

# Genetic Analysis of Feather Pecking and Mortality in Laying Hens



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- **About 8-10 % total mortality of birds until 80 weeks of age**
- **Minimizing bird losses is important**
  - **from an economical point of view**
  - **from the animal welfare point of view**
- **Mortality as a compound trait, is highly dependent on environmental conditions and also depends on social interactions with other birds**
- **A high level of feather pecking has been found to be correlated with high mortality from cannibalism**



- **Feather pecking is one of the most obvious welfare problems in laying hens**
- **Observed in all types of housing systems for commercial laying hens**
  - **Feather damage**
  - **Increase of food consumption for higher maintenance energy requirement**
  - **Skin injury and infection diseases**
  - **Mortality**



## Feather pecking

is a multifactorial problem caused by both genetic and environmental factors

### Genetics

- Breed and lines
- Layer vs. Broiler
- Selection for high egg production
- Early sexual maturity
- Low body weight

### Environments

- Group size
- Light intensity
- Diet and feed structure
- Type of litter
- Ambient temperature

# Goals

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- **The objective of this research work is to estimate genetic parameters of mortality and feather cover score**
- **Genome wide association study based on a Genome-Wide Chicken Array to identify SNPs and genes associated with aforementioned traits**



## Animals and husbandry

- **Brown layer hens kept under cage systems**
  - **3 different cage sizes**
  - **3 to 13 hens from one sire per cage**
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- **Number of hens: 32523**
  - **Number of sires: 538**
  - **Number of cages: 5337**



# Material and Methods



## Animals and husbandry



**Aggressor and victim in one family**



## Recording of phenotypic traits

- Feather pecking behaviour
  - *Plumage condition at the age of 45 and 70 weeks*
    - *Feather score: 1 (low plumage quality) to 9 (high plumage quality)*
- Mortality
  - *Cumulative until 45 weeks of age (%)*
  - *and from 46 to 70 weeks of age (%)*
- Performance traits
  - *Egg performance (g/d) at the age of 45 and 70 weeks*







## Bivariate analysis using sire model for estimation of genetic parameters

$$y_{ijklmn} = \varphi + \alpha_i + \alpha\beta_{ij} + \lambda_k + \gamma_l + \rho_m + \varepsilon_{ijklmn}$$

$y$  = Plumage condition, Mortality

$\varphi$  = Overall mean effect

$\alpha_i$  = Fixed effect of poultry house

$\beta_j$  = Fixed effect of tier+site+lane

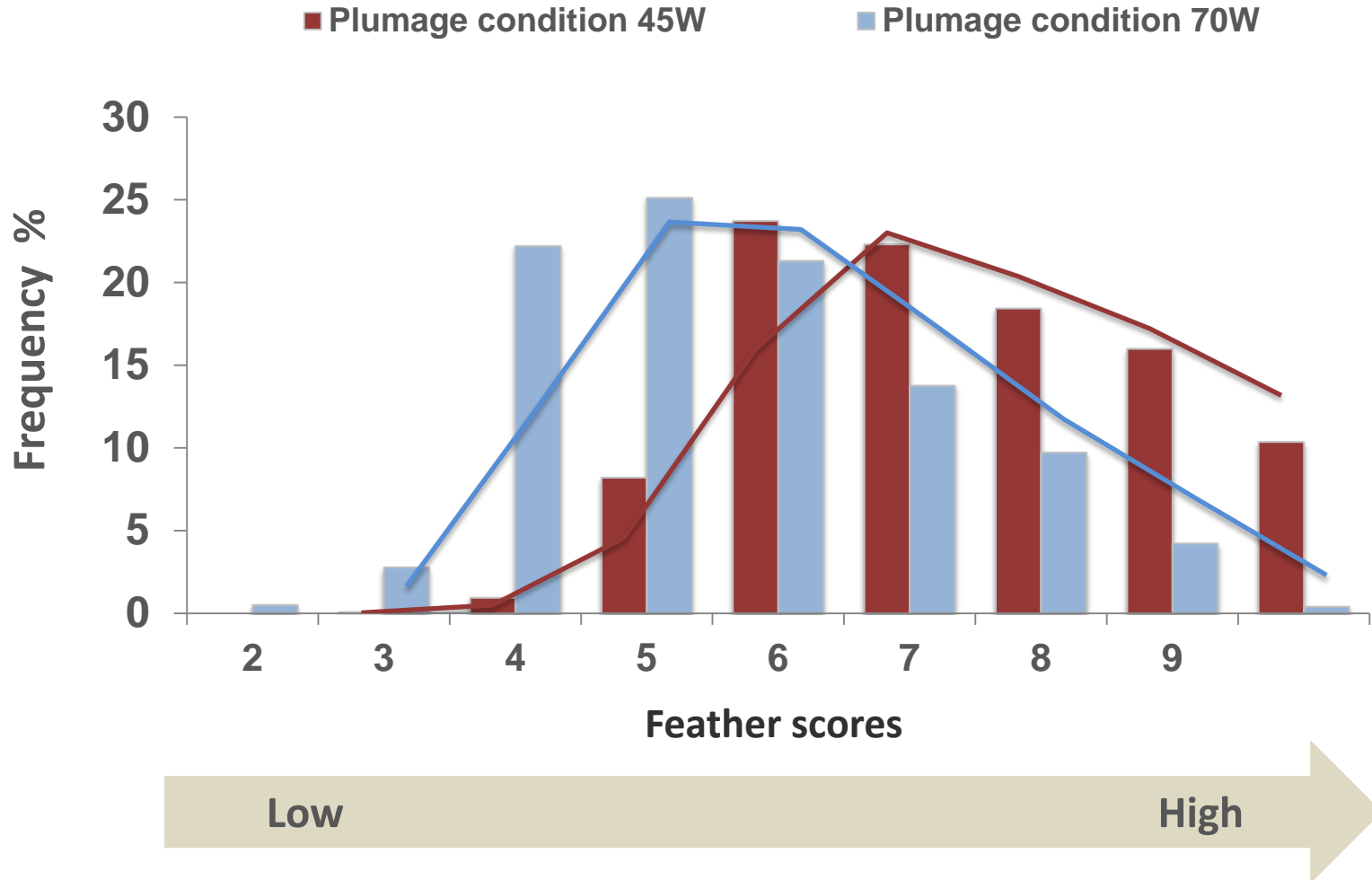
$\lambda_k$  = Fixed effect of breeding line

$\gamma_l$  = Random effect of sire

$\rho_m$  = Random effect of common environment

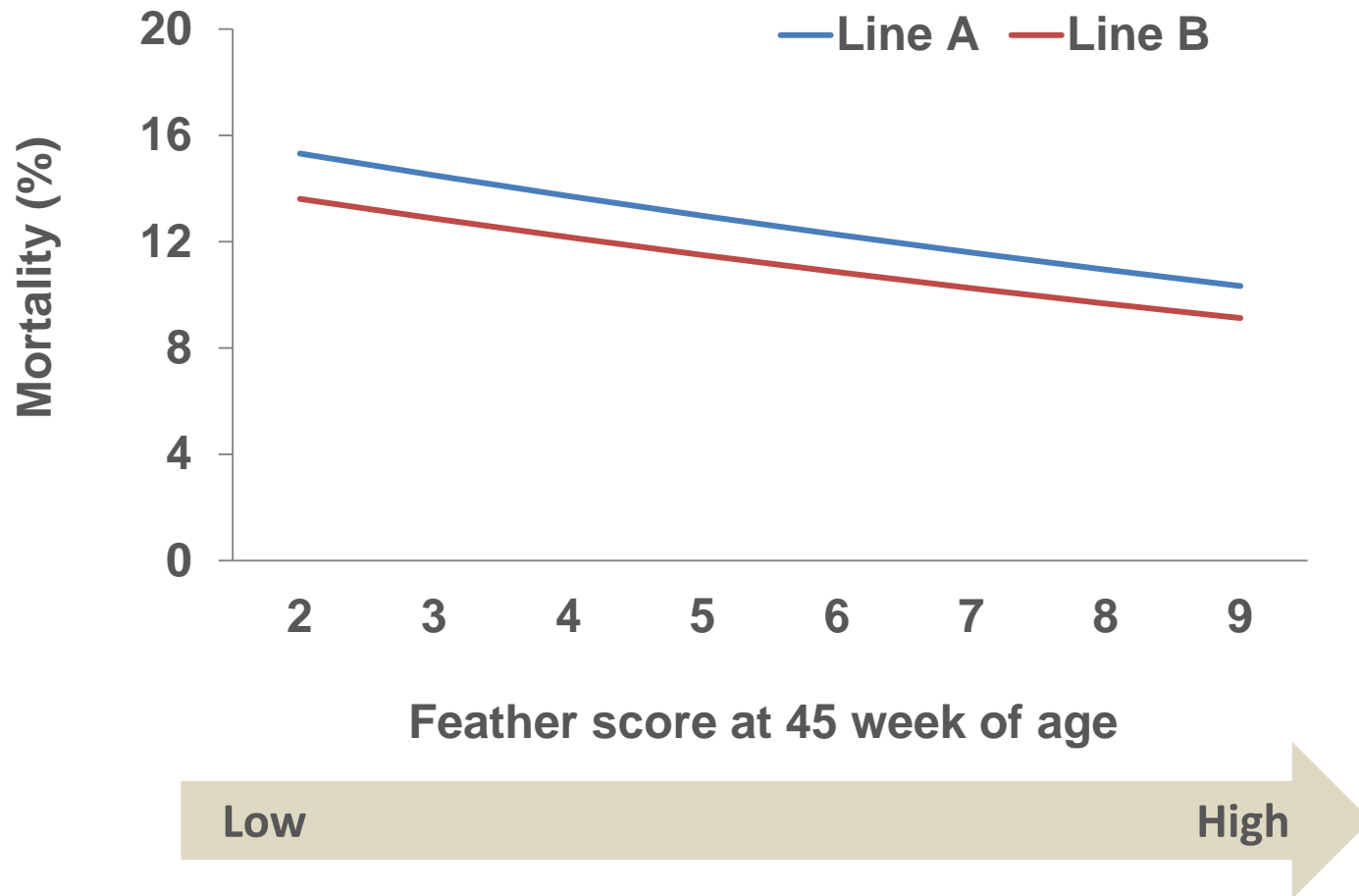
$\varepsilon_{ijklmn}$  = Is random residual effect

# Results



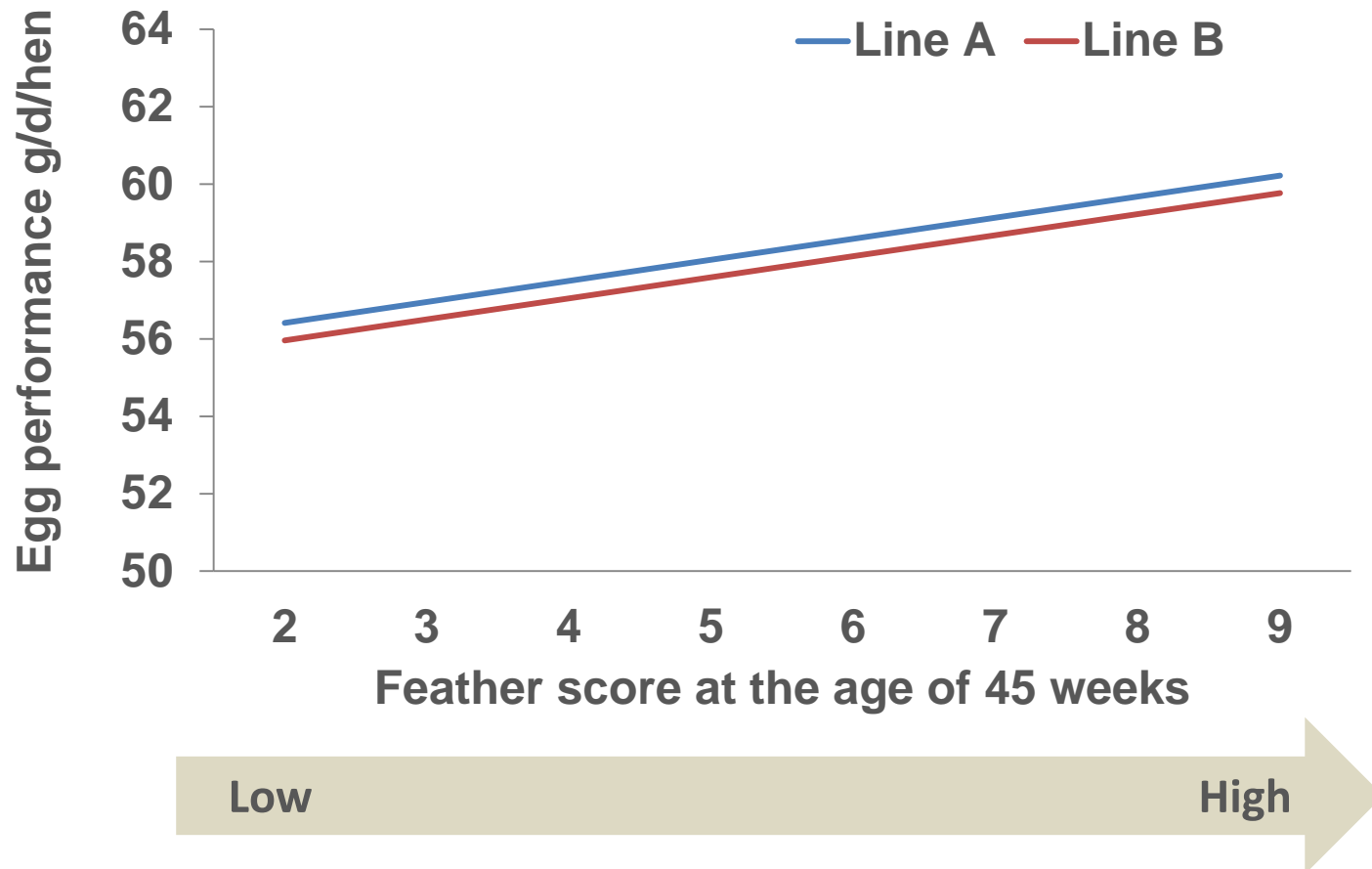


## The effect of Plumage condition on mortality



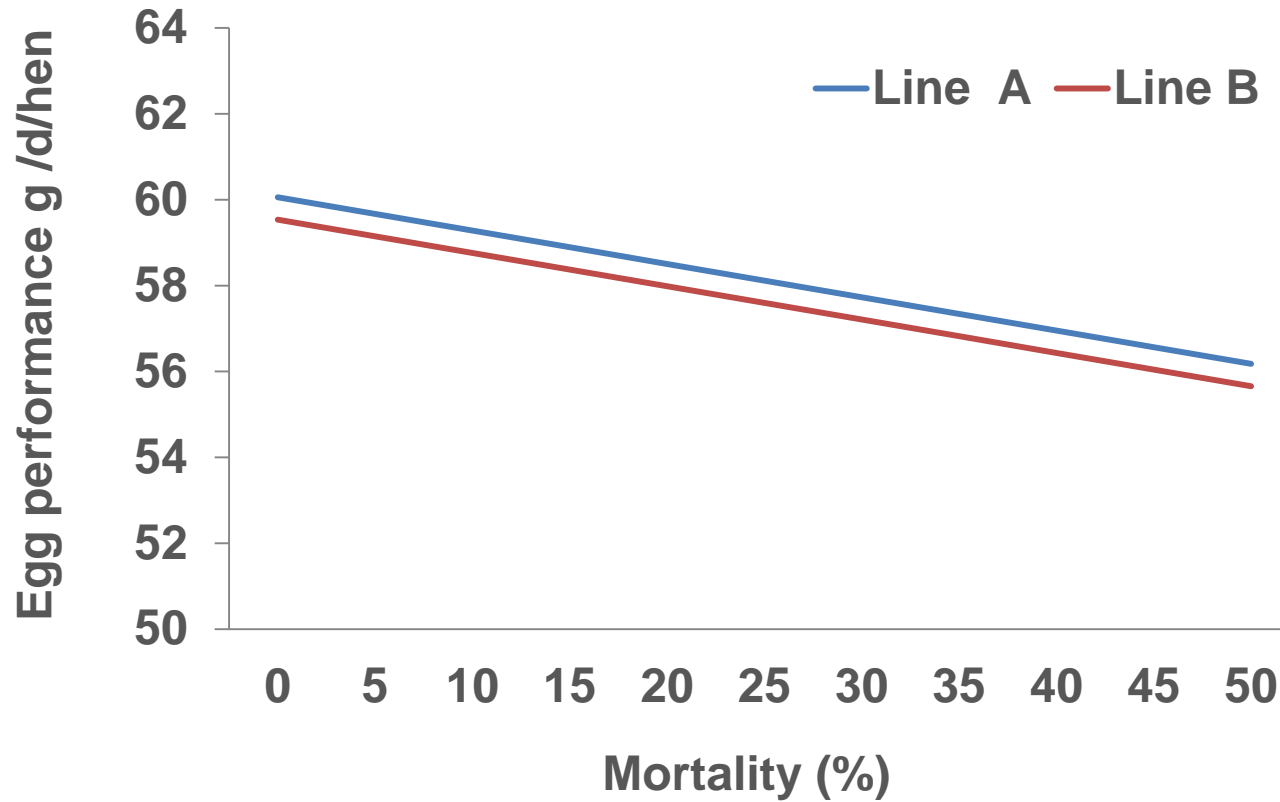


## The effect of feather score on egg performance





## The effect of mortality on egg performance





Estimation of genetic parameters for mortality and plumage condition at the age of 45 weeks using a bivariate analysis (sire model)

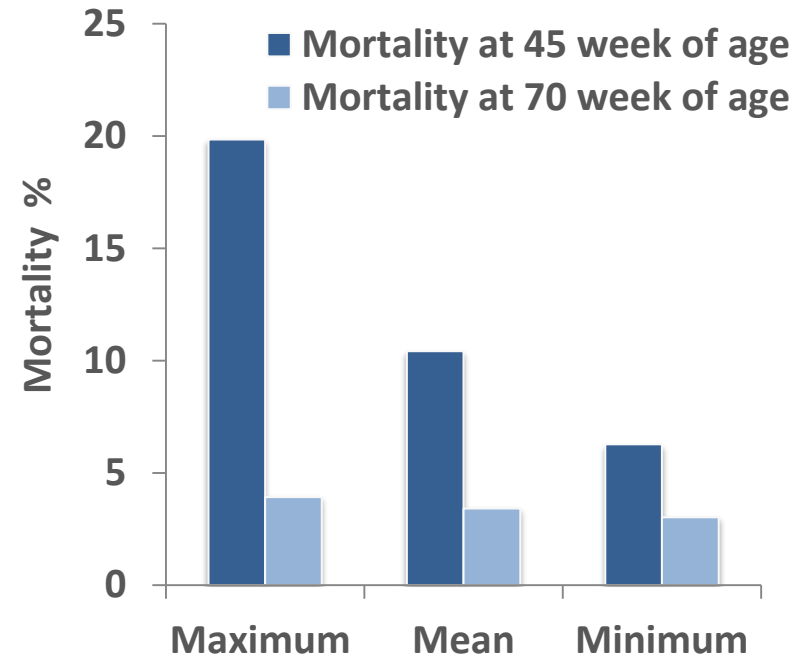
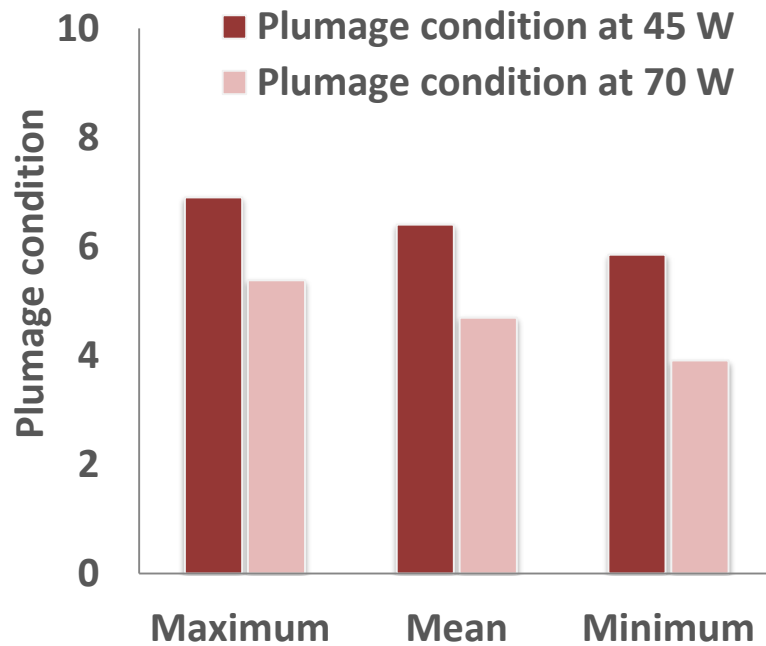
Traits	Mortality	Plumage condition
Mortality	0.20 (0.007)	-0.22 (0.156)
Plumage condition		0.29 (0.019)



Estimation of genetic parameters for mortality and plumage condition at the age of 70 weeks using a bivariate analysis (sire model)

Traits	Mortality	Plumage condition
Mortality	<b>0.019</b> <b>(0.004)</b>	<b>0.24</b> <b>(0.375)</b>
Plumage condition		<b>0.080</b> <b>(0.024)</b>

# Results



Mean, minimum and maximum of breeding values for mortality and feather score



## Further analyses

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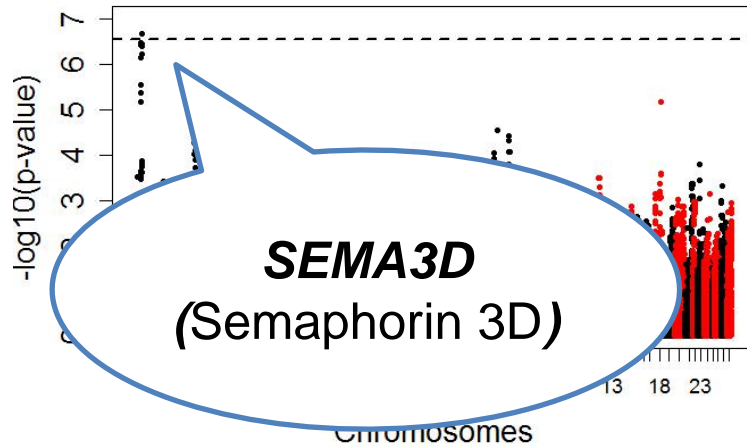
- **Based on the results (breeding values) from the bivariate analysis of mortality and feather score:**
  
- **Genome-wide association study**
  
- **Genomic data:**
  - 296 cocks genotyped with Affymetrix Axiom<sup>®</sup> Genome-Wide Chicken Array
  - ~ 335.000 SNPs on autosomal chromosomes after quality checks
  
- **Model : Single Marker Regression (with correction for stratification in the population)**

# Results

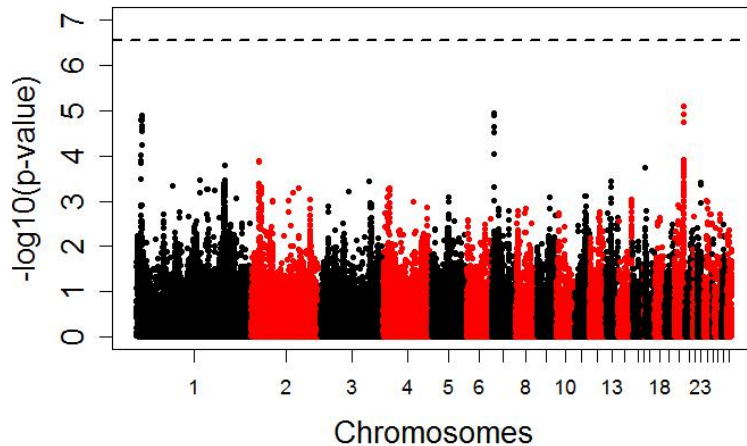


## Mortality

### SNPs in Gene Regions

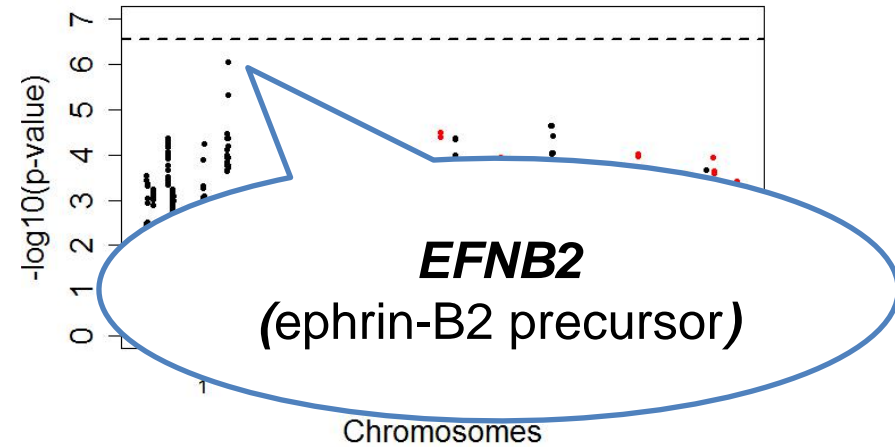


### SNPs outside Gene Regions

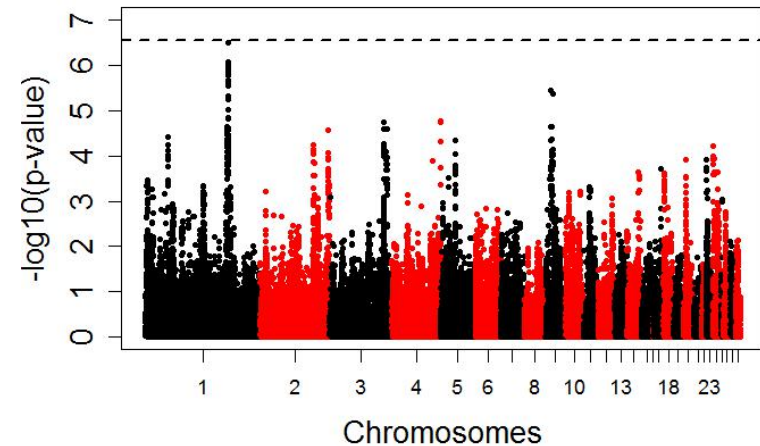


## Plumage condition

### SNPs in Gene Regions



### SNPs outside Gene Regions



# Conclusions

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- **Estimated heritabilities for mortality and plumage condition were low to moderate**
- **Selection for good plumage condition result in higher liveability and performance**
- **Even though the heritability is low, high reproductive performance and low generation interval in chicken make it feasible to select animals successfully for higher plumage condition (feather pecking) and survival ability**
- **GWAS resulted in the detection of two candidate genes SEMA3D and EFNB2**



Thank you very much  
for your attention





## Genome-wide association study

- **Data:**
  - 296 cocks genotyped with Affymetrix Axiom<sup>®</sup> Genome-Wide Chicken Array
  - ~ 335.000 SNPs on autosomal chromosomes after quality checks
  - Breeding values for mortality and feathering

- **Model :**           **Correction for stratification by including effects for principal components (70% variation explained)**

$$y = Xb + Wu + e$$

with

y = breeding values

X = design matrix for single marker regression

W = design matrix for fixed PC effects

b = vector with intercept and regression coefficient

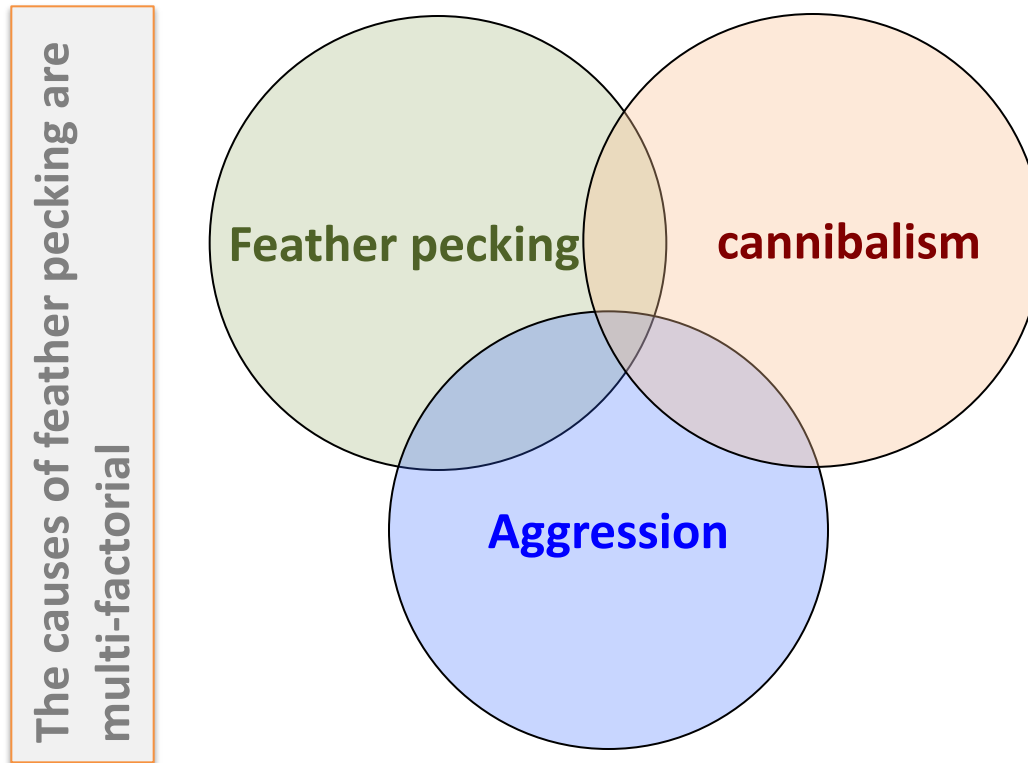
u = vector with fixed PC effects

e = vector of random residual effects with  $e \sim N(0, I\sigma_g^2)$

# Introduction



Feather pecking, cannibalism and aggression (AG) are supposed to have different motivational backgrounds

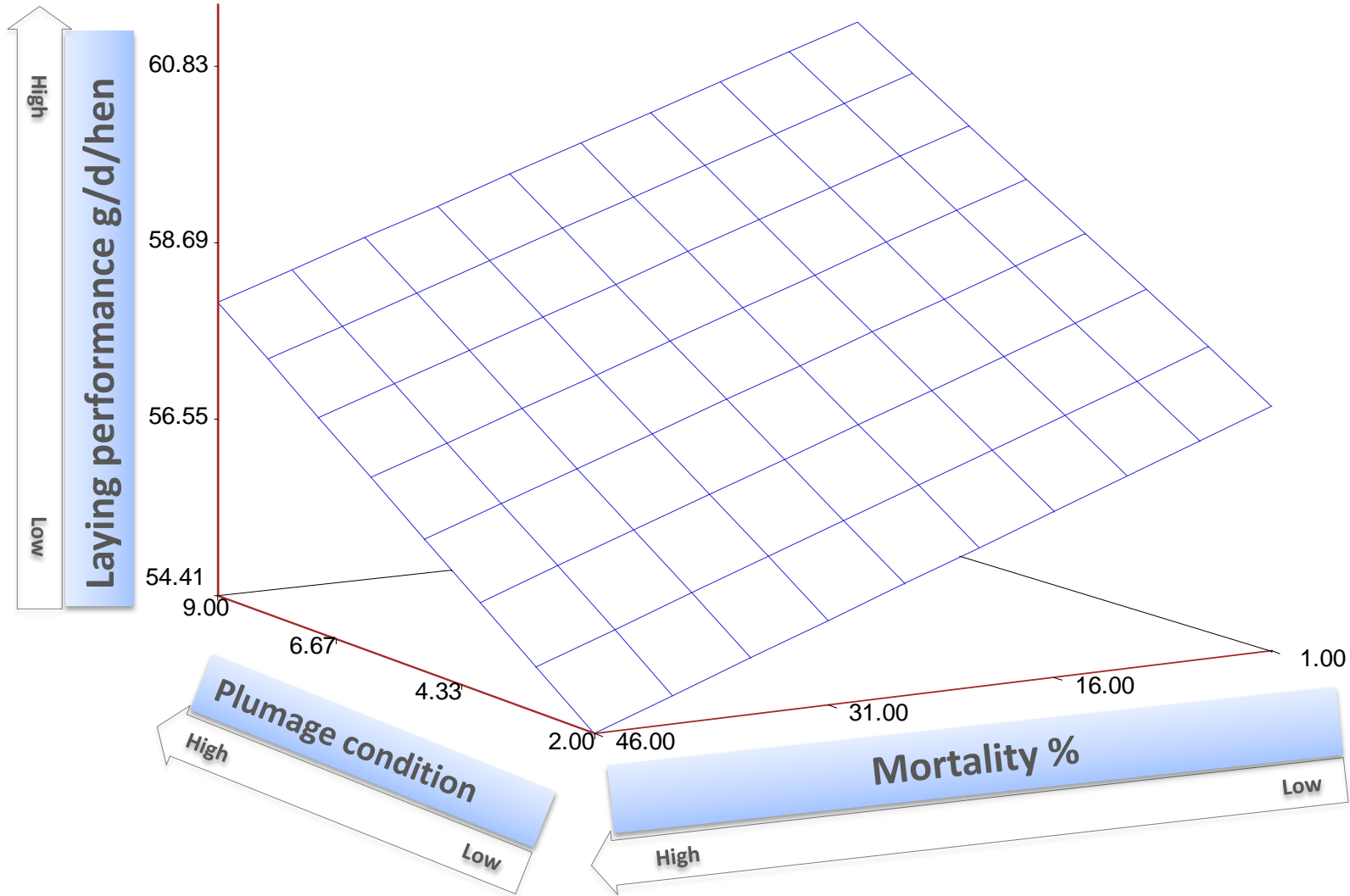


Nevertheless some interactions occur, where one behaviour leads to another, indicated by the overlapping areas.

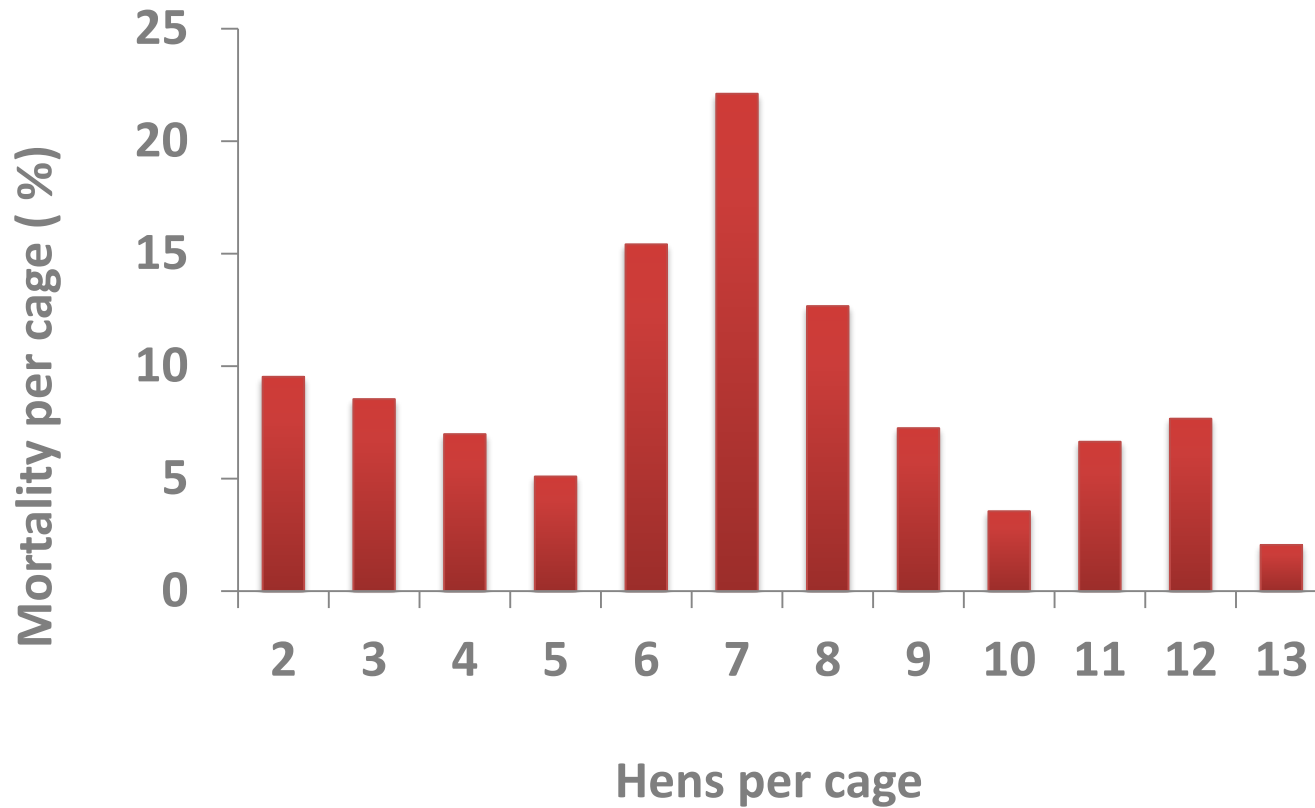
# Result



## The effect of Plumage condition on mortality and performance



# Result



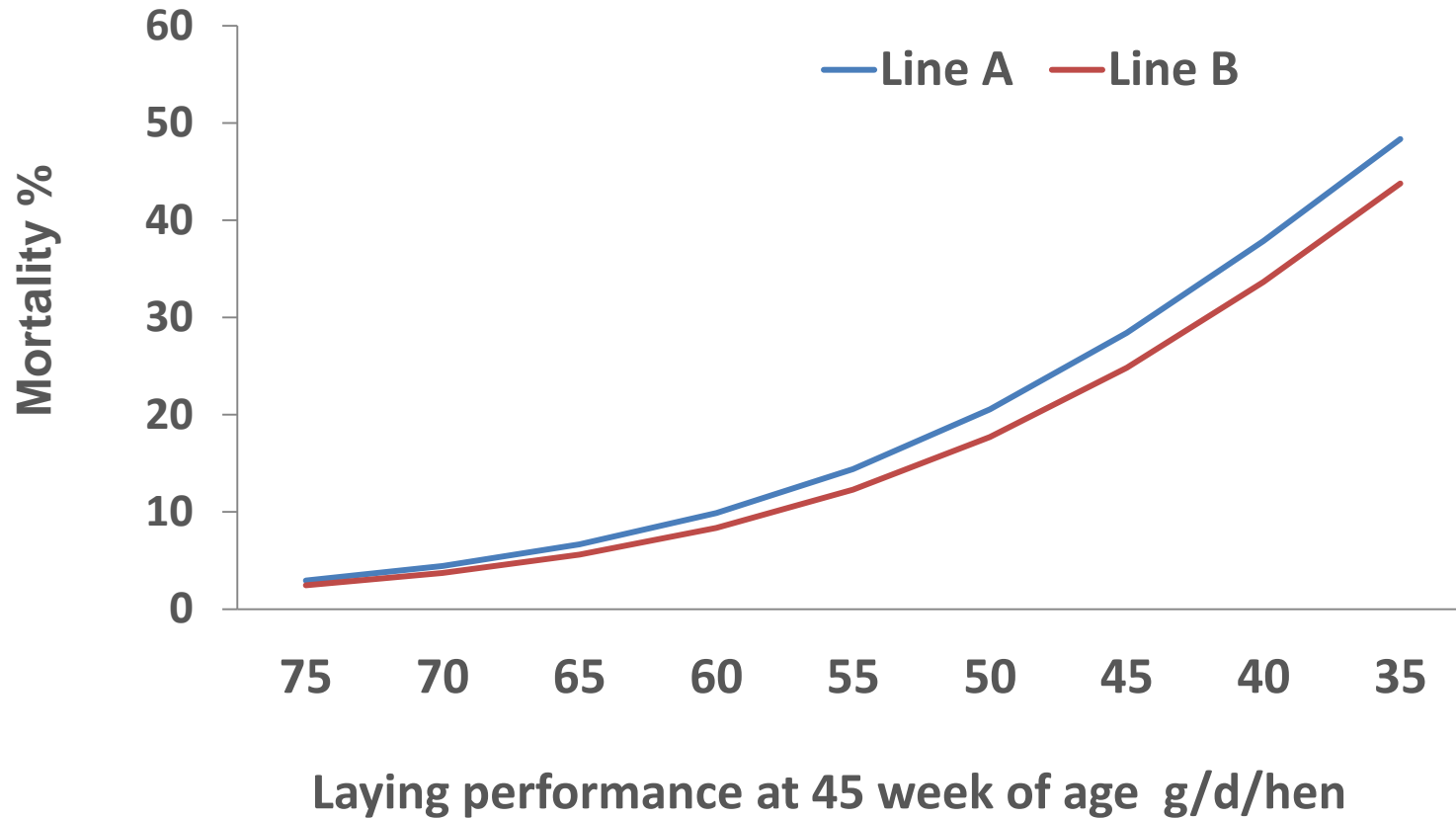
The effect of cage density on total morality



# Result



## The association between of laying performance and mortality





Estimation of genetic parameters for mortality ,  
plumage condition and egg performance at 45 week  
of age using a multivariate analysis (sire model)

Traits	Mortality	Plumage condition	Egg performance
Mortality	<b>0.15</b> <b>(0.007)</b>	<b>-0.2289</b>	<b>-0.127</b>
Plumage condition		<b>0.355</b> <b>(0.019)</b>	<b>0.125</b>
Egg performance			<b>0.2041</b>



Estimation of genetic parameters for mortality ,  
plumage condition and egg performance at 70 week  
of age using a multivariate analysis (sire model)

Traits	Mortality	Plumage condition	Egg performance
Mortality	<b>0.15</b> <b>(0.004)</b>	<b>0.17</b> <b>(0.300)</b>	<b>0.21</b> <b>(0.266)</b>
Plumage condition		<b>0.29</b> <b>(0.020)</b>	<b>0.074</b> <b>(0.118)</b>
Egg performance			<b>0.24</b> <b>(0.017)</b>

# Introduction

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- **mortality is caused is caused by diseases agents and parasites**
- **injuries through aggression, flightiness, feather pecking and cannibalism under stressful environmental situation such as caging of birds in commercial multiple bird cages (Graig and Muir, 1996; Muir, 1996)**
- **A high level of feather pecking has been found to be correlated with high mortality from cannibalism**



**A group selection (Graig and Muir, 1996; Muir, 1996) based on mortality and other indirect traits such as injury occurrence (analysed as either a binary or an ordered categorical trait) and feather cover score can be performed, provided that these traits are heritable and correlated to mortality**

# Material and Methods



Statistical model for estimation of genetic parameters (univariately using generalized sire model)

$$\text{Logit}(\pi_{rstv}) = \eta_{rstv} = \log(\pi_{rstv} / 1 - \pi_{rstv}) = \varphi + \alpha_r * \beta_s * \lambda_t + \gamma_v + \rho_v$$

$\eta_{rst}$  = linear predictor

$\pi_{rst}$  = Probability of fertility; or probability of hatchability for fertile eggs, or probability of EEM, MEM and LMM

$\varphi$  = Overall mean effect

$\alpha_r$  = Fixed effect of poultry house

$\beta_s$  = Fixed effect of tier+site+lane

$\lambda_t$  = Fixed effect of breeding line

$\rho_v$  = Random effect of common environment sire



## ■ Genomewide association study

- 296 cocks genotyped with Affymetrix Axiom<sup>®</sup> Genome-Wide Chicken Array
- ~ 335.000 SNPs on autosomal chromosomes after quality checks
- Breeding values for mortality and feathering

## ■ Model I: Mixed model approach: Single Marker Regression with correction of polygenic effects

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{g} + \mathbf{e}$$

with

$\mathbf{y}$  = breeding values

$\mathbf{X}$  = design matrix for marker regression

$\mathbf{Z}$  = design matrix for random polygenic effect

$\mathbf{b}$  = vector with intercept and regression coefficient

$\mathbf{g}$  = vector of random polygenic effects with  $g \sim N(0, G\sigma_g^2)$

$\mathbf{e}$  = vector of random residual effects with  $e \sim N(0, I\sigma_e^2)$

$\mathbf{G}$  = genomic relationship matrix



## Means, minimum and maximum of different trials

<b>Number of hens per sire</b>	<b>6.07 (2-13)</b>
<b>Plumage condition at 45 weeks of age</b>	<b>6.08 (2-9)</b>
<b>Plumage condition at 70 weeks of age</b>	<b>4.67 (1-9)</b>
<b>Mortality (at 45 and 70 weeks of age)</b>	<b>11.0 (0-100)</b>