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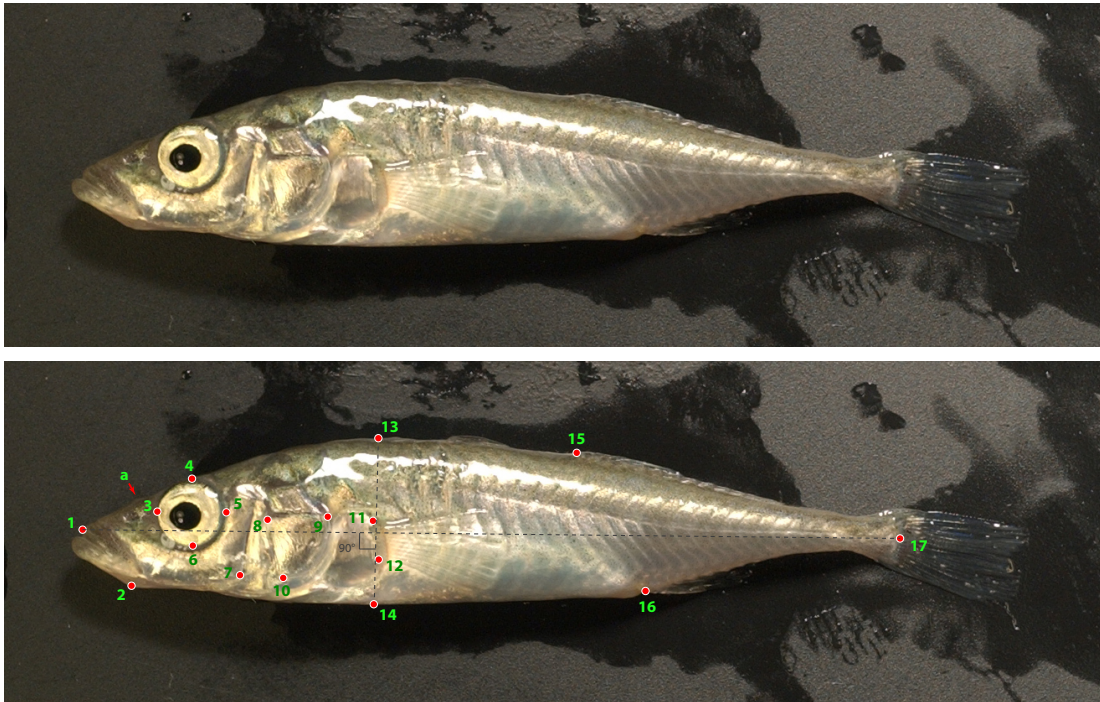
Supplemental Information

Genetic Coupling of Female Mate Choice

with Polygenic Ecological Divergence

Facilitates Stickleback Speciation

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1. anterior tip of the upper jaw (anterior-most extent of the premaxilla; see a, below)
 2. posterior-ventral corner of the lower jaw (border between the angular-articular and quadrate bones)
 3. anterior-most point (edge) of the orbit
 4. dorsal-most point (edge) of the orbit
 5. posterior-most point (edge) of the orbit
 6. ventral-most point (edge) of the orbit
 7. inner corner of the preoperculum
 8. anterior-dorsal corner of the operculum
 9. posterior-dorsal corner of the operculum
 10. ventral corner of the operculum
 11. dorsal insertion of the pectoral fin
 12. ventral insertion of the pectoral fin
 13. dorsum of the trunk over the pectoral fin midpoint
 14. ventrum of the trunk under the pectoral fin midpoint
 15. anterior insertion of the dorsal fin
 16. anterior insertion of the anal fin
 17. posterior midpoint of the caudal peduncle
- a. posterior end of the premaxilla's ascending process (the premaxilla is V-shaped)

Figure S1. Locations of 17 landmarks used in morphometric analysis. Related to Figure 1.

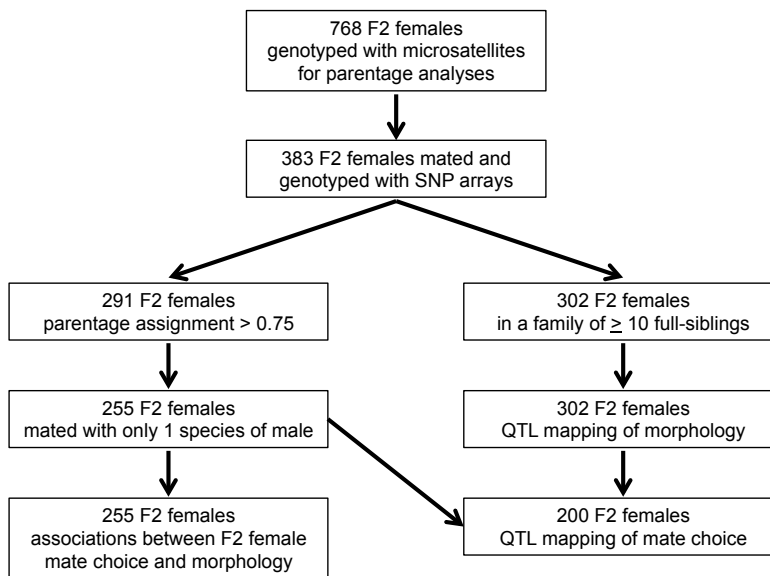
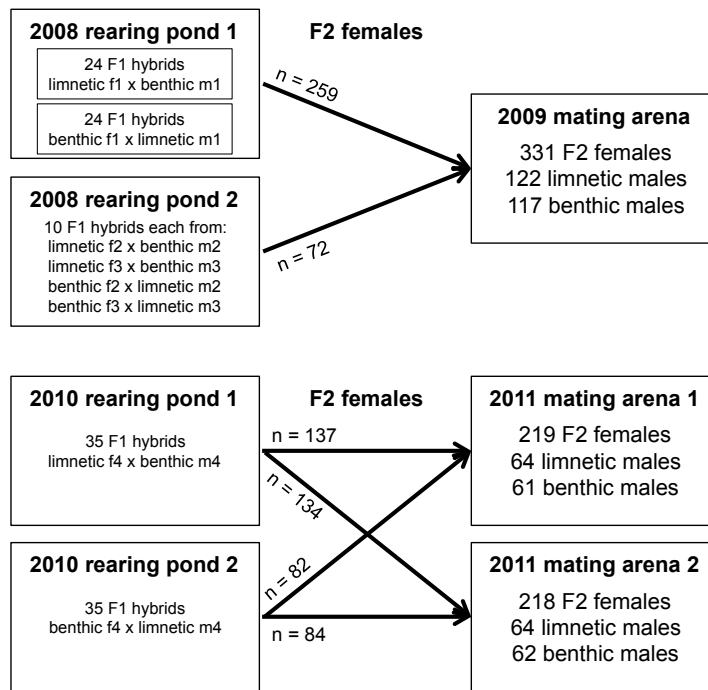


Figure S2. Overview of experimental design and analysis. Related to STAR Methods.

Landmark	PC2	LD1
x1	0.216	26.839
y1	-0.317*	4577.351*
x2	0.221	-744.582
y2	-0.272*	3823.246*
x3	0.030	221.469
y3	0.111	3577.608*
x4	-0.083	722.195
y4	0.023	3117.165*
x5	-0.166	242.918
y5	0.137	2624.617
x6	-0.061	-231.759
y6	0.208	3100.080
x7	-0.004	-589.378
y7	-0.054	2447.137
x8	-0.125	211.181
y8	0.184	2010.066
x9	-0.060	220.541
y9	0.149	1341.069
x10	-0.020	-571.613
y10	0.040	1866.242
x11	0.071	92.302
y11	0.076	659.106
x12	0.019	-420.228
y12	0.025	514.774
x13	0.048	1215.315
y13	0.229	550.743
x14	0.042	-1044.044
y14	-0.369*	579.358
x15	-0.203	1069.442
y15	0.277*	-1922.137
x16	0.256	-726.822
y16	-0.314*	-2864.858
x17	-0.179	181.686
y17	-0.133	-6244.713*

Table S1. Scaling of principal component axis 2 (PC2) and linear discriminant function 1 (LD1) by morphological landmarks. Related to Figure 1. Note that for visualization purposes, LD1 scores are multiplied by -1 so that directionality corresponds with PC2; a more benthic phenotype is indicated by higher and positive numbers. For each analysis, the top five landmarks are indicated with an asterisk.

Trait	n	LOD	Chr	Position (cM)	Nearest SNP	Mean ± SE (LL)	Mean ± SE (LB)	Mean ± SE (BB)
mate choice	200	4.5	14	22.43	chrXIV:1713227	0.641 ± 0.08	0.706 ± 0.04	0.863 ± 0.06
mate choice	200	4.61	21	8	chrXXI:9373717	0.58 ± 0.06	0.83 ± 0.05	0.614 ± 0.11
discriminant function	302	4.83	12	17	chrXII:7504339	-0.15 ± 0.13	0.249 ± 0.08	0.54 ± 0.13
discriminant function	302	4.23	14	8.1	chrXIV:4632223	-0.228 ± 0.17	0.279 ± 0.08	0.393 ± 0.12
PC2	302	4.04	4	30.76	chrIV:11367975	-0.012 ± 0.008	0.012 ± 0.004	0.019 ± 0.006
PC2	302	6.67	7	47	chrVII:26448674	0.02 ± 0.007	0.015 ± 0.005	-0.013 ± 0.008
centroid size	302	6.97	9	47.8	chrIX:19745222	4.868 ± 0.12	5.074 ± 0.04	5.133 ± 0.08
x2*	302	3.93	7	60	chrUn:29400087	-1.208 ± 0.004	-1.21 ± 0.002	-1.198 ± 0.004
y2*	302	9.99	4	32	chrIV:11367975	-0.309 ± 0.003	-0.328 ± 0.002	-0.334 ± 0.003
x3	302	4.45	1	32.3	chrI:15145305	-1.101 ± 0.002	-1.094 ± 0.001	-1.089 ± 0.002
x4	302	5.13	16	30.9	chrXVI:12111717	-0.881 ± 0.002	-0.889 ± 0.001	-0.891 ± 0.002
x5*	302	4.54	15	6	chrXV:505537	-0.666 ± 0.003	-0.675 ± 0.002	-0.669 ± 0.003
y5	302	4.21	4	24.9	chrIV:15721538	0.099 ± 0.002	0.101 ± 0.001	0.108 ± 0.001
x6	302	3.96	16	29.5	chrXVI:13588796	-0.877 ± 0.002	-0.885 ± 0.002	-0.885 ± 0.003
y6*	302	4.14	9	30.2	chrIX:18942598	-0.111 ± 0.003	-0.103 ± 0.002	-0.105 ± 0.003
y15*	302	5.3	2	27	chrII:19324477	0.499 ± 0.005	0.5 ± 0.004	0.479 ± 0.005
x16	302	5.49	7	60	chrUn:29400087	1.906 ± 0.006	1.883 ± 0.004	1.854 ± 0.007
x17	302	4.92	1	32.8	chrI:14261764	3.369 ± 0.004	3.38 ± 0.003	3.392 ± 0.004

Table S2. Significant QTL loci for mate choice and morphology. Related to Figures 2 and 3. For each QTL, the table shows the number of F2 females used in analysis (n), log odds ratio (LOD), chromosome (Chr), position in centiMorgans (cM), nearest SNP, and mean and standard errors (SE) for the trait estimated in each genotype category – limnetic homozygote (LL), heterozygote (LB), and benthic homozygote (BB). QTL significance ($\alpha=0.1$) was determined based on 10,000 permutations. The landmark coordinates significantly associated with mate choice are highlighted with an asterisk.

Marker	Genotyped	Chr	Forward primer (5' to 3')	Reverse primer (5' to 3')
LG1_7.59	2009, 2011	1	TGGACGAGTGCCAACATAAA	TTTTGGCAGCTCGGAATATC
LG1_27.1	2009	1	GAAGGAGGTTGGACATAAAGG	CTGCCTGCTTCTCAAATACC
Stn27	2009, 2011	2	TCCTCTGGGACAGTTGAGC	CTGAGAAGCTGCAGGAAGCC
Stn20	2009, 2011	2	CCAGATCATGTGTAACGGC	AAGGCTCAGCTGTGATCTGG
Stn32	2009, 2011	3	CAGATTTCTCTCCAGACGG	TGTATGCGCAGTGAGTAGGG
Stn45	2009, 2011	4	ACGAGGGTTTGAGTCTCTCC	GTTGTTCAATCCATCCGTCC
Stn309	2009, 2011	4	AACTGTGCAGATCTATGCCG	GGAAGTTGTAAAGAAAGGCCG
Stn241	2009, 2011	5	GACCTCCAGAACCAGGAAGG	CTTTACCAAGGTGAGGGACG
Stn85	2009, 2011	8	ACAGGACACCAGTGTAGCCC	ATGAGCGTGTCTCTTTCCC
Stn98	2009	8	CAAAGTGCACACTACGTGCG	AGTGAATAAAGGGAACCCG
Stn225	2009, 2011	9	AACATCGGAGACCACTGACG	ACGAGGCAACTTCCTTCTGC
Stn119	2009, 2011	10	CTCTACTGCTTCTCCATGC	TGAGCCTTCACAGACCACC
LG11_4.0	2009, 2011	11	GGCCATTAGAGTCATCAAGC	GCACATGAGTGAGAGTGTGC
Gac7033	2009, 2011	11	AGGTGGATTGGTTTTCTG	GGACGCTCGCTCTTTC
Stn148	2011	13	AACCCTTACTCAACTCAGCCC	GAGGAACTTCATTTGGCAGC
Stn163	2009, 2011	14	GAGAAGACAACAGGGAAGCG	CGCCTGCAGTCAACCTACC
LG15_13.4	2011	15	CAGGGTTTCACTTCAACC	CACAGAATGGCTGATTACGC
Stn344	2009, 2011	17	TTTGTTGGGATCTGGAGACG	GAGCTCTTCAAGCTGGTTCC
Stn305	2011	18	TGATCCAACGGTCAGATTCC	GTTACCTGGCGAGGACG
Stn290	2009, 2011	19	CATCCAGAGCCTGTTTGAGG	TCACGGACTGTGGATCAGC
Stn194	2009, 2011	19	ACACTCTGCTCTCGCTCCG	TGAAAGGCTTACTGTTCCG

Table S3. Microsatellite markers used for parentage assignments. Related to Figures 1 and 2. For each marker, the mate choice experiment year in which that marker was genotyped, the chromosome (Chr), and the primer sequences are given.