SUISAG

Genomic Prediction in two Swiss populations

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Gemeinsam für die
**SCHWEINE-
GENERATION**
von morgen

25 JAHRE

Outline

- genomic breeding programs:

  - Swiss Large White dam line (SLW)

  - Swiss Large White sire line (Premo)

  - Swiss Landrace dam line (SLR)

- New health Index: longevity

Swiss pig breeding populations

➢ SLW: typical dam line since 2002

- genomic prediction since 2016

- start with 1000 reference animals (focus on accuracy of predictions > 50%)

➢ Premo: sire line since 2002

- genomic prediction together with SLW since 2016

➢ SLR: regular import from France since 2008

- genomic prediction since 2023

- start with at least1000 reference animals (focus on accuracy of predictions > 50%)

Reference animals (March 2023)

Reproduction

Breed	No. genotyped	No. Ref. Sows	R^2 NBA	No. Ref. Boars	R^2 NBA
SLW	9'327	3'073	0.61	660	0.81
SLR	3'488	1'347	0.55	193	0.73

Production

Breed	No. genotyped	No. Ref. Anim	R^2 ADG	R^2 FC	R^2 LMC
SLW	9'327	3'973	0.67	0.73	0.77
Premo	13'657	1'342	0.70	0.79	0.86
SLR	3'488	670	0.71	0.76	0.80

Conformation

Breed	No. genotyped	No. Ref. Anim	R^2 Teats	R^2 Teats inverted	R^2 Inner hoof
SLW	9'327	3'289	0.85	0.76	0.70
Premo	13'657	840	0.85	0.75	0.68
SLR	3'488	949	0.84	0.74	0.68

➢ **Reproduction**
- The size of the reference population for SLW is currently 2.5 times bigger than for SLR.

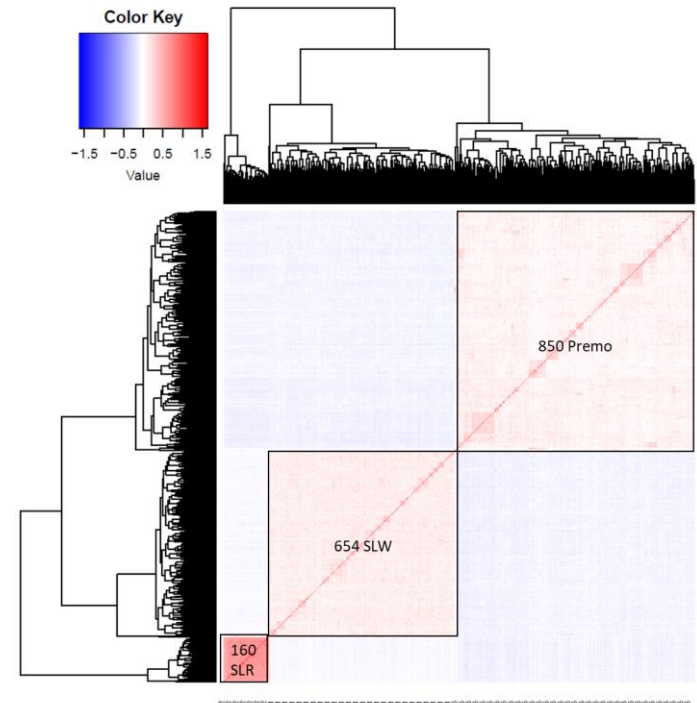➢ **Production und conformation** fewer SLR reference animals.

Genomic relationship matrix (GRM)

- SLW and Premo: common starting population in 2002
- SLR : separate breed, genotype frequencies clearly different from SLW and Premo
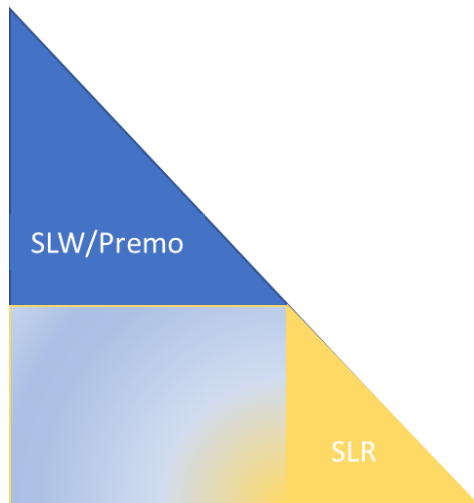
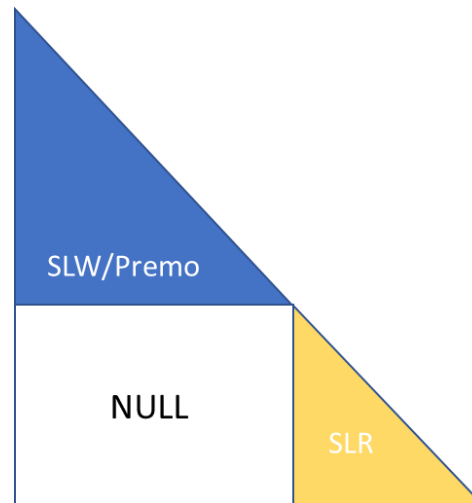Birth year 2004-2005

Birth year 2017

GRM structure for GEBV
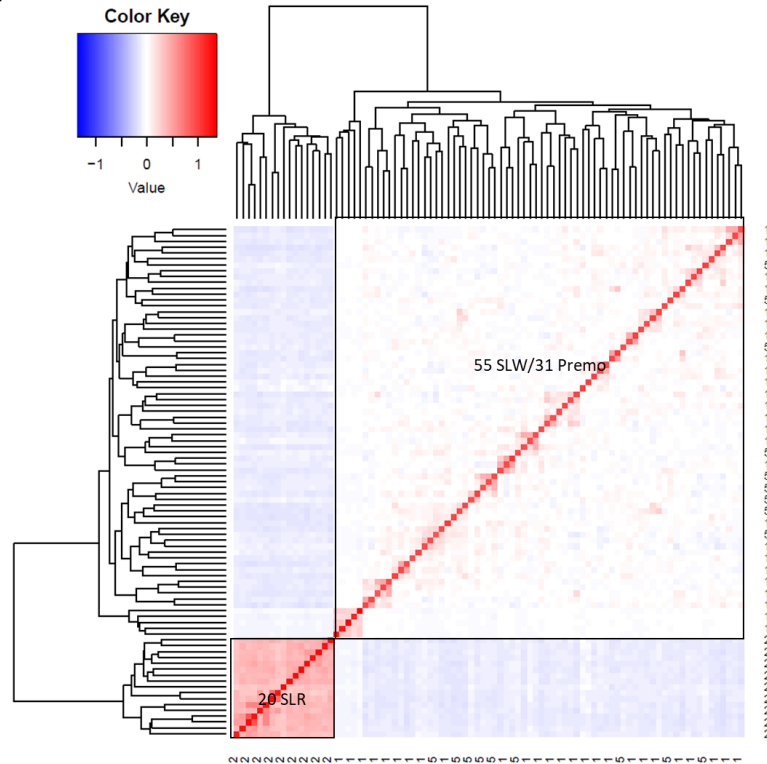
V1. a shared GRM

V1. shared	SNP ID		
Breed	1	2	3
SLW			
Premo			
SLR			

V2. a shared GRM for SLW und Premo and a nonshared GRM for SLR

V2. nonshared SLR	SNP ID_1			SNP ID_2		
Breed	1	2	3	1	2	3
SLW						
Premo						
SLR						

V3. three nonshared GRM

| V3. nonshared	SNP ID_1			SNP ID_5			SNP ID_2		
Breed	1	2	3	1	2	3	1	2	3
SLW									
Premo									
SLR									
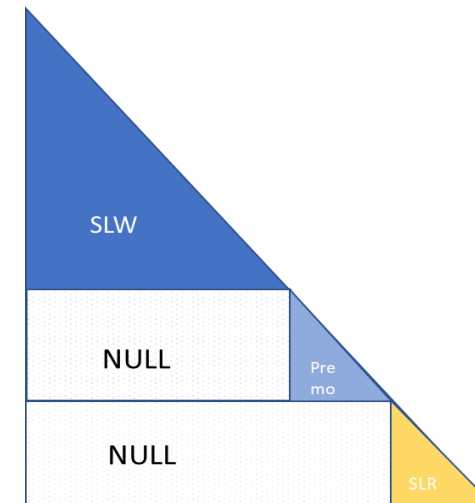
- Due to different population structure in both LW compared to LR, the variant 2 is optimal to construct the GRM.

Genomic relationship matrices for our different indices

➢ **Reproduction**
- 2 separate GRM: SLW and SLR.
- Premo-genotypes are excluded and GEBV is implemented for two dam lines.
- Premo-young sows and boars receive the pedigree EBV (EBV) afterwards.
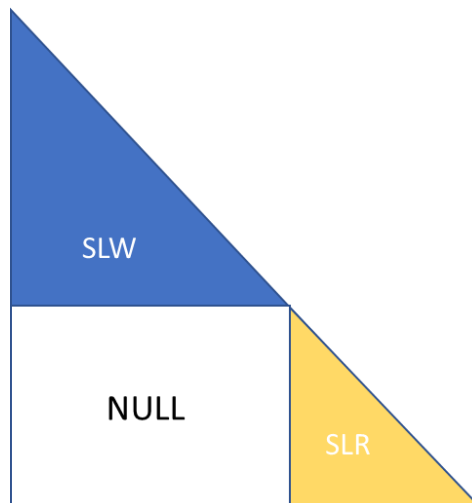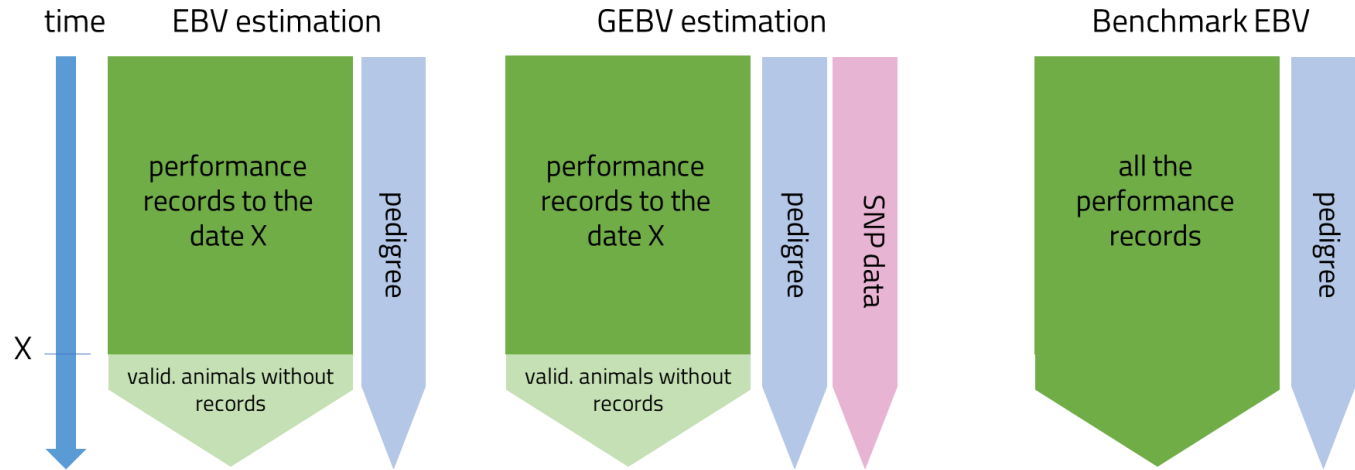
➢ **Production und conformation**
- 2 separate GRM: SLW/Premo and SL
- SLW und Premo benefit from each other, and their relationships are therefore considered (coming from a common population).
- A separate GRM for SLR like the reproduction.
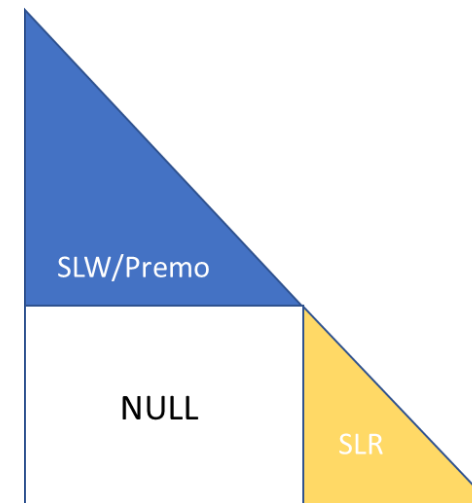
Validation procedure: how good and exact are genomic predictions?

time — EBV estimation

performance records to the date X

pedigree

valid. animals without records

X

EBV = Pedigree BLUP

GEBV estimation

performance records to the date X

pedigree

SNP data

valid. animals without records

GEBV = Genomic BLUP

Benchmark EBV

all the performance records

pedigree

- EBV_{bm} = Pedigree BLUP
- Deregressed EBV_{bm}

sire — **dam**
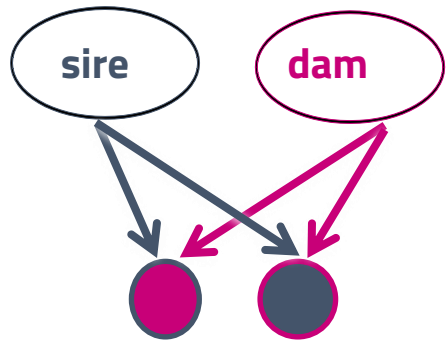
BV = ½ BV sire + ½ BV dam
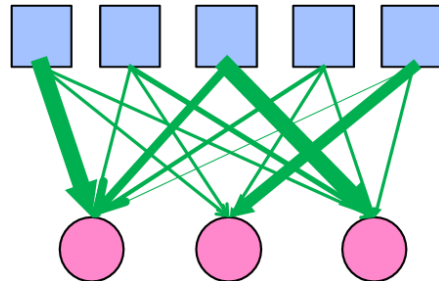
- How much is the gain from GEBVs? relative improvement:

$$RelImp = cor((Dr)EBV_{bm}, GEBV) / cor((Dr)EBV_{bm}, EBV)$$

- How accurate are the GEBVs (bias)?

$$(Dr)EBV_{bm} = m + b * GEBV + e$$

Final set of parameters: historical data and H-inverse

➤ Reproduction

Historical data	
Pedigree	Birth year 2004
Genotypes	Birth year 2006
Records	Litter date 2010
Scaling parameter for Invers of H-matrix (G – A_{22})	
GRMs	2 separate GRMs (SLW und SLR)
Scal. factors	*w:0.15, t:1.1, o: 0.8

Part of Hinverse = $tau[a + b((1-w)G + wA_{22})]^{-1} - omega*A_{22}^{-1}$

- Weight (w) to make G invertible
- Tau (t) for the reduced genetic variance
- Omega (o) for different depth of pedigree

➤ Production und conformation

Historical data	
Pedigree	Birth year 2004
Genotypes	Birth year 2006
Records	End of test 2010
Scaling parameter for Invers of H-matrix (G – A_{22})	
GRMs	2 separate GRMs (1.SLW/Premo shared and 2. SLR)
Scal. factors	SLW/Premo: w:0.15, t:1.1, o: 0.9 SL R : w:0.10, t:1.0, o: 0.5

*w, t and o are weight, tau and omega for A_{22}- and G-Matrices in software hginv

Results from validation studies I: Reproduction

Table 1 Accuracy of predictions of GEBVs for reproduction traits and reproduction index by breeds

	NBA	PS	Traits weighted in Repro index
205 SLW			
Rel. Improvement (with / without SNP)	**2.00**	**1.67**	**1.94**
Slope with SNP (bias)	**0.97**	**0.91**	**0.94**
218 SLR			
Rel. Improvement (with / without SNP)	**1.29**	**1.08**	**1.17**
Slope with SNP (bias)	**1.31**	**0.94**	**1.13**

*relative improvement is supposed to be > 1.
$^\$$Slope as bis criteria is supposed to be close to 1.

➢ **NBA** higher gain in accuracy
➢ **FAR** little gain in accuracy

➢ GEBVs for SLR
  ▪ 29% of the ranking of the selection candidates is more accurate than pure pedigree breeding values.
  ▪ Breeding value differences are generally estimated to be greater later with performance data.

Results from validation studies II: Produktion

Table 2 Accuracy of predictions of GEBVs for production traits and reproduction index by breeds

	FC	IMF	LMC	ADG	Traits weighed in Prod index
175 SLW					
Rel. Improvement (with / without SNP)	1.22	1.37	1.41	1.29	1.31
Slope with SNP (bias)	1.04	1.52	1.12	0.99	1.17
202 Premo					
Rel. Improvement	1.26	1.21	1.55	1.44	1.32
Slope with SNP (bias)	1.10	1.28	0.89	1.13	1.13
98 SLR					
Rel. Improvement	0.97	0.97	1.07	1.13	1.08
Slope with SNP (bias)	1.24	0.78	1.17	1.01	0.98

*relative improvement is supposed to be > 1.
$Slope as bis criteria is supposed to be close to 1.

➢ SLW und Premo:
  ▪ 30% gain in accuracy.
  ▪ Breeding values differences are underestimated on average.

➢ SL:
  ▪ 8% more precise ranking of the selection candidates.
  ▪ GEBVS are estimated with less bias on average.

Conclusions

➤ GEBVs gives SLR an accuracy gain of almost 17% for reproduction, 8% for production and 15% for conformation on average.

➤ Starting with >1400 SLR reference sows in reproduction, slightly fewer reference animals in production and significantly fewer reference animals in conformation. The accuracy of the GEBVs for SLR will increase over time with more reference animals.

➤ The definitive introduction of the new GEBVs, considering the genotypes of SLR in our data band SuisData: **22. Juni 2023**.

Longevity

- Current related health traits in our breeding program
  - Piglet survival until weaning
  - Litter quality: weight of piglet (under < 1 kg) und stillborn piglets
  - Conformation traits (healthy legs, teats)
  - Marker selection for ColiF4 and coli ColiF18 resistant

- New
  - Longevity as indicator for productive lifetime

Which trait is a better indicator for productive lifetime?

Example:

A Sow with <u>finished</u> carrier with 3 litters

A Sow with <u>ongoing</u> carrier with 3 litters

Merkmal	VR12		VR13		VR14		LL	AW
Kodierung	erleben [1]	ableben [0]	erleben [1]	ableben [0]	erleben [1]	ableben [0]	[0,0,...,1]	[Summe der Würfe]
Wurf 1	-	-	-	-	-	-	0|0	1|1
Wurf 2	1|1	-	-	-	-	-	0|0	2|2
Wurf 3	-	-	1|1	-	-	-	1|0	3|3
Wurf 4	-	-	-	-	NA	0	-|	-|
Wurf 5	-	-	-	-	-	-	-|	-|

NA = no litter information

Assumptions:

Sows without litter information to <u>210 days</u> after the last farrowing are assumed to no productive anymore.

- <u>30 days</u> weaning to the next service.
- <u>120 days</u> gestation length.
- <u>40 Tage</u> lactating.
- <u>20 Tage</u> delay to receive the litter data.

Trait	h² (SE)
Stayability 12 (VR12)	0.04 (0.007)
Stayability 13 (VR13)	0.06 (0.008)
Stayability 14 (VR14)	0.09 (0.010)
Longevity (LL)	**0.03** (0.002)
No. of Litters (AW)	**0.14** (0.011)

- The longevity trait has a low heritability (3%), but it shows the highest predictability even without known own contributions.

- Due to the low heritability, little breeding change is expected.

- **Publish as index** (mean 100 and standard deviation of 20).

- Since Jan. 2024 in SUISAG databank.

VIELEN DANK!

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Fragen?