Unspecific, maintenance, growth and fat deposition dependent feed efficiency in Duroc pigs

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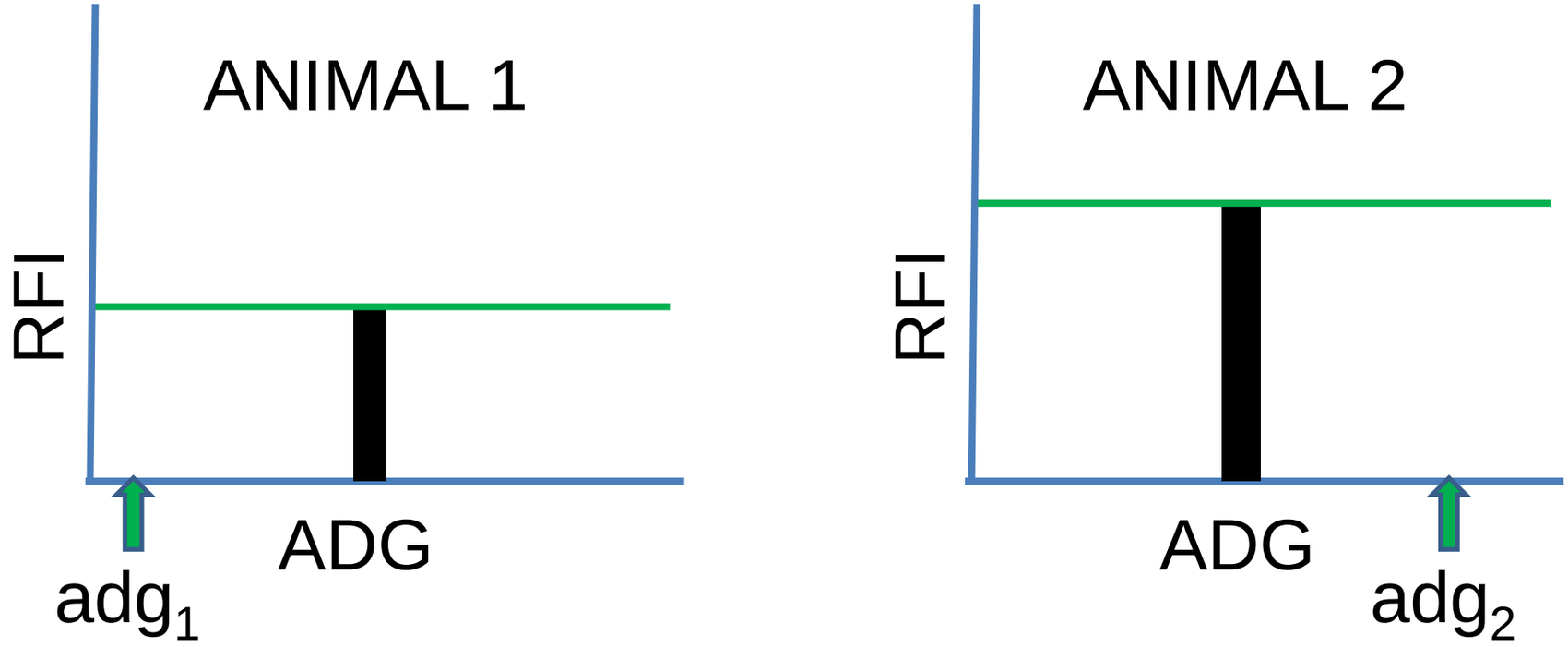
Residual Feed Intake (FI)

$$FI_{klpij} = BATCH_k + AGE_{ij} * \beta_{age} + ADG_{ij} * \beta_{ADG,E_l} + MBW_{ij} * \beta_{MBW,E_l} + BF_{ij} * \beta_{BF,E_l} + c_p + a_i + p_i + e_{klpij}$$

RFI



RFI = Kg of food consumed above/bellow requirements

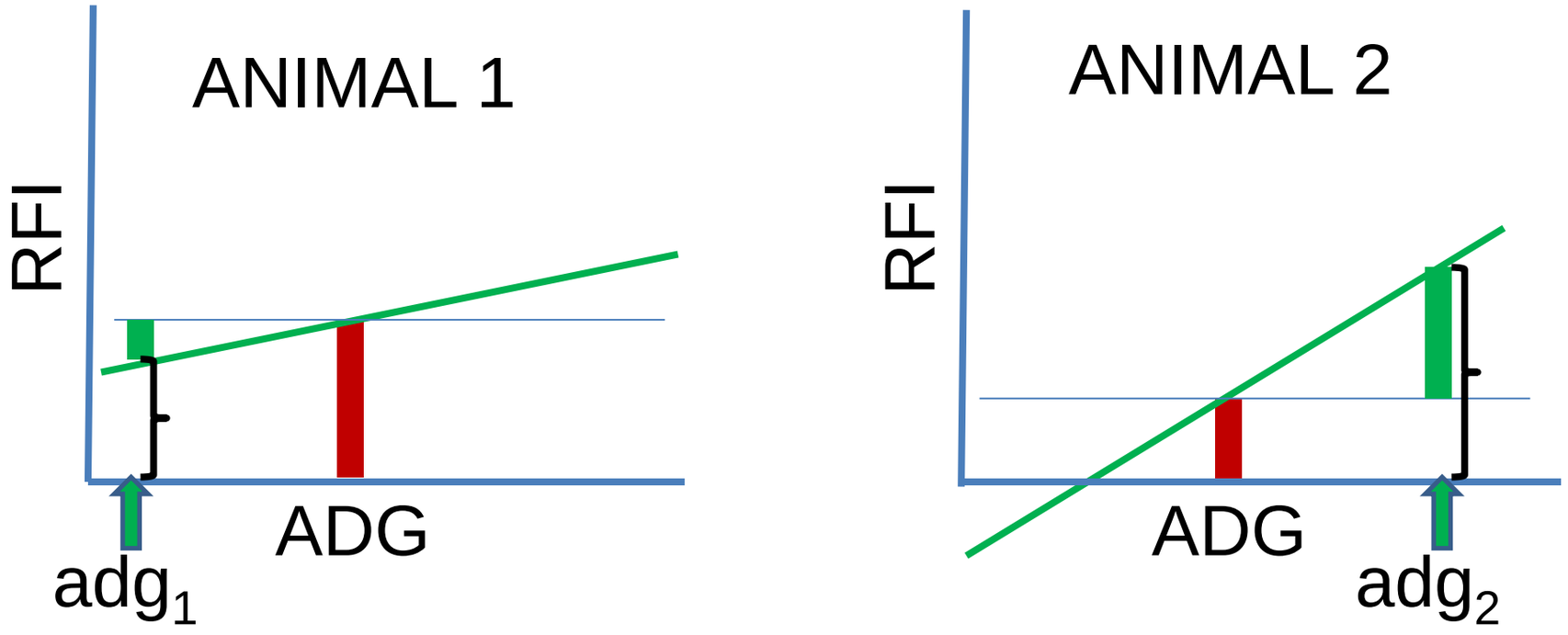
Requirements = F(ADG, MBW, BF)

The same function for all the animals in a group

Random Regression Models (RR)

$$FI_{klpij} = BATCH_k + AGE_{ij} * \beta_{age} + ADG_{ij} * \beta_{ADG,E_l} + MBW_{ij} * \beta_{MBW,E_l} + BF_{ij} * \beta_{BF,E_l} + c_p +$$

$$(a_{0,i} + p_{0,i}) + ADG_{ij} * (a_{1,i} + p_{1,i}) + MBW_{ij} * (a_{2,i} + p_{2,i}) + BF_{ij} * (a_{3,i} + p_{3,i}) + e_{klpij}$$



Kg of food above/below requirements – regardless (ADG, MBW or BF)

Kg of food above/below requirements per Kg of ADG (independent of individual ADG deviation)

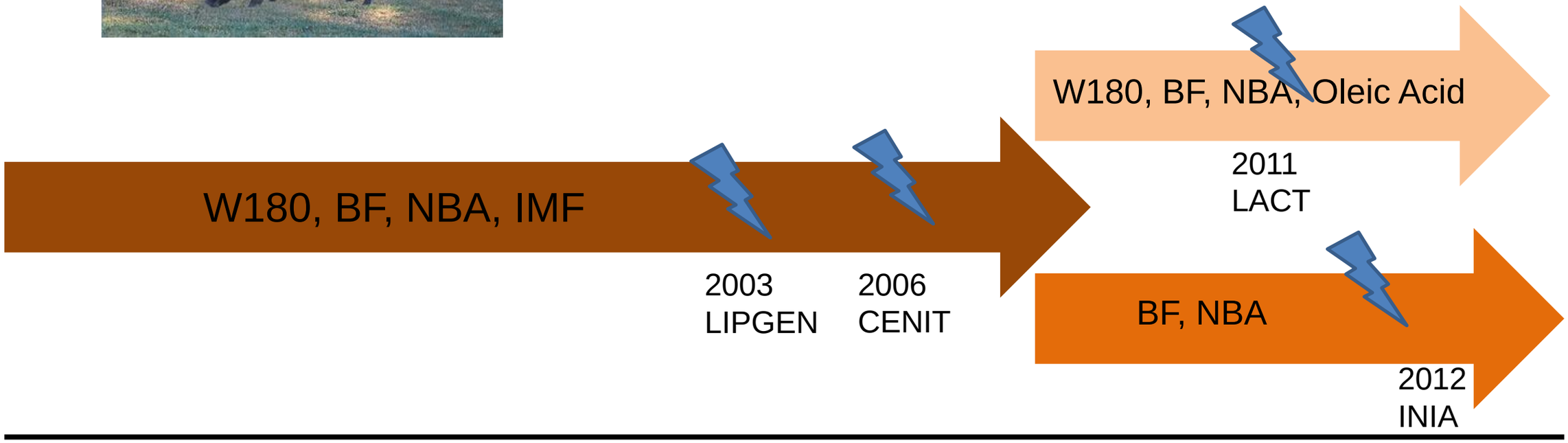
Kg of food above/below requirements given the observed ADG

OBJECTIVES

- Does individual variation in the use of feed per unit of ADG, MBW or BF explain a relevant part of FI variability?

- Is there any genetic control of the variability of these slopes?

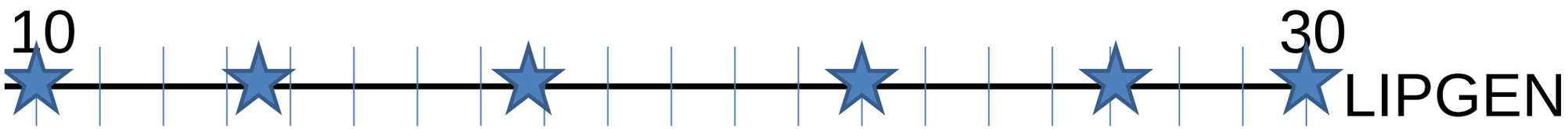
DUROC POPULATION

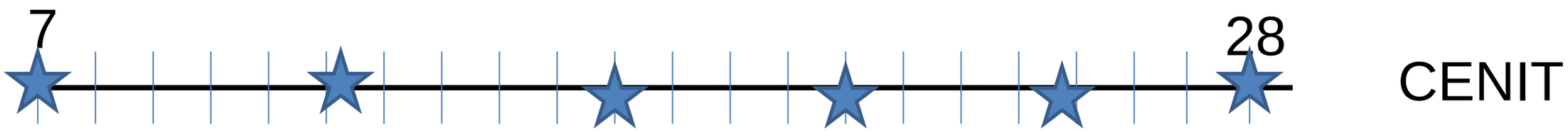


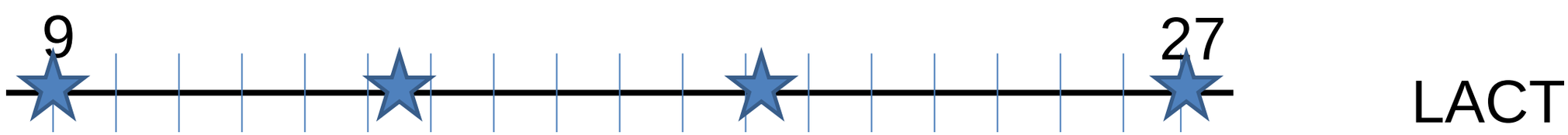
SELECCIÓN
BATALLÉ

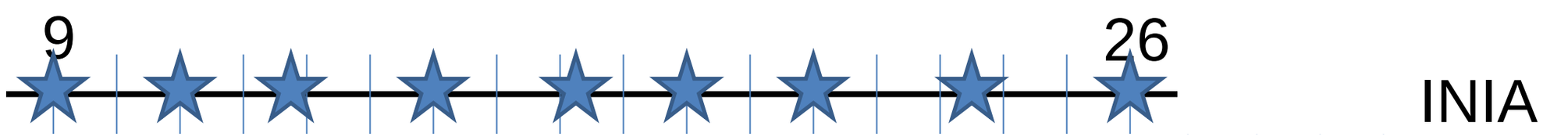
Feed Intake Recording

Control Periods – WEEKS



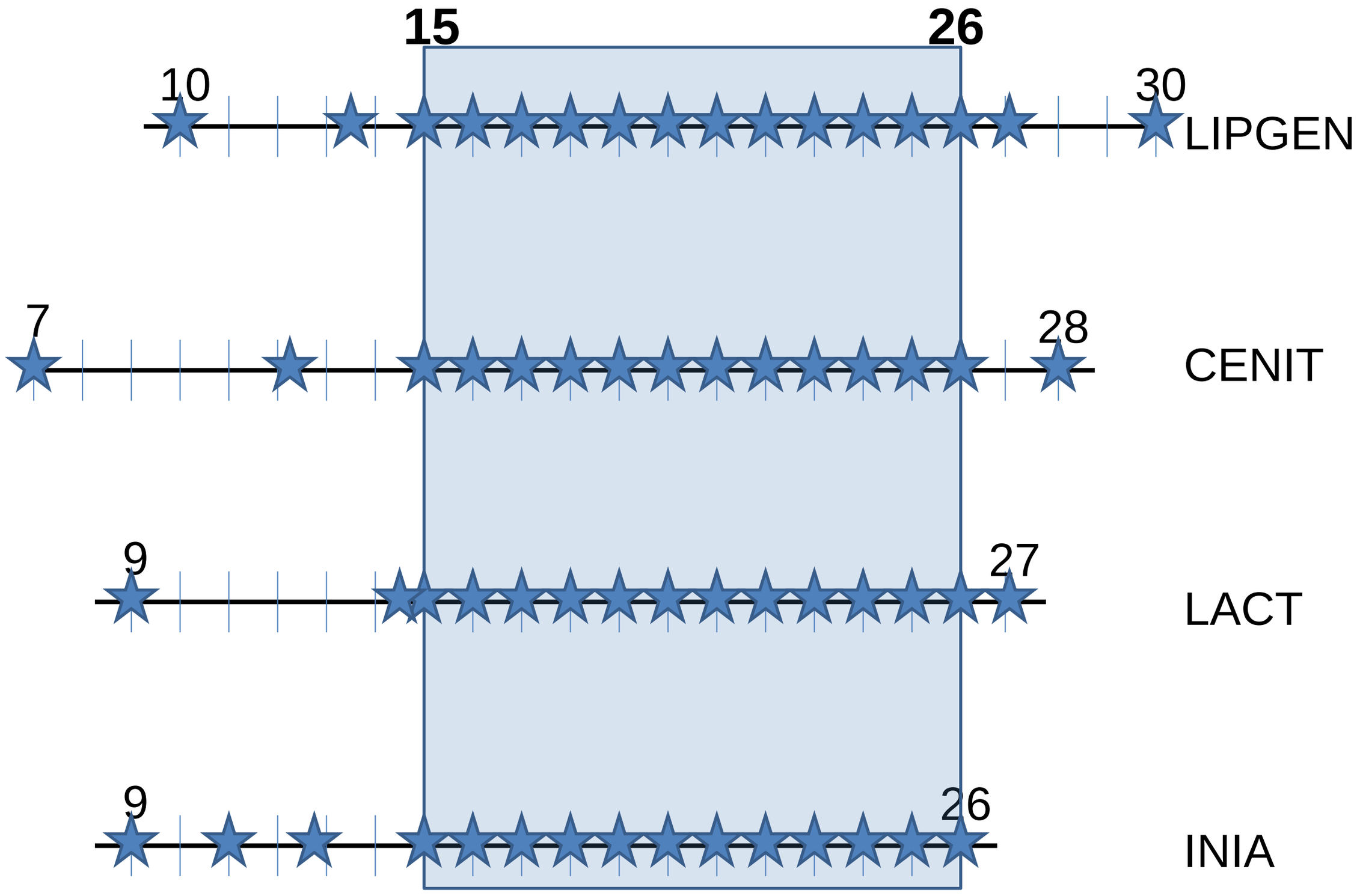






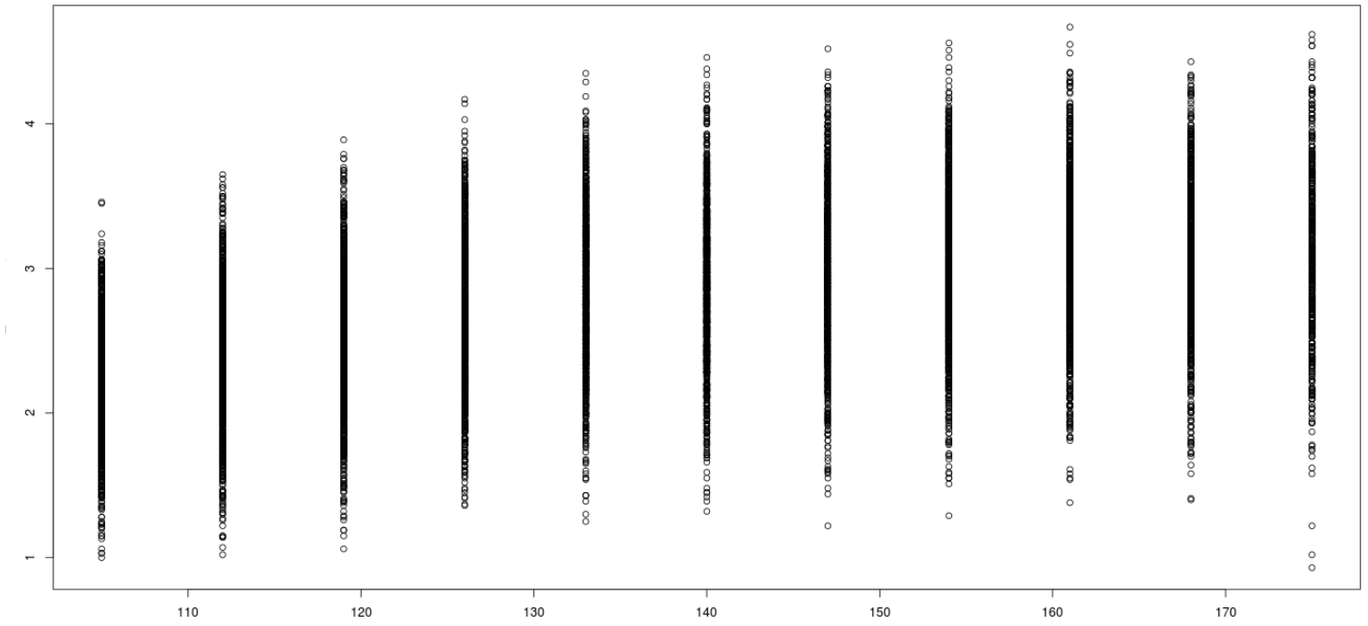
Control Periods - WEEKS

3 Coef. Legendre Random Regression



Weekly Daily Average DATA

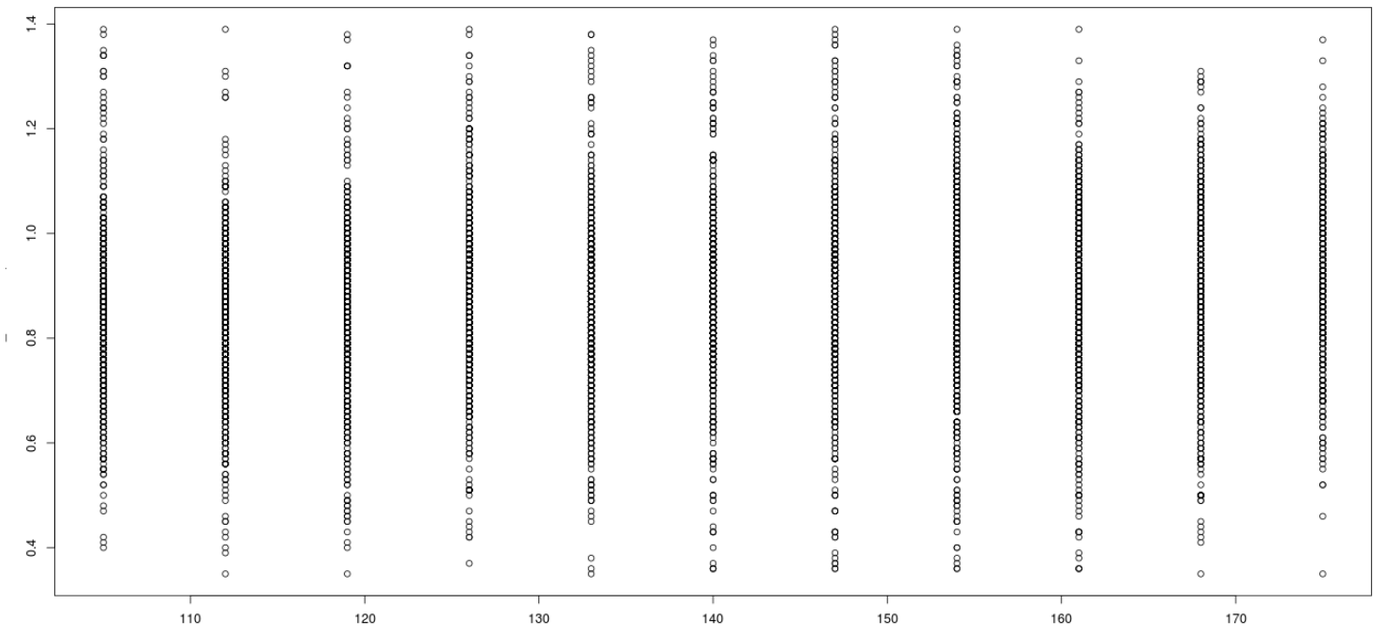
FI (kg)



VAR. = 0.33 Kg^2

Days

ADG (kg)



VAR.= 0.02 Kg^2

Days

Forward inclusion of RR model terms

HME -log(Marginal Likelihood)

Deviance = E(-2log(L))

	-log(p(y|Model))	Deviance
Int	663,036	1339524
Int+MBW	652,358	1316501
Int+ADG	660,763	1334189
Int+BF	662,254	1336188

FI variance explained by the RR model components

AGE	int	int + MBW	int + ~~DG~~	Int + ~~RF~~
105	0.012(0.005)	0.022(0.008)	0.013(0.003)	0.014(0.002)
119	0.012(0.005)	0.018(0.005)	0.013(0.003)	0.015(0.002)
126	0.012(0.005)	0.019(0.005)	0.014(0.003)	0.016(0.003)
140	0.012(0.005)	0.024(0.006)	0.015(0.004) **~Const.**	0.018(0.003) **~Const.**
147	0.012(0.005)	0.028(0.008)	0.015(0.004)	0.020(0.003)
161	0.012(0.005)	0.041(0.013)	0.016(0.004)	0.021(0.003)
175	0.012(0.005)	0.060(0.020)	0.017(0.004)	0.024(0.004)

GENETIC PARAMETERS

		Int	Int+MBW	Int+ADG	Int+BF
h^2	**Intercept**	0.14(0.02)	0.18(0.04)	0.12(0.03)	0.15(0.02)
	Slope*	0.40(0.01)	0.38(0.08)	0.56(0.13)	
Genetic Correlation		0.39(0.21)	0.71(0.19)	0.89(0.07)	

*** additive genetic variance / total individual variance**

EXPECTED RESPONSES

- SIMULATION

$$RFI_i = 0 + a_{1i} + p_{1i}$$

$$MBW_{ij} = 0 + a_{2i} + p_{2i} + e_{2ij}$$

$$(\frac{FI}{MBW})_i = 0 + a_{3i} + p_{3i}$$

$$FI_{ij} = 0.03 * MBW_{ij} + RFI_i + (\frac{FI}{MBW})_i * MBW_{ij} + e_{4ij}$$

$$\boldsymbol{a_i} \sim \boldsymbol{MVN}\left(\mathbf{0}, \begin{bmatrix} 0.02 & 0 & 0.001 \\ 0 & 2.45 & 0 \\ 0.001 & 0 & 0.0003 \end{bmatrix}\right)$$

$$\boldsymbol{p_i} \sim \boldsymbol{MVN}\left(\mathbf{0}, \begin{bmatrix} 0.02 & 0 & 0.002 \\ 0 & 1.94 & 0 \\ 0.002 & 0 & 0.0004 \end{bmatrix}\right)$$

$$e_{2ij} \sim N(0, 0.97)$$

$$e_{4ij} \sim N(0, 0.075)$$

EXPECTED RESPONSES

- GENETIC EVALUATIONS
  - TRADITIONAL RFI

$$FI_{ij} = \beta * MBW_{ij} + a_{1i} + p_{1i} + (\frac{FI}{MBW})_i * MBW_{ij} + e_{4ij}$$

  - RR on MBW

$$FI_{ij} = \beta * MBW_{ij} + a_{1i} + a_{3i} * MBW_{ij} + p_{1i} + p_{3i} * MBW_{ij} + e_{4ij}$$

EXPECTED RESPONSES

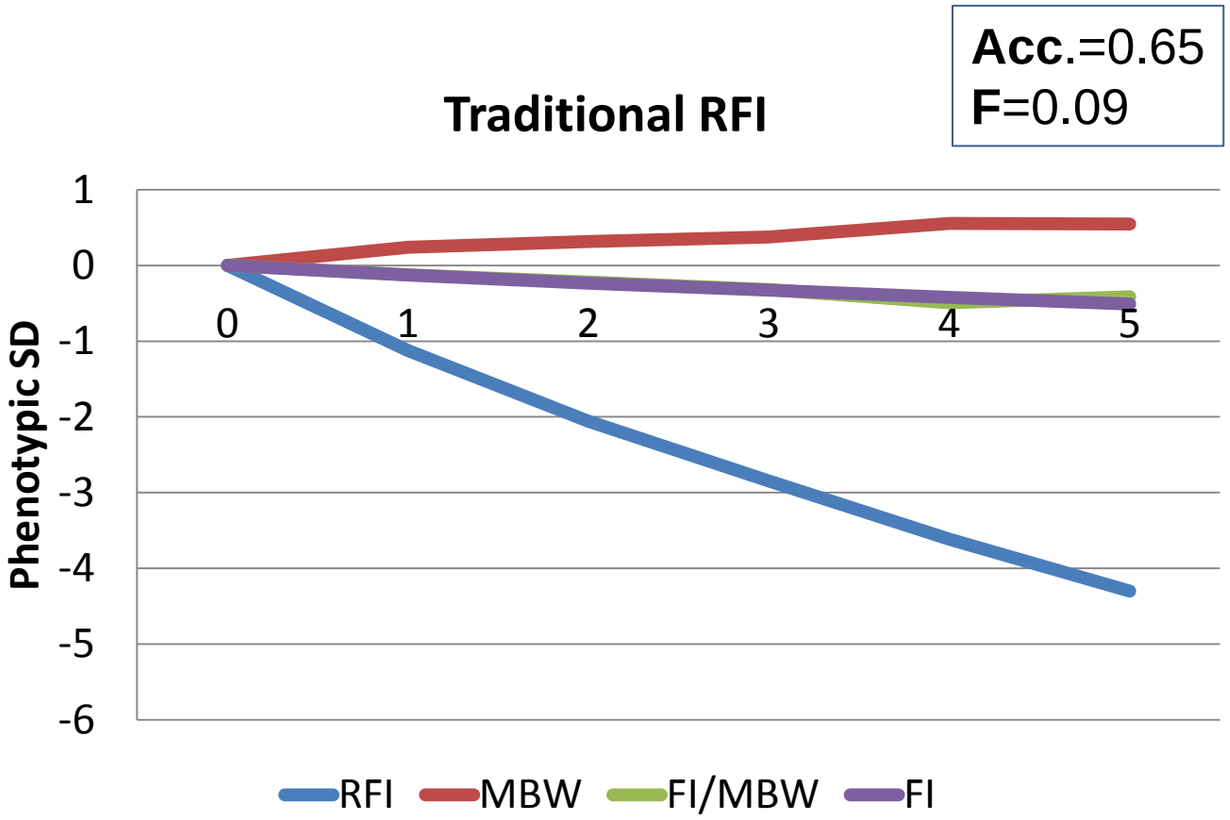
- SELECTION INDEXES
  - TRADITIONAL RFI

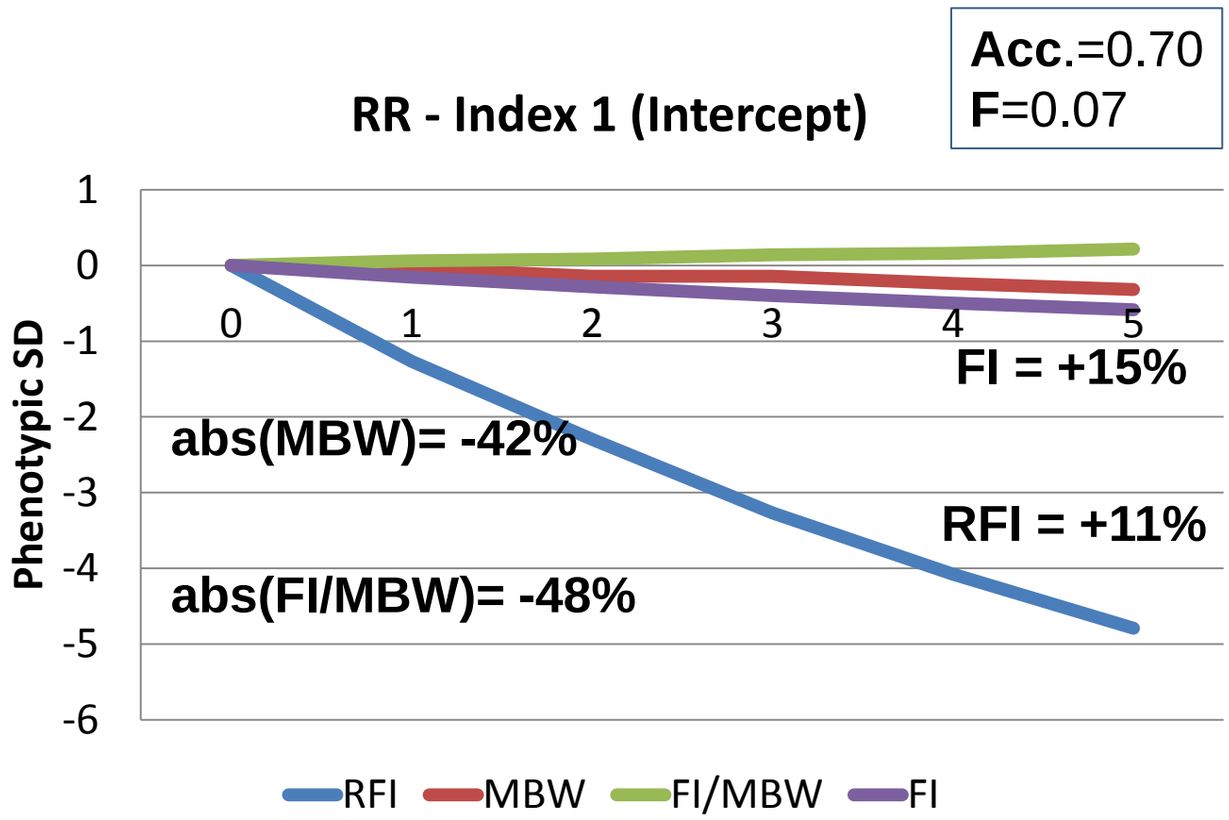
$$FI_{ij} = \beta * MBW_{ij} + a_{1i} + p_{1i} + (\frac{FI}{MBW})_i * MBW_{ij} + e_{4ij}$$

  - RR on MBW

$$FI_{ij} = \beta * MBW_{ij} + a_{1i} + a_{3i} * MBW_{ij} + p_{1i} + p_{3i} * MBW_{ij} + e_{4ij}$$

EXPECTED RESPONSES





CONCLUSIONS

- Variability of **FI per unit of MBW** is the only **relevant component explaining variation in FI**.
  - In agreement with experimental results.

- **Heritability** under **RR model on MBW is higher** than under “traditional” RFI definition.
  - Higher response on reducing RFI and FI
  - Lower changes in MBW and FI/MBW
    - Of interest in **maternal lines** to keep their robustness
    - Further research is needed

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