

Cluster Analysis on Across Country Genetic Correlations for Conformation Traits in Holstein Cattle Breed

Mara BATTAGIN¹ (✉)

Flavio FORABOSCO²

Mauro PENASA¹

Martino CASSANDRO¹

Summary

The aim of this paper is to investigate across country genetic correlations of conformation traits of 21 Holstein bull populations, using cluster analysis. Data consisted of across country genetic correlations of 18 conformation traits estimated by Interbull for the April 2011 routine genetic evaluation. For cluster analysis, the distance measure (d_{ij}) between countries i and j was calculated as $d_{ij}=1-rG_{ij}^2$, where rG_{ij} is the genetic correlation between countries i and j . Traits showed different mean distances with the lowest value for udder depth (0.062) and the highest for locomotion (0.441). For traits with similar definition further investigation is needed to understand differences within cluster. Also, more attention needs to be paid to countries that define or record traits differently from what is suggested by World Holstein Friesian Federation.

Key words

conformation traits, dairy international evaluation, genetic correlations, cluster analysis

Abbreviation keys

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 = The United States of America; ZAF = South Africa.

¹ University of Padova, PhD School in Animal and Food Science, Department of Animal Science, Viale dell'Università 16, 35020 Legnaro (PD), Italy

✉ e-mail: mara.battagin@studenti.unipd.it

² Interbull Centre, Box 7023 S-75007 Uppsala, Sweden

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Aim

International genetic evaluation of dairy bulls for conformation traits began in August 1999 with data from 10 countries. Now the number of countries is 21 and new conformation traits are evaluated (Interbull, 2011a). Genetic correlations across country are needed to estimate international BV of sires. Genetic correlations can be used to evaluate similarities between countries. The cluster analysis could provide a clear picture of distances between countries and the quality of traits harmonization. The objective of this paper is to investigate across country genetic correlations of 18 conformation traits of 21 Holstein bull populations, using cluster analysis.

Material and methods

Data consisted of across country genetic correlations (r_G) of 18 Holstein conformation traits estimated by Interbull for the April 2011 routine genetic evaluation (Interbull, 2011a). Genetic correlations were estimated during the previous test run using deregressed national BV from 21 countries. Not all countries sent information for the 18 traits (Interbull, 2011a). Traits are shown in Table 1 and they are grouped in dimensional, directional, general and mammary.

Hierarchical clustering was performed using the CLUSTER procedure of SAS (SAS Inst. Inc., Cary, NC) to visualize the similarity between countries for each conformation trait. The distance measure (d_{ij}) between countries i and j was calculated as $d_{ij}=1-rG^2_{ij}$, where rG_{ij} is the genetic correlation between countries i and j . The d_{ij} was inversely proportional to rG_{ij} . Dendrograms were plotted using the TREE procedure of SAS (SAS Inst. Inc., Cary, NC).

Table 1. Number of clusters (n) and descriptive statistics of distance for conformation traits

Trait	n	mean	SD ¹	min	max
Dimensional					
Stature	21	0.135	0.113	0.020	0.510
Rump width	21	0.192	0.166	0.040	0.640
Body depth	21	0.260	0.207	0.059	0.806
Chest width	21	0.299	0.217	0.078	0.904
Directional					
Rump angle	21	0.093	0.076	0.020	0.328
Rear leg set	21	0.224	0.188	0.020	0.708
Foot angle	20	0.345	0.211	0.135	0.916
Rear leg rear view	20	0.377	0.229	0.116	0.848
General					
Body condition score	11	0.330	0.223	0.098	0.750
Angularity	19	0.385	0.219	0.135	0.863
Locomotion	12	0.441	0.226	0.190	0.916
Mammary					
Udder depth	20	0.062	0.037	0.020	0.154
Teat length	20	0.092	0.102	0.020	0.422
Front teat placement	21	0.108	0.097	0.020	0.392
Rear teat placement	18	0.149	0.196	0.020	0.779
Fore udder	21	0.268	0.198	0.078	0.863
Rear udder height	21	0.278	0.164	0.078	0.708
Udder support	21	0.318	0.236	0.098	0.971

¹ Standard Deviation

Results and discussion

Mean distance between countries within trait is reported in Table 1. Low value denotes similarities between countries for the given trait. Among the four groups, mammary traits showed the lowest mean distance with values that ranged from 0.062 for udder depth to 0.318 for udder support. Dimensional came after mammary traits, with the lowest value for stature (0.135) and the highest for chest width (0.299). Among directional traits, rump angle showed the lowest (0.093) and rear leg rear view the highest distance (0.377). The general group showed the highest values, with mean distance of 0.441 for locomotion. Schneider and Fikse (2008) found similar results using principal components analysis. Low mean distance between countries and a small number of principal components needed to explain variation of a trait (Schneider and Fikse, 2008), could be attributed to similar trait definition and similar genetic background of the animals. An example of different trait definition is presented in Figure 1a, where two main clusters can be identified for stature: one groups countries (BEL, CAN, JPN, FRA, DFS, NLD, DEU, ESP, EST, FRR, CZE, HUN, GBR, USA, ITA and POL) that scored stature from top of the spine in between hips to ground as defined by World Holstein Friesian Federation (WHFF, 2008) and one groups the remaining countries (CHE, CHR, NZL, AUS and ZAF), three of which (CHE, CHR and NZL) scored stature from top of the withers or shoulders to ground. Both these two countries belong to South hemisphere where different management systems and genotype by environment interaction could affect their correct allocation in the cluster. For traits with homogeneous definition such as rump angle (Figure 1b), differences between clusters could be attributed to model definition, heritability and genotype by environment interactions (Schneider and Fikse, 2008).

Udder depth (Figure 2a) exhibited the lowest mean distance among all conformation traits. The dendrogram showed two distinct; the first sub-cluster group included AUS, GBR, BEL, FRR, DFS, NLD, USA, CHE, CHR, FRA and JPN and the second sub-cluster included CAN, CHE, CHR, FRA, JPN, CAN, CZE, DEU, ZAF, EST, ESP, POL, HUN and ITA. The order of the countries inside each sub-cluster can change because there can be two or more pairs of countries with the same minimum distance. Rear teat placement (Figure 2b) showed an unexpected dendrogram compared to other traits: ITA and FRR largely contributed to the increase of the mean distance although ITA defined this trait as suggested by WHFF. An investigation is needed to understand why these two countries are detached from others. For mammary traits results are comparable with Schneider and Fikse (2008).

General group included two traits recently evaluated by Interbull: body condition score (BCS) and locomotion. Results for BCS (Figure 3a) are comparable with the pilot study conducted by Lawlor and Klei (2008). There are two distinct clusters for countries that use BCS (BEL, CHE, NLD, GBR, CZE, DEU and DFS) and countries that use a best predictor (FRA, ITA, USA and FRR). Dendrogram for locomotion (Figure 3b) differed from results obtained by Lawlor and Klei (2008). Lawlor and Klei (2008) found large distance for BEL, because the country definition of locomotion was bone quality, but since January 2009 BEL has sent rear leg rear view trait as predictor of locomotion (Interbull, 2011a). Locomotion exhibited the highest mean distance among

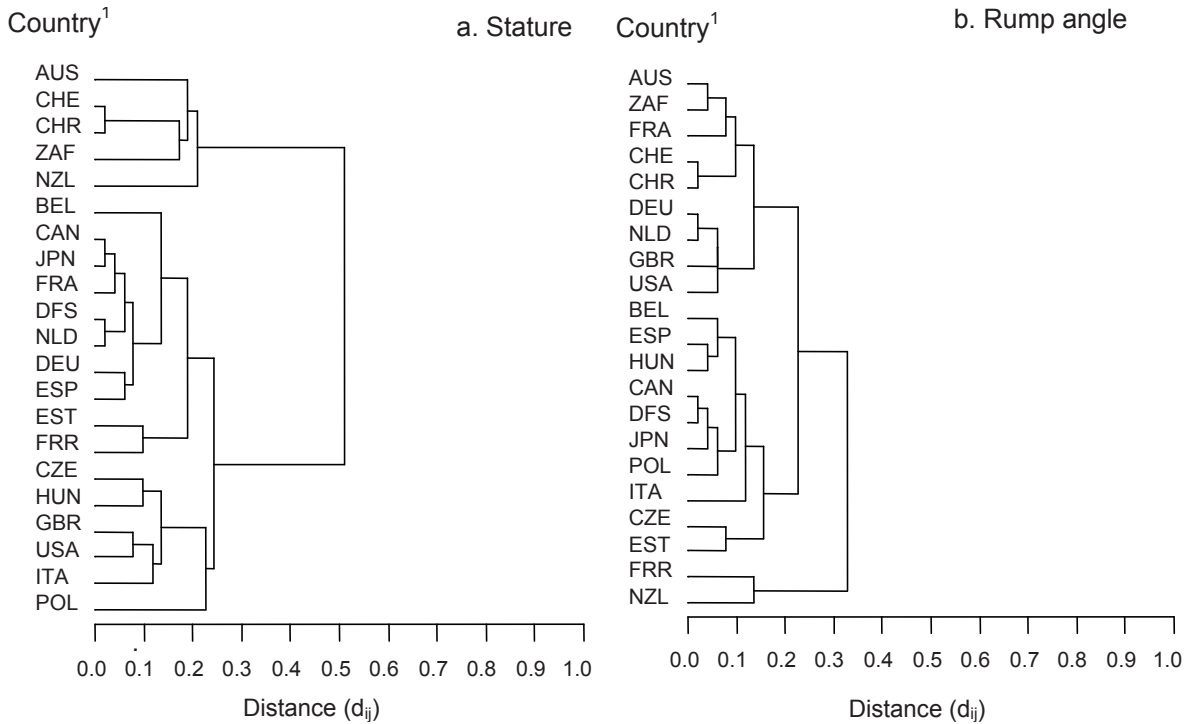


Figure 1. Dendrograms of stature (a) and rump angle (b).

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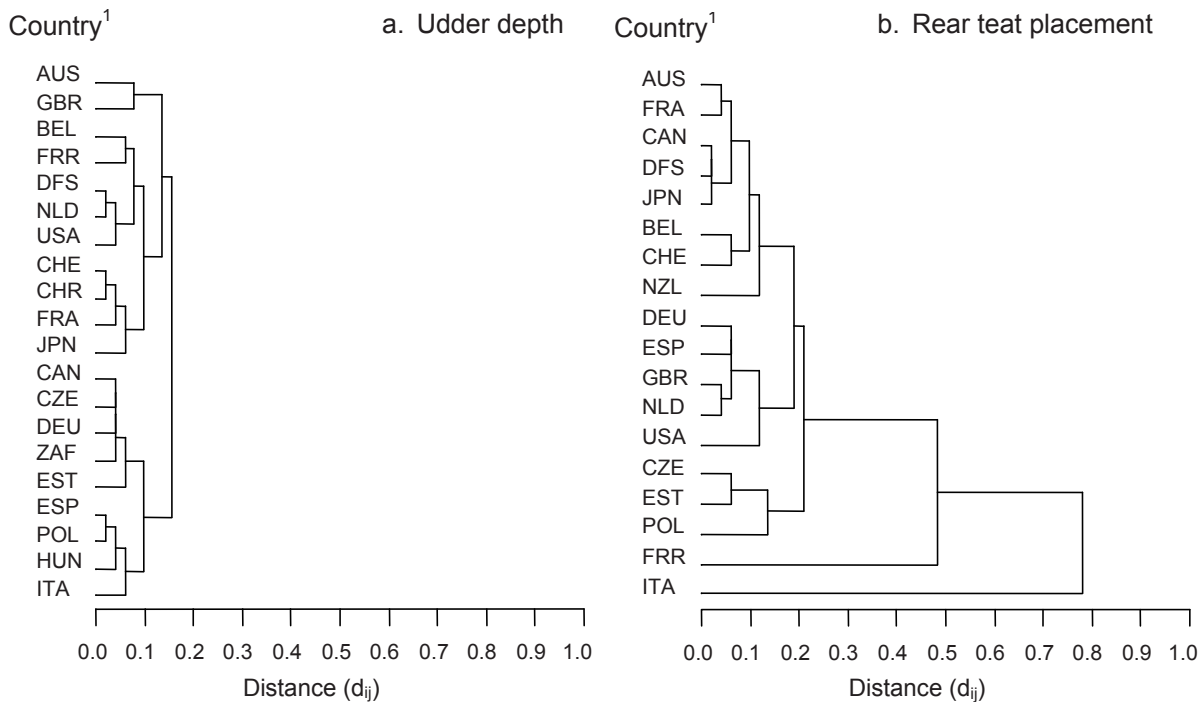


Figure 2. Dendrograms of udder depth (a) and rear teat placement (b).

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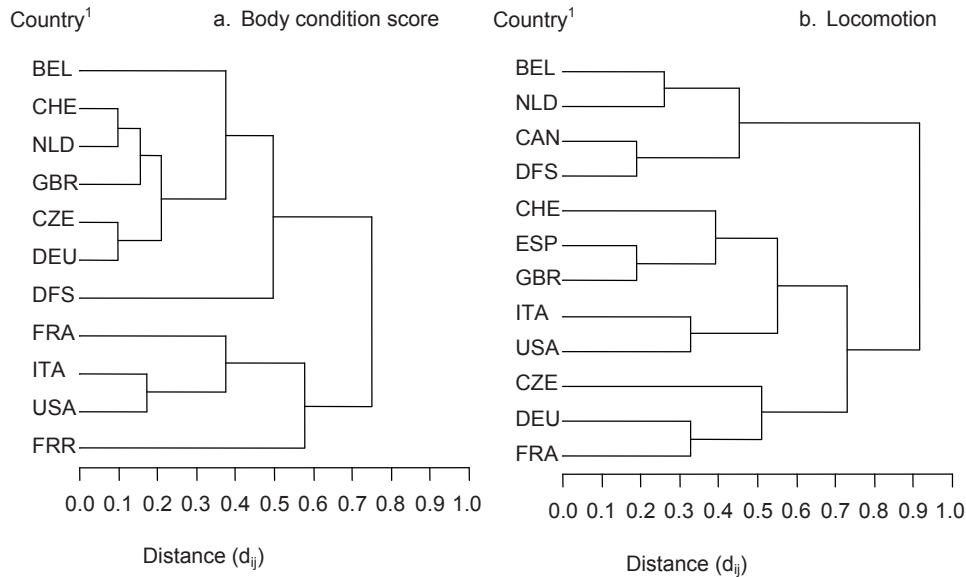


Figure 3. Dendrograms of body condition score (a) and locomotion (b).

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all conformation traits, and the different definitions of this trait among countries can explain the high value. NLD, DFS, GBR, DEU and FRA use locomotion, CHE and ESP use feet and legs score, ITA uses a “subjective functionality score”, USA uses “mobility” and BEL uses “rear leg rear view” as measure for locomotion (Lawlor and Klei, 2008; Interbull, 2011b).

Conclusions

The cluster analysis provided a clear picture of countries distances and the quality of traits harmonization. For traits with similar definition further investigation is needed to understand differences within cluster. New traits (BCS and locomotion), are more influenced by non-genetic factors, which results in larger distances among countries. More attention has to be paid to countries that define or record traits differently from what suggested by WHFF.

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