Session 13 e-mail: kstachow@uoguelph.ca

An in-depth pedigree analysis of Canadian Holstein Cattle

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Objective

- Analyze the pedigree of purebred Canadian Holstein cattle to assess past and current levels of inbreeding and genetic diversity

Materials and Methods

- Pedigree of 8 765 141 animals born between 1883 and 2008 was analyzed.
- CFC, EVA and Pedig software were used.
- The following parameters were estimated:
  - Pedigree Completeness Index
  - Inbreeding: regular and accounting for missing records
  - Effective population size
  - Effective number of founders
  - Effective number of founder genomes
  - Effective number of non-founders
  - Effective number of ancestors
  - Genetic diversity loss

Results

Figure 1. Pedigree completeness index calculated for 5, 10, 15, 20, 25, and 30 generations back on time.

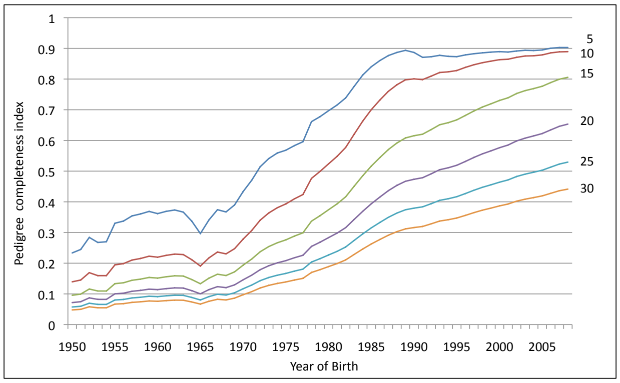


Figure 2. Average inbreeding coefficients: regular inbreeding (reg) and inbreeding estimated accounting for missing pedigree records by VanRaden method (vr).

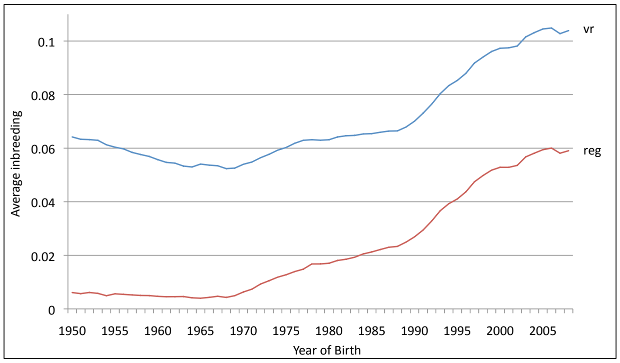


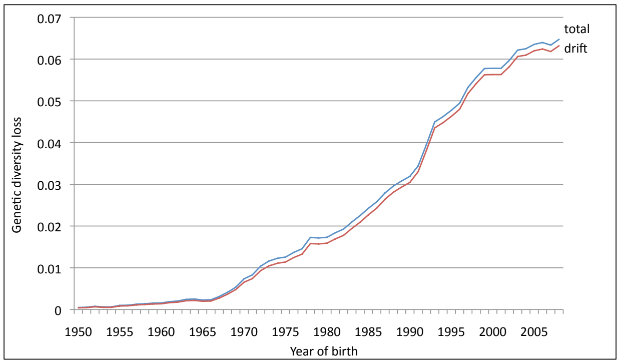
Table 1. Ancestors with the highest contributions to inbreeding of animals born between 1998 and 2008.

#	Name	Year of Birth	% of inbreeding contributed	% of inbreeding accumulated
1	Round Oak Rag Apple Elevation	1965	19.3	19.3
2	Hanoverhill Starbuck	1979	10.6	29.9
3	Pawnee Farm Arlinda Chief	1962	10.6	40.5
4	S-W-D Valiant	1973	7.2	47.7
5	Madawaska Aerostar	1985	5.9	53.6
6	To-mar Blackstar-et	1983	5.1	58.7
7	Osborndale Ivanhoe	1952	4.7	63.4
8	Walkway Chief Mark	1978	3.5	66.9
9	Wisconsin Admiral Burke Lad	1934	2.4	69.3
10	A B C Reflection Sovereign	1946	1.9	71.2

For animals born between 1998 and 2008 the following parameter estimates were obtained:

- Effective population size - 60
- Effective number of founders - 320
- Effective number of founder genomes – 8.2
- Effective number of non-founders – 8.5
- Effective number of ancestors – 16

Figure 3. Genetic diversity loss in the population: total and due to genetic drift (drift).



Conclusions

- Good quality and depth of pedigree was observed.
- High levels of inbreeding were estimated when missing pedigree records were accounted for.
- Small effective population size and small effective number of founder genomes were estimated for recent years.
- Very few ancestors needed to explain the gene pool of the current population.
- Genetic drift was the main cause of genetic diversity loss in the population.
- There exists a need for controlling inbreeding and effective population size by optimizing mating system and by introducing animals less related to the current population.

Acknowledgments

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Appendix

Formulas used:

- Pedigree Completeness Index

$$PCI = \frac{4C_{Sire}C_{Dam}}{C_{Sire}C_{Dam}} \qquad C = \frac{1}{d}\sum_{i=1}^{d} a_i$$

- Effective population size

$$N_e = \frac{1}{2\Delta F_y L}$$

- Effective number of founders

$$f_e = \sum_{j \in FOUND} \left(\frac{\sum_{i \in G} t_{ij}}{n_g} \right)^{-2}$$

- Effective number of founder genomes

$$f_{ge} = \frac{1}{2\overline{f_g}}$$

- Effective number of non-founders

$$N_{enf} = \left(\frac{1}{f_{ge}} - \frac{1}{f_e} \right)^{-1}$$

- Effective number of ancestors

$$N_a = \left(\sum_{i=1}^{n_a} p_i^2 \right)^{-1}$$

- Genetic diversity lost

$$1 - GD = \frac{1}{2f_e} \, or \, \frac{1}{2f_{ge}} \, or \, \frac{1}{2N_{enf}}$$

Symbols and abbreviations used:

- C_{sire}, C_{dam} – indexes for paternal and maternal contribution
- a_i – proportion of ancestors known in generation i
- d – number of generation traced
- F_y – average inbreeding coefficient in given year(s)
- L – average generation interval
- *FOUND* – set of ID numbers for founders
- G – set of ID numbers for group considered
- n_g – number of individuals in the group
- t_{ij} – the fraction of genes that individual i inherited from founder j
- f_g – coancestry in group g
- p_i – marginal genetic contribution of ancestor i to the population
- n_a – number of ancestors