

Table S1. Results of analysis of deviance (ANODEV) of binomial generalized linear model for recapture data.

Source	df	Δ Deviance	Residual df	Residual Deviance	Likelihood Ratio	p-value
Null			11	255.23		
Site	2	126.01	9	129.21	2.31×10^{27}	< 0.001
Cross type	3	117.04	6	12.17	2.60×10^{25}	< 0.001
Site*Cross type	6	12.17	0	0	439.44	0.058

Table S2. Analysis of deviance (ANODEV) table for generalized linear model of recapture weight by mean egg weight, site, cross type, and all possible interactions. Model was specified using the Gamma family and identity link. Null deviance for the model was 232.72 on 1241 degrees of freedom (df), and residual deviance was 142.21 on 1218 df. Δ dev refers to change in deviance, and LR refers to likelihood ratio.

Source	df	Δ dev	F	LR	p-value
NULL					
Egg weight	1	8.46	69.90	68.75	< 0.001
Site	2	53.86	222.52	4.97×10^{11}	< 0.001
Cross type	3	10.72	29.5	212.41	< 0.001
Egg weight*Site	2	1.04	4.31	1.68	0.014
Egg weight*Cross type	3	8.82	24.28	82.11	< 0.001
Site*Cross type	6	6.34	8.73	23.78	< 0.001
Egg weight*Site*Cross type	6	1.28	1.76	1.89	0.100

Table S3. ANOVA table for linear model of recapture length by mean egg weight, site, cross type, and all possible interactions. LR is the likelihood ratio, MS is mean squares, SS is sums of squares, df is degrees of freedom.

Source	df	SS	MS	F	LR	p-value
Egg weight	1	2311	2310.7	76.62	1.63×10^{10}	< 0.001
Site	2	13044	6522	216.27	4.69×10^{68}	< 0.001
Cross type	3	3098	1032.8	34.25	1.64×10^{18}	< 0.001
Egg weight*Site	2	244	121.9	4.044	5.23	0.018
Egg weight*Cross type	3	2972	990.5	32.85	9.25×10^{18}	< 0.001
Site*Cross type	6	1086	181	6.00	1.37×10^5	< 0.001
Egg weight*Site*Cross type	6	272	45.3	1.50	0.19	0.170
Residual	1216	36670	30.2			

Table S4. Intercept and slope values for regression lines generated using results of generalized linear model (recapture weight) and linear model (recap length), and predicted recapture (Pred) weight and length at mean egg weight value (93.2 mg) with standard error (SE(pred)), for each site by cross type combination. Slope and intercept were calculated using coefficients from model results. Intercept value is theoretical recapture weight or length if mean egg weight was 0, and slope is the change in recapture weight (g) or length (mm) for every 10 mg increase in mean egg weight.

Site x Cross	Recapture Weight				Recapture Length			
	Intercept	Slope* 10	Pred	SE(pred)	Intercept	Slope* 10	Pred	SE(pred)
1 Wild	0.29	0.06	0.836	0.0353	32.17	1.20	43.4	0.659
2 Wild	0.61	0.08	1.33	0.0407	43.31	0.79	50.7	0.477
3 Wild	0.65	0.08	1.391	0.0484	39.12	1.25	50.7	0.544
1 Farm	1.26	-0.02	1.042	0.049	48.641	-0.23	46.5	0.747
2 Farm	1.77	-0.03	1.48	0.0516	54.54	-0.27	52.1	0.548
3 Farm	0.89	0.11	1.911	0.065	47.07	0.91	55.6	0.547
1 F♀hyb	-1.07	0.22	0.997	0.0566	18.77	2.89	45.7	0.952
2 F♀hyb	-0.43	0.19	1.374	0.0509	27.18	2.54	50.9	0.61
3 F♀hyb	-3.14	0.49	1.47	0.0714	-3.46	5.86	51.1	0.716
1 W♀hyb	0.96	0.0001	0.965	0.0367	42.28	0.35	45.5	0.6
2 W♀hyb	1.87	-0.04	1.535	0.039	56.29	-0.36	52.9	0.402
3 W♀hyb	1.35	0.07	2.023	0.0609	48.61	0.91	57.1	0.47

Table S5. ANOVA table for linear model of recapture condition factor by mean egg weight, site, cross type, and all possible interactions. Abbreviations of terms are defined as in Table 2.

Source	df	SS	MS	F	LR	p-value
Egg weight	1	0.003	0.003	0.872	0.54	0.350
Site	2	0.289	0.145	42.195	9.83×10^{15}	< 0.001
Cross type	3	0.145	0.048	14.065	3.40×10^7	< 0.001
Egg weight*Site	2	0.003	0.002	0.496	0.21	0.610
Egg weight*Cross type	3	0.045	0.015	4.333	28.91	0.005
Site*Cross type	6	0.058	0.010	2.803	9.46	0.010
Egg weight*Site*Cross type	6	0.064	0.011	3.086	23.68	0.005
Residuals	1216	4.168	0.003			

Table S6. Results of Procrustes ANOVA of overall fish shape by centroid size (Csize), site, and cross type. Sums of squared Procrustes distances are used as a measure of SS (sums of squares) with this approach. SS are calculated sequentially. Z-scores (effect sizes) indicate standard deviation of observed SS for each term relative to the mean of the distribution of resampled SS values (note that the values from the resampled distribution are log-transformed by the function prior to the estimation of effect sizes). Rsq is the amount of variation explained by each term, MS is mean squares, and LR is likelihood ratio.

Source	df	SS	MS	Rsq	F	Z	p-value	LR
Csize	1	0.026	0.026	0.089	85.71	7.16	< 0.001	2.27x10 ¹⁴
Site	2	0.022	0.011	0.073	35.42	7.98	< 0.001	3.00x10 ¹²
Cross type	3	0.025	0.008	0.086	27.78	9.36	< 0.001	9.26x10 ¹⁵
Residuals	727	0.222	0.0003	0.75				
Total	733	0.296						

Table S7. Mean number of parr marks (at grand mean of standard length= 45.2 mm), mean length, and mean width of marks in mm (at grand mean ln(standard length)= 3.08 mm), for each cross type by site combination. SE is the standard error of the mean estimate. Emmeans are estimated marginal means, calculated using the *emmeans* package in R.

Cross type	Site	Mean Number of Marks		Mean Length of Marks		Mean Width of Marks	
		emmean	SE	emmean	SE	emmean	SE
Wild	1	9.56	0.63	0.53	0.05	0.61	0.06
Farm	1	9.92	0.54	0.48	0.04	0.49	0.05
F♀hyb	1	8.85	0.37	0.49	0.03	0.62	0.04
W♀hyb	1	8.81	0.75	0.64	0.06	0.66	0.07
Wild	2	8.18	0.39	0.61	0.03	0.72	0.04
Farm	2	9.04	0.38	0.58	0.03	0.63	0.04
F♀hyb	2	8.92	0.36	0.56	0.03	0.70	0.03
W♀hyb	2	8.84	0.42	0.57	0.04	0.69	0.04
Wild	3	9.48	0.36	0.62	0.03	0.72	0.03
Farm	3	9.16	0.44	0.62	0.04	0.67	0.04
F♀hyb	3	9.38	0.39	0.59	0.03	0.69	0.04
W♀hyb	3	7.42	0.58	0.67	0.05	0.74	0.06