Population structure and genetic diversity of four Swiss sheep breeds

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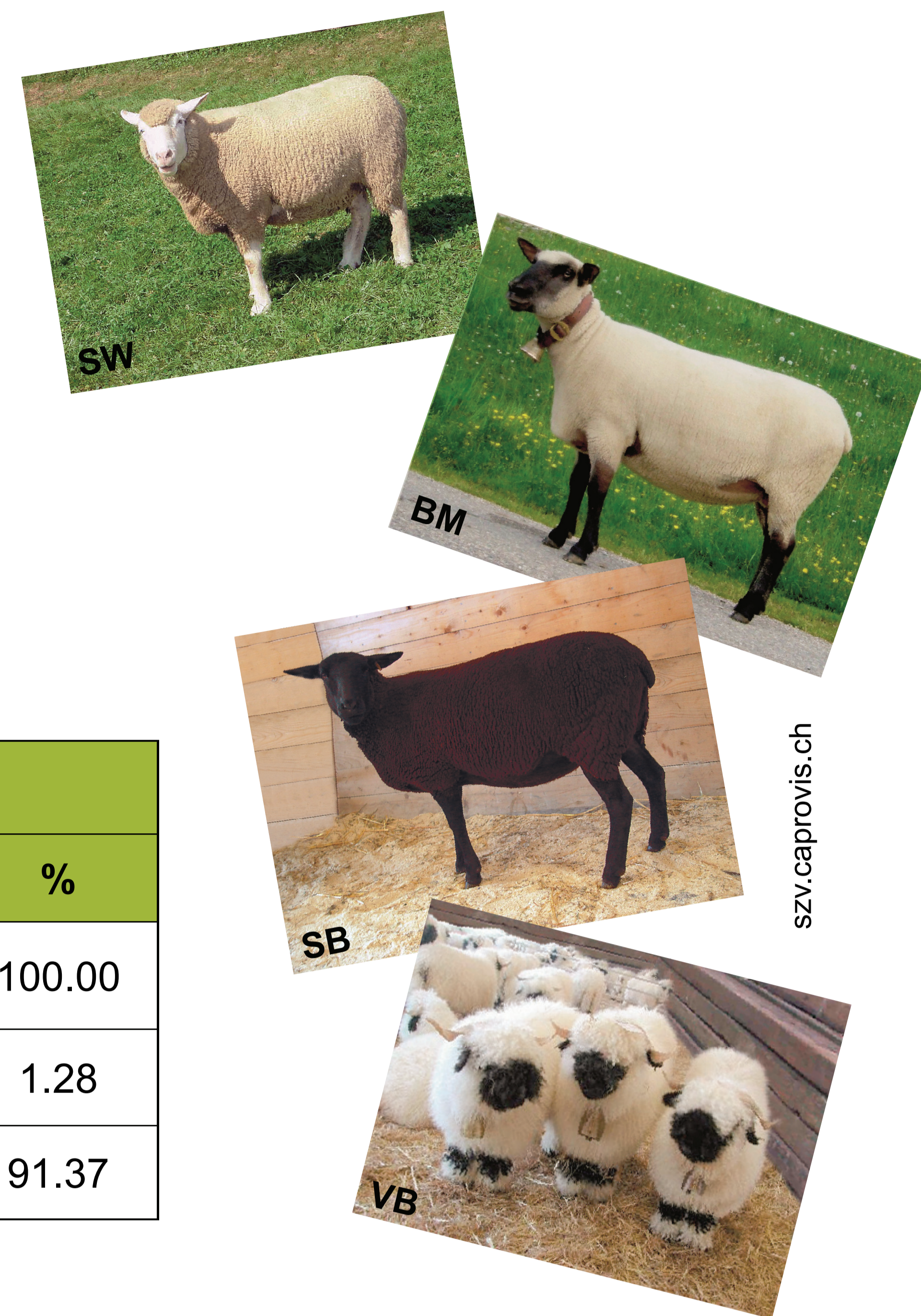
Introduction

The pedigree data of the four largest Swiss sheep breeds – Swiss White Mountain sheep (SW), Brown-Headed Meat sheep (BM), Swiss Black-Brown Mountain sheep (SB) and Valais Blacknose sheep (VB) – was evaluated in the context of their population structure and genetic diversity within population.

Material and Methods

The full pedigree of all herdbook individuals born in the years 1996-2008 (Table 1) was analysed with the software tools CFC (Sargolzaei et al. 2006), PEDIG (Boichard 2002) and POPREPORT (Groeneveld et al. 2009).

Table 1: Pedigree records

	SW		BM		SB		VB	
	animals	%	animals	%	animals	%	animals	%
animals in the pedigree	519'711	100.00	167'527	100.00	156'603	100.00	152'545	100.00
founder	8'503	1.64	1'737	1.04	998	0.64	1'949	1.28
inbred animals	395'982	76.19	151'307	90.32	144'513	92.28	139'384	91.37

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Results

Pedigree completeness of 90% and above, considering 1 to 6 generations, was found for BM and SB. For VB completeness varied between 80% to above 90%, whereas completeness for SW varied between 70% to 90%.

All four breeds showed an increasing trend for average inbreeding coefficients (Figure 1), and a decreasing trend for effective population size.

Futhermore, a decreasing trend was found for the number of founder equivalents, the effective number of ancestors and for the number of founder genome equivalents (Figure 2).

The decrease in genetic diversity is further supported by the increasing marginal gene contribution of the most important ancestors. For the VB population, e.g., 19.8% of the present gene pool is explained by one animal only.
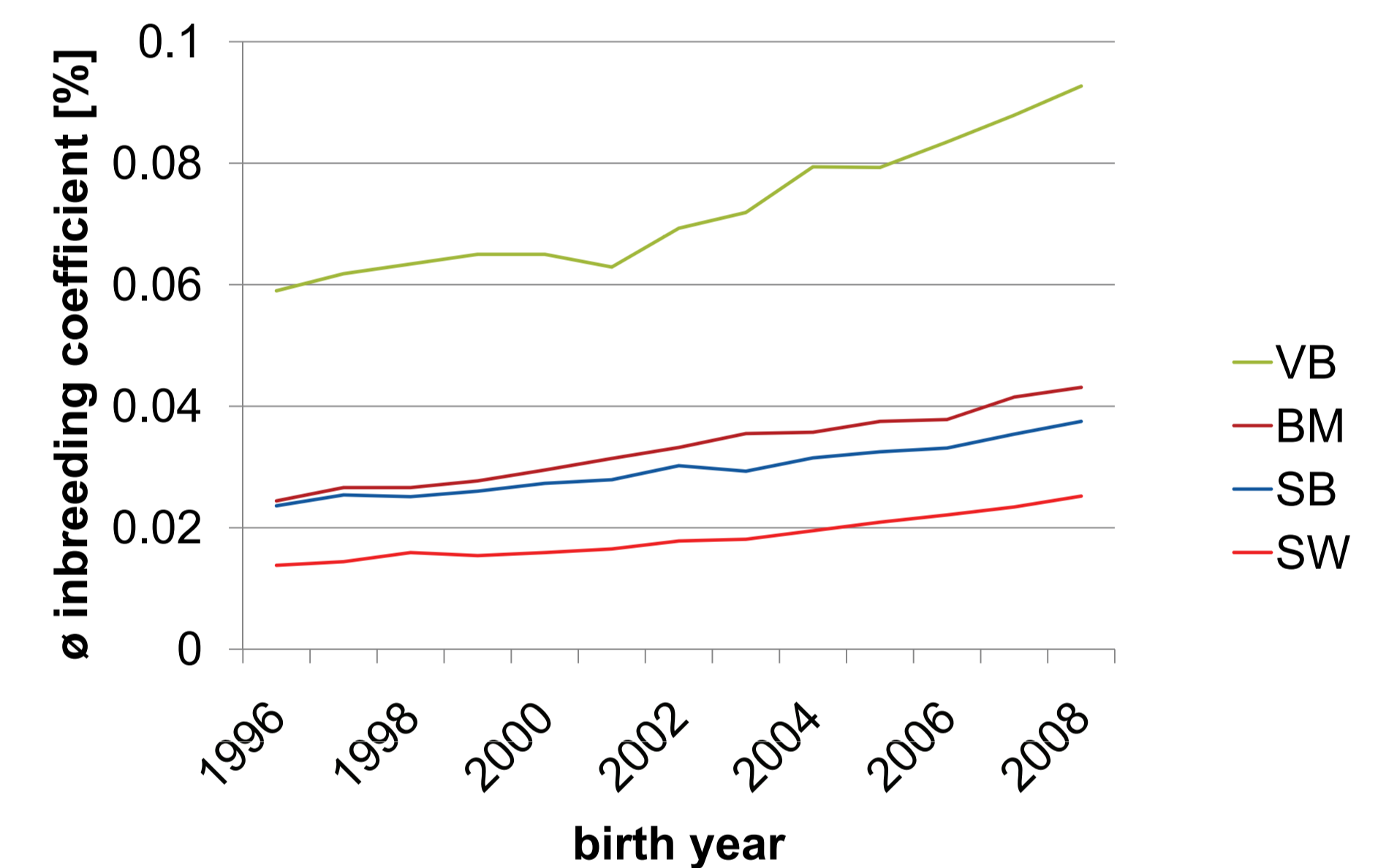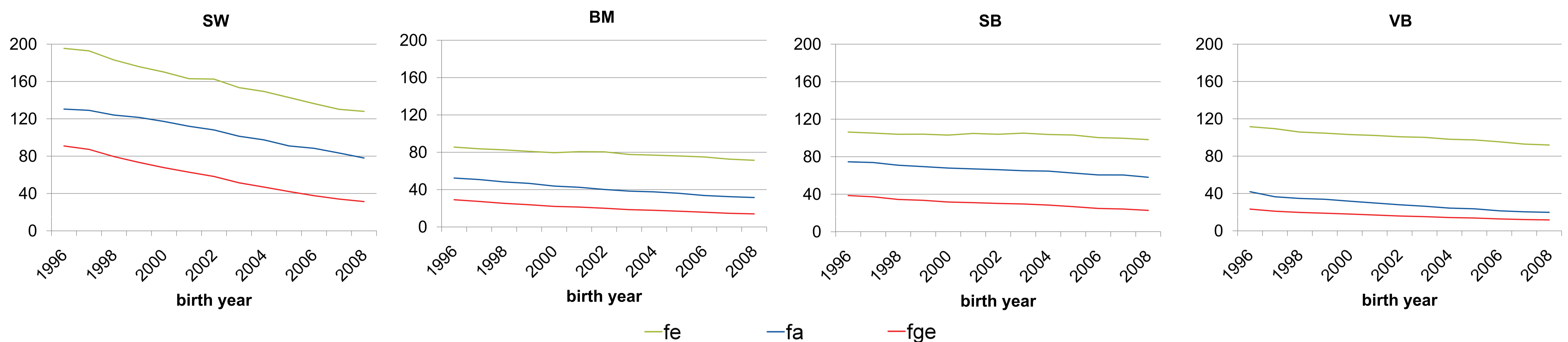

Figure 1: Trend of inbreeding coefficient

Figure 2: Number of founder equivalents (f_e), effective number of ancestors (f_a) and number of founder genome equivalents (f_{ge})

Conclusion

Specific strategies to ensure long-term genetic diversity are only proposed for VB. Thus, sires with superior breeding values, and under average relationship to the dams, i.e. sires in the left upper rectangular, should be first used for breeding. Sires on the right side should only be mated selectively to dams (Figure 3).

→horizontal blue line: breeding value 100 = population average
→vertical blue line: average relationship between sires and dams 2010

For the other three breeds a regular monitoring of genetic diversity is proposed.
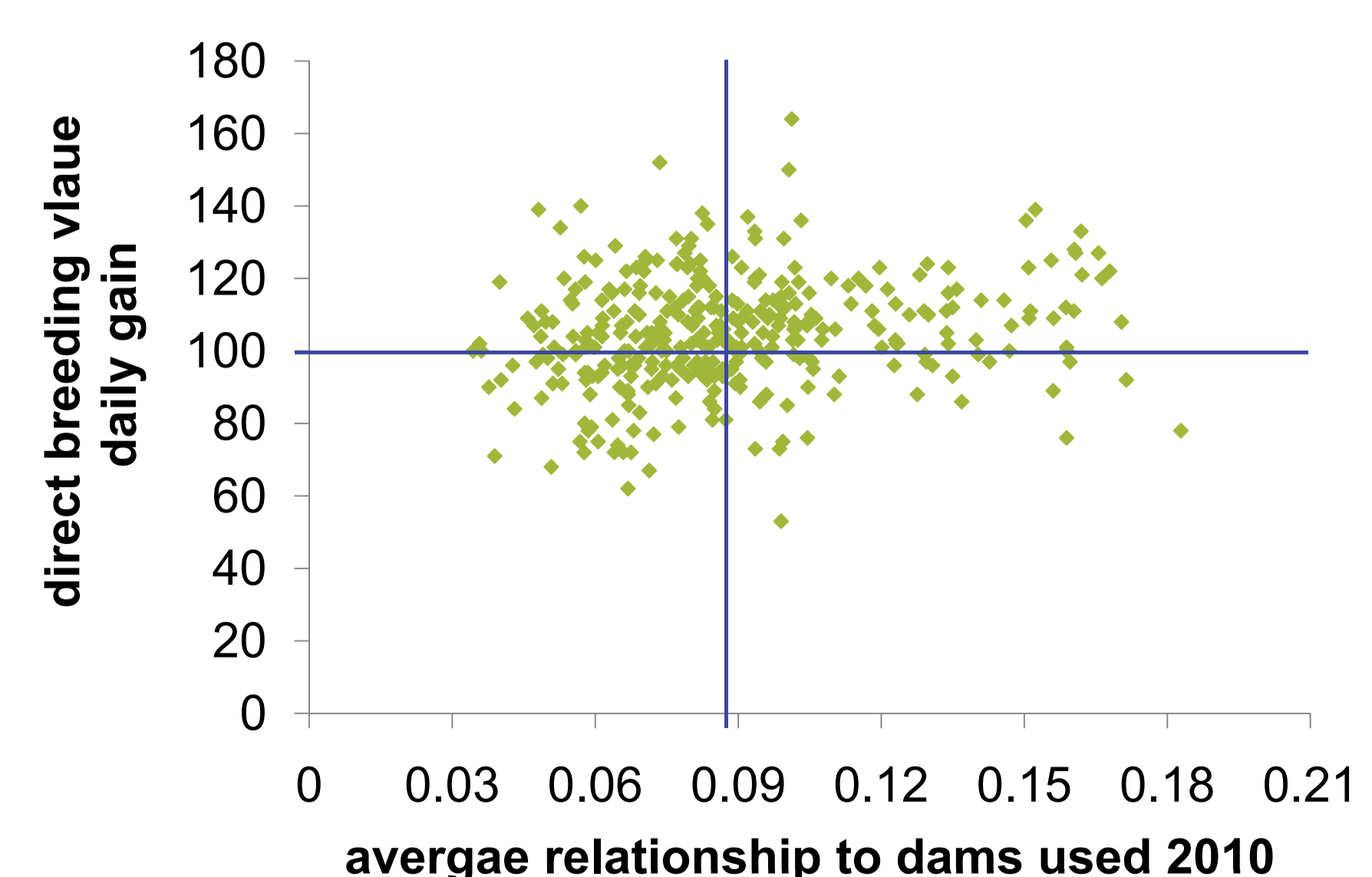

Figure 3: Breeding values for the trait "daily gain" plotted against the average relationship of sires to dams

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