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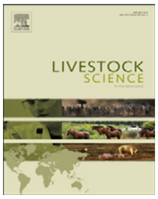

Pedigree analysis of the Hungarian Thoroughbred population

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ABSTRACT

The aim of the study was to analyse the pedigree information of Thoroughbred horses which were participating in gallop races between 1998 and 2010 in Hungary. Among the 3043 individuals of the reference population there were imported animals from foreign countries (e.g. Germany, England or Ireland) and horses that were born in Hungary. The number of complete generations was 15.64 (varied between 0 for the founders and 25.20), the mean number of full generations was 6.69, and the mean maximum generations were 28.96. The number of founders was 1062, and the effective number of founders was 42. Two hundred and thirty-two founders were born before 1793 (when the stud book of the Thoroughbred breed was closed), therefore these founders are considered as true founders of the breed. These 232 founders were responsible for 88.58% of the gene pool in the reference genome. The significant difference between the number of founders and effective number of founders indicate that the genetic diversity decreased greatly from the founders to the reference population. The number of ancestors was 908 and only 6 of them were responsible for 50% of the genetic diversity in the examined population. The effective number of ancestors was 15.32. From the ratio of the effective number of founders and effective number of ancestors we concluded to a bottleneck effect that characterizes the pedigree under study. Generation interval was more than a year longer for stallions (12.17) than it was for mares (10.64). More than 94% of the individuals in the pedigree were inbred, and the average inbreeding of the population was 9.58%. Considering the changes of the inbreeding status of the examined population 4 large time periods were appointed. The first lasted until 1780, the second period was from 1780 until 1952, the third period was between 1946 and 1998 and the last one was from 1998 until 2008. Rate of inbreeding in the last generation was 0.3%, which forecasts further increase in inbreeding. The effective population size was above 100 in the last 30 generations, proving the genetic diversity did not decrease by a level that would make long-term selection impossible.

1. Introduction

The Thoroughbred breed is known as one of the fastest horse breeds in the world. The breed was bred in England, during the 18th century, from native (celtic), and imported (oriental) horses. The first General Stud Book (which contained 237 mares and 169 stallions) was published in 1792, and it was closed in 1793. Since then, only individuals that were comprised in the original stud book (or are descendants of those) are allowed in breeding. Genetic improvement of the breed followed a consistent, strict breeding scheme for centuries, while the only breeding goal was the better performance of the horses at horse races (Fehér, 1990). The breed has had 4 early main founder stallions, namely: *Byerly Turk*, *Godolphin Arabian*,

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Darley Arabian and *Curwen Bay Barb* (Cunningham et al., 2001), that had a great impact on today's Thoroughbred population. Outside of the races, Thoroughbred horses are also widely used in crossings.

Thoroughbreds were imported to Hungary from England since the 1780s and races for Thoroughbred horses were organized from 1814 on. From the 1820s, the number of the imported Thoroughbreds started to raise and the first official racetrack was opened in 1827.

The Hungarian Thoroughbred Stud Book was first published in 1823 (Fehér, 1990). Since then, imported horses entered the Hungarian Stud Book with a status approved and recognized by the International Stud Book Committee (2011). The horses must have racehorse identity card and official pedigree certificate issued by the officially recognized Stud Book Authority of the country of origin deposited in the office of Hungarian Stud Book Management. The current rules of entry to the Hungarian Stud Book for Thoroughbreds are following the International Agreement on Breeding, Racing and Wagering (2012). As it follows, the Hungarian Thoroughbred population is a subpopulation of the English–Irish population (further information is given in the Results and Discussion part).

In pedigree analysis, information about the animal's ancestors and collateral relatives is used to carry out analyses to estimate parameters, which characterize the genetic structure and diversity of the populations (Maignel et al., 1996). Pedigree analysis has an important role in breeding programmes, which aim to maintain genetic diversity of endangered populations (either wild or domesticated species). In case of livestock, pedigree analysis is used to calculate several population parameters, in the interest of sustainable breeding.

Such analyses are specifically important in case of populations, which were bred under high selection pressure and closed stud books for centuries. Based on pedigree data, breeding values and inbreeding coefficients might be estimated as well as many other parameters that characterize a population.

2. Aims

The objective of this study was to characterize the Hungarian Thoroughbred population, based on pedigree information. Such an analysis is important both in preservation of genetic diversity of populations and during improvement of a livestock by selection.

3. Materials and methods

3.1. The database

The pedigree of the horses was recorded with the "Equihun Pedigree Builder" software (written by the first author). The software is capable of recording all relevant information about the individuals, to check the pedigrees for errors, and to export all information about the individuals in any format we might have needed later.

For the purpose of our analysis, the reference population was defined as horses that were born between 1998 and 2008. These horses represent the last generation of racehorses in Hungary at the 2010 racing year. To establish the database, we used information from the Hungarian Stud Books (volumes I–XXVIII), as well as information from on-line databases (〈www.pedigreequery.com〉, 〈www.tesiopower.com〉, 〈www.abrakmester.hu〉, 〈www.nlkft.hu〉).

The database comprised the following information about the horses: name, unique identification number, date of birth, colour, gender, parents, country of origin, breed (Thoroughbred), breeder, mare family and additional information.

We used the Pedigree Viewer programme (Kinghorn, 1994) to verify if the set-up of the database is appropriate for the analysis, and also if there are any errors left in the data files. The analysis was carried out with the ENDOG software, developed by Gutiérrez and Goyache (2005).

3.2. Calculated parameters

3.2.1. Pedigree completeness

Pedigree completeness expresses how many generation-equivalent information we have on average in any individual's pedigree. The number of maximum generations known and number of full generations known were also calculated in our analysis.

Pedigree completeness determines how accurately the inbreeding coefficient can be estimated, therefore it has a high influence on the validity of the estimated values.

3.2.2. Generation interval (L)

Generation interval is defined as the average age of the parents, when their offsprings that were used in breeding are born. This parameter was estimated for the whole pedigree, and also for the reference population separately. Generation intervals were estimated on 4 different paths separately in this study: sire–daughter, sire–son, dam–daughter and dam–son ways.

3.2.3. Number of founders and effective number of founders

Founders are defined as animals in the pedigree, without known parents. Number of founders is dependent on the available pedigree information, and increases exponentially with the number of known generations. Founders are responsible for all genetic variability in the reference population. The unknown parents of those individuals that have known ancestors only on one parental line are also considered as founders.

Effective number of founders (f_e) is defined as the number of founders that are expected to generate the same genetic variability as that observed in the population under study, given, all founders equally contribute to the genetic diversity of the reference population (James, 1972; Lacy, 1989).

3.2.4. Number of ancestors and effective number of ancestors

Number of ancestors is the minimum number of individuals in the pedigree, which explains the total genetic variability in the reference population. Unlike the number of founders, number of ancestors does not increase rapidly with the number of generations and it is