




Using crossbred genomics in a breeding program for pigs

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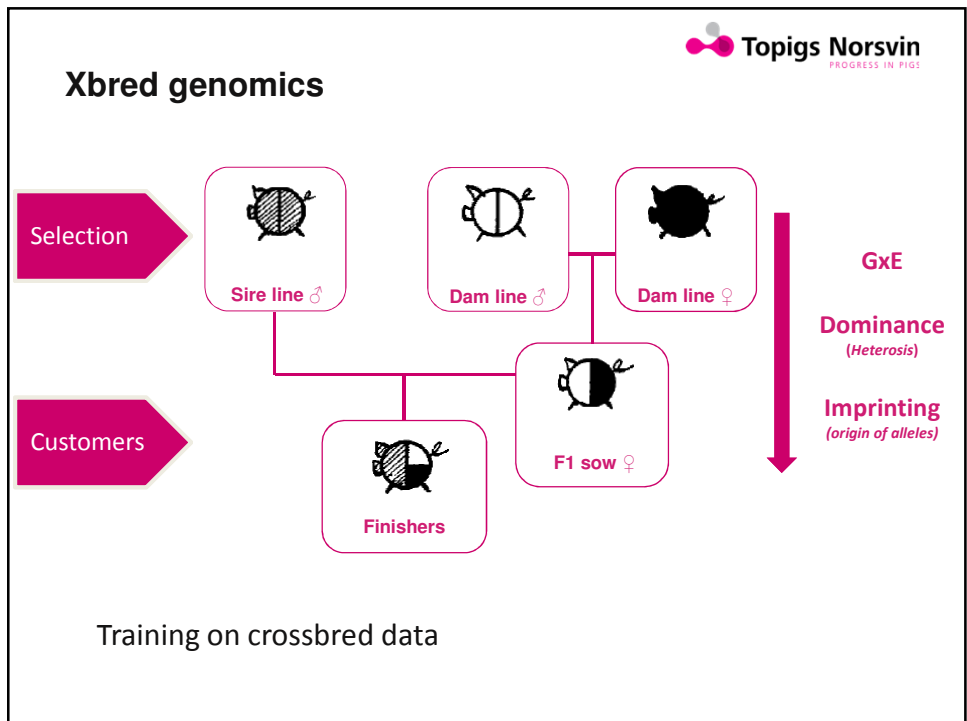
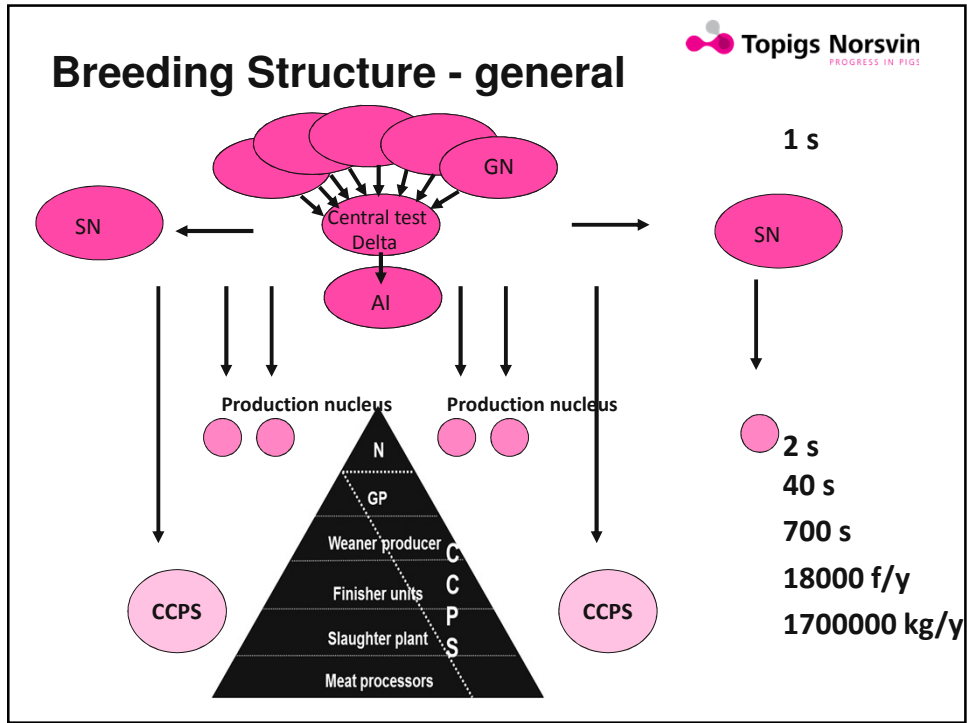


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Breeding Program



We shall **double** annual genetic progress on commercial level. Our key partners' performance shall impact our genetic progress.



Xbred genomics

- Breeding value estimation
- Optimizing breeding program

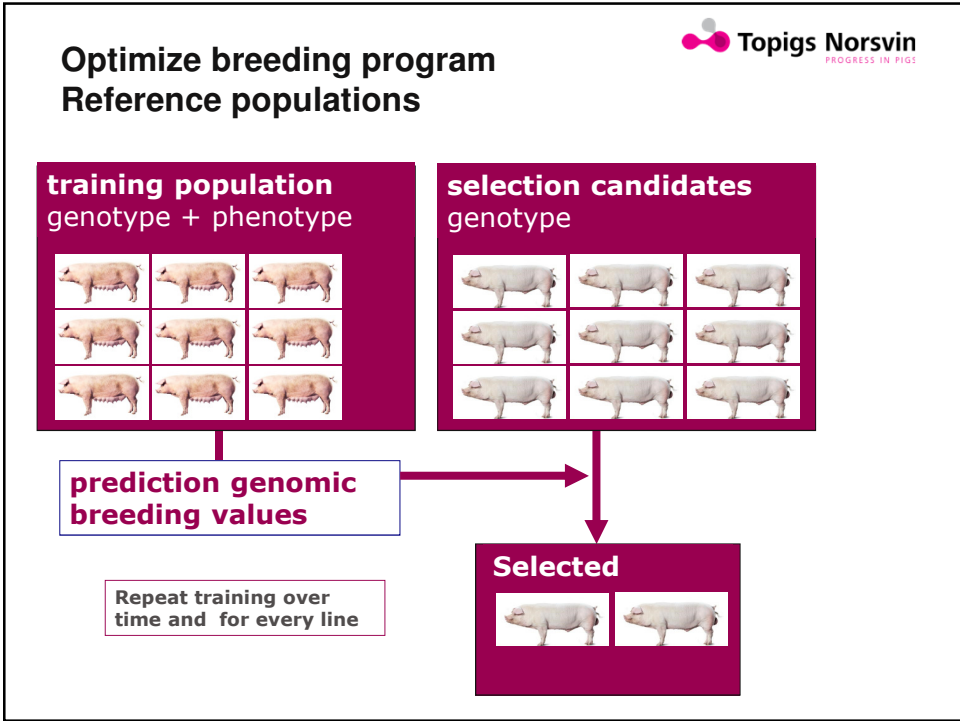
Breeding value estimation

- MixBLUP
- APY
- Testing adding crossbred genotypes

- Increased running time
→ Adapt selection procedures

- Lines with different historic trends and genetic parameters
→ Test Metafounders





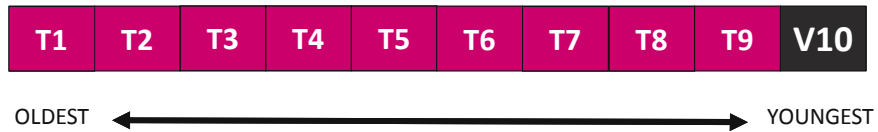
Training / reference population

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- Size of reference population =
 - number of years
 - * number of phenotyped + genotyped animals
 - * **degradation** of information over generations

The concept


- Split the data in 10 blocks of equal size
- Sorted by date of birth
- V10: youngest 10% animals as validation animals



Training per block


1b	T1	T2	T3	T4	T5	T6	T7	T8	T9	V10
2b	T1	T2	T3	T4	T5	T6	T7	T8	T9	V10
3b	T1	T2	T3	T4	T5	T6	T7	T8	T9	V10
4b	T1	T2	T3	T4	T5	T6	T7	T8	T9	V10
5b	T1	T2	T3	T4	T5	T6	T7	T8	T9	V10
6b	T1	T2	T3	T4	T5	T6	T7	T8	T9	V10
7b	T1	T2	T3	T4	T5	T6	T7	T8	T9	V10
8b	T1	T2	T3	T4	T5	T6	T7	T8	T9	V10
9b	T1	T2	T3	T4	T5	T6	T7	T8	T9	V10


Equal size of reference population
and decreasing relationship between Training and Validation populations

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Training per block

Block	# training animals	# validation animals	Age diff. (V - T animals)	Accuracy	Bias
All	17,282	1,921	2.32	0.57	0.90
T90	1,921	1,921	0.31	0.43	1.02
T80	1,921	1,921	0.66	0.39	0.96
T70	1,921	1,921	1.02	0.47	0.95
T60	1,921	1,921	1.40	0.38	0.83
T50	1,921	1,921	1.75	0.42	1.04
T40	1,921	1,921	2.08	0.42	1.00
T30	1,921	1,921	2.53	0.40	0.99
T20	1,921	1,921	3.99	0.35	1.02
T10	1,921	1,921	7.16	0.25	0.76

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- ## Optimizing breeding program
- ~~SelIndex~~
 - SelAction
 - MTINDEX

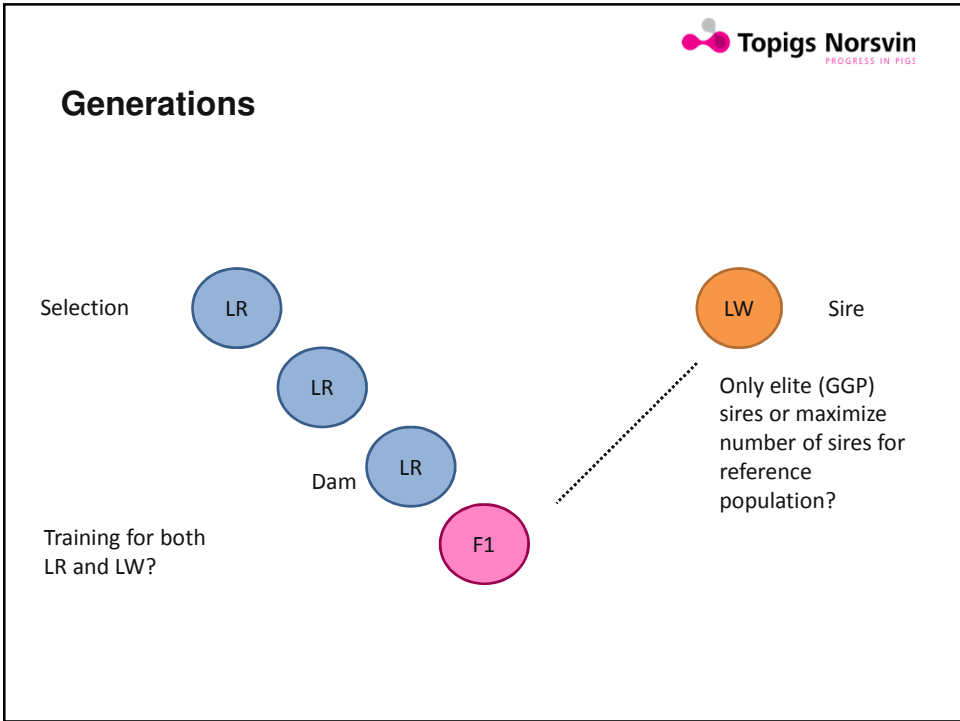
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MTINDEX

- Marker information simulated as:
 - second trait with $h^2 = 1.0$
 - r_g dependent on reference population size based on Daetwyler

- Allows for varying:
 - h^2 between purebreds and crossbreds (data quality)
 - r_{PC} between traits
 - size of reference population

- Does NOT include:
 - Degradation of training information over time
 - Effect of distance training population to selection population ?





Topigs Norsvin appreciates the work being done in WUR / B4F on crossbred genomics

