# Genomic prediction of heterosis for egg production traits in white Leghorn crosses

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# Heterosis

- Heterosis is an essential element of crossbreeding schemes

- Problem: selection of suitable parental lines

- Prediction has a long history with inconsistent results
    - limited number of markers/small data sets

# Aim

Does genome-wide difference in allele frequency

between pure lines

predict heterosis in white Leghorns?

# Data

- 11 pure lines - genotype
- Allele frequency at 60K SNP loci
- 47 crosses - phenotype
- Egg number, egg weight, survival

# Theory

- Heterosis is proportional to the squared difference in allele frequency (SDAF) between the parental lines

$$\text{Heterosis}_{ij} = \sum_l d_l \boxed{(p_{i,l} - p_{j,l})^2}$$

$$\text{Heterosis}_{ij,l} = d_l (p_{i,l} - p_{j,l})^2$$

$d$ : dominance deviation

$P_{i,l}$ : allele frequency at locus $l$ in parental line $i$

$P_{j,l}$ : allele frequency at locus $l$ in parental line $j$

(Falconer & Mackay, 1996)

# Model

- Regress crossbred phenotypes on SDAF

$$\mathrm{y}_{\mathrm{ijklm}} = \mu + \mathrm{sire\text{-}line}_{\mathrm{i}} + \mathrm{dam\text{-}line}_{\mathrm{j}} + \beta \cdot \mathrm{SDAF}_{\mathrm{ij}} + \ldots + e_{ijklm}$$

$$\Rightarrow \hat{\beta}_{\mathrm{trait}}$$

$$\text{Predicted heterosis}_{\mathrm{trait,\,ij}} = \hat{\beta}_{\mathrm{trait}} \times \mathrm{SDAF}_{\mathrm{ij}}$$

- Observed heterosis *($y^{\#}$)*:crossbred phenotypes corrected for parental means

# Accuracy of prediction

- Correlation between observed and predicted heterosis
- Cross-validation
  - Predict heterosis for crosses left out of the estimation of $\beta$
  - Leave-one-out strategy

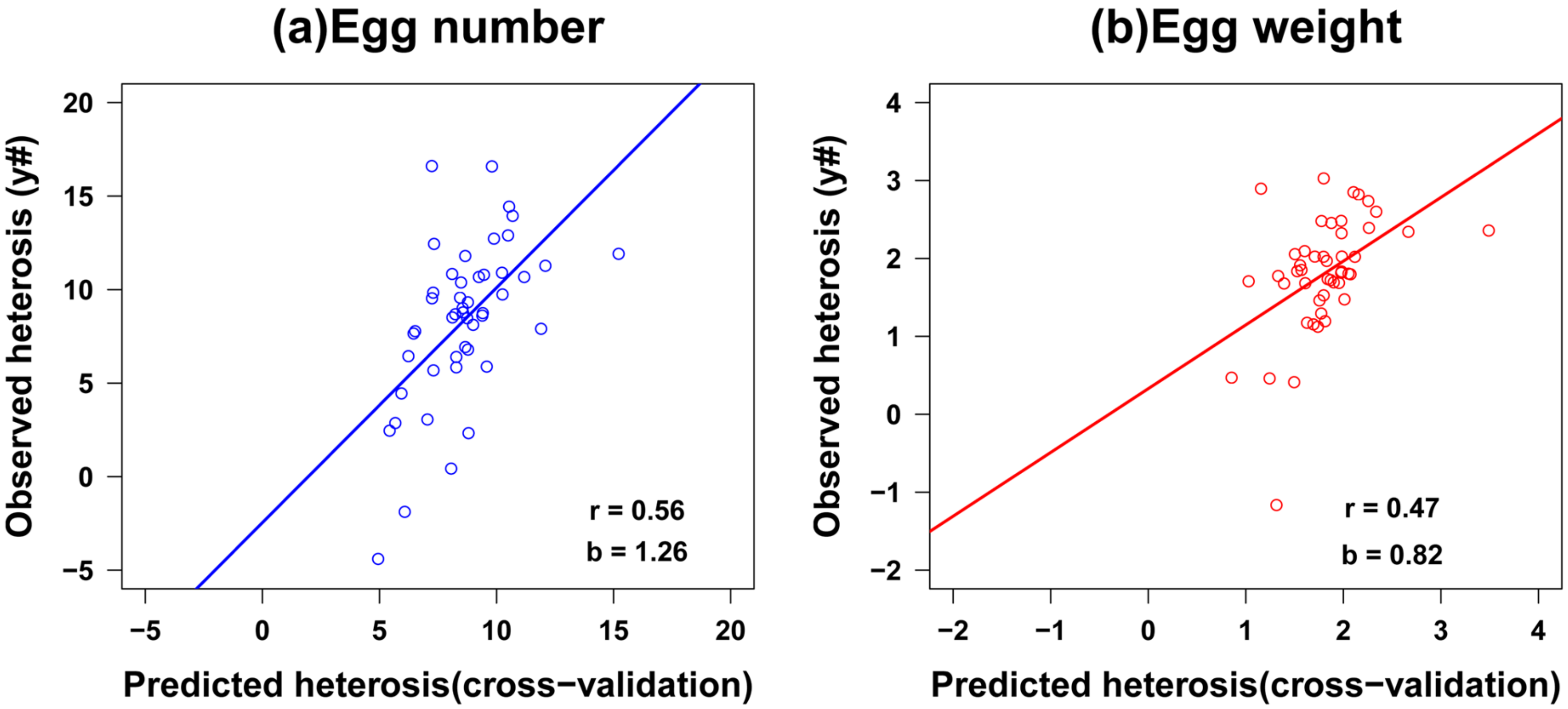
# Estimated heterosis due to SDAF

| **Trait** | $\widehat{\beta}$ | **se($\widehat{\beta}$)** | **p value** |
|---|---|---|---|
| Egg number | 103.5 | 16.8 | >0.001 |
| Egg weight | 22.3 | 2.2 | >0.001 |
| Survival days | -42.1 | 25.9 | 0.10 |

SDAF explains heterosis:

- Egg number: 5.2 – 11.7 eggs
- Egg weight: 1.1 – 2.5g

# Cross validation



# Heterosis prediction

- SDAF predicts heterosis in egg traits with an accuracy of ~0.5

- SDAF did not predict heterosis in survival days
    - limited variation in survival days

# Benefits of predicting heterosis

- Two-step selection

    1. Select a subset of crosses based on predicted heterosis

    2. Field-test only selected crosses

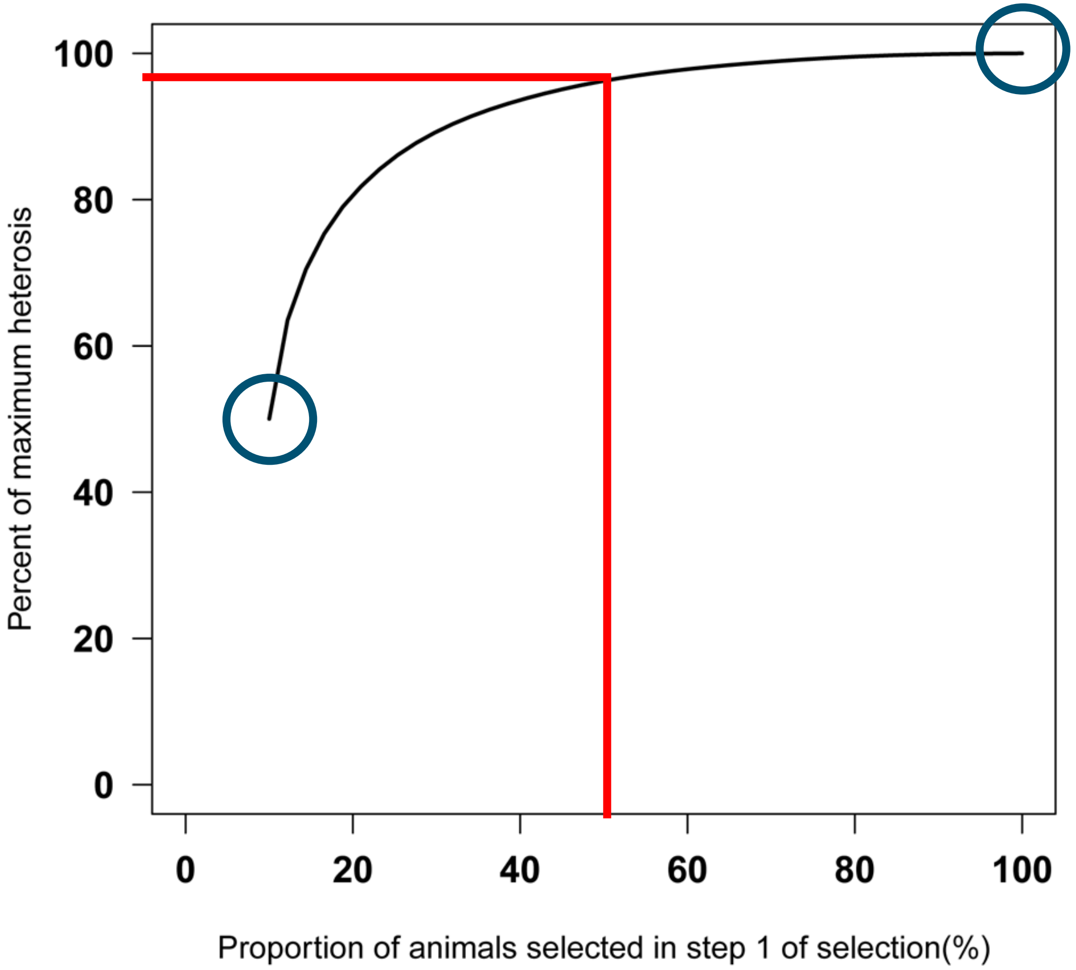
# Benefits of predicting heterosis

- Two-step selection:

$\rho_{\text{pred heterosis}} = 0.5$

Final selected prop =10%

96% of total heterosis



# Observed heterosis

- Crossbred phenotypes corrected for sire-line, dam-line and systematic effects

$$y_{ijklm} = \mu + \text{sire-line}_i + \text{dam-line}_j + \boxed{\beta \cdot \text{SDAF}_{ij}} + \ldots + e_{ijklm}$$

$\text{sire-}\hat{\text{l}}\text{ine}_i$ $\quad$ $\text{dam-}\hat{\text{l}}\text{ine}_j$ = pure-line means

- SDAF partitions crossbred phenotypes into pure line means and heterosis

# Conclusions

- The squared difference in allele frequency predicts heterosis ($\rho$= ~ 0.5)

- Reduce field tests by 50% with only 4% loss in heterosis

- Heterosis can be predicted even without pure-line phenotypes


Thankyou

- The squared difference in allele frequency predicts heterosis

- Reduce field tests by 50% with only 4% loss in heterosis

- Heterosis can be predicted even without pure-line phenotypes

See Amuzu-Aweh et al 2013 (Heredity, in press)

# SDAF between lines

| | S1 | S2 | S3 | S4 | S5 | D1 | D2 | D3 | D4 | D5 | D6 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| S1 | | 0.004 | 0.095 | **0.094** | **0.082** | **0.089** | **0.082** | **0.072** | **0.085** | **0.082** | **0.073** |
| S2 | | | 0.094 | 0.094 | 0.080 | **0.085** | **0.080** | **0.070** | **0.083** | 0.079 | **0.071** |
| S3 | | | | 0.105 | 0.099 | **0.112** | **0.095** | **0.091** | **0.098** | **0.101** | **0.090** |
| S4 | | | | | 0.085 | **0.113** | **0.092** | **0.089** | 0.089 | **0.101** | **0.085** |
| S5 | | | | | | **0.103** | **0.056** | **0.060** | **0.058** | **0.089** | **0.057** |
| D1 | | | | | | | 0.096 | 0.078 | **0.096** | 0.048 | **0.068** |
| D2 | | | | | | | | 0.032 | 0.029 | 0.083 | 0.061 |
| D3 | | | | | | | | | 0.041 | 0.066 | 0.055 |
| D4 | | | | | | | | | | **0.081** | **0.060** |
| D5 | | | | | | | | | | | **0.050** |
| D6 | | | | | | | | | | | |

# Observed heterosis

- Crossbred phenotypes corrected for sire-line, dam-line and systematic effects

$$\mathrm{y}_{\mathrm{ijklm}} = \mu + \mathrm{sire\text{-}line}_{\mathrm{i}} + \mathrm{dam\text{-}line}_{\mathrm{j}} + \beta \cdot \mathrm{SDAF}_{\mathrm{ij}} + \ldots + e_{ijklm}$$

$$\mathrm{y}^{\#}{}_{\mathrm{ijklm}} = \mathrm{y}_{\mathrm{ijklm}} - \hat{\mu} - \mathrm{sire\text{-}}\hat{\mathrm{l}}\mathrm{ine}_{\mathrm{i}} - \mathrm{dam\text{-}}\hat{\mathrm{l}}\mathrm{ine}_{\mathrm{j}} - \ldots$$

$$\text{Observed heterosis}_{\mathrm{trait,ij}} = \overline{\mathrm{y}}^{\#}{}_{\mathrm{trait,\,ij}}$$

Done for each cross independently