

Genomic relationship among InterGenomics populations

Genomische Verwandtschaftsbeziehungen der heutigen (InterGenomics) Braunviehpopulationen

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Zusammenfassung

Das europäische Braunvieh ist bekannt für seine Langlebigkeit, Funktionalität, Anpassungsfähigkeit, Leichtkalbigkeit, Beanspruchbarkeit, Krankheitsresistenz und Fügsamkeit. Das Braunvieh hat sich weltweit verbreitet und ist sehr beliebt in Europa. Wir haben beschlossen, die genomischen Verwandtschaftsbeziehungen zwischen den heutigen (InterGenomics) Populationen zu analysieren. Es wurden genomische Proben aus den Ländern: Österreich, Schweiz, Deutschland, Frankreich, Italien, Slowenien und den USA zueinander in Verbindung gebracht. Der durchschnittliche IBD (Identity-by-descent) zwischen den Populationen war sehr ähnlich, in der Mehrzahl der Populationen lag er bei 0.05. Gleichzeitig lag der maximale IBD zwischen zwei Individuen auf einem sehr engen Intervall von 0.50 (Österreich – Slowenien) bis 0.60 (Deutschland – Italien und Schweiz – USA). Die maximalen IBD's zwischen individuellen Paaren bestätigen den Spermaaustausch zwischen den Ländern, der statt findet um in den einzelnen Ländern qualitativ hochwertige Zuchtstiere zu züchten. Ein Nachteil dieser genomischen Verwandtschaftsschätzung ist, dass keine Aussage zur Richtung der Einführung der Vätertiere in verschiedene Populationen getroffen werden kann.

Abstract

The European Brown Swiss breed is noted for its longevity, functionality, adaptability, calving ease, strength, disease resistance and docility. The Brown Swiss breed is raised worldwide and is very popular in Europe. We decided to found out the genomic relationship among nowadays (InterGenomics) populations. The average IBD among populations was very similar where among the majority of populations were 0.05. Likewise, the maximum IBD between two individuals were on very narrow interval from 0.50 to 0.60. All maximum IBD between individual pairs confirm "exchange" of sire semen among countries to produce sire-sons for improving within county Brown Swiss population. Disadvantage of maximum IBD genomic relationship estimation is the unknown direction of sire introduction among populations.

Introduction

The European Brown Swiss breed is noted all over Europe for its longevity, functionality, adaptability, calving ease, strength, disease resistance and docility. The Brown Swiss breed is raised worldwide, but it is very popular in Europe where the highest numbers of Brown head are raised and top selective results have been reached. Brown Swiss is raised also in the USA and it has been the source of new blood lines which have renewed the original European Alpine Brown Breed (www.brown-swiss.org). Despite the fact that Brown Swiss cattle were widespread from its

homeland through the World and it was used for improving local populations we decided to found out the genomic relationship among nowadays (InterGenomics) populations.

Materials and methods

SNP genotypes (BovineSNP50 BeadChip, Illumina, San Diego, CA) were available for 5755 Brown Swiss bulls via the InterGenomics project operated at the Interbull. These bulls originated from seven countries: (Austria (487), France (115), Germany (1642), Italy (1151), Slovenia (181), Switzerland (1347), and the United States of America (832). Samples were divided by countries based on ear tag identification number where county code is included, too. Genotyping was performed in the Qualitas AG Zug (Switzerland). SNPs were further edited as follows: SNPs were considered if a marker call rate was higher than 95%, minor allele frequencies higher than 0.05, the departure from the Hardy-Weinberg equilibrium at a threshold of $P < 0.0001$, and finally, SNPs that could not be mapped or that were on the X chromosome were also excluded, leaving a final set of SNPs. The imputation method proposed by VanRaden et al. (2010) and its associated program (FindHap; VanRaden, 2010, <http://aipl.arsusda.gov/software/findhap/>) were used. The *Bos taurus* genome assembly UMD 3.1 was used to determine the SNP position within each autosome. Genome-wide relationships between individuals were estimated using the PLINK software (Purcell et al. 2007) as genome-wide identity-by-descent (IBD) estimates for all pairs of individuals.

Results and discussion

Identity-by-descent (IBD) is a fundamental concept in genetics and refers to alleles that are descended from a common ancestor in a base population. In modern applications, IBD relationships are estimated from genetic markers for individuals without any known relationship (Powell et al, 2010). The average IBD (Table 1) among Brown Swiss individuals within InterGenomics populations were similar among the majority of the populations i.e., 0.05. The lowest value (0.04) was observed between Germany and Switzerland populations and the highest (0.07) value between France and USA populations. Likewise, the maximum IBD between two individuals were on very narrow interval from 0.50 (Austria – Slovenia individual pair) to 0.60 (Germany – Italy and Switzerland – USA individual pairs). All maximum IBD between individual pairs confirm use of sire semen from other countries populations to produce sire-sons with the manner to improve within county Brown Swiss population. Disadvantage of this kind (maximum IBD) genomic relationship estimation is the unknown direction of sire introduction among populations.

	AUT	CHE	DEU	FRA	ITA	SVN	USA
AUT		0.05	0.05	0.05	0.05	0.06	0.06
CHE	0.59		0.04	0.05	0.05	0.05	0.06
DEU	0.55	0.59		0.05	0.05	0.05	0.05
FRA	0.59	0.54	0.52		0.06	0.06	0.07
ITA	0.55	0.59	0.60	0.54		0.06	0.06
SVN	0.50	0.50	0.53	0.50	0.52		0.06
USA	0.58	0.60	0.59	0.59	0.59	0.52	

AUT – Austria, **CHE** – Switzerland, **DEU** – Germany, **FRA** – France, **ITA** – Italy, **SVN** – Slovenia, **USA** – United States of America

Table 1: Average IBD (above diagonal) and maximum IBD (below diagonal) among Brown cattle "InterGenomics" populations

References

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