

# Crossbred SNP effects depending on the breed-of-origin

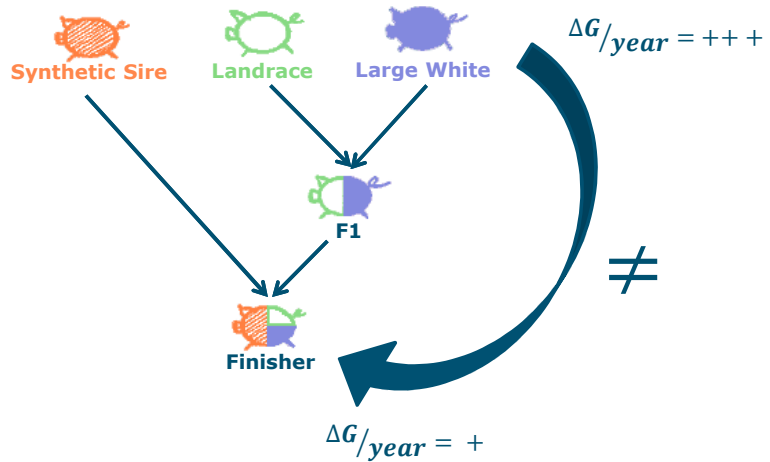
July 12, Claudia A. Sevillano

Breed4Food SEMINAR



## Background: Breeding Structure

- (1) Management (GxE)
- (2) Trait differences
- (3) Genetic backgrounds

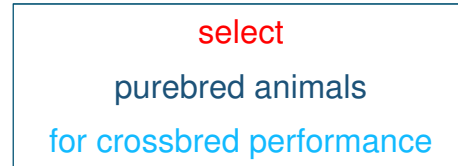
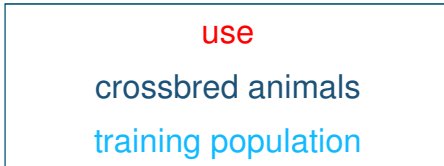


## Background: Breeding Goal



Aim: Select purebreds for crossbred performance

Idea: Improve prediction by using **crossbred performance**

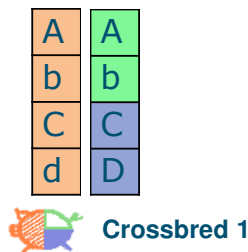


## Breeding Goal

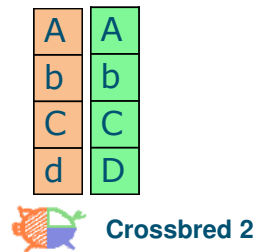


Idea: Improve prediction by using **crossbred performance**

+ assuming effects of SNPs are **breed-specific**






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## Results BOA-model

**Average daily gain**

<i>Model</i>	$h^2_{PB}$	$h^2_{CB}$	$r_{g_{PB-CB}}$	$r_{IH}$
 BOA	0.15	0.30	0.73(0.09)	<b>0.090</b>
G	0.18	0.29	0.66(0.08)	<b>0.099</b>
 BOA	0.23	0.30	0.56(0.18)	<b>0.153</b>
G	0.23	0.29	0.44(0.12)	<b>0.147</b>
 BOA	0.21	0.30	0.62(0.10)	<b>0.148</b>
G	0.23	0.29	0.49(0.08)	<b>0.140</b>

## Hypothesis

SNP-allele effect for crossbred performance **depends on the breed-of -origin.**

Present study

- To show if they are different
- To show how they are different

How?

- Association study by breed-of-origin for **Average Daily Gain.**

# Methodology

1. Back-solve SNP-allele effects for CB performance.



2. Calculate % variance explained by non-overlapping blocks of SNPs.

- Build blocks of SNPs.

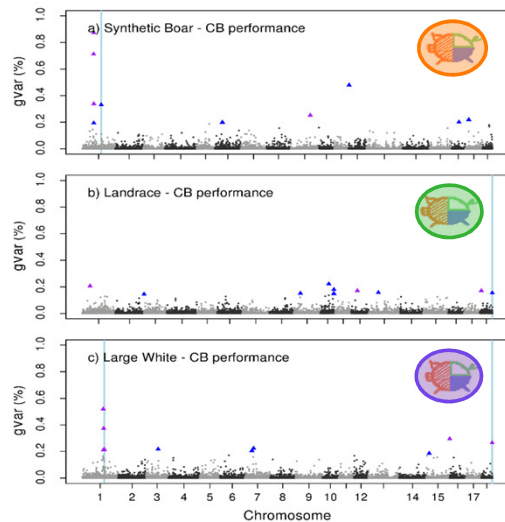
*Nonrandom association between alleles at two loci in the CB population (P-value<0.01)*

Arlequin (Excoffier et al., 2005).

Breed of Origin	#	Mean	Median	Mean Kb
S	5631	7.3	5.0	335.0
LR	7592	5.4	4.0	237.6
LW	6767	6.3	5.0	272.1



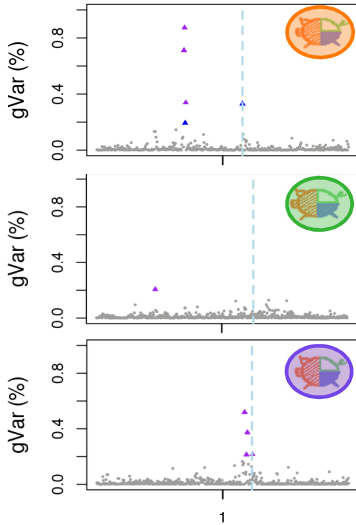
# Results



■ The genetic variance explained by a genomic region associated to crossbred performance is different depending on the breed it was inherited from.



# MC4R



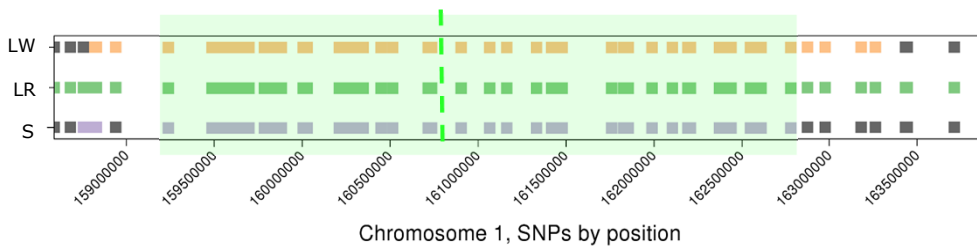
- The **MC4R gene** is expressed in the hypothalamus and affects feed intake and energy expenditure.
- A mutation in the protein coding region of the gene (*m allele*) **increases feed intake and growth.**

Breed of Origin	<i>m</i>	<i>w</i>
S	0.81	0.19
LR	0.11	0.89
LW	0.44	0.56

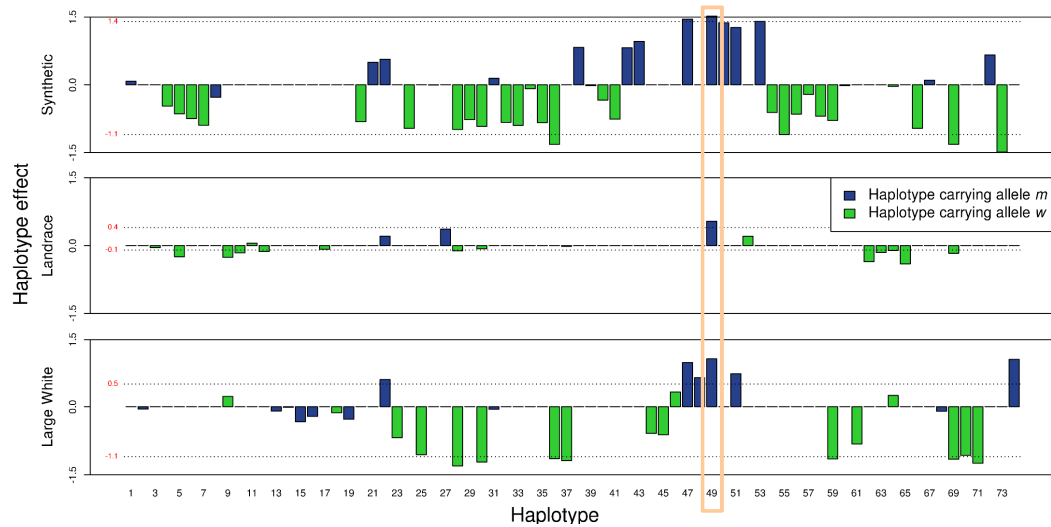


# Blocks with MC4R

- Block across breeds containing the MC4R
  - 31 SNPs -> 74 haplotypes
  - 31 SNPs + MC4R -> 74 different haplotypes



## Results



## Summary

- Variance % of a genomic region associated to crossbred performance is **different depending on the breed-of-origin**.
  - Differences in allele frequencies across breeds.
- Pairs of **identical haplotypes** (both carrying either the *m* or *w* allele), although from different breed-of-origin have **different effects**.
  - Epistasis or unobserved differences between the haplotypes

## Hypothesis 2

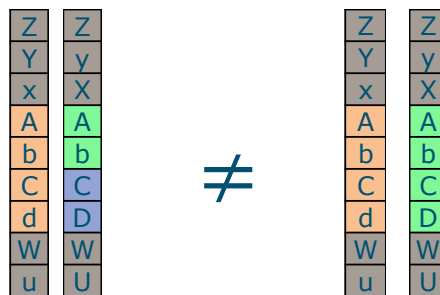
Effect of **haplotypes associated** with crossbred performance are **different depending on the breed.**

**Majority** of the genomic regions **are not or weakly associated** with crossbred performance.

Further study

- **NEW Model:**  
SNPs strongly associated with crossbred performance (breed-specific effects) + rest of the SNPs (effects are the same across breeds).

## Modified-BOA model



**Selection of SNPs strongly associated with crossbred performance:**

top LD blocks explain together

5% and 10%

of the total genetic variance

in each breed-of-origin






Crossbred 1



Crossbred 2

## Results Objective 2

<i>Model</i>	$h_{PB}^2$ <i>Non-sel / Sel</i>	$h_{CB}^2$ <i>Non-sel / Sel</i>	$r_{gPB-CB}$ <i>Non-sel / Sel</i>	$r_{IH}$
 10%-BOA	0.01 / 0.10	0.02 / 0.26	0.00 / 0.74	<b>0.100</b>
BOA	0.15	0.30	0.73	<b>0.090</b>
G	0.18	0.29	0.66	<b>0.099</b>
 10%-BOA	0.02 / 0.16	0.02 / 0.26	0.00 / 0.96	<b>0.177</b>
BOA	0.23	0.30	0.56	<b>0.153</b>
G	0.23	0.29	0.44	<b>0.147</b>
 10%-BOA	0.02 / 0.14	0.02 / 0.26	0.99 / 0.74	<b>NA</b>
BOA	0.21	0.30	0.62	<b>0.148</b>
G	0.23	0.29	0.49	<b>0.140</b>

## Conclusions

- The modified-BOA model (seem) to **improve** predictions of **crossbred performance** for purebred animals belonging to the most **divergent** paternal breed.



# Thank you

