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# Using phenotypes of three-breed cross to improve breeding value estimation of purebred animals

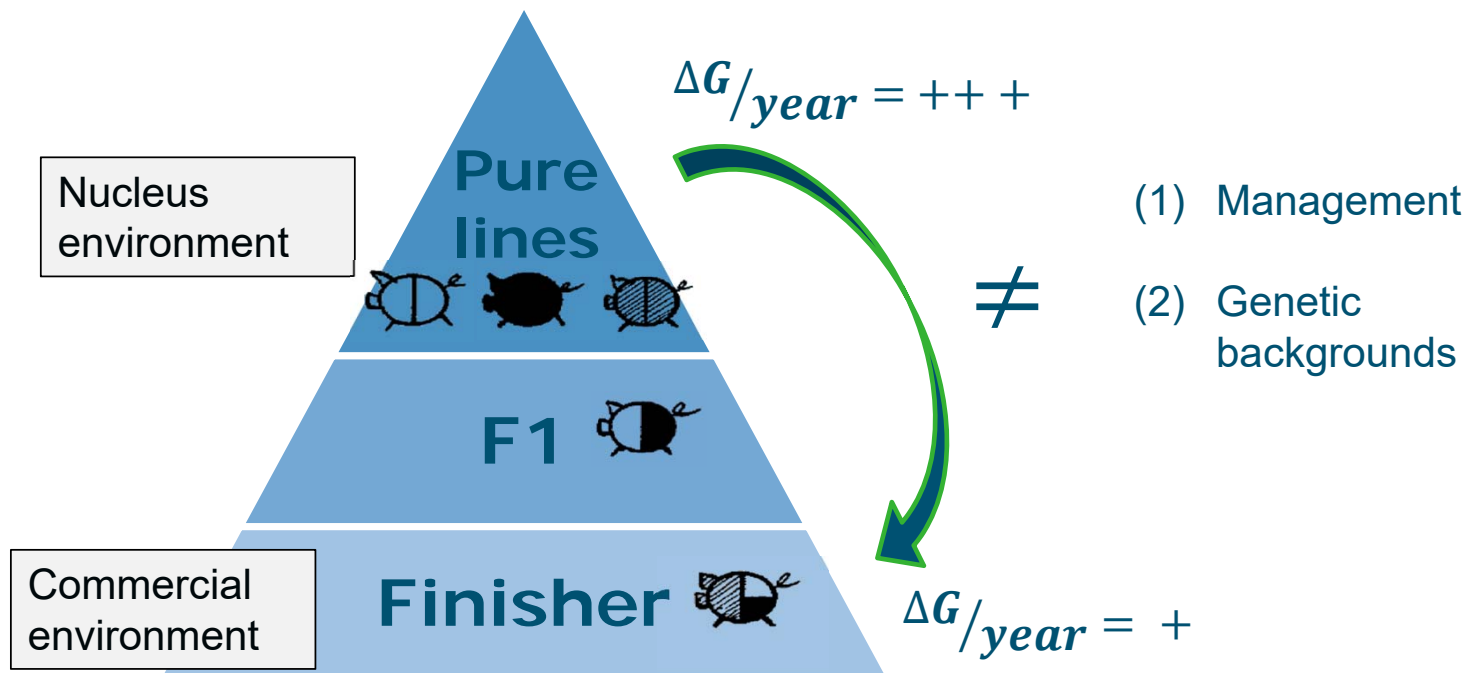
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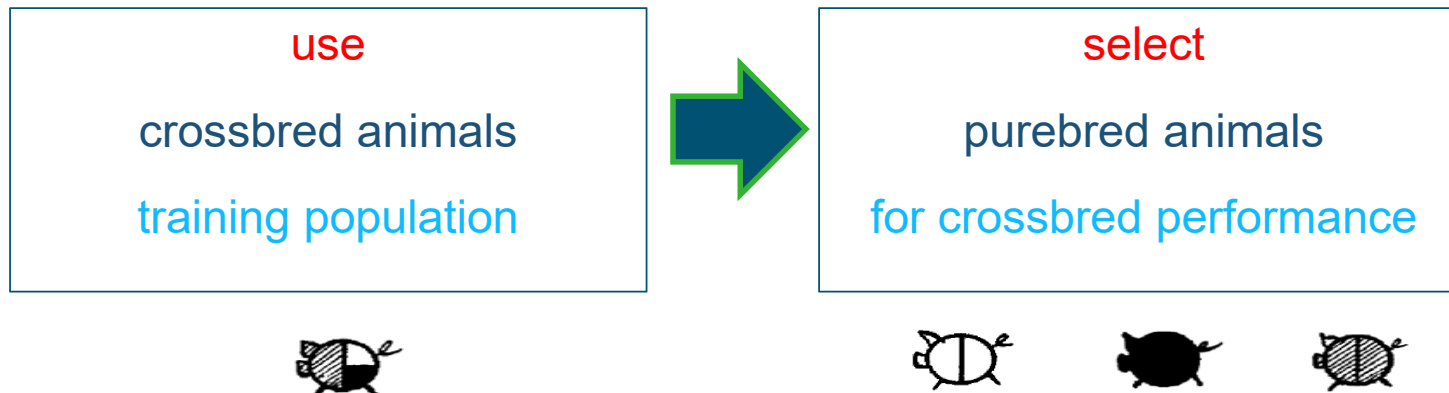
# Finisher traits



# Crossbreds in Genomic prediction

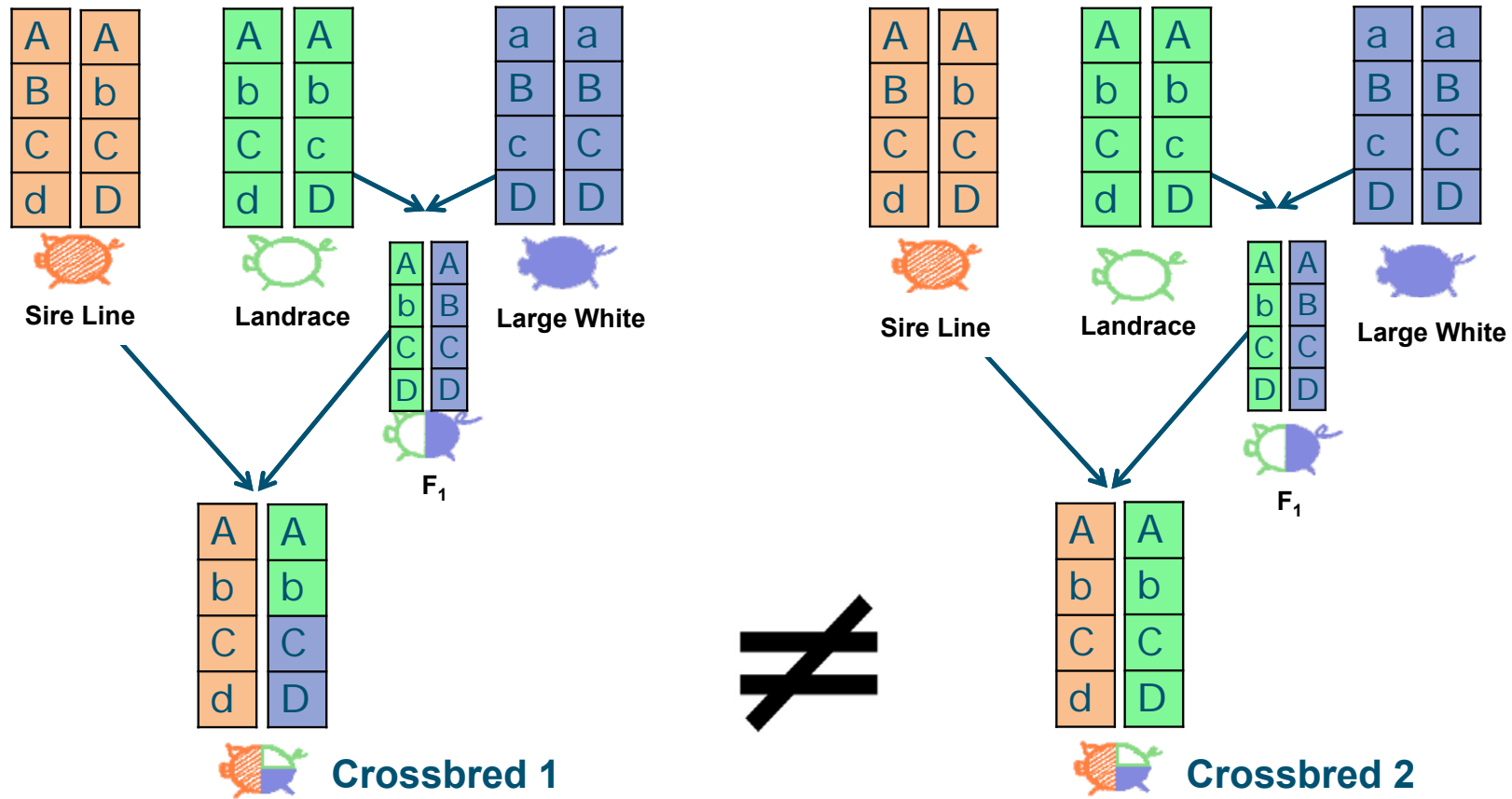


Aim: Improve accuracy of purebred breeding values estimates  
Idea: Selection of pure lines based on **crossbred performance**



Effects of SNPs may be breed-specific because of different genetic backgrounds

# Breed specific SNP effects



# Model for purebred and crossbred performance with G-matrix (**G model**)

Multivariate (4-traits):

	<i>Response variable</i>	<i>Fixed effects</i>	<i>Litter effect</i>	<i>Additive effect</i>	<i>Residual</i>
(Sire Line) 1.	$y_S$	$X_S b_S$	$W_S u_S$	$Z_S a_S$	$+ e_S$
(Landrace) 2.	$y_{LR}$	$X_{LR} b_{LR}$	$W_{LR} u_{LR}$	$Z_{LR} a_{LR}$	$+ e_{LR}$
(Large White) 3.	$y_{LW}$	$X_{LW} b_{LW}$	$W_{LW} u_{LW}$	$Z_{LW} a_{LW}$	$+ e_{LW}$
(Crossbred) 4.	$y_{CB}$	$X_{CB} b_{CB}$	$W_{CB} u_{CB}$	$Z_{CB} a_{CB}$	$+ e_{CB}$

# Model for purebred and crossbred performance with partial relationship matrices (**BOA model**)

Multivariate (4-traits):

	<i>Response variable</i>	<i>Fixed effects</i>	<i>Litter effect</i>	<i>Additive effect</i>	<i>Residual</i>
(Sire Line) 1.	$y_S$	$= X_S b_S$	$+ W_S u_S$	$+ Z_S a_S$	$+ e_S$
(Landrace) 2.	$y_{LR}$	$= X_{LR} b_{LR}$	$+ W_{LR} u_{LR}$	$+ Z_{LR} a_{LR}$	$+ e_{LR}$
(Large White) 3.	$y_{LW}$	$= X_{LW} b_{LW}$	$+ W_{LW} u_{LW}$	$+ Z_{LW} a_{LW}$	$+ e_{LW}$
(Crossbred) 4.	$y_{CB}$	$= X_{CB} b_{CB}$	$+ W_{CB} u_{CB}$	$+ Z_{CB} c_{CB}^{(S)} + Z_{CB} c_{CB}^{(LR)} + Z_{CB} c_{CB}^{(LW)}$	$+ e_{CB}$

Christensen et al. Genet Sel Evol (2015) 47:98

# Assigning breed-of-origin of alleles in three-breed cross pigs

Vandenplas *et al. Genet Sel Evol* (2016) 48:61  
DOI 10.1186/s12711-016-0240-y



RESEARCH ARTICLE

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## Assigning breed origin to alleles in crossbred animals



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RESEARCH ARTICLE

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## Empirical determination of breed-of-origin of alleles in three-breed cross pigs



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Background

New approach






Results part1

Results part2

Conclusions

# Assigning breed-of-origin of alleles in three-breed cross pigs

## Data

Sire Line 	Landrace Line 	Large White Line 	F1 	Finishers 	Total
2825	4179	7183	1354	1723	17,264

## Results

Paternal	Maternal			Total
Sire Line	LR Line	LW Line	Total	
49.6	23.0	22.7	45.7	95.2

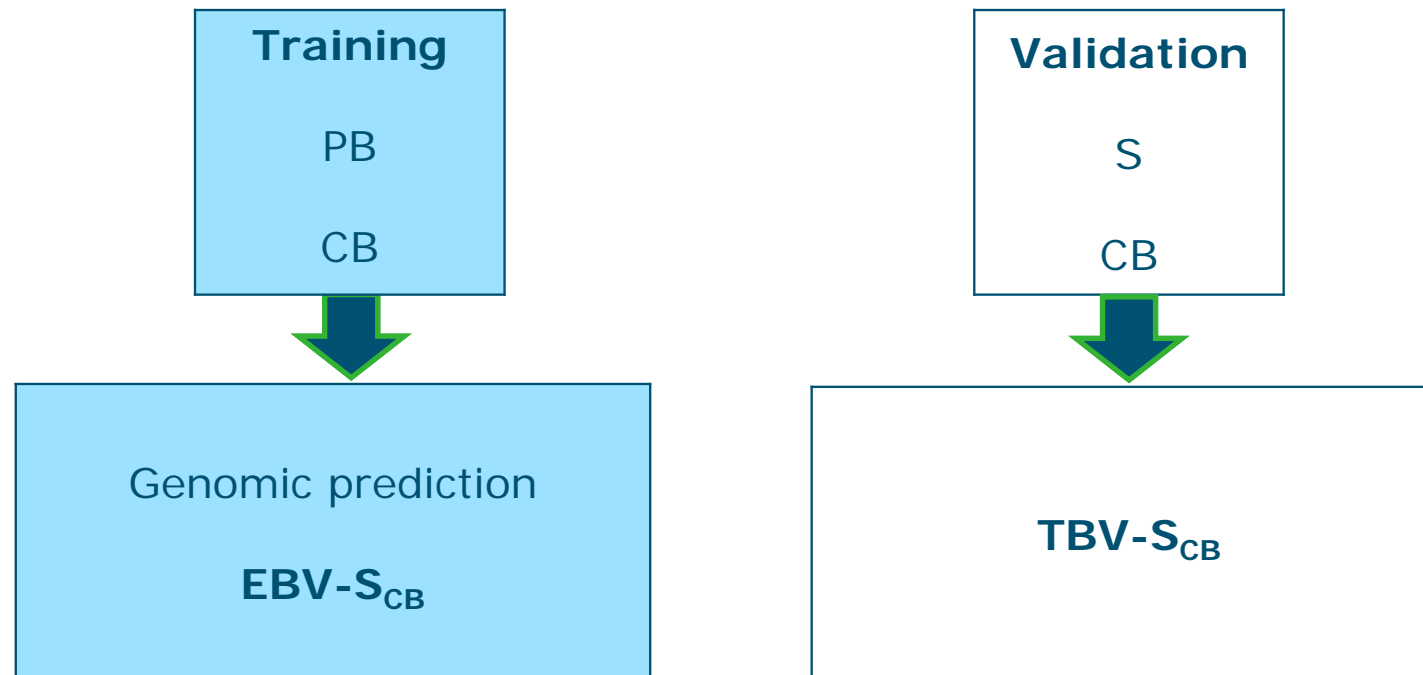
- Average assignment of the alleles were similar across the 18 chromosomes.
- Average assignment rates were also similar across finishers.



# Validation of the model

Sire line

Cross-validation (4X)



# Results

## Average daily gain

Model	$h_S^2$	$h_{CB}^2$	$r_{g_{S-CB}}$	$r_{IH}$
BOA	0.23	0.33	0.49	<b>0.11</b>
G matrix	0.28	0.33	0.52	<b>0.08</b>

## Back fat

Model	$h_S^2$	$h_{CB}^2$	$r_{g_{S-CB}}$	$r_{IH}$
BOA	0.31	0.28	0.74	<b>0.20</b>
G matrix	0.36	0.37	0.73	<b>0.24</b>

## Loin depth

Model	$h_S^2$	$h_{CB}^2$	$r_{g_{S-CB}}$	$r_{IH}$
BOA	0.42	0.26	0.53	<b>0.17</b>
G matrix	0.47	0.23	0.57	<b>0.21</b>

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# Conclusions

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Assign of breed-of-origin of alleles

- **Breed-of-origin of alleles** of three-breed cross animals **can be derived**.
- It is **feasible** to use **breed-specific SNP effects models** in genomic prediction.

Model for purebred and crossbred performance

- **No big improvements** with **BOA model**, maybe because of high  $r_{gPB-CB}$  and limited training data size.

# THANK YOU



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