



## Short communication

# Pedigree analysis in the German Paint Horse: Genetic variability and the influence of pedigree quality



Margot Siderits\*, Roswitha Baumung, Birgit Fuerst-Waltl

University of Natural Resources and Life Sciences, Department of Sustainable Agricultural Systems, Division of Livestock Science, Gregor-Mendel-Str. 33, A-1180 Vienna, Austria

## ARTICLE INFO

*Article history:*

Received 13 April 2012

Received in revised form

22 August 2012

Accepted 25 October 2012

*Keywords:*

Paint Horse

Genetic variability

Pedigree analysis

Inbreeding

## ABSTRACT

Pedigree information of the German Paint Horse was analysed in order to assess genetic variability within this population. A data set consisting of 14,313 horses was provided by the German Paint Horse Breeding Association. Three reference populations of registered Paint horses born in Germany between the years 2000 and 2009 (1), between 2000 and 2009 based on a manually improved pedigree (2) and between 1990 and 1999 (3) were defined. For all three reference populations the quality of pedigree information, average inbreeding coefficients, effective number of founders, effective number of ancestors, effective number of founder genomes and most important ancestors were analysed. One aim of this study was to compare the results before and after the pedigree was improved. The current Paint Horse population in Germany (reference population 2) has an average number of complete generation-equivalent of 4.77. Average inbreeding coefficients are 0.49% for all and 0.41% for five considered generations. The number of founders for the current population is 4341. The effective number of founders is 963, the effective number of ancestors is 186.1 and the effective number of remaining genomes in the reference population is 118.5. Half of the gene pool of the current German population is explained by 120 animals. These rather high values indicate a good genetic diversity within the breed. However, results have to be interpreted carefully as depth of pedigree and the rather low average generation equivalent of the German Paint Horse have to be taken into account.

© 2012 Elsevier B.V. All rights reserved.

## 1. Introduction

With 13,592 herd book animals registered annually, the Paint Horse is the second-largest horse breed in the United States. Germany has the third largest breeding population (563 herd book animals registered annually) after the United States, which is the country of origin, and Canada (APHA, 2010a). While the coat pattern is essential, Paint Horses also have strict bloodline requirements (APHA, 2010b). To be eligible for registry, a Paint's sire

and dam must be registered with the American Paint Horse Association, the American Quarter Horse Association, or the Jockey Club (Thoroughbreds).

A prerequisite for decisions in livestock development and breeding programmes is the extensive knowledge of breed characteristics (FAO, 2007). Pedigree analysis is one method towards this aim as it enables the estimation of genetic variability and its evolution over time utilising pedigree information (Maignel et al., 1996). Especially in horse breeds, pedigree information often is of rather high quality. In contrast, routinely evaluated performance data for genetic variance analyses or genomic data, both also allowing the study of genetic variability, may not be easily available. Hence, pedigree analysis was often performed

\* Corresponding author. Tel.: +43 664 580 15 68.

E-mail address: [margot.siderits@gmx.at](mailto:margot.siderits@gmx.at) (M. Siderits).

to describe the genetic variability and to gain knowledge of the structure of various horse breeds (e.g. [Cervantes et al., 2008](#); [Valera et al., 2005](#); [Zechner et al., 2002](#)).

The concept of pedigree analysis goes back to the work of [Wright and McPhee \(1925\)](#). The first proposal to analyse probabilities of gene origin in an approximate approach was made by [Dickson and Lush \(1933\)](#); [James \(1972\)](#) described a procedure how to compute genetic contributions of individuals to later generations from pedigrees. For larger pedigrees, so called gene drop simulations may be applied ([MacCluer et al., 1986](#)). Detailed descriptions of measures for genetic variability were provided by [Boichard et al. \(1997\)](#).

The knowledge of different genetic variability measures and of the structure of this breed will certainly be beneficial for further breeding schemes in the German sub-population. Apart from that this work has a focus on the impact of pedigree depth and completeness on various measures of genetic variability.

## 2. Material and methods

### 2.1. Data

Information on 2364 animals registered in the German Paint Horse stud book and their ancestors was provided by the Paint Horse Club Germany (PHCG), the responsible German Breeding Association. The pedigree consisted of 14,313 individuals. Each complete record included the registration code of the individual, its sire and its dam, as well as name, sex, breed, birth year, birth place, coat colour and coat pattern. Data preparation was carried out by means of the Software Package SAS 9.2 (2003).

### 2.2. Measures of genetic variability

Several measures of genetic variability were calculated from the pedigree data. The effective number of founders ( $f_e$ ) is defined as the number of equally contributing founders (animals with unknown ancestors in the pedigree) that would be expected to produce the same genetic diversity as in the population under study ([Lacy, 1989](#)). This parameter is the reciprocal of the probability that two randomly drawn genes in the population under study originate from the same founder ([James, 1972](#)). The effective number of ancestors ( $f_a$ ) is the minimum number of ancestors, not necessarily founders, explaining the complete genetic diversity of a population ([Boichard et al., 1997](#)). The parameter  $f_a$  accounts for the losses of genetic variability produced for the unbalanced use of reproductive individuals producing bottlenecks. Only the marginal contribution of an ancestor that is not explained by other ancestors chosen before must be considered ([Boichard et al., 1997](#)). The effective number of founder genomes ( $N_g$ ) accounts for both unequal contributions of founders and random loss of alleles caused by genetic drift ([Lacy, 1989](#)).

Quality of pedigree information was described by the average complete generation equivalent ([Boichard et al., 1997](#)). [Maignel et al. \(1996\)](#) reported the complete generation equivalent as the best way to describe pedigree

information. Inbreeding coefficients were computed according to [VanRaden \(1992\)](#) considering all available and five generations in the pedigree ( $F_A$ ,  $F_5$ ), respectively. All calculations of measures describing genetic variability were carried out using the Fortran software package PEDIG ([Boichard, 2002, 2007](#)).

### 2.3. Reference populations

In order to be able to perform a pedigree analysis, reference populations had to be defined. In accordance to [Baumung and Sölkner \(2002\)](#), reference populations contained animals potentially contributing to the next generation. Hence, reference population 1 (RP 1) was defined by registered animals born in Germany between the years 2000 and 2009. To analyse the effect of increasing the quality and depth of the current German pedigree records, the 30 most important ancestors based on the original pedigree were identified. By means of the internet database [www.allbreedpedigree.com](http://www.allbreedpedigree.com), their parents, grandparents and great-grandparents were manually added to the existing pedigrees if missing. Additionally, registration numbers of some animals were corrected to be consistent and in accordance with the above mentioned Internet source. Missing links between animals were thus filled and new records could be created. Finally, the revised pedigree consisted of 14,570 records. To demonstrate the changes in the calculated measures depending on pedigree completeness, the second reference population (RP 2) was defined in the same way as the first using the improved pedigree however. The third reference population (RP 3), including 679 horses, was based on animals born in Germany between 1990 and 1999 and served as a historical analogy. The improved pedigree was also used for RP 3.

## 3. Results and discussion

### 3.1. Pedigree completeness

The quality of the pedigree information for the RPs 1–3 is illustrated in [Fig. 1](#). The completeness level in the second generation was 99.9%, 99.9% and 99.6% for RPs 1, 2 and 3, respectively. These high levels drop in the following generations. From the fourth generation on the difference between the calculated parameters before and after enlarging and improving the pedigree is evident. After five generations only 38% of the ancestors are known for the current population and the original pedigree. Improving the pedigree (RP 2) resulted in 45% of known ancestors per generation. For animals born in Germany in the years 1990–1999 (RP 3), 28% of the ancestors are known after five generations. The maximum number of traceable generations was 12, 15 and 14 for RPs 1, 2 and 3, respectively. For several other horse breeds, deeper pedigrees were reported. For Spanish Arab horses born between 1995 and 2004, the completeness of the pedigree information was higher than 90% until the sixth generation ([Cervantes et al., 2008](#)). In the Noriker breed, an Austrian draught horse, the maximum number of traceable generations was 31 for the breeding

Download English Version:

<https://daneshyari.com/en/article/5790448>

Download Persian Version:

<https://daneshyari.com/article/5790448>

[Daneshyari.com](https://daneshyari.com)