

Genetic and genome-wide analysis of longitudinal egg-production data in laying hens

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- ▀ Background**
- ▀ Variance components for egg production**
- ▀ Dynamics of genetic correlations**
- ▀ Adding genomics to the picture**
- ▀ Conclusions**

Life of a layer chicken is longitudinal



Feed temperature ventilation disease...

Hatch

Start laying

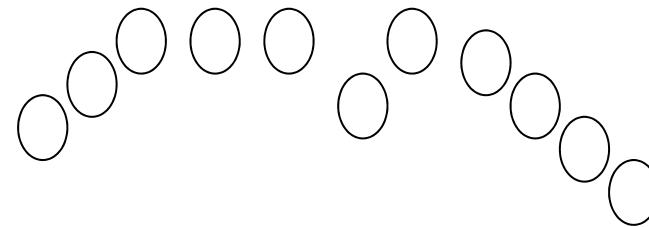
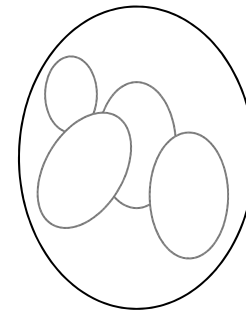
Keep laying

Keep laying

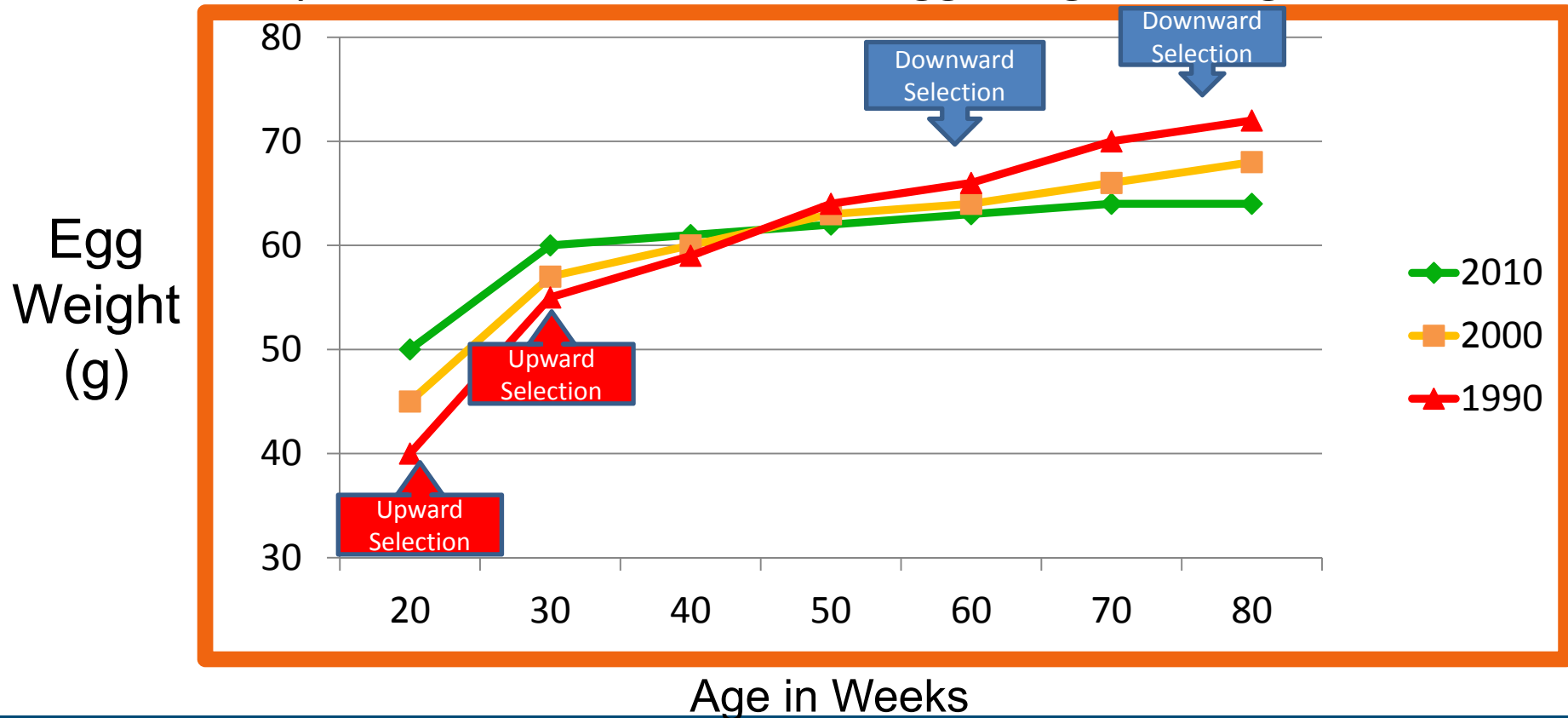
Retire



- Single measurement
- Changes over time



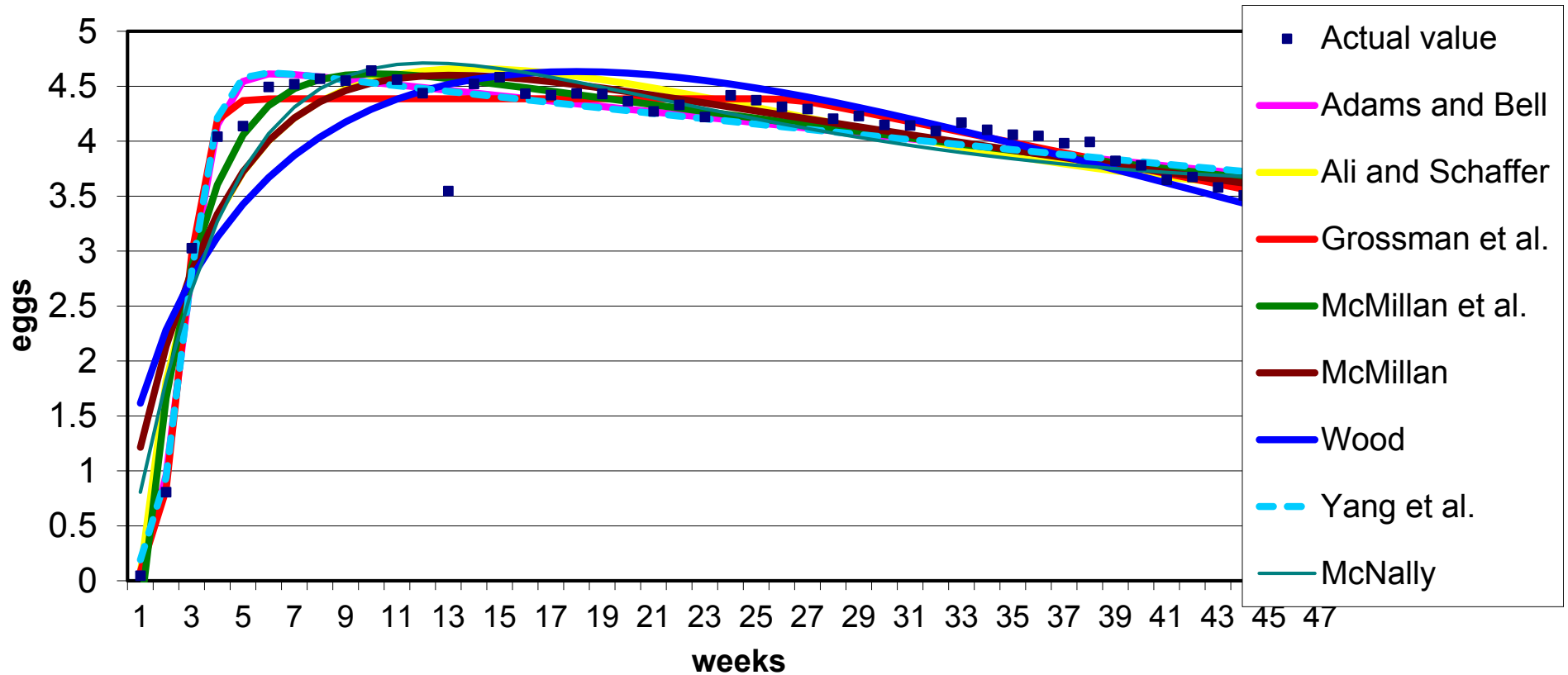
Hy-Line Brown Selection for Egg Weight Change



- ▀ **Single trait model for cumulative data**
- ▀ **Repeatability model**
- ▀ **Fixed regression model**
- ▀ **Multitrait model**
- ▀ **Random regression model**



On a flock level chicken data looks like dairy cows



Egg



No egg

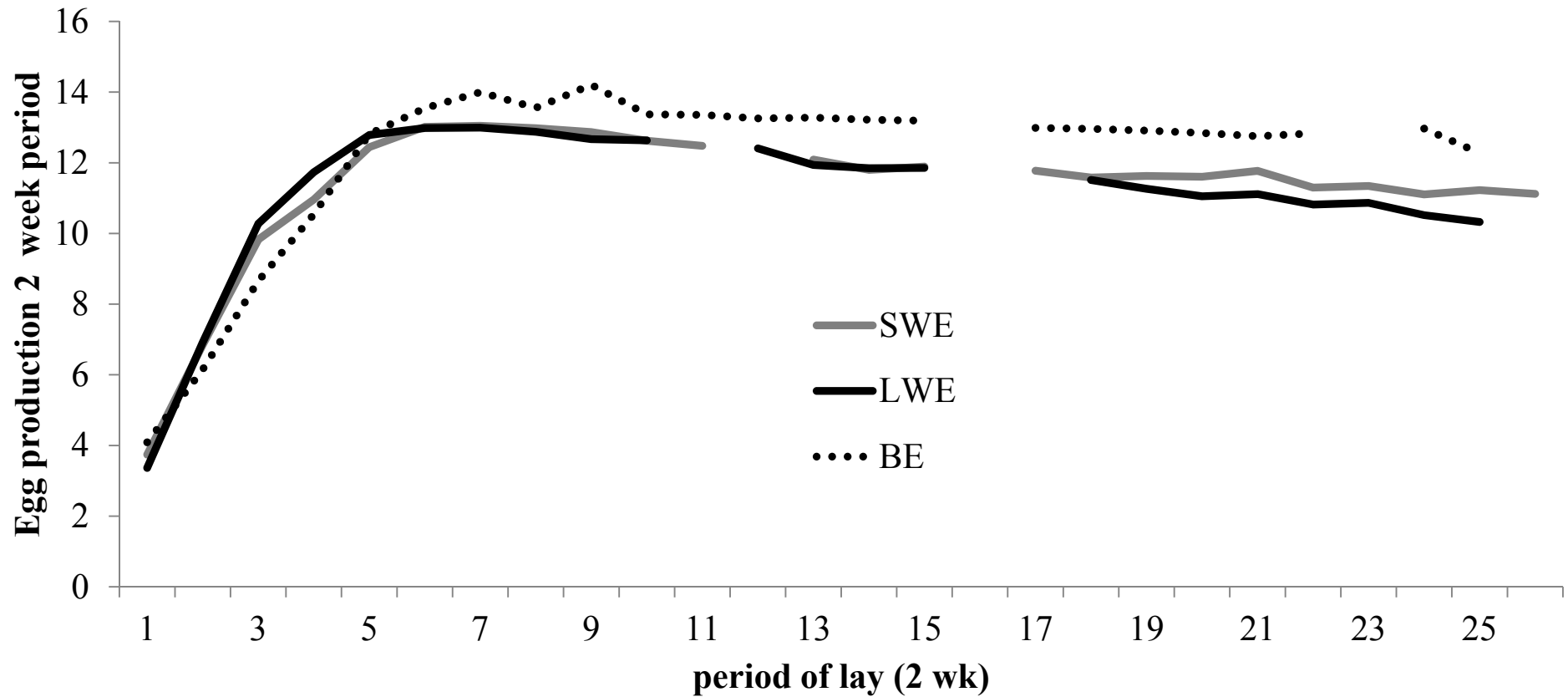


- ▀ **Express egg production as weekly, bi-weekly or monthly records**
- ▀ **Assume normally distributed**

Study 1

Variance components for egg production

- **Small white-egg (SWE) line**
26,719 birds 307,462 bi-weekly records
- **Large white-egg (LWE) line**
31,531 birds 379,786 bi-weekly records
- **Brown-egg (BE) layer**
31,059 birds 372,288 bi-weekly records
- Daily records from first egg to **47 wk of lay**
- **6 generations**



Biweekly
egg
production

Additive
genetic
effects

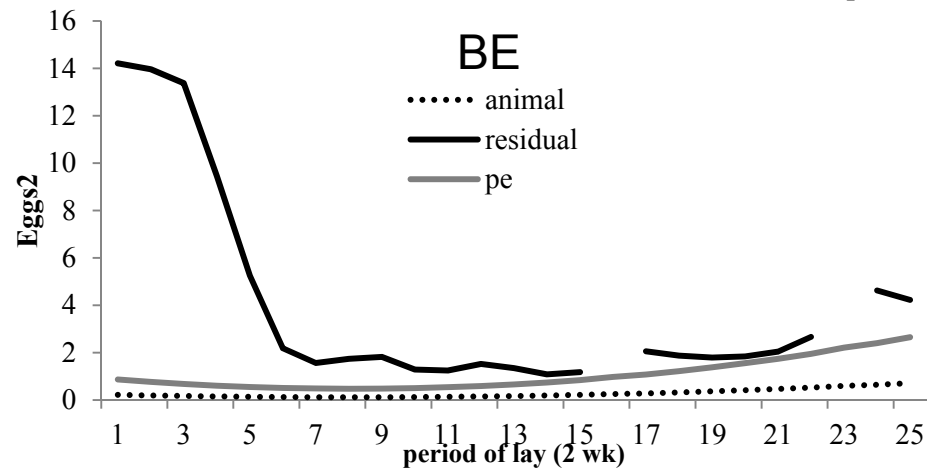
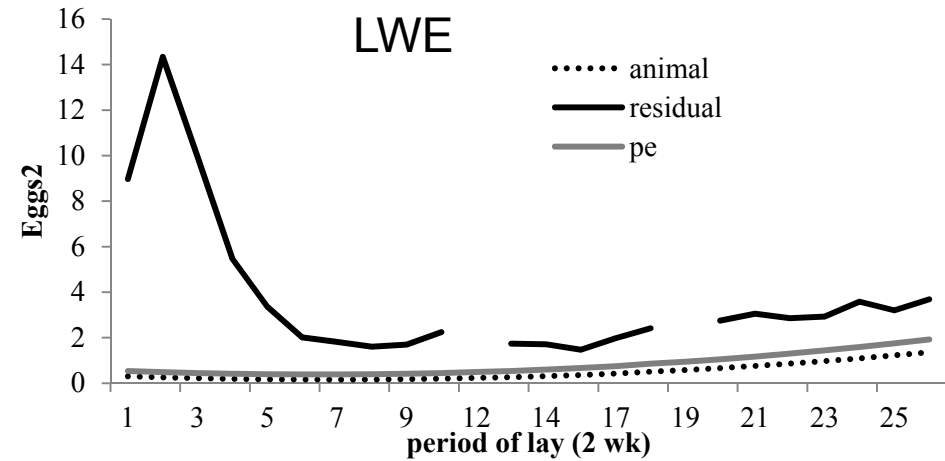
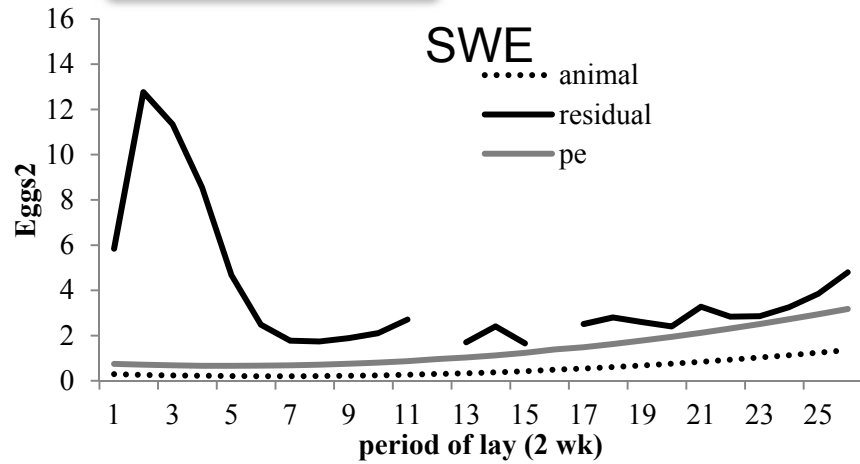
Residual

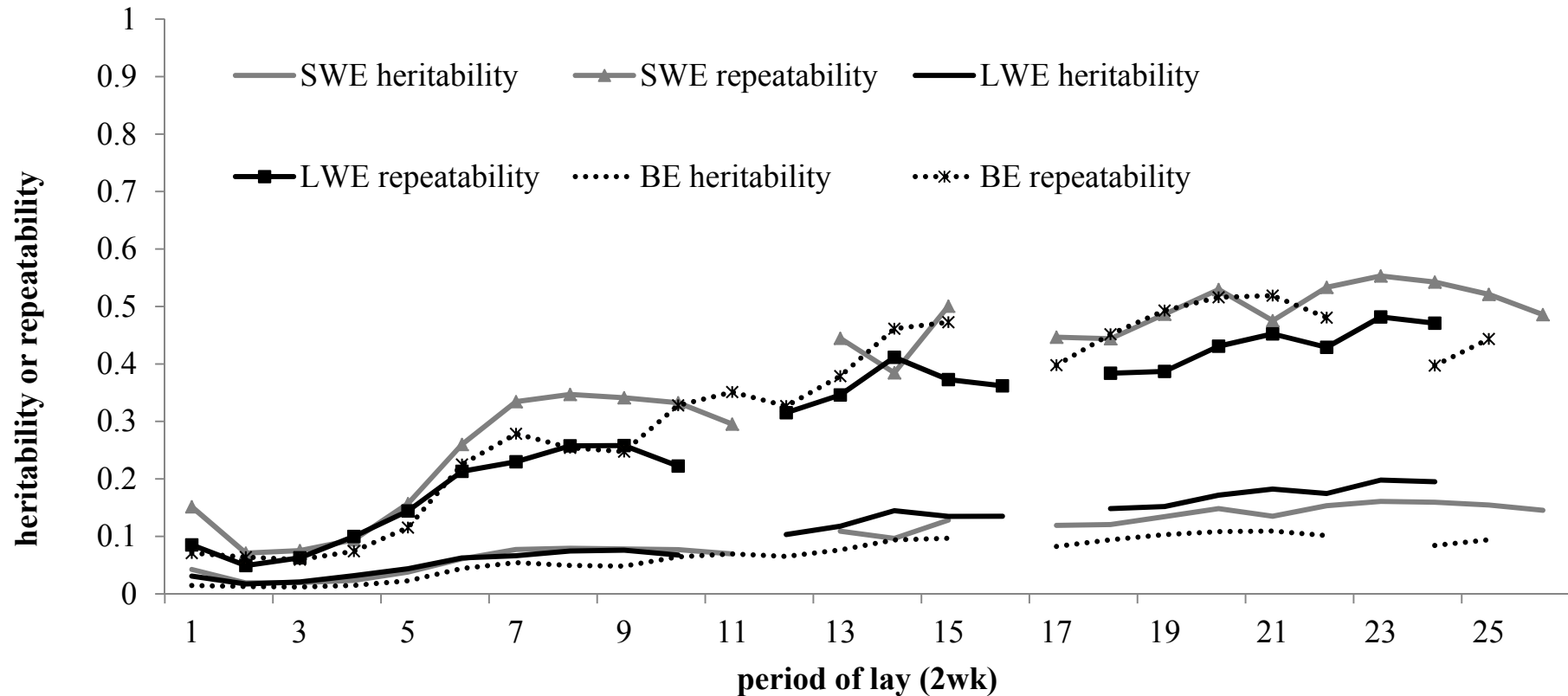
$$y_{ikl} = HY_i x \sum_{m=0}^{n_1} b_m z_{klm} + \sum_{m=0}^{n_2} a_{km} z_{klm} + \sum_{m=0}^{n_3} p_{km} z_{klm} + e_{ikl}$$

Hatch week
-age

Permanent
Environment

Variance components





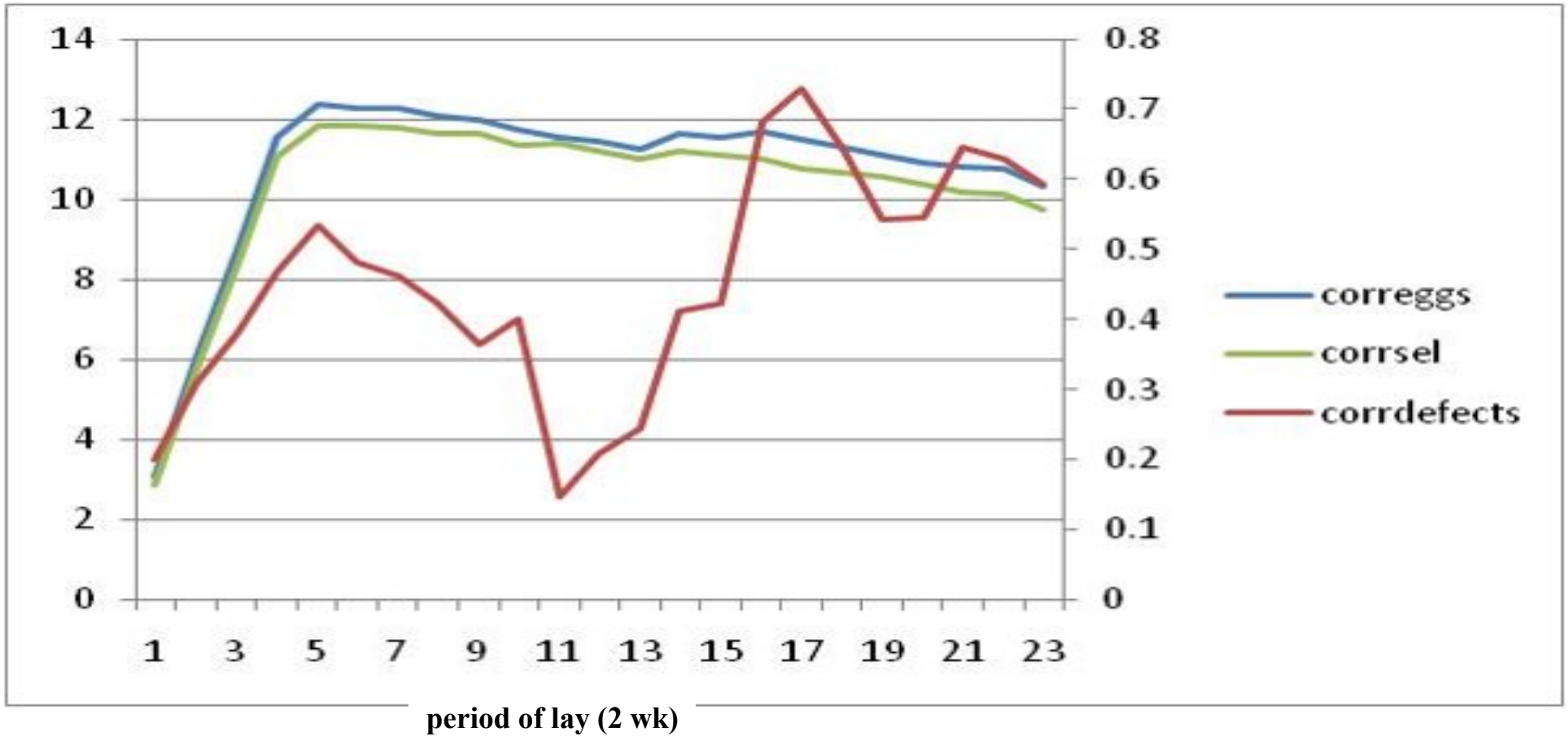
- ▀ **Linear polynomial for genetic component gave a good description of the data in all 3 lines**
- ▀ **Similar shape of variance components to higher order polynomials**
- ▀ **Interpretable parameters**
- ▀ **We can keep it simple!**

Study 2

Dynamics of genetic correlations

- ▀ **Egg number and egg defects**
- ▀ **13,475 animals**
- ▀ **6 generations**
- ▀ **137,998 biweekly records**

Genetic correlation between egg number and number of defects is **0.061**



Biweekly
egg
production

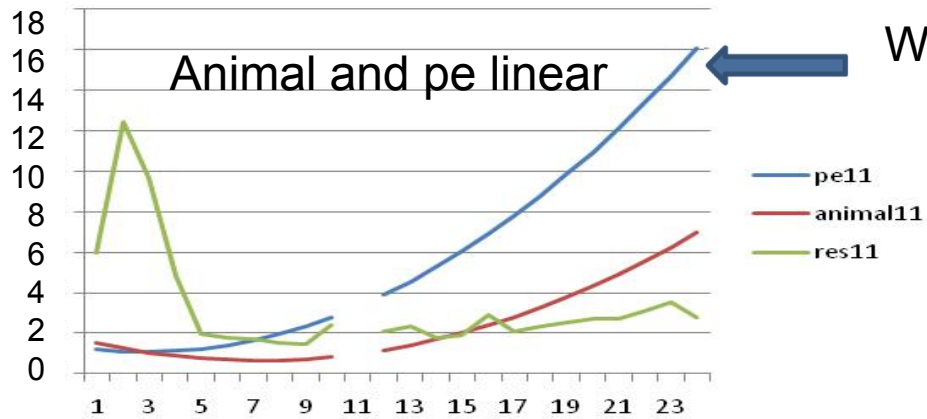
Additive
genetic
effects

Residual

$$y_{ijkn} = hatchgen_i * \sum_{m=1}^5 b_m z_{mn} + \sum_{m=0}^{m_1} a_{jkm} z_{mn} + \sum_{m=0}^{m_2} p_{jm} z_{mn} + e_{ijkn}$$

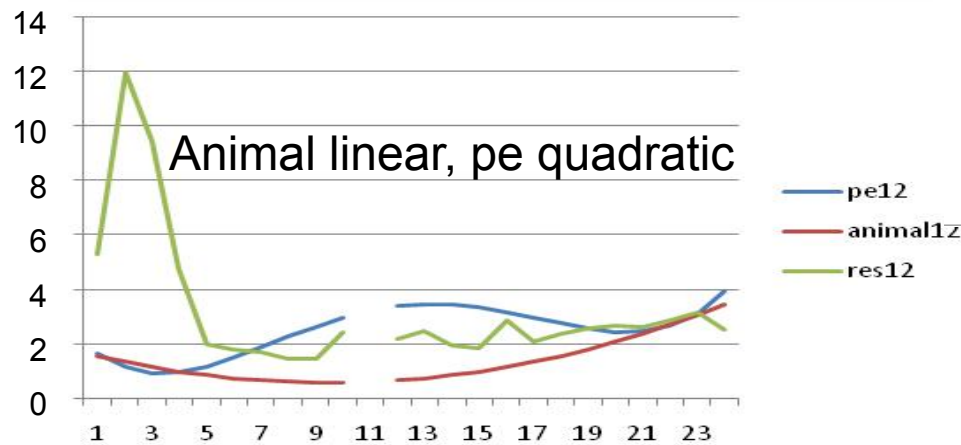
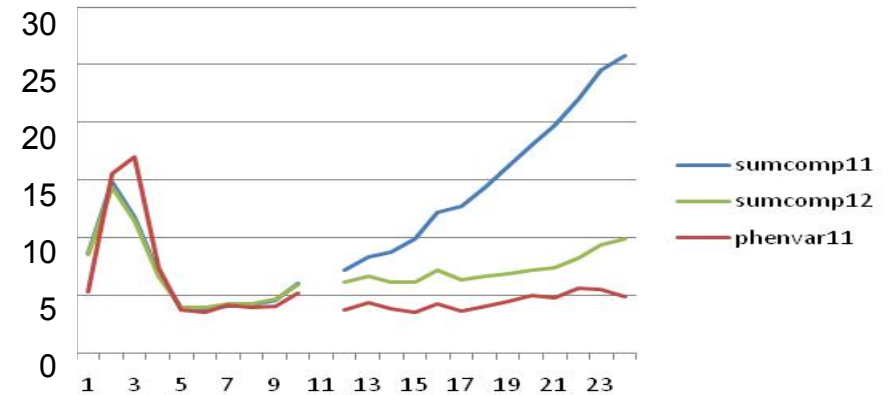
Hatch week
-age

Permanent
Environment



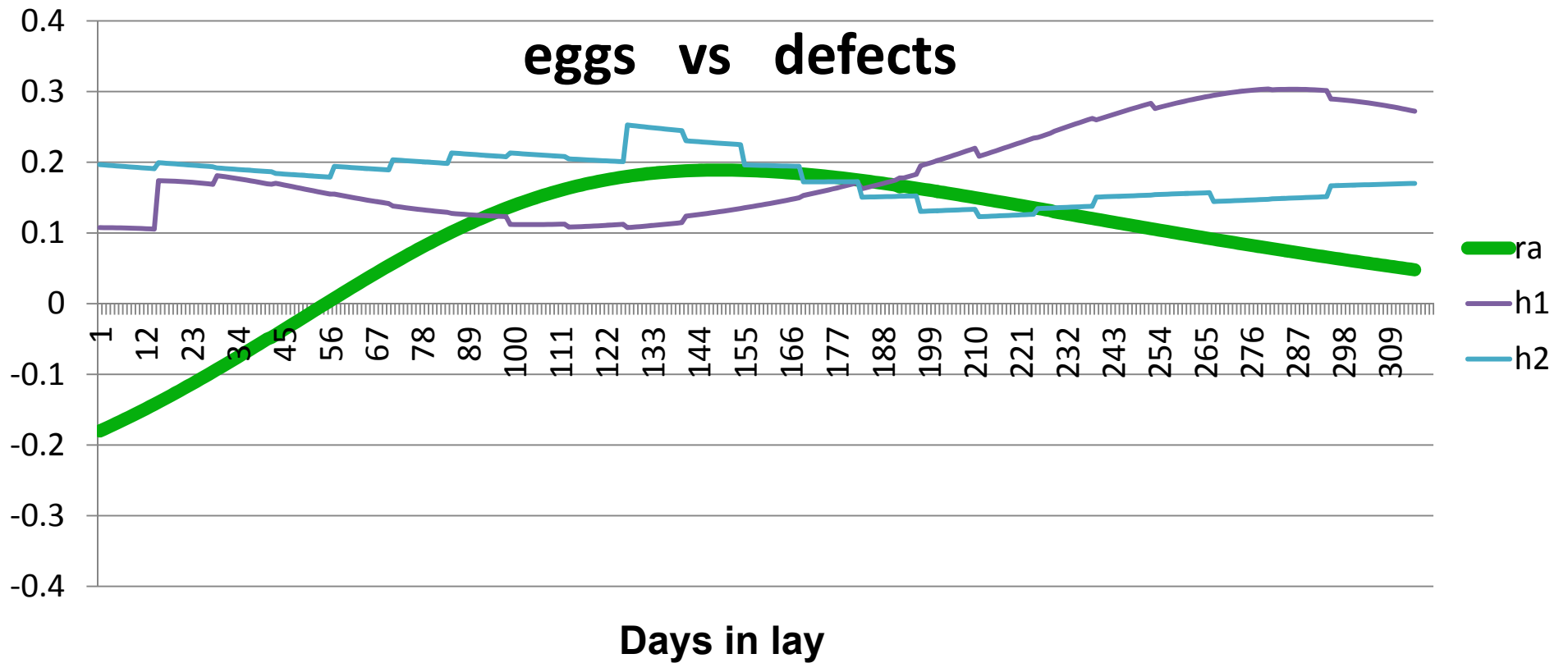
Way too high

Sum of variance components was overall phenotypic variance



Based on these pictures we went for animal linear and quadratic pe

$R_g=0.061$



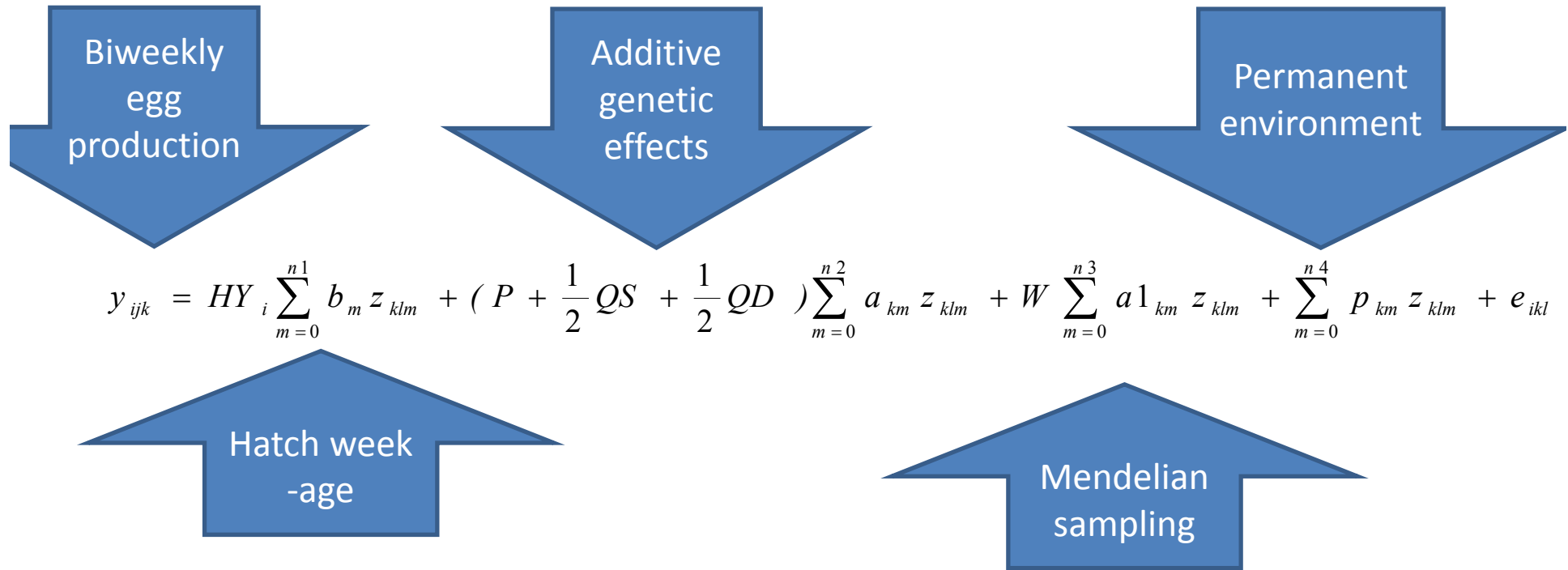
- ▮ **Life is more complicated than linear**
- ▮ **Genetic correlations change over time**

Study 3

Adding genomics to the picture

- ▀ **Estimate variance components using genomic relationship information**
- ▀ **Evaluate predictive ability of random regression reduced animal model with genomic relationships**

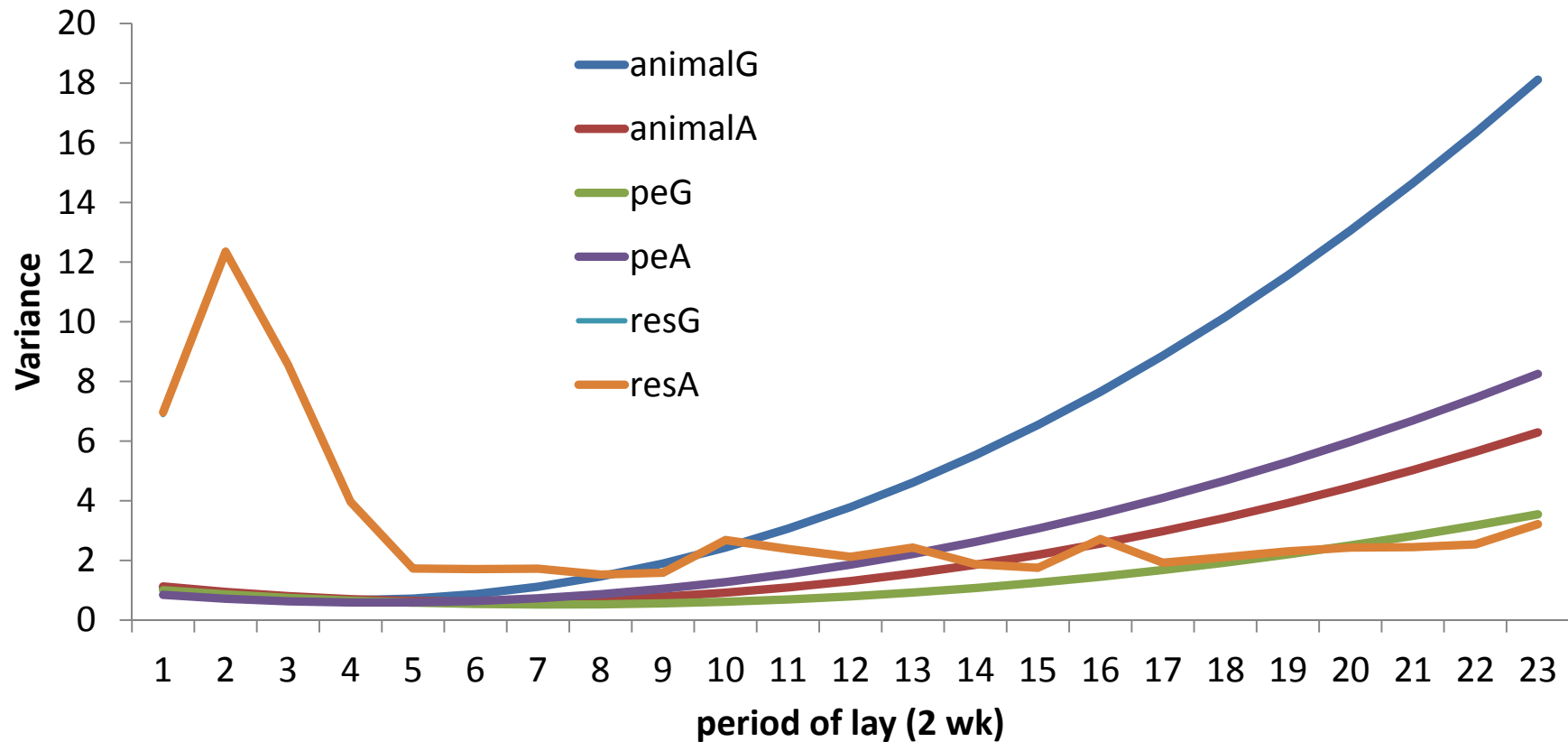
- ▲ Brown egg-layer line, 5 generations**
- ▲ 24,430 segregating SNPs**
- ▲ Data**
 - ▲ daily egg production up to 46 weeks in lay accumulated into 85,462 biweekly records
 - ▲ 17,570 records on genotyped hens
 - ▲ other records on their non-genotyped progeny
- ▲ Validation on 288 genotyped and phenotyped individuals from generation 6 with 5,787 biweekly records**



n1=5, n2 to n4=1 or 2

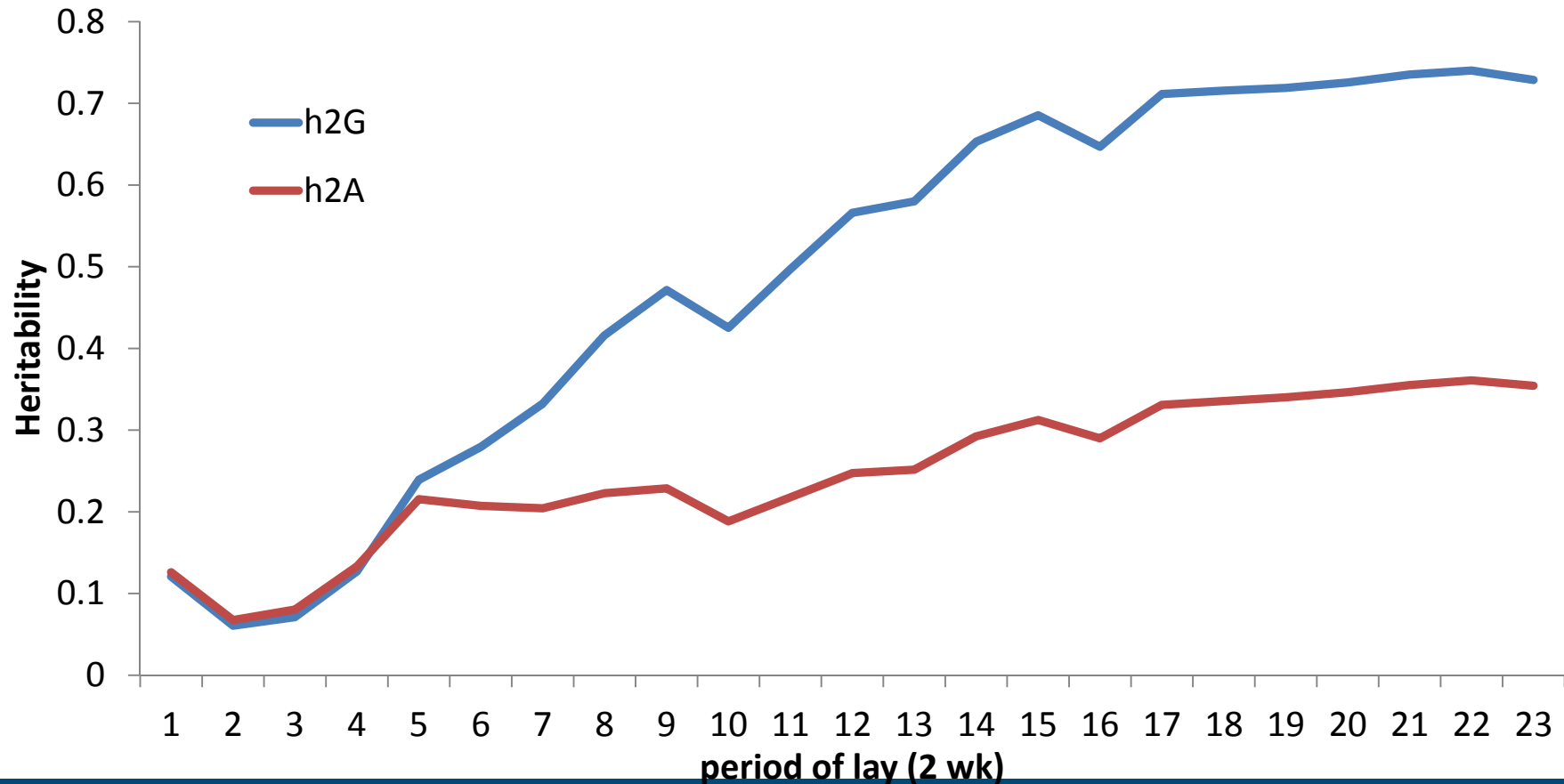


Variance components with linear regression for additive and permanent environmental effects



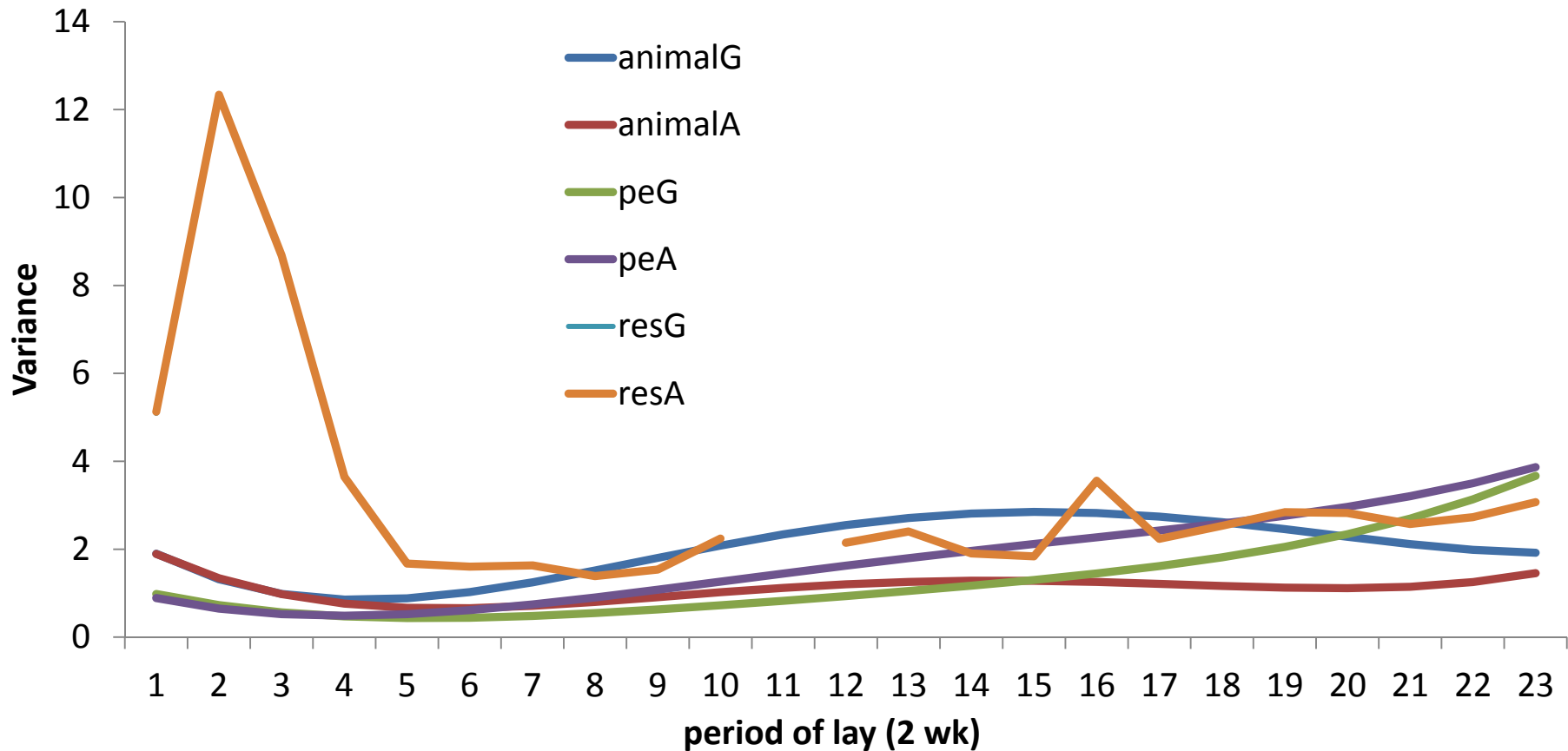


Heritability with linear regression for additive and permanent environmental effects





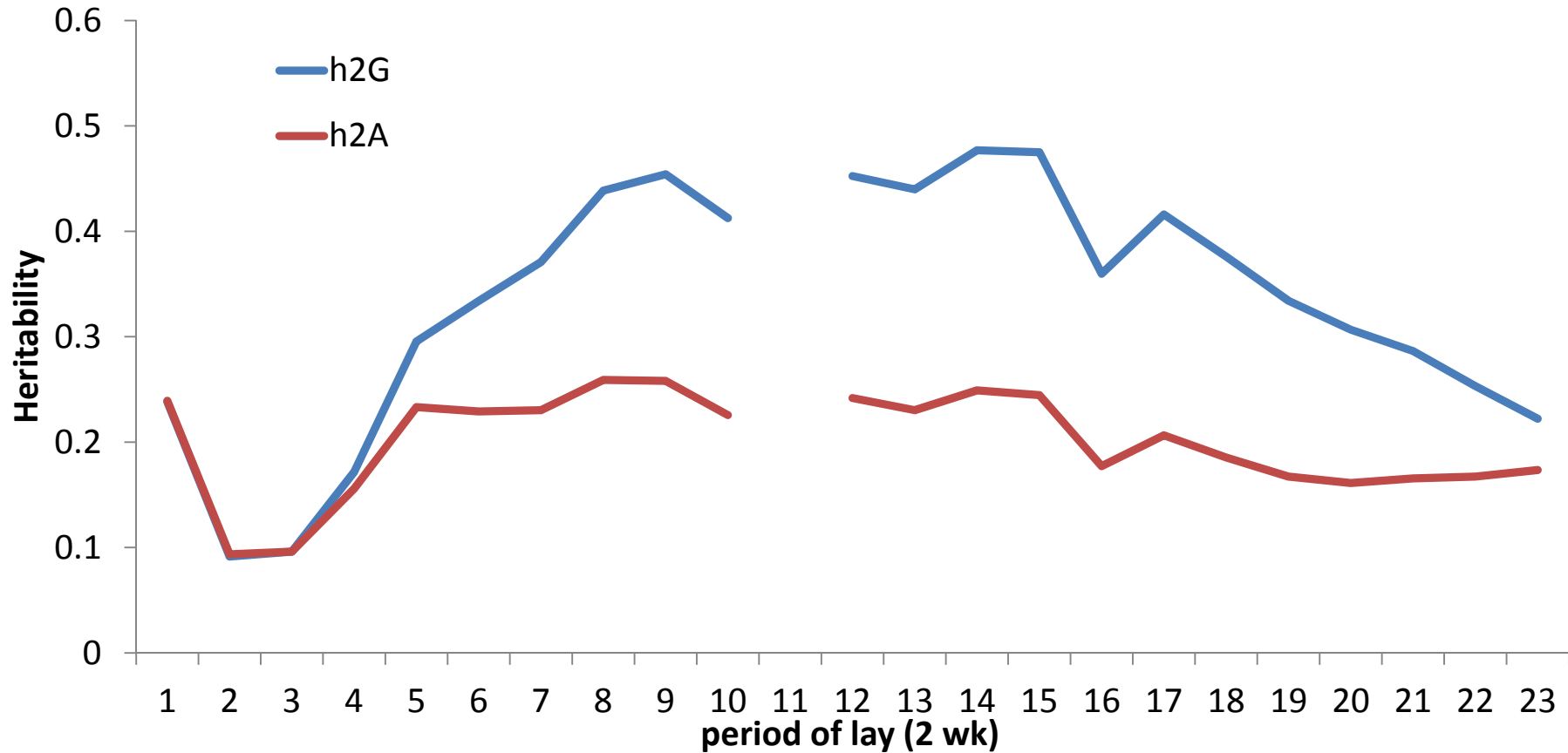
Variance components with quadratic regression for additive and permanent environmental effects





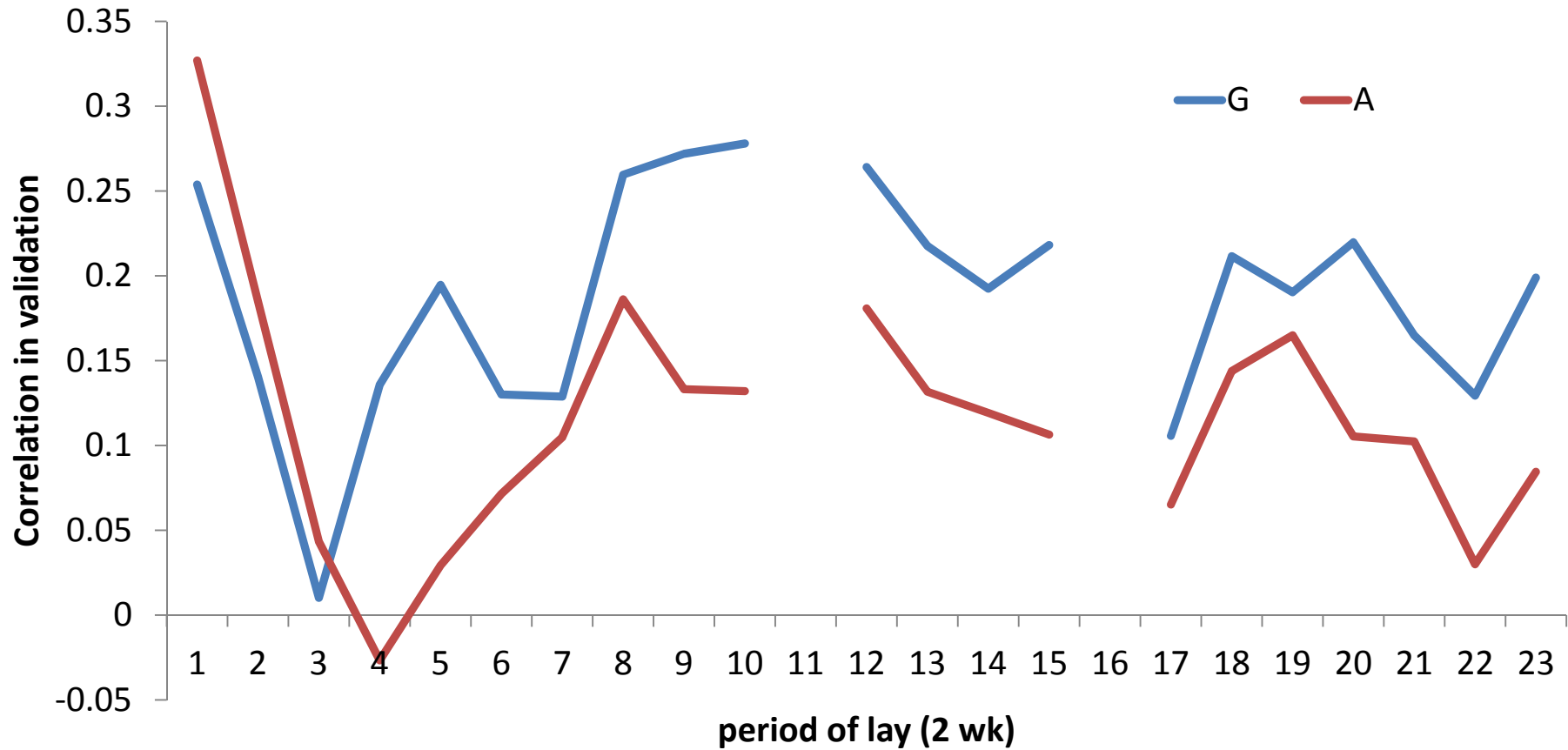
Hy-Line

Heritability with quadratic regression for additive and permanent environmental effects





Accuracy with quadratic regression for additive and permanent environmental effects



- ▀ Prediction of total egg number was more accurate with genomic than with pedigree relationships (0.26 vs. 0.16)
- ▀ Random Regression Models can be used for evaluation of egg production
- ▀ No one model fits all traits
- ▀ Variance components change over time
- ▀ Genetic correlations are dynamic

- **RRM can be utilized in breeding programs using genomic information**
- **Practical implementation will depend upon reducing computing and genotyping costs; both of which are reducing at a breathtaking rate**



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