Relevance of genotyping crossbred pigs for selection of nucleus purebred pigs for finisher traits
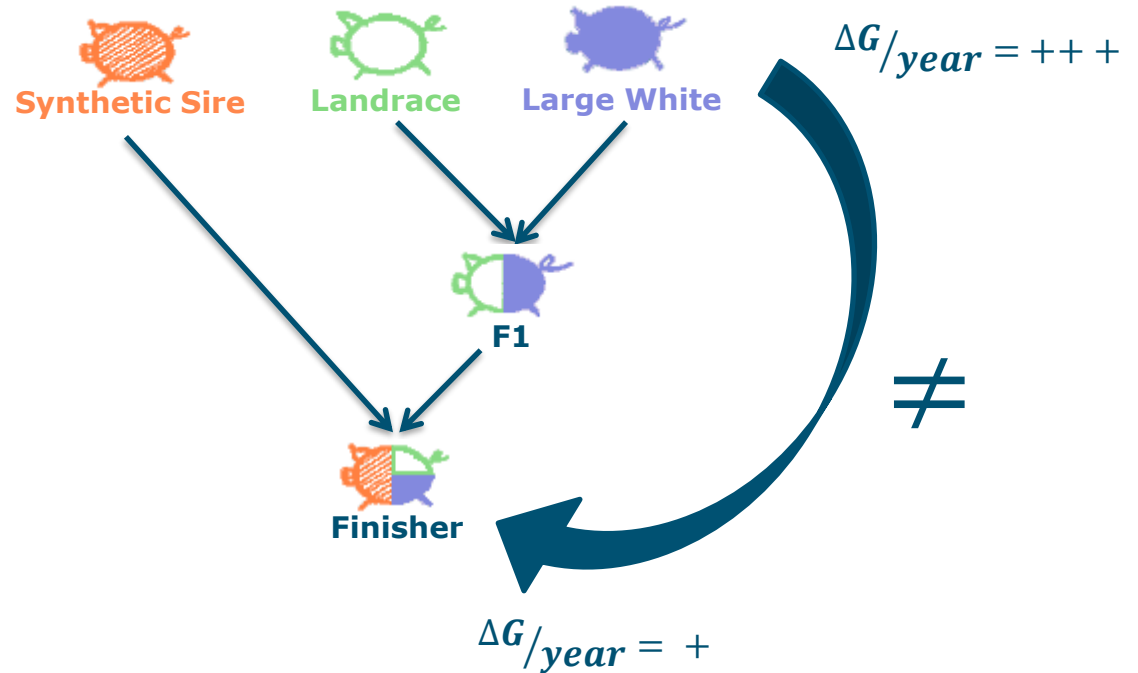
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Background: Breeding Structure

(1) Management (GxE)

(2) Trait differences

(3) Genetic backgrounds

Background: Breeding Goal

Aim: Select purebreds for crossbred performance

Idea: Improve prediction by using crossbred genomic information

use
crossbred animals
training population

select
purebred animals
for crossbred performance

Background: Mixed models in ssGBLUP

- Pedigree is unable to consider relationships with or across base populations.

- Conflict to combine pedigree with genomic relationships.

Additive Relationship

- Defined within populations (Breed of origin approach)

- Defined across populations (Metafounders approach)

Background:Breed of origin approach (BOA)

Partial relationship matrices

(assuming base populations are unrelated

and effects of SNPs are breed-specific)

	S1	S2	CB1	CB2
S1	PB-PB		PB-CB_S	
S2				
CB1	CB_S-PB		CB_S-CB_S	
CB2				

	LW1	LW2	CB1	CB2
LW1	PB-PB		CB_{LW}-PB	
LW2				
CB1	PB-CB_{LW}		CB_{LW}-CB_{LW}	
CB2				

	LR1	LR2	CB1	CB2
LR1	PB-PB		PB-CB_{LR}	
LR2				
CB1	CB_{LR}-PB		CB_{LR}-CB_{LR}	
CB2				

A	A
b	b
C	C
d	D

$\neq$

A	A
b	b
C	C
d	D

Crossbred 1   **Crossbred 2**

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UNIVERSITY & RESEARCH

100years

Background:Breed of origin approach (BOA)

Partial relationship matrices

(assuming base populations are unrelated

and effects of SNPs are breed-specific**)**

Three-way crossbred:

+8% accuracy, r_{pc} 0.44
-9% accuracy, r_{pc} 0.66
+6% accuray, r_{pc} 0.49
(Sevillano et al. 2018 Front genet)

Two-way crossbred:

+13% accuracy, r_{pc} 0.59 and 0.73 (H^{-1})
(Xiang et al., 2016, J Anim Sci)

+0% accuracy, r_{pc} 0.88
(Lopes et al., 2017, Gent Sel Evol)
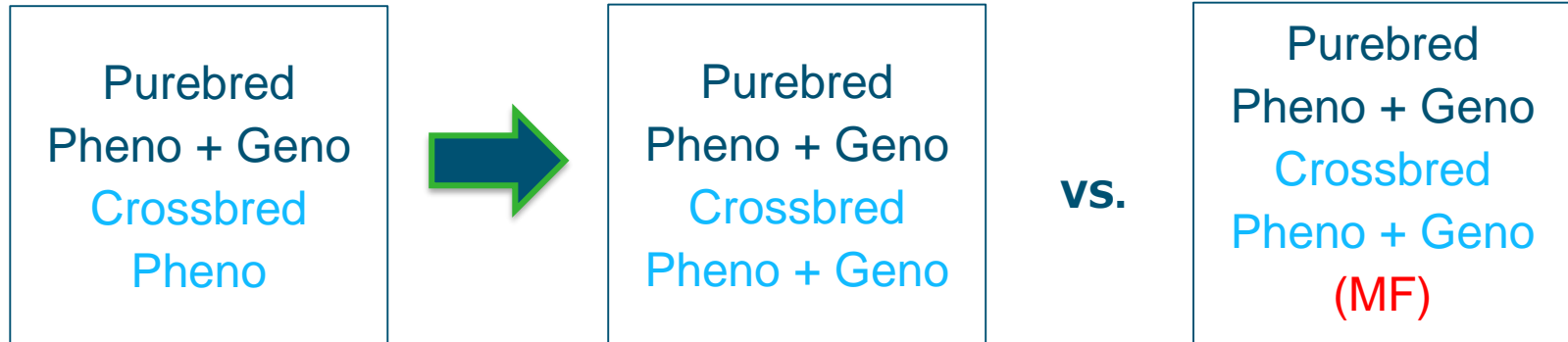
Background: Metafounders approach (MF)

Relationship matrix

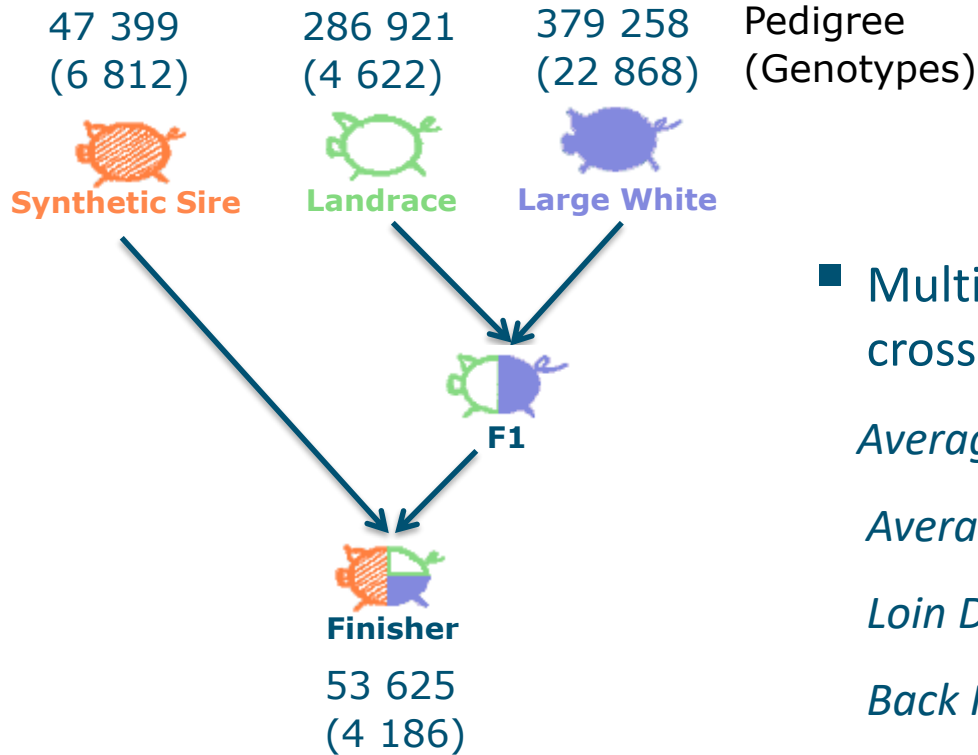(assuming base populations are related)

- Metafounder = represents an ancestral population.

- Ancestral populations may be connected and therefore related.

Objective

Show the added value of using CB genomic information in the training population with or without the MF approach

Purebred		Purebred		Purebred
Pheno + Geno	➡	Pheno + Geno	**vs.**	Pheno + Geno
Crossbred		Crossbred		Crossbred
Pheno		Pheno + Geno		Pheno + Geno
				(MF)

Data & Model

Topigs Norsvin
PROGRESS IN PIGS

47 399
(6 812)

286 921
(4 622)

379 258
(22 868)

Pedigree
(Genotypes)

Synthetic Sire

Landrace

Large White

F1

Finisher

53 625
(4 186)

- Multivariate ssGBLUP: Purebred & crossbred

Average Daily Gain (ADG) *(r_{pc} 0.78)*

Average Daily Feed Intake (ADFI) *(r_{pc} 0.75)*

Loin Depth *(r_{pc} 0.81)*

Back Fat Thickness *(r_{pc} 0.82)*

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100years
1918 — 2018

Validation

Synthetic Sire

TBV of Sires for Crossbred performance

(Average of "individual offspring deviation")

correlation

EBV of Synthetic sires for Crossbred performance

ssGBLUP with metafounders

1. Assume one MF per breed

2. Compute relationships between MF

   Covariances of base allelic frequencies across populations→ Generalized least square *(Garcia-Baccino et al., 2017 Genet Sel Evol)*

3. Use those MF in ssGBLUP

   $H^{\Gamma-1}$ *(Legarra et al., 2015 Genetics)*

Results

	Geno PB	Geno PB + CB	Geno PB + CB (MF)
ADG	0.53	0.55	0.57
ADFI	0.62	0.60	0.60
Back Fat	0.56	0.53	0.58
Loin Depth	0.49	0.44	0.50

	Geno PB to Geno PB + CB	Geno PB to Geno PB + CB (MF)
ADG	+4%	+8%
ADFI	-2%	-2%
Back Fat	-6%	+4%
Loin Depth	-10%	+3%

Conclusion

- Including CB genomic information seems to be beneficial for prediction accuracy

when genomic and pedigree information are properly aligned as achieved with the MF approach

Thank you