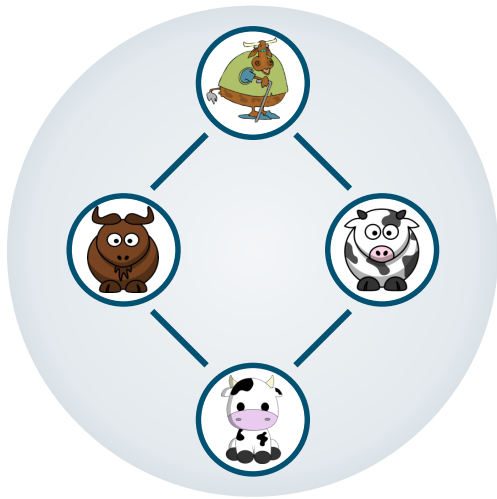


Not all inbreeding is depressing

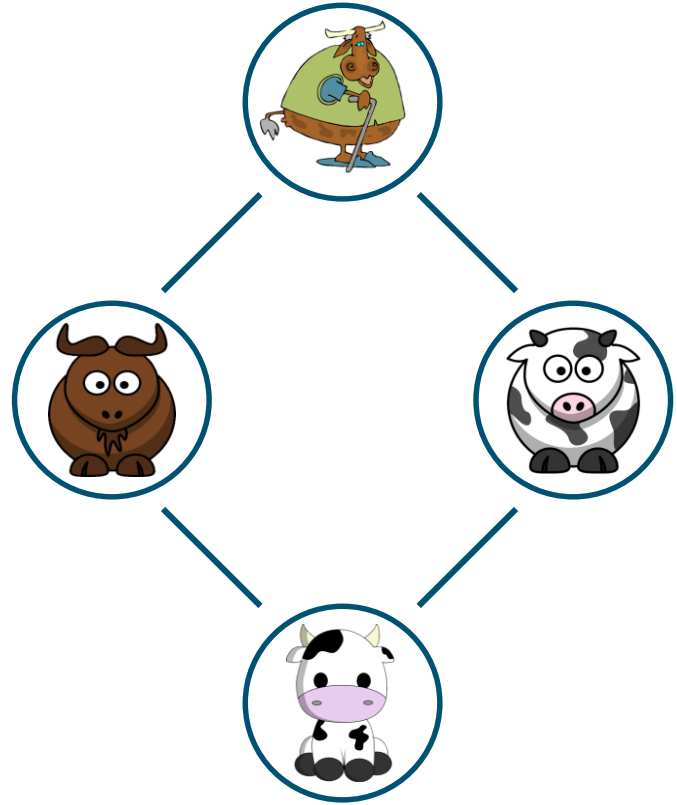
Harmen Doekes, R.F. Veerkamp, P. Bijma, S.J. Hiemstra, G. de Jong and J.J. Windig

EAAP 2019



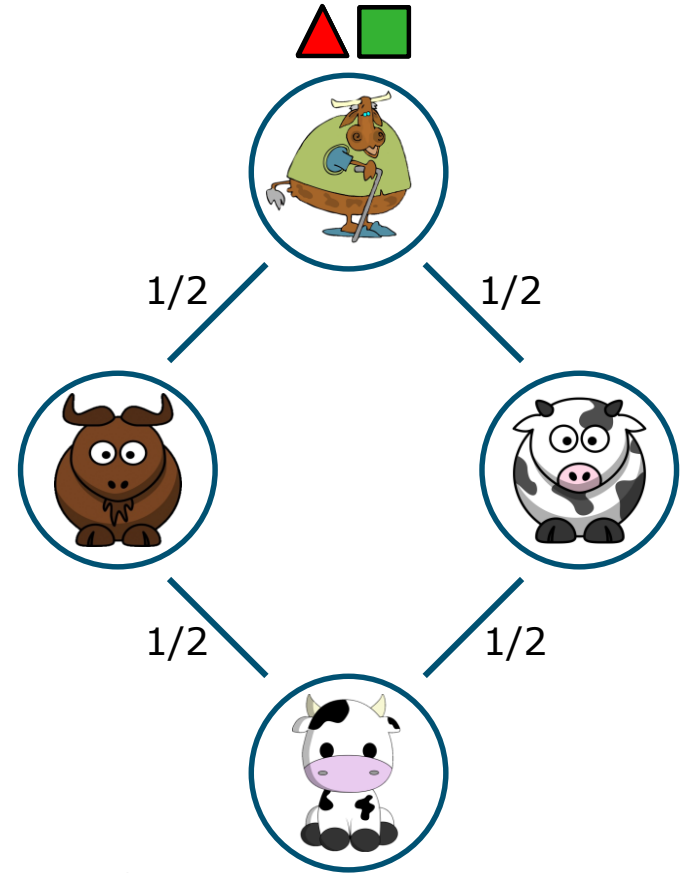
Inbreeding

- The mating between relatives
- F = probability alleles are “identical by descent” (IBD)



Inbreeding

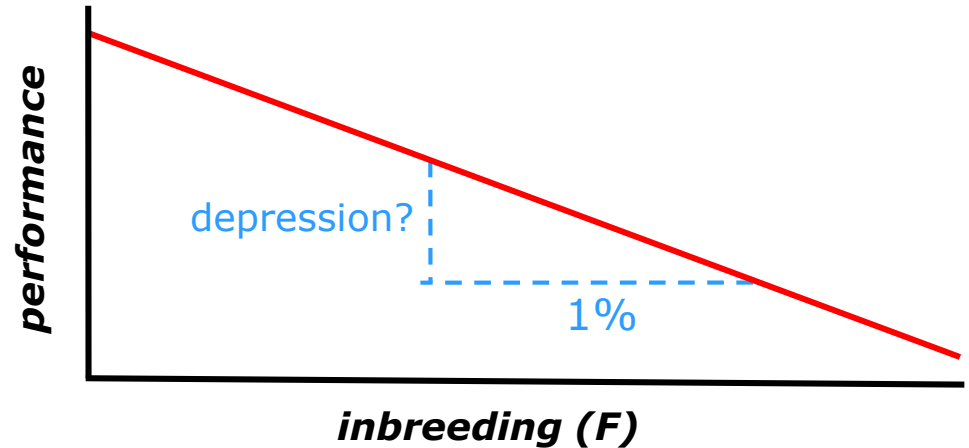
- The mating between relatives
- F = probability alleles are “identical by descent” (IBD)



$$F = \left(\frac{1}{2}\right)^3 \left\{ \right.$$

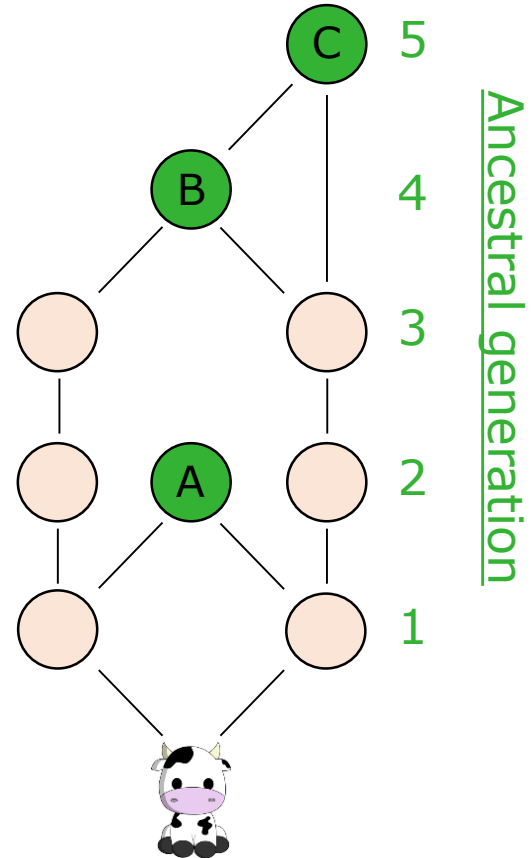
Inbreeding depression

- Decrease in performance due to inbreeding
- Cause: increased homozygosity of deleterious recessive alleles
- Depression expressed per 1% increase in F



Recent and ancient inbreeding

- Hypothesis: recent F more harmful than ancient F , because of **purging**
- **Purging** = removal of deleterious recessive alleles by selection



Data

- 38,792 first-parity cows, calved 2012-2016
- Phenotypes:
 - Protein yield (305-d)
 - Calving interval
 - SCS day 151-400
 - (+ 6 other traits)



Inbreeding

- Total inbreeding based on:
 - Pedigree (mean NCG = 6.2)
 - Regions of homozygosity (ROH), using 75k genotypes

- Split total inbreeding into components based on age of inbreeding (3 methods)

Model

- For total inbreeding:

$$y_{ijk} = \mu + HY_i + month_j + \alpha * age_k + \beta * F_k + cow_k + e_{ijk}$$

Results total inbreeding

- Unfavourable effect for all traits
- Pedigree and ROH similar results

Trait	<i>F</i> based on	
	Pedigree	ROH
Protein yield	-1.27	-1.20
Calving interval	0.46	0.48
SCS day 151-400	0.86	0.86

 P < 0.05

 P < 0.01

Model

- For total inbreeding:

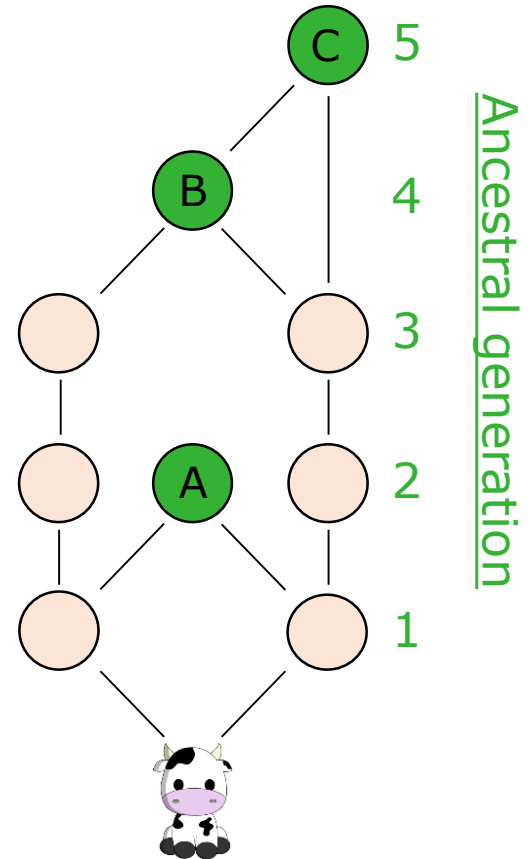
$$y_{ijk} = \mu + HY_i + month_j + \alpha * age_k + \beta * F_k + cow_k + e_{ijk}$$

- For n age-based components:

$$y_{ijk} = \mu + HY_i + month_j + \alpha * age_k + \sum_{l=1}^n \beta_l * F_{kl} + cow_k + e_{ijk}$$

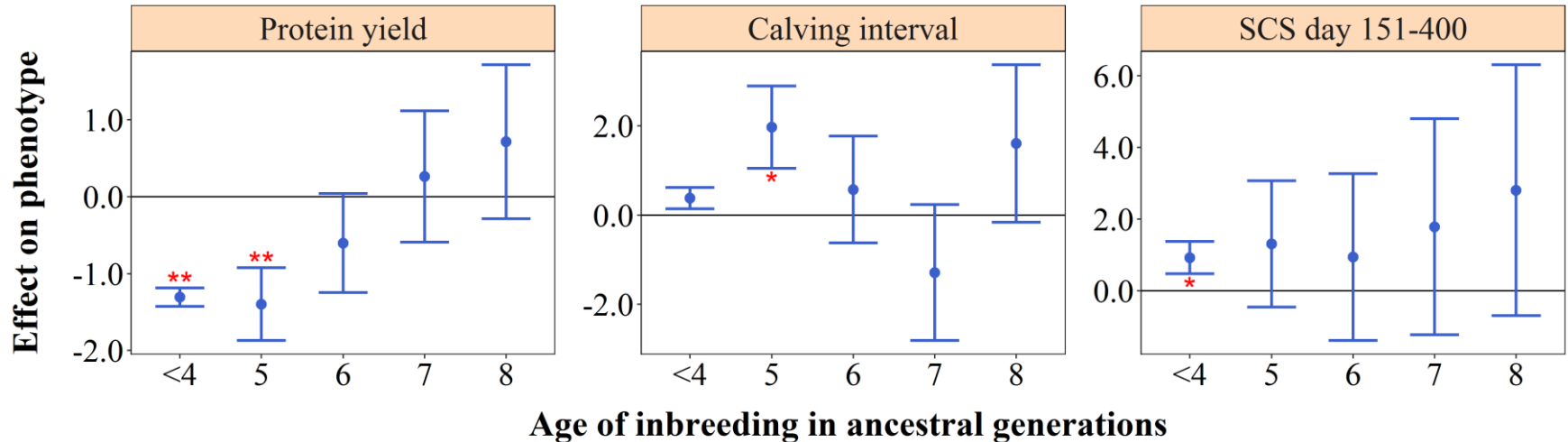
Method 1: generation-based

- Total inbreeding:
 - F_{tot} = inbreeding on A, B & C
- Split F_{tot} into generation-based components:
 - $F_{\leq 4}$ = inbreeding on A & B
 - F_5 = inbreeding on C
 - Etc.



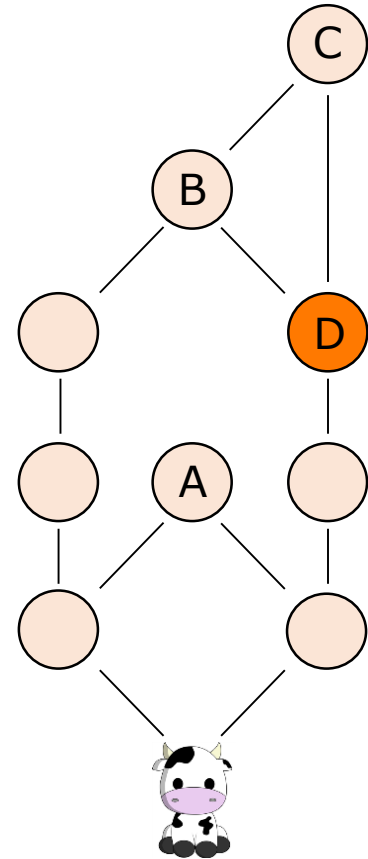
Results 1: generation-based

- For yield traits, inbreeding on recent generations more harmful
- For other traits, no clear difference across generations



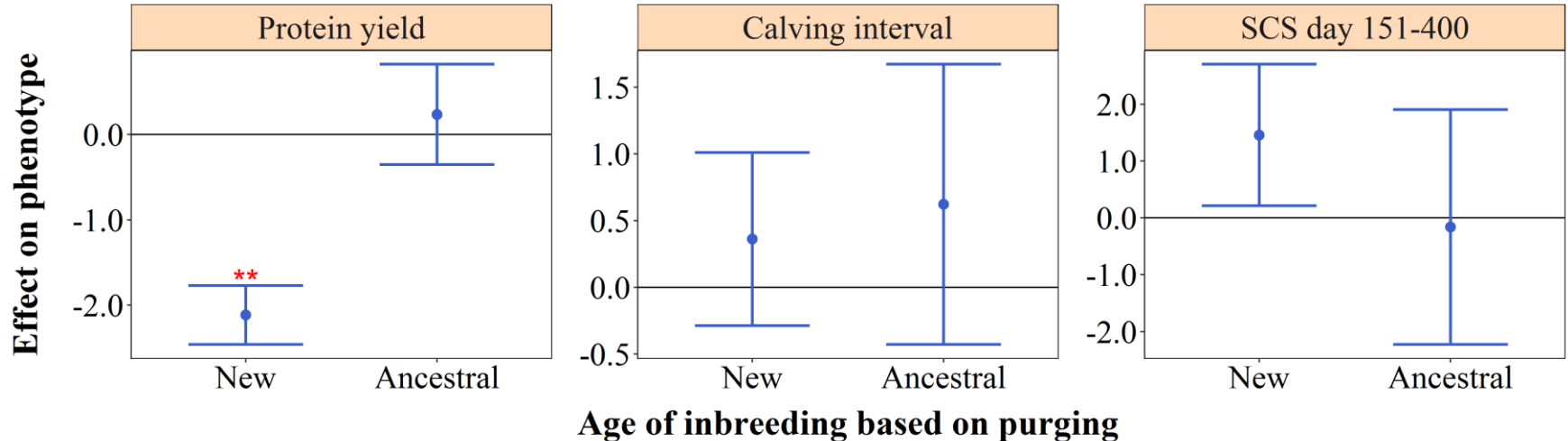
Method 2: purging-based

- If ancestors were inbred, purging
- Split F_{tot} into purging-based components:
 - $F_{ancestral}$ = “purged” inbreeding
 - F_{new} = “unpurged” inbreeding



Results 2: purging-based

- For 7 out of 9 traits, new inbreeding more harmful than ancestral
- Difference most evident for yield traits

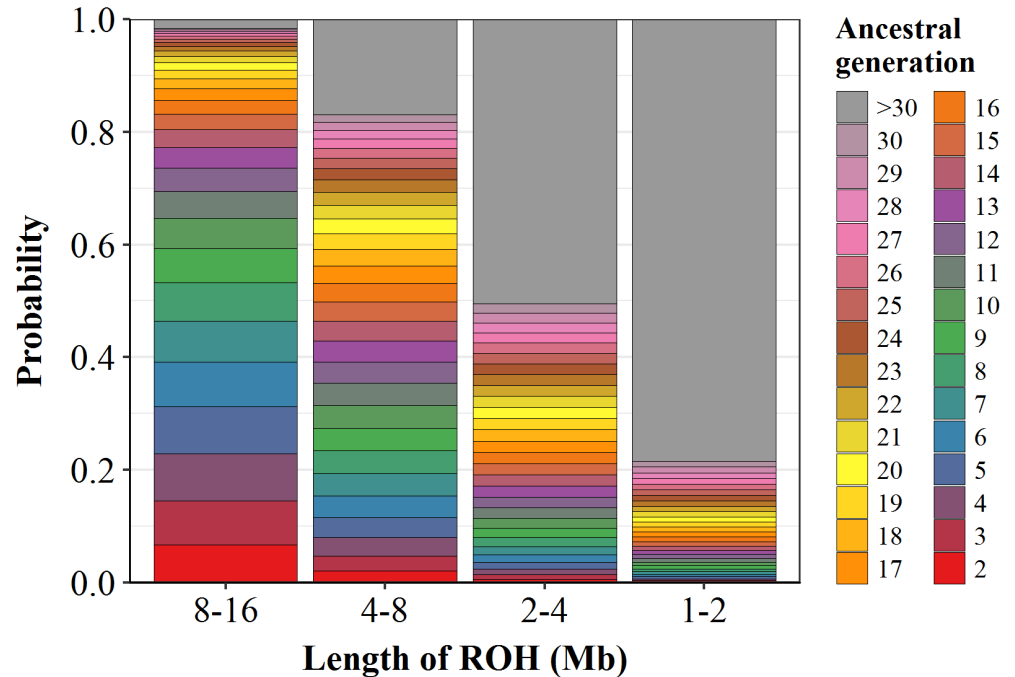


Method 3: ROH-based

- Longer ROHs = more recent inbreeding

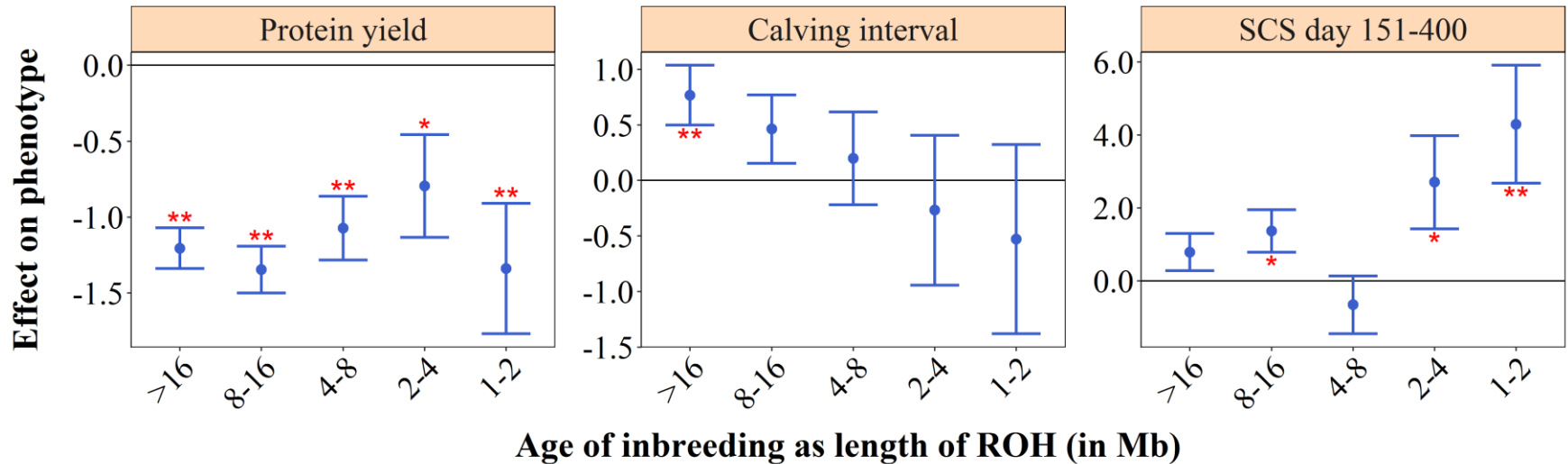
- Five length classes:

- ≥ 16 Mb
- 8-16 Mb
- 4-8 Mb
- 2-4 Mb
- 1-2 Mb



Results 3: ROH-based

- Results differ across traits
- Overall, both long and short ROH contribute to depression

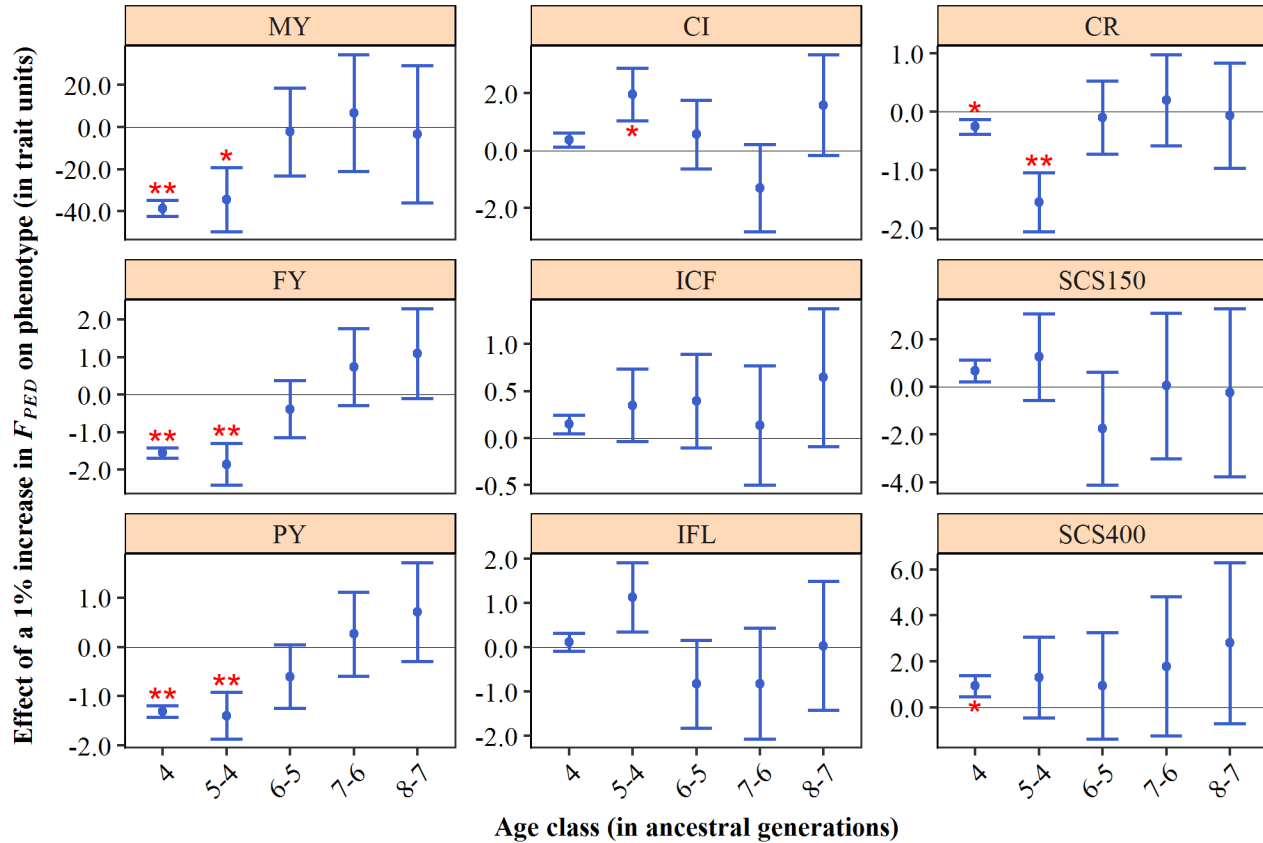


Take home messages

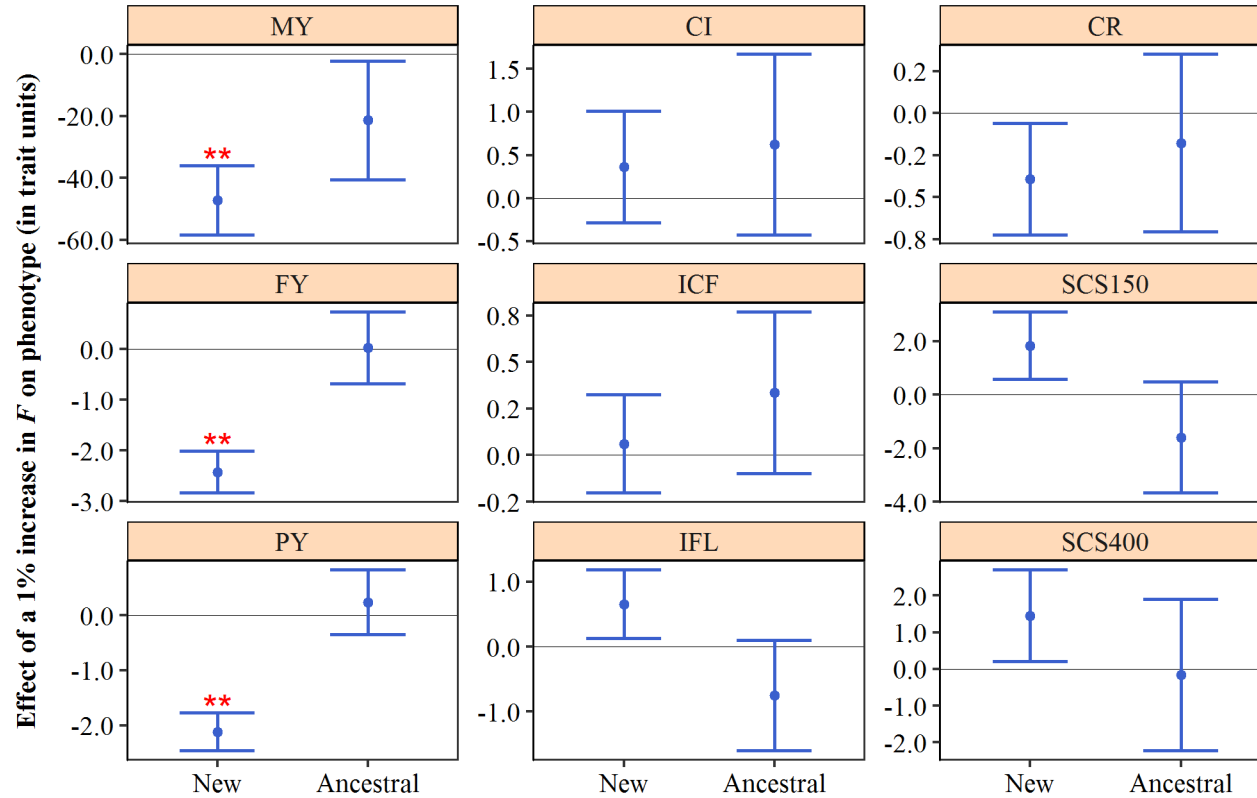
- Inbreeding depression for all traits
- Not all inbreeding is depressing
- Next: assess purging with genomic time series (?)



Generation based (all traits)

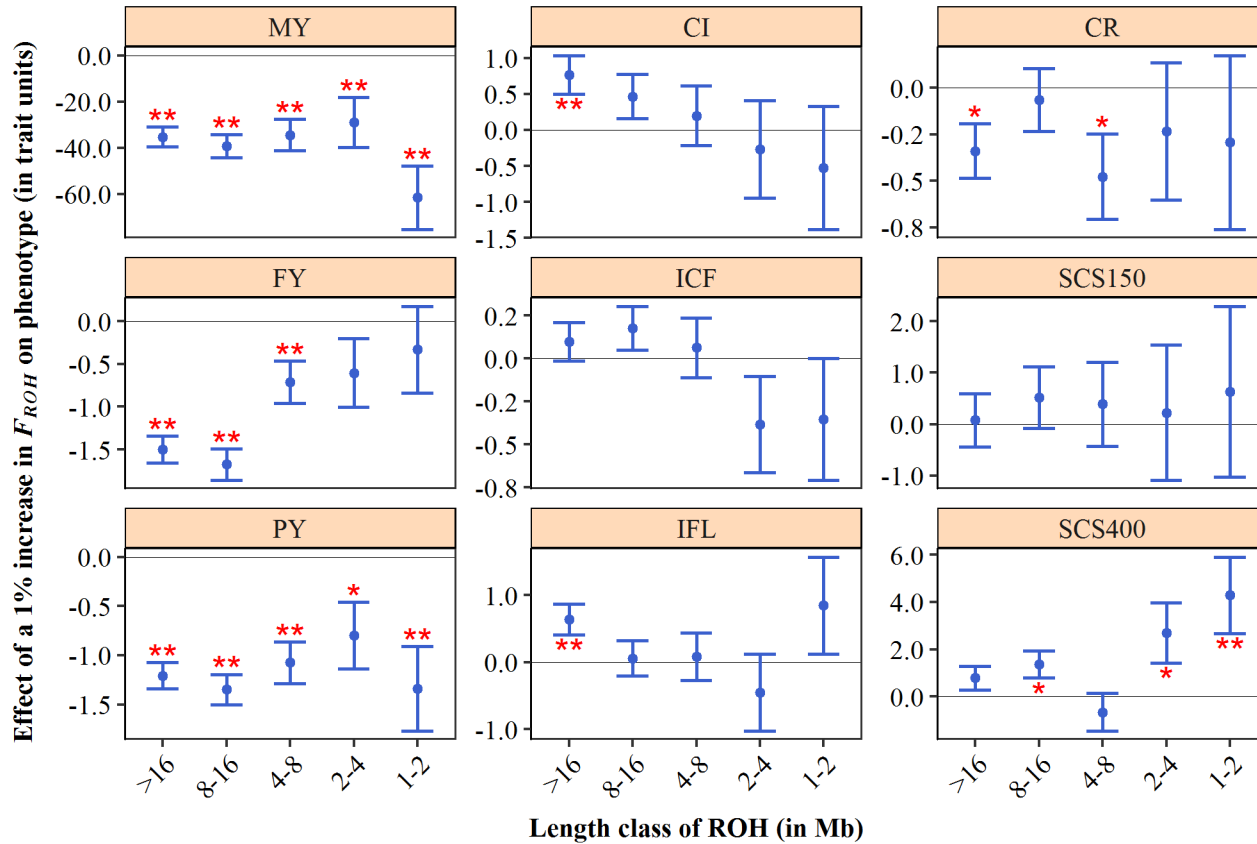


Purging based (all traits)

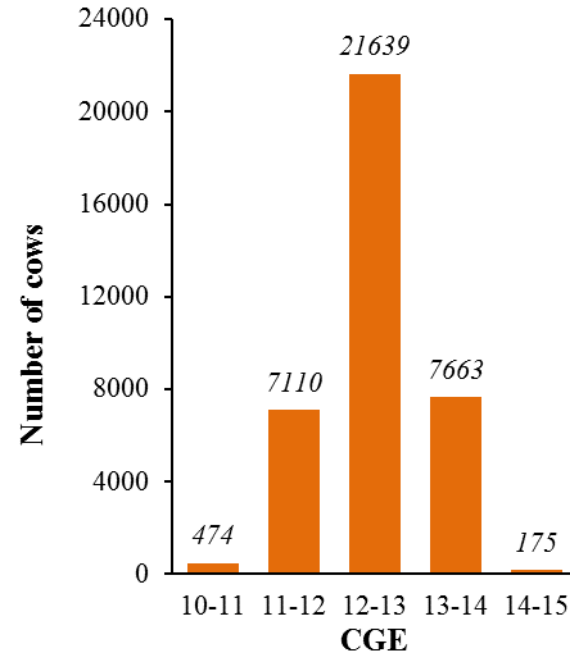
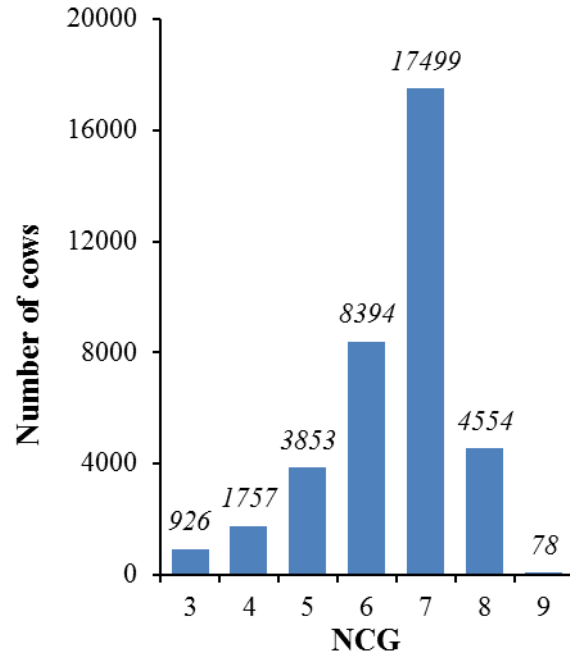


Kalinowski's new and ancestral inbreeding

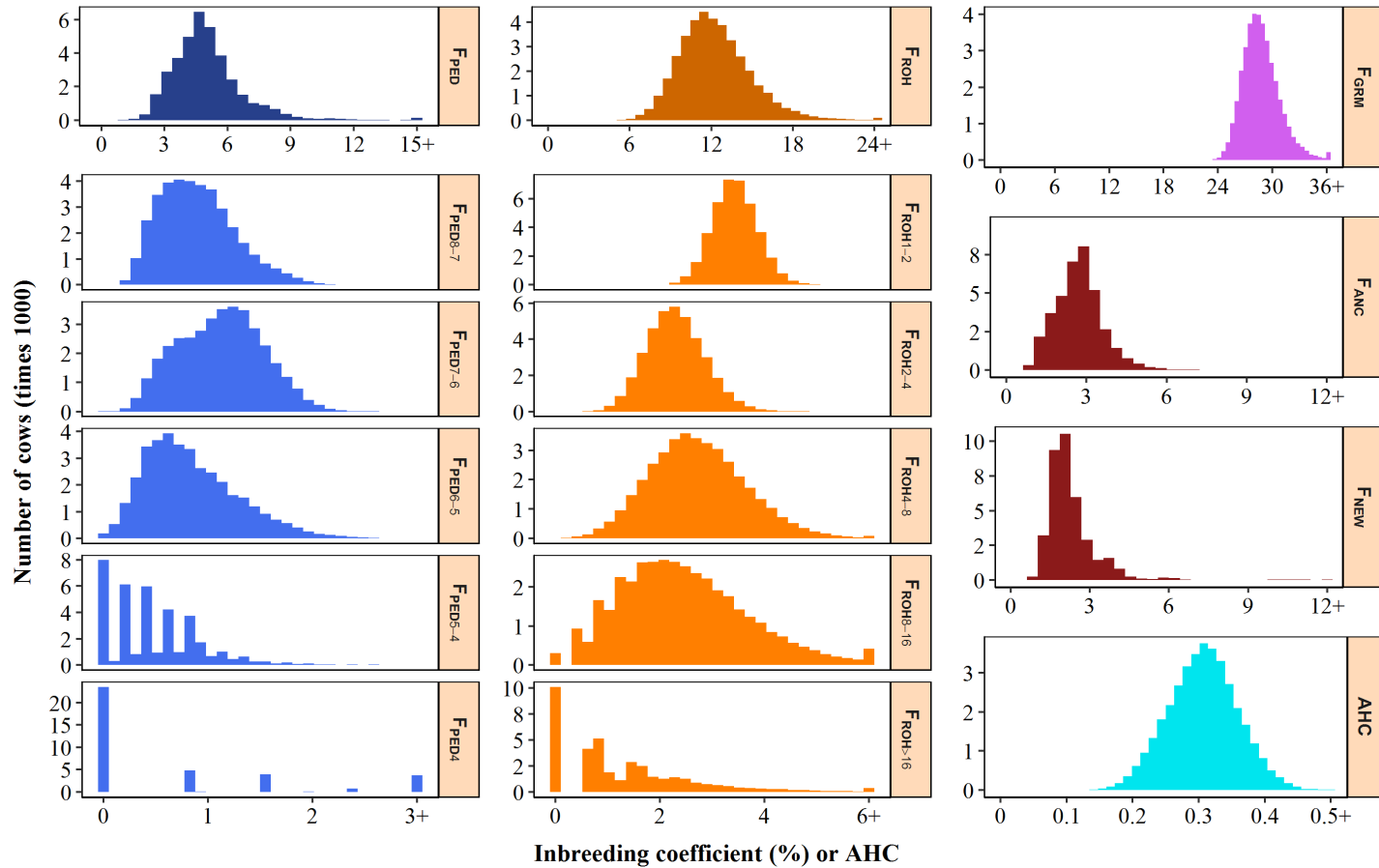
ROH based (all traits)



Pedigree completeness



Distributions of F -measures



Differences in population (+/- 2 SD of F)

Trait	F_{PED}			F_{ROH}			F_{GRM}		
	Low	High	Diff	Low	High	Diff	Low	High	Diff
MY	8,229	7,953	-274	8,284	7,898	-386	8,293	7,889	-404
FY	347.6	336.4	-11.2	349.1	334.9	-14.2	348.7	335.3	-13.4
PY	287.6	278.4	-9.2	289.4	276.6	-12.8	289.5	276.5	-13.0
CI	392.3	395.7	3.4	391.4	396.6	5.2	391.4	396.6	5.2
IFL	39.4	40.4	1.0	38.5	41.3	2.8	38.1	41.7	3.6
CR	64.9	62.7	-2.2	65.2	62.4	-2.8	65.3	62.3	-3.0
SCS400	1,578	1,584	6	1,576	1,586	10	1,576	1,586	10

Phenotypes

Group	Trait
Yield	Milk yield (305-d)
	Fat yield (305-d)
	Protein yield (305-d)
Fertility	Calving interval
	Interval calving to first insemination
	Interval first to last insemination
	Conception rate
Udder health	SCS day 1-150
	SCS day 151-400
