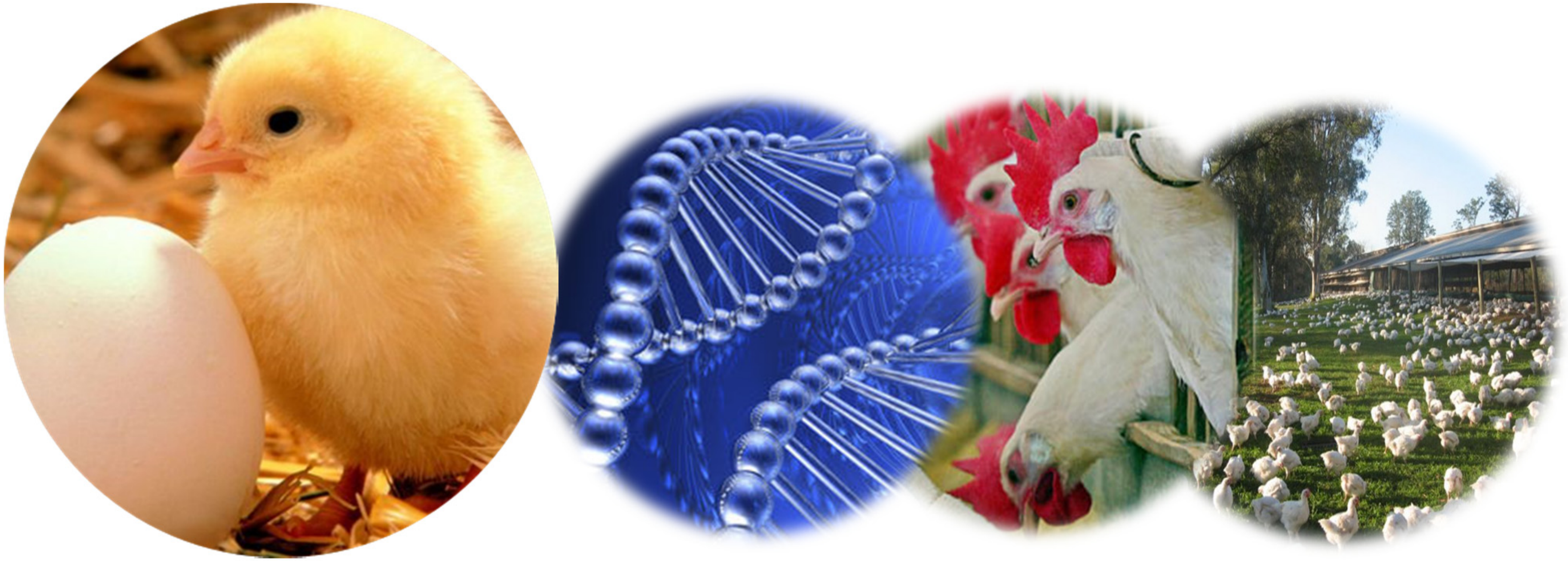
Sire-based genomic prediction of heterosis in White Leghorn crossbreds

EN Amuzu-Aweh

H Bovenhuis, D-J de Koning and P Bijma



WAGENINGEN UR For quality of life

SLU SVERIGES LANTBRUKSUNIVERSITET

European Commission ERASMUS MUNDUS

EGS ABG

ISA A Hendrix Genetics Company

BREED4FOOD

- Heterosis is an essential element of crossbreeding schemes

- Which parental lines should be mated to maximize benefits from heterosis?

- Can we predict heterosis?
  - long history with inconsistent results
  - based on limited number of markers/small data sets

Prediction of heterosis with 60K SNPs:

- $\frac{\sum_{n=1}^{N}\left(p_i - p_j\right)^2}{N}$ predicts heterosis with an accuracy of 0.5

  (Amuzu-Aweh et al., 2013)

- We are able to identify suitable pure-line combinations

  Exploit line-level heterosis

  Reduce dependency on field trials of crossbreds

p_i = allele frequency in sire line, p_j = allele frequency in dam line

WAGENINGEN UR
For quality of life

Research question

Can we exploit heterosis at the sire level?

- Utilise the variation between sires from the same pure-line
- Benefit more from heterosis

Derive equation to predict heterosis

- Assumptions:

  Heterosis is due to dominance deviations *(d)*

  d at each locus is independent of the allele frequency

$$Heterosis = \boxed{\left[(p_i - p_j)^2\right.} + \boxed{\left.(p_{s_i} - p_i)(1-2p_j)\right]} \bullet d$$

- Heterosis is a function of heterozygosity excess due to between- and within-line differences in allele frequencies

p_i = allele frequency in sire line , p_{si} = allele frequency in the sire
p_j = allele frequency in dam line

Data:

- ~3 450 sires from 4 lines genotyped at 60K SNPs
- 6 dam lines with known allele frequencies
- Phenotypic records from 16 crosses

    35 000 egg number records (EN)

    26 000 egg weight records (EW)

Model:

$$y_{s_i j} = \mathrm{sire\_line_i} + \mathrm{dam\_line_j} + \beta \boxed{\bar{x}_{s_i j}} + \ldots + e_{s_i j}$$

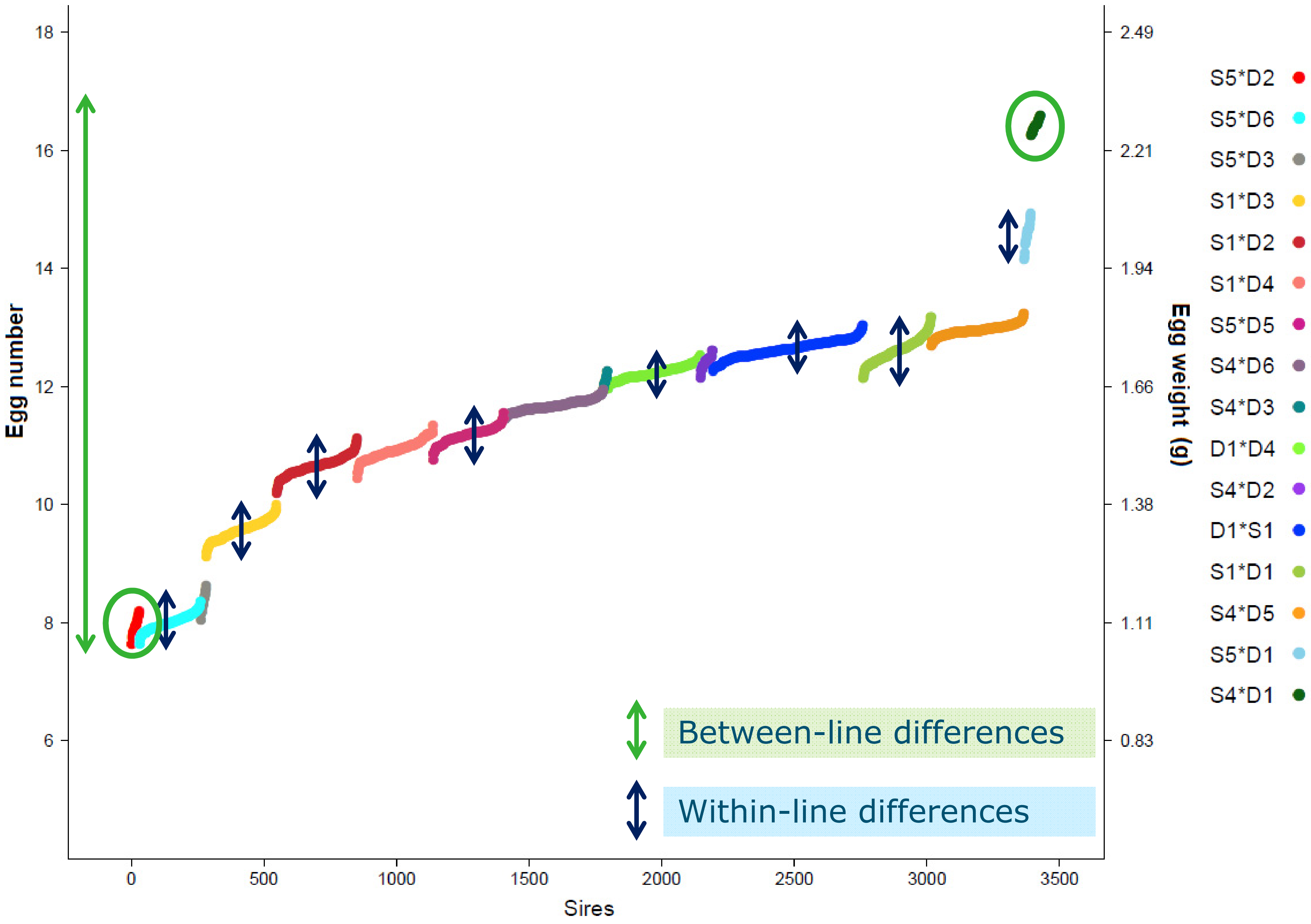
$$\bar{x}_{s_i j} = \frac{\sum_{n=1}^{N} \left[(p_i - p_j)^2 + (p_{s_i} - p_i)(1 - 2p_j) \right]}{N}$$

Results

- $\overline{x}_{s_i j}$ ranged from 0.08 to 0.18
- $\hat{\beta}_{EN} = 93.5$ (s.e = 18.3)
- $\hat{\beta}_{EW} = 12.9$ (s.e = 2.7)

$$\text{Predicted heterosis}_{\text{trait}, s_i j} = \hat{\beta}_{\text{trait}} \cdot \overline{x}_{s_i j}$$

Predicted heterosis for Egg number and Egg weight



Between-line differences

Within-line differences

Variance explained by components of $\boldsymbol{x}$

$$x_{s_i j} = \left[(p_i - p_j)^2 + (p_{s_i j} - p_i)(1 - 2p_j)\right]$$

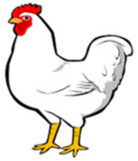
- Between-line accounted for 99.00%
- Within-line accounted for 0.72%

Individual sire information did not explain much

Variance explained by components of x

- Regression on the between- and within-line components

	Egg number			Egg weight		
	Estimate	Se	p-value	Estimate	se	p-value
Full x						
β	93.5	18.3	3.4 E-7	12.9	2.7	1.1 E-6
Components						
β_1	92.5	19.3	2.2 E-6	12.9	2.8	4.7 E-7



Ongoing…

Single SNP regression on $x_{s_i j}$

- Identified ~12K SNPs significant for predicting heterosis
- Larger variance between sires
- Bigger values of predicted heterosis

Conclusions

- Heterosis can be predicted at the sire level
- Within-line sire variance contributes little to heterosis
- However, if sire genotypes are available, variance can be exploited
- Method may work better if genomic regions affecting heterosis are identified

Thanks for your attention

Acknowledgements:

WAGENINGEN UNIVERSITY
WAGENINGEN UR
Animal Breeding & Genomics Centre

SVERIGES LANTBRUKSUNIVERSITET
SLU

European Commission
ERASMUS MUNDUS

EGS
ABG

ISA
A Hendrix Genetics Company

HENDRIX GENETICS

BREEDFOOD

Conclusions

- Heterosis can be predicted at the sire level
- Within-line sire variance contributes little to heterosis
- However, if sire genotypes are available, variance can be exploited
- Method may work better if genomic regions affecting heterosis are identified