

Estimation of allele frequency for Arachnomelia in Austrian Fleckvieh (Simmental) cattle

C. Fuerst¹, B. Heidinger², B. Fuerst-Waltl², R. Baumung²

¹ ZuchtData EDV-Dienstleistungen GmbH, Vienna, Austria.

² University of Natural Resources and Applied Life Sciences (BOKU) Vienna, Austria.

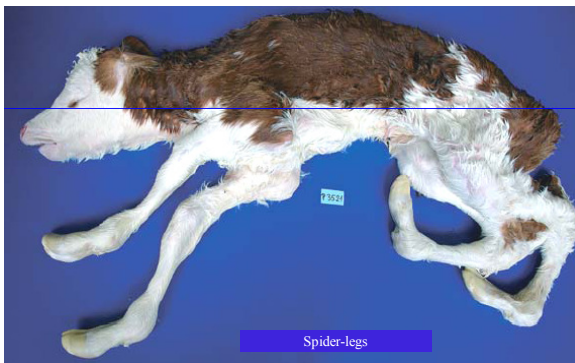


Summary

- mean allele frequencies for birth years 1992-1996 and 2002-2006 were 0.08% and 0.49%, respectively
- increasing trend of allele frequencies until 2005
- indirect gene-test since 2006 keeps frequencies on low level
- for monitoring allele frequencies a program which takes all generations and identified non-carriers into account is recommended

1. What is arachnomelia?

- also known as spider-legs
- lethal autosomal genetic disorder
- malformation of limbs, back and head in cattle
- described in Brown Swiss and Holstein
- similar symptoms observed in Fleckvieh in the 1970s
- again observed in the German-Austrian Fleckvieh population in 2006



Affected calf (source: Meier et al., 2007)

2. Goal

- getting an overview of the current situation in the German-Austrian Fleckvieh population by calculating genetic contributions of possible carriers
- estimating carrier-probabilities and allele frequencies with different computer programs based on gene counting and gene dropping methods

3. Data

3.1 List of carriers and pedigree data

- list of all potential carriers and identified non-carriers (indirect gene-test) consisting of 925 carriers (2008)
- 43,028,033 pedigree records of all German-Austrian Fleckvieh cattle

3.2 Reference populations

- reference populations were 1,452,957 purebred cattle born in Austria between 1992 and 1996 and 3,001,631 animals born between 2002 and 2006
- further analyses for single birth years were carried out

4. Methods

4.1 Gene counting method

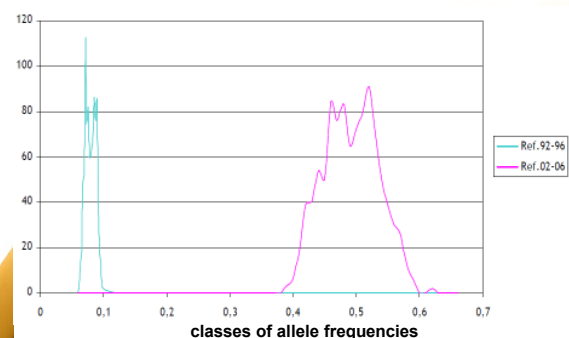
- deterministic approach proposed by Allaire et al. (1982)
- Fortran program written by Lidauer and Essl (1994) considering 6 generations per animal (**Li**)
- SAS program written by Fuerst (2008) taking all generations into account (**Fü 1**), which additionally allows to consider identified non-carriers (**Fü 2**)

4.2 Gene dropping method

- Fortran program developed by Baumung (2008) based on the stochastic gene dropping approach (**Ba**)
- 1,000 repetitions of gene dropping runs

5. Results

Number of observed gene-dropping results for different classes of allele frequencies and reference populations 1992-1996 and 2002-2006



Carrier probabilities (twice allele frequencies) per birth year estimated with different methods

