Evaluation of selection strategies including genomic breeding values in pigs

A.M. Haberland[1], F. Ytournel[1], H. Luther[2], H. Simianer[1]

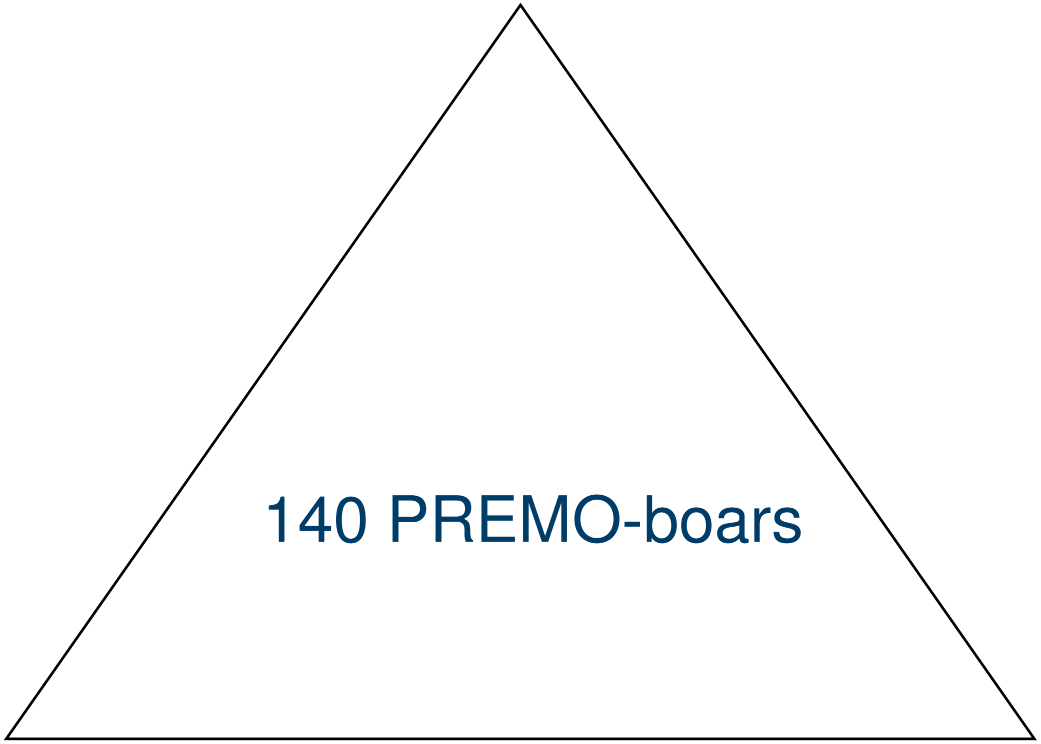
[1]Department of Animal Sciences, Animal Breeding and Genetics Group, Georg-August-University Göttingen, Germany
[2]SUISAG, Allmend, Sempach, Switzerland

Introduction

- Three-way crossbreeding scheme of the Swiss breeding association *SUISAG*
- terminal sire-line PREMO® (140 boars in AI)
- small breeding nucleus of 250 breeding sows
  ➔ risk of inbreeding

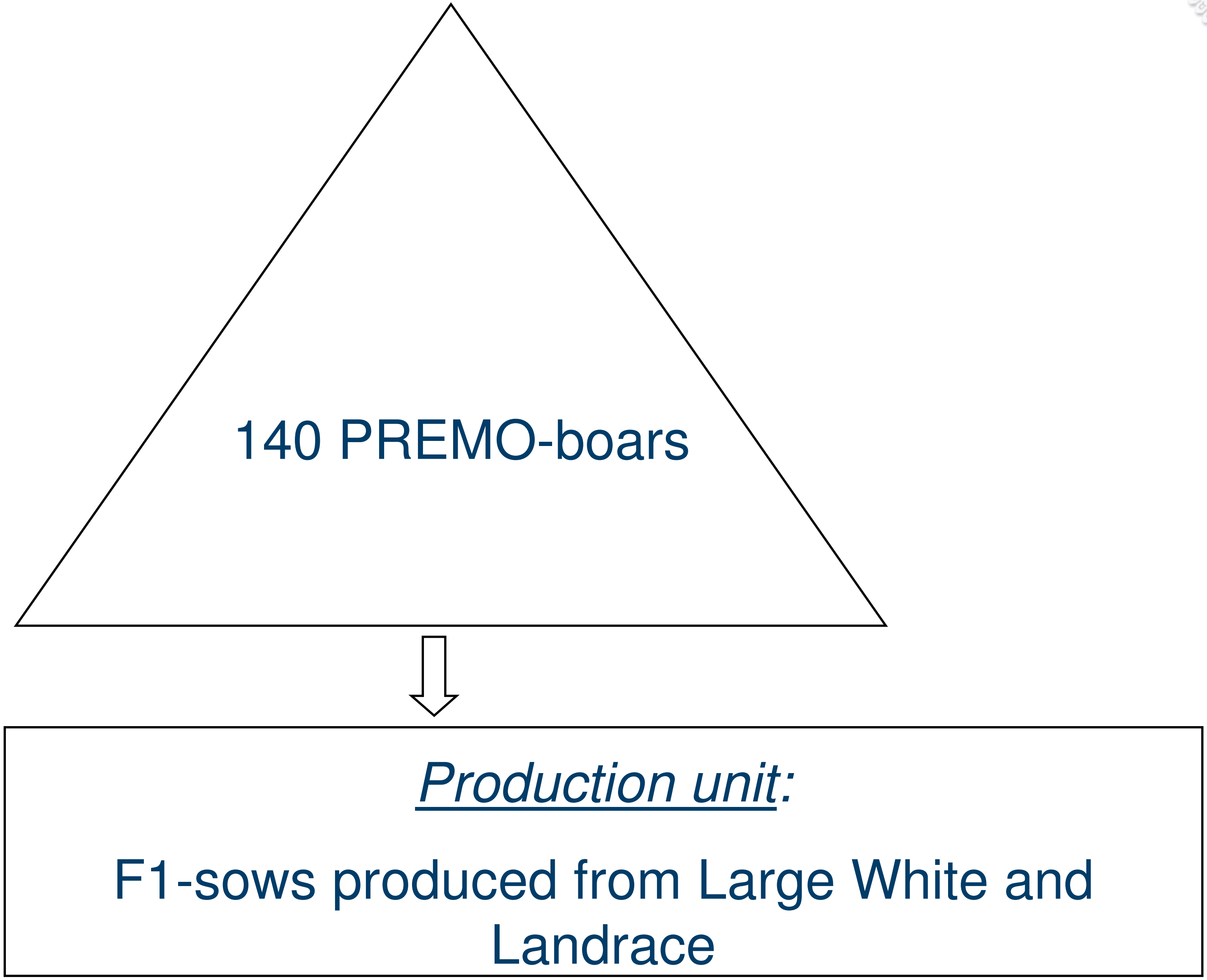
Foto: SUISAG

Selection groups



140 PREMO-boars

Selection groups



140 PREMO-boars

Production unit:

F1-sows produced from Large White and Landrace

Selection groups

Breeding unit:

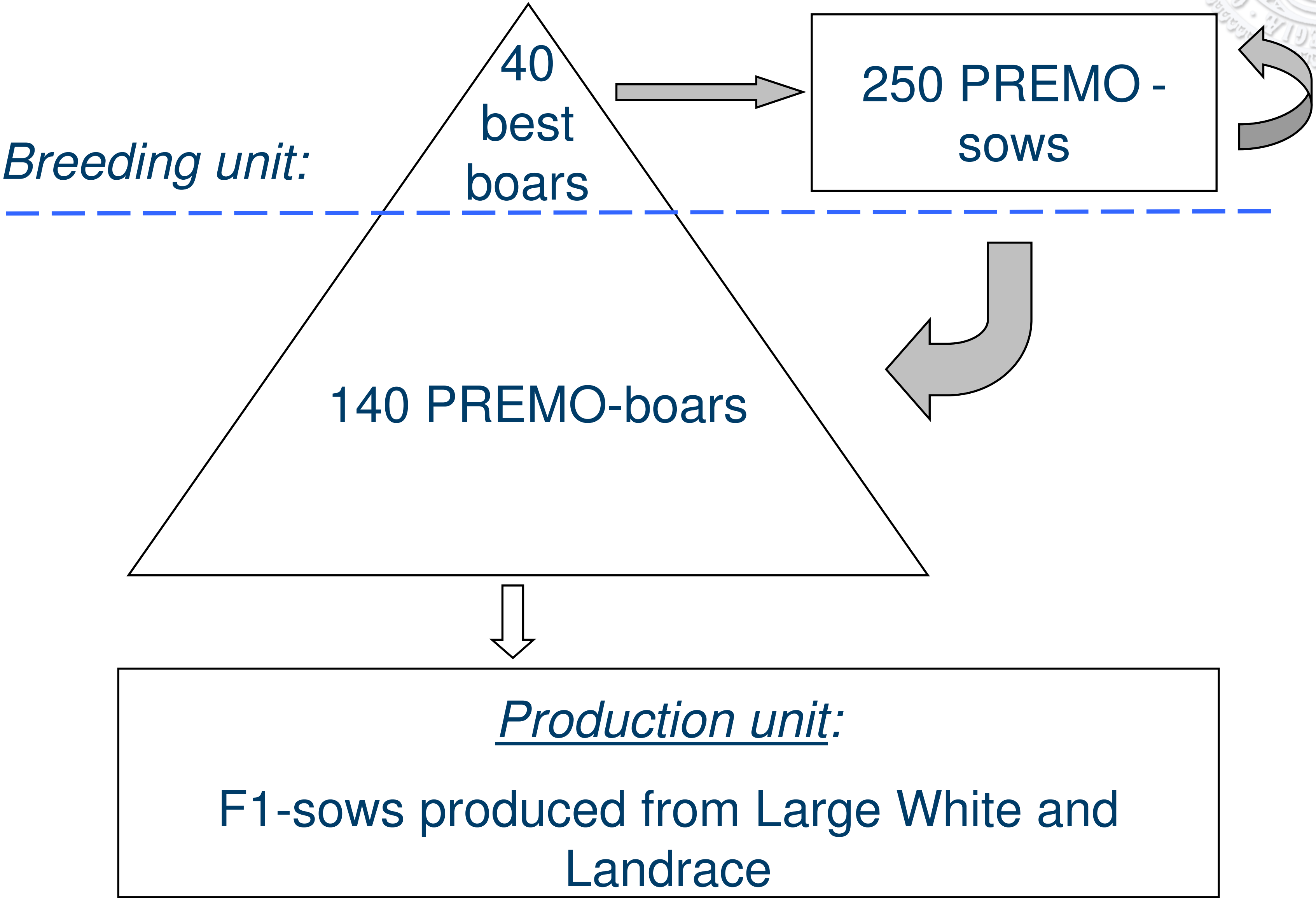
40
best
boars

140 PREMO-boars

Production unit:

F1-sows produced from Large White and Landrace

Selection groups



Breeding unit:

40 best boars

250 PREMO - sows

140 PREMO-boars

Production unit:

F1-sows produced from Large White and Landrace

Introduction

- 40 young boars selected out of 1,200 candidates according to
  - pedigree
  - own performance
    (daily gain, backfat thickness)
  - station test of two full sibs
    (lean meat percentage, daily gain, feed conversion rate, fat quality, intramuscular fat, drip loss, pH_1, pH_{30}, reflectance)

➔ low reliability of selection index ($r^2 = 0.32$)

Motivation

Can we increase the reliability of selection and the genetic gain transferred by the young boars by integrating information on genomic breeding values into the selection index?

Foto: Eimer

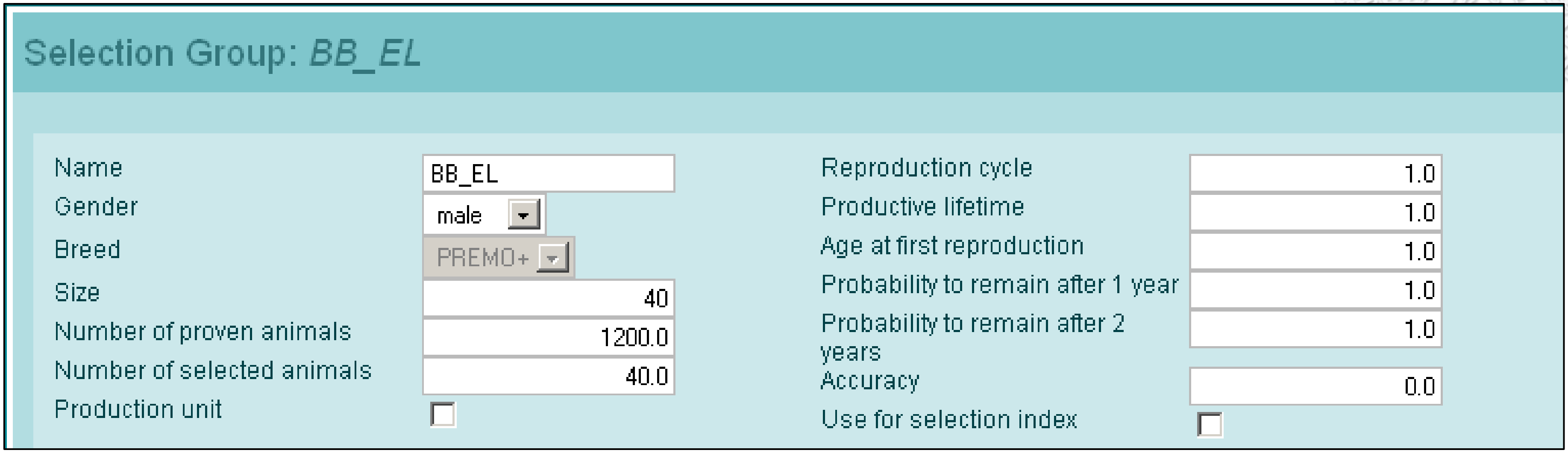
Materials and methods

- modeling of the population with ZPLAN+
- software ZPLAN+ is based on
  - selection index theory
  - gene-flow method
  - economic modeling

Foto: SUISAG

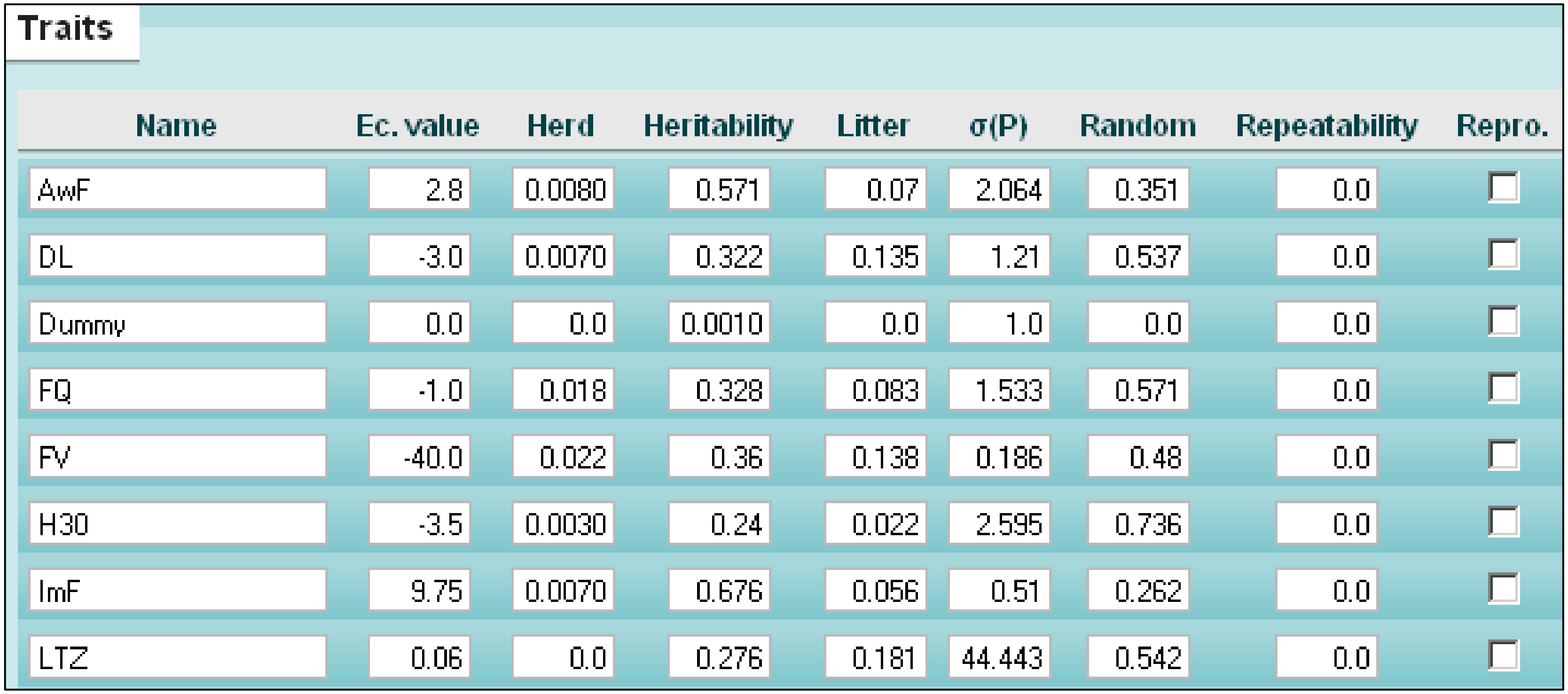
➔ deterministic calculation of output parameters (selection intensity, generation interval, accuracy of the index, discounted returns, genetic gain)

Modeling in ZPLAN+



Selection Group: *BB_EL*

Name	BB_EL	Reproduction cycle	1.0
Gender	male	Productive lifetime	1.0
Breed	PREMO+	Age at first reproduction	1.0
Size	40	Probability to remain after 1 year	1.0
Number of proven animals	1200.0	Probability to remain after 2 years	1.0
Number of selected animals	40.0	Accuracy	0.0
Production unit	☐	Use for selection index	☐



Traits

Name	Ec. value	Herd	Heritability	Litter	σ(P)	Random	Repeatability	Repro.
AwF	2.8	0.0080	0.571	0.07	2.064	0.351	0.0	☐
DL	-3.0	0.0070	0.322	0.135	1.21	0.537	0.0	☐
Dummy	0.0	0.0	0.0010	0.0	1.0	0.0	0.0	☐
FQ	-1.0	0.018	0.328	0.083	1.533	0.571	0.0	☐
FV	-40.0	0.022	0.36	0.138	0.186	0.48	0.0	☐
H30	-3.5	0.0030	0.24	0.022	2.595	0.736	0.0	☐
ImF	9.75	0.0070	0.676	0.056	0.51	0.262	0.0	☐
LTZ	0.06	0.0	0.276	0.181	44.443	0.542	0.0	☐

Materials and methods

- Assumption:

  genomic breeding values (GEBVs) available for 10 traits of the breeding goal

- How to consider this information in selection index?

  definition of ‚genomic traits‘ linked to their corresponding breeding goal traits via genetic correlation of 1

Heritability and reliability

	h^2_{con}	r^2	h^2_{500}	h^2_{1000}
Lean Meat Percentage	0.57	0.71	0.26	0.41
Drip Loss	0.32	0.39	0.16	0.28
Fat Quality	0.33	0.48	0.19	0.32
Feed Conversion Rate	0.36	0.41	0.17	0.29
H30	0.24	0.36	0.15	0.27
Intramuscular Fat	0.68	0.44	0.18	0.31
Daily Gain_Field	0.28	0.42	0.17	0.30
Daily Gain_Station	0.25	0.38	0.16	0.28
pH1	0.20	0.27	0.12	0.21
Daily Gain_Carcass	0.34	0.47	0.19	0.32

$$h_N^2 = \frac{Nr^2}{Nr^2 + k}$$

Daetwyler et al., 2008

Materials and methods

Scenario	Index Sources
Young boars	*Pedigree, field test, station test of 2 full sibs*
Older boars	*Station test of 6 progeny, 40 records of end-products (GI = 2.6 yrs)*
GS_500	*Genomic Breeding Value (N= 500)*
convent. + GS_500	*Pedigree, field test, station test of 2 full sibs and GEBV*
GS_1000	*Genomic Breeding Value (N= 1,000)*
convent. + GS_1000	*Pedigree, field test, station test of 2 full sibs and GEBV*

Materials and methods

Scenario	**Index Sources**
Young boars	***Pedigree, field test, station test of 2 full sibs***
Older boars	***Station test of 6 progeny, 40 records of end-products (GI = 2.6 yrs)***
GS_500	***Genomic Breeding Value (N= 500)***
convent. + GS_500	***Pedigree, field test, station test of 2 full sibs and GEBV***
GS_1000	***Genomic Breeding Value (N= 1,000)***
convent. + GS_1000	***Pedigree, field test, station test of 2 full sibs and GEBV***

Materials and methods

Scenario	Index Sources
Young boars	*Pedigree, field test, station test of 2 full sibs*
Older boars	*Station test of 6 progeny, 40 records of end-products (GI = 2.6 yrs)*
GS_500	***Genomic Breeding Value (N= 500)***
convent. + GS_500	*Pedigree, field test, station test of 2 full sibs and GEBV*
GS_1000	*Genomic Breeding Value (N= 1,000)*
convent. + GS_1000	*Pedigree, field test, station test of 2 full sibs and GEBV*

Materials and methods

Scenario	Index Sources
Young boars	*Pedigree, field test, station test of 2 full sibs*
Older boars	*Station test of 6 progeny, 40 records of end-products (GI = 2.6 yrs)*
GS_500	*Genomic Breeding Value (N= 500)*
convent. + GS_500	***Pedigree, field test, station test of 2 full sibs and GEBV***
GS_1000	*Genomic Breeding Value (N= 1,000)*
convent. + GS_1000	*Pedigree, field test, station test of 2 full sibs and GEBV*

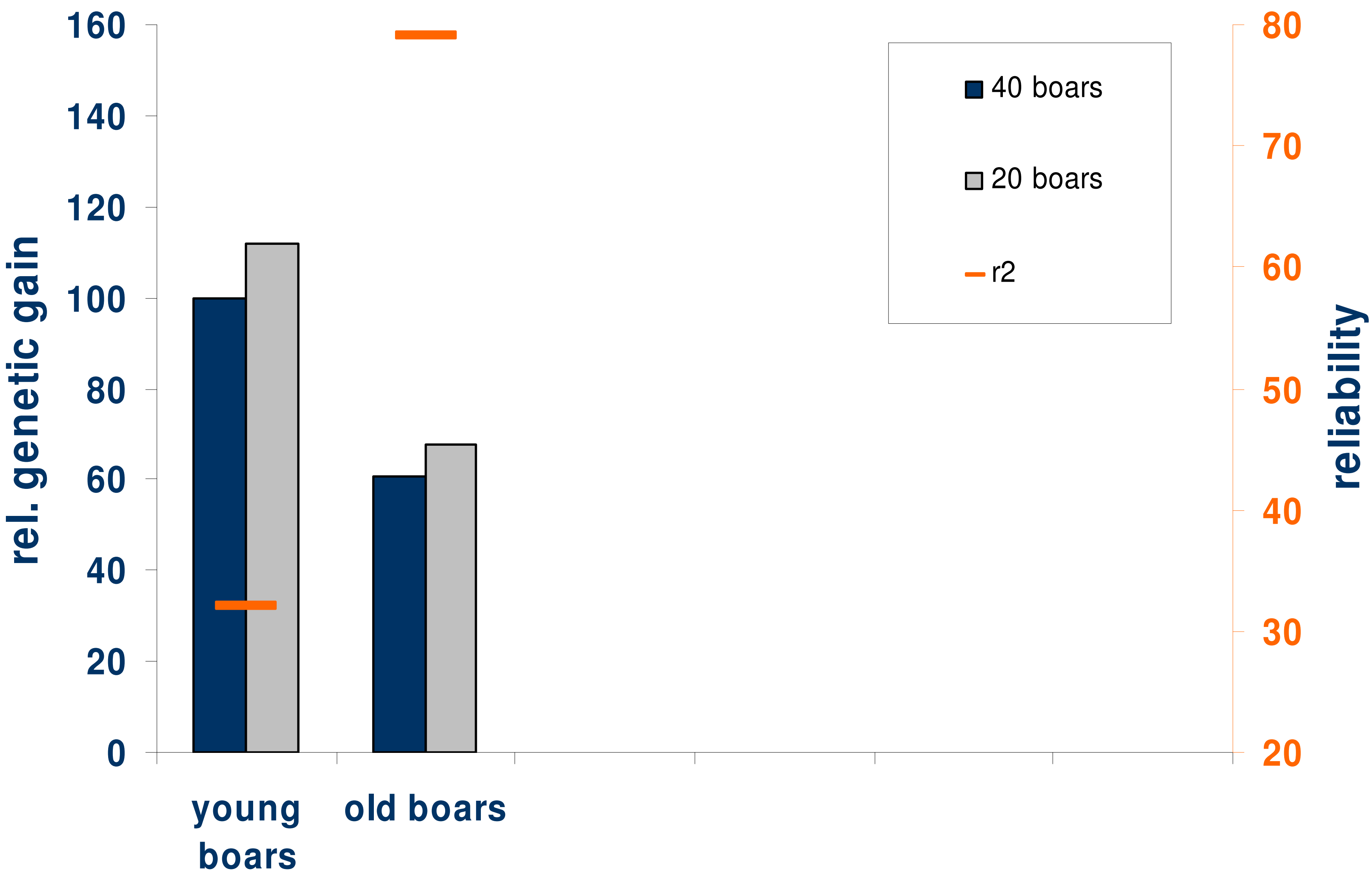
Materials and methods

Scenario	Index Sources
Young boars	*Pedigree, field test, station test of 2 full sibs*
Older boars	*Station test of 6 progeny, 40 records of end-products (GI = 2.6 yrs)*
GS_500	*Genomic Breeding Value (N= 500)*
convent. + GS_500	*Pedigree, field test, station test of 2 full sibs and GEBV*
GS_1000	***Genomic Breeding Value (N= 1,000)***
convent. + GS_1000	*Pedigree, field test, station test of 2 full sibs and GEBV*

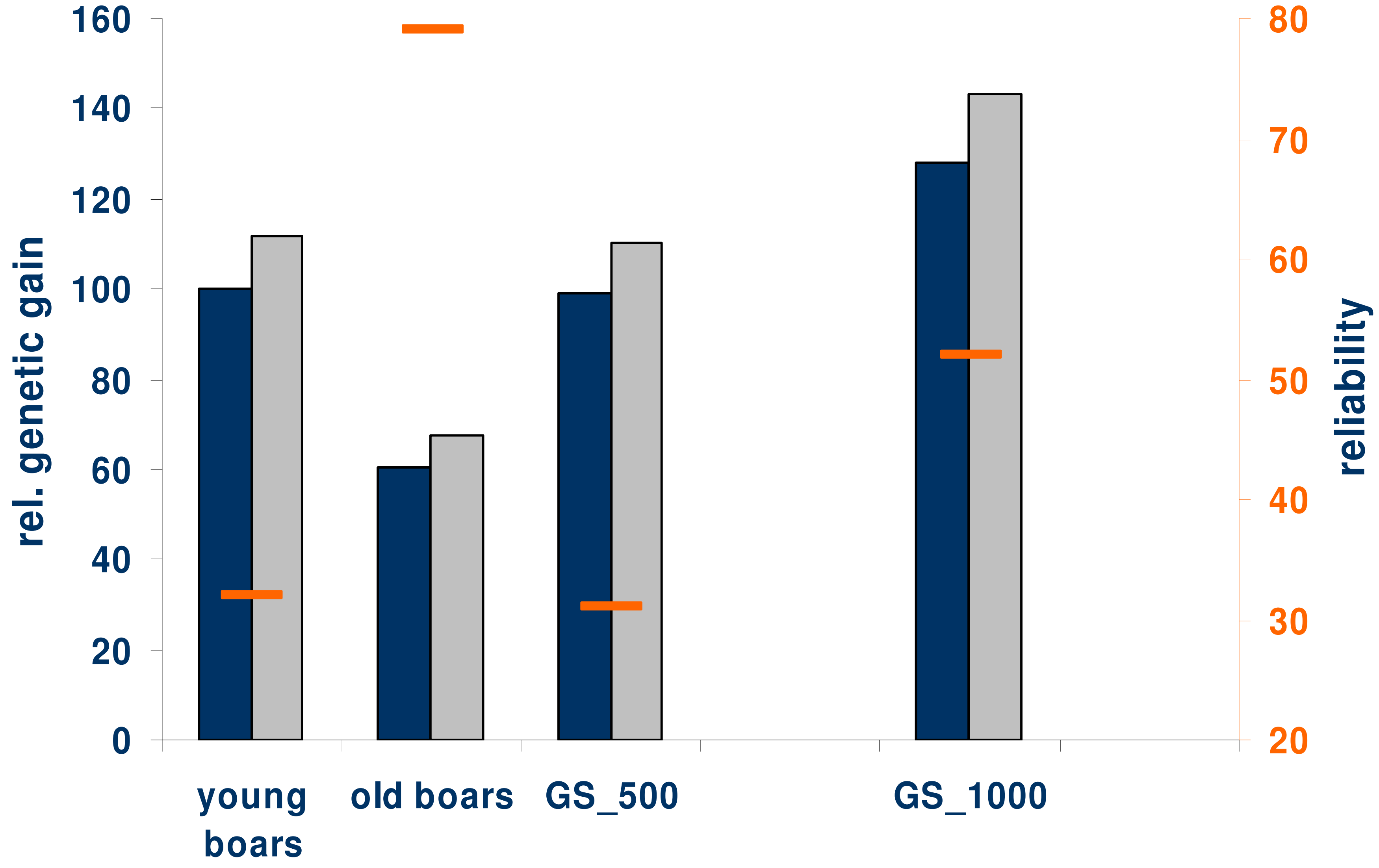
Materials and methods

Scenario	Index Sources
Young boars	*Pedigree, field test, station test of 2 full sibs*
Older boars	*Station test of 6 progeny, 40 records of end-products (GI = 2.6 yrs)*
GS_500	*Genomic Breeding Value (N= 500)*
convent. + GS_500	*Pedigree, field test, station test of 2 full sibs and GEBV*
GS_1000	*Genomic Breeding Value (N= 1,000)*
convent. + GS_1000	*Pedigree, field test, station test of 2 full sibs and GEBV*

Results

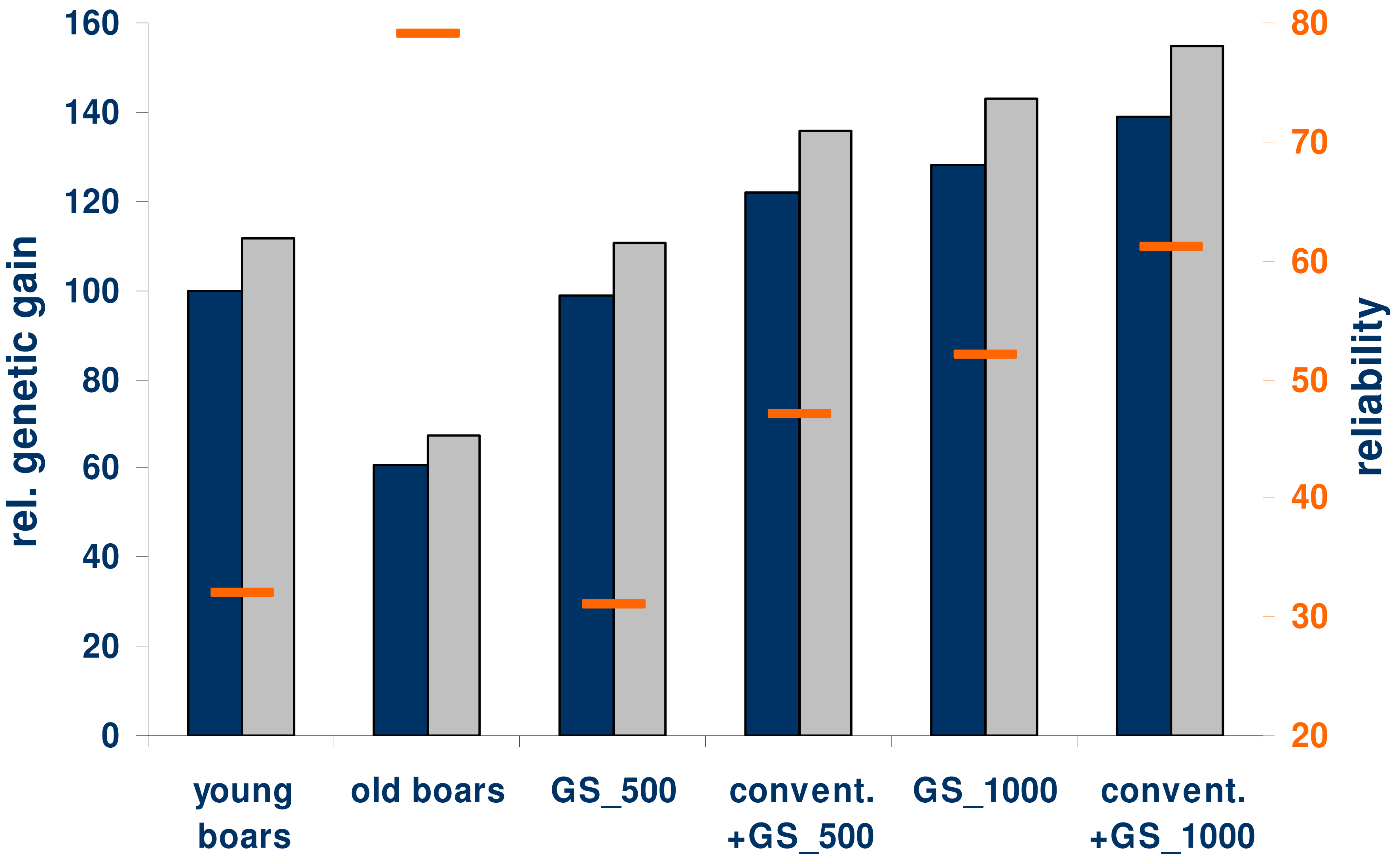

160
140
120
100
80
60
40
20
0
rel. genetic gain
80
70
60
50
40
30
20
reliability
40 boars
20 boars
r2
young boars
old boars

Results



160
140
120
100
80
60
40
20
0
rel. genetic gain
80
70
60
50
40
30
20
reliability
young boars
old boars
GS_500
GS_1000

Results


160
140
120
100
80
60
40
20
0
rel. genetic gain
80
70
60
50
40
30
20
reliability
young boars
old boars
GS_500
convent. +GS_500
GS_1000
convent. +GS_1000

Conclusions

- Young boars can be selected more accurately by integrating genomic information into the selection index

  $r^2_{(N=500)} = 47\%$; $r^2_{(N=1000)} = 61\%$ ($r^2_{conv} = 32\%$)

- Accurate estimation of GEBVs remains precondition

- Calibration set of 500 progeny-tested boars seems more realistic than 1,000 animals in calibration set

Thank you for your attention

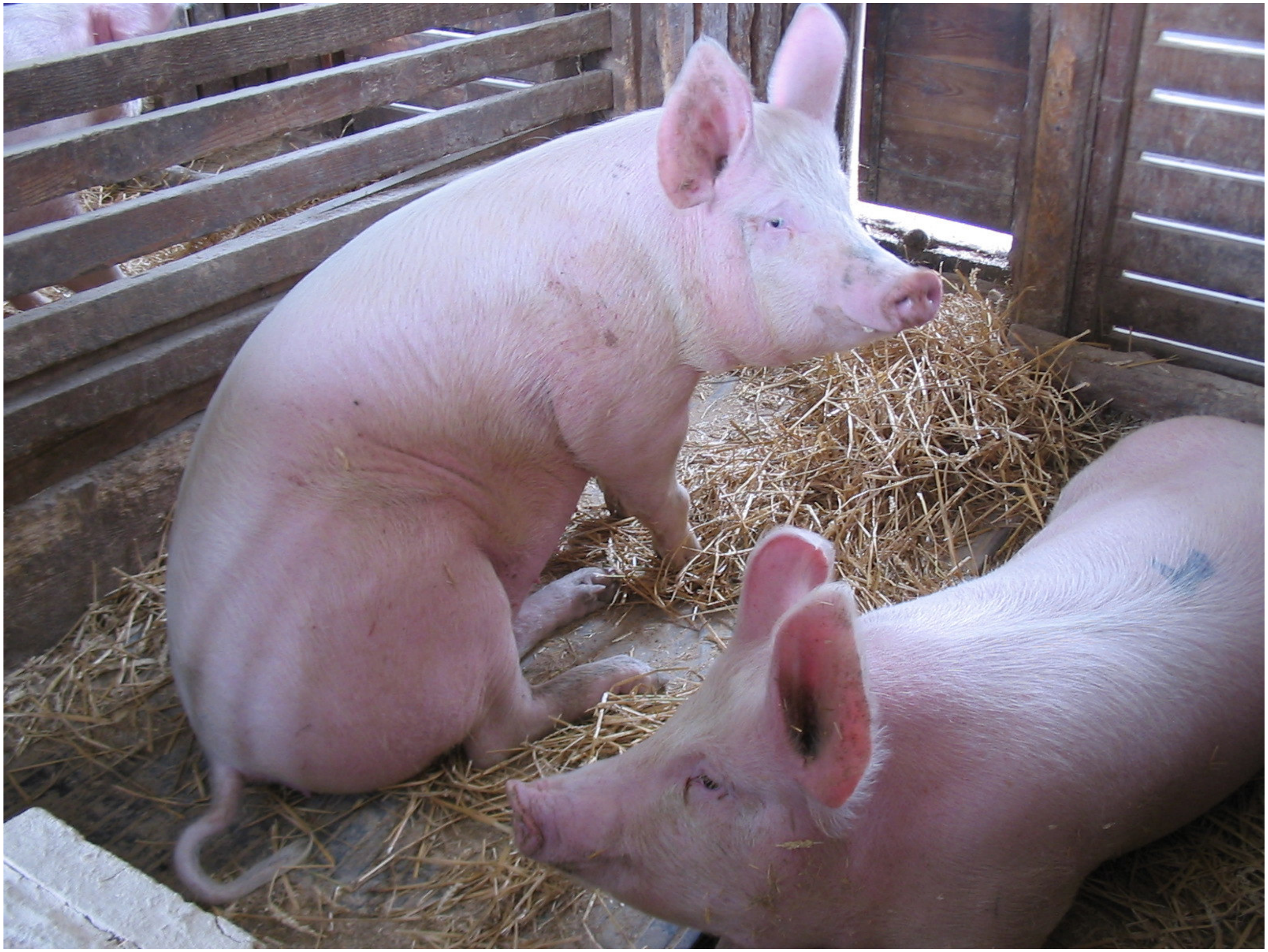


Foto: Eimer

Acknowledgments

This study was part of the FUGATO *plus* brain project.

We thank our partners for financial support:

Bundesministerium
für Bildung
und Forschung

FBF

LOHMANN
TIERZUCHT

Increase in inbreeding

$$\Delta F = \frac{1}{2N_e}$$

$$N_e = \frac{4 * N_f * N_m}{N_f + N_m}$$

$$N_f = 250$$

$$N_m = 40 \quad or \quad 20$$

# selected males	N_e	ΔF
20 boars	138	0.4%
40 boars	74	0.7%

Results (genetic gain & reliability)

Scenario	40 boars (of 1,200)	20 boars (of 1,200)	r^2 (%)
Young boars	11.5	12.8	32
Older boars	7.0	7.8	79
GS_500	11.4	12.7	31
convent. + GS_500	14.0	15.6	47
GS_1000	14.7	16.4	52
convent. + GS_1000	15.9	17.8	61