS) è un indicatore dello stato energetico e della mobilizzazione del tessuto adiposo delle bovine durante la lattazione. Negli ultimi decenni il BCS è stato utilizzato come indicatore indiretto della fertilità, dello stato di salute e del benessere delle bovine da latte. L'Associazione Nazionale Allevatori di razza Frisona (ANAFI) registra i dati del BCS sulla popolazione bovina dal 2007, ma la valutazione genetica per questo carattere non è ancora ufficiale. La globalizzazione del mercato di seme dei tori da latte, iniziata negli anni '80, ha portato ad un aumento a livello internazionale dei legami genetici (di parentela) tra animali, rendendo possibile la valutazione genetica internazionale dei tori. Utilizzare le valutazione genetiche nazionali per un toro in un Paese diverso da quello di origine o di produzione delle figlie porta a valutazioni genetiche fuorvianti, perciò, nel 1983 è stato fondato il centro di valutazione genetica internazionale dei tori da latte (Interbull). Lo scopo di Interbull è quello di consentire il confronto internazionale tra i tori provati in diversi Paesi. Il BCS è stato valutato per la prima volta da Interbull nel 2009. La prima valutazione ufficiale ha coinvolto 11 Paesi, tra cui l'Italia, che ha partecipato utilizzando il carattere angolosità come misura indiretta del BCS. Quando 2 o più Paesi partecipano alle valutazioni internazionali con caratteri simili, la correlazione genetica tra questi Paesi sarà bassa e di conseguenza le classifiche dei tori saranno influenzate. Risultano quindi importanti, per i Paesi che aderiscono ad Interbull, l'utilizzo di caratteri omogenei e la partecipazione alle valutazioni internazionali con la misura diretta dei diversi caratteri (nel caso della Frisona Italina l'utilizzo del BCS). I principali obiettivi della tesi sono stati: lo studio dello stato delle valutazioni internazionali per il carattere BCS e per i 3 caratteri morfologici complessivi, la stima delle componenti di varianza del BCS, le sue correlazioni genetiche con i caratteri produttivi e morfologici ed infine l'analisi dei risultati della prima valutazione internazionale per il BCS utilizzando la misura diretta del carattere nei tori valutati in Italia. La prima analisi ha messo in evidenza l'eterogeneità nel modo di definire i caratteri morfologici generali, dovuta ai diversi obiettivi di selezione genetica tra i Paesi aderenti ad Interbull. Le differenze per il BCS sono dovute principalmente all'utilizzo di caratteri indiretti, quali angolosità e muscolosità. Le correlazioni genetiche stimate da Interbull evidenziano le differenze tra i Paesi e l'utilizzo dell'analisi di raggruppamento (*cluster analysis*) ha evidenziato come i cambiamenti adottati a livello nazionale ed internazionale influenzano le correlazioni genetiche tra i Paesi. Diversi Paesi hanno inoltre reso ufficiale la valutazione genomica dei propri animali, mentre Interbull sta sviluppando la metodologia per fornire indici genomici internazionali ai Paesi membri. La varianza genetica

additiva della Frisona Italiana per il BCS è bassa ma in linea con quanto riportato in letteratura. La correlazione genetica del BCS con la produzione di latte è moderata, indicando che vacche produttive tendono ad essere magre. Le correlazioni con il contenuto di grasso e proteina e il rapporto grasso/proteina sono invece trascurabili. Il BCS sembra essere indipendente dalla maggior parte dei caratteri morfologici, ad eccezione dei caratteri "forza e vigore", "arti posteriori visti di lato" e "altezza attacco posteriore della mammella". Il BCS ha una forte correlazione con l'angolosità, anche se negli anni l'intensità del legame è diminuita a causa del cambio di definizione dell'angolosità (2009). Anche per il carattere locomozione la varianza genetica stimata nella popolazione Frisona Italiana è bassa, ma le correlazioni con gli altri caratteri sono più forti e favorevoli. L'utilizzo del BCS nelle valutazioni internazionali permette di aumentare le correlazioni genetica della Frisona Italiana con gli altri Paesi aderenti ad Interbull per il BCS di questa razza, di conseguenza aumenta il numero dei tori italiani nelle classifiche estere. Allo stesso tempo, nella classifica italiana, aumenta il numero dei tori dei Paesi che utilizzano direttamente il BCS nella valutazione internazionale. Il trend genetico per il carattere BCS nella popolazione Frisona è sfavorevole per i tori di tutti i Paesi aderenti ad Interbull.

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List of Publications

This thesis is based on the work contained in the following papers, referred to by Roman numerals in the text:

I. M. Battagin, F. Forabosco, J. H. Jakobsen, M. Penasa, T. J. Lawlor, and M. Cassandro. 2012. International genetic evaluation of Holstein bulls for overall type traits and body condition score. Journal of Dairy Science 95(8), 4721-4731.

II. M. Battagin, F. Forabosco, M. Penasa, and M. Cassandro. 2013. Cluster analysis on across-country genetic correlations for overall type traits and body condition score of Holstein bulls. Livestock Science 151, 108-114.

III. M. Battagin, C. Sartori, S. Biffani, M. Penasa, and M. Cassandro. Genetic parameters for body condition score, locomotion, angularity and production traits in Italian Holstein cattle (*under revision* – Journal of Dairy Science).

IV. Short Communication: Genetic relationship of body condition score, and locomotion with type traits in Italian Holstein cattle (*draft*).

V. M. Battagin, S. Biffani, M. Penasa, and M. Cassandro. 2013. Results of the first international genetic evaluation for body condition score in Italian Holstein Friesian (submitted for the poster session of the XX Congress of Animal Science and Production Association - Bologna, June 11-13, 2013).

Abbreviations

ANAFI = Italian Holstein Breeder Association
ANG = angularity
AUS = Australia

BCS = body condition score
BEL = Belgium
BRF = British Friesian

CAN = Canada
CHE = Swiss black and white Holstein population
CHR = Swiss red Holstein population
CZE = Czech Republic

DEU = Germany
DFR = Dutch Friesian
DFS = Denmark-Finland- Sweden (joint evaluation)
DNK = Denmark

EAAP = European Association for Animal Production
ESP = Spain
EST = Estonia

F:P = fat to protein ratio
FNP = Final point
FRA = France black and white Holstein population
FRR = France red Holstein population

GBR = United Kingdom and Ireland (joint evaluation)
HUN = Hungary
HYS = herd-year-season

IBV = international breeding value
ICAR = International Committee for Animal Recording
IDF = International Dairy Federation
ILQ = Italian selection index of milk quality
ILQM = Italian selection index of milk quality and udder health
INTERBULL = International Bull evaluation services
IRL = Ireland
ITA = Italy

JPN = Japan

LOC = locomotion

MACE = multiple-trait across country evaluation
MRY = Meuse Rhine Yssel
MY = milk yield (kg/d)

NLD = The Netherlands
NZL = New Zealand

OCS = overall conformation score
OFL = overall feet and legs
OUS = overall udder score

PFT = Italian selection index of production, functionality and type
POL = Poland

RDC = Ayrshire

UK = United Kingdom
USA = United States of America

WHFF = World Holstein Friesian Federation

General Introduction

Italian Holstein Friesian breed and its national evaluation

The Italian Holstein Breeder Association (**ANAFI**, Cremona, Italy) is the body that performs genetic evaluation, promotion, valorization and diffusion of the Italian Holstein Friesian since 1945. Like each national association of breed, ANAFI manages the genealogical book of the breed and is the body responsible of the genetic improvement of the breed.

Production traits were the first group of traits subjected to genetic selection. Over the years, milk yield was the trait that played the most important role in the genetic improvement mainly of this breed. The strong selection pressure on milk production makes Holstein Friesian the "dairy type" breed par excellence all over the world. The Italian Holstein population is the first dairy breed in Italy, with 1.128.626 cows controlled in 12,922 herds, and with an average milk production of 9.011 kg of milk/lactation (AIA; 2012).

Conformation was one of the first non-production traits scored and included in the selection indexes of dairy cattle populations around the world (White, 1974; Powell and Norman, 2006; Shook, 2006). From 2000, type traits gained interest as early predictors of functional traits, such as longevity, and they were used to reduce problems of health and fertility in dairy cattle (Mark, 2004; Miglior et al., 2005; Shook, 2006). The Italian Holstein population followed the international deterioration of cows' efficiency, with an increment of costs due to health problems, the high level of somatic cells and the lower feet and legs functionality (Biffani et al., 2002).

Italian Holstein Selection Index

In 1993, the Italian selection index for milk quality (**ILQ**) was implemented with conformation traits related to the udder health (**ILQM**: quality of milk and udder health), with 80% of weight attributed to production traits and 20% to udder heath (ANAFI, 2012b). To stop the decline of functionality, the Italian Holstein selection index has been changed at the beginning of 2002 (Biffani et al., 2002). The new index for Production, Functionality, and Type (**PFT**) reduced the emphasis of production traits (from 80 to 60%) and increased those of functional traits (from 20 to 40%). In 2009 the definition of PFT was update including the aggregate index for fertility, with 10% of weight, and changing the ratio of production to functionality from 60:40 to 49:51 (Canavesi et al., 2009).

International genetic evaluation of dairy bulls

The increasing trade of dairy bull semen, started in 1980s, has led to the increase of genetic links among countries (Powell et al., 1994; Interbull, 2001). Nonetheless, using the genetic evaluations made by one country to evaluate bulls from another country without appropriate conversion is not a good way to compare animals. The differences in breeding objectives and genetic levels across countries may lead to different performances of genetic materials in different environments. In 1983 the International Bull Evaluation Service (**Interbull**, Sweden) was established by the European Association for Animal Products (**EAAP**), the International Dairy Federation (**IDF**), and the International Committee for Animal Recording (**ICAR**) in response to the need for universal comparison criteria of animals across countries (Interbull, 2011c).

Before the establishment of Interbull, for estimating genetic merit of bulls in importing countries, the following regression was recommended by IDF: $EBV_{IMP}=a + b(EBV_{EXP})$, where the intercept (*a*) was the difference in base between the two countries and the scaling factor (*b*) was the ratio of standard deviations of evaluations in the two countries (Powell and Sieber, 1992). The method of conversion equations was improved by Interbull using the Goddard (1985) and Wilmink et al. (1986) procedures. Following, conversion equations were replaced by the multiple-trait across county evaluation (**MACE**) method, but they are still estimated, using the international genetic evaluations instead of the national genetic evaluations as starting values.

Multiple-trait across country evaluation (MACE)

In 1985 Shaeffer developed the first BLUP based method for international genetic evaluation of sires (**MCE**). To solve the problem of some improbable assumptions of MCE (i.e. genetic correlations across countries set to one), Schaeffer, in 1994, extended the MCE model to a MACE. The MACE uses deregressed national EBV as input values to predict international breeding values for bulls of all participating countries. In MACE, similar traits evaluated in different countries are considered different traits. Therefore, it is possible to consider different heritability value for each country and genetic correlations less than one. Moreover, bulls could rank differently in different countries because genotype by environment interaction is allowed.

Over the last 18 years the international evaluation method was refined. A time edit for the birth date of bulls was added to ensure that the base populations are similar for all countries (Weigel and Banos, 1997; de Jong, 2003). Then, the effective daughter contributions (Fikse and Banos, 2001) replaced the number of daughters as weighting factor, 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 reduce problems related to phantom groups (Jakobsen and Dürr, 2012). Other improvements are development and implementation of multiple-trait MACE (Nilforooshan, 2011) and inclusion of genomic information in the evaluation of dairy breeds (VanRaden and Sullivan, 2010; Sullivan et al., 2012; Zumbach et al., 2012).

The first international evaluation took place in August 1994 and included milk production data from the European Nordic countries for the Holstein and Ayrshire breeds. Currently, three official evaluations per year are performed, and 40 traits, grouped in 7 major categories, 6 breeds, and 30 member countries are involved in the routine evaluation for dairy bulls (Interbull, 2012b). 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 score (**OUS**) and overall feet and legs (**OFL**).

Type traits and harmonization

At a national level, type traits are scored as linear traits, composite traits and/or general characteristics. The scoring system for linear traits describes the conformation objectively, from one biological extreme to the other (Shook, 2006), and each trait depicts only one specific part of the cow (ICAR, 2011). Composite traits are groups of linear traits related to one specific area (e.g., frame, dairy strength, udder, feet and legs), and weighed according to the breeding objective of each country (ICAR, 2011). General characteristics are phenotypic assessments and subjective scores that are given for the desirability of the cow according to the national breeding goal (ICAR, 2011).

The World Holstein Friesian Federation (**WHFF**) and ICAR are the bodies involved in the harmonization of animals identification, performance recording for animals, and exchange of information among countries (ICAR, 2012; WHFF, 2012). The improvements of animals' genetic comparison across countries start from the development of common guidelines, with the aim to reduce errors due to different recording systems across countries. For conformation traits, this process started in 1986 at the conference of the European Confederation of black and white breed societies (WHFF,2012), where the harmonization of type traits was one of the main topics. The first report established guidelines for 12 linear traits. During the years, standard definition was developed for other traits, reaching 16 traits, and the number of countries participating in type traits harmonization also increased.

ANAFI has been collecting data on conformation traits since 1971. Initially, the evaluation consisted of assigning a score to a number of anatomical regions of the cow and a final overall merit score. In 1984, the linear system was introduced with the aim of objectively describing the conformation of the animal, from one biological extreme to the other, and a 1 to 50 point scale system was adopted (ANAFI, 2012c). In 1993, the conformation scoring system was adapted to the guidelines provided by WHFF (2008). Currently, all first lactation cows belonging to registered herds are evaluated once for type traits.

Body Condition Score and Locomotion

Two of the most recent traits included in the WHFF guidelines of type traits are body condition score (**BCS**) and locomotion (**LOC**). Body condition reflects the degree of apparent adiposity of the cow; it is a visual measure of the covering of fat covering the tail head and rump. Body condition score has gained notable interest in the last decades as an important management tool in the dairy herd because it can be used as an indicator of overall energy status and of adipose stores mobilization during lactation (Roche et al., 2009). Moreover, BCS can be used as a predictor of the reproduction, health, and welfare status of cows (Boettcher et al., 1998; Roche et al., 2009; Dal Zotto et al., 2007; Zink et al., 2011).

Like other linear traits, different scales were used by each country. WHFF suggests a scale from 1 to 9, ITA used a scale from 1 to 5, other countries, like USA, used a scale from 1 to 50 (Dechow et al. 2004). Regardless of the scale, low values of BCS are given to very thin animals, and high values to very fat ones. ANAFI started to collect data for BCS in 2007 and definition is slightly different from the one of WHFF. The most important areas are rump and loin, in particular the fat reserves of thurl region, the angularity of hips and pins, and the prominence of spinous processes (Edmonson et al., 1989; ANAFI, 2012c).

The first international genetic evaluation for BCS was carried out in 2009 and involved 11 countries. Seven countries used direct measures of BCS and the remaining 4 used a best predictor, which was angularity (**ANG**) for Italy and France black and white, dairy form for USA, and muscularity for France Red Holstein (Interbull, 2012a). During the following years other countries jointed the Interbull evaluation for BCS, namely Czech Republic in 2010 and Japan in 2011. In 2012 United Kingdom and Ireland started to send data separately, and France black and white started to send BCS data instead of ANG (Interbull, 2012b).

Locomotion evaluates the length of the step and direction of rear legs in movement. Locomotion has been defined and investigated since 1980s as predictor of lameness, reproductive performance, and foot and leg diseases which could be responsible for reduction of animal welfare, economic losses for the farmer, and involuntary culling (Boettcher et al., 1998; van der Waaij et al., 2005; Onyiro et al., 2008). ANAFI collects data for LOC since 2009, using a scale from 1 to 50 points. Low values are given for lame animals, while high values for animals with an excellent LOC (ANAFI, 2012c). The direction of the scale used by ANAFI follows the guidelines of WHFF (2008), and it is reversed compared to the scale reported in literature (Manson and Leaver, 1988; Boettcher et al., 1998; Van Dorp et al., 2004).

Locomotion entered the Interbull portfolio in 2009, but 6 out of 10 countries that started the international evaluation for this trait used other related type traits (e.g., rear leg set rear view or feet and legs) as best predictors (Interbull, 2012a).

Overall traits

Currently, linear traits for the Holstein breed are expected to be similarly defined across countries because of the harmonization process developed by WHFF (Mark, 2004), whereas overall traits are heterogeneous and depend on the specific national breeding goals (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 (Miglior et al., 2004, 2007; Canavesi et al., 2006; Lawlor, 2012). When similar traits evaluated in two 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).

Aims of the thesis

The general aims of the thesis were to study the status of international genetic evaluation of body condition score (BCS) and overall traits (Papers I and II), to estimate genetic variance of BCS and estimated its genetic correlations with related traits in Italian Holstein Friesian (Papers III and IV), and finally reported the results of the first international genetic evaluation with BCS as direct trait in Italian Holstein bulls (Paper V). In more details, the study was conducted following two major lines: the international evaluation and the national evaluation.

For the international evaluation, data from Interbull were used. In the first step, an overall investigation was done to clarify differences and similarities among countries that participated to the international evaluation for BCS, overall conformation score (OCS), overall udder score (OUS), and overall feet and legs (OFL). Publication policy, and the use of IBV at national levels were discussed, and the status of genomic evaluation for these traits was documented. In the second step, a deeper analysis on the progress in traits harmonization over time for those traits was done.

For the national evaluation, field data from Italian Holstein Breeder Association (ANAFI) were used. Heritability of BCS was estimated and the genetic and phenotypic correlations of BCS with locomotion (LOC), production traits (milk yield, fat and protein content, and fat to protein ratio), and type traits were estimated. Understanding if BCS is a heritable characteristic could address future national breeding strategies to improve this trait in the Italian Holstein population. After the investigation on the status of international evaluation for BCS, and after the estimation of national genetic parameters for BCS, in the last step of this thesis the results of the first international evaluation using BCS as direct trait were analyzed.

International genetic evaluation of Holstein bulls for overall type traits and body condition score

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Abstract

The study documents the procedures used to estimate genetic correlations among countries for overall conformation (OCS), overall udder (OUS), overall feet and legs (OFL), and body condition score (BCS) of Holstein sires. Major differences in traits definition are discussed, in addition to the use of international breeding values (IBV) among countries involved in international genetic evaluations, and similarities among countries through hierarchical clustering. Data were available for populations from 20 countries for OCS and OUS, 18 populations for OFL, and 11 populations for BCS. The IBV for overall traits and BCS were calculated using a multi-trait across-country evaluation model. Distance measures, obtained from genetic correlations, were used as input values in the cluster analysis. Results from surveys sent to countries participating in international genetic evaluation for conformation traits showed that different ways of defining traits are used: the overall traits were either computed from linear or composite traits or defined as general characteristics. For BCS, populations were divided into 2 groups: one scored and evaluated BCS, and one used a best predictor. In general, populations were well connected except for Estonia and French Red Holstein. The average number of common bulls for the overall traits ranged from 19 (OCS and OUS of French Red Holstein) to 514 (OFL of United States), and for BCS from 17 (French Red Holstein) to 413 (the Netherlands). The average genetic correlation (range) across countries was 0.75 (0.35 to 0.95), 0.80 (0.41 to 0.95), and 0.68 (0.12 to 0.89) for OCS, OUS, and OFL, respectively. Genetic correlations among countries that used angularity as best predictor for BCS and countries that scored BCS were negative. The cluster analysis provided a clear picture of the countries distances; differences were due to trait definition, trait composition, and weights in overall traits, genetic ties, and genotype by environment interactions. Harmonization of trait definition and increasing genetic ties could improve genetic correlations across countries and reduce the distances. In each national selection index, all countries, except Estonia and New Zealand, included at least one overall trait, whereas none included BCS. Out of 18 countries, 9 have started genomic evaluation of conformation traits. The first were Canada, France, New Zealand, and United States in 2009, followed by Switzerland, Germany, and the Netherlands in 2010, and Australia and Denmark-Finland-Sweden (joint evaluation) in 2011. Six countries are planning to start soon.

Key words: overall conformation trait, body condition score, international evaluation, cluster analysis

Introduction

Conformation was one of the first nonproduction traits scored and included in the selection indices of dairy cattle populations around the world (White, 1974; Powell and Norman, 2006; Shook, 2006). Conformation is often referred to as an early predictor of functional traits, such as longevity, and it is used to reduce the deterioration of health and fertility in dairy (Mark, 2004; Miglior et al., 2005; Shook, 2006), dual-purpose (Sölkner et al., 2000), and beef cows (Forabosco et al., 2004). At a national level, type traits are scored as linear traits, composite traits, or general characteristics. The scoring system for linear traits describes the conformation objectively, from one biological extreme to the other (Shook, 2006), and each trait depicts only one specific part of the cow (ICAR, 2011). Composite traits are groups of linear traits related to one specific area (e.g., frame, dairy strength, udder, feet and legs) and are weighted according to the breeding objective of each country (ICAR, 2011). General characteristics are phenotypic assessments and subjective scores are given for the desirability of the cow according to the national breeding goal (ICAR, 2011). The World Holstein Friesian Federation (**WHFF**) and International Committee for Animal Recording (**ICAR**) established specific guidelines for definition of conformation traits, data recording, genetic evaluation, and publication of type proofs for bulls.

The term “overall traits” will be used hereafter to summarize conformation traits that are not linearly scored and that are internationally evaluated; namely, overall conformation (**OCS**), overall udder (**OUS**), and overall feet and legs (**OFL**).

One of the newest traits recognized by WHFF is BCS, defined as “the covering of fat over the tail head and rump” (WHFF, 2008). Body condition score reflects the degree of apparent adiposity of the cow and it can be used as an indicator of overall energy status; changes in BCS reflect mobilization of adipose tissue stores during lactation (Roche et al., 2009). In addition, BCS is an important management trait in the dairy herd as it can be used as a predictor of the reproduction, health and welfare status of cows (Dal Zotto et al., 2007; Roche et al., 2009; Bastin et al., 2010).

The International Bull Evaluation Service (**Interbull**, Uppsala, Sweden) was established in 1994 to provide international estimated breeding values (**IBV**) for dairy bulls. The multiple across-country evaluation (**MACE**) method, developed by Schaeffer (1994) and refined in the following years (Sigurdsson et al., 1996; Sullivan, 1999; Fikse and Banos, 2001), uses deregressed national EBV as input values to predict IBV for bulls of all participating countries. Interbull is developing methodology to include the genomic information in the evaluation of dairy breeds (VanRaden and Sullivan, 2010; Sullivan et al., 2012; Zumbach et al., 2012).

The first routine international genetic evaluation for conformation traits of Holstein bulls was carried out in 1999 and involved 10 countries. Currently, 19 countries participate in the evaluation that includes 18 linear traits and 3 overall traits (OCS, OUS, and OFL) recorded on 5 breeds (Interbull, 2011b). International genetic evaluation for BCS was added to the service portfolio in January 2009 with data on Holstein bulls from 10 countries (Interbull, 2011b).

Linear traits for the Holstein breed are expected to be similarly defined across countries because of the harmonization process developed by WHFF (Mark, 2004), whereas overall traits are heterogeneous and depend on the specific national breeding goals (Shook, 2006). Recently, countries participating in international genetic evaluations have discussed the efficiency of MACE to evaluate overall traits when those traits are not consistently defined across countries (Canavesi et al., 2006). When trait definitions vary between countries, the genetic correlations are low (Miglior et al., 2004). Then, domestic bulls (or bulls with daughters in a specific country) are favoured over foreign bulls (or bulls with only daughters that are not in the specific country; Canavesi et al., 2006). Previous research has suggested the use of linear traits to derive overall traits instead of using general characteristics or subjective scores in international genetic evaluations (Miglior et al., 2004; Canavesi et al., 2006).

The objectives of this study were (1) to report differences and similarities among countries for overall traits (OCS, OUS, and OFL) and BCS in the Holstein breed; (2) to discuss the publication policy and use of IBV at national levels among member organizations involved in the routine international evaluation; and 3) to document the status of genomic evaluation for these traits.

Materials and Methods

National Evaluation Procedures

A survey on OCS, OUS, OFL, and BCS of Holstein cattle was sent to countries participating in international genetic evaluation. The main aim of the survey was to collect detailed information on composition, computation, and use of overall traits in the selection index, and to document the progress of genomic evaluation in member countries. In addition, supplementary information about the publication policy of the above traits was retrieved.

International Genetic Evaluation

Data. Twenty populations [Australia (**AUS**), Belgium (**BEL**), Canada (**CAN**), Czech Republic (**CZE**), Denmark-Finland-Sweden (**DFS**), Estonia (**EST**), French Black and White (**FRA**) and Red (**FRR**) Holstein, Germany (**DEU**), Hungary (**HUN**), Italy (**ITA**), Japan (**JPN**), New Zealand (**NZL**), Spain (**ESP**), Swiss Black and White (**CHE**) and Red (**CHR**) Holstein, Poland (**POL**), the Netherlands (**NLD**), the United Kingdom and Ireland (**GBR**), and the United States (**USA**)] provided information on Holstein bulls to compute the April 2011 routine international genetic evaluation for OCS and OUS (Table 1). For OFL and BCS, data were from 18 (Table 1) and 11 (Table 2) populations, respectively.

Procedure. International genetic evaluations can be divided into 2 main steps: (1) deregression, within-country sire variance estimation, and correlation estimation between countries; and (2) deregression, within-country sire variance estimation, and breeding value prediction. Step 1 as applied to Holstein conformation traits is described. To be included in the international evaluation, Interbull required country of first test proofs of AI bulls with at least 10 daughters, or 10 effective daughter contributions in at least 10 herds. Only Holstein bulls born from 1970 onward were included for correlation estimation. The quality of international genetic evaluations depends on the quality of national data. For this reason, a national genetic evaluation model for conformation traits must pass the trend validation test (Boichard et al., 1995) for stature and fore udder attachment and be within the limit of 5% change in sire standard deviation between 2 succeeding official evaluations (Jakobsen and Hjerpe, 2006). In addition, countries are encouraged to verify changes in genetic evaluations (Klei et al.,

Table 1. Information on overall conformation (OCS), overall udder (OUS), and overall feet and legs (OFL) across countries in international genetic evaluations

Country[1]	Classification[2]			Common bulls[3]	Heritability[3]		
	OCS	OUS	OFL		OCS	OUS	OFL
AUS	C	C	bp[4]	207	0.300	0.300	0.210
BEL	C	L	L	213	0.359	0.238	0.132
CAN	C	L	L	361	0.261	0.247	0.152
CHE	na[5]	na[5]	na[5]	170	0.253	0.210	0.165
CHR	C	L	L	123	0.340	0.370	0.220
CZE	C	L	L	297	0.252	0.197	0.121
DEU	C	C	C	379	0.260	0.225	0.182
DFS	L	L	L	343	0.300	0.250	0.200
ESP	L	L	C	283	0.240	0.250	0.150
EST	C	S	S	34	0.270	0.310	0.140
FRA	L	L	S	264	0.300	0.300	0.100
FRR	C	S	-	19	0.310	0.410	-
GBR	C	S	S	455	0.310	0.259	0.153
HUN	S	S	S	253	0.200	0.120	0.150
ITA	L	L	C	423	0.240	0.280	0.100
JPN	C	S	S	110	0.270	0.200	0.130
NLD	C	S	S	495	0.300	0.340	0.170
NZL	L	L	-	203	0.190	0.230	-
POL	L	L	L	250	0.280	0.150	0.100
USA	C	L	L	514	0.310	0.230	0.170

[1] AUS = Australia; BEL = Belgium; CAN = Canada; CHE = Switzerland (Black and White Holstein); CHR = Switzerland (Red Holstein); CZE = Czech Republic; DEU = Germany; DFS = Denmark-Finland-Sweden; ESP = Spain; EST = Estonia; FRA = France (Black and White Holstein); FRR = France (Red Holstein); GBR = United Kingdom and Ireland; HUN = Hungary; ITA = Italy; JPN = Japan; NLD = the Netherlands; NZL = New Zealand; POL = Poland; USA = United States. [2] Method to define traits: S = subjective; L = computed from linear traits; C = computed from a set of composite traits or composite traits and linear traits. [3] Mean number of common bulls for OCS, OUS, and OFL, and heritability provided by the countries participating in April 2011 international multiple-trait across-country routine evaluation (MACE). [4] BP = best predictor. [5] NA = not available.

Table 2. Information on BCS across countries

Country[1]	Trait definition	Data since	Evaluation[2]		Common bulls[3]	heritability
			NN	INT		
AUS	covering of fat over the tail head and rump	na[4]				
BEL	covering of fat over the tail head and rump	2006	x	x	195	0.370
CHE	linear score (Edmonson et al., 1989)	1992	x	x	135	0.171
CHR	covering of fat over the tail head and rump	2005				
CZE	covering of fat over the tail head and rump	2006	x	x	195	0.275
DEU	covering of fat over the tail head and rump	2005	x	x	278	0.247
DFS[5]	covering of fat over the tail head and rump	2002	x	x	175	0.230
ESP	covering of fat over the tail head and rump	2002	x			
EST	covering of fat over the tail head and rump	2008				
FRA	Subjective visual assessment	2009	x	bp	225	0.280
FRR				bp	17	0.360
GBR	relative fatness or body condition of the cow	1996	x	x	377	0.268
HUN	na[4]	2005				
ITA	pelvic and lumbar region	2007		bp	na[4]	0.230
JPN	covering of fat over the tail head and rump	2007				
NLD	covering of fat over the tail head and rump	1998	x	x	413	0.350
NZL	Visual estimate of body fat reserves	2000	x			
POL	covering of fat over the tail head and rump	2008				
USA	scored as dairy form or angularity (1-50). 1 is low dairy form or very fat; 50 is high dairy form or very thin.	na[4]		bp	380	0.310

[1] AUS = Australia; BEL = Belgium; CHE = Switzerland (Black and White Holstein); CHR = Switzerland (Red Holstein); CZE = Czech Republic; DEU = Germany; DFS = Denmark-Finland-Sweden; ESP = Spain; EST = Estonia; FRA = France (Black and White Holstein); FRR = France (Red Holstein); GBR = United Kingdom and Ireland; HUN = Hungary; ITA = Italy; JPN = Japan; NLD = the Netherlands; NZL = New Zealand; POL = Poland; USA = United States. [2] × = countries that had national (N) or international (INT) evaluation for BCS; BP = countries that used a best predictor. [3] Mean number of common bulls for BCS and heritability provided by the countries participating in April 2011 international multiple-trait across-country routine evaluation (MACE). [4] NA = not available. [5] Only Denmark evaluated BCS.

2002) before submitting data to Interbull. National EBV were first deregressed within country to obtain variables independent of all effects included in the international sire model (Sigurdsson and Banos, 1995). Then, genetic parameters (sire variance within country and genetic correlations between countries) were estimated by Interbull at the test run in January 2011, with the expectation maximization (EM) algorithm for REML procedure described by Klei and Weigel (1998).

Because of computational limits, genetic correlations were estimated from subsets of data, and at most 10 countries at a time were included, using only bulls that had multiple proofs in different countries plus full-sibs or three-quarter sibs of such bulls. Countries were grouped into triplets, with the USA as the link between any other 2 groups. Genetic correlations for all country pairs were estimated by considering all possible combinations of triplets.

Heritability values used for the international evaluations were those provided by the countries. Pedigree was traced back as far as possible to increase across-country connections. Genetic groups for unidentified parents were defined according to national origin, breed and birth year of the bull, and path of selection (sires, maternal grandsires, and maternal granddams). Minimum group size was set to 30 (Interbull, 2011d).

Cluster Analysis

Data used in the cluster analysis consisted of across-country genetic correlations estimated by Interbull during the January 2011 test run and used for the April 2011 routine genetic evaluation (Interbull, 2011a). Hierarchical clustering was performed using the CLUSTER procedure (SAS Institute, 2008) to visualize the similarity between countries for OCS, OUS, OFL, and BCS. The distance (d_{ij}) between countries *i* and *j* was calculated as $d=1-rG^2$, where rG_{ij} is the genetic correlation between countries *i* and *j*. Dendrograms were plotted using the TREE procedure (SAS Institute, 2008).

Results and Discussion

Trait Definition

Overall Conformation. Out of 20 populations, 12 included composite traits, 6 used linear traits, and only 1 subjectively described the OCS (Table 1). The most common traits used in the composition of OCS were OUS and OFL (Table 3). The weight of OUS and OFL ranged from 30 to 50% and from 15 to 35%, respectively (data not shown). Dairy strength was adopted by 4 populations and given a weight ranging from 10 to 25%; 3 populations used overall dairy type (from 10 to 30% of weight) and frame (from 15 to 25%). Other traits included in the composition were overall body including rump, overall teats, aspect, front and capacity, and overall development (Table 3).

Among the 18 linear traits evaluated by Interbull (Interbull, 2011b), only BCS was not included by any population, whereas 2 traits that were not internationally evaluated were used: chest depth and topline. Both ITA and ESP used 15 linear traits, followed by FRA (10), DFS (7), and POL (3). The most common traits were rump width, followed by rump angle, angularity, and stature (Table 3).

The differences in OCS definition led to differences in how countries publish the IBV for this trait (Miglior et al., 2007). For example, GBR had 2 OCS, 1 for domestic and 1 for international use. The GBR international index for OCS is linearly composed of several type traits and it is a good predictor of the US index for OCS. Since 2004, CAN has adopted a blending approach for IBV of overall traits, which optimizes the use of all information from Interbull evaluations (Miglior et al., 2004).

Overall Udder. Out of 20 populations, 11 computed OUS from linear traits, 2 used composite traits, and 6 assessed OUS subjectively as visual judgment of overall udder (Table 1). All linear traits related to udder and evaluated by Interbull (Interbull, 2011b) were included in the computation. Udder depth, rear udder height, and udder support were included by 10 populations, front teat placement and fore udder attachment by 8, and rear teat placement and teat length by 5 (Table 3). In addition, other traits were used that are not internationally evaluated; namely, udder width, rear udder width, udder texture, udder balance, fore udder length, and teat thickness (Table 3). Overall udder in DEU is a combination of a subjective score (25% of the weight) and linear traits evaluated by Interbull (75% of the weight; Table 3). Despite the differences in the OUS composition, this trait was quite homogeneous. Countries that composed OUS by linear traits gave from 15 to 45% of weight to udder depth, 10 to 22% to udder support, and 10 to 20% to rear udder height. Among countries that assessed OUS subjectively, FRR and NLD referred to an overall visual judgment of udder, and GBR and JPN focused attention on the strength and quality of the fore and rear udder attachments and of the central ligament and on udder texture.

Overall Feet and Legs. Neither FRR nor NZL evaluated OFL. Of the remaining 18 populations, 7 computed OFL using linear traits, 2 using composite traits, 7 scored this trait subjectively, and 1 used a best predictor (Table 1). When OFL was composed of linear traits, rear leg set side view, rear leg set rear view, and foot angle traits were used by 6 populations, and locomotion by 3 (Table 3). To assess OFL, other traits not evaluated by Interbull were used; namely, hock quality, bone quality, body quality, and height of hoof (Table 3). Canada included defective characteristics in its composition of OFL (Holstein Canada, 2011). Two countries (ITA and DEU) combined subjective measurements with linear traits and they gave 50 to 55% of weight to functionality of feet and legs (ITA) and feet and legs score (DEU). Linear traits included by these countries were rear leg set side view, rear leg set rear view (ITA and DEU), foot angle (DEU), locomotion, hock quality (DEU), and hoof depth (ITA; Table 3). When OFL was assessed as a general characteristic, locomotion was recorded by FRA and GBR, whereas JPN evaluated the length of legs in relation to the depth of body, standing wide apart, clean-cut and strong with light and sound walk. Both NLD and ESP gave an overall judgment of feet and legs, whereas AUS did not evaluate OFL nationally and sent to Interbull "side view foot diagonal" as a best predictor.

BCS. Body condition score is one of the newest traits evaluated by Interbull and is defined by WHFF as "the covering of fat over the tail head and rump" (ICAR, 2011). Table 2 lists the

Table 3. Traits used by countries for the definition of OCS, OUS and OFL

Country[1]	Trait[2]		
	OCS	OUS	OFL
BEL	ODE, ODT, OFL, ORU, OUS	FTP, FUA, RTP, RUH, RUW, TLN, UBL, UDT, USP, UTX	BNQ, FAN, RLR, RLS
CAN	DST, OFL, ORU, OUS	Soft, high, wide and strongly attached, good teat length and placement (linear traits)	Widely placed legs, intermediate curvature, and a step foot with a deep heel (linear traits and defective characteristics)
CHR	OFL, ORT, OTE, OUS	FUA, FUL, RUH, UDT, USP, UTX	FAN, HHF, HKQ, LOC, RLR, RLS
CZE	DST, FRM, OFL, OUS	FTP, FUA, RTP, RUH, TLN, UDT, USP, UWD	BDQ, FAN, LOC, RLR, RLS
DEU	OBR, ODT, OFL, OUS	FTP, FUA, RTP, RUH, TLN, UDT, USC, USP	FAN, FLS, HKQ, LOC, RLR, RLS
DFS	ANG, BDP, CWD, RAN, RWD, STA, TOP	FTP, FUA, RTP, RUH, TLN, TTK, UBL, UDT, USP	BNQ, FAN, HKQ, RLR, RLS
ESP	ANG, BDP, CWD, FAN, FTP, FUA, RAN, RLR, RLS, RUH, RWD, STA, TLN, UDT, USP	FTP, FUA, RUH, UDT, USP	FAN, RLR, RLS, SFL
EST	OFL, OUS	WHFF	WHFF
FRA	CDP, FTP, LOC, RTP, RUH, RWD, STA, TLN, UDT, USP	FTP, RTP, RUH, TLN, UDT, USP	Visual assessment of locomotion
FRR	ASP, OUS	Visual assessment of animals	-
GBR	LON, OFL, OUS	Strength and quality of the fore and rear udder attachment, strength of central ligament, udder texture	Shape and quality of legs and feet, resulting in good locomotion.
ITA	ANG, BDP, CWD, FAN, FTP, FUA, LOC, RAN, RLR, RLS, RUH, RWD, STA, UDT, USP	FTP, FUA, RUH, UDT, USP	FLF, HHD, RLR, RLS
JPN	DST, FRM, OFL, OUS	Udder being strongly attached and fully capacious, and quarters well-balanced, fine texture	Length well proportioned with the depth of body, standing wide apart, clean-cut and strong with light and sound walk
NLD	DST, FRM, OFL, OUS	Overall judgment of the udder	Overall judgment of feet and legs
NZL	Traits pertaining dairy conformation including those body linear traits	Traits pertaining to the udder including those udder linear traits	-
POL	ANG, RAN, RWD	FTP, FUA, RUH, TLN, UDT, USP, UWD	FAN, RLR, RLS
USA	DST, F&C, OFL, ORU, OUS	FTP, FUA, RTP, RUH, RUW, UDT, USP	FAN, LOC, RLR, RLS

[1] BEL = Belgium; CAN = Canada; CHR = Switzerland (Red Holstein); CZE = Czech Republic; DEU = Germany; DFS = Denmark-Finland-Sweden; ESP = Spain; EST = Estonia; FRA = France (Black and White); FRR = France (Red Holstein); GBR = United Kingdom and Ireland; ITA = Italy; JPN = Japan; NLD = The Netherlands; NZL = New Zealand; POL = Poland; USA = The United States of America. [2] ANG = angularity; ASP = aspect; BDP = body depth; BDQ = body quality; BNQ = bone quality; CDP = chest depth; CWD = chest width; DST = dairy strength; F&C = front and capacity; FAN = foot angle; FLF = feet and legs functionality; FLS = feet and legs score; FRM = frame; FTP = front teat placement; FUA = fore udder; FUL = fore udder length; HHD = hoof depth; HHF = height of hoof; HKQ = hock quality; LOC = locomotion; LON = longevity; OBR = overall body including rump; ODE = overall development; ODT = overall dairy traits; OFL = overall feet & legs; ORU = overall rump; OTE = overall teats; OUS = overall udder; RAN = rump angle; RLR = rear leg set rear view; RLS = rear leg set side view; RTP = rear teat placement; RUH = rear udder height; RUW = rear udder width; RWD = rump width; SFL = subjective feet and legs; STA= stature; TLN = teat length; TOP = topline; TTK = teat thickness placement back; UBL = udder balance; UDT = udder depth; USC = udder score; USP = udder support; UTX = udder texture; UWD = udder width; WHFF = World Holstein Friesian Federation definition.

populations that took part in the international evaluation for BCS as well as populations that did not send BCS data to Interbull but had recordings of the trait or had only national evaluation. Out of 11 populations that have international evaluation, 5 used the WHFF definition to describe this trait, 1 described BCS as “the relative fatness or body condition of the cow,” 1 used the linear scale of Edmonson et al. (1989), and 4 used best predictors: angularity (FRA and ITA), opposite of angularity (USA), and muscularity (FRR). Angularity was defined differently by FRA, ITA, and USA; FRA used a “subjective visual assessment of animals,” ITA followed the definition of WHFF (the angle and spring of the ribs), and USA the sharpness and flatness of bone. Muscularity is intended by FRR as the opposite of angularity. Out of the 8 populations that did not participate in international evaluation for BCS, 6 defined the trait as indicated by WHFF, 1 (NZL) used a visual estimate of cow body fat reserves, and 1 (HUN) had no information available (Table 2).

Genetic Ties

Genetic ties among populations are an important factor when estimating genetic correlations, and an increase in the number of common bulls increases the precision of the estimation (Interbull, 2011d). Generally populations were well connected, except for EST and FRR. The average number of common bulls for the overall traits ranged from 19 (OCS and OUS of FRR) to 514 (OFL of USA), and for BCS from 17 (FRR) to 413 (NLD). For overall traits, the strongest connection, on average, was between USA and CAN (1,216), USA and GBR (986), and USA and NLD (968). For BCS, the highest numbers of common bulls were between USA and GBR (918), USA and NLD (738), and GBR and NLD (725).

Heritability and Genetic Correlation

Heritabilities, as provided by the national evaluation centers (Tables 1 and 2), ranged from 0.190 (NZL) to 0.359 (BEL) for OCS, 0.120 (HUN) to 0.410 (FRR) for OUS, 0.100 (FRA, ITA and POL) to 0.220 (CHR) for OFL, and 0.171 (CHE) to 0.370 (BEL) for BCS.

The matrices of across-countries genetic correlations are available on the Interbull website (Interbull, 2011a). The average genetic correlation across countries was 0.75, 0.80, and 0.68 for OCS, OUS, and OFL, respectively. For OCS, values ranged from 0.35 (POL-NZL) to 0.95 (CHE-CHR); the populations with the highest and the lowest average estimates were GBR (0.83) and POL (0.61), respectively. Genetic correlations for OUS ranged from 0.41 (AUS-DFS) to 0.95 (CAN-CHE/ USA); the highest and lowest average estimates were 0.87 (CHE and USA) and 0.63 (POL), respectively. For OFL, genetic correlations ranged from 0.12 (AUS- DFS) to 0.89 (CHE-CHR), and the highest and lowest average estimates were 0.75 (USA) and 0.35 (AUS), respectively. Genetic correlations for BCS showed negative values between populations that used angularity as best predictor (FRA, ITA, USA) and populations that scored BCS (CHE, CZE, DEU, DFS, GBR, and NLD). The negative correlations were due to differences in trait definitions; that is, BCS had low scores for skinny cows and high scores for fat cows, whereas angularity had low values for cows that lacked angularity and high values for those with very angular and open ribs. The FRR population was positively correlated with populations that scored BCS because this country uses muscularity as best predictor. Genetic correlations ranged from −0.50 (DFS-FRA) to 0.95 (CHE-NLD and DEU-CZE/NLD). The average genetic correlation in absolute value was 0.77, with the highest estimate for CZE, DEU, and NLD (0.82) and the lowest for FRA (0.64).

Across-country genetic correlations were less than unity for several reasons: different origins of the data and trait definitions, interaction between genotype and country-environment, differences in national genetic procedures, weak genetic ties, and erroneous identification of bulls between countries (Mark, 2004).

Cluster Analysis

Overall Conformation. Figure 1a depicts the dendrogram of OCS: AUS, NZL, and POL were the most distant from the rest of the countries. Australia and NZL were grouped in the same cluster, probably because the environment and the production systems are alike, leading to similar breeding goals, and because of the high number of common bulls. The high distance of POL could be explained by a difference in trait definition, as only 3 linear traits were used in the composition of OCS (Table 3), and by the relative low number of bull ties (on average, 234 common bulls). Three of the main clusters linked are CZE, HUN, EST (first cluster); DEU, GBR, NLD, USA and DFS (second cluster); and ESP, FRA, ITA (third cluster). All those populations, except HUN, defined OCS from linear or composite traits (Table 1); CZE, EST, DEU, GBR, NLD, and USA gave 35 to 40% of weight to OUS and 15 to 30% to OFL. The DFS population did not include traits related to udder and feet and legs in the computation of OCS, and could be tied with these populations because of the high number of common bulls, which ranged from 506 (DEU) to 724 (NLD). The populations with the highest number of linear traits included in the computation were ESP, ITA, and FRA (Table 3).

The 2 Swiss populations, Black and White (CHE) and Red and White (CHR), were the 2 most similar for OCS, probably because they have common ancestors, and they were linked to CAN and JPN. The definition of OCS for CAN and CHR was similar (Table 3), whereas JPN defined OCS as did CZE and NLD, with small difference on the weights, but showed the highest genetic correlations with CHE (0.91), CHR (0.89), and CAN (0.91). Another branch of the dendrogram was composed of BEL and FRR. They gave different definitions of OCS (Table 3), but “aspect” of FRR was a general trait that could include the traits computed by BEL; moreover, the number of Red and White bulls in BEL was high, which could explain the similarity with FRR population. The cluster analysis for OCS shows that countries with similar trait definition are usually linked, but the number of common bulls also influences the position of a country in the genetic tree.

Overall Udder. The cluster of OUS (Figure 1b) showed 2 main branches. In the first branch, POL, AUS, and NZL were the most distant countries. The high distance of POL is due to very low genetic correlations between POL and the other populations, which ranged from 0.55 (FRA) to 0.73 (DEU). Trait definition of POL is similar to that of the countries that defined OUS from linear traits (Table 3). Australia and NZL were better linked to other countries for this trait than for OCS, and DEU could be linked with NLD because of the high number of common bulls and with GBR because of the similarity of trait definition: the traits that DEU used in the computation were related to the subjective definition that GBR gave (Table 3). Canada and CHE showed the lowest distances and were linked with USA and JPN. The trait definition was similar for CAN (Holstein Canada, 2011) and JPN, and related to the linear traits used by USA (Table 3).

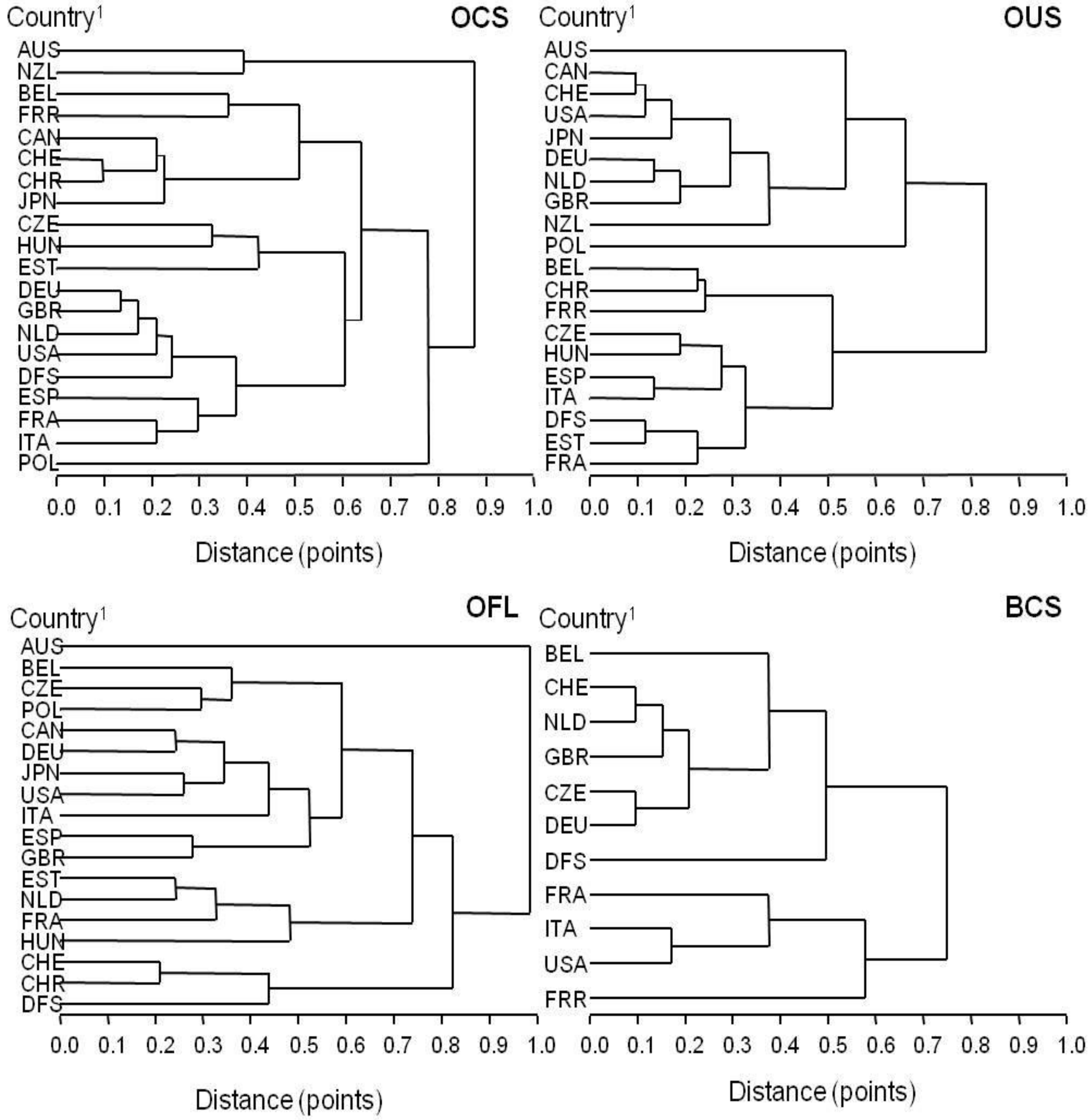

Figure 1. Dendrograms from cluster analysis of (a) overall conformation (OCS), (b) overall udder (OUS), (c) overall feet and legs (OFL) and (d) BCS, using distances calculated from genetic correlations among countries for the April 2011 Interbull (Uppsala, Sweden) routine evaluation for Holstein breed. Countries: AUS = Australia; BEL = Belgium; CAN = Canada; CHE = Switzerland (Black and White Holstein); CHR = Switzerland (Red Holstein); CZE = Czech Republic; DEU = Germany; DFS = Denmark-Finland-Sweden; ESP = Spain; EST = Estonia; FRA = France (Black and White Holstein); FRR = France (Red Holstein); GBR = United Kingdom and Ireland; HUN = Hungary; ITA = Italy; JPN = Japan; NLD = the Netherlands; NZL = New Zealand; POL = Poland; USA = United States.

The second branch was composed of BEL, CHR, FRR, linked with CZE, HUN, ESP, ITA, and DFS, EST and FRA. The red populations (CHR and FRR) are in the same cluster with BEL. The high number of Red and White bulls in BEL could explain the similarity with CHR and FRR. Both ITA and ESP used the same linear traits (Table 3) and they were linked with CZE and HUN. Population CZE computed OUS using the same traits of ITA and ESP, with the addition of 3 other traits (udder width, fore udder attachment, and teat length). Hungary was linked with CZE and ITA because of the high number of common bulls. Denmark-Finland-Sweden and EST were very similar: DFS used linear traits in the computation, whereas EST used a subjective description. The FRA population had the highest genetic correlation with DFS and composed OUS using linear traits similar to those used by DFS (Table 3).

Among overall traits, the average genetic correlation across countries was highest for OUS, suggesting a good harmonization in trait definition. We did not, however, observe a clear distinction between populations that defined OUS from linear traits and populations that used a subjective scoring.

Overall Feet and Legs. The most distant population in the cluster of OFL (Figure 1c) was AUS, followed by the cluster of CHE, CHR, and DFS. Australia used “side view foot diagonal” as the best predictor of OFL, whereas CHE, CHR, and DFS computed OFL from linear traits. The similarity of traits used could explain the link between DFS and the 2 Swiss populations. Populations that defined OFL subjectively (i.e., EST, NLD, FRA, and HUN) were grouped in one cluster (Table 3). Another branch was formed by BEL, CZE, and POL. They used a composition of linear traits with small differences among populations (Table 3). The FRR population did not have an international evaluation of OFL; thus BEL, clustered with FRR for OCS and OUS, changed cluster for OFL.

Spain had the highest number of common bulls with GBR (516); ITA followed the GBR and ESP pair, and it was linked to JPN, USA, CAN, and DEU. Japan defined OFL subjectively, whereas USA gave 50% of the weight to locomotion, ITA and DEU gave 50% of the weight to “feet and legs score” and “feet and legs functionality,” and CAN used linear traits, respectively (Table 3).

Compared with OCS and OUS, OFL showed the highest distance between countries. Trait definition influenced this higher distance because the “subjectivity” in trait definition was more pronounced.

BCS. As reported in the paragraph on trait definition, we observed 2 groups of populations that participated in international evaluation for BCS, 1 that scored and used BCS, and 1 that used a best predictor (Table 2). This distinction is clearly depicted by the cluster analysis (Figure 1d). Italy, USA, and FRA, all using angularity as the best predictor, had a maximum distance of 0.38; FRR was the most distant due to the use of muscularity. The other branch was composed of DFS and BEL, followed by GBR, NLD, CHE, and CZE, and DEU having DFS as the most distant of this group. Of the 3 countries that comprised DFS, only Denmark sent data for BCS evaluation. Our results for BCS were comparable to those of the pilot study conducted by Lawlor and Klei (2008); in their work, BEL was linked with USA in the cluster of populations that used a best predictor, but since August 2010 the genetic evaluation of BCS in BEL was modified (Interbull, 2011b), which could explain the different allocation of this population.

Selection Indices

Out of 18 populations, 16 included at least one overall trait in its own selection index, whereas no population included BCS. Out of these 16 populations, 8 included OCS, 11 included OUS, and 12 included OFL. Australia, CHR, FRA, and FRR included only OCS; CZE included only OFL; DEU, DFS, ESP, GBR, HUN, JPN, and NLD included OUS and OFL; and the other populations (BEL, ITA, POL, and USA) included all overall traits. The dynamism of the selection index leads to a reduction of the emphasis of production traits, which ranged from 60 to 100% in the study of Leitch (1994), increasing the importance of durability, health, and reproduction traits. Within durability, conformation traits provided the largest contribution (Miglior et al., 2005).

The major reasons for including OCS in the selection index were to improve functional traits (Sewalem et al., 2004) and increase height (FRA, FRR), because of the influence on survival (AUS) and lifetime profitability (BEL), positive correlation with longevity (CHE), breeders' desire for a balance of type and production (ITA), as an important subindex in sire of dam selection (POL), and for profit (USA). The OUS and OFL traits were included in the selection index mainly to improve longevity (DFS, ESP, GBR, ITA), to improve lifetime profitability (BEL) and productivity (JPN), for breeders' desire (ESP, NLD), for profit (USA) and cost reduction (DFS), to improve functional traits (DEU, ITA) and workability (DFS), and as an important subindex in sire of dam selection (POL). Moreover, OUS was important to prevent pathologies of udder (ESP, GBR, ITA), and OFL as a good predictor of feet and leg problems [e.g., lameness and digital dermatitis (GBR)] and because of the relationship with fertility (ITA). The survey answers confirmed the importance of conformation to improve functional herd life; that is, the ability of the cow to delay involuntary culling (Schneider et al., 2003) despite longevity being included in the selection index (Forabosco et al., 2009).

Publication of Overall Traits

Most member countries published EBV for overall traits both in magazines and on websites (12 for OCS, 13 for OUS, 11 for OFL), whereas 5, 4, and 3 published EBV only on websites for OCS, OUS, and OFL, respectively, and 1 country published the EBV only in magazines. The EBV for BCS was published on websites by 6 populations, and 2 published both on websites and in magazines. The majority of populations published the EBV 3 times per year (10 populations for OCS and OUS, 9 for OFL, and 5 for BCS), whereas 3 populations (OCS and OUS), 2 populations (OFL), and 1 population (BCS) published the EBV 2 times per year. The remaining populations published EBV more than 3 times per year.

Genomic Evaluation

Among 20 populations, 10 have started using genomic evaluation of conformation traits. The first populations (CAN, FRA, FRR, NZL, and USA) started in 2009, followed by CHE, DEU, and NLD in 2010 and AUS and DFS in 2011. Six populations are planning to start genomic evaluation soon (CZE, ESP, GBR, ITA, JPN, and POL). Different methods are used by countries to combine genomic breeding values and genomic reliabilities. Genomic evaluation for conformation is likely to change rapidly and a new survey in a few years would probably give very different results.

Conclusions

Across-country genetic correlations are useful in evaluating differences among countries, and cluster analysis contributes to the interpretation of the correlation matrix. Genetic correlations were always <1, which could be the consequence of different origins of the data and trait definition, interaction between genotype and country-environment, differences in national genetic procedures, weak genetic ties, and erroneous identification of bulls between countries. The differences for overall traits were mostly due to the heterogeneity in trait definitions as countries use linear traits, composite traits, or a subjective description. For BCS, the differences were due to the use of angularity and muscularity as best predictors. The international organizations ICAR and WHFF have developed guidelines for trait definitions for the linear traits that are widely used all over the world, whereas no guidelines have yet been developed for the composite traits. Overall traits are important in selection indices to improve functional traits, and their definition depends on the specific breeding goals in each country. It may be advantageous for national evaluation centers to follow international standards in computing their own overall traits from the MACE linear traits instead of using overall traits with no international standards. National genomic evaluation for type traits has been adopted by some countries and other members are planning to adopt it in the near future. At the international level, Interbull is developing the methodology required to provide international comparisons of genomically enhanced breeding values to member organizations.

Acknowledgments

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

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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.

Keywords: Body condition score, Cluster analysis, Holstein, Overall type trait.

Introduction

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

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).

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.

Materials and methods

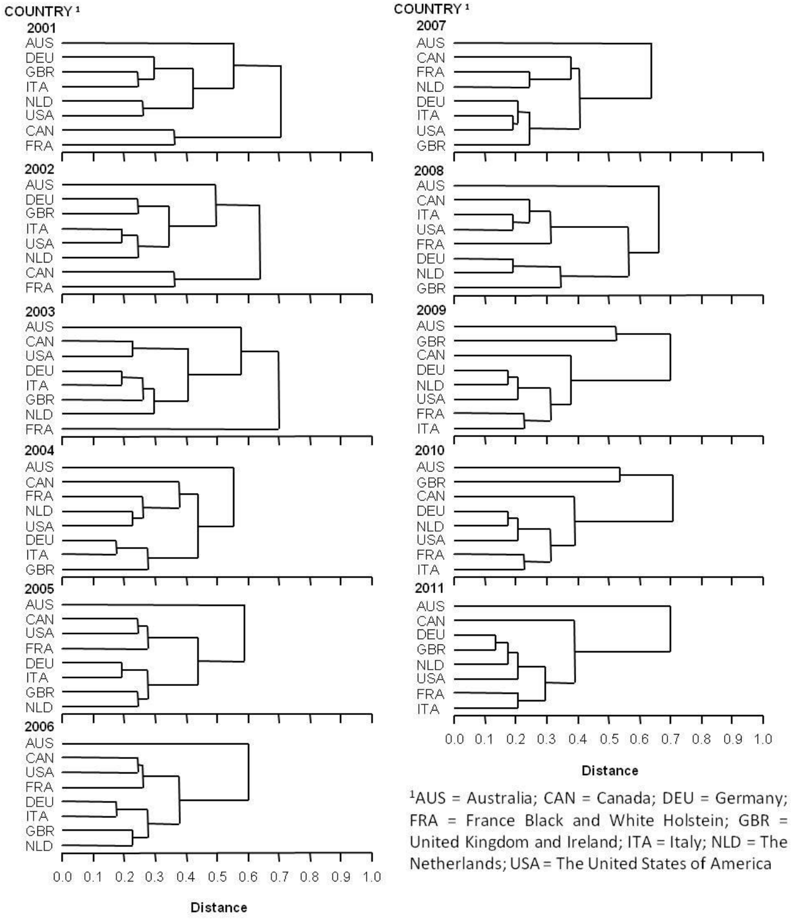
The genetic correlations among 8 reference member countries [Australia (AUS), Canada (CAN), France Black and White Holstein (FRA), Germany (DEU), Italy (ITA), The Netherlands (NLD), the United Kingdom and Ireland (GBR), and the United States (USA)], estimated by Interbull from 2001 to 2011, were the 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. The number of common bulls changed during the years and is different for each trait considered and for each pair of countries (data not shown).

Hierarchical cluster analysis was performed using the CLUSTER procedure (SAS, 2008). The distance (d_{ij}) between countries *i* and *j* was calculated as $d_{ij} = 1\text{-}rG^2_{ij}$, where rG_{ij} is the genetic correlation between countries *i* and *j*. Dendrograms were plotted using the TREE procedure (SAS, 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).

Results and discussion

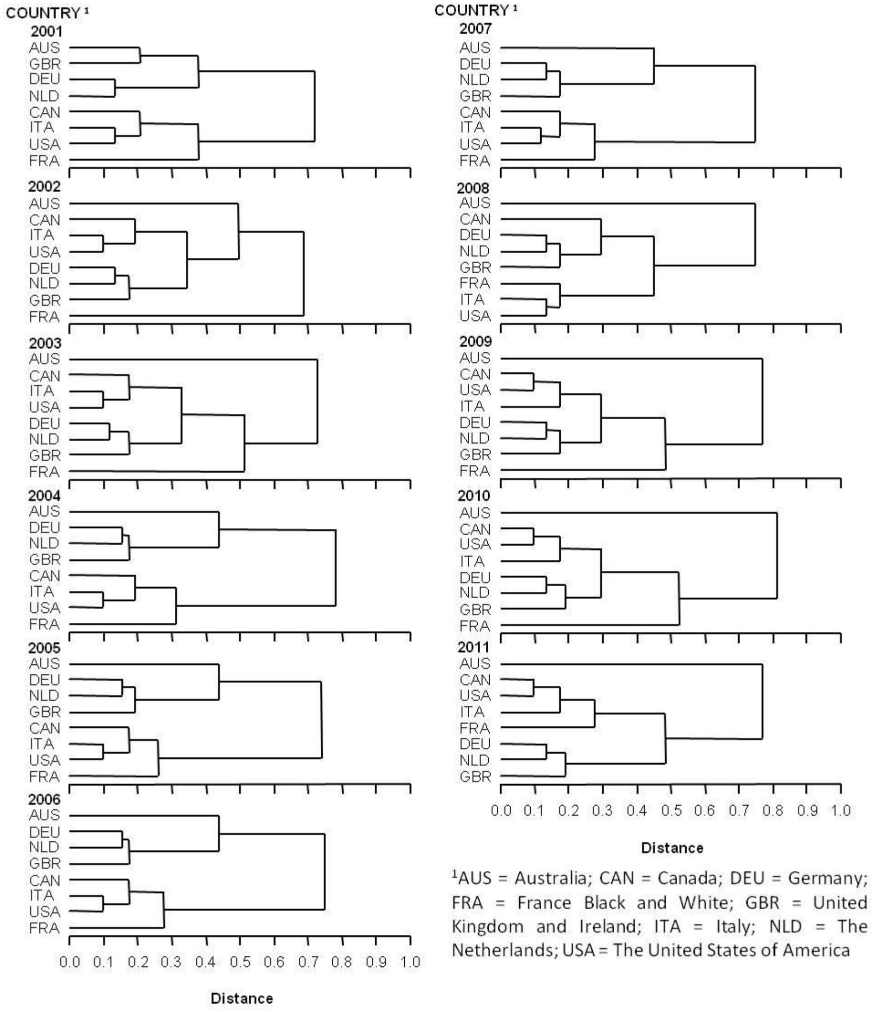
Overall Conformation Score. The 8 reference countries used the following definitions for OCS in May 2001: final score as individual trait (CAN and ITA), overall score as composite trait (FRA, GBR and NLD), overall score as individual trait (USA), general appearance (AUS), and relative total breeding 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

Figure 1. Dendrograms for overall conformation score using distances derived from across-country genetic correlations estimated by Interbull from 2001 to 2011.



¹AUS = Australia; CAN = Canada; DEU = Germany; FRA = France Black and White Holstein; GBR = United Kingdom and Ireland; ITA = Italy; NLD = The Netherlands; USA = The United States of America

Figure 2. Dendrograms for overall udder score using distances derived from across-country genetic correlations estimated by Interbull from 2001 to 2011



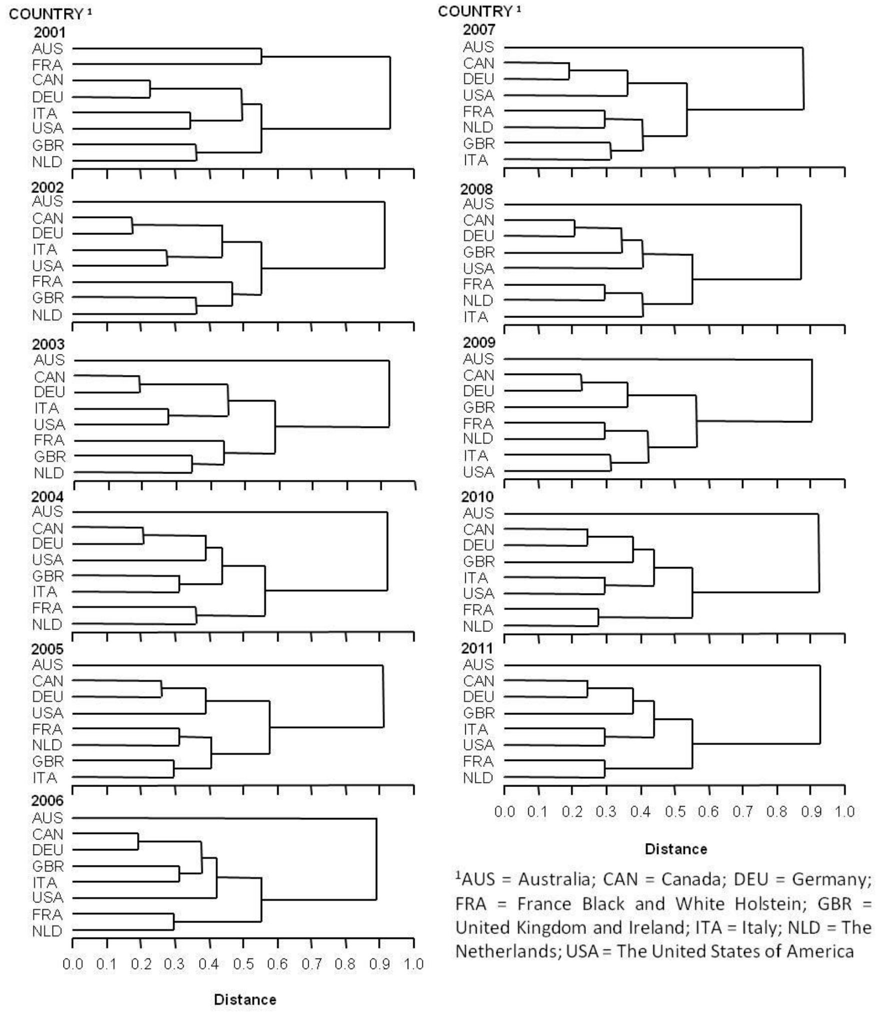
¹AUS = Australia; CAN = Canada; DEU = Germany; FRA = France Black and White; GBR = United Kingdom and Ireland; ITA = Italy; NLD = The Netherlands; USA = The United States of America

(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.

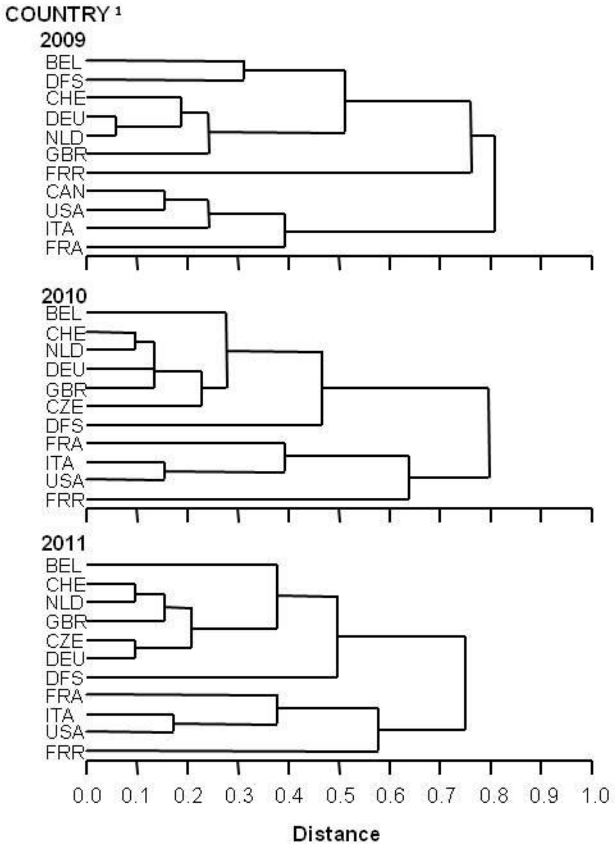
Overall Udder Score. In 2001, the OUS was defined as mammary system (AUS and CAN), overall udder as composite trait (DEU, FRA, GBR, ITA and USA), and a qualification of the total udder as composite trait (NLD). The genetic correlations across countries were generally higher for OUS than OCS, and the changes were less pronounced; for example, the structure of the clusters remained the same from 2004 to 2007 (Fig. 2). Australia showed the lowest genetic correlations (mean value of 0.70), whereas the countries with the highest genetic correlations were USA and ITA (mean value of 0.86). In 2001, there were 2 main clusters: the first grouped AUS, GBR, DEU and NLD, and the second ITA, USA, CAN and FRA.

Figure 3. Dendrograms for overall feet and legs using distances derived from across-country genetic correlations estimated by Interbull from 2001 to 2011.



[1]AUS = Australia; CAN = Canada; DEU = Germany; FRA = France Black and White Holstein; GBR = United Kingdom and Ireland; ITA = Italy; NLD = The Netherlands; USA = The United States of America

Figure 4. Dendrograms for body condition score using distances derived from across-country genetic correlations estimated by Interbull from 2009 to 2011.



[1] BEL = Belgium; CAN = Canada; CHE = Switzerland Black and White Holstein; CZE = Czech Republic; DEU = Germany; DFS = Denmark-Finland-Sweden; FRA = France Black and White Holstein; FRR = France Red Holstein; GBR = United Kingdom and Ireland; ITA = Italy; NLD = The Netherlands; USA = The United States of America.

The change in trait definition made by AUS in 2002 seemed to influence the cluster (Fig. 2), whereas the modifications made by NLD (November, 2001), GBR (August, 2002) and FRA (November, 2003) did not lead to changes in the structure of clusters.

Overall feet and legs. In 2001, the OFL was defined as a composite (BEL, DEU, FRA, GBR, ITA and NLD) and individual (CAN) trait. Australia used ‘‘side view foot diagonal’’ as best predictor of OFL. In 2001, there were 2 main clusters: the first included CAN, DEU, ITA, USA, GBR and NLD, and the second AUS and FRA (Fig. 3).

For OFL, AUS was even more distant than for the other 2 composite traits. On average, the correlation between AUS and the other countries was 0.41 for the whole period. Australia had the highest genetic correlations with FRA, but the correlation decreased from 0.67 (in 2001) to 0.36 (in 2011). In 2001, FRA had low correlations with other countries: the lowest genetic correlation was 0.40 (CAN) and the highest was 0.70 (ITA). In 2002, FRA changed OFL definition from ‘‘composite trait’’ to ‘‘locomotion’’, and the genetic correlations increased (the maximum value was 0.80 with ITA). As a consequence, FRA changed group in the cluster (Fig. 3). Italy has made 2 changes in trait definition: (1) in November 2003, the OFL changed from a composite to an individual trait (Interbull, 2011b) and ITA moved from the cluster with USA to the new cluster with GBR (Fig. 3); and (2) in March 2007, the definition changed again, with a consequent decrease of genetic correlations with all countries except AUS and FRA. In 2008, ITA was linked to FRA and NLD, and since 2009 it has been linked to USA. Other changes were the gradual increase in genetic correlation between CAN and USA, from 0.73 (in 2001) to 0.83 (in 2011), and between NLD and FRA, from 0.47 (in 2001) to 0.84 (in 2011). For OFL, CAN and DEU clustered together from 2001 to 2011 (Fig. 3).

Body condition score. The cluster analysis (Fig. 4) well depicts the difference in trait definitions among countries. In 2009, countries that sent information on BCS (the BCS countries) to Interbull were in one cluster, whereas countries that sent angularity (ANG, the ANG countries) as predictor of BCS were clustered in another group. Within the group of ‘‘BCS countries’’, it is clear that DFS, FRR and BEL exhibited the lowest average genetic correlations: 0.73, 0.74 and 0.81, respectively. In 2010, FRR changed group and did not clearly belong to one or another group for the trait definition. France Red Holstein used ‘‘muscularity’’ (the opposite of ANG) instead of BCS, and it could be placed in either of the two groups (Lawlor and Klei, 2008). In 2007, BEL was in the group of ‘‘ANG countries’’ (Lawlor and Klei, 2008). In BEL, BCS has been collected since 2006; in the first year, the variability of the BCS scoring system among recorders was high (Bastin et al., 2007), whereas in the following years recorders became more familiar with the scoring system and the country changed cluster. Low correlations between DFS and other countries that used BCS could be because only Denmark evaluated this trait.

The genetic correlations between countries that used ANG as best predictor of BCS were high (from 0.78 to 0.92). Canada used ANG as best predictor for BCS in 2009, but in the following years it did not submit data for this trait. Among the remaining three countries, ITA and USA showed the strongest ties (Fig. 4).

Conclusion

The cluster analysis over the years showed that the changes in evaluation procedure and trait definition influenced the genetic correlations across countries. Therefore, further efforts are needed to improve the harmonization of type traits and BCS among members. The overall traits can be computed using linear traits to reduce the variance due to different ways of defining the traits. For BCS, as for other linear traits, it may be advantageous for national evaluation centers to follow international standards provided by the International Committee for Animal Recording (ICAR).

Authors contributions

M. Cassandro designed the research. M. Battagin performed the statistical analyses and wrote the first draft of the manuscript. F. Forabosco and M. Penasa were involved in drafting the paper. All authors contributed to the interpretation and discussion of the results.

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Genetic parameters for body condition score, locomotion, angularity and production traits in Italian Holstein cattle

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Abstract

The objectives of this research were to estimate genetic parameters for body condition score (BCS) and locomotion (LOC), and to assess their relationships with angularity (ANG), milk yield (MY), fat and protein content, and fat to protein content ratio (F:P) in the Italian Holstein Friesian breed. The Italian Holstein Friesian Cattle Breeders Association (ANAFI) collects type traits data once on all registered first lactation cows. Body condition score and LOC were introduced in the conformation scoring system in 2007 and 2009, respectively. (Co)variance components for the traits were estimated with a Bayesian approach via a Gibbs sampling algorithm and an animal model. Heritability estimates were 0.114 and 0.049 for BCS and LOC, respectively. The genetic correlation between BCS and LOC was weak (-0.084) and not different from zero; therefore the traits seem to be genetically independent, but further investigation on the linearity of this relationship is needed. Angularity was strongly negatively correlated with BCS (-0.612), and strongly positively correlated with LOC (0.650). The genetic relationship of MY with BCS was moderately negative (-0.386), and was moderately positive (0.238) with LOC. These results indicate that high producing cows tend to be thinner and to have better locomotion than low producing cows. The genetic correlation of BCS with fat content (0.094) and F:P (-0.014) was very low and not different from zero, and with protein content (0.173) was low but different from zero. Locomotion was weakly correlated with fat content (0.071), protein content (0.028), and F:P (0.074), and correlations were not different from zero. Phenotypic correlations were low and generally smaller than the genetic counterparts ranging from -0.241 (BCS with ANG) to 0.245 (LOC with ANG). Before including BCS and LOC in the selection index of the Italian Holstein breed, the correlations with other traits currently used to improve type and functionality of animals need to be investigated.

Key words: body condition score, locomotion, angularity, genetic parameter

Introduction

The Italian Holstein Friesian Cattle Breeders Association (ANAFI, Cremona, Italy) has been collecting data on conformation traits since 1971. Initially, the evaluation consisted of assigning a score to a number of anatomical regions of the cow and a final overall merit score. In 1984, the linear system was introduced with the aim of objectively describing the conformation of the animal, from one biological extreme to the other, and a 1 to 50 point scale system was adopted (ANAFI, 2012b). In 1993, the conformation scoring system was adapted to the guidelines provided by the World Holstein Friesian Federation (WHFF, 2008). Body condition score (**BCS**) and locomotion (**LOC**) were introduced in the Italian linear trait classification program in 2007 and 2009, respectively. Currently, all first lactation cows belonging to registered herds are evaluated once for type traits, BCS, and LOC.

Body condition score is a visual measure of fat covering over the pelvic and lumbar regions, and its scoring is based on a 1 (very thin) to 5 (very fat) scale, with 0.25 point increments. In particular, the fat reserves of the thurl region, the angularity of hips and pins, and the prominence of spinous processes are evaluated (Edmonson et al., 1989; ANAFI, 2012b).

Body condition score has gained notable interest in the last decades as an important management tool in the dairy herd because it can be used as an indicator of overall energy status and predictor of reproduction, health, and welfare of the cow (Roche et al., 2009; Zink et al., 2011). Not all countries (including Italy) have a national evaluation for BCS, and angularity (**ANG**), defined as the angle and spring of the ribs (ranging from 1, lacks of angularity, to 50, very angular; WHFF, 2008), is currently used by the majority of the countries as the best predictor of BCS in the international genetic evaluation for the Holstein breed (Battagin et al., 2012).

Locomotion evaluates the length of the step and direction of rear legs in movement, and its scoring is based on a 1 (lame) to 50 (excellent) scale, with 1 unit increments: score 5 is given to short strides and severe abduction; score 25 to normal strides and slight abduction; and scores greater than 40 to long strides without abduction (ANAFI, 2012b). The direction of the scale follows the guidelines of WHFF (2008), and it is the opposite of those reported in the literature (Manson and Leaver, 1988; Boettcher et al., 1998; Van Dorp et al., 2004). Locomotion has been defined and investigated since the 1980s as a predictor of lameness, reproductive performance, and foot and leg diseases, all of which could be responsible for reduction of animal welfare, economic losses for the farmer, and involuntary culling (Boettcher et al., 1998; van der Waaij et al., 2005; Onyiro et al., 2008). Locomotion entered the Interbull portfolio in 2009, but 6 out of 10 countries that started the international evaluation for this trait use other related type traits (e.g., rear leg set, rear view, or feet and legs) as best predictors (Interbull, 2012a).

The aims of this study were to estimate genetic parameters for BCS and LOC in the Italian Holstein population, and to assess their phenotypic and genetic correlations with ANG and production traits. Understanding if BCS and LOC are heritable could address future breeding strategies to improve these traits in the Italian Holstein population.

Materials and Methods

Data and Editing

Information on BCS and ANG from July 2007 to June 2012, and on LOC from February 2009 to June 2012 were recorded by ANAFI once on first lactation cows. Only animals with known parents and with age at scoring between 20 and 38 mo were retained in the dataset. Herd-year-season (**HYS**) classes were formed and those including less than 5 cows were discarded. Also, records from classifiers who scored less than 100 animals were removed. The date of scoring of BCS and LOC for a given cow was matched with the closest test-day milk record if there was a milk record within 16 d of the BCS or LOC scoring date (similar to Dal Zotto et al., 2007). A test-day milk record included data on milk yield (**MY**, kg/d), fat and protein content (%), and fat to protein content ratio (**F:P**). Test-day milk records falling outside mean ± 3.5 SD were discarded from the dataset.

Following editing of the data as above, 500,053 records were available for further analyses. To reduce computer memory and time requirements, 5 samples of 1,000 herds each were randomly selected using the SURVEYSELECT procedure of SAS (SAS Inst. Inc., Cary, NC).

Means and variances of the traits were very similar across samples, and a preliminary assessment of variance components showed that estimates of genetic and phenotypic parameters were very comparable among samples (data not shown); therefore only results from one dataset (DATA1) were reported. Because the recording of LOC started 1.5 yr later than that of BCS, fewer records were available for this trait. Hence, a subset of LOC records (DATA2) was extracted from DATA1, and cows included in classes of HYS and CL with less than 5 and 100 contemporary animals, respectively, were removed from the dataset. Table 1 summarizes the descriptive statistics of the data before and after sampling. Sampled herds accounted for 66,808 and 44,218 cows, progeny of 4,982 and 3,799 sires, and were spread over 4,296 and 2,676 classes of HYS in DATA1 and DATA2, respectively. Animals were scored by 31 (DATA1) and 27 (DATA2) classifiers. The pedigree files for the analysis of BCS, ANG, and production traits (253,602 animals) and LOC (197,787 animals), included animals with phenotypic records and all their known ancestors up to 10 generations back.

Table 1. Means (SD) for body condition score, locomotion, angularity, milk yield, fat and protein contents, and fat to protein ratio (F:P) of data before and after sampling

Trait	Before sampling (n = 500,053)[1]	DATA1 (n = 66,808)[2]	DATA2 (n = 44,218)
BCS	3.01 (0.46)	3.01 (0.46)	2.99 (0.46)
Locomotion	23.46 (6.27)	23.49 (6.19)	23.48 (6.19)
Angularity	28.09 (5.15)	28.05 (5.14)	28.29 (5.16)
Milk yield, kg/d	30.48 (6.65)	30.28 (6.63)	30.62 (6.63)
Fat, %	3.59 (0.72)	3.59 (0.72)	3.60 (0.74)
Protein, %	3.33 (0.33)	3.33 (0.33)	3.33 (0.33)
F:P	1.08 (0.21)	1.08 (0.21)	1.08 (0.21)

[1] n = 331,654 for locomotion. [2] n = 44,368 for locomotion.

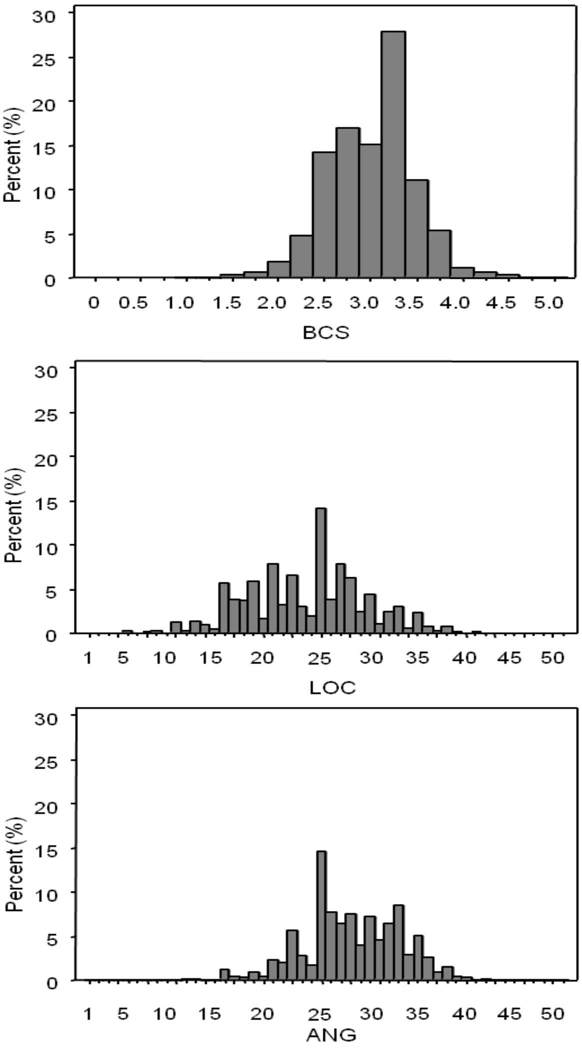
Parameter Estimation

Heritability estimates were obtained under single-trait animal models, using DATA1 for BCS, ANG, MY, fat content, protein content, and F:P, and DATA2 for LOC. The fixed systematic effects considered in the analyses were age of the cow at scoring (19 classes of one month each, from 20 to 38 mo), DIM (12 classes, the first being a class from 5 to 30 d, the central being classes of 30 d each, and the last being a class from 335 to 364 d), classifier (31 classifiers for BCS and ANG, and 27 for LOC), and milk yield (4 classes: <25 kg/d, 25 to 29 kg/d, 30 to 33 kg/d, and >34 kg/d). The classifier and milk yield effects were not included in the analysis of production traits. The general form of the model was as follows:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Z_1hys} + \mathbf{Z_2cl} + \mathbf{Z_3a} + \mathbf{e},$$

where **y** was the vector of observations for BCS, ANG, LOC, MY, fat content, protein content, or F:P; **β** was the vector of fixed effects as previously described; **hys** was the vector of random effects of herd-year-season of classification; **cl** was the vector of random effects of classifier; **a** was the vector of random effects of additive genetic animal; and **e** was the vector of random residuals. **X** and $\mathbf{Z_i}$ (i = 1 to 3) were incidence matrices of appropriate order relating the corresponding effects to the dependent variable. The random effects **hys**, **cl**, **a**, and **e** were assumed to be normally distributed with null means, and to be mutually uncorrelated. Genetic effects **a** were correlated between relatives and had variance $\mathbf{A}\sigma^2_a$, where **A** was the additive genetic relationship matrix among animals and σ^2_a was the genetic variance for animal effects. Non-genetic effects **hys**, **cl**, and **e** were uncorrelated between animals, with variances σ^2_{hys}, σ^2_{cl}, and σ^2_e, respectively.

Figure 1. Distribution of body condition score (BCS), locomotion (LOC), and angularity (ANG).



Genetic and phenotypic correlations between BCS and LOC, and of BCS and LOC with ANG and production traits were assessed through bivariate animal models, using the same datasets of the previous analysis. Systematic and random effects were identical to the univariate approach and for each random effect a (co)variance structure between traits was assumed.

(Co)variance components were estimated with a Bayesian approach via Gibbs sampling algorithm (Geman and Geman, 1984) using the GIBBS3F90 program (Misztal, 2008). The Gibbs sampler performed 480,000 iterations and the initial 30,000 samples were discarded as burn-in. The posterior means of (co)variance components were estimated using 4,500 samples (i.e., one every 100 samples of the remaining 450,000 iterations). The convergence of Gibbs samples was assessed by visual inspection of trace plots. The posterior mean was used as a point estimate of (co)variance components and related parameters. Lower and upper limits of the 95% highest probability density region for the posterior SD (PSD95%) for variance components, heritabilities, and phenotypic and genetic correlations were estimated from the Gibbs samples. Heritability was defined as the ratio of additive genetic variance to phenotypic variance, which was the sum of additive genetic, HYS, CL, and residual variances for BCS, LOC, and ANG, and the sum of additive genetic, HYS, and residual variances for MY, fat and protein contents, and F:P. Because in practice selection heritability is usually estimated on a "within-herd" basis, and a lack in differences among classifiers is assumed, heritabilities have been also computed as the ratio of additive genetic variance to the sum of additive and residual variances. Additive genetic correlations were the ratio of the covariance of two traits to the product of their additive genetic SD. Finally, phenotypic correlations were computed as the ratio of phenotypic covariance of two traits to the product of their phenotypic SD.

Results

Descriptive Statistics

Means and SD for the analyzed traits were very similar before and after sampling (Table 1). Before sampling, means (SD) for BCS, LOC, and ANG were 3.01 (0.46), 23.46 (6.27), and 28.09 (5.15), respectively; LOC had the highest coefficient of variation (CV; 27%) followed by ANG (18%) and BCS (15%). Milk yield, fat content, protein content, and F:P averaged 30.48 (6.65) kg/d, 3.59 (0.72) %, 3.33 (0.33) %, and 1.08 (0.21), respectively, in agreement with the official statistics reported by ANAFI (2012a). The distributions of BCS, LOC, and ANG followed a normal distribution, as depicted in Figure 1. About 28% of cows were scored 3.25 for BCS. The distributions of LOC and ANG showed greater variation than that of BCS, and approximately 14% of cows received a score of 25 for these traits. Locomotion had in prevalence scores lower than 25, whereas ANG had the opposite. Milk yield, fat and protein contents, and F:P were normally distributed (data not shown).

Genetic Parameters

Considering the CV of the 4,500 Gibbs samples of all traits after the single-trait analyses, the effect accounting for the greatest variation among samples was the classifier (CV of 32.0%), followed by the additive genetic (8.7%), the HYS (3.3%), and the residual (1.4%) effects. Locomotion was the trait with the highest values of samples CV. Analyses carried out using bivariate models resulted in similar estimates (results not shown). In general, residual variance was the component that the model was better able to assess.

Heritability estimates for BCS, LOC, and ANG were 0.114 (PSD95%: 0.094 to 0.134), 0.049 (PSD95%: 0.035 to 0.063), and 0.098 (PSD95%: 0.081 to 0.116), respectively (Table 2). Regarding production traits, protein and fat content exhibited the highest heritability, namely 0.251 (PSD95%: 0.226 to 0.276) and 0.163 (PSD95%: 0.141 to 0.185), respectively, whereas MY and F:P the lowest, namely 0.108 (PSD95%: 0.092 to 0.124) and 0.109 (PSD95%: 0.091 to 0.128), respectively (Table 2). The correspondent within-herd heritabilities were 0.158 (PSD95%: 0.134 to 0.182) for BCS, 0.056 (PSD95%: 0.040 to 0.072) for LOC, 0.120 (PSD95%: 0.099 to 0.140) for ANG, 0.162 (PSD95%: 0.138 to 0.185) for MY, 0.343 (PSD95%: 0.310 to 0.376) for protein content, 0.216 (PSD95%: 0.187 to 0.245) for fat content, and 0.141 (PSD95%: 0.118 to 0.164) for F:P (data not shown).

The genetic correlation between BCS and LOC was weak (-0.084) and not different from zero (Table 3). Body condition score showed a strongly negative genetic correlation with ANG (-0.612) and a moderately negative genetic correlation with MY (-0.386), whereas genetic correlations of BCS with fat (0.094) and F:P (-0.014) were very low and not different from zero (Table 3). The genetic correlation between BCS and protein content (0.173) was low, but different from zero. The genetic correlation between LOC and ANG was strongly positive (0.650), and moderately positive with MY (0.238), whereas the genetic relationships with fat content (0.071), protein content (0.028), and F:P (0.074) were weak and not different from zero.

Phenotypic correlations were low and generally smaller than the genetic counterparts. The estimates ranged from -0.241 (BCS with ANG) to 0.245 (LOC with ANG), and were of the same sign as the correspondent genetic correlations, with the exception of the relationships between BCS and MY, and BCS and LOC, which were also significantly different from zero.

Discussion

Within-herd heritability estimates were slightly greater than heritabilities, and, the increment in estimates ranged between 14% (for LOC) and 50% (MY), consistently with the relative incidence of the quotes of variance for HYS and CL effects on the total phenotypic variance. The heritabilities for BCS were consistent with previous findings in Holstein cows. Estimates ranging from 0.10 to 0.34 were reported in literature by Pryce et al. (2000), Dechow et al. (2001), Gallo et al. (2001), Van Dorp et al. (2004), Zink et al. (2011), and Buttchereit et al. (2012). In a recent study, Buttchereit et al. (2011) used random regression models to assess heritability of BCS across lactation for 682 first parity Holstein cows from a dairy research herd in Germany; the estimates decreased from 0.59 at the beginning of the lactation to 0.40 after 4 mo from calving. Loker et al. (2011) estimated heritabilities for BCS that were between 0.14 and 0.26 using random regression models on field data recorded on first lactation Holsteins in Canada, with the highest values in mid-lactation and an average value of 0.22. Dechow et al. (2004) suggested that BCS has the lowest heritability at early lactation and the highest at mid-lactation. Early lactation is a critical period for cows that experience a negative energy balance resulting in mobilization of body tissue (Roche et al., 2009). Loker et al. (2011) argued that the low heritability at this stage could be due to the importance of fat mobilization for cow metabolism. The ability to mobilize tissue reserves has been subjected to evolutionary pressures such that early lactation tissue mobilization has been genetically conserved. As reported by Van Dorp et al. (2004) and Dal Zotto et al. (2007), the discrepancies across studies regarding the heritability for BCS could be due to a number of factors such as differences in scale used for scoring the traits, the statistical model, breeds, number of records per animal, accuracy and consistency among classifiers, data editing and the method of calculating heritability. The additive genetic variances estimated in our study were similar to those of Loker et al. (2011) and Buttchereit et al. (2012). The estimates of Loker et al. (2011) ranged between 0.02 and 0.04, whereas that of Buttchereit et al. (2012) was 0.032. Conversely, the additive genetic variance for BCS of Italian Holsteins estimated by Gallo et al. (2001) using a repeatability animal model on test-day records was 0.044, which is higher than our result. Possible reasons for this difference could be related to the data used to obtain the genetic variance. For instance, the study of Gallo et al. (2001) was based on a much smaller number of recorded animals (1,344 in 25 herds) than our work, and was conducted on different lactations and on repeated records collected by one classifier. Besides these differences, another key point could be the time span (10 yr) between the two studies and the genetic selection that occurred in this period. In particular, the selection to increase production traits and to obtain more “dairy type” cows (i.e., more angular) could have indirectly reduced genetic variance for BCS.

The heritabilities for LOC were slightly lower compared to findings of Boelling and Pollott (1998), Van Dorp et al. (2004), van der Waaij et al. (2005), Boelling et al. (2007), Onyiro and Brotherstone (2008), and Laursen et al. (2009), who reported estimates of heritability between

0.06 and 0.11. The heritabilities for LOC were higher compared with Zink et al. (2011), who found a heritability of 0.03 in first-parity Czech Holsteins. The differences in heritability estimates likely depend on the trait definition (lameness or locomotion), the type of trait recorded (binary or continuous), the model used (threshold or linear), and the effects included in the analysis. Regarding the trait definition, LOC was mainly described either as degree of lameness (Van Dorp et al., 2004) or as the walking ability of an individual, depending on the consequences of foot or leg disorders (Boelling and Pollott, 1998). In agreement with the national recording system, our study referred to the definition of LOC given by Boelling and Pollott (1998). Regarding the type of traits and the model applied, binary traits analyzed via threshold models using an underlying continuous scale instead of the observed binary scale have often reported greater values of heritability (Laursen et al., 2009). Onyiro and Brotherstone (2008) found that the type of housing and the amount of time spent in housing explained a significant amount of variation of LOC, but it is not always easy to get comprehensive information on these aspects during routine LOC collection. Another factor that could influence the estimation of heritability is the quality of trait recording, since the classifier could have a strong impact on the variability of the scored trait, especially when the trait is relatively new in the scoring system (Veerkamp et al., 2002). Interestingly, in the current study, classifier and LOC were respectively the effect and the trait with the greatest variation in Gibbs samples estimates.

Heritabilities estimated for ANG and production traits were lower than the official values reported by ANAFI (Interbull, 2012c). For ANG, the explanation could be the depth of data used. Specifically, the present study only used records from 2007 to 2012, whereas ANAFI used data since 1997 and assessed heritabilities using a multiple-trait animal model that includes all the conformation traits routinely recorded (Interbull, 2012c). Previous estimates of heritability for ANG were moderate and ranged from 0.19 to 0.33 (Pryce et al., 2000; Dechow et al., 2003; Zink et al., 2011). A slightly closer value to the heritability estimated for ANG in the current study was found by Van Dorp et al. (2004), who assessed heritability of 0.11 for the trait. The low heritability for MY, and fat and protein contents of the current study could be the consequence of the use of only one record per cow, whereas the official analysis performed by ANAFI (2012a) uses a random regression model including repeated records across lactations. The heritability of F:P was lower compared with Buttchereit et al. (2011 and 2012) and Loker et al. (2012). Buttchereit et al. (2011) found heritabilities ranging from 0.20 to 0.54 for F:P, with the highest values at the beginning of lactation and at the end of the recording period. Loker et al. (2012) reported heritability of 0.42 for F:P, which is much higher than our estimate. Buttchereit et al. (2012), using repeated records of F:P, found a heritability of 0.30. As previously observed by Buttchereit et al. (2010), the high heritability of F:P in early lactation could be due to the large repeatability of this trait in this phase.

Correlations between BCS and LOC

The phenotypic correlation between BCS and LOC was very low (0.093) but different from zero, whereas the genetic correlation between these traits (-0.084) was not different from zero. Van Dorp et al. (2004) found negative phenotypic (-0.17) and genetic (-0.27) correlations

Table 2. Estimates of herd-year-season of classification (σ^2_{hys}), classifier (σ^2_{cl}), additive genetic (σ^2_a), and residual (σ^2_e) variance, and heritability (h^2) for body condition score, locomotion, angularity, milk yield, fat and protein contents, and fat to protein ratio (F:P). The 95% posterior SD intervals for heritability are within parentheses

Trait	σ^2_{hys}	σ^2_{cl}	σ^2_a	σ^2_e	h^2
Body condition score	0.027 (0.026; 0.029)	0.035 (0.014; 0.056)	0.025 (0.021; 0.029)	0.134 (0.131; 0.138)	0.114 (0.094; 0.134)
Locomotion	3.163 (2.853; 3.474)	1.358 (0.443; 2.273)	1.857 (1.327; 2.387)	31.362 (30.760; 31.965)	0.049 (0.035; 0.063)
Angularity	2.390 (2.217; 2.564)	2.255 (0.878; 3.631)	2.565 (2.109; 3.021)	18.862 (18.464; 19.259)	0.098 (0.081; 0.116)
Milk yield, kg/d	13.773 (13.053; 14.492)		4.412 (3.744; 5.080)	22.842 (22.286; 23.389)	0.108 (0.092; 0.124)
Fat, %	0.127 (0.120; 0.134)		0.083 (0.072; 0.095)	0.302 (0.293; 0.312)	0.163 (0.141; 0.185)
Protein, %	0.022 (0.021; 0.024)		0.021 (0.019; 0.023)	0.040 (0.039; 0.042)	0.251 (0.226; 0.276)
F:P	0.009 (0.009; 0.010)		0.005 (0.004; 0.005)	0.028 (0.027; 0.029)	0.109 (0.091; 0.128)

Table 3. Estimates of genetic (r_g) and phenotypic (r_p) correlations of body condition score and locomotion with angularity, milk yield, fat and protein contents, and fat to protein ratio (F:P). The 95% posterior SD intervals for genetic and phenotypic correlations are within parentheses

Traits	Body condition score		Locomotion	
	r_g	r_p	r_g	r_p
Body condition score	–	–	-0.084 (-0.271; 0.103)	0.093 (0.047; 0.138)
Angularity	-0.612 (-0.530; -0.694)	-0.241 (-0.189; -0.294)	0.650 (0.521; 0.778)	0.245 (0.221; 0.269)
Milk yield, kg/d	-0.386 (-0.291; -0.481)	0.043 (0.023; 0.064)	0.238 (0.068; 0.407)	0.132 (0.107; 0.156)
Fat, %	0.094 (-0.008; 0.196)	0.043 (0.033; 0.054)	0.071 (-0.117; 0.259)	0.015 (0.002; 0.027)
Protein, %	0.173 (0.086; 0.261)	0.113 (0.122; 0.144)	0.028 (-0.145; 0.201)	0.042 (0.028; 0.055)
F:P	-0.014 (-0.129; 0.101)	-0.016 (-0.005; -0.026)	0.074 (-0.123; 0.271)	-0.004 (-0.016; 0.008)

between BCS and LOC, but with high standard error of estimate for the genetic relationship (0.14). Those authors concluded that, phenotypically, cows with high BCS also had better LOC (Van Dorp et al., 2004). Our phenotypic correlation would support this comment, but the correlation is very weak, so it is not possible to draw a clear conclusion from this result.

Correlations of BCS with ANG and Production Traits

The genetic correlation between BCS and ANG (dairy form) was strong and negative (-0.612), and confirmed findings reported in the literature (-0.47 to -0.87) by Veerkamp and Brotherstone (1997), Dechow et al. (2003), and Dal Zotto et al. (2007), whereas the phenotypic relationship was much weaker (-0.241).

The genetic correlation between BCS and MY was moderate and negative, indicating that cows that produce high levels of milk in early lactation are genetically incline to lose more BCS. Phenotypically, the relationship between BCS and MY was close to zero. Overall, a range of moderate to weak negative genetic correlations between BCS and milk production have been reported in literature (-0.13 from Pryce and Harris, 2006; -0.40 from Dal Zotto et al., 2007; and -0.28 from Loker et al., 2012).

The genetic correlation between BCS and fat content was slightly positive and not different from zero, whereas between BCS and protein content was still slightly positive but different from zero. The respective phenotypic correlations were positive and different from zero. Loker et al. (2012) found similar genetic correlations of BCS with fat and protein content (0.06 and 0.23, respectively, with a posterior SD of 0.05). The genetic correlation between BCS and F:P was negative but not different from zero, whereas the phenotypic correlation was slightly negative and different from zero. Buttchereit et al. (2011) found positive albeit not significant genetic correlations between BCS and F:P. Loker et al. (2012) found a genetic correlation of -0.12 between BCS and F:P, with a posterior SD of 0.06. Loker et al. (2012) analyzed the relationship between BCS and production traits using a random regression animal model; in early lactation, the genetic correlation of BCS was strongest and negative with F:P, strongest and positive with protein content, and weak with fat content (Loker et al., 2012). Both BCS and F:P are indicators of cow energy status, and are expected to be negatively correlated. Due to high energy demand from increased milk production in early lactation, cows incur an energy deficit: the lipolysis increases (reducing BCS) and the mobilization of fatty acids results in an increased fat synthesis in the udder. At the same time, due to inadequate feed intake, there could be insufficient protein synthesis that increase F:P (Grieve et al., 1986; Buttchereit et al., 2010). Loker et al. (2012) also showed that during the lactation the genetic correlation between BCS and fat changes sign (even if it was significant only at 95 and 125 DIM), whereas the correlation of BCS and protein, high and positive at the beginning of lactation, tends to reduce over time but remains positive, as a consequence of the change in cow metabolism. These previous findings could explain genetic correlations of the present work.

Correlations of LOC with ANG and Production Traits

The genetic correlation between LOC and ANG was high (0.650), whereas the phenotypic correlation was weak (0.245), but still positive and different from zero, indicating that angular cows had better locomotion, both genetically and phenotypically. Boettcher et al. (1998)

estimated an opposite and moderately strong genetic correlation between clinical lameness and dairy form, indicating that increased sharpness was associated with increased clinical lameness. Van Dorp et al. (2004) found very low genetic (-0.07) and phenotypic (-0.01) correlations between LOC and dairy form but they used data recorded in different lactations.

The genetic and phenotypic correlations between LOC and MY were moderately positive and different from zero, indicating that cows with good locomotion tend to produce more milk, which could mean that genetically healthier cows are better milk producers, have better walking ability, and are less genetically predisposed to diseases such as lameness (Van Dorp et al., 2004). Previous studies reported desirable relationships between traits related to locomotion (e.g., clinical lameness or feet and leg score), even if of a low magnitude (Boettcher et al., 1998; Van Dorp et al., 2004; Pérez-Cabal et al., 2006). The genetic correlations of LOC with fat content, protein content, and F:P were low and not different from zero, indicating that those traits are genetically independent.

Conclusions

The additive genetic variances of BCS and LOC were low but in agreement with estimates reported in literature. Body condition score and LOC seem to be genetically independent of each other, but further investigation on the linearity of this relationship is needed. Body condition score showed a strong genetic correlation with its predictor (ANG). The genetic relationships of BCS and LOC with MY were moderate to low, and indicated that high producing cows tend to be thinner and to have better locomotion than low producing cows. The correlations of BCS and LOC with fat and protein content and F:P were almost negligible. Body condition score and LOC are susceptible to genetic improvement, but before including the two traits in the selection index of the Italian Holstein breed, the correlations with other traits currently used to improve type and functionality of cows need to be investigated.

Authors’ Contributions

MC planned and supervised the research; MB performed the statistical analyses; MB and CS wrote the first draft of the manuscript; SB provide data and suggestions for statistical analyses; MP edited the manuscript. All authors contributed to the discussion of the results and commented on the manuscript.

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Short Communication: Genetic relationship of body condition score, and locomotion with type traits in Italian Holstein cattle

draft

Abstract

The aim of this study was to estimate phenotypic and genetic correlations of body condition score (BCS) and locomotion (LOC) with linear type traits officially scored in Italian Holstein cows. The Italian Holstein Friesian Cattle Breeders Association (ANAFI) collects type traits data once on all registered first lactation cows. Body condition score and LOC were introduced in the conformation scoring system in 2007 and 2009, respectively. (Co)variance components for the traits were estimated with a Bayesian approach via a Gibbs sampling algorithm and an animal model. The genetic correlation between BCS and most of type traits are not significantly different from zero, except for angularity (-0.492), rear leg set side view (-0.432), rear udder height (-0.249), and chest width (0.256). All genetic correlations between LOC and type traits were different from zero, except for rump angle and teat length. The positive and significant genetic correlations of LOC with type traits ranged from 0.404 (rear teat position) to 0.980 (feet and legs functionality). The only one negative genetic correlation was with rear legs set side view (-0.298). Based on the results from the present study, the inclusion of BCS and LOC in the selection index has to be carefully discussed.

Key words: Body condition score, Locomotion, Type trait, genetic correlation

Short Communication

The group of type traits is evaluated by breeder associations worldwide since several decades. Type traits are used as tool of indirect selection to improve functionality of cows (Miglior et al., 2005). Even if in the last years there has been a growing interest in direct evaluation of fertility, longevity and health, type traits are still recorded and used in selection index. The Italian Holstein PFT (Productivity, Functionality and Type) Selection Index give 23% of the weight to conformation traits, namely 4% to type, 13% to udder composite index, and 6% to feet and legs composite index. Type index includes 15 linear traits related to body (i.e. stature, strength, body depth, angularity, rump angle, rump width, rear legs side view, feet and legs functionality, front udder, rear udder height, udder support, udder depth and front teat position); udder index includes 5 linear traits related to udder (i.e. fore udder attachment, rear attachment height, central ligament, udder floor, teats placement); and feet and legs index includes 4 traits related to feet and legs (i.e. feet and legs functionality, hoof depth, rear leg rear view, rear leg set side view).

Since 1993, the Italian Holstein breed linear type scoring system is adapted to the guidelines provided by the World Holstein Friesian Federation (WHFF, 2008), and includes 19 linear type traits, 2 general characteristics (conformation and functionality of feet and legs) and a final point (**FNP**; Table 1). The aim of this study was to estimate phenotypic and genetic correlations of body condition score (**BCS**) and locomotion (**LOC**) with linear type traits officially scored in Italian Holstein cows.

Information about type traits for Italian Holstein cattle was made available by the Italian Holstein Friesian Cattle Breeders Association (ANAFI, Cremona, Italy). Data editing followed those of BCS and LOC of 3rd contribution (see “data and editing” paragraph, of “material and methods” section). Summarizing, records with missing sire and dam information were omitted, as well as records in class of herd-year-season (**HYS**) of classification with <5 cows. Records from classifiers who scored less than 100 animals were removed. Animals with age at scoring between 20 and 38mo and DIM > 5 days were retained. One sample of animals was used for genetic parameters estimation (the DATA2 of 3rd contribution). Sampled herds accounted for 44,218 cows, progeny of 3,799 sires, and spread over 2,676 classes of HYS. Animals were scored by 27 classifiers. The pedigree files for the analysis included 197,787 animals with phenotypic records and all their known ancestors up to 10 generations back.

Genetic parameters were obtained under tri-traits animal models. The model used included the fixed systematic effects of age of the cow at scoring (19 classes of one month each, from 20 to 38 mo), DIM (12 classes, the first being a class from 5 to 30 d, the central being classes of 30 d each, and the last being a class from 335 to 364 d), classifier (27 levels), and milk yield (4 classes: <25 kg/d, 25 to 29 kg/d, 30 to 33 kg/d, and >34 kg/d). The general form of the model was as follows:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{hys} + \mathbf{Z}_2\mathbf{cl} + \mathbf{Z}_3\mathbf{a} + \mathbf{e},$$

where **y** was the vector of observations for BCS, LOC, and type traits; **β** was the vector of fixed effects as previously described; **hys** was the vector of random effects of herd-year-season of classification; **cl** was the vector of random effects of classifier; **a** was the vector of random effects of additive genetic animal; and **e** was the vector of random residuals. **X** and $\mathbf{Z}_\mathbf{i}$ (i = 1 to 3) were incidence matrices of appropriate order relating the corresponding effects to the dependent variable. The random effects **hys**, **cl**, **a**, and **e** were assumed to be normally distributed with null means, and to be mutually uncorrelated. Genetic effects a were correlated between relatives and had variance $\mathbf{A}\boldsymbol{\sigma}^2_\mathbf{a}$, where **A** was the additive genetic relationship matrix among animals and $\boldsymbol{\sigma}^2_\mathbf{a}$ was the genetic variance for animal effects. Non-genetic effects hys, cl, and e were uncorrelated between animals, with variances $\boldsymbol{\sigma}^2_\mathbf{hys}$, $\boldsymbol{\sigma}^2_\mathbf{cl}$, and $\boldsymbol{\sigma}^2_\mathbf{e}$, respectively.

Genetic and phenotypic correlations between BCS, LOC, and type traits were assessed through tri-traits animal models, using the same datasets of the previous analysis. For each random effect a (co)variance structure between traits was assumed. (Co)variance components were estimated with a Bayesian approach via Gibbs sampling algorithm (Geman and Geman, 1984) using the GIBBS3F90 program (Misztal, 2008). The Gibbs sampler performed 480,000 iterations and the initial 30,000 samples were discarded as burn-in. The posterior means of (co)variance components were estimated using 4,500 samples (i.e., one every 100 samples of the remaining 450,000 iterations). The convergence of Gibbs samples was assessed by visual inspection of trace plots. The posterior mean was used as a point estimate of (co)variance components and related parameters. Lower and upper limits of the 95% highest probability density region for the posterior SD (**PSD95%)** for variance components, heritabilities, and phenotypic and genetic correlations were estimated from the Gibbs samples.

Heritability was defined as the ratio of additive genetic variance to phenotypic variance, which was the sum of additive genetic, HYS, CL, and residual variances. Because in practice selection heritability is usually estimated on a "within-herd" basis, and a lack in differences

Table 1. Means, standard deviation (SD) and definition of Body Condition Score, Locomotion and conformation traits of 44,218 Holstein.

Trait	Mean	SD	Definition (from 1 to 50[1])
Frame			
Stature	32.26	6.70	Measured from top of the spine between hips to ground
Chest width	28.07	6.01	Measured from the inside surface between the top of the front legs
Body depth	31.08	5.80	Distance between the top of spine and bottom of barrel at last rib, the deepest point
Angularity	28.29	5.16	Angle and spring of the ribs
Rum angle	25.25	6.22	Measured as the angle of the rump structure from hooks (hips) to pins
Rump width	26.97	6.73	Distance between the most posterior points of pin bones
Conformation	25.70	5.72	Standard of breed (feet and legs, and udder are not included)
Feet and Legs			
Rear leg set, side view	26.20	5.62	Angle measured at the front of the hock, side view
Rear leg set, rear view	25.64	6.36	Direction of the rear feet, rear view
Locomotion	23.48	6.19	Length of the step and direction of rear legs in movement
Foot angle	25.25	5.77	Angle at the front of the rear hoof measured from the floor to the hairline at the right hoof
Feet & legs functionality	23.34	5.84	Functionality of feet and legs
Udder			
Fore udder attachment	24.35	6.27	Strength of the attachment of the fore udder to the abdominal wall.
Rear udder height	27.23	6.20	Distance between the bottom of the vulva and the milk secreting tissue
Udder depth	28.53	7.76	Distance from the lowest part of the udder floor to the hock
Rear udder width	30.17	6.71	Width of the high part of udder
Central ligament	29.31	6.17	Depth of cleft, measured at the base of the rear udder
Front teat placement	24.41	5.36	Position of the front teats from center of quarter, viewed from the rear
Teat length	22.74	5.56	Length of the front teat
Rear teat placement	27.24	9.00	Position of the rear teats from center of quarter, viewed from the rear
Final point	80.09	2.21	final point (20% structure, 20% dairy strength, 20% feet and legs, 40% udder)
Body condition score	2.99	0.46	Visual measure of the covering of fat over the pelvic and lumbar regions

[1] Body condition score from 1 to 5, and final point from 50 to 100

among classifiers is assumed, heritabilities have been also computed as the ratio of additive genetic variance to the sum of additive and residual variances. Heritabilities for BCS and LOC were calculated as the means of all Gibbs samples estimated in the 19 trivariate analyses.

Additive genetic correlations were the ratio of the covariance of two traits to the product of their additive genetic SD. Finally, phenotypic correlations were computed as the ratio of phenotypic covariance of two traits to the product of their phenotypic SD.

Table 1 summarizes the descriptive statistics of the type traits after sampling of herds. The FNP is a phenotypic and subjective assessment of cow that weighted 4 general characteristics of animals (20% structure, 20% dairy strength, 20% feet and legs, and 40% udder). The scale of FNP range from 50 (insufficient) to 100 (excellent), with 1 point increment. The scale are divided in 6 classes: 1) insufficient, from 50 to 69 points; 2) sufficient, form 70 to 74; 3) good, from 75 to 79; 4) more than good, from 80 to 84; 5) very good, from 85 to 89, and 6) excellent, from 90 to 100. Cows with a FNP lower than 70 are not enrolled in the genealogic book, while a fist lactation cow can have a maximum FNP equal to 88. Cows of this study had a mean (SD) FNP equal to 80.09 (2.21), and nearly the 60% of cows were in the 4th class of FNP, denoting that cows of this dataset were classified as more than good animals. For most of the traits the mode was 25, except for stature, body depth, rump width and udder support, with a mode of 35 and rear teat placement with a mode of 15. Cows were tall (stature: 32.26 ± 6.70), had a deepest body (body depth: 31.08 ± 5.80), the udder tend to be wide (udder width: 30.17 ± 6.71) and the central ligament was well defined and strong (central ligament: 29.31 ± 6.17).

Heritability estimates for all traits are given in Table 2, along with the posterior PSD95%. The estimation was 0.090 and 0.051 for BCS and LOC, respectively. Heritability ranged from 0.085 (rump width) to 0.207 (stature) for traits related to frame, from 0.043 (rear leg set, rear view) to 0.062 (feet and legs functionality) for traits related to feet and legs, and from 0.047 (rear udder width) to 0.157 (udder depth) for traits related to udder. Final point had a heritability of 0.186.

Within-herd heritability estimates were slightly greater than heritabilities, and the increment in estimates ranged between 13% (for rear leg set, side view) to 43% (rear udder width). Heritabilities for type traits estimated in the current study are smaller compare to the officials (Interbull, 2012c). Authors decided to estimate random components for HYS and CL because those two effects were partially overlap. Different models were tested, with different association of HYS and CL effects (e.g. HYS as fixed or random without CL effect, or using the combination of HYS and CL effects). For example, heritabilities estimated for stature ranged from 0.269 to 0.272 if only genetic additive and residual variances were included in the phenotypic variance. Heritabilities ranged from 0.207 to 0.246 if all the variances (HYS, genetic additive, and residual) were included in the phenotypic variance. Other reasons for the lowest estimates are: 1) the narrow range of years used: type traits were scored since 1997, but in this study only data from 2009 were used, and 2) the model used: for the official evaluation of type traits, a multiple traits animal model were used (Interbull, 2012c).

Table 2. Estimates of herd-year-season of classification (σ^2_{hys}), classifier (σ^2_{cl}), additive genetic (σ^2_{a}), residual (σ^2_{e}) variances and heritability (h^2) for body condition score, locomotion and type traits. The 95% posterior SD intervals are within parentheses

Traits	σ^2_{hys}	σ^2_{cl}	σ^2_{e}	σ^2_{a}	h^2
Frame					
Stature	4.642 (4.242; 5.042)	6.123 (1.543; 10.704)	24.609 (23.593; 25.625)	9.217 (7.924; 10.510)	0.207 (0.173; 0.241)
Chest width	3.221 (2.925; 3.518)	4.683 (1.187; 8.179)	23.115 (22.453; 23.777)	4.002 (3.236; 4.769)	0.115 (0.091; 0.138)
Body depth	2.921 (2.654; 3.189)	4.239 (1.101; 7.377)	21.168 (20.508; 21.828)	4.217 (3.435; 5.000)	0.130 (0.104; 0.156)
Angularity	2.273 (2.060; 2.487)	2.011 (0.483; 3.540)	19.695 (19.221; 20.170)	2.430 (1.920; 2.940)	0.092 (0.072; 0.112)
Rump angle	1.749 (1.520; 1.978)	3.571 (0.892; 6.251)	29.451 (28.577; 30.325)	5.592 (4.574; 6.609)	0.139 (0.113; 0.164)
Rump width	3.721 (3.378; 4.065)	7.772 (2.031; 13.513)	30.614 (29.835; 31.393)	3.897 (3.048; 4.747)	0.085 (0.064; 0.106)
Conformation	2.271 (2.037; 2.504)	2.656 (0.678; 4.634)	21.811 (21.120; 22.503)	4.748 (3.919; 5.577)	0.151 (0.124; 0.178)
Feet and legs					
Rear leg, side view	2.120 (1.891; 2.349)	2.061 (0.496; 3.627)	26.862 (26.365; 27.359)	1.484 (1.086; 1.882)	0.046 (0.033; 0.058)
Rear leg, rear view	2.962 (2.670; 3.253)	4.844 (1.273; 8.415)	31.343 (30.770; 31.916)	1.766 (1.275; 2.256)	0.043 (0.031; 0.056)
Locomotion	3.175 (2.860; 3.490)	1.748 (0.436; 3.061)	31.309 (30.702; 31.917)	1.934 (1.379; 2.490)	0.051 (0.036; 0.065)
Foot angle	2.505 (2.257; 2.754)	5.296 (1.273; 9.319)	25.706 (25.225; 26.187)	1.596 (1.174; 2.018)	0.046 (0.033; 0.059)
Feet & legs functionality	2.847 (2.571; 3.123)	1.675 (0.378; 2.971)	27.073 (26.516; 27.630)	2.097 (1.563; 2.632)	0.062 (0.046; 0.078)
Udder					
Fore Udder Attachment	2.602 (2.319; 2.884)	2.949 (0.718; 5.180)	30.856 (30.080; 31.631)	4.296 (3.431; 5.162)	0.106 (0.084; 0.127)
Rear Udder Height	3.146 (2.844; 3.448)	3.754 (0.936; 6.571)	28.702 (28.031; 29.373)	3.174 (2.465; 3.882)	0.082 (0.063; 0.101)
Udder Depth	4.849 (4.362; 5.336)	4.919 (1.169; 8.670)	41.966 (40.520; 43.413)	9.646 (7.898; 11.393)	0.157 (0.128; 0.186)
Rear Udder Width	3.681 (3.357; 4.005)	9.036 (2.422; 15.651)	27.705 (27.155; 28.254)	1.990 (1.478; 2.501)	0.047 (0.033; 0.061)
Central ligament	2.058 (1.827; 2.289)	5.392 (1.357; 9.427)	29.219 (28.615; 29.823)	2.530 (1.940; 3.120)	0.065 (0.048; 0.081)
Front teat placement	1.676 (1.488; 1.865)	6.980 (1.844; 12.117)	23.744 (23.259; 24.229)	1.755 (1.303; 2.208)	0.052 (0.037; 0.067)
Teat length	1.468 (1.296; 1.640)	3.393 (0.788; 5.999)	22.919 (22.385; 23.453)	2.645 (2.084; 3.205)	0.087 (0.068; 0.107)
Rear teat placement	4.704 (4.184; 5.224)	16.439 (3.969; 28.909)	61.281 (59.897; 62.665)	6.022 (4.616; 7.428)	0.068 (0.050; 0.086)
Final Point	0.391 (0.353; 0.429)	0.172 (0.030; 0.313)	3.247 (3.130; 3.364)	0.869 (0.724; 1.015)	0.186 (0.155; 0.216)
Body condition score	0.023 (0.021; 0.025)	0.040 (0.012; 0.068)	0.142 (0.138; 0.146)	0.020 (0.016; 0.024)	0.090 (0.069; 0.111)

Estimates of genetic and phenotypic correlations of BCS with type traits are given in Table 3. Genetic correlations were significantly different from zero for chest width, angularity, rear leg set (side view) and rear udder height. Body condition score had moderately negative genetic correlations with angularity (-0.492), rear leg set side view (-0.432) and rear udder height (-0.249) and positive genetic correlation with chest width (0.256). The genetic correlation with angularity was less strong in this study compared with that published in the 3rd contribution (i.e. -0.612). This is due to the change of angularity definition that occurs in 2009. Until 2009 angularity was scored looking in prevalence the rear of animals, while from 2009, angularity is scored as the angle and the spring of the ribs. In this study only data from 2009 were considered, while in the previous data from 2007 were used. Phenotypic correlations of BCS with type traits were significantly different form zero with final score, all traits (except rump angle) related to frame, all traits (except foot angle) related to feet and legs, and for rear udder height, udder depth and front teat position (Table 3). Body condition score had moderately positive phenotypic correlations with stature (0.183), chest width (0.313), body depth (0.212), rump width (0.102), conformation (0.082), rear leg set rear view (0.107), feet and legs functionality (0.112), front teat position (0.100) and final score (0.069), and moderately negative phenotypic correlations with angularity (-0.218), rear leg set side view (-0.102), rear udder height (-0.076), and udder depth (-0.071). Body condition score is not a real conformation trait and the covariance with type traits could be the result of genetic selection for the desired dairy cow or due to pleiotropic effects (Kadermideen and Wegmann, 2003).

Estimates of genetic and phenotypic correlations of LOC with type traits are given in Table 3. All genetic correlations were different from zero, except for rump angle and teat length. The positive and significant genetic correlations of LOC with type traits ranged from 0.404 (rear teat position) to 0.980 (feet and legs functionality). The high genetic correlation with feet and legs functionality was expected, because in the definition of feet and legs functionality, LOC was one of the aspects evaluated, together with bone quality, position, pastern, and consistency of feet and legs. The only one negative genetic correlation was with rear legs set side view (-0.298). The phenotypic correlations of LOC with type traits were significantly different from zero for all traits except of rump angle and rear teat position. All the phenotypic correlations were positive and ranged from 0.047 (udder depth) to 0.772 (feet and legs functionality). The only negative phenotypic correlation of LOC was with rear leg set side view (-0.158). Generally, estimates of genetic and phenotypic correlations between LOC and type traits were favourable.

In conclusion BCS seems to be genetically independent with most of type traits, except for chest width, angularity, rear leg set side view and rear udder height, while LOC shows favourable genetic correlations with type traits. Body condition score and LOC were recently added to the scoring system of Italian Holstein Friesian and their inclusion in the selection index has to be discussed also in function of their correlation with type traits.

Table 3. Estimates of genetic (rg) and phenotypic (rp) correlations of body condition score and locomotion with type traits

Traits	**Body condition score**		**Locomotion**	
	r_g	r_p	r_g	r_p
Frame				
Stature	-0.018 (-0.141; 0.105)	0.183 (0.107; 0.25)	0.612 (0.486; 0.738)	0.211 (0.164; 0.257)
Chest width	0.256 (0.125; 0.388)	0.313 (0.245; 0.381)	0.537 (0.402; 0.672)	0.256 (0.214; 0.297)
Body depth	0.097 (-0.041; 0.235)	0.212 (0.141; 0.283)	0.483 (0.341; 0.625)	0.257 (0.215; 0.298)
Angularity	-0.492 (-0.618; -0.366)	-0.218 (-0.275; -0.160)	0.624 (0.493; 0.754)	0.247 (0.217; 0.276)
Rump angle	0.066 (-0.080; 0.211)	0.033 (-0.031; 0.096)	0.080 (-0.099; 0.258)	0.015 (-0.019; 0.049)
Rump width	-0.097 (-0.253; 0.058)	0.103 (0.021; 0.186)	0.585 (0.439; 0.730)	0.217 (0.170; 0.265)
Conformation	-0.132 (-0.267; 0.004)	0.082 (0.020; 0.143)	0.772 (0.681; 0.863)	0.452 (0.424; 0.479)
Feet and legs				
Rear leg set, side view	-0.434 (-0.590; -0.278)	-0.102 (-0.162; -0.042)	-0.298 (-0.486; -0.110)	-0.158 (-0.188; -0.128)
Rear leg set, rear view	0.119 (-0.059; 0.297)	0.107 (0.034; 0.179)	0.832 (0.747; 0.917)	0.506 (0.472; 0.539)
Foot angle	0.123 (-0.048; 0.294)	0.054 (-0.039; 0.146)	0.858 (0.775; 0.940)	0.549 (0.518; 0.579)
Feet and legs functionality	0.050 (-0.108; 0.209)	0.112 (0.061; 0.164)	0.980 (0.956; 1.005)	0.772 (0.759; 0.786)
Udder				
Fore udder attachment	0.062 (-0.086; 0.210)	0.025 (-0.032; 0.082)	0.525 (0.380; 0.670)	0.211 (0.181; 0.241)
Rear udder height	-0.249 (-0.403; -0.096)	-0.076 (-0.141; -0.011)	0.708 (0.589; 0.828)	0.227 (0.194; 0.260)
Udder depth	0.020 (-0.128; 0.168)	-0.071 (-0.136; -0.006)	0.455 (0.299; 0.611)	0.047 (0.013; 0.081)
Rear udder width	-0.097 (-0.276; 0.081)	0.027 (-0.067; 0.121)	0.606 (0.455; 0.757)	0.244 (0.194; 0.293)
Central ligament	-0.004 (-0.168; 0.160)	-0.023 (-0.099; 0.053)	0.692 (0.558; 0.826)	0.148 (0.104; 0.192)
Front teat placement	-0.132 (-0.302; 0.039)	0.100 (0.009; 0.190)	0.100 (-0.094; 0.295)	0.127 (0.077; 0.177)
Teat length	0.034 (-0.127; 0.195)	-0.027 (-0.098; 0.044)	0.512 (0.354; 0.669)	0.112 (0.073; 0.150)
Rear teat placement	-0.072 (-0.240; 0.095)	-0.034 (-0.123; 0.056)	0.404 (0.228; 0.580)	0.030 (-0.021; 0.081)
Final score	-0.044 (-0.175; 0.087)	0.069 (0.023; 0.116)	0.869 (0.812; 0.927)	0.554 (0.533; 0.575)

Results of the first international genetic evaluation for body condition score in Italian Holstein Friesian

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Abstract

The aim of this study was to summarize the results of the Interbull test-run of October 2012 where BCS information for Italian Holstein was used, and compare those results with the official run of December 2012. Interbull sent the results of test-run to each country participating to the international evaluation. The available information were: 1) traits definition, 2) changes in national and international procedure, 3) genetic correlations across countries, and 4) international breeding values of all bulls evaluated. Ranks were different for each country that participated to the international evaluation for a specific trait (e.g. there were 14 ranks of bulls for Holstein and BCS trait). Also results of December 2012 official-run were made available, these results were joint whit those of the test-run for the common bulls between the two analysis. The most important change occurred for the test-run was the trait used by Italy. Italy participates to the official international evaluation for BCS since 2009 using ANG as best predictor of BCS. For the test-run of October 2012, Italy sent BCS as direct trait. The change of trait used by Italy lead to an increment of its genetic correlations with other countries. The mean genetic correlations of Italy with other countries was 0.87 for the test-run, and 0.71 for the official-run. In October, the weakest genetic correlation (absolute value) for Italy was with Belgium (0.78) and the strongest with France black and white Holstein (0.96). With the countries that used BCS as direct trait, the most visible increments of genetic correlations occurred with Swiss black and white Holstein (from 0.66 to 0.91), Germany (from 0.69 to 0.94), Czech Republic (0.71 to 0.94), and France black and white Holstein (from 0.75 to 0.96). Among countries that used a best predictor, the genetic correlation with France red Holstein increased (from 0.51 to 0.81), while that with United States decreased (from 0.91 to 0.77). When Italy used directly BCS for the international evaluation, the number of Italian top-bulls increased in all ranks, particularly the number of top-1% bulls in ranks of Ireland (from 11 to 31), Swiss (from 10 to 29), and United States (from 1 to 19). At the same time, in the Italian rank, the number of top bulls of countries that use BCS as direct trait increased when also Italy used BCS (e.g. in the test-run rank of Italy there were 113 top-1% black and white bulls from Netherlands, while in the official-run they were only 36). The number of bulls from countries that used a best predictor was lowest when Italy used the direct trait, the most evident result was of bulls from United States, they were 224 in the Italian rank of test-run, and they doubled in the rank of official-run (445). The genetic trend of bulls for BCS was unfavourable for all countries (based on the Italian rank). Italian bulls had an unfavourable genetic trend, and for most of the years considered the trend was negative, even if in line with those of other countries.

Abbreviations: ANG = angularity; BCS = body condition score; BEL = Belgium; CHE = Swiss black and white Holstein; BRF = British Frisian; CZE = Czech Republic; DEU = Germany; DFR = Dutch Frisian; DFS = Denmark, Finland, Sweden (joint evaluation); DNK = Denmark; FRA = France black and white Holstein; FRR = France red Holstein; IRL = Ireland; ITA = Italy; JPN = Japan; MRY = Meuse Rhine Yssel; NLD = The Netherlands; RDC = Ayrshire; UK = Great Britain; USA = The United State of America.

Introduction

The first international genetic evaluation for BCS was carried out in 2009 and involved 11 countries. Seven countries used direct measures of BCS and the remaining 4 used a best predictor, which was ANG for ITA and FRA, dairy form for USA, and muscularity for FRR (Interbull, 2012a). During the following years other countries jointed the Interbull evaluation for BCS, namely CZE in 2010 and JPN in 2011. In 2012 UK and IRL started to send data separately, and FRA started to send data of BCS instead ANG (Interbull, 2012b). For the test-run of October 2012 also ITA sent BCS as direct trait, and for that test-run only 2 out of 14 countries (USA and FRR) used a best predictor. The aim of this paper was to summarize the results of the October 2012 Interbull test-run, where ITA used BCS information, and to compare those results with the official-run of December 2012.

Materials and methods

National information

Body condition score was recorded on all first lactation cows during the routine linear traits evaluation. It was introduced in the linear traits scoring system in 2007, and up to now about 1 million of cows have been scored at an age between 20 and 38 months. For each cow only one record in first lactation was collected. For the genetic evaluation a single trait animal model was used with the fixed effects of age at calving, stage of lactation, and herd-year-season of classification (**HYS**). The minimum size of HYS was set to 5 animals. The only random effect was the animal, and genetic groups were used in the pedigree. Genetic parameters used in test-run evaluation were those estimated by Gallo et al. (2001), namely 0.29 for heritability and 0.044 for genetic variance.

Test-run

All breeding values for bulls with at least 10 daughters in 10 herds were sent to Interbull for the test-run of October 2012. As for the other traits, BCS was evaluated by Interbull with the Multiple Across Country Evaluation (**MACE**) method. National EBV were deregressed within country to obtain variables independent from all effects included in the international sire model (Sigurdsson and Banos, 1995), then genetic parameters (sire variance within country and genetic correlations between countries) were estimated with the expectation maximization (EM) algorithm for REML procedure described by Klei and Weigel (1998).

Heritability used for the international evaluations were those provided by the countries, whereas genetic correlations across countries were estimated in test-runs when new or modified data are submitted from a country (Interbull, 2011d).

Pedigree was traced back as far as possible in order to increase across-country connections. Genetic groups for unidentified parents were defined according to national origin, breed and year of birth of the bull, and path of selection (sires, maternal grand-sires, and maternal grand-dams). Minimum group size was set to 30 (Interbull, 2011b).

Results from Interbull

Interbull sent the results of test-run to each country participating in the International evaluation. The information available were: 1) traits definition, 2) changes in national and international procedure, 3) genetic correlations across countries, and 4) international breeding values of all bulls evaluated. Ranks are different for each country that participated to the international evaluation for a specific trait (e.g. there were 14 ranks of bulls for Holstein and BCS trait). Also results of December 2012 official-run were made available, these results were joint whit those of the test-run for the common bulls between the two analysis.

Results and discussion

For Holstein breed, 57,750 bulls were evaluated by Interbull during the test-run of October 2012. Of these bulls, 94.59% were black and white, 4.72% red Holstein and the remaining 0.69% was represented by other Holstein populations (MRY, BRF, DFR, RDC). United States was the country with the highest number of bull (44.89%), followed by NLD (14.15%), DEU (12.67%), FRA (7.52%), and DNK (5.97%). Italy had 4.30% of bulls.

Genetic ties among populations are in Table 1. Considering the number of common bulls, FRR had the lowest average number of common bulls (15), whereas NLD had the highest (459). The strongest connection was between USA and UK (1,017), USA and NLD (885), and UK and NLD (821). Italy had the highest number of common bulls with USA (769), NLD (662), and UK (623). France red Holstein had the lowest average number of ¾ sib bulls (19), and DEU had the highest (675). The strongest connections were between DEU and USA (1,295), USA and NLD (1,276), and USA and UK (1,263). The number of ¾ sib bulls of ITA reflected that of common bulls. Increase in the number of common bulls leads to a higher precision of the across country genetic correlations (Interbull, 2011d).

The most important change occurred for the test-run was the trait used by Italy. Italy participates to the official international evaluation for BCS since 2009 using ANG as best predictor of BCS. For the test-run of October 2012, Italy sent BCS as direct trait, whereas USA and FRR used a best predictor, which were dairy form and muscularity, respectively (Table 2). The change of trait performed by Italy was well observable in the matrix of genetic correlations (Table 2). Across country genetic correlations estimated for the test-run of October 2012 are reported below diagonal, while those estimated for the official-run of December 2012 are reported above diagonal. The mean genetic correlation of ITA and other countries was 0.87 in test-run, and 0.71 in official-run. In October, the weakest genetic correlation (absolute value) for ITA was with BEL (0.78) and the strongest with FRA (0.96). The most visible increments of genetic correlations, with the countries that used BCS as direct trait, occurred with CHE (from 0.66 to 0.91), DEU (from 0.69 to 0.94), CZE (0.71 to 0.94), and FRA (from 0.75 to 0.96). Among countries that used a best predictor, the genetic correlation with France red Holstein increased (from 0.51 to 0.81), while that with United States decreased (from 0.91 to 0.77). Increments in degree of genetic correlations with FRR could be due to the direction of the scale of muscularity and BCS. Low values represent thin animals, without fat deposition (BCS) or with a reduced muscle mass (muscularity), while

Table 1. Common bulls (below diagonal) and ¾ sib bulls (above diagonal).

Country[1]	% bulls[2]	Country[1]												
		BEL	CHE	DEU	DFS[3]	FRA	GBR	ITA	NLD	USA	CZE	FRR	JPN	IRL
BEL	0.34		166	312	198	200	340	258	470	335	163	26	72	201
CHE	0.69	163		262	144	130	250	212	257	288	114	6	67	159
DEU	12.67	254	183		699	696	799	826	1195	1295	659	47	363	278
DFS[3]	5.97[2]	153	119	270		346	547	386	703	605	351	2	153	229
FRA	7.52	169	113	179	109		433	405	568	676	373	8	267	170
GBR	3.12	321	242	419	303	204		669	1043	1263	427	18	230	455
ITA	4.30	249	199	445	316	202	623		708	842	436	17	228	274
NLD	14.15	488	246	674	446	256	821	662		1276	624	62	242	424
USA	44.89	261	230	430	289	190	1017	769	885		653	19	500	350
CZE	1.13	127	89	403	195	173	283	345	505	415		19	213	152
FRR		25	5	34	2	7	15	16	45	13	15		0	8
JPN	1.68	42	38	61	60	53	82	93	78	107	69	0		69
IRL	0.24	199	168	231	169	142	509	280	402	328	126	6	47	

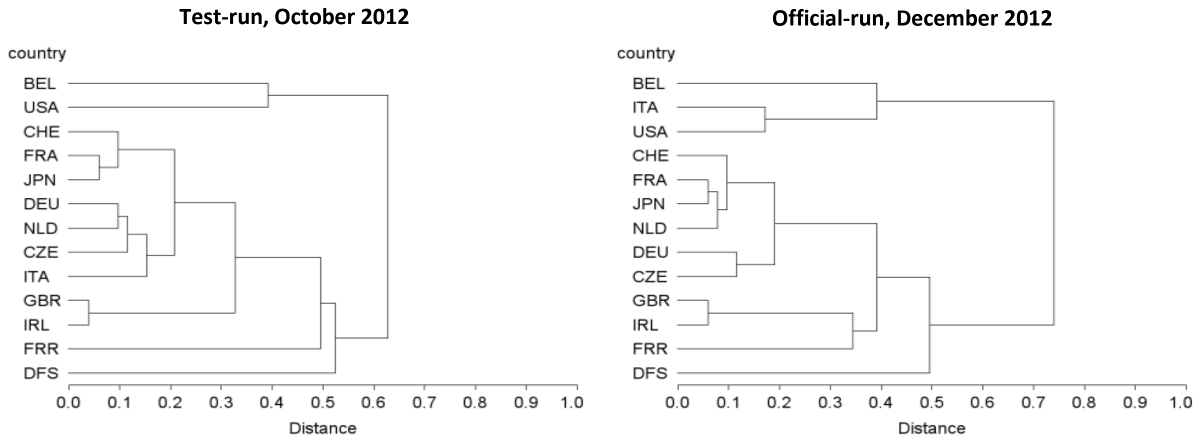
[1] BEL = Belgium; CHE = Swiss, Black and White; DEU = Germany; DFS = Denmark, Finland and Sweden (only Denmark send data for BCS evaluation); FRA =France, black and white Holstein; GBR = Great Britain; ITA = Italy; NLD = The Netherlands; USA = The United States of America; CZE = Czech Republic; FRR = France, red Holstein; JPN = Japan; IRL = Ireland. [2] In the remaining quota, the most important part is represents by bulls from Canada (2.67 %). Other countries had less than 0.5 % of bulls. [3] Only bulls from Denmark.

Table 2. Countries participating in Interbull evaluation for Body Condition score (BCS); Trait used by each country, and across county genetic correlations estimated by Interbull for the test-run of October 2012 (below diagonal) and for the official-run of December 2012 (above diagonal).

Country[1]	Trait[2]	Country[1]												
		BEL	CHE	DEU	DFS	FRA	GBR	ITA	NLD	USA	CZE	FRR	JPN	IRL
BEL	BCS(0901)		0.75	0.77	0.68	0.72	0.77	0.78	0.77	0.79	0.79	0.65	0.72	0.71
CHE	BCS(0901)	0.75		0.93	0.73	0.96	0.95	0.66	0.95	0.72	0.9	0.8	0.95	0.91
DEU	BCS(0901)	0.79	0.92		0.79	0.93	0.94	0.69	0.95	0.74	0.94	0.87	0.94	0.88
DFS	BCS(0901)	0.65	0.72	0.79		0.79	0.75	0.61	0.76	0.60	0.78	0.71	0.80	0.72
FRA	BCS(1204)	0.74	0.95	0.94	0.78		0.95	0.75	0.96	0.74	0.90	0.80	0.97	0.92
GBR	BCS(0901)	0.77	0.94	0.93	0.74	0.94		0.75	0.92	0.77	0.86	0.85	0.95	0.97
ITA	BCS(1210)	0.75	0.91	0.94	0.77	0.96	0.91		0.73	0.91	0.71	0.51	0.76	0.71
NLD	BCS(0901)	0.76	0.95	0.95	0.77	0.96	0.92	0.92		0.72	0.93	0.83	0.96	0.86
USA	DFO(0901)	0.78	0.73	0.74	0.63	0.75	0.77	0.77	0.73		0.74	0.58	0.77	0.75
CZE	BCS (1001)	0.78	0.89	0.94	0.77	0.91	0.89	0.94	0.94	0.74		0.78	0.92	0.78
FRR	MUS(0901)	0.73	0.71	0.86	0.71	0.83	0.84	0.81	0.83	0.61	0.78		0.79	0.81
JPN	BCS(1112)	0.77	0.95	0.94	0.82	0.97	0.94	0.95	0.94	0.78	0.93	0.8		0.93
IRL	BCS(1204)	0.69	0.9	0.87	0.69	0.9	0.98	0.84	0.88	0.68	0.82	0.8	0.89	

[1] BEL = Belgium; CHE = Swiss, Black and White; DEU = Germany; DFS = Denmark, Finland and Sweden (only Denmark send data for BCS evaluation); FRA =France, black and white Holstein; GBR = Great Britain; ITA = Italy; NLD = The Netherlands; USA = The United States of America; CZE = Czech Republic; FRR = France, red Holstein; JPN = Japan; IRL = Ireland. [2] BCS = body condition score; DFO = dairy form; MUS = muscularity. In parenthesis the years (first two digits) and month (second two digits) from which the county started to use the current trait.

Figure 1: Cluster analysis using across countries genetic correlations calculated by Interbull on the test-run of October 2012 and on the official-run of December 2012.



Test-run, October 2012

Official-run, December 2012

[1] BEL = Belgium; CHE = Swiss, Black and White; DEU = Germany; DFS = Denmark, Finland and Sweden (only Denmark send data for BCS evaluation); FRA =France, black and white Holstein; GBR = Great Britain; ITA = Italy; NLD = The Netherlands; USA = The United States of America; CZE = Czech Republic; FRR = France, red Holstein; JPN = Japan; IRL = Ireland.

Table 3. Top Italian black and white bulls in 1%, 100 and 50 positions of different ranks for the test-run evaluation of October 2012 (OCT) and the official-evaluation of December 2012 (DEC).

Rank[1]	Top 1%		Top 100		Top 50	
	OCT	DEC	OCT	DEC	OCT	DEC
BEL	8	7	2	1	-	-
CHE	29	10	5	2	3	2
DEU	16	7	4	2	2	1
DFS	28	14	2	1	1	-
FRA	19	5	5	2	2	2
GBR	22	7	5	2	2	1
ITA	16	3	4	-	2	-
NLD	24	10	4	2	3	2
USA	19	1	2	-	1	-
JPN	17	6	4	2	2	2
CZE	13	3	4	2	3	1
FRR	21	17	4	2	2	1
IRL	31	11	5	1	2	1

Table 4. Top black and white bulls in 1%, 100 and 50 positions of Italian rank for the test-run evaluation of October 2012 (OCT) and the official-evaluation of December 2012 (DEC).

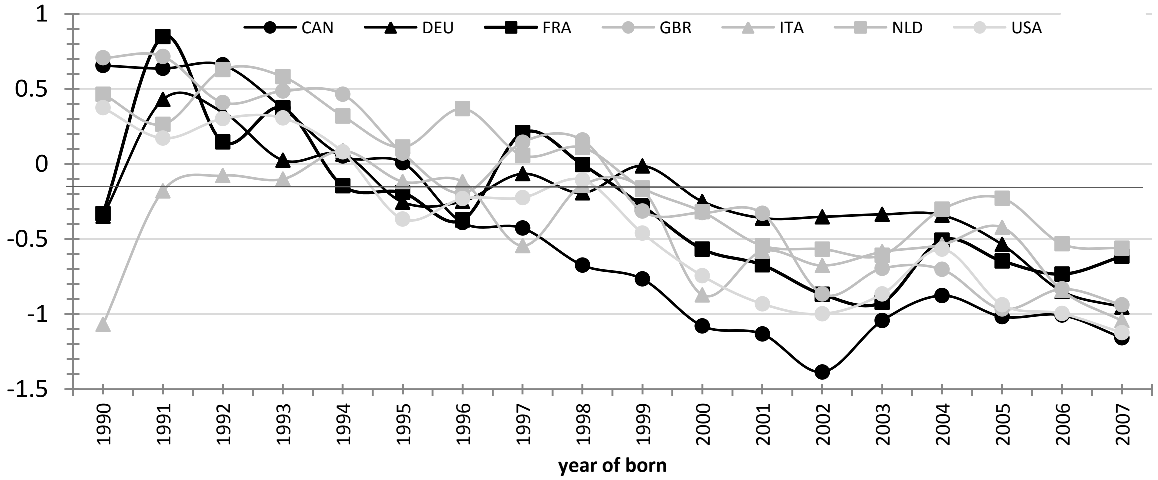
Country[1]	Top 1%		Top 100		Top 50	
	OCT	DEC	OCT	DEC	OCT	DEC
AUS	2	1	1	1	1	1
AUT	2	-	-	-	-	-
BEL	3	2	-	-	-	-
CAN	17	14	5	5	2	3
CHE	6	2	1	1	1	-
CZE	13	2	4	-	3	-
DEU	55	5	10	-	5	-
DNK	34	10	11	1	6	-
FRA	18	1		-	-	-
GBR	36	23	17	11	9	6
ITA	16	3	4	-	2	-
JPN	3	-	-	-	-	-
NLD	113	36	17	3	8	2
NZL	3	1	-	-	-	-
USA	224	445	30	78	13	38

[1] AUS= Australia; AUT: Austria; BEL = Belgium; CAN = Canada; CHE = Swiss, Black and White; CZE = Czech Republic; DEU = Germany; DFS = Denmark, Finland and Sweden (only Denmark send data for BCS evaluation); DNK = Denmark; FRA =France, black and white Holstein; FRR = France, red Holstein; GBR = Great Britain; ITA = Italy; IRL = Ireland*;* JPN = Japan; NLD = The Netherlands; USA = The United States of America.

high values represent fat animals (BCS) or with a good muscle mass (muscularity). On the other side, ANG is related to the angle and spring of the ribs and its relationship with muscularity could be weak. In fact, genetic correlations between FRR and countries that scored BCS were strongest than those of USA. The genetic correlation between ITA and BEL changed slightly. Belgium showed different behaviour in previous works: in 2007 (Lawlor and Klei, 2007) it clustered with USA, whereas in the following years (2nd contribution) it grouped with countries that used BCS as direct trait, and in the last 2 evaluations, the test-run of October and the official-run of December, it clustered again with USA (Figure 1). One of the most important results of the test-run evaluation is reported in Table 3. When Italy used directly BCS for the international evaluation, the number of top-bulls increased in all ranks, particularly the number of top-1% bulls in ranks of IRL (from 11 to 31), CHE (from 10 to 29), and USA (from 1 to 19). The same results were found in top-100 bulls and top-50 bulls (Table 3). At the same time, in the Italian rank (Table 4) the number of top bulls from countries that used BCS as direct trait increased when also ITA used BCS (e.g. in Italian' test-run rank there were 113 top-1% black and white bulls from NLD, while in the official-run they are only 36). The number of bulls of countries that used a best predictor was lowest when ITA used the direct trait. The most evident result was of USA bulls: they were 224 in the Italian test-run rank, and they doubled in the official-run rank (445). The same results were found in top-100 and top-50 positions of Italian rank (Table 4).

Figure 2 depicts the genetic trend of bulls for BCS, based on Italian rank. Clear unfavourable genetic trend was found for all countries. Bulls with worst performance for BCS were from CAN, while bulls born in 2006 and 2007, from DNK, NLD and FRA, showed better, even though negative, performances. Italian bulls had an unfavourable genetic trend and, for most of the years considered, it was negative, even if in line with bulls from other countries.

Figure 2. Genetic trend using EBV in the Italian scale for bulls originated by Canada (CAN), Germany (DEU), France (FRA), Great Britain (GBR), Italy (ITA), the Netherlands (NLD) and United States of America (USA).



Conclusions

Using BCS as direct trait improved the Italian Holstein genetic correlations with other countries that participate to international evaluation for BCS. When ITA used BCS as direct trait, the number of Italian bulls increased in the top positions of other countries rank, and at the same time, in the Italian rank increased the number of bulls of those countries that used BCS as well. Clear unfavourable genetic trend was found for all countries. Italian bulls had an unfavourable genetic trend and, for most of the years considered, it was negative, even if in line with bulls from other countries.

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General conclusions

Correspondence to the aims of the thesis, the main conclusions were that at international levels, using directly body condition score (BCS) instead a best predictor, increased the across-country genetic correlations, and increased the number of Italian bulls in top positions of other countries ranks. Before including BCS as direct trait in the international evaluation, a national evaluation has to become official. Given the data recorded by the Italian Holstein Friesian Breeder Association, a national genetic evaluation of BCS is possible.

In more details, the investigation performed among countries that participated to the international evaluation showed that differences for overall traits were mostly due to the heterogeneity in trait definitions. For BCS, the differences were due to the use of angularity and muscularity as best predictors. Overall traits are important in selection indices to improve functional traits, and their definition depends on the specific breeding goals in each country. National genomic evaluation for type traits has been adopted by some countries and other members planned to start in following years. Across country genetic correlations were useful in evaluating differences among countries. The cluster analysis over the years showed that changes in Interbull evaluation procedure and trait definition influenced the genetic correlations across countries.

The additive genetic variances of BCS and LOC were low but in agreement with estimates reported in literature. The genetic relationships of BCS and LOC with milk yield were moderate to low, and indicated that high producing cows tend to be thinner and to have better locomotion than low producing cows. The correlations of BCS and LOC with fat and protein content and fat to protein ratio were almost negligible. Body condition score seemed to be genetically independent with most of type traits, except for chest width, angularity, rear leg set side view and rear udder height. It showed a strong genetic correlation with its predictor, although this correlation decreased during the years, due to the change in definition of angularity occurred in 2009. Locomotion showed favourable genetic correlations with type traits, and the strongest relationship was with feet and legs functionality.

Clear unfavourable genetic trend was found for all countries that participated to the Interbull evaluation for BCS of Holstein Friesian. Italian bulls had an unfavourable genetic trend too, and for most of the years considered, it was negative, even if in line with bulls from other countries.

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