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 necessarily 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)

$r_{G_{FvS}} = 0.58$ (95 % CI 0.39-0.76)
STABILITY OF G-MATRIX

 générations et test stations analysées en traits distincts (21 traits)
h² range: 0.04 – 0.71

Total de 46 corrélations génétiques:
8 sign. positive (0.39 – 0.89)
16 sign. negative (-0.97 – -0.45)
22 did not differ from zero (-0.54 – 0.54)
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)
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.
<table>
<thead>
<tr>
<th></th>
<th>G96F</th>
<th>G99F</th>
<th>G99Sa</th>
<th>G99Sb</th>
<th>G02F</th>
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</thead>
<tbody>
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<tr>
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<td>-0.40</td>
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<td>G02Sa</td>
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<td>-0.91</td>
<td>-0.85</td>
<td>-0.91</td>
<td>0.71</td>
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</tbody>
</table>
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)
<table>
<thead>
<tr>
<th>POPULATION I</th>
<th></th>
<th>Gen. corr.</th>
<th>Corr. btw breeding values</th>
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</thead>
<tbody>
<tr>
<td>Parent trait</td>
<td>Offspring trait</td>
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<td></td>
</tr>
<tr>
<td>G98F</td>
<td>G01F</td>
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<tr>
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<td>G04F</td>
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<tr>
<td>G01F</td>
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<tr>
<td>G01F</td>
<td>G04Sb</td>
<td>-0.54</td>
<td>-0.13</td>
</tr>
</tbody>
</table>
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. The Finnish Ministry of Agriculture and Forestry and the Kone Foundation.

Thank you.


www.mtt.fi/fishgenetics