Izlaganje sa znanstvenog skupa
Conference paper

UTILISING SOMATIC CELL SCORE RESULTS IN THE SELECTION OF HOLSTEIN-FRIESIAN BREEDING BULLS (METHODOLOGICAL RESEARCH IN HUNGARY)

J. Vági

Summary

Somatic cell score evaluation of Hungarian dairy herds started in 1988. A mastitis control system is available as a regular service from 1991. It cover almost every high breeding value dairy Holstein-Friesian population.

Genetic investigations tell that there is a close genetics correlation between the mastitis frequency and the somatic cell score (especially in the case of infective mastitis). In the case of selection for decreasing milk somatic cell count both clinic and subclinic mastitis frequency may be decreased, but often differently for genotypes.

The aim of the present investigation is to derive somatic cell score by means of logarithmic transformation processed by the methods described in the literature and making use of Holstein-Friesian population data sets in a comparative evaluation for further population genetics, breeding value estimation and practical utilisation purposes.

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J. Vági, University of Agricultural Sciences, Institute of Animal Husbandry, Department of Applied Animal Genetics and Breeding H-2103 Gödöllo, Hungary

comparative evaluation for further population genetics, breeding value estimation and practical utilisation purposes.

Material and methods

The somatic cell count of milk is hardly applicable directly to genetic investigations, since its variations is multiplicative to the environmental effects, its distribution is asymmetrical and proportional to the mean value. The investigation data of milk somatic cell count should be transformed to result in linear and additive picture of environmental effects, transformed principal data with normal, stabiliseable variance.

The above requirements are completed by the logarithmic transformation of somatic cell count results, and the data gained such way are called sometic cell score (or linear somatic cell score, by some authors). The logarithmic transformation is primary and principal precondition of utilising the somatic cell count in genetic programmes.

The methods applied are summarised below:

First Ali and Shook (1981) were who counted somatic cell score (SCS) characteristics applying natural logarithm transformation to somatic cell count (SCC) by the formula

$$SCS = \frac{[\ln(SCC/1000)]}{0.69315} - 3.6439$$

The natural based logarithm is used, for example, in Finland in parallel with the decimal based logarithm transformation.

Decimal based logarithm transformation is currently used in all Scandinavian countries and Denmark.

Binary based logarithm transformation is used in the greatest Holstein-Fries breeding countries like USA, Canada, Germany ,The Netherlands, etc. In Germany, however, Bavarian breeders prefer to use decimal based logarithm transformation.

In the different logarithmic transformations the magnitudes of the somatic cell scores are interpreted unambiguously.

The production control aim somatic cell score data are used to produce mean values for given lactation periods and sections of lactations. The means used are simple mathematical or geometrical, as well as corrected and weighted mean values.

Data on 1-3 parity production and 1-9 month test-day production were collected from purebred and crossbred herds of more than six thousand cows.

Results

The practical test of somatic cell score characteristics determined by different methods allows us to draw the conclusions as follows:

1.) Both decimal, natural and binary based logarithms are applicable to perform logarithmic transformations. The most important difference is in interpretation of somatic cell score in deriving somatic cell number. The decimal based logarithm seems more known and usual for the first sight, while the natural is more accepted scientifically. However, the compilation of the result of both method is more complicated as compared to the binary based logarithmic transformation. The somatic cell score values obtained by the binary based logarithm transformation means a duplication of cell count at each cell score increase.

2.) In the case of all the three logarithm transformation normal distribution or near-normal distribution is experienced. With the techniques mentioned, the value of variance is stabilised. The main sources of variance, such as stock, lactation number, section, year, season, first calving age of cow, genotype, etc. are elucidated and analysed easily and the population genetics parameters, such as heritability, repeatability, phenotype and genetic correlations, can be also determined.

3.) Until the Hungarian correction factors of the first calving age, lactation section and lactation number will be elaborated, the lactation somatic cell score is determined practically from the first nine - or occasionally the 6-9 - month production monitoring data by using simple mathematical mean of somatic cell score values. The application of geometry mean the lactation somatic cell score will not expose normal distribution.

In brief it can be concluded that the applicaton of binary based logarithm transformation accepted in the most important Holstein-Fries production countries seems the most practicable in Hungary. The parameter makes the evaluation of the results according to genotypes simpler and more applicable in international comparison.

PRIMJENA REZULTATA SCORA SOMATSKIH STANICA U ODABIRU HOLSTEIN-FRIZIJSKIH RASPLODNIH BIKOVA
(Metodološko istraživanje u Mađarskoj)

Sažetak

S procjenom scora somatskih stanica u mađarskih mliječnih stada započelo se 1988. Sustav kontrole mastitisa postoji kao redovita služba od 1991. Njime je obuhvaćena gotovo čitava Holstein - frizijska mliječna populacija visoke rasplodne vrijednosti.

Genetska istraživanja pokazuju da postoji uska genetska povezanost između učestalosti mastitisa i zbroja somatskih stanica (osobito u slučaju infektivnog mastitisa). U slučaju odabira za smanjenje broja somatskih stanica mlijeka može se smanjiti i klinička i supklinička učestalost mastitisa, ali različito za genotipove.

Cilj je ovog istraživanja bio dobiti zbroj somatskih stanica pomoću logaritamske transformacije izvedene metodama opisanim u literaturi te služeći se skupovima podataka o Holstein-frizijskoj populaciji u komparativnoj procjeni genetike buduće populacije, procjeni rasplodnih vrijednosti kao i u svrhu praktične primjene.