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Survival of the Currently Fittest – Genetics of Rainbow Trout Survival Across Time and Space

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PRACTICAL IMPORTANCE

- Survival of farmed fish an important animal welfare issue (10-20 % mortality)
- Nutrient effluent due to carcasses dissolving into sea and excess feed given
-  Increased profitability of the industry

THEORETICAL CHALLENGES

- Fitness traits (survival, fecundity) commonly assumed to have low or zero heritability (e.g. Fisher 1930, Roff & Mosseau 1987, Merilä & Sheldon 1999)

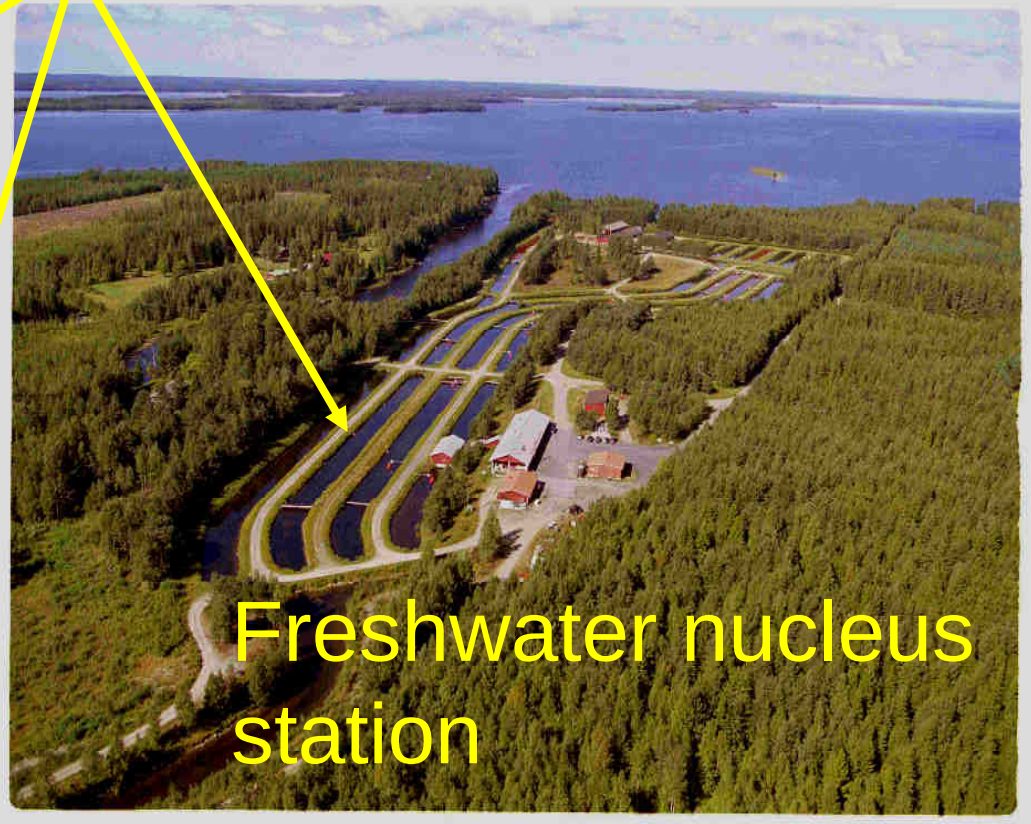
- Multiple mortality agents do not necessarely share genetic determination

  -reduced genetic variation and/or increased residual variation (e.g. Price & Schluter 1991, Houle 1992, Merilä & Sheldon 1999)

Individual tagging of fingerlings

Sea test station A

Sea test station B



Freshwater nucleus station

Fish present at end of grow-out season = Survived

DATA STRUCTURE

- 10 year-classes 1995-2004
- 121 905 individuals
- Common base population.
- Three sub-populations, 3-4 successive generations.
- 109-341 full-sib families in each year-class
- 48-168 sires and 79-252 dams
- Nested paternal or partial factorial designs.

ANALYSES

1. Is the assumption of low heritability fulfilled?

   - heritability of overall survival across the whole dataset

   - 2 traits, freshwater and sea survival

2. Does the G-matrix remain stable in space and time?

   - heritabilities and genetic correlations between generations and environments

   - 21 separate survival traits, survival in each generation and in each of the three test stations.

OVERALL SURVIVAL

- Mean survival 71 %, min-max: 50 % - 84 %
- Overall survival during grow-out

  Freshwater nucleus $h^2 = 0.17$ (± 0.02)

  Sea test stations $h^2 = 0.08$ (± 0.02)
- $r_{G\ FvsS} = 0.58$ (95 % CI 0.39-0.76)

STABILITY OF G-MATRIX

- Generations and test stations analyzed as separate traits (21 traits)

  h^2 range: 0.04 – 0.71

- Total of 46 genetic correlations:

  8 sign. positive (0.39 – 0.89)

  16 sign. negative (-0.97 – -0.45)

  22 did not differ from zero (-0.54 – 0.54)

POPULATION I

- Genetic correlations between generations at the freshwater station were positive

  (mean = 0.34, range: 0.13 – 0.52)

- The negative correlations occurred only between the freshwater station and the sea stations

  (mean = -0.08, range: -0.54 – 0.73)

POPULATION IIa AND IIb

- The patterns of both PopIIa and PopIIb differed from that of PopI, but do resemble each other.

- Both PopIIa and PopIIb were characterized by a single generation that is negatively correlated with the other generations.

	G96F	G99F	G99Sa	G99Sb	G02F
G99F	**-0.83**				
G99Sa	**-0.72**	**0.97**			
G99Sb	**-0.74**	**0.95**	**0.94**		
G02F	0.54	**-0.45**	-0.40	-0.41	
G02Sa	**0.89**	**-0.91**	**-0.85**	**-0.91**	**0.71**

VALIDATION OF GENETIC CORRELATIONS

Correlation between breeding values of parents estimated

1. from the observations of their own generation

and

2. from their offspring's generation only (≈realized breeding values)

POPULATION I			
Parent trait	Offspring trait	Gen. corr.	Corr. btw breeding values
G98F	G01F	**0.52**	**0.44**
G98F	G01Sa	0.02	**0.17**
G98F	G01Sb	0.24	0.34
G01F	G04F	0.13	0.08
G01F	G04Sa	-0.15	-0.08
G01F	G04Sb	-0.54	**-0.13**

CONCLUSIONS

- Genetic architecture of survival varies across time and space.
- Significant genetic variation in specific cohorts was revealed after analysing the splitted data.

IMPLICATIONS

- Overall survival can be selected
  - not a perfect measure of general resistance
  - causes to specific resistance?

Hard working FGFRI staff at the Tervo station.

Members of BGE, EGE and GDI –groups at MTT Agrifood Research Finland.

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Thank you.

*The whole story: Vehviläinen, Kause, Quinton, Koskinen & Paananen (2008) Survival of the Currently Fittest – Genetics of Rainbow Trout Survival Across Time and Space.

Genetics, in press

www.mtt.fi/fishgenetics