

Introduction

- Runs of homozygosity (ROH) have been used to assess inbreeding and its impact
- It is hypothesized that recent inbreeding is more harmful than its old counterpart
- No clear definition of recent and ancient inbreeding is currently available
 - ✓ Current methods are largely based on heuristic criteria
 - ✓ Number of generations from common ancestor from pedigree
 - ✓ Length of ROH segments: Longer ROH reflect new inbreeding

Material and Methods

Proposed grid search approach

- It is based on the hypothesis that recent inbreeding has more deleterious effects on traits
- A profile of the effects of recent and old inbreeding could be obtained by moving the cut-off threshold based on specified number of generations or ROH segments length
- Threshold will be identified as the point where recent inbreeding has a larger effect on the trait compared to old inbreeding
- The proposed method can be applied using pedigree or ROH segment information
- Thresholds are population and trait specific
- The proposed method was compared to the Ancestral inbreeding approach (Kalinowski et al., 2000), fixed Predefined thresholds, and Model-based clustering (Pemberton et al., 2012)

Data

- Line 1 Hereford cattle population data set ($F_{ped} = 29\%$)
- Pedigree: 25 equivalent complete generations (11 to 29)
- 50k SNP marker panel (30,810 SNPs); 785 genotyped animals
- 4 growth traits: birth (BW), weaning (WW), yearling (YW) weights, ADG

Results

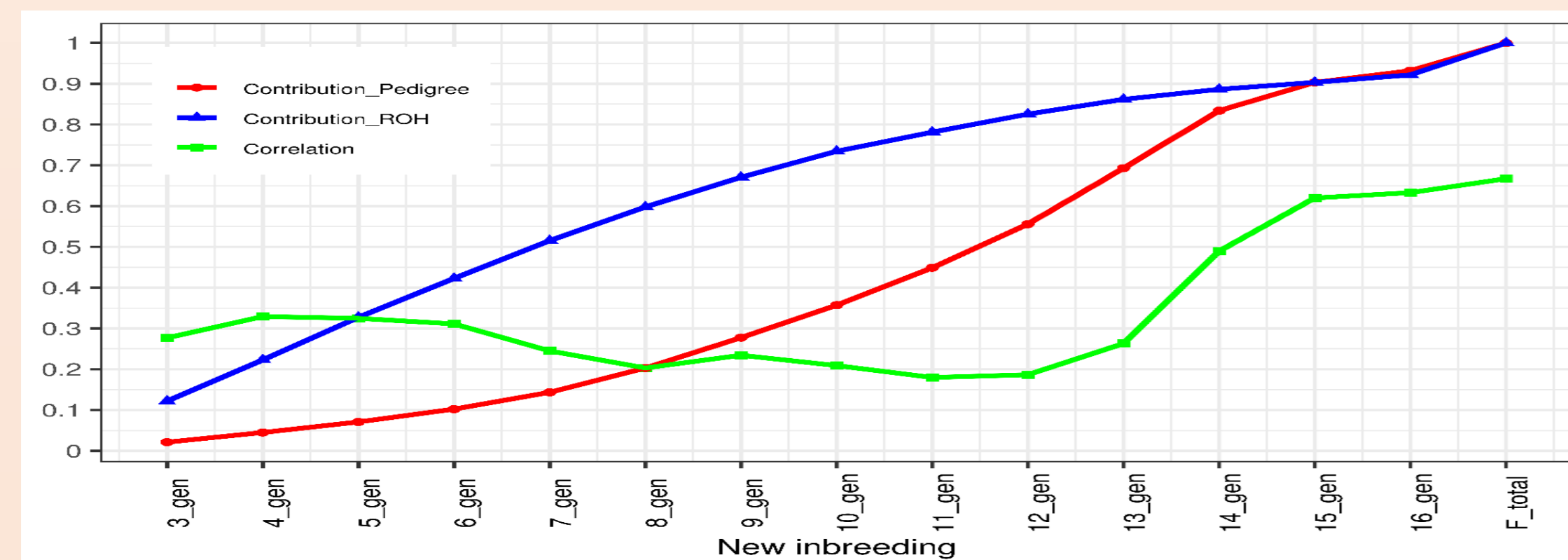


Figure 1: Contribution of recent inbreeding based on pedigree (red line) and ROH (blue line) to total inbreeding and their correlation (green line) as a function of the number of ancestral generations used to define new inbreeding

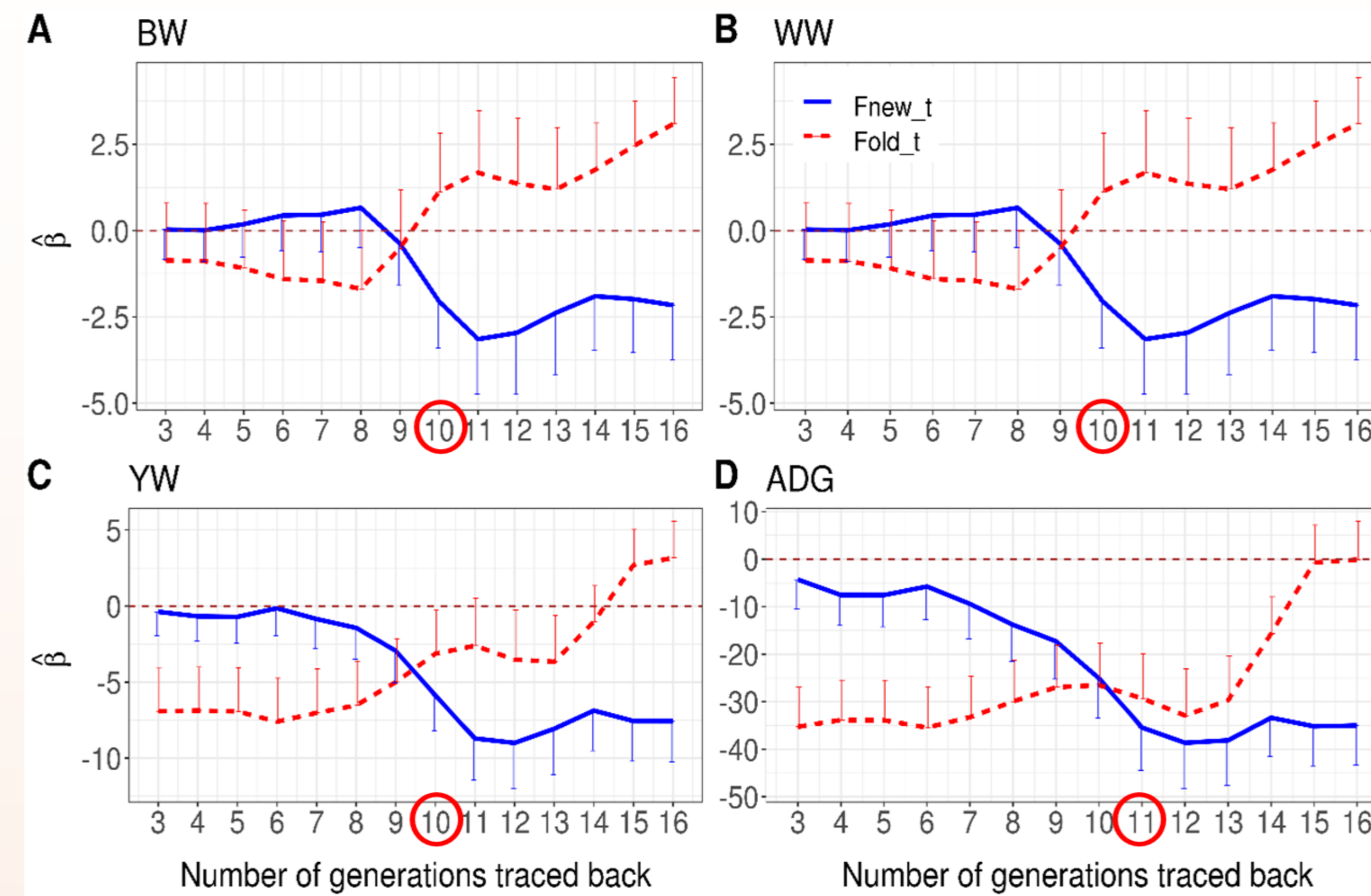


Figure 2: Estimates of regression coefficient associated with new (F_{new_t}) and old (F_{old_t}) inbreeding as a function of the position of the threshold (number of generations)

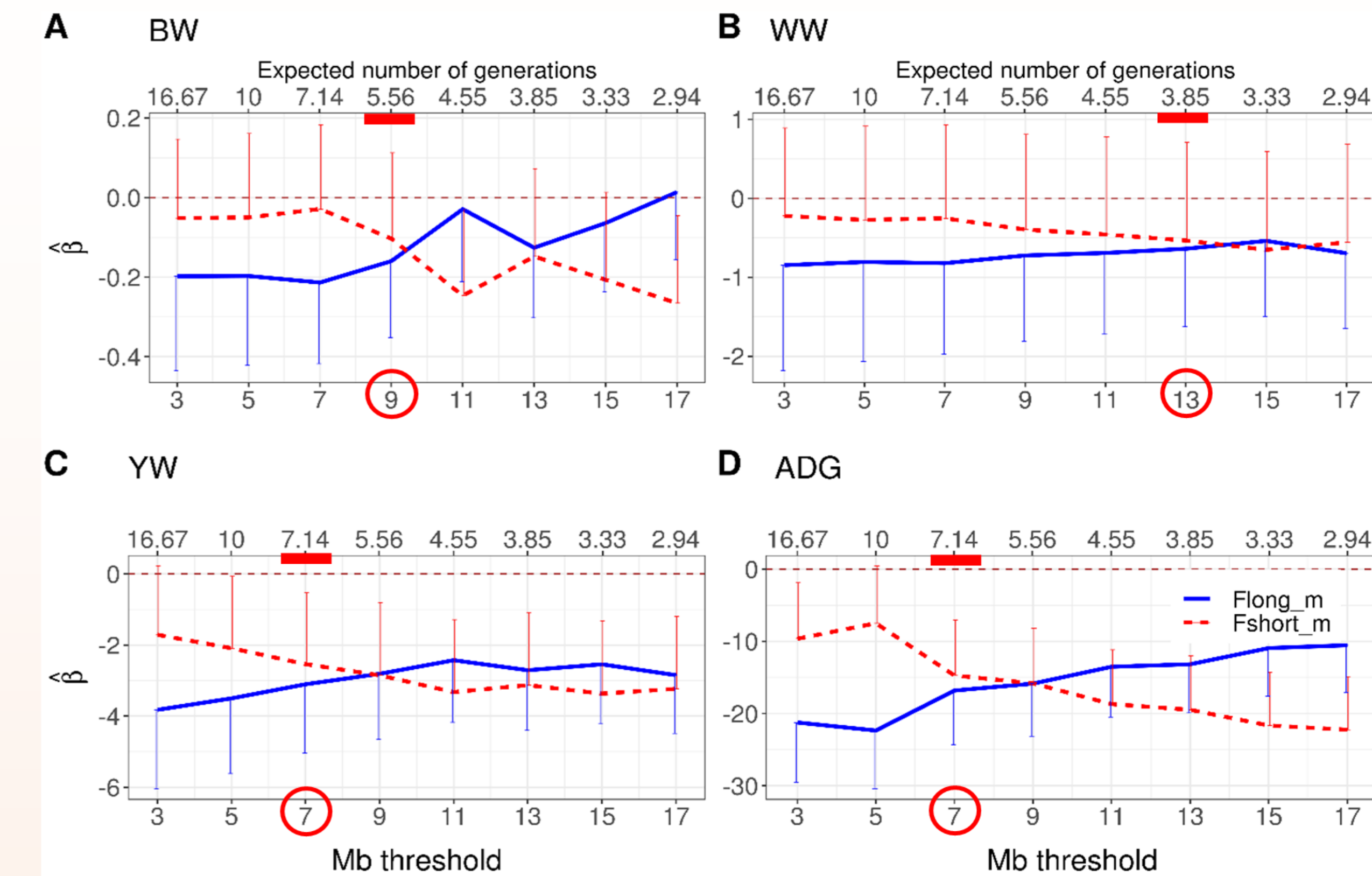


Figure 3: Estimates of regression coefficients associated with new (F_{long_m}) and old (F_{short_m}) inbreeding as a function of the position of the threshold (ROH length in Mb)

Trait	Pedigree-based	Criterion				ROH-based	Criterion			
		Adj.R2	RMSE	AIC	BIC		Adj.R2	RMSE	AIC	BIC
BW	Kalinowski	0.1561	4.1822	4294.78	4433.10	ROH_Mclust	0.15583	4.1829	4295.01	4433.34
	Ped_5_Lit	0.1553	4.1841	4295.45	4433.78	ROH_5_Lit	0.15566	4.1833	4295.16	4433.48
	Ped_10_gen*	0.1580	4.1776	4293.12	4431.44	ROH_9_Mb*	0.15588	4.1828	4294.97	4433.29
WW	Kalinowski	0.5418	22.6225	6741.76	6884.40	ROH_Mclust	0.53964	22.6759	6745.23	6887.87
	Ped_5_Lit	0.5402	22.6625	6744.36	6887.00	ROH_5_Lit	0.53946	22.6802	6745.52	6888.15
	Ped_10_gen*	0.5436	22.5781	6738.87	6881.51	ROH_13_Mb*	0.53962	22.6762	6745.25	6887.89
YW	Kalinowski	0.8448	31.3207	6744.06	6884.56	ROH_Mclust	0.84299	31.5019	6751.99	6892.49
	Ped_5_Lit	0.8441	31.3937	6747.26	6887.76	ROH_5_Lit	0.84304	31.4976	6751.80	6892.30
	Ped_10_gen*	0.8449	31.3088	6743.54	6884.04	ROH_7_Mb*	0.84299	31.5025	6752.01	6892.52
ADG	Kalinowski	0.8427	0.1366	-726.03	-590.06	ROH_Mclust	0.84202	0.1369	-723.05	-587.08
	Ped_5_Lit	0.8437	0.1361	-730.21	-594.24	ROH_5_Lit	0.84205	0.1368	-723.15	-587.18
	Ped_11_gen*	0.8441	0.1359	-732.16	-596.19	ROH_7_Mb*	0.84211	0.1368	-723.43	-587.46

Table 1. Model comparisons between the proposed and existing methods to classify inbreeding into new and old inbreeding based on pedigree and ROH information (* indicates thresholds from the proposed method)

- Contribution of ROH based new inbreeding to total inbreeding is higher compared to the pedigree counterpart at the same number of generations
- The threshold for separating new and old inbreeding was 10 to 11 and 4 to 7 generations using pedigree and ROH information, respectively
- Thresholds to classify inbreeding into new and old classes were trait specific and varied with the sources of information
- The proposed grid search method seems to perform at least as good as existing approaches

Conclusions

- ROH segments tend to capture earlier the harmful effects of recent inbreeding compared to pedigree information
- For some traits old inbreeding could still have a significant contribution to inbreeding depression (YW, ADG)
- Optimum management designs should consider the age of inbreeding in their mating scheme

References

- Kalinowski et al. 2000. *Conserv. Biol.* 14: 1375-1384.
Pemberton et al. 2012. *Am. J. Hum. Genet.* 91: 275-292.