Characterization of the Global Brown Swiss Cattle Population Structure

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Abstract

Genetic diversity in the Brown Swiss population was characterized by examining some population genetic parameters such as the level and the rate of inbreeding, population size, generation intervals, average relatedness, effective number of founders and ancestors. Pedigree records for 181.094 Brown Swiss individuals were obtained from 22 countries. The mean inbreeding coefficient for the Brown Swiss population was 0,77% and the average generation interval for the whole population was 6,5 years. The highest average generation interval was in the sire-son pathway with a value of 8,7 years. The pedigree population had 1,1% mean average relatedness. The effective number of founders and the effective number of ancestors was 141 and 88, respectively.

Keywords: Brown Swiss, pedigree analysis, inbreeding

1. Introduction

One way to describe genetic variability and its evolution across generations is through the analysis of pedigree information. Inbreeding trend, effective number of founders, effective number of ancestors and effective population size are some measures of genetic variation based on pedigree information (Boichard *et al.*, 1997).

experiences Through the from the international genetic evaluations of dairy bulls of six major breeds run by Interbull for 15 years it has been possible to study the global dairy pedigrees. Updates to the global dairy pedigrees housed by Interbull are a continuous process complemented with the newest young bulls as well as corrections in existing al., information (Philipsson et 2009). Currently, Interbull is setting up a database for storage of more complete pedigree including information on bull dams.

This study is focused on the pedigree analysis of Brown Swiss cattle populations from 22 countries from around the world. Seven of these populations have been joined to form a common reference population for a global genomic evaluation of dairy traits in this breed.

The objectives of this study were to assess the genetic diversity of the Brown Swiss cattle population in terms of genetic variation, population structure and identification of the most important individuals for genomic analysis.

2. Materials and Methods

2.1 Description of data

Pedigree information of 181.094 (71.497 males and 109.597 females) Brown Swiss cattle, which was based on sires and their ancestors, was used. Animals originated from 22 different countries, seven of them reported higher number of animals to Interbull (Table 1).

Country	Number of Individuals
Austria	28.997
France	746
Italy	8.064
Germany	103.464
Slovenia	863
Switzerland	29.476
USA	9.033
Others	451
Total	181.094

Table 1. List of the major reporting countriesand number of animals they contributed with.

The contributing countries were mainly from Europe and North America and the three most represented countries were Germany (103.464), Switzerland (29.476) and Austria (28.997). The animals in the pedigree had reported or constructed birth years between 1906 and 2009. Out of 181.094 individuals, 36.895 individuals had missing birthdates. For these individuals birthdates were constructed by looking at the birthdates of their parents and offspring.

2.2 Analysis procedures

The pedigree was checked and edited to ensure integrity of the data, e.g. individuals listed as sire and dam or offspring with dates of birth before those of their parents were edited.

The Pedigree analysis was carried out using the computer program ENDOG v4.6 (Gutierrez and Goyache, 2005). Parameters like individual inbreeding coefficient, average relatedness, effective number of founders, effective number of ancestors and other parameters were calculated by ENDOG v4.6.

2.3 Definitions

Inbreeding coefficient (F) is the probability that two alleles from the same locus are identical copies of an ancestral allele (Wright, 1931).

Average Relatedness (AR) is twice the probability that a randomly picked allele from an individual is identical by descent with another allele from a different individual (Dunner et al., 1998).

Generation Interval (L) is defined as the average age of parents when their offspring, which become parents themselves, are born (Gutierrez et al., 2003).

Effective Number of Founders (f_e) can be defined as the number of equally contributing individuals that would give rise to the same genetic diversity as in the reference population under study (Lacy, 1989).

Effective Number of Ancestors (f_a) is the minimum number of individuals (founders or not) that explain the complete genetic diversity in a reference population (Sölkner et al., 1997).

3. Results and Discussions

3.1 Inbreeding coefficient (F)

The mean inbreeding coefficient (F) of the Brown Swiss population under study was 0,77%. Figure 1 shows that mean inbreeding coefficient increased from 0,02% (for animals born between 1950 and 1954) to 2,89% (for individuals born between 2000 and 2004). The increase in inbreeding coefficient since mid-1970s was swifter compared with the earlier periods.



Figure 1. Mean inbreeding coefficient per group of 5 years period.

These findings illustrate higher level of inbreeding (in the last periods) in the pedigree population under study than most other cattle populations in different parts of the world; it should be noted that the pedigree used was based on AI sires and their ancestors, not a complete pedigree. Mean inbreeding for recently newborn individuals was less than 1% in Spanish beef cattle breeds (Gutierrez et al., 2003) and less than 1,5% for Irish dairy and beef breeds (Mc Parland et al., 2007).

3.2 Average Relatedness (AR)

The mean average relatedness calculated for the total pedigree population was 1,10%. Peixoto et al. (2010) reported the same AR (1,10%) for the Guzerat breed in Brazil while AR for most Spanish beef breeds (between 0,10% and 0,73%) was a bit lower (Gutierrez et al., 2003).

The average relatedness between the pedigree individuals increased periodically and reached 4,59% for animals born between 2000 and 2004. As Figure 2 shows there has been a sharp increase in mean average relatedness since 1970, except the decline between 1985 and 1989, until recent years. These results indicate that the relationship between newly born animals is increasing, though the increase is lower in the later periods.



Figure 2. Mean average relatedness per group of five years period.

3.3 Generation Interval (L)

The average generation interval for the total pedigree population was 6,56. This interval is considerably higher compared with those reported for Danish dairy cattle (between 4,6 and 5 years), Spanish beef cattle (mostly less than 5,5 years) or Italian beef cattle ranging from 4,93 to 5,35 (Sorensen et al., 2005; Gutierrez et al., 2003; Bozzi et al., 2006). This high generation interval could be as a result of the constructed birthdates.

The highest average generation interval was in the sire-son pathway with a value of 8,73 years. Table 2 shows that the lowest average generation interval was recorded in the damdaughter pathway.

	Generation	Interval
Type of Path	Number of Individuals	Interval
Sire-Son	18.784	8,73
Sire-Dau	83.503	7,81
Dam-Son	18.689	5,26
Dam-Dau	74.499	4,93
Average		6,56

Table 2. Average generation Interval for thefour ancestral pathways.

3.4 Founders and Ancestors

The number of founders was counted to be 41.011, corresponding to 22,65% of the total pedigree population. The number of ancestors (founders or not) was 36.795, which was 20,32% of the whole population.

The effective number of founders of the pedigree population was 141. Compared with the total number of founders, the number of effective founders, i.e. number of equally contributing founders that would be expected to produce the same genetic diversity as in the population under study (Gutierrez and Goyache, 2005), was low.

This suggests that the vast majority of the founders had low and unequal contribution to the genetic variability of the reference population which led to loss due to unequal contribution of founders (Lacy, 1989).

The minimum number of ancestors (not necessarily founders) that would explain the whole genetic diversity of the reference population was 88. This effective number of ancestors is lower than the effective number founders, which indicates that there might have been genetic bottleneck in the pedigree population (Boichard et al., 1997).

The analysis of the top genetically contributing founders showed that most of these founders were sires, i.e. 14 out of the top 20. This can be explained by the fact that the number of offspring produced per sire was much higher than the number of offspring per dam (as shown in this study). The highest contributing founder sire had 3,22% genetic contribution while the highest contributing founder dam had 1,75% genetic contribution (see table 3). The overwhelming majority of founders for the total reference population were from the US subpopulation.

The top 20 founders contributed 23% of the genetic variation in the pedigree population. The relatively higher effective number of founders and effective number of ancestors seen in this population explains the low genetic contribution made by top founders and ancestors.

Table 3. Description of most importantfounders.

	Genetic Contribution
First Founder	3,22%
Second Founder	2,61%
Third Founder	2,36%
First Founder Dam	1,75%
Top Ten Founders	17,42%
Top Twenty Founders	22,84%

4. Conclusions

As shown in this study, there has been decrease in the genetic variation of the Brown Swiss populations. Breeders should be aware of this situation and breeding systems should be designed to maintain the genetic variation of the Brown Swiss populations. Future research should be made on a complete global Brown Swiss pedigree to assess the genetic variation in the Brown Swiss populations.

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