Genotype-by-environment interaction for uniformity of growth in rainbow trout

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Why is uniformity important?

- Uniform fish schools benefical for sea food value chain: Homogeneous products; Reduced dominance hierarchies; Increased growth, animal welfare and survival
- Traits with intermediate optimum: fillet lipid%, body shape
- Uniformity can genetically change, if genetic variation
- Quantified by within-family residual variation

Family 1: Uniform

Family 2: Heterogeneous

Potential for genotype-by-environment interaction

Nucleus: Freshwater **Commercial production: Sea**

Does GxE interfere selective breeding?
Or not?

Objectives

- Quantify genetic variation for uniformity of body weight in two environments
- Estimate genetic correlation between mean body weight and uniformity of growth in two environments
- Quantify the degree of genotype re-ranking for uniformity

Sae-Lim et al. 2015. Genetic (co)variance of rainbow trout body weight and its uniformity across production environments. *Genetics Selection Evolution* 47:46.

Sae-Lim P, Gjerde B, Nielsen HM, Mulder H & Kause A. 2015. A review of genotype-by-environment interaction and microenvironmental sensitivity in aquaculture species. *Reviews in Aquaculture*, in press.

Panya Sae-Lim's
Project STABLEFISH

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Data (no pre-selection at tagging)

	Subpopulation I		Subpopulation II	
	1996	1999	1997	2000
Number of parents and families				
Sires, dams	57, 129	37, 94	65, 79	95, 121
Sires per dam, mean (range)	1.00 (1-1)	1.00 (1-1)	2.41 (1-3)	1.63 (1-3)
Dams per sire, mean (range)	2.26 (1-4)	2.54 (1-4)	2.93 (1-5)	2.06 (1-5)

Statistical analysis

- Double hierarchical generalized linear model (DHGLM) (Rönnegård et al. 2010; Felleki et al. 2012)

Model factors

- Fixed effects: YearClass x Sex x Maturity x Farm
- Random effects: Sire x Dam; Family tank

A bivariate analysis with two models:

1) Mean model: *Body weight*

2) Variance model: *Squared residuals from model 1*

Two response variables analysed:

1) Body weight

2) Log transformed body weight

Average body weight, Nucleus: 1094g; Sea: 1050g

Relationship between mean BW and uniformity

Trait	r_g (SE)	
	Raw data	Log-transformed
Within environment		
$BW_{Nucleus}$ – $Uniformity_{Nucleus}$	0.30 (0.15)	
BW_{Sea} – $Uniformity_{Sea}$	0.79 (0.13)	

High mean - High variance

High mean - Low scaled variance (log variance; CV)
Fish become more uniform / less sensitive with increasing body weight

Genetic variation for uniformity in two environments

Parameter	Environment	
	Nucleus	Sea
Raw BW data		
CV_G - Coefficient of genetic variation %	21.0	19.0
h^2, heritability	0.011	0.010
c^2, family tank ratio	0.005	0.004

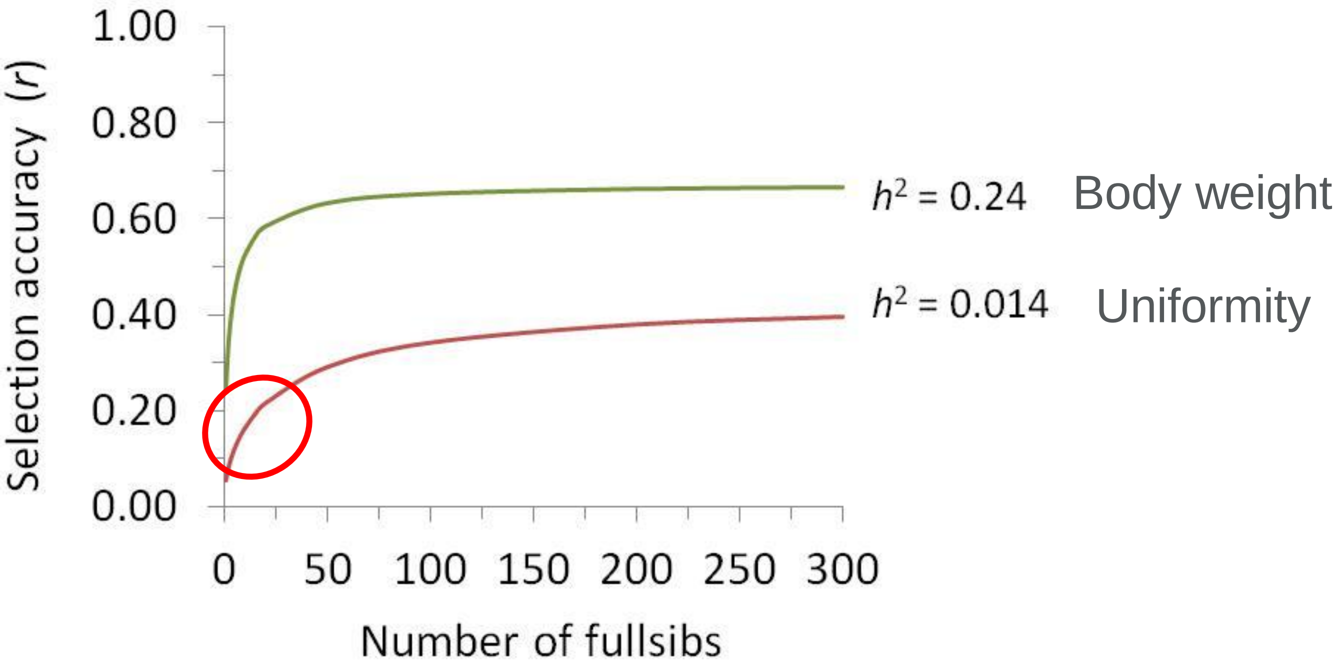
High CV_G ⇨ High potential for genetic change (R)

Low h^2 ⇨ Low selection accuracy, high number of relatives needed

$$R = i r_{IH} \sigma_A$$

i = selection intensity
r_{IH} = selection accuracy
σ_A = genetic standard deviation

Accuracy and selection response in uniformity



Expected genetic response in uniformity when 10% selected

Family size	**Residual variance of BW reduced**
20	-5%
40	-9%
80	-11%
160	-13%

→ Genetic responses expected but large number of fullsibs needed

Genotype re-ranking across two environment

Trait	r_g (SE)	
	Raw data	Log-transformed
Genotype re-ranking		
$BW_{Nucleus} – BW_{Sea}$	0.70 (0.06)	
$Uniformity_{Nucleus} – Uniformity_{Sea}$	0.56 (0.20)	

Moderate re-ranking for mean and raw variance

When variation scaled for mean, complete re-ranking!

Testing at multiple enviroments needed

Uniformity has two parts:
1) One related to the mean
2) One independent of the mean

Practical implications

- Uniformity not included into the selection index, why?

1) Genetic trend for log-uniformity flat or downward, fish are not becoming more sensitive (This study; Janhunen et al. 2012. *PLoS ONE* 7(6): e38766

2) We practice two-stage selection, the smallest of each family are left untagged (Martinez et al. 2006. *Aquaculture* 254: 195-202)

3) Not an easy trait to improve

Conclusions

- Uniformity diplays stronger re-ranking than growth itself
- Uniformity of growth can be improved, but not an easy trait to select:

  Multiple environments

  Large fullsib families

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