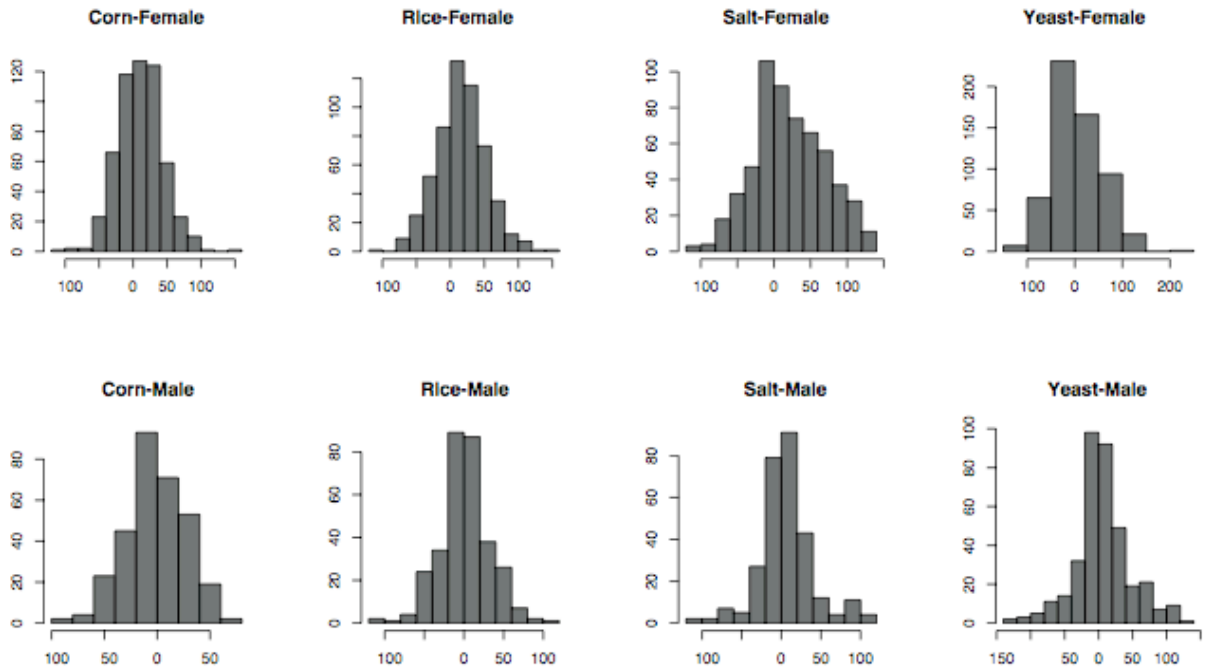
SUPPLEMENTARY MATERIAL

(for the submitted manuscript: Punzalan et al., Comparing the intersex genetic correlation for fitness across novel environments in the fruit fly, *Drosophila serrata*)

S1. Frequency distribution of environment- and sex-specific competitive fitness.

Competitive fitness (x-axis) was calculated as the difference in the number of wild-type (i.e. focal) vs. orange-eyed competitor offspring emerging from a given vial.



S2. The additive genetic variance-covariance (G) matrix of sex- and environment-specific competitive fitness. Estimation was performed using a full-rank unconstrained covariance matrix at the inbred-line level, and a reduced rank (five dimension factor analytic) covariance matrix at the inbred-line x reference line level. Labels denote the environment (C, R, S and Y, indicating corn, rice, salt and yeast respectively) followed by sex (F and M, indicating female and male respectively). Genetic variances are given along the diagonal (bold), with covariances below and correlations (italicized) above.

	CF	CM	RF	RM	SF	SM	YF	YM
CF	**152.76**	*-0.60*	*0.03*	*-1.00*	*0.10*	*-0.87*	*-0.41*	*-0.17*
CM	-128.12	**276.65**	*-0.69*	*1.00*	*0.12*	*0.77*	*0.51*	*0.68*
RF	-1.63	-166.33	**217.99**	*0.51*	*0.32*	*0.42*	*0.27*	*-0.17*
RM	-156.78	170.10	48.92	**81.78**	*-1.00*	*0.36*	*0.23*	*-0.43*
SF	28.85	28.15	85.63	-233.51	**396.51**	*0.63*	*-1.00*	*-0.59*
SM	-94.50	91.77	34.70	9.57	81.89	**70.17**	*0.28*	*-1.00*
YF	-68.89	104.15	42.44	16.04	-287.61	-4.68	**152.67**	*0.22*
YM	-30.72	223.49	-55.32	-76.33	-260.30	-251.33	37.80	**442.68**

S3. Asymptotic standard errors corresponding to genetic (co)variances and correlations in Table S2. Labels denote the environment (C, R, S and Y, indicating corn, rice, salt and yeast respectively) followed by sex (F and M, indicating female and male respectively).

	CF	CM	RF	RM	SF	SM	YF	YM
CF	**120.44**	*0.60*	*0.61*	*0.00*	*0.61*	*1.38*	*0.90*	*0.57*
CM	108.33	**194.07**	*0.48*	*0.00*	*0.51*	*1.10*	*0.74*	*0.46*
RF	107.39	123.54	**183.82**	*1.06*	*0.59*	*1.19*	*0.27*	*0.53*
RM	108.96	135.54	129.85	**83.53**	*0.00*	*1.87*	*0.23*	*1.20*
SF	143.99	163.87	165.14	172.25	**286.34**	*1.27*	*0.00*	*0.61*
SM	113.38	126.92	140.86	124.18	184.82	**107.25**	*1.57*	*0.00*
YF	124.10	140.94	142.96	154.40	198.71	151.95	**179.98**	*0.74*
YM	142.59	181.47	166.23	204.13	229.44	167.18	194.56	**301.73**

S4. Multivariate genetic variance for male and female fitness in novel environments, estimated separately by reference line.

Given the significant inbred line x reference interaction in the global estimation of **G** (i.e. when combining data across reference lines), we tested the genetic basis of fitness separately for each of the three reference lines. The same factor analytic modeling approach was used in which a series of nested likelihood ratio tests were conducted to determine whether the removal of a dimension significantly worsened the fit of the model (Hine and Blows 2006). Likelihood convergence problems prevented the fitting of models with more than five dimensions. Statistical support for two dimensions was found for reference lines 1 and 2, and marginally non-significant support for one dimension for reference line 3 (Table S4).

Table S4. Model fit statistic for test of the dimensionality of fitness across four novel environments, conducted separately for each of the three reference lines. AIC indicates Akaike's Information Criterion.

Reference line	Number of dimensions	-2 log likelihood	Number of parameters	AIC	P-Value
1	5	11871.54	38	11947.5	0.9929
	4	11871.79	34	11939.8	0.7367
	3	11874.55	29	11932.6	0.5762
	2	11879.30	23	11925.3	0.0437
	1	11893.75	16	11925.8	0.0072
	0	11914.72	8	11930.7	--
2	5	12269.52	38	12345.5	0.9810
	4	12269.94	34	12335.9	0.7835
	3	12272.40	29	12330.4	0.3250
	2	12279.35	23	12325.4	0.0490
	1	12293.47	16	12323.5	0.0311
	0	12310.38	8	12326.4	--
3	5	11453.64	38	11527.6	0.9999
	4	11453.67	34	11521.7	0.6666
	3	11456.88	29	11512.9	0.3964
	2	11463.13	23	11507.1	0.4353
	1	11470.07	16	11500.1	0.0766
	0	11484.27	8	11500.3	--