Estimating genetic parameters for DGE and IGE on survival time in crossbred layers using genomic information

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Acknowledgement

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Nieuwe technologie
mogelijk maken

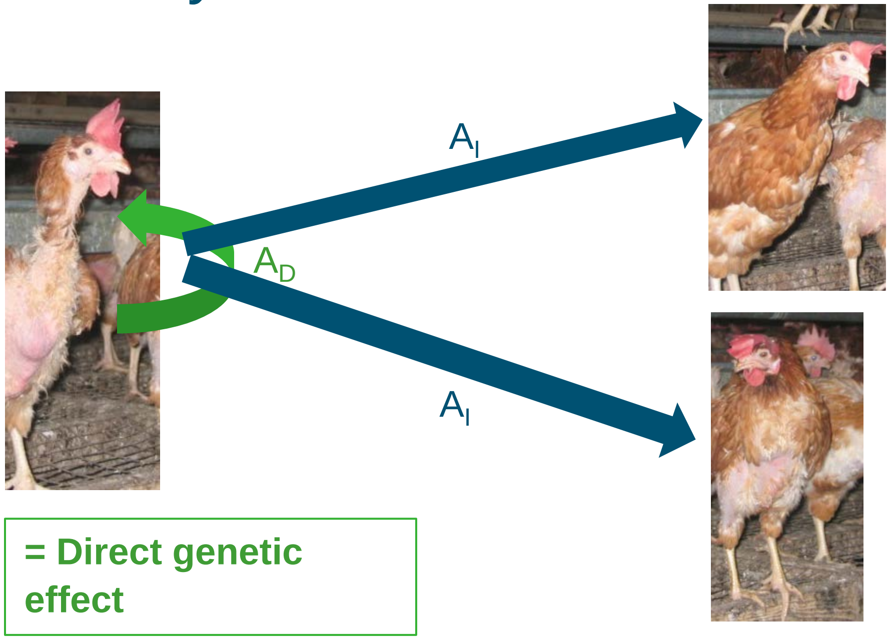
Genomic solutions for socially-affected traits: Genetic architecture and improvement of survival in cannibalistic laying hens

Survival in layers

- Mortality due to cannibalism
- Worldwide problem
- Legislation
- Survival depends on behaviour group members

DGE and IGE

- Socially-affected trait

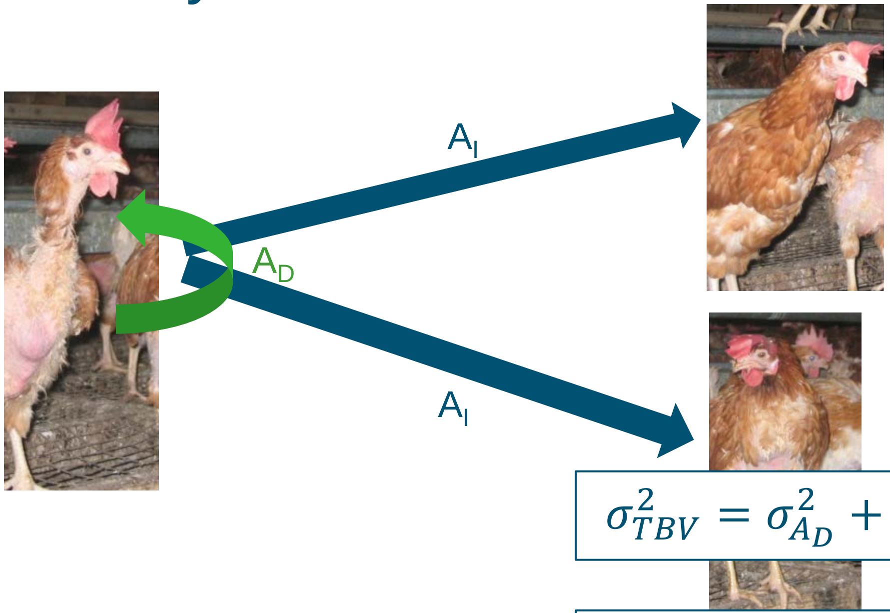


= Social or Indirect genetic effect

= Direct genetic effect

DGE and IGE

- Socially-affected trait

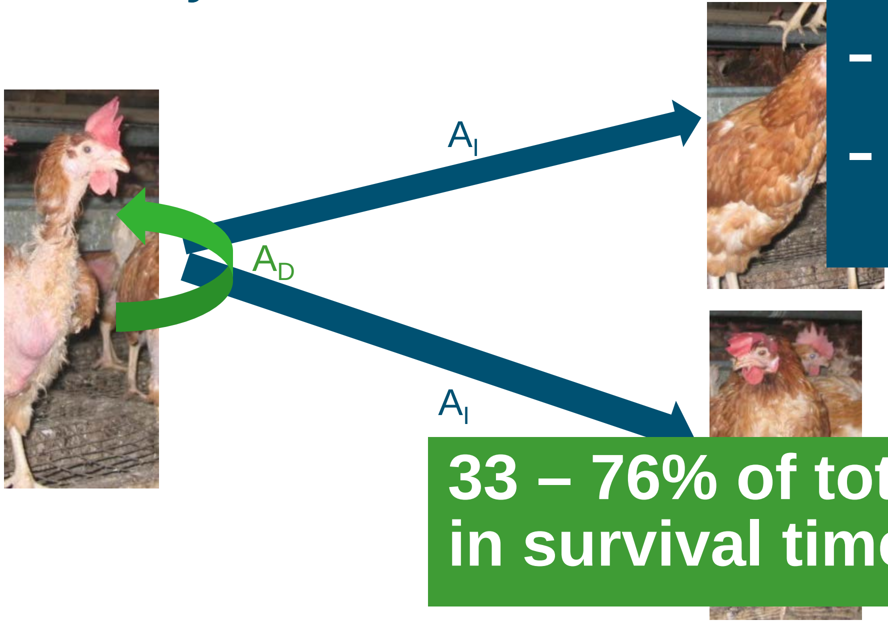


$$\boxed{\sigma^2_{TBV} = \sigma^2_{A_D} + 2(n-1)\sigma_{A_{DI}} + (n-1)^2\sigma^2_{A_I}}$$

$$\boxed{T^2 = \sigma^2_{TBV}/\sigma^2_P}$$

DGE and IGE

- Socially-affected trait



Data structure is important

- **Group housing**
- **Variation in relatedness**

33 – 76% of total heritable variation in survival time

Bijma et al., 2007; Ellen et al., 2008; Peeters et al., 2012

Commercial poultry breeding

- Recurrent testing
    - Housed in sire family groups
    - Dam unknown
- Problem: DGE and IGE fully confounded
- ➢ Solution: genomic information
    - Identify dam
    - Variation in relatedness

Aim

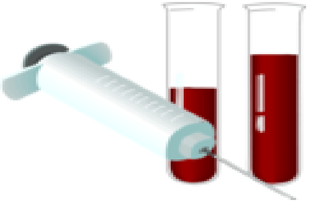
To evaluate the potential benefit of using **genomic information** to estimate **DGE** and **IGE** on survival time in **crossbred** layers

Three models

1. Sire model with A matrix
2. Sire model with H matrix
3. DGE-IGE model with H matrix

Data

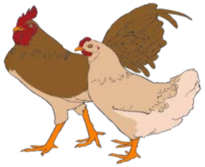
- N = 7,290
- Intact beaks
- 5 sibs/cage
- 4 crosses (W1WA, W1WB, W1WC, W1WD)



- Crossbreds: ~20 weeks of age
- Sires & Dams genotypes
- 60 K SNP chip

Data description

Cross	Cages	# hens	# genotyped hens	# sires	# genotyped sires
W1WA	386	1,930	1,889	54	51
W1WB	388	1,940	1,816	57	55
W1WC	334	1,670	1,545	48	42
W1WD	350	1,750	1,672	50	48



- ~20 dams/sire
- Dam unknown
- Pedigree reconstruction
- ~35,000 SNPs

Sire model

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}s + \mathbf{Vc} + \mathbf{e}$$

- y = survival time for each individual hen
- b = Fixed effect
  - barn*row*level
- s = random sire effect
- c = rand

Output

- $\sigma^2_{A_{TBV}} = 4\sigma^2_{sire}$
- T^2

Sire models

1. A matrix
2. Genotypes of sires ’ H matrix calc grm (Calus, 2015)

DGE-IGE model

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z_D a_D} + \mathbf{Z_I a_I} + \mathbf{Vc} + \mathbf{e}$$

- Random effects
  - a_D = direct genetic effect
  - a_I = indirect genetic effect
  - c = random cage effect
- H matrix
  - Genotypes of crossbreds
  - Reconstructed pedigree

Output

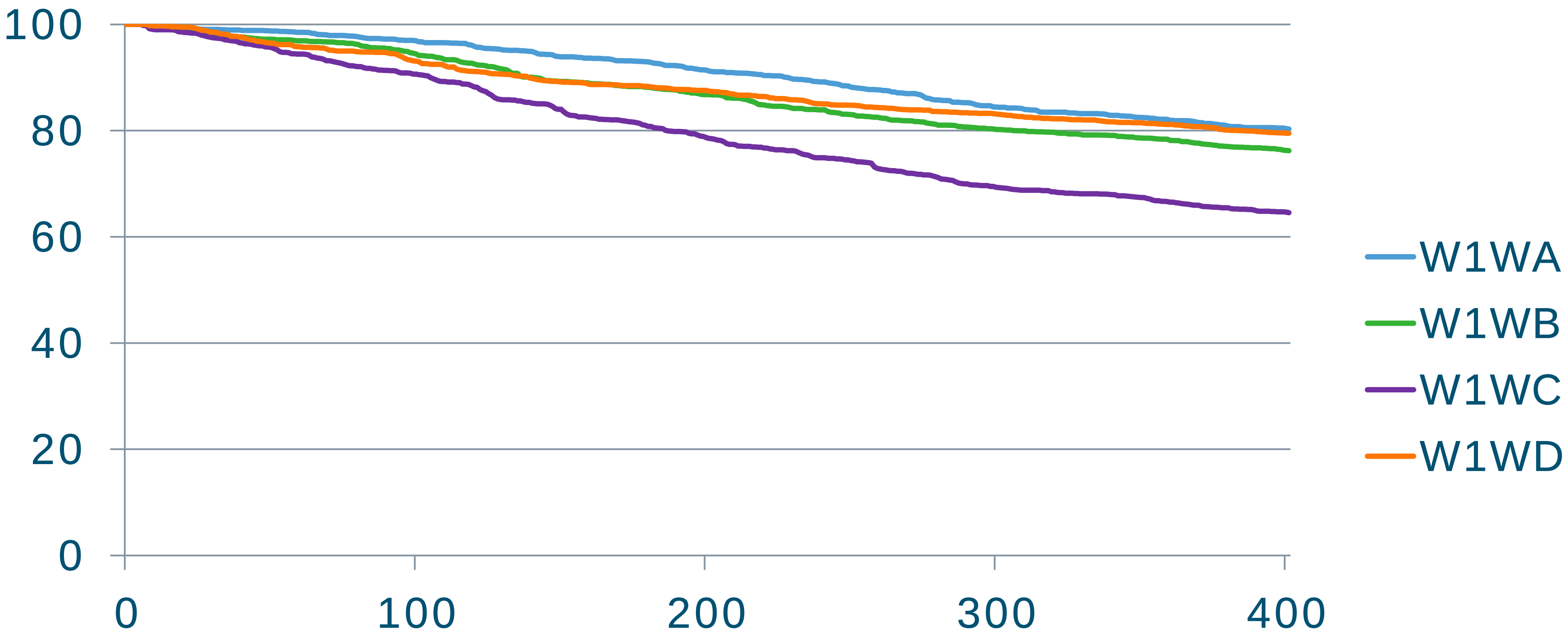
- $\sigma^2_{A_D}, \sigma^2_{A_I} /\# \sigma_{A_{DI}}$

Cross validation

- Per sire family
    - Phenotypes of crossbreds are set to missing
    - Predicted using EBVs
- Rank correlation between predicted and observed phenotypes
- On a sire level

Ellen et al., 2010

Results – survival



Results – sire model with A matrix

Cross	σ_{A_T}	T^2
W1WA	14	0.03 œ0.04
W1WB	35	0.11 œ0.06
W1WC	61	0.25 œ0.09
W1WD	49	0.21 œ0.09

Results – sire model with H matrix

Cross	σ_{A_T}	T^2	T^2
W1WA	14	0.03 œ0.04	0.03 œ0.04
W1WB	35	0.11 œ0.06	0.09 œ0.06
W1WC	61	0.25 œ0.09	0.25 œ0.09
W1WD	49	0.21 œ0.09	0.21 œ0.09

Results – DGE-IGE model

Cross	σ_{A_T}	T^2	**r**$_A$
W1WC	87	0.49 œ0.09	-0.21 œ0.29

- Problem with converging
- To estimate DGE and IGE variation in relatedness should be increased

Cross validation

	Rank correlation	
Cross	Sire - A matrix	Sire - H matrix
W1WA	0.16 œ0.13	0.15 œ0.13
W1WB	-0.02 œ0.13	-0.15 œ0.13
W1WC	0.20 œ0.14	0.39 œ0.12
W1WD	0.41 œ0.12	0.14 œ0.14

- No evidence genomic information improves EBVs
- Improve cross validation – better utilize data

Take home message

- Genomic information helps to estimate DGE and IGE separately
- In this data: no evidence genomic information improves EBVs
- Current sire models can be used to improve survival time in laying hens