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Genetic analysis of joint diseases in Swedish Rottweiler and Bernese Mountain Dog

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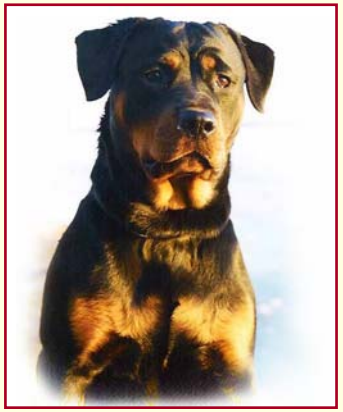
Objectives

- ✓ To estimate the amount of genetic variation in hip dysplasia (HD) and elbow dysplasia (ED)
- ✓ To assess genetic trends for HD and ED
- ✓ To evaluate whether genetic groups were needed in the model for prediction of breeding values
- ✓ To develop a statistical model for routine prediction of breeding values for HD and ED in Swedish dogs

What is HD and ED?

- ✓ Two of the most common hereditary disorders in dogs
- ✓ Growth disorders of the bone, causing arthrosis in the joint
- ✓ Painful for dogs, costly for dog owners
- ✓ Heritability estimates ranging from 0.2 to 0.6 for HD and 0.1 to 0.8 for ED



Genetic control programmes

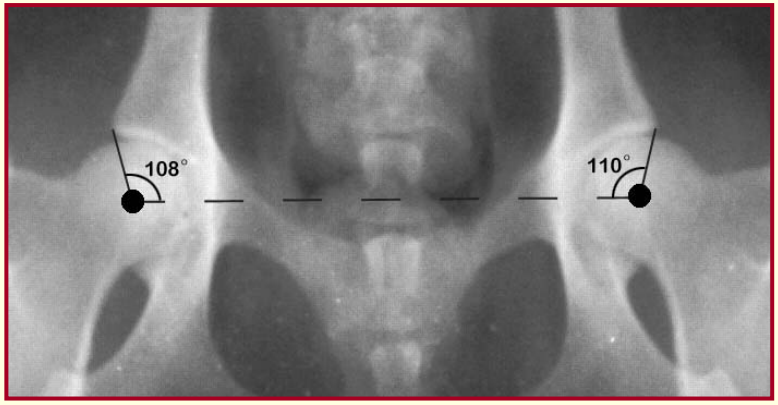
Centralized evaluation and recording of screening results for HD and ED

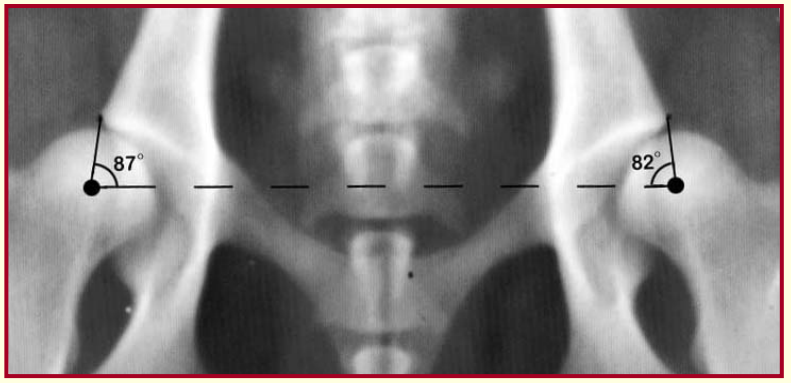
Breeding programmes based on mass selection

- ✓ Limited possibilities for measuring differences among phenotypically normal dogs
- ✓ Influence of various environmental factors, e.g. age at screening, sedation method

HD grading

HD grade		
Until 1999	Since 2000	**HD score**
	A	1.0
Normal		1.3
	B	2.0
	C	2.5
Grade I		2.6
	D	3.0
Grade II		3.1
Grade III		3.6
	E	3.7
Grade IV		4.5





ED grading

ED grade	ED score
Normal	1.0
Grade I	2.0
Grade II	2.6
Grade III	3.2

Materials

Screening results and pedigree information from the Swedish Kennel Club.

Data also included: dates of birth and screening, sex of the dog, panelist and veterinary clinic.

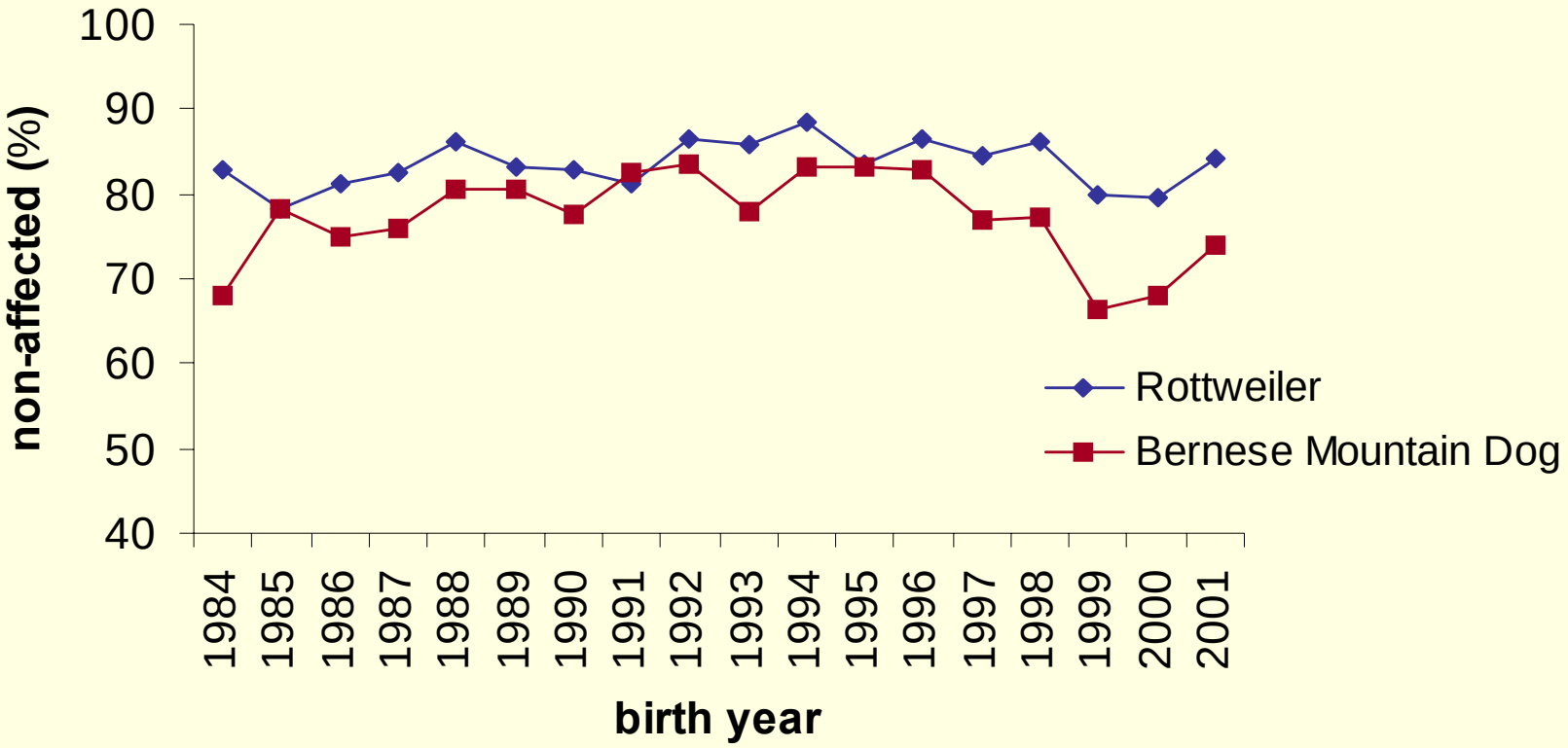
14 693 records of HD

11 842 records of ED

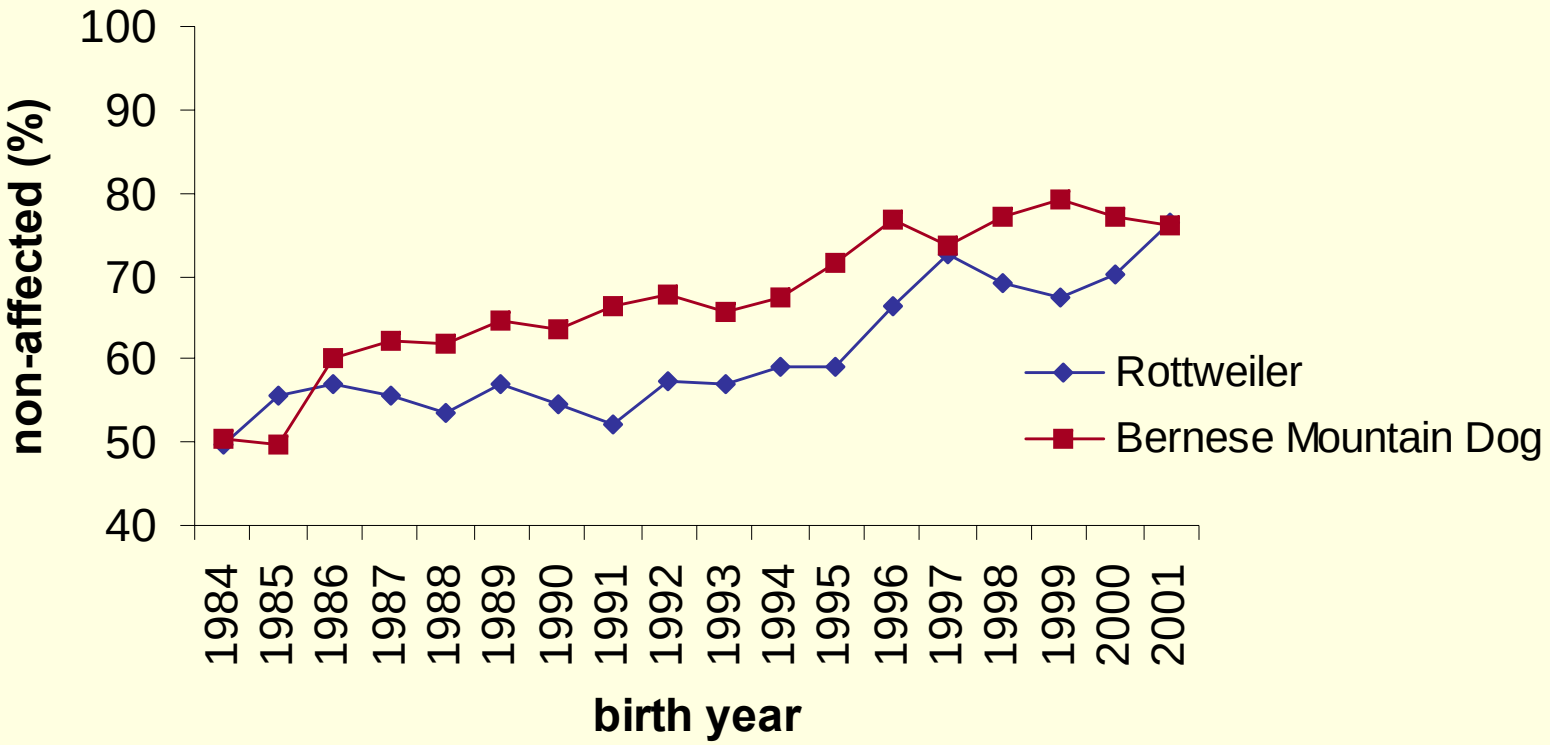
8221 records of HD

7963 records of ED

Phenotypic trends for HD



Phenotypic trends for ED



Methods

- ✓ Mixed linear animal model
- ✓ Estimation of variance components using AI-REML
- ✓ Prediction of breeding values using BLUP
- ✓ DMU software

Model 1:

$Y = \mu + \text{sex} + \text{birth month} + \text{age} + \text{year of examination} + \text{clinic}\times\text{year of examination} + a + e$

Methods (cont.)

- ✓ Extended model for prediction of breeding values also included genetic group effects

Model 2:

$Y = \mu + \text{sex} + \text{birth month} + \text{age} + \text{year of examination} + \text{genetic group} + \text{clinic} \times \text{year of examination} + a + e$

F-test to evaluate the need for genetic groups in the model

Heritabilities and genetic correlations

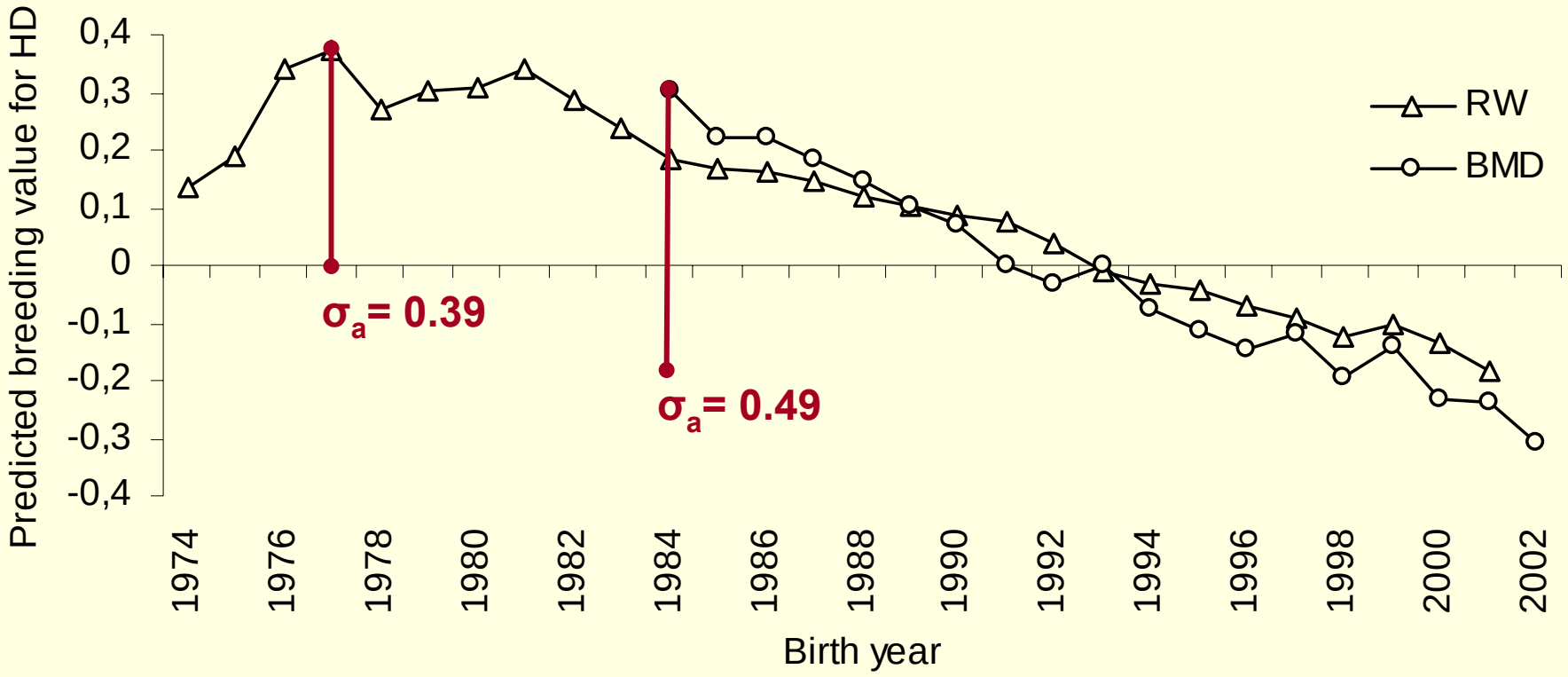
Breed	HD score		ED score
	0.38	**0.23**	0.34
	0.42	**0.06**	0.38

Genetic group effects

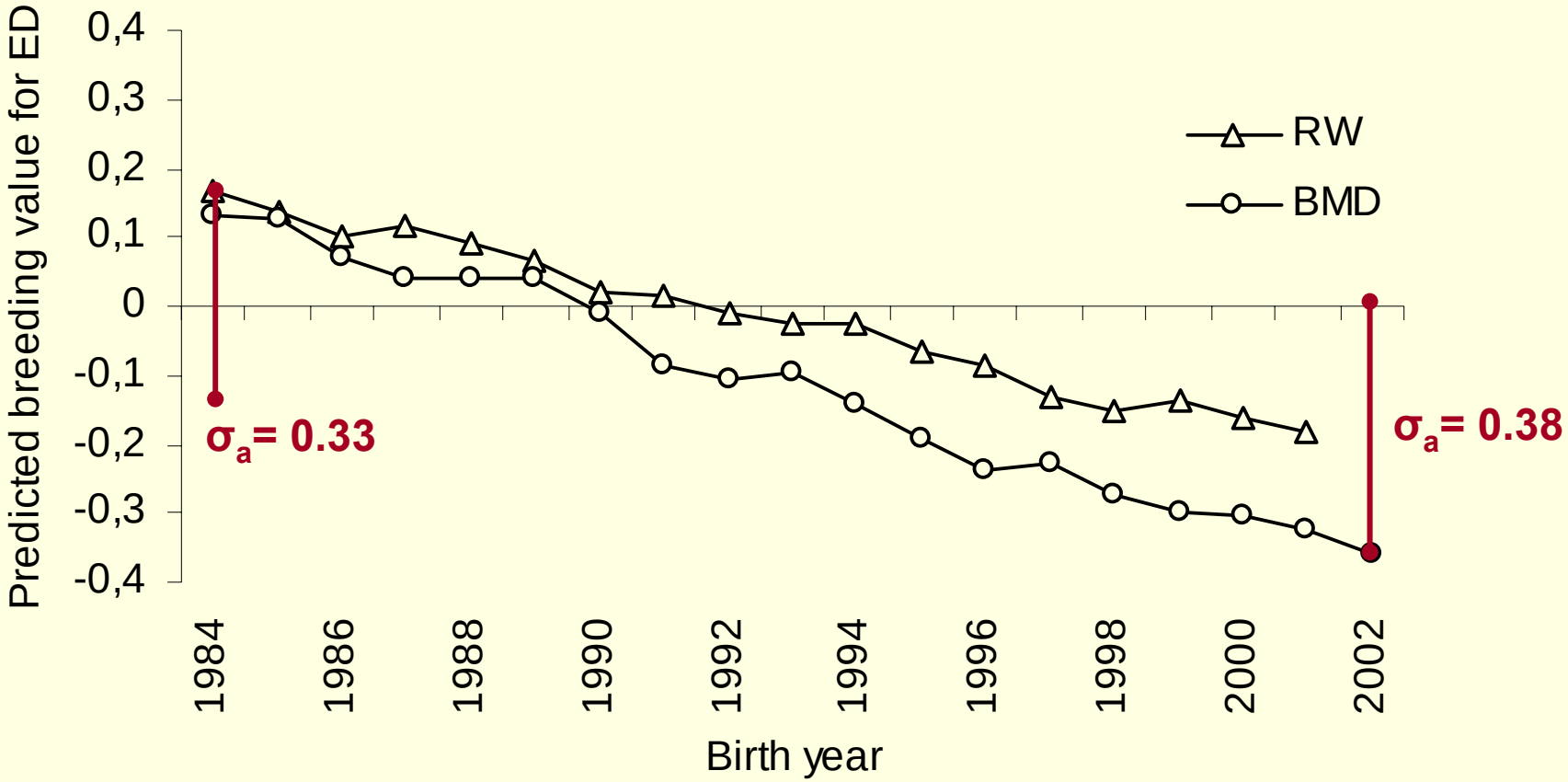
- ✓ Estimates of genetic group effects were small
- ✓ None of the F-values were significant

	HD score	ED score
Breed	Pr>F	Pr>F
	0.72	0.22
	0.60	0.22

Genetic trends for HD

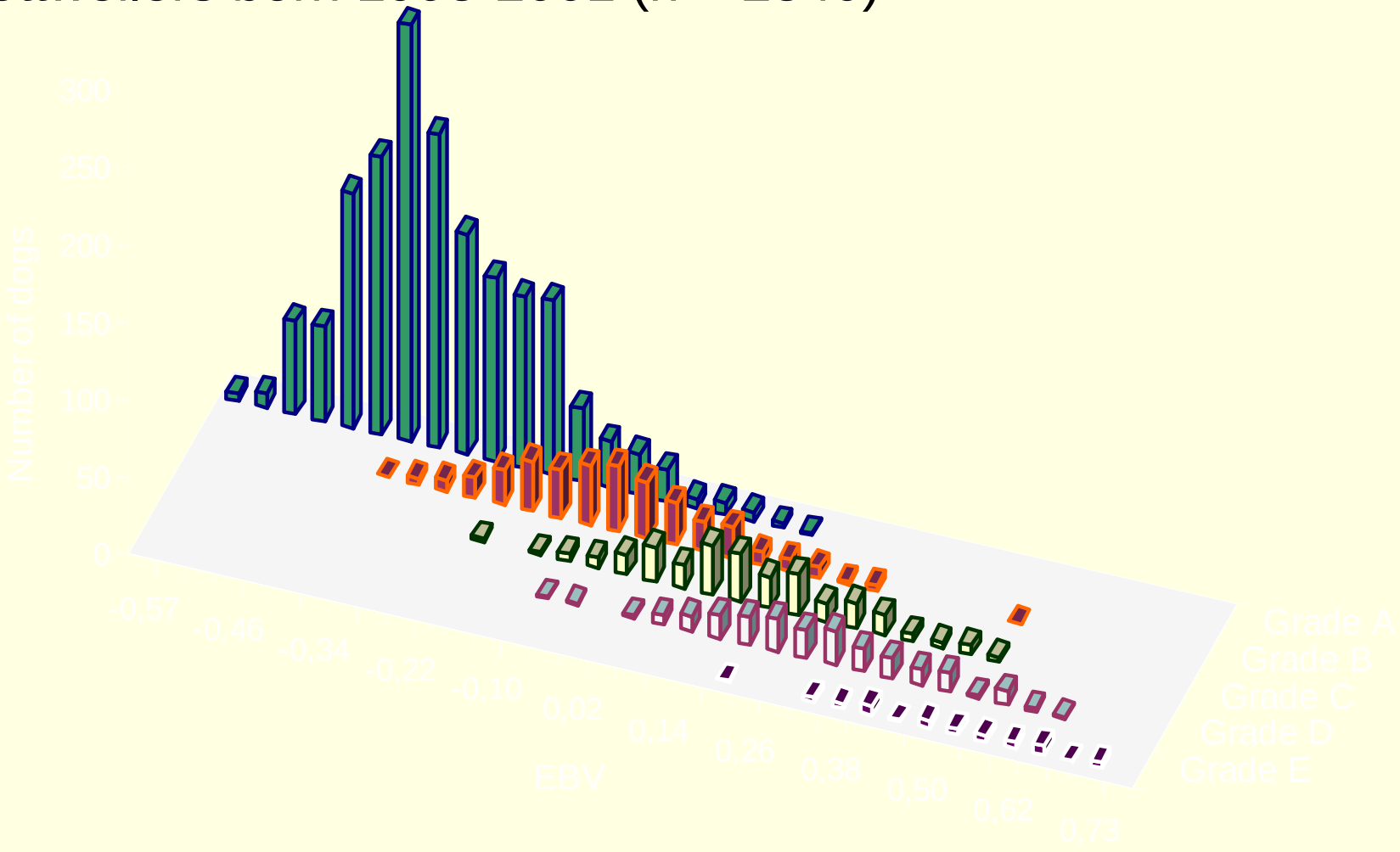


Genetic trends for ED



Distribution of EBVs

Distribution of predicted breeding values (EBV) for HD in Rottweilers born 1998-2001 (n = 2340)



Conclusions

- ✓ There is considerable genetic variation in HD and ED in both breeds
- ✓ The genetic trends indicated a genetic improvement
- ✓ Dogs with the same phenotypic record get different breeding values
- ✓ A model without genetic groups is recommended for routine prediction of breeding values for HD and ED

Reference to original article:

Malm S., Fikse W.F., Danell B., Strandberg E. 2008. Genetic variation and genetic trends in hip and elbow dysplasia in Swedish Rottweiler and Bernese Mountain Dog. *J. Anim. Breed. Genet.*, **125(5)**, DOI: 10.1111/j.1439-0388.2008.00725.x