Genetic heterogeneity of residual variance in the GIFT strain of Nile tilapia

Jovana Marjanovic, Han Mulder, Hooi Ling Khaw, and Piter Bijma

WAGENINGEN UR
For quality of life
SLU
Swedish University of Agricultural Sciences
EGS ABG
Erasmus Mundus
WorldFish

Acknowledgement

www.egsabg.eu

www.wageningenur.nl

www.slu.se

www.worldfishcenter.org

Background

- **Animal breeding** - improvement of the **mean** level of traits
- Genetically Improved Farmed Tilapia (GIFT)
- Genetic gain >100% through 12 generations of selection on BW
- Aims - improve the mean of a trait, but also reduce its **variability**

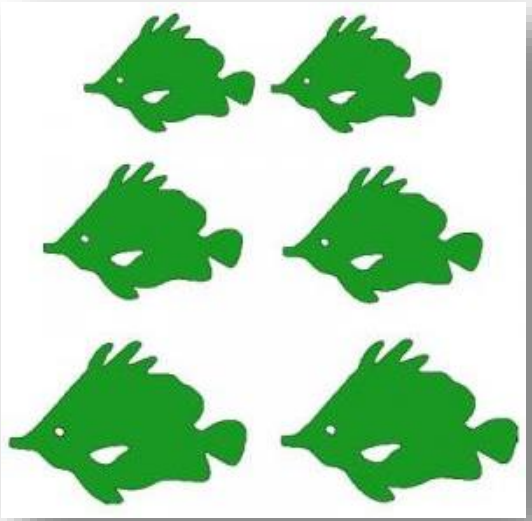
Background

- Large variation around the optimal value -> negative effects
- **Competition** -> size differences

- **CV** of body weight as an indicator of the level of competition
- In GIFT, CV ~**40%-60%**

How to deal with variability?

- **Grading** – sorting fish in a groups according to their size



- **Disadvantages**
  - Labour
  - Expenses
  - Welfare
  - Temporary effect

Breeding for uniformity

- Alternative to grading

- Genetic heterogeneity of environmental (residual) variance

- **Common assumption** – homogeneous Var(E)

$$Var(P)=Var(A)+Var(E)$$

- **Empirical evidence** – substantial genetic Var(E)

$$Var(E)=A+E'$$

Var(E) as a heritable trait

- Quantitative trait
- We can select for more uniform fish
- GIFT – large size differences among individuals
- Genetic background of this variability?

Objectives

- **Estimate**
  - genetic variance in residual variance of harvest weight and body size traits (length, depth and width)
  - genetic correlation between the mean and the variance

- By applying double hierarchical generalized linear models (DHGLM)

Objectives

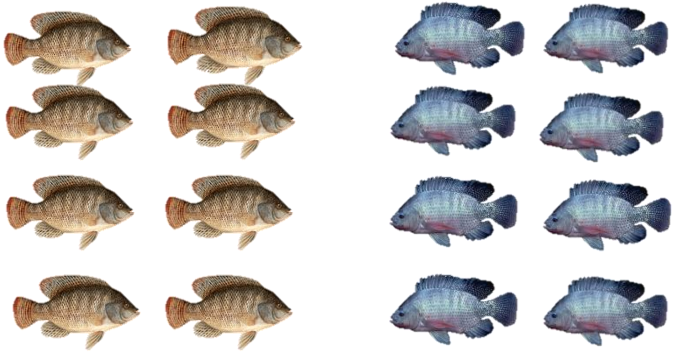
- **Investigate** the effect of Box-Cox transformation of harvest weight on
  - genetic variance in uniformity
  - mean-variance correlation

Data

- The GIFT strain of Nile tilapia
- Harvest weight and body size traits
- IGE experiment
- Jitra Aquaculture Extension Centre
- Three batches (2009-2011)

Data

16 individuals



Data

Data overview	
Number of individual observations	6,090
Number of families	107
Number of groups	446
Number of observations per family per group	892
Pedigree	34,517

Box-Cox transformation

$$\mathbf{y}^{(\lambda)} = \frac{\mathbf{y}^{\lambda} - 1}{\lambda}$$

- Normalize distribution of the data
- Harvest weight
- λ=0.34
- New variable BC-HW

Statistical analysis – DHGLM

- Uses individual observations
- Mean and the residual variance can be modelled jointly
- Residual variance is modelled on the exponential scale
- Essentially a bivariate model
- Iterates between **linear mixed model** for the phenotypic records and **generalized linear mixed** model for the residual variance

Statistical analysis - DHGLM

$$\begin{cases} \mathbf{y} = \mathbf{Xb} + (\mathbf{Z_P} + \mathbf{Z_M})\mathbf{u} + \mathbf{Vc} + \mathbf{Sk} + \mathbf{Um} + \mathbf{e} \\ \mathbf{\Psi} = \mathbf{Xb_v} + (\mathbf{Z_P} + \mathbf{Z_M})\mathbf{u_v} + \mathbf{Vc_v} + \mathbf{Sk_v} + \mathbf{Um_v} + \mathbf{e_v} \end{cases}$$

- $\mathbf{y}$ – HW, BC-HW, length, depth or width

$$\boldsymbol{\phi_i} = \hat{\mathbf{e}}_\mathbf{i}^2/(\mathbf{1} - \mathbf{h_i})$$

$$\boldsymbol{\Psi_i} = \log(\hat{\boldsymbol{\sigma}}^2_{e_i}) + (\{[\hat{\boldsymbol{\sigma}}^2_{e_i}/(\mathbf{1} - \boldsymbol{h_i})] - \hat{\boldsymbol{\sigma}}^2_{e_i}\}/\hat{\boldsymbol{\sigma}}^2_{e_i})$$ (Felleki et al.,2012)

- fixed effects – sex, batch, pond and their interaction with age at harvest

Results

Genetic parameters - harvest weight

Parameter	HW	BC-HW
h^2	0.25 (0.04)	0.31 (0.05)
g^2	0.13 (0.02)	0.15 (0.02)
k^2	0.10 (0.02)	0.10 (0.02)
m^2	0.02 (0.01)	0.02 (0.01)

Genetic parameters - body size traits

Parameter	Length	Depth	Width
h^2	0.30 (0.05)	0.32 (0.05)	0.25 (0.05)
g^2	0.15 (0.02)	0.16 (0.02)	0.27 (0.02)
k^2	0.10 (0.01)	0.08 (0.01)	0.10 (0.02)
m^2	-	0.02 (0.01)	-

GCV – variance level

	HW	BC-HW	Length	Depth	Width
σ_A^2	0.34 (0.07)	0.24 (0.05)	0.16 (0.04)	0.18 (0.04)	0.20 (0.05)
GCV, %	58	49	39	42	45

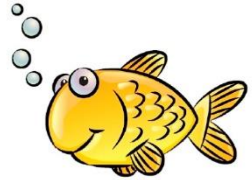
- GCV – genetic coefficient of variation; $\mathrm{GCV} = \sigma_A^2/\mu$
- For exponential model GCV is close to $\sqrt{\sigma_A^2}$

Genetic correlations between mean and the variance

	HW	BC-HW	Length	Depth	Width
r_A	0.60 (0.09)	0.21 (0.14)	0.11 (0.16)	0.37 (0.13)	0.20 (0.15)

Conclusion

Thank you!



- Substantial genetic variation in uniformity
- GCV = **39% - 58%**
- Distribution of the data has an impact on genetic heterogeneity
- After Box-Cox transformation σ^2_A in uniformity ↓
- $\mathbf{r_A}$ between mean and the variance of HW~0.60

WAGENINGEN UR
For quality of life

jovana.marjanovic@wur.nl