

Supplement B: Power and Sensitivity of Admixture Estimates

First we created 1,000 genomes each for pure, F₁, F₂, and backcrossed individuals. From each genome, genotypes at seven unlinked, diploid markers were randomly sampled to compare known admixture levels with estimates calculated from only a few markers. Estimates were observed to be accurate for the pure and F₁ individuals, but less accurate for the F₂ and backcross individuals (Figure A.1.1).

Next, analyses were performed again using only individuals (for ova diameter, egg energy concentration, and sperm motility) or families (for embryonic survival, juvenile growth, juvenile survival, and high-velocity swimming endurance) that were estimated to be genetically pure or F₁. For each analysis, we used the final models identified in the initial analyses. In general, the conclusions drawn for admixture were consistent with those using the full data set. The details follow.

Embryonic Survival

The conclusions drawn from using all of the data were the same as those from using only the pure and F₁ families.

Supplementary Table S.B.1. Results for regression analysis of embryonic survival using only F₁ and pure individuals. The model included familial average ancestry (Avg. % WCT) and temperature as fixed effects, as well as both dam and sire as random effects.

Random effect	Variance			
Dam	1.0866			
Sire	0.3321			
Fixed effect	Estimate	SE	Z-value	P
Intercept	4.16677	0.40275	10.346	$< 2 \times 10^{-16}$
Avg. % WCT	−1.90032	0.91105	−2.086	0.0370
Temperature	−0.05914	0.03036	−1.948	0.0515

Supplementary Table S.B.2. Results for regression analysis of juvenile growth using only F1 and pure individuals. The model included familial average ancestry (Proportion WCT) as the only fixed effect and both dam and sire as random effects.

Random effect	Variance
Dam	0.0096028
Sire	0.0013147

Fixed effect	Estimate	SE	df	<i>t</i> -value	<i>P</i>
Intercept	0.59535	0.02577	22.165	23.101	$< 2 \times 10^{-16}$
Proportion WCT	0.38047	0.06761	21.048	5.627	1.375×10^{-5}

Supplementary Table S.B.3. Results for regression analysis of juvenile survival using only F1 and pure individuals. The model included familial average ancestry (Avg. % WCT) and tank density as the only fixed effects, as well as both dam and sire as random effects.

Random effect	Variance
Dam	0.2046
Sire	0.2634

Fixed effect	Estimate	SE	Z-value	<i>P</i>
Intercept	1.227516	0.377588	3.251	0.00115
Avg. % WCT	0.128288	0.480181	0.267	0.78934
Tank density	0.006435	0.004184	1.538	0.12406

Supplementary Table S.B.4. Results for regression analysis of juvenile survival using only F1 and pure individuals. The model included tank density as the only fixed effect and both dam and sire as random effects.

Random effect	Variance
Dam	0.2074
Sire	0.2621

Fixed effect	Estimate	SE	Z-value	<i>P</i>
Intercept	1.265557	0.351463	3.601	0.000317
Tank density	0.006234	0.004128	1.510	0.130968

High-Velocity Swimming Endurance

In the initial analysis, Rainbow Trout were compared with hybrid trout. Because no differentiation was made among hybrid classes, no sensitivity analysis was needed.

Ova Diameter

The analysis was dominated by pure Rainbow Trout, and the removal of hybrid individuals that were not F₁s resulted in only three remaining data points. Because the sample size was so small, the analysis was not performed.

Egg Energy Concentration

The conclusions did not change.

Supplementary Table S.B.5. Results for regression analysis of egg energy concentration using only F₁ and pure individuals. The model included dam ancestry (Proportion WCT) as the only fixed effect and both dam and sire as random effects.

Random effect	Variance				
Dam	0.2314				

Fixed effect	Estimate	SE	df	<i>t</i> -value	<i>P</i>
Intercept	8.8579	0.1126	26.5570	78.671	$< 2 \times 10^{-16}$
Proportion WCT	-1.1099	0.3403	25.6440	-3.262	0.00312

Sperm Motility

The final model did not include admixture as a parameter.