Effectiveness of genomic prediction of boar taint components in Pietrain sired breeding populations

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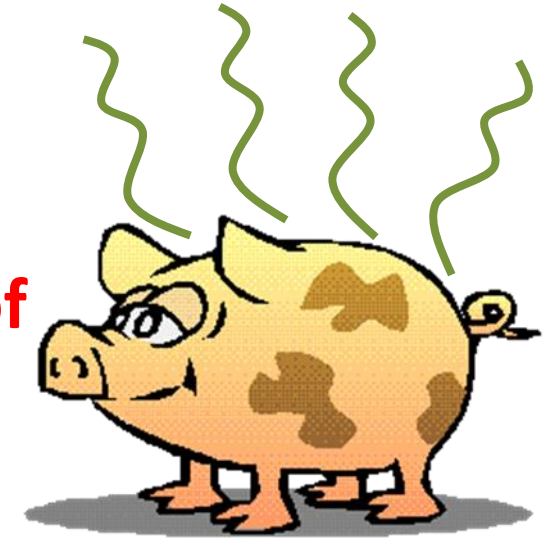
Boar taint ?



- **„… unpleasant flavour and odour of porcine meat“**

- Androstenone (5α-androst-16-ene-3-on) + Skatole (3-methylindol) + others (indole, phenol, …)

- Ban of surgical castration of piglets until 2018

→ Fattening of entired boars

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Background

- Pig breeding organizations
  - Selection of boars with low incidence of boar taint
  - Set up Pietrain breeding lines

  - BUT: costly phenotyping and small Pietrain populations

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Background

- Pig breeding organizations
  - Selection of boars with low incidence of boar taint
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  - BUT: costly phenotyping and small Pietrain populations

Objective: Genomic selection across breeding organizations

- using data of cross-bred boars

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Objectives-details

1. Combine the data sets of two boar taint related projects of Pietrain-sired progenies

2. Investigation and comparison of the genetic structure of the different local cross-bred Pietrain-populations

3. Evaluation of genomic prediction accuracy for boar taint components within Pietrain-sired populations

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Population structure

Population	No. boars	Type of cross	Project	Year
E1	241	Pi x F1	ENZEMA	Nov. 2009 – Dec. 2010
E2	236	Pi x F1		
E3	120	Pi x F2		
G1	213	Pi x F1	GOGS	Oct. 2012 – May 2013
G2	262	Pi x DL		

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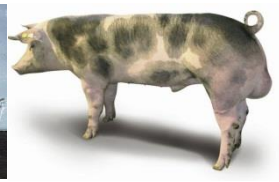
Animals


- Project EN-Z-EMA (E): **597** crossbred boars
  - Androstenone (And): GC-MS (Gracia-Regueiro & Diaz 1989)
  - Skatole (Ska): RP-HPLC (Dehnhard et al. 1993)
  - **Lab.: IME, Fraunhofer Institut, Schmallenberg**

- Project GOGS (G): **475** crossbred boars
  - And: rapid enzyme immunoassay (Claus et al. 1997)
  - Ska: UPLC - HPLC Hillenbrand (2000)
  - **Lab.: Tiergesundheitsdienst Bayern**

Genotypes

- Genotypes
  - DNA isolation from muscle samples
  - Quality control: call rate > 0.95, MAF > 0.01
  - Project E:
    - Typing of DNA with porcineSNP60 Illumina BeadChip v2
    - **Lab: Life & Brain, Bonn**
  - Project G:
    - Typing of DNA with porcineSNP60 Illumina BeadChip v1
    - **Lab: GeneControl, Poing**

Genotypes

- Genotypes
  - DNA isolation from muscle samples
  - Quality control: call rate > 0.95, MAF > 0.01

After quality control:

- 1077 boars
- 42’063 SNP markers

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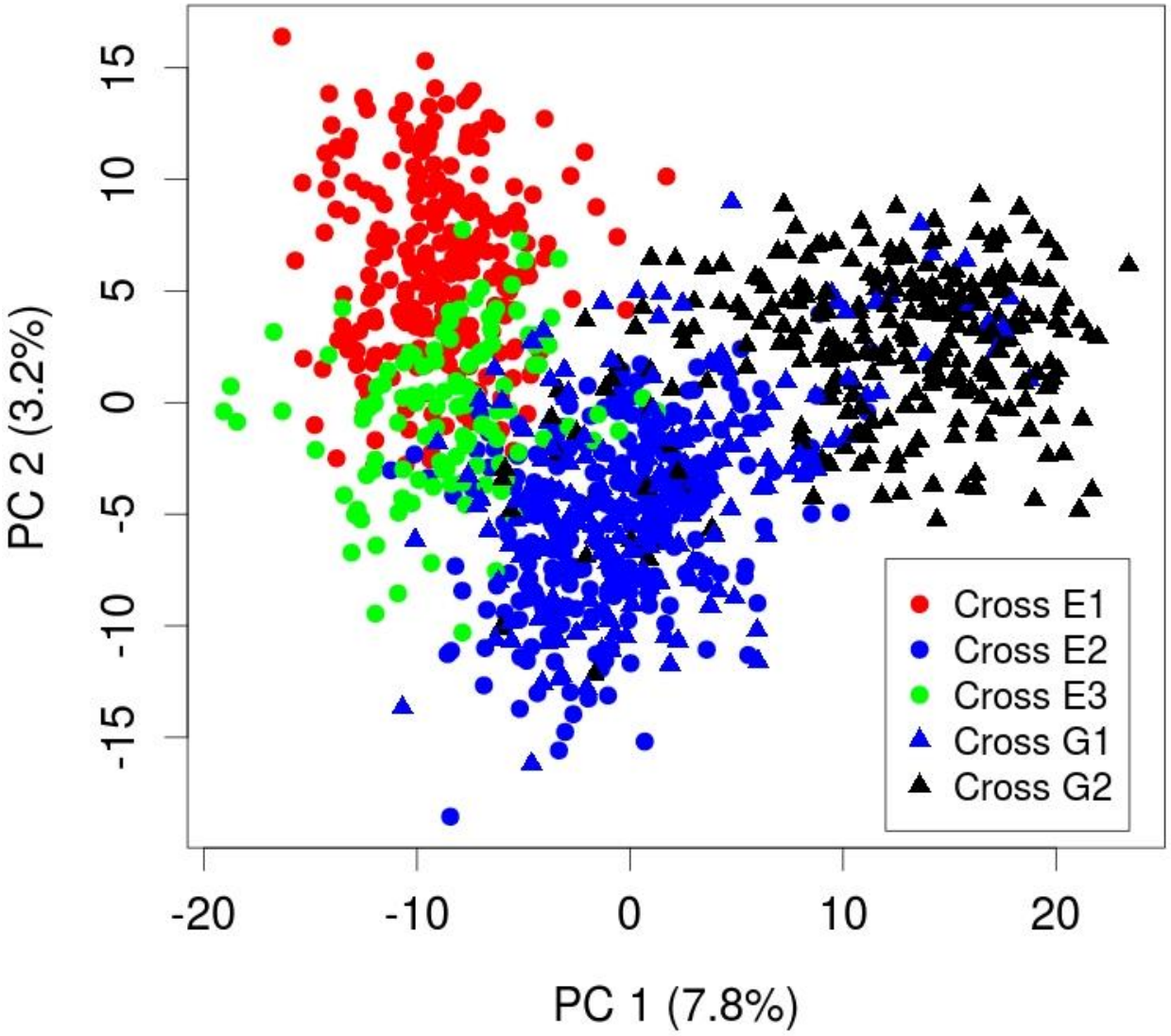
Population structure



Genetic variation

- Estimation of the F_{ST} values across the regional populations (Weir 1996)

$$F_{ST} = \frac{\sum_i n_i(\tilde{p}_i - \bar{p})^2/(r-1)\bar{n}}{\bar{p}(1-\bar{p})}$$

	●E1	●E2	▲G1	▲G2	●E3
●E1-F2	241	$1.23E^{-02}$	$1.26E^{-02}$	$1.92E^{-02}$	$1.44E^{-02}$
●E2-F2		236	$0.52E^{-02}$	$1.18E^{-02}$	$1.38E^{-02}$
▲G1-F2			213	$0.97E^{-02}$	$1.53E^{-02}$
▲G2-F1				266	$2.29E^{-02}$
●E3-F3					120

Genomic Selection (GS)

- Breeding value (BV) estimation: multivariate sire model
  - Wombat (Meyer 2006)
  - Estimation within the project groups

- Genomic BV estimation: ridge regression BLUP
  - R package: rrBLUP (Endelmann et al. 2011)
  - EBV = Zu + e
  - u ~ N(0, G σ^2_a), G: genomic relationship matrix (vanRaden 2008)

Accuracy of GS

- derived from 5-fold cross-validation
- Sampling number: 5000

1. r_{MP}: Correlation between observed and estimated breeding values

2. $r_{GS} = \frac{r_{MP}}{\sqrt{\overline{r_{EBV}}}}$ (Lande & Thompson 1990, Dekkers 2007)

   - $\overline{r_{EBV}}$: mean accuracy of the conventional breeding value

3. $r_{PEV} = \sqrt{1 - \left(PEV/\sigma_g^2\right)}$ (Henderson 1975)

Scenarios

S1: CV across all groups of local populations

S2: CV within each local population

S3: Calibration (C) in one population and validation (V) in another population

a) C- and V-population are genetically close related

b) C- and V-population are genetically less related

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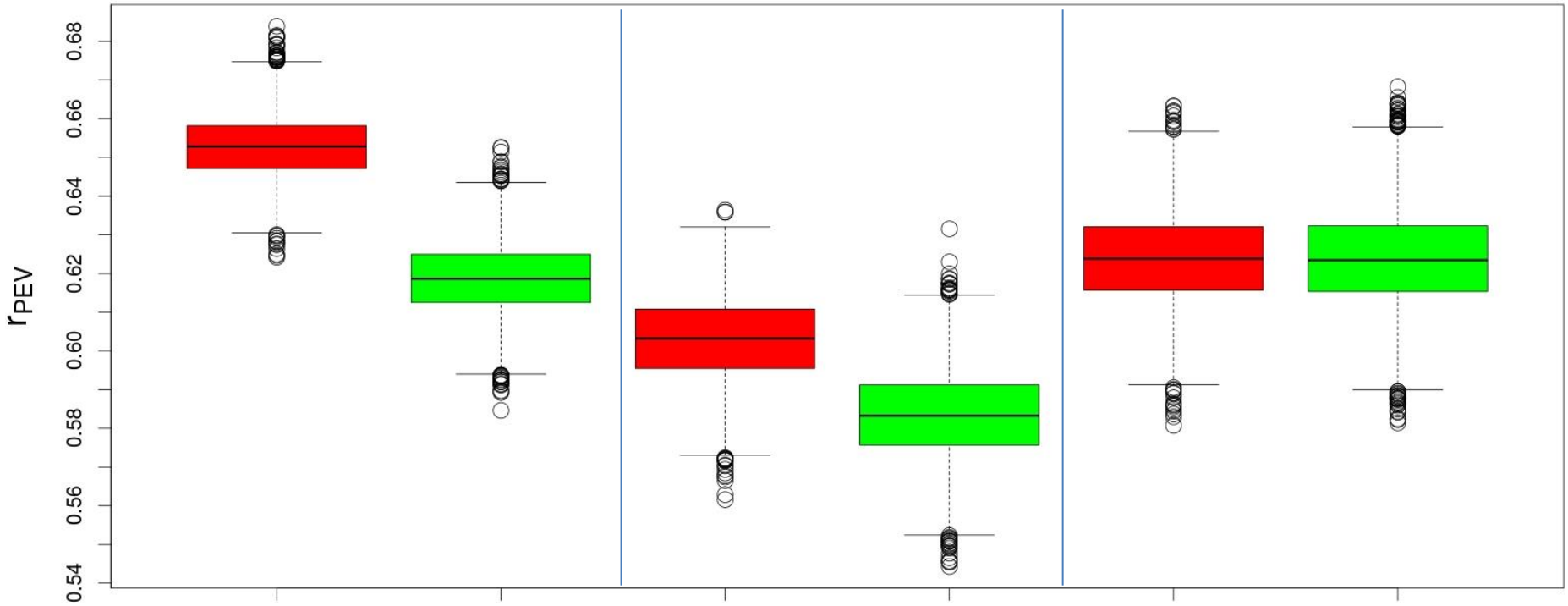
Heritability and accuracy of estimated breeding values

Data	N	Trait	h^2	r_{EBV}
All ENZMA	597	AND	0.58	0.76
		SKA	0.52	0.72
●E1	241	AND	0.63	0.78
		SKA	0.61	0.77
●E2	236	AND	0.67	0.81
		SKA	0.61	0.77
●E3	120	AND	*	*
		SKA	*	*
All GOGS	481	AND	0.58	0.77
		SKA	0.42	0.66
▲G1	214	AND	0.70	0.78
		SKA	0.57	0.71
▲G2	267	AND	0.40	0.66
		SKA	0.30	0.58

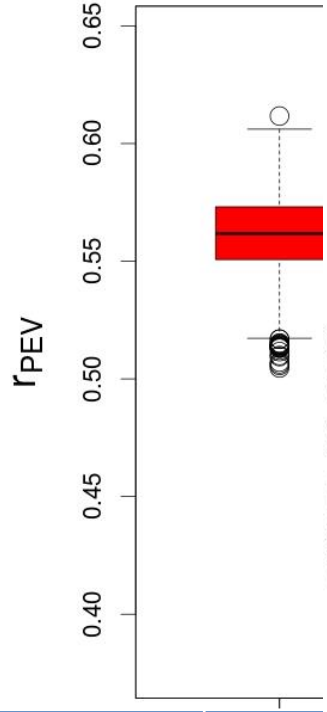
*Algorithm did not converge

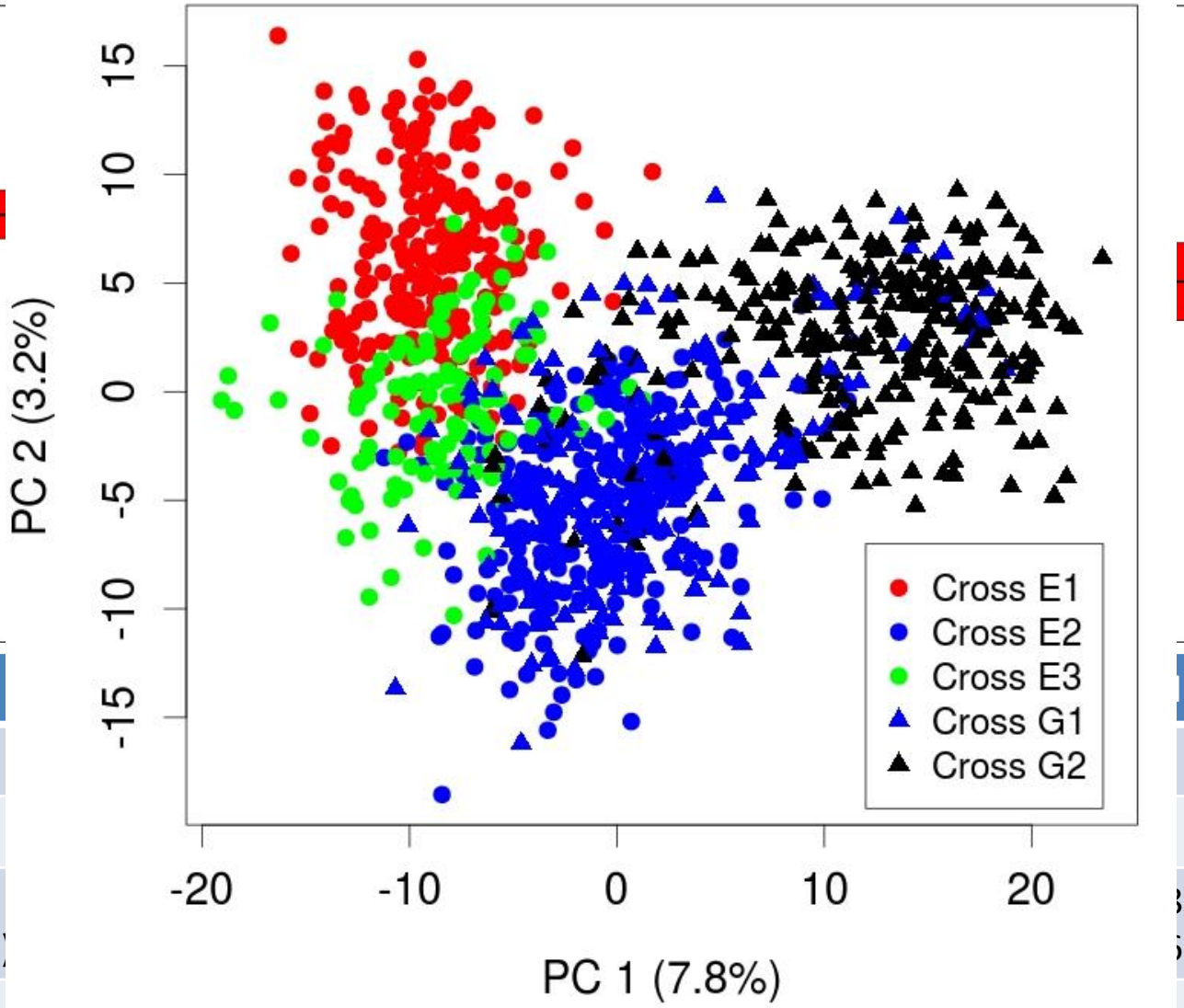
Scenario 1: 5-fold cross validation across the data sets

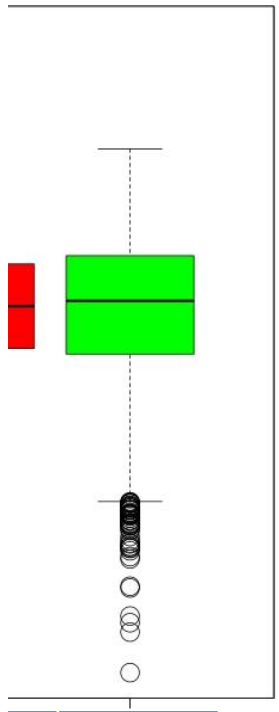


	And	Ska	And	Ska	And	Ska
Pop	All		ENZMA		GOGS	
Val./Cal.	862/215		478/120		380/95	
r_{MP}	0.56 (±0.05)	0.49(±0.05)	0.56(±0.06)	0.51(±0.07)	0.54(±0.07)	0.55(±0.07)
$r_{MP}/\sqrt{r_{EBV}}$	0.64	0.58	0.64	0.60	0.62	0.68

Scenario 2: 5-fold cross validation within each cross

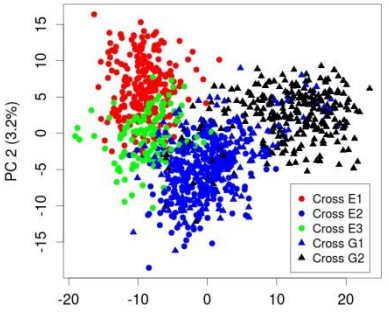


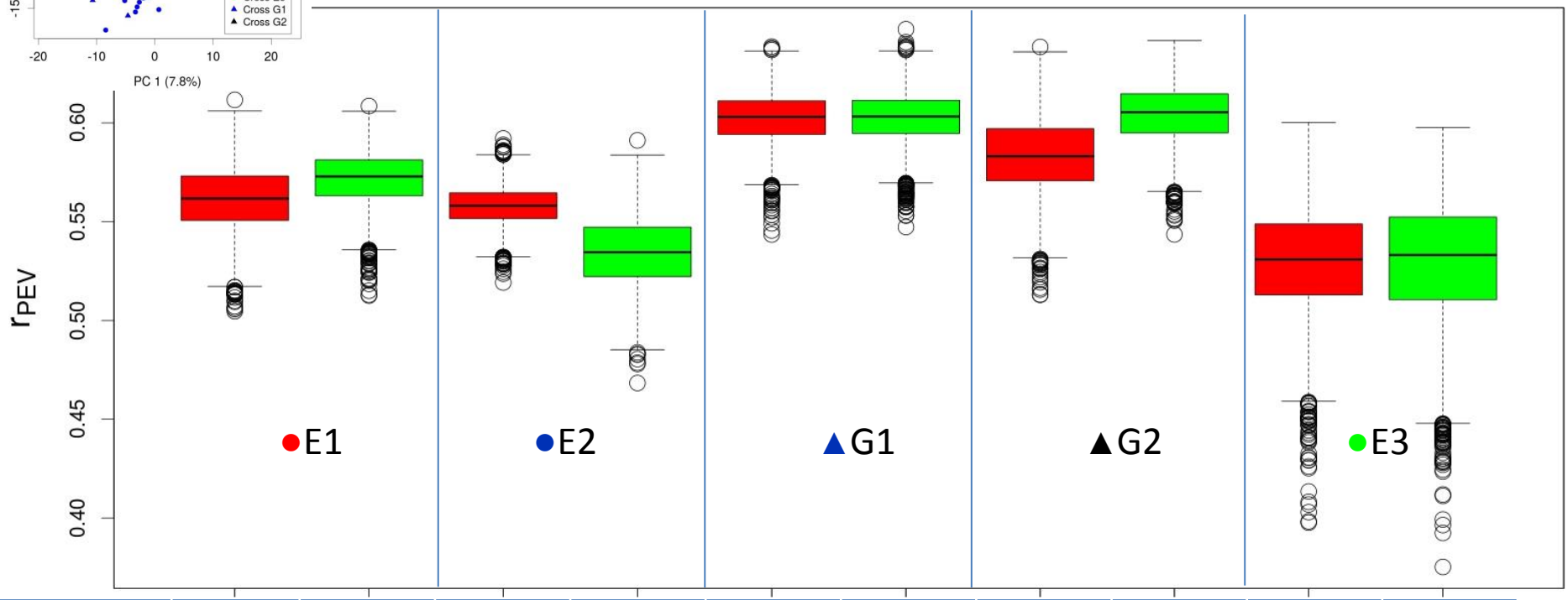




	And									Ska
Pop.									E3	
									120*	
r_{MP}	0.51 (0.10)									0.42 (0.14)
$r_{MP}/\sqrt{r_{EBV}}$	0.58	0.60	0.74	0.57	0.69	0.74	0.53	0.64	0.55	0.49

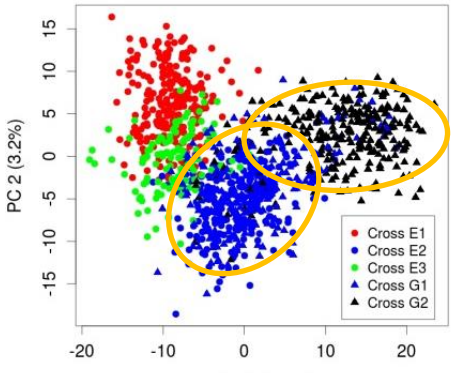
Scenario 2: 5-fold cross validation within each cross

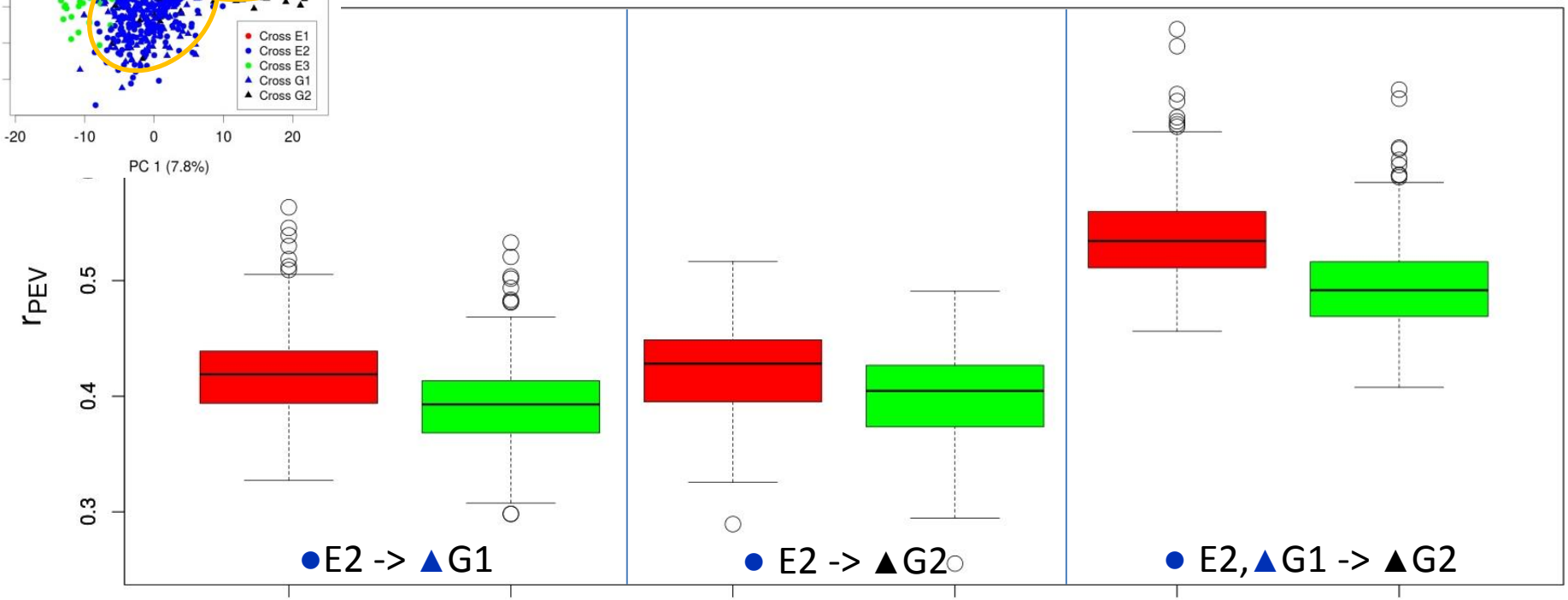




	And	Ska	And	Ska	And	Ska	And	Ska	And	Ska
Pop.	●E1		●E2		▲G1		▲G2		●E3	
	242		236		213		262		120*	
r_{MP}	0.51 (0.10)	0.53 (0.11)	0.67 (0.08)	0.50 (0.10)	0.61 (0.09)	0.60 (0.09)	0.47 (0.10)	0.52 (0.09)	0.48 (0.16)	0.42 (0.14)
$r_{MP}/\sqrt{r_{EBV}}$	0.58	0.60	0.74	0.57	0.69	0.74	0.53	0.64	0.55	0.49

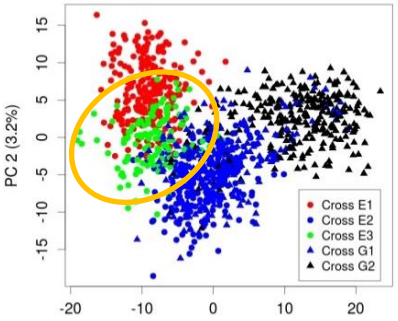
Scenario 3a: Forward prediction

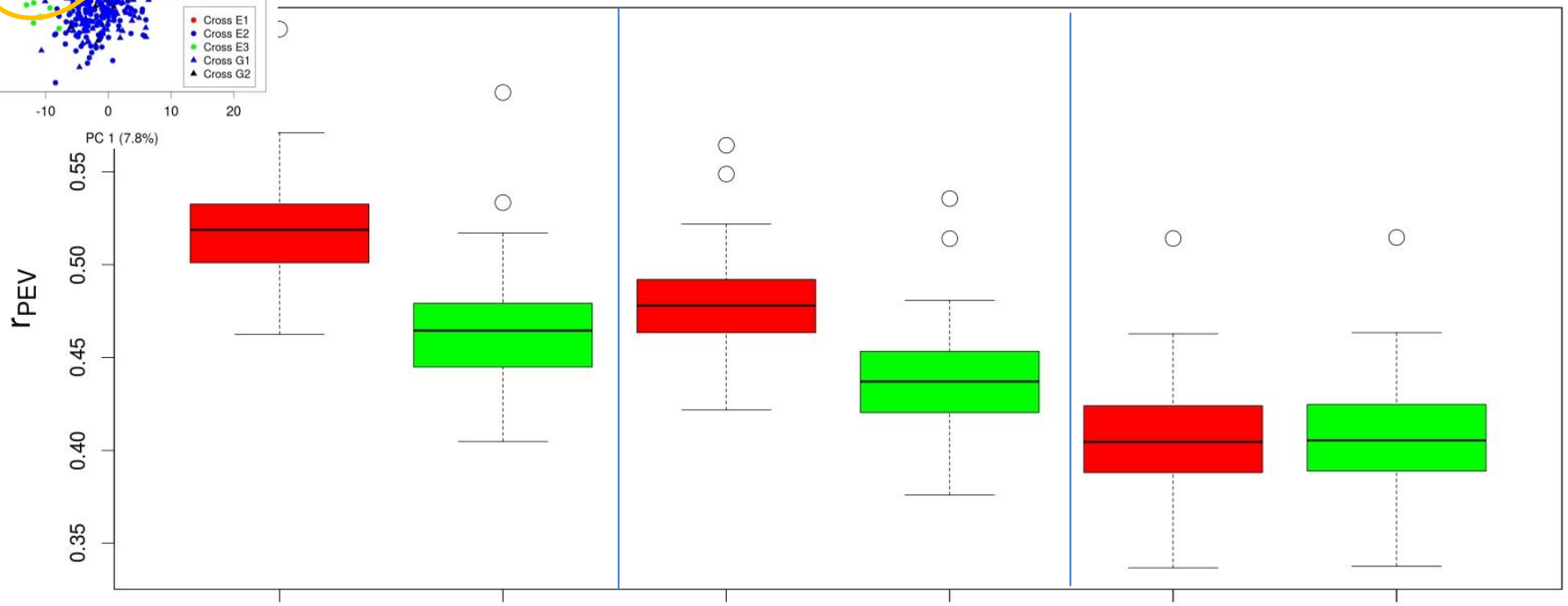




	And	Ska	And	Ska	And	Ska
Calib.	●E2	●E2	●E2	●E2	●E2, ▲G1	●E2, ▲G1
Valid.	▲G1	▲G1	▲G2	▲G2	▲G2	▲G2
r_{MP}	0.28	0.06	0.10	0.11	0.34	0.26
$r_{MP}/\sqrt{r_{EBV}}$	0.32	0.07	0.11	0.13	0.39	0.31

Scenario 3b: Forward prediction





	And	Ska	And	Ska	And	Ska
Calib.	E1,E2,G1,G2	E1,E2,G1,G2	E2,G1,G2	E2,G1,G2	G1, G2	G1, G2
Valid.	●E3	●E3	●E3	●E3	●E3	●E3
r_{MP}	0.26	0.13	0.20	0.10	0.20	-
$r_{MP}/\sqrt{r_{EBV}}$	0.30	0.16	0.23	0.12	0.23	-

Summary and conclusion

- Genomic selection against boar taint using information from commercial crossbreds is promising (= $r_{\overline{EBV}}$)
- Genetic differences between regional populations
  - Calibrations **cannot** be transferred between subpopulations without considerable **loss of accuracy**

- Perspectives:
  - Combining pure- and cross-bred information
    - Investigation of the relationship between fertility traits and boar taint
  - Enlarge the data set

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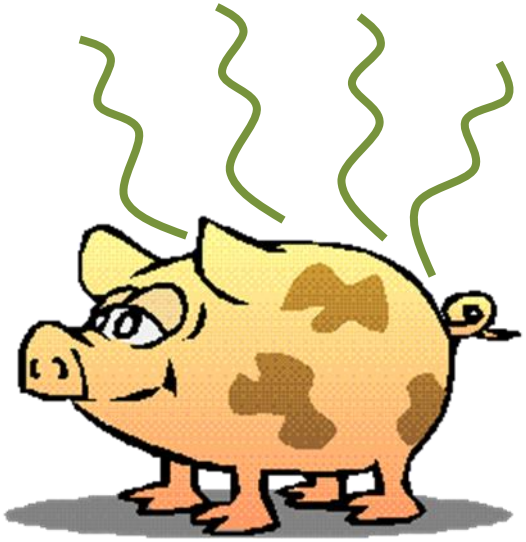
LfL Tierzucht



Thank you for your attention!

Bundesministerium für Ernährung, Landwirtschaft und Verbraucherschutz

Bundesanstalt für Landwirtschaft und Ernährung

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