Poznań University of Life Sciences
Uniwersytet Przyrodniczy w Poznaniu

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Different models for estimation of litter size variability phenotypes

Jan Dobrzański

E. Sell-Kubiak, T. Szwaczkowski, H.A. Mulder, E.F. Knol

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LITTER SIZE

- Crucial trait for pig breeders
- In Large White differences up to 20 piglets
- High variability affects profitability and animal welfare

VARIABILITY PHENOTYPES

- Accurate phenotypes of variability are needed
- Formerly variance, standard deviation or genetic coefficient of variation were used as phenotypes
- Litter size variability can be explored with residual variance

RESIDUAL VARIANCE

$$\mathrm{TNB} = \mathrm{FYS} + \mathit{animal} + p + e$$

- Gathers the environmental effects that can’t be measured by known factors
- Has a genetic component
- Can be used to increase uniformity of traits

AIM

To define and compare new phenotypes for variability of total number born (varTNB) in Large White using the residual variance.

DATA

- 246 799 observations of litters from 1998-2014
- 53 804 Large White sows
- Average litter size 13.57 (SD 3.45)
- > 3 piglets
- 2 < observations per sow

STATISTICAL MODELS

BM: $\mathrm{TNB} = \mathrm{FYS} + animal + p + e$

BM**P**: $\mathrm{TNB} = \mathrm{FYS} + \textbf{parity} + animal + p + e$

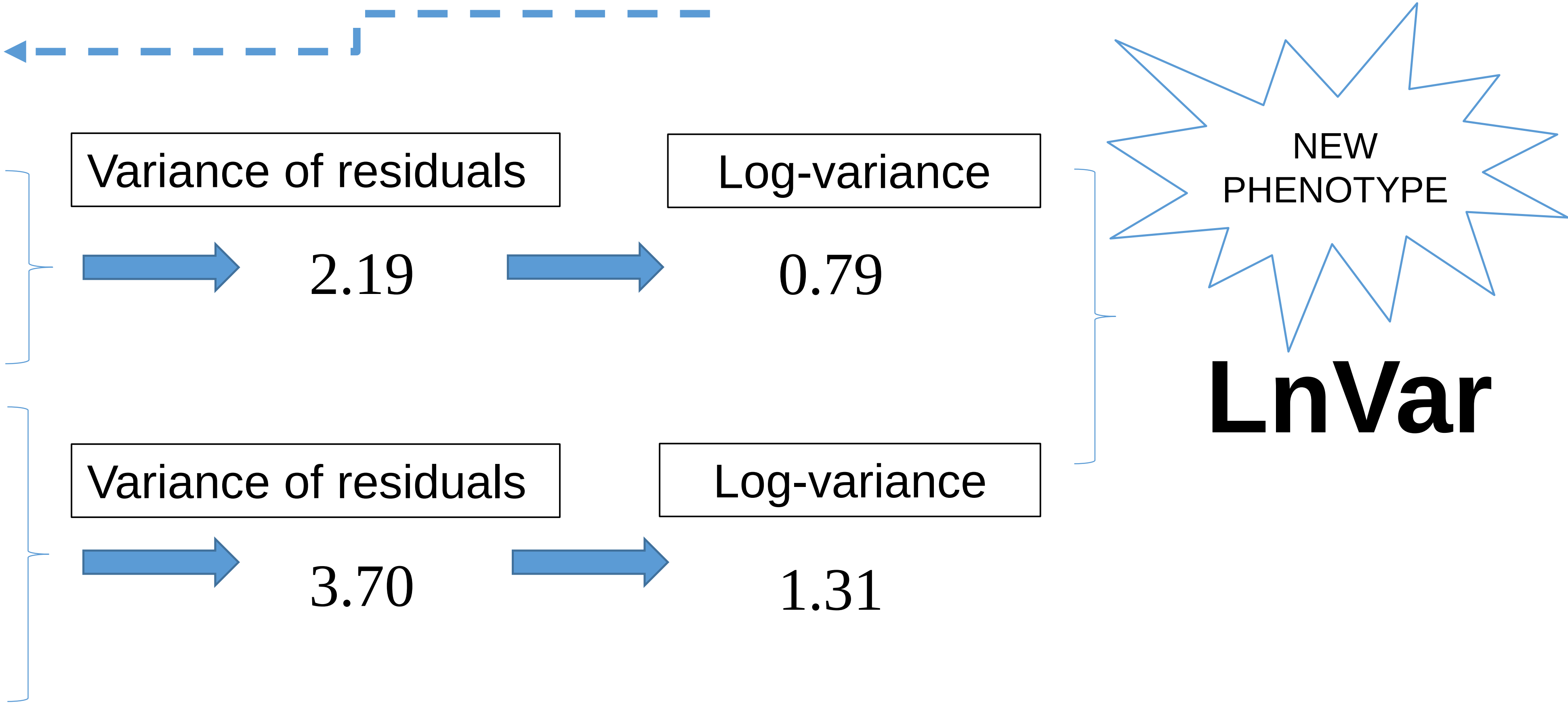
RRM: $\mathrm{TNB} = \mathrm{FYS} + \textbf{parity*} + animal^{*} + p^{*} + e$

*with 3rd order Legendre polynomials

DEFINING THE NEW PHENOTYPES

$$\mathrm{TNB} = \mathrm{FYS} + animal + p + \boxed{e}$$

Sow ID	Residual
1	1.07
1	1.12
1	3.66
2	0.66
2	2.42
2	4.55
2	0.38



Variance of residuals → 2.19 → Log-variance → 0.79

Variance of residuals → 3.70 → Log-variance → 1.31

NEW PHENOTYPE

LnVar

THREE NEW PHENOTYPES

- LnVarBM

- LnVarBMP

- LnVarRRM

STATISTICAL ANALYSIS

$$\mathrm{LnVar} = \mathrm{FYS}_1 + \mathit{animal} + e$$

VARIANCE COMPONENTS

Estimate	**LnVarBM**	**LnVarBMP**	**LnVarRRM**
Additive genetic	0.026 (0.004)	0.028 (0.004)	0.028 (0.004)
Residual	1.23 (0.01)	1.29 (0.01)	1.26 (0.01)
Heritability	0.021 (0.004)	0.021 (0.004)	0.021 (0.004)

LnVar's have genetic component, thus can be used in selection

GENETIC CORRELATIONS

	LnVarBM	**LnVarBMP**	**LnVarRRM**
LnVarBM	**-**	0.98 (0.008)	0.95 (0.008)
LnVarBMP	0.83 (0.001)	**-**	0.98 (0.008)
LnVarRRM	0.82 (0.001)	0.93 (0.008)	**-**

GENETIC CORRELATIONS

Effect		**LnVarBM**	**LnVarBMP**	**LnVarRRM**
Additive genetic	**mTNB**	0.62 (0.06)	0.58 (0.06)	0.57 (0.06)

Increase in litter size will result in increase in it’s variability

GENETIC COEFFICIENT OF VARIATION

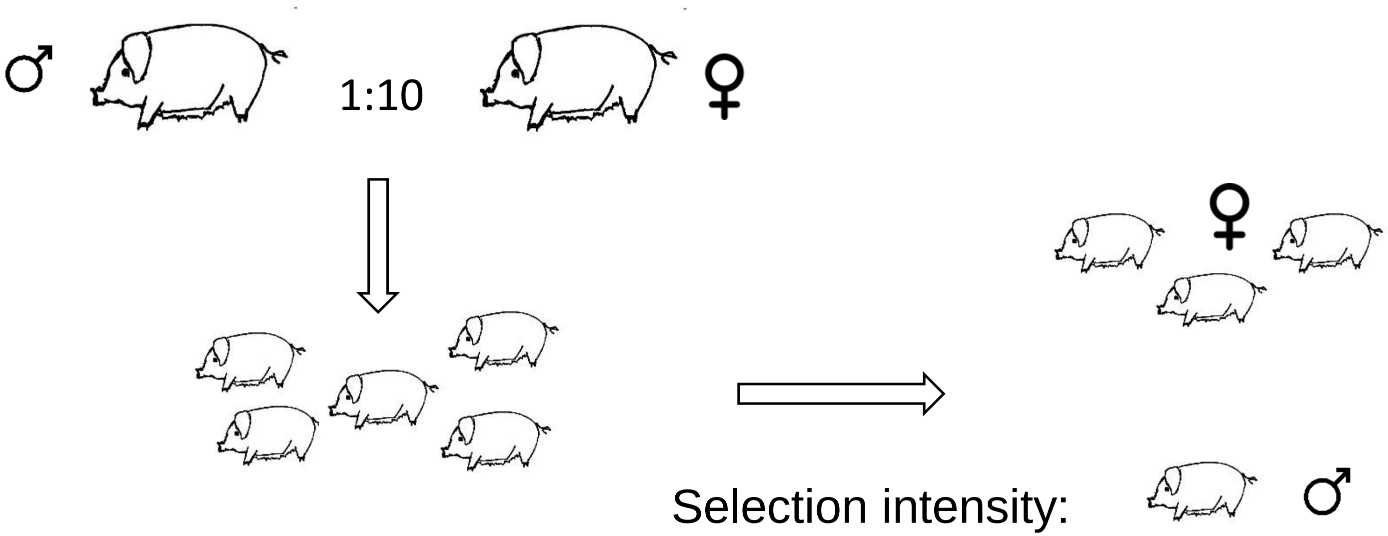
Estimate	**LnVarBM**	**LnVarBMP**	**LnVarRRM**
GCV_{SDe}	0.081	0.083	0.083

Litter size variability can be reduced by 8% of residual variance SD per generation

SIMULATION ANALYSIS

ASSUMPTIONS

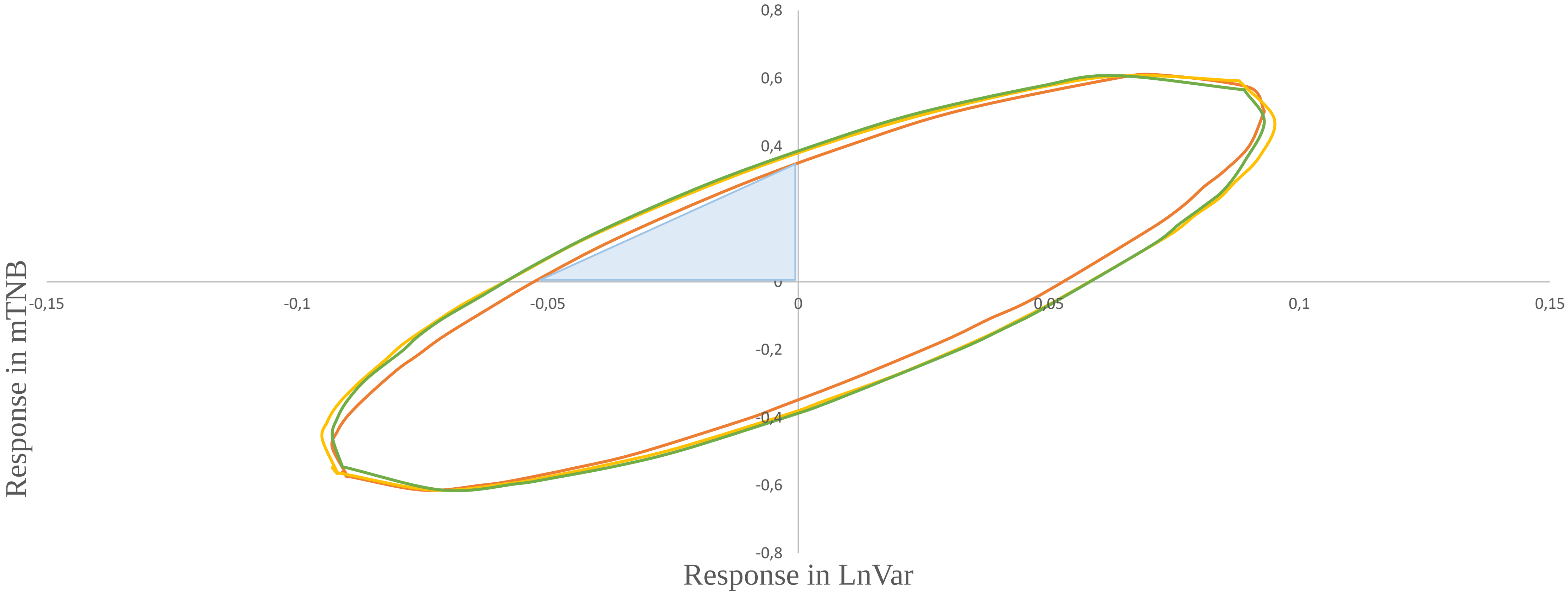
Breeding schemes based on variance components from LnVar’s



Selection intensity:
Female -> 0.167
Male -> 0.0167

Selection index based on: own performance, BLUP, half and full-sib information

ELLIPSE OF RESPONSE



With appropriate selection index litter size can increase with decrease in it’s variability

CONCLUSIONS

- LnVar’s for TNB are low heritable
- Created phenotypes are genetically the same trait
- Litter size and it’s variability is positively correlated
- It’s possible to ↓ varTNB and ↑ TNB

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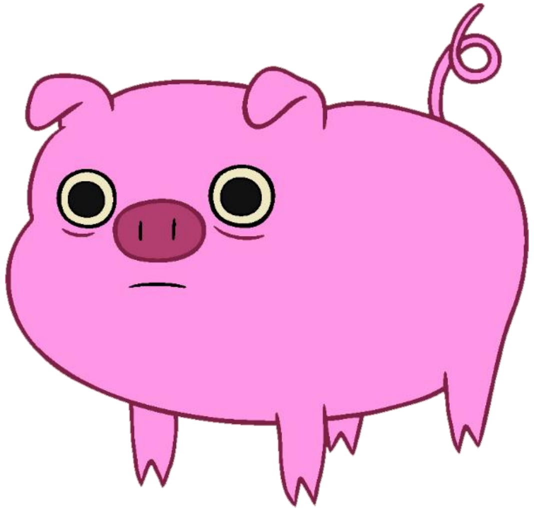
THANK YOU FOR YOUR ATTENTION



Bivariate analysis between LnVar and mTNB

$$\begin{bmatrix}\mathbf{LnVar}\\ \mathbf{mTNB}\end{bmatrix}=\begin{bmatrix}\mathbf{X}_{\mathbf{Ln}} & \mathbf{0}\\ \mathbf{0} & \mathbf{X}_{\mathbf{mTNB}}\end{bmatrix}\begin{bmatrix}\mathbf{b}_{\mathbf{Ln}}\\ \mathbf{b}_{\mathbf{mTNB}}\end{bmatrix}+\begin{bmatrix}\mathbf{Z}_{\mathbf{Ln}} & \mathbf{0}\\ \mathbf{0} & \mathbf{Z}_{\mathbf{mTNB}}\end{bmatrix}\begin{bmatrix}\mathbf{a}_{\mathbf{Ln}}\\ \mathbf{a}_{\mathbf{mTNB}}\end{bmatrix}+\begin{bmatrix}\mathbf{e}_{\mathbf{Ln}}\\ \mathbf{e}_{\mathbf{mTNB}}\end{bmatrix},$$

where **LnVar** is a vector of the analyzed LnVar obtained from a certain model (LnVarBM, LnVarBMP, or LnVarRRM); mTNB is a vector of observation on mean TNB per sow; $\mathbf{b}_{\mathrm{Ln}}$ and $\mathbf{b}_{\mathrm{mTNB}}$ are vectors of fixed effects of farm_year_season of the first farrowing on **LnVar** and **mTNB**; $\mathbf{a}_{\mathrm{Ln}}$ and $\mathbf{a}_{\mathrm{mTNB}}$ are vectors of random additive genetic effects on **LnVar** and **mTNB**, and $\mathbf{e}_{\mathbf{LnVar}}$, $\mathbf{e}_{\mathbf{mTNB}}$ are residuals.

Trivariate analysis between LnVar’s

$$\begin{bmatrix}\mathbf{LnVarBM}\\ \mathbf{LnVarBMP}\\ \mathbf{LnVarRRM}\end{bmatrix}=\begin{bmatrix}\mathbf{X}_{\mathbf{BM}} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{X}_{\mathbf{BMP}} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{X}_{\mathbf{RRM}}\end{bmatrix}\begin{bmatrix}\mathbf{b}_{\mathbf{BM}}\\ \mathbf{b}_{\mathbf{BMP}}\\ \mathbf{b}_{\mathbf{RRM}}\end{bmatrix}+\begin{bmatrix}\mathbf{Z}_{\mathbf{BM}} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{Z}_{\mathbf{BMP}} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{Z}_{\mathbf{RRM}}\end{bmatrix}\begin{bmatrix}\mathbf{a}_{\mathbf{BM}}\\ \mathbf{a}_{\mathbf{BMP}}\\ \mathbf{a}_{\mathbf{RRM}}\end{bmatrix}+\begin{bmatrix}\mathbf{e}_{\mathbf{BM}}\\ \mathbf{e}_{\mathbf{BMP}}\\ \mathbf{e}_{\mathbf{RRM}}\end{bmatrix},$$

where **LnVarBM, LnVarBMP, LnVarRRM** are vectors of the analyzed LnVar obtained from a certain model; $\mathbf{b}_{\mathrm{BM}}$ $\mathbf{b}_{\mathrm{BMP}}$ and $\mathbf{b}_{\mathrm{RRM}}$ are vectors of fixed effects of farm_year_season of the first farrowing on certain **LnVar**; $\mathbf{a}_{\mathrm{BM}}$, $\mathbf{a}_{\mathrm{BMP}}$, and a_{RRM} are vectors of random additive genetic effects on **LnVar** and $\mathbf{e}_{\mathrm{BM}}$, $\mathbf{e}_{\mathrm{BMP}}$ and $\mathbf{e}_{\mathrm{RRM}}$ are residuals on LnVar.