



Influence of pedigree on effective population size in European Red Dairy Cattle

Jakimowicz, M.¹; Nyman, S.²; Szyda, J.¹; Suchocki, T.¹; De Koning, D.-J.²

¹Wroclaw University of Environmental and Life Sciences, Department of Genetics, THETA Biostatistic Group

²Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, PO Box 7023, SE-750 07 Uppsala, Sweden.



Aim of study

Estimate the effective population size (N_e) of the simulated population, using the inbreeding coefficients estimated based on actual pedigree information.



Importance of effective population size

Effective population size

- one of the most important parameter in population genetics and conservation biology
- translates census sizes of a real population into the size of an idealized population showing the same rate of loss of genetic diversity as the real population under study.

Red Dairy Cattle

- Spread across whole Europe
- Very suitable breed to crossbreed other cattle breeds with
- Organised in trans-national breeding programs
- Well adapted to local conditions





Data

- Simulated data
- Three populations
 - different numbers of animals
 - different effective numbers of founders
- Inbreeding coefficients —> based on actual pedigree information



Inbreeding Coefficients

- Meuwissen method based on decomposition of the additive genetic relationship matrix
- VanRaden approach based on the tabular method taking into account missing relatives

N_e based on individual increase in inbreeding

$$\Delta F = 1 - \sqrt[t]{1 - F_i} \quad (1)$$

- t - equivalent complete generation
- F_i is the inbreeding coefficient for the individual.

$$\bar{N}_e = \frac{1}{2\bar{\Delta F}}, \quad (2)$$

- $\bar{\Delta F}$ - average increase in inbreeding for population

N_e based on regression coefficients

$$\Delta F = \frac{b}{1 - (F_t - b)} \quad (3)$$

- F_t - mean F for population
- b - regression coefficient
 - individual inbreeding values over the individual equivalent complete generations
 - individual inbreeding values over the year of birth
 - individual inbreeding values over the generation

Results - individual increase in inbreeding

# of individuals	method	mean delta F	sd delta F	Ne	Ne sd
20	Meuweissen	0.042	0.061	11.781	3.787
	VanRaden	0.116	0.078	4.294	0.725
12537	Meuweissen	0.001	0.005	847.225	58.852
	VanRaden	0.012	0.020	41.505	0.863
	VanRaden4	0.019	0.026	26.404	0.455
19610	Meuweissen	0.003	0.007	195.496	3.966
	VanRaden	0.011	0.016	44.316	0.512
	VanRaden4	0.011	0.016	44.316	0.512

Results - regression coefficient (equivalent complete generations)

# of individuals	method	mean delta F	Ne
20	Meuweissen	4.125	2.063
	VanRaden	2.008	1.004
12537	Meuweissen	46.517	23.259
	VanRaden	-1.999	-0.999
	VanRaden4	-4.017	-2.009
19610	Meuweissen	58.738	29.369
	VanRaden	1.419	0.709
	VanRaden4	-3.585	-1.793



Summary

- Reexamine methodology
- Further research is necessary

THANK YOU FOR YOUR ATTENTION

Biostatistics Group
Department of Genetics
Wrocław University of Environmental
and Life Sciences
<http://theta.edu.pl>

