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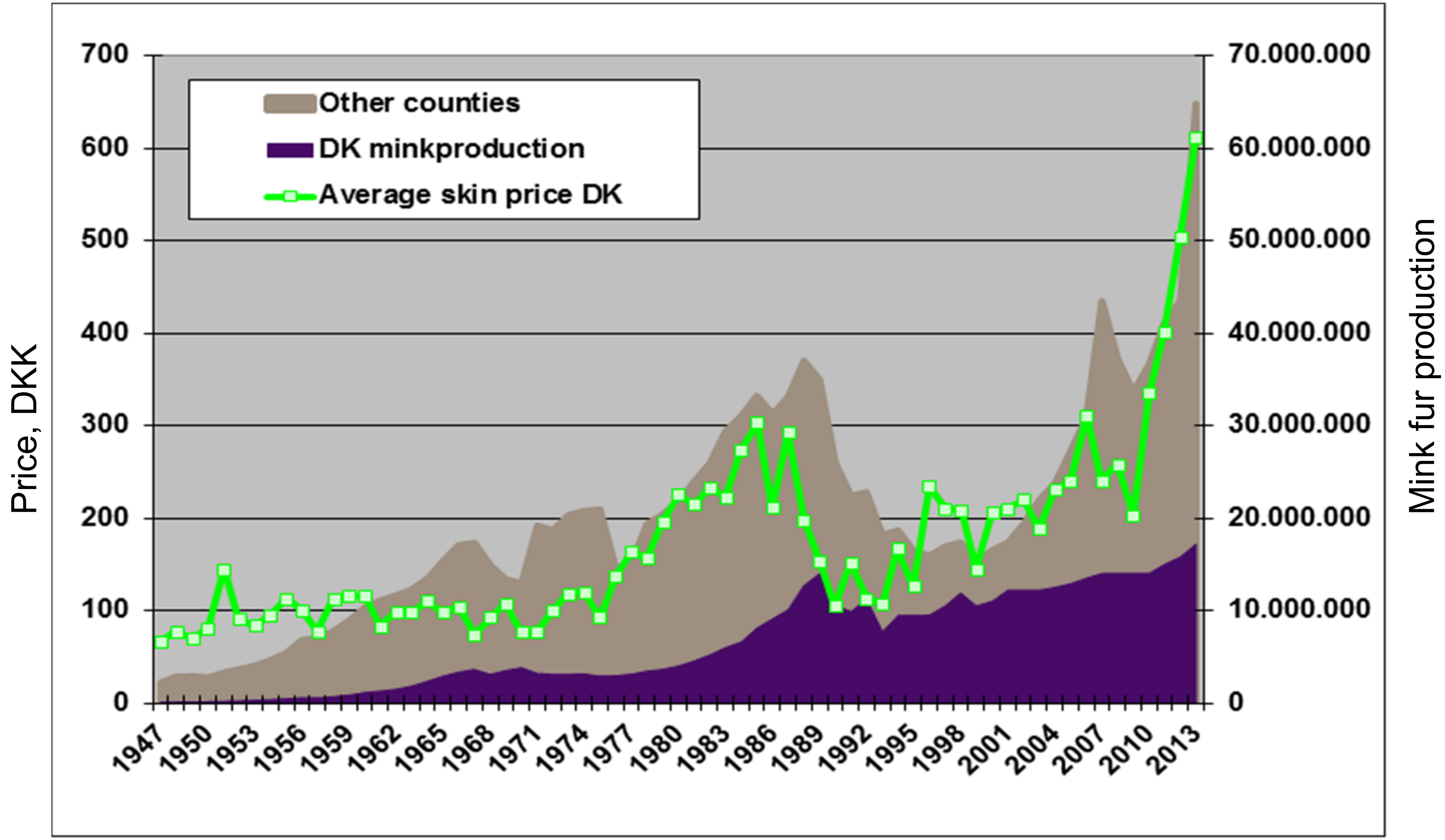
Longitudinal analysis of residual feed intake in mink using random regression with heterogeneous residual variance

Mahmoud Shirali, Vivi Nielsen, Steen Møller & Just Jensen

Mink Breeding

- **Denmark:**
  - World second mink fur producer
    - 17.2 Million skin (2012-2013)
  - Fur farming is Denmark's third largest type of animal farming

Mink Fur Production and Price



Denmark world second largest mink skin producer

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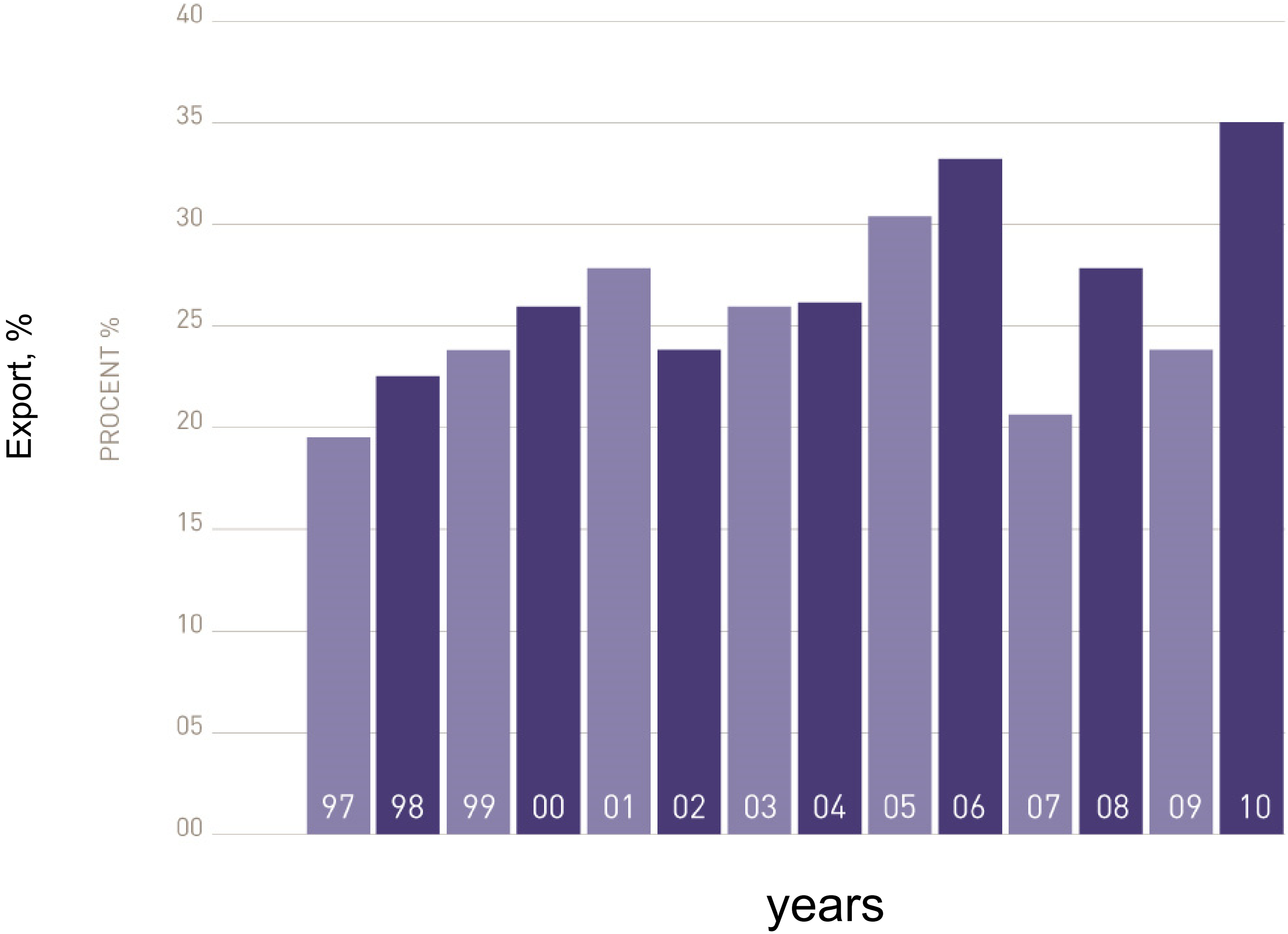
Fur skins are Denmark's largest export commodity to China



Mink breeders & feed efficiency

- **Mink breeders:**
  - Include feed efficiency in mink breeding program
- **Improvement in efficiency:**
  - Increased compatibility of fur production
    - 40-50% skin cost
  - Reduced nutrient excretion (environmetal pollution)

Year	Feed produced, t	Protein of feed, t	Nitrogen of feed, t
2012 - 2013	801.891	123.501	19.760

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Feed intake

Objective

Dissect the genetic background of longitudinal residual feed intake (RFI) and body weight (BW)

- ***Accurate method for feed efficiency***
- ***Least phenotype recording***

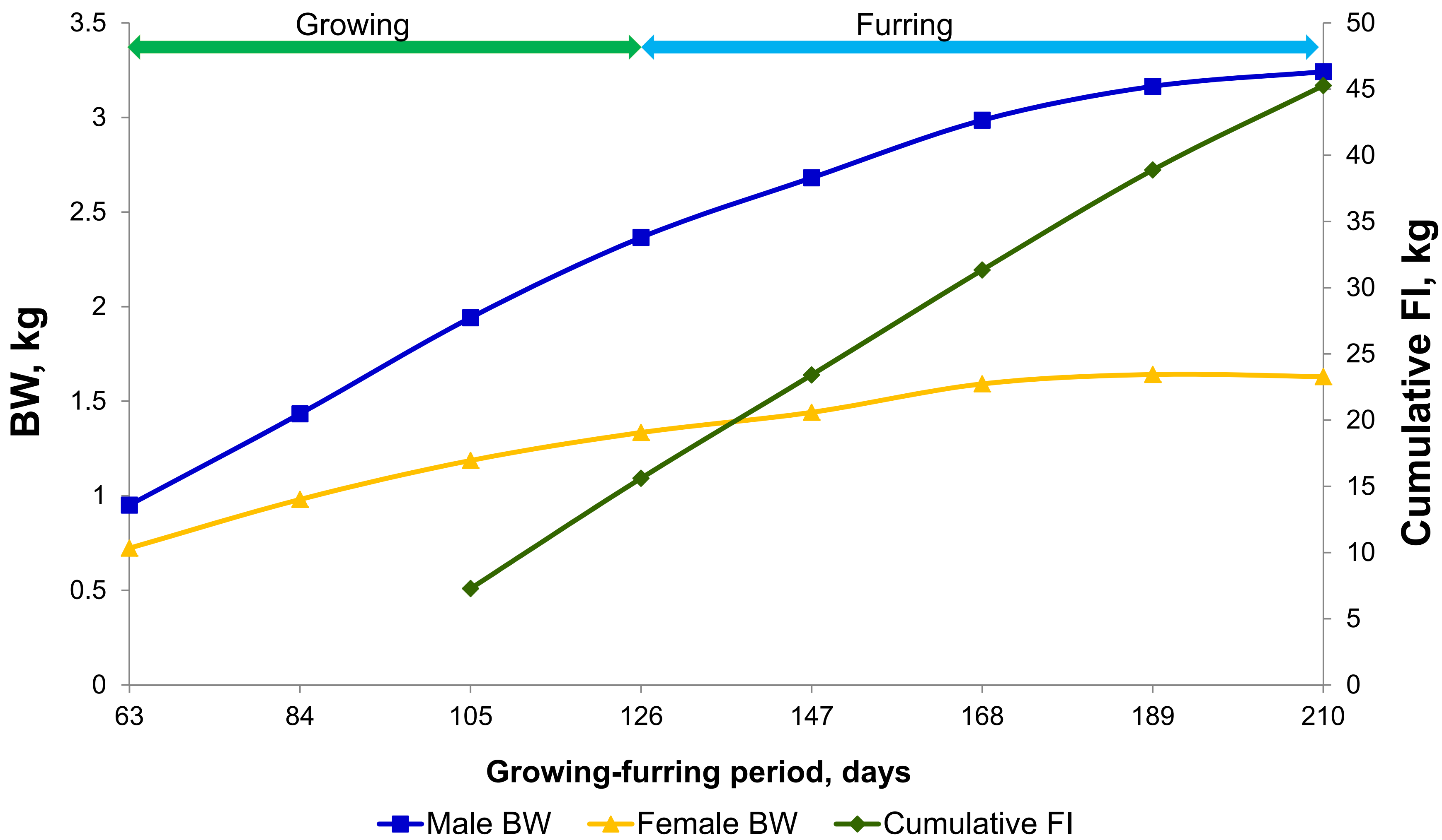
Data

- **2139 cages**
  - Pairs of one male and one female

- **Cumulative feed intake per cage**
  - 6 measurements
  - From 105 – 210 days of age (15 to 30 weeks of age)
  - Every three weeks

- **Body weight per animal**
  - 8 measurements
  - From 63 – 210 days of age (9 to 30 weeks of age)
  - Every three weeks

Body weight and feed intake curve



Method

- **Univariate models**
- **Random Regression**
  - Legendre polynomials
- **Gibbs Sampling**

Random regression-Legendre polynomials

RFI Male & Female

$$\boldsymbol{CFI\ cage}_{ijklm} = YL_i + b_1(BW_{Male\ k}) + b_2(BW_{Female\ l})$$

$+ l_{q1}(t)'r_i$ *Fixed part, LP_0, LP_1, LP_2*

G = 4 × 4

$+ l_{q2}(t)'a_k$ *Male, LP_0, LP_1*

$+ l_{q2}(t)'a_l$ *Female, LP_0, LP_1*

P = 4 × 4

$+ l_{q2}(t)'p_k$ *Male PE, LP_0, LP_1*

$+ l_{q2}(t)'p_l$ *Female PE, LP_0, LP_1*

$+ e_{ijklm}$ *Heterogeneous, 6 levels*

Random regression-Legendre polynomials

- **BW_{male} & Bw_{female}**

$$y_{ijkm} = YL_i$$

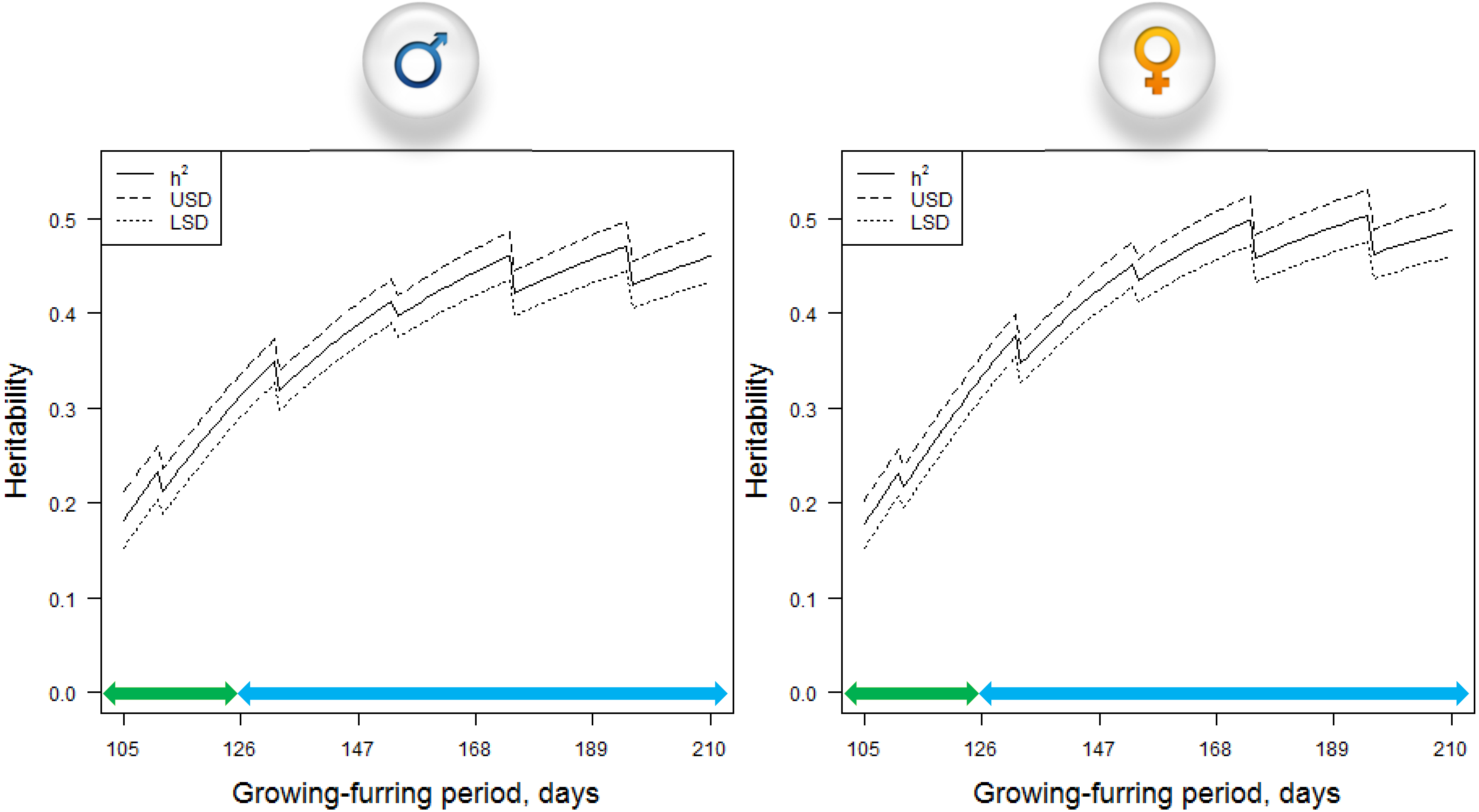
$+ l_{q1}(t)' r_i$ *Fixed part, LP_0, LP_1, LP_2*

G = 3 × 3 ⇒ $+ l_{q1}(t)' a_k$ *Genetic effect, LP_0, LP_1, LP_2*

P = 3 × 3 ⇒ $+ l_{q1}(t)' p_k$ *PE, LP_0, LP_1, LP_2*

$+ e_{ijkm}$ *Heterogeneous, 8 levels*

Genetic background of RFI



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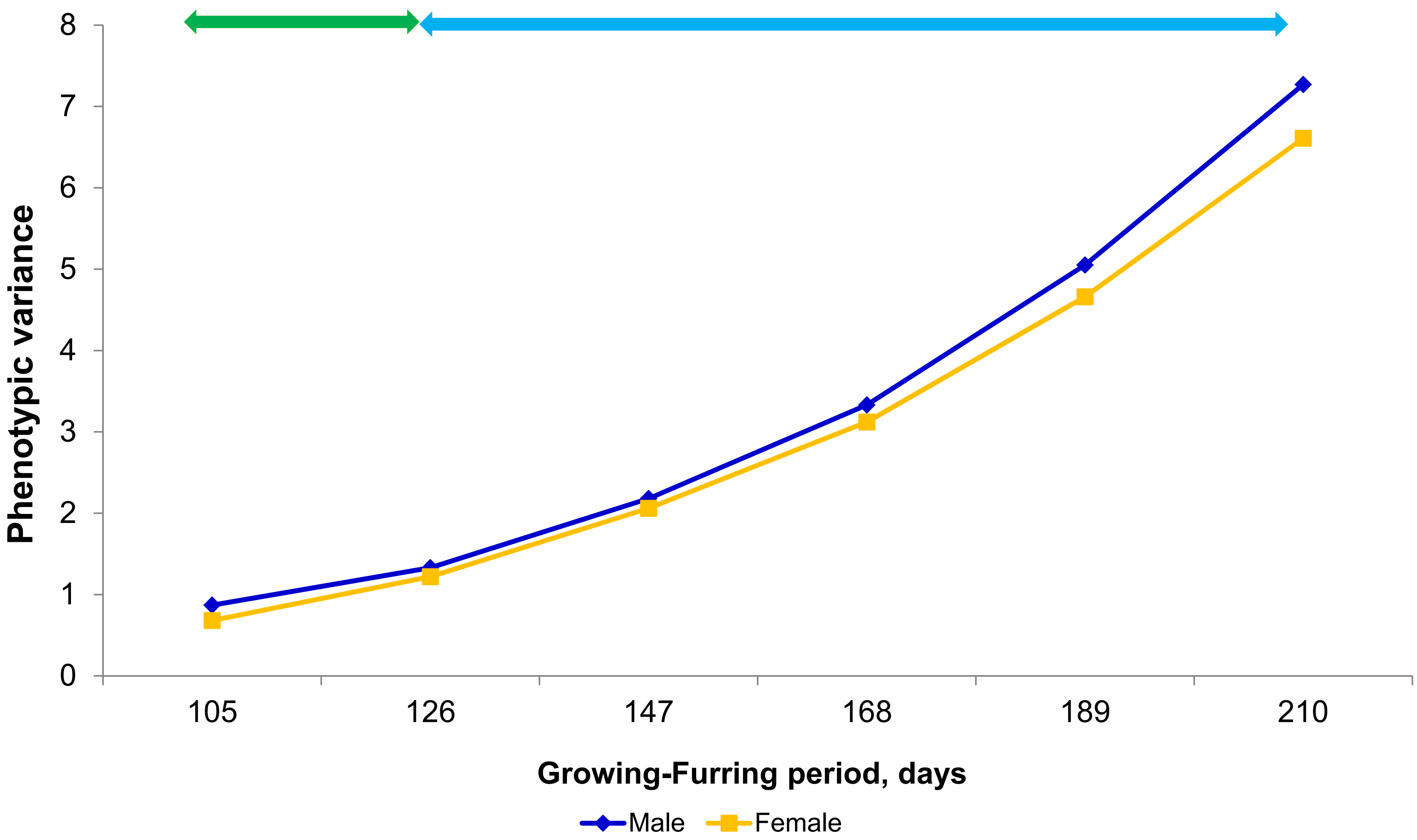
Phenotypic variance of RFI



Genetic correlations among RFI

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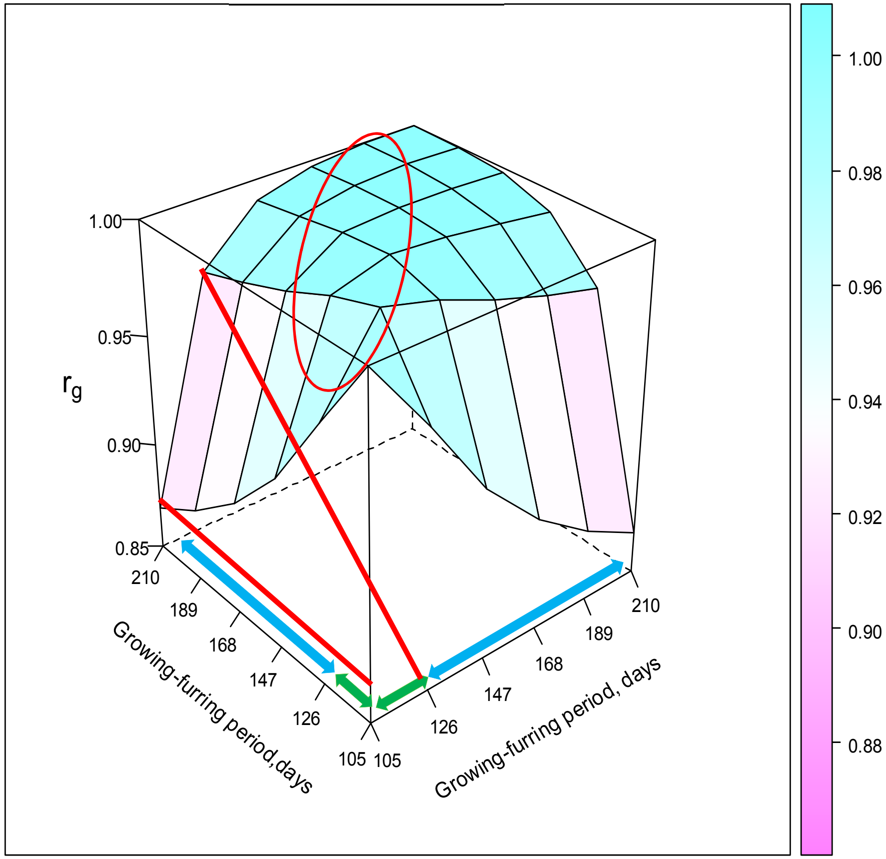

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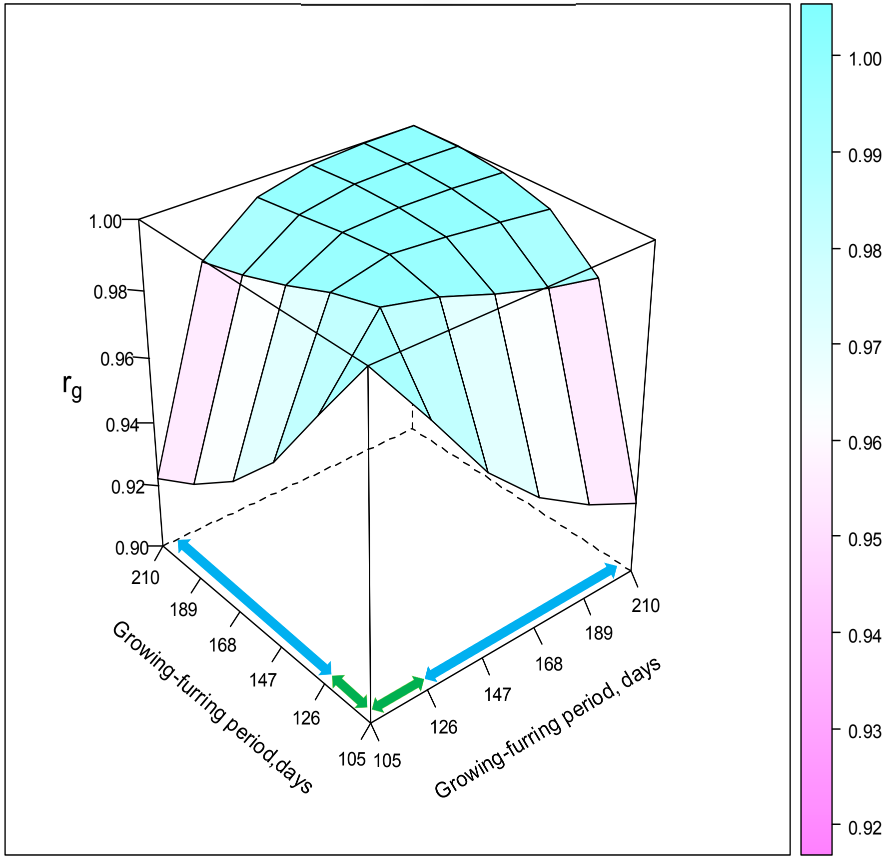

Phenotypic correlations among RFI

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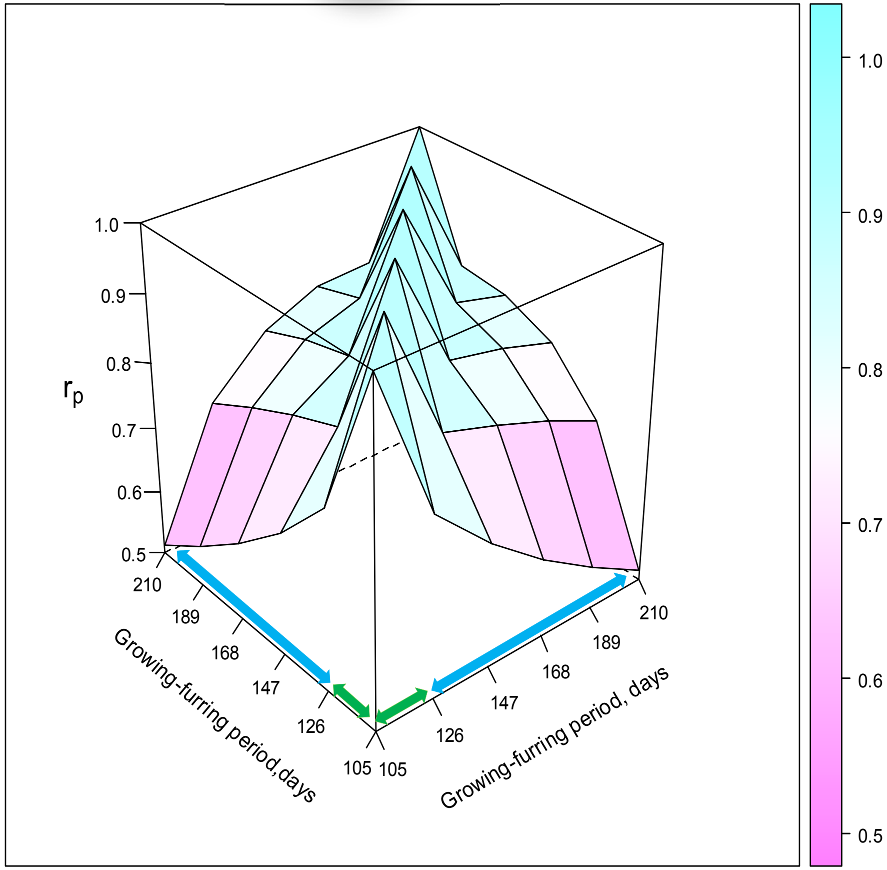

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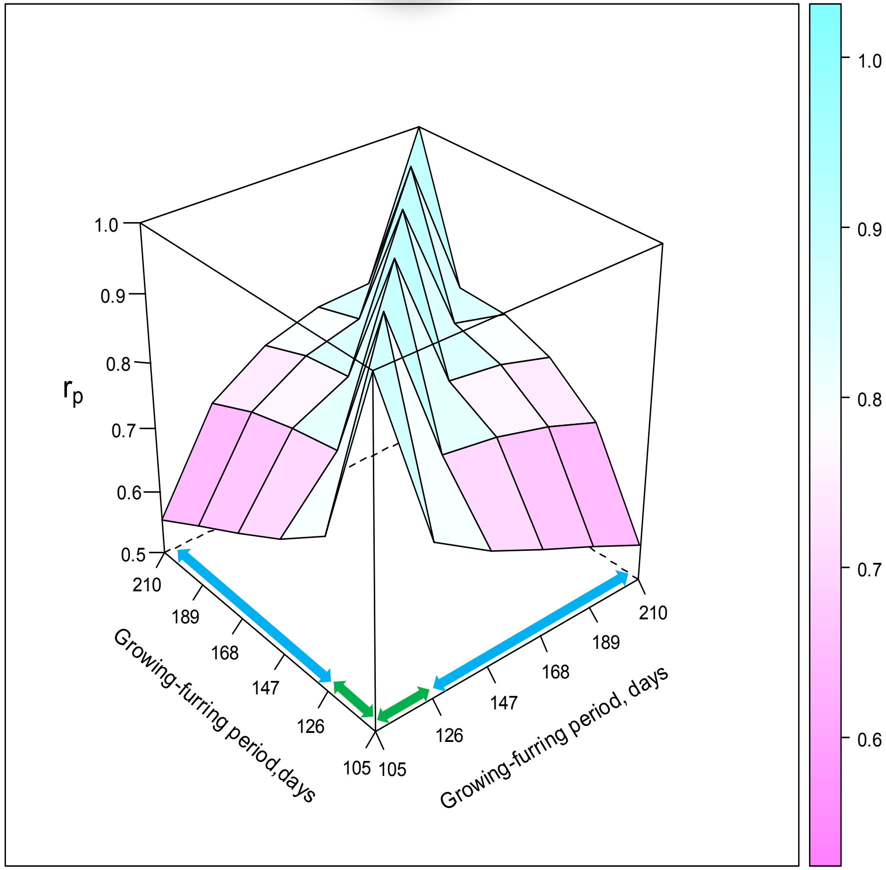
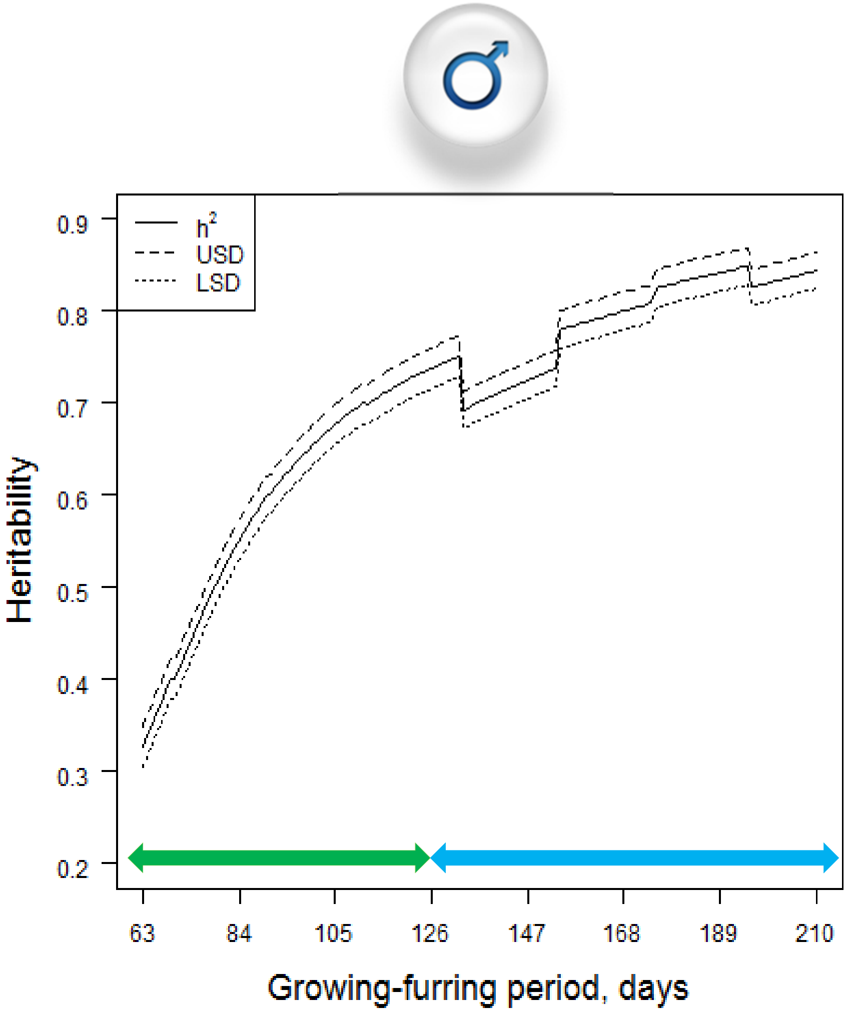
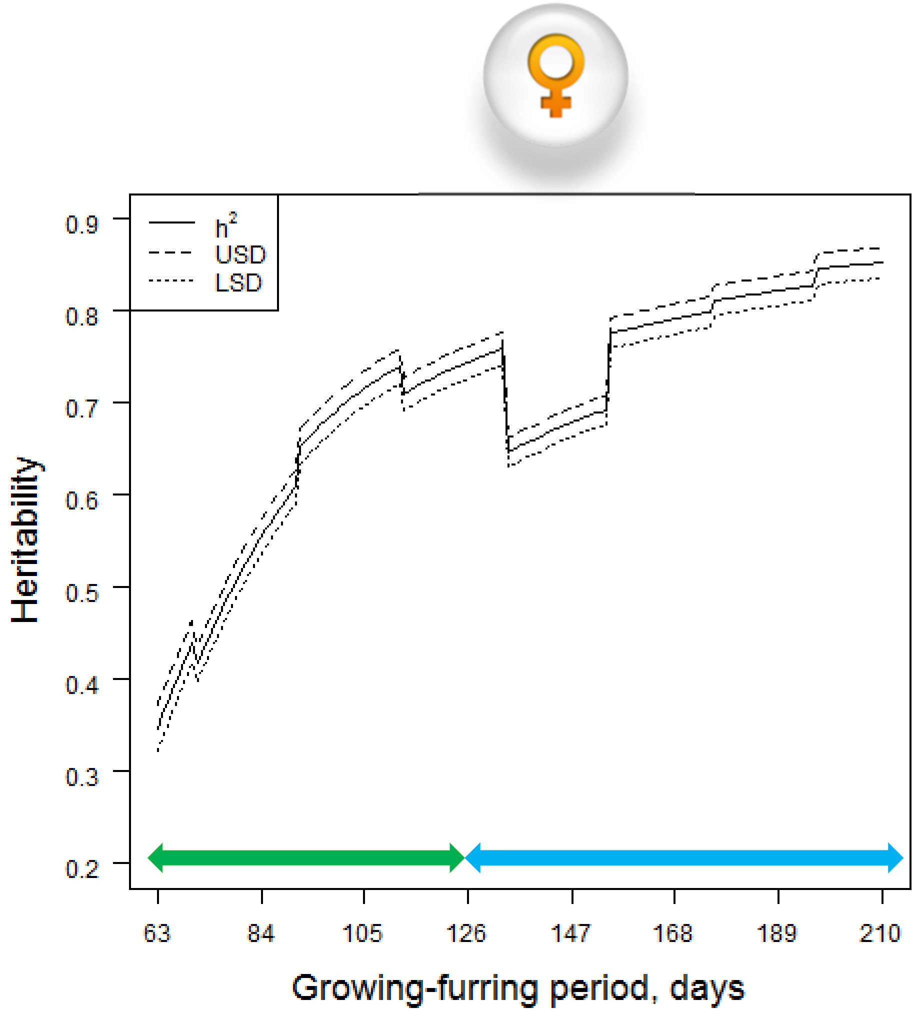
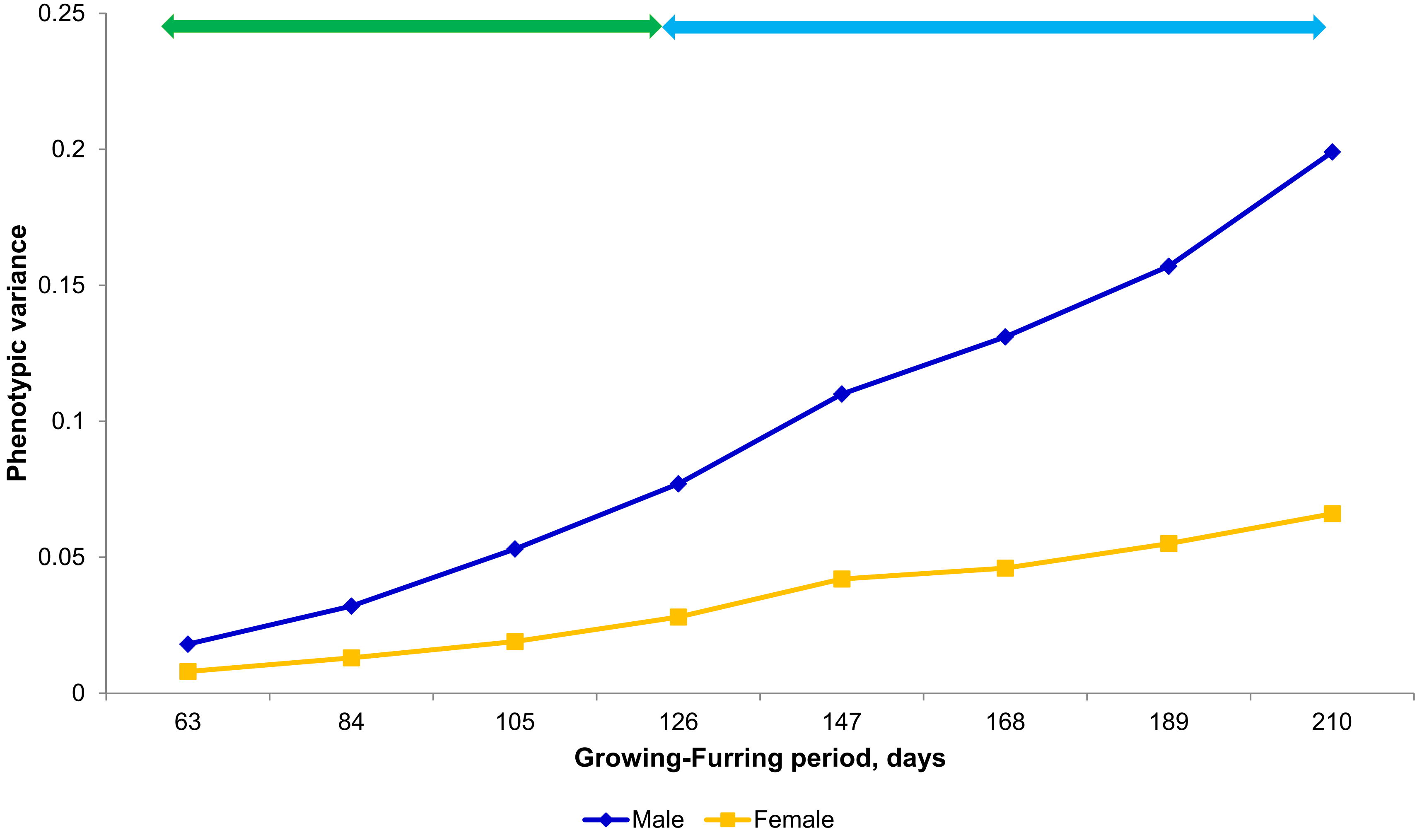


Genetic background of BW





Phenotypic variance of BW



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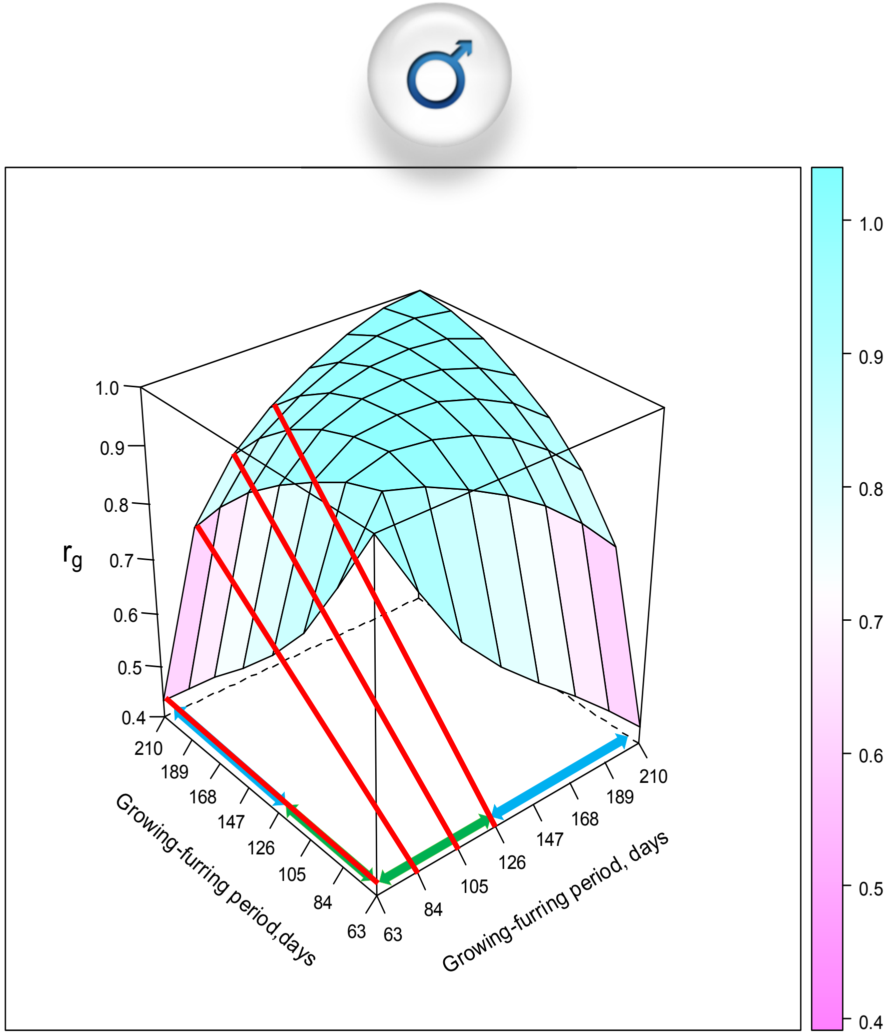
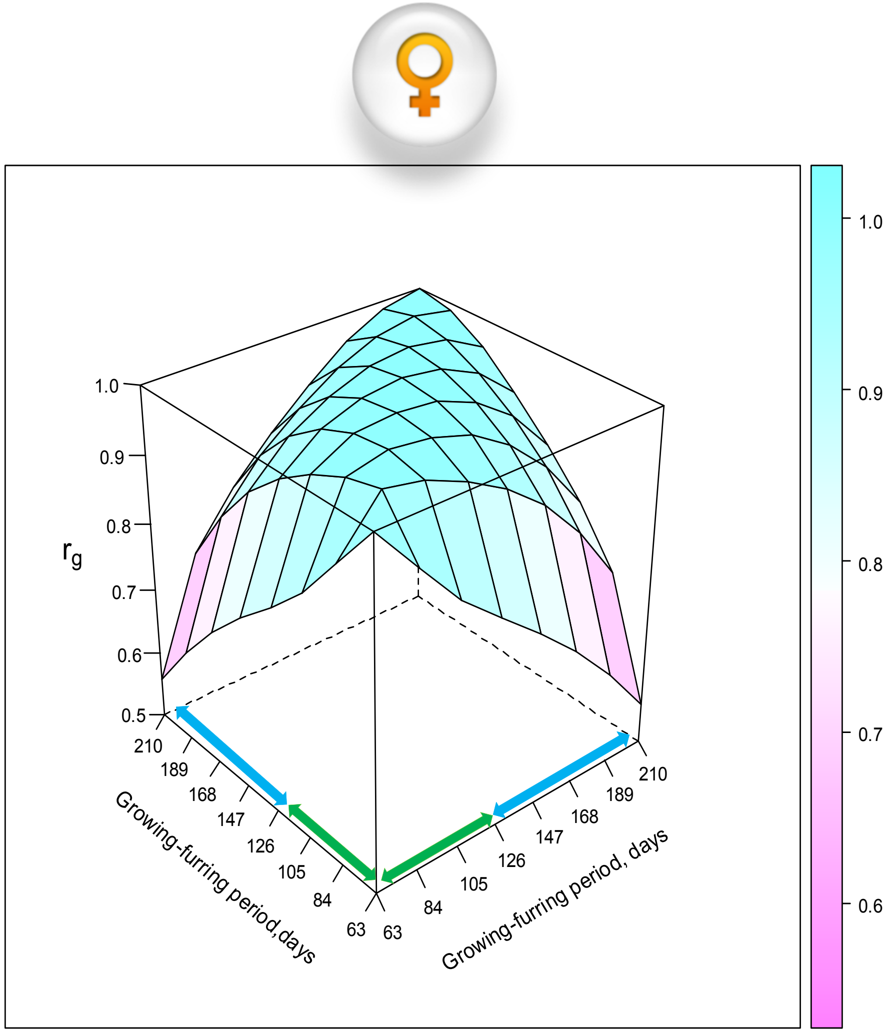
Genetic correlations among BW





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Phenotypic correlations among BW

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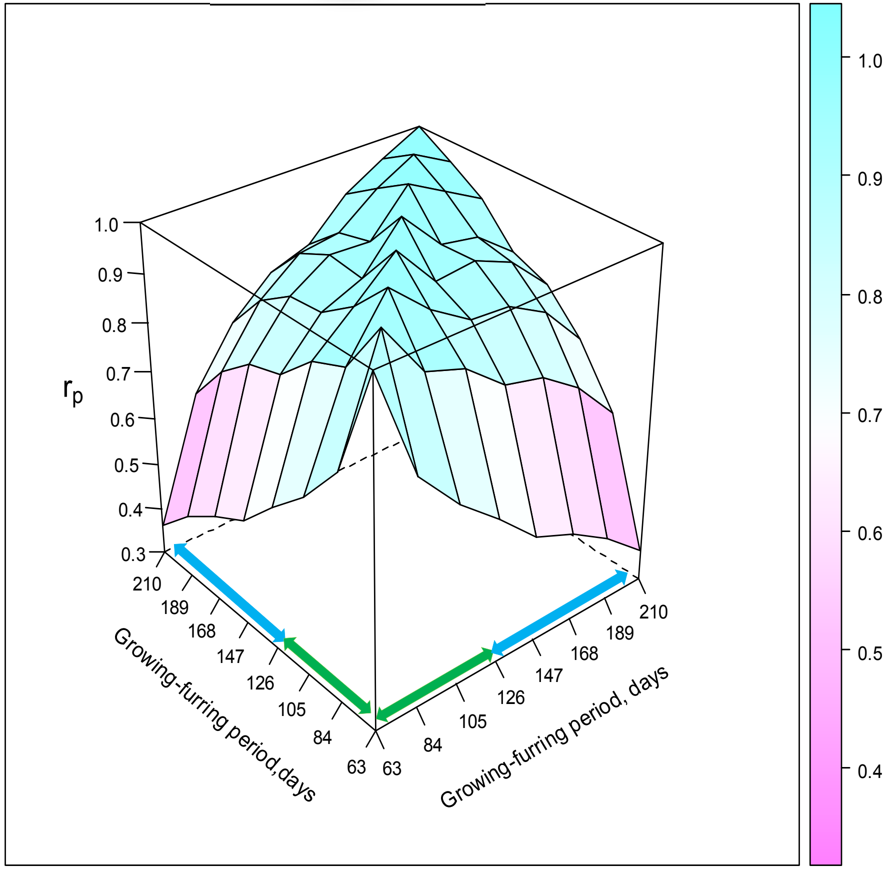

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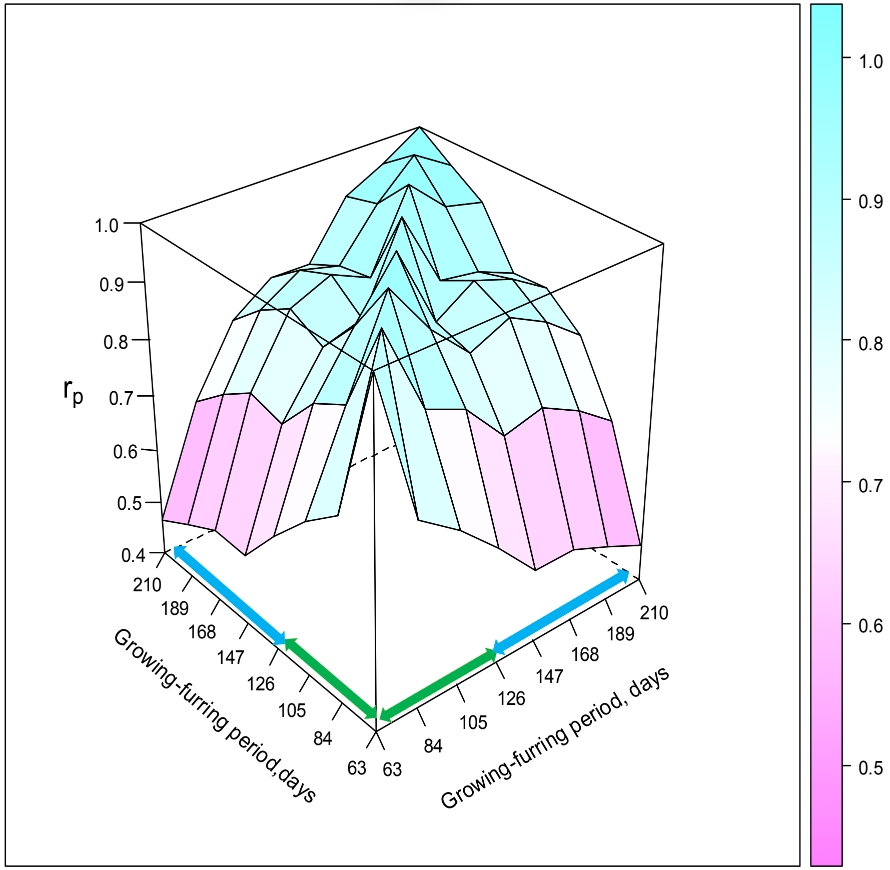


Selection index theory

- **Accuracy of selection based on different recording strategies**

$$r_{a,I} = \frac{\sqrt{\boldsymbol{b}\ \boldsymbol{P}\ \boldsymbol{b}'}}{\sqrt{\boldsymbol{a}\ \boldsymbol{G}\ \boldsymbol{a}'}}$$

$\boldsymbol{r_{a,I}}$ = accuracy of index

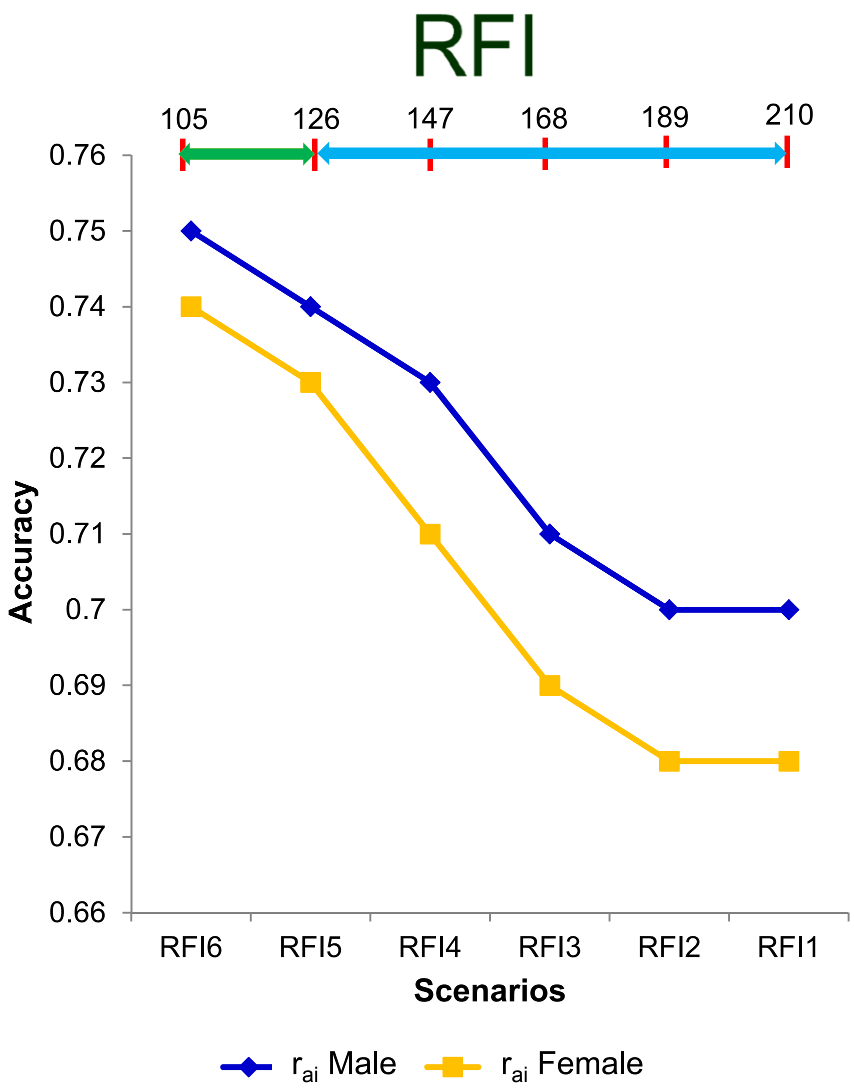
$\boldsymbol{b}$ = n×1 vector of weighing factors for each record

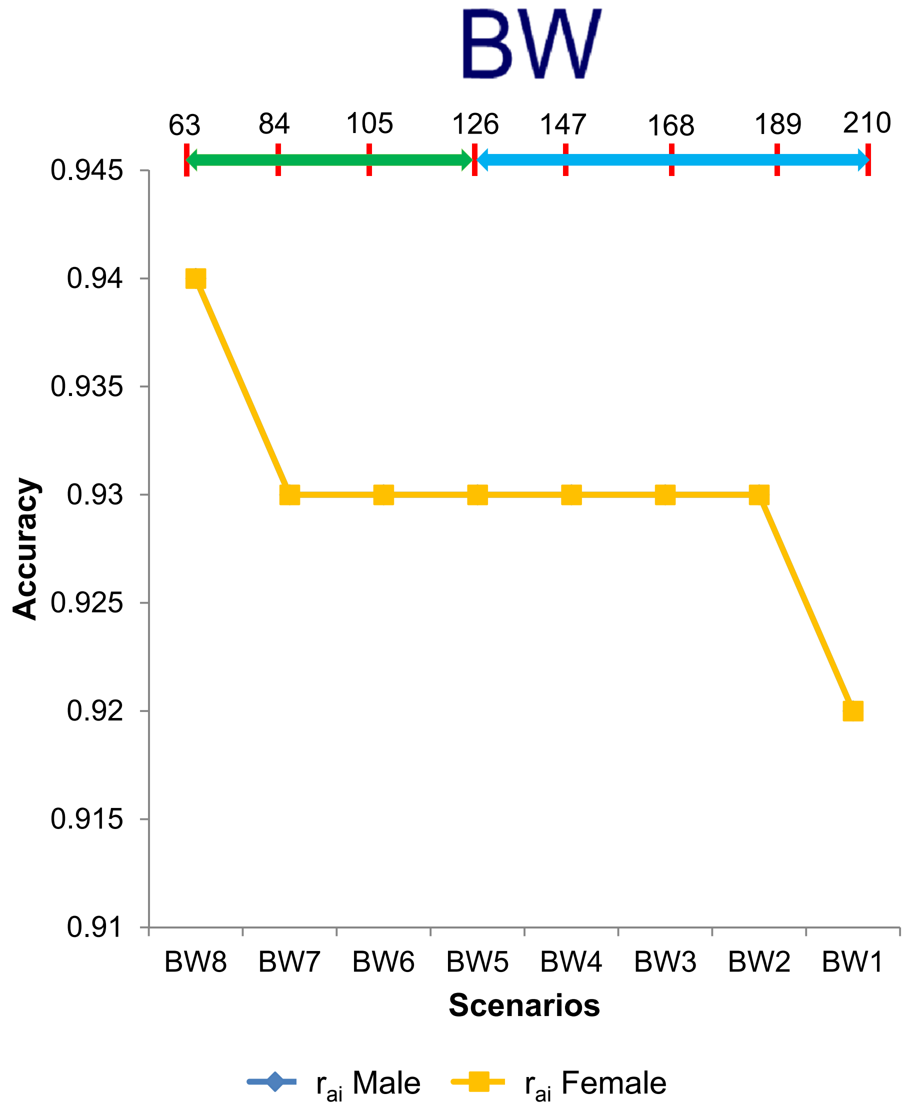
$\boldsymbol{P}$ = n×n matrix of phenotypic (co)variance among records of each trait

$\boldsymbol{a}$ = n×1 vector of relative economic values for each record with only the pelting RFI and BW (210 days) considered to have one economical weight and other time points to be zero

$\boldsymbol{G}$ = n×n matrix of genetic (co)variance among all records of each trait

Selection Indices





Conclusion

Feed efficiency can be improved substantially by selection at the later stages of growth

Different genes can be associated with feed efficiency and body weight during the growing-furring period

Random regression models are suitable for dissecting the genetic background of RFI & BW

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