Genetic parameters for uniformity of harvest weight and body size traits in the GIFT strain of Nile tilapia

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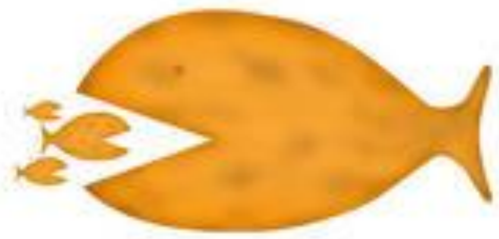
Background

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

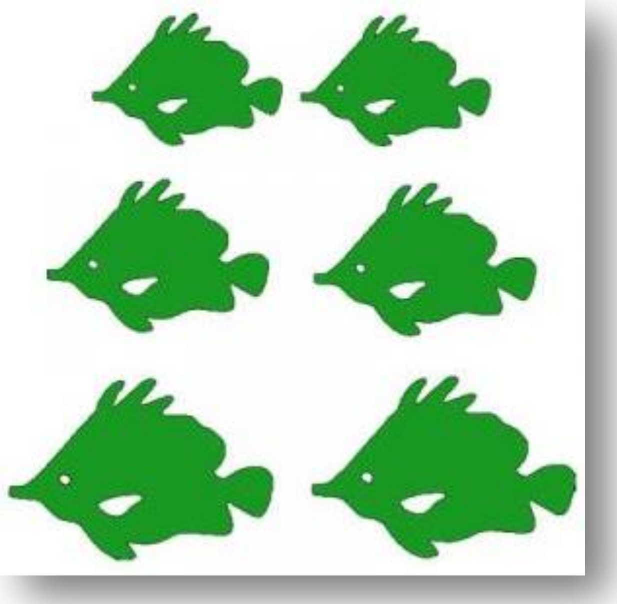
Background

- Variation around the optimal value -> negative effects on the output of a production system
- **Competition** = size differences among individuals
- **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 environmental (residual) variance

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

- **Empirical evidence** – substantial genetic variation in environmental variance

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

Var(E) as a heritable trait

- Quantitative trait
- We can select for more uniform individuals
- 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
- Apply double hierarchical generalized linear models (DHGLM)

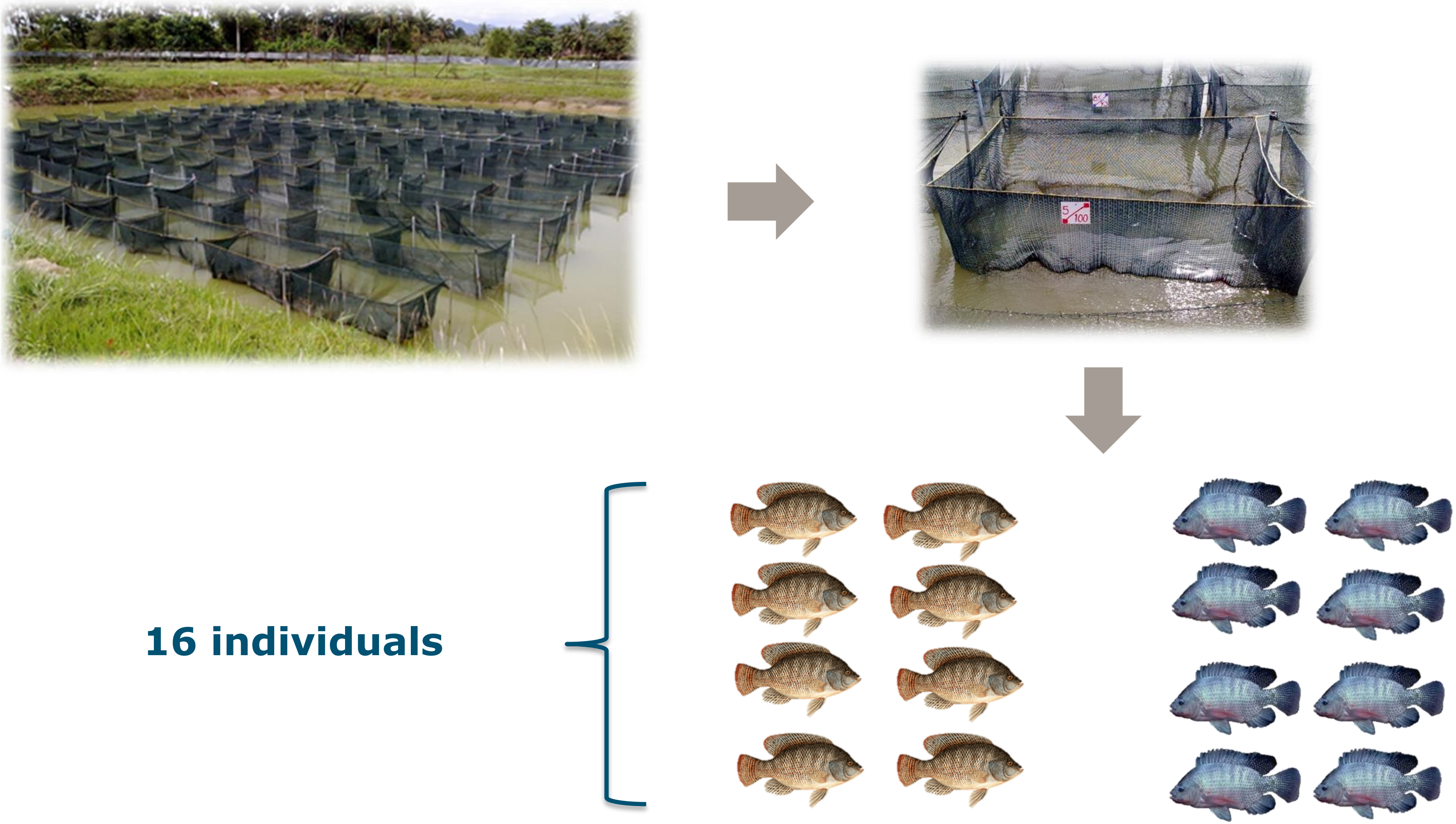
Objectives

- **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

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

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

- $\mathbf{y}$ – harvest weight, Box-Cox transformed harvest weight, length, depth or width

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

$$\boldsymbol{\Psi_i} = \mathbf{log}\left(\hat{\boldsymbol{\sigma}}_{\boldsymbol{e_i}}^\mathbf{2}\right) + (\{[\hat{\boldsymbol{\sigma}}_{\boldsymbol{e_i}}^\mathbf{2}/(\mathbf{1} - \boldsymbol{h_i})]\text{-}\hat{\boldsymbol{\sigma}}_{\boldsymbol{e_i}}^\mathbf{2}\}/\hat{\boldsymbol{\sigma}}_{\boldsymbol{e_i}}^\mathbf{2})$$

(Felleki et al.,2012)

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

Box-Cox transformation

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

- Normalize distribution of the data
- Make variance more stable
- Improve validity of Pearson correlation between the variables
- λ=0.34
- New variable BC-HW

Results

Genetic parameters - harvest weight

Parameter	Harvest weight (untransformed)	Harvest weight (Box-Cox)
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 $\sqrt{\sigma_A^2}$
- Very good opportunity for selection for uniformity

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)

- Genetic correlation - mean harvest weight and variability of body size traits near zero

Conclusion

- 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 decreased, but remained considerable
- Correlation between mean and the variance of HW~0.60 - necessity for index selection
- Correlation between mean HW and variance of body size traits near 0