Supplemental Information

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SI Text

Quantitative Genetic Models. We fitted the following six models using either VCE 6.0.2, a program for restricted maximum likelihood (REML) estimation of variance components, or the software package MCMCglmm run in R 2.10.1, which implements a Bayesian approach using Monte Carlo-Markov Chain methods.

Model I: Five-trait permanent environment model in VCE. For Model 1, we used single observations as the unit of phenotypic data (i.e., 3,776 courtship rates, 3,168 unpaired response scores, 3,958 extrapair response scores, paternity of 2,253 eggs, and 202 measurements of extrapair siring success). For each of the five traits we fitted all of the relevant fixed effects (Table S2). Repeated measures on the same individual are taken into account by including individual identity as a random effect that is not linked to the pedigree (see Table S1 for sample sizes). Any individual consistency that is not accounted for by other random effects (e.g., additive genetic effects) will be attributed to individual identity and can be considered a permanent environment effect. To explore which random effects should be included in the final model, we started with separate single-trait models, including an additive genetic effect, a maternal effect (modeled by mother identity, not linked to the pedigree), an early-rearing environment effect (foster-pair identity), a late-rearing environment effect (peer-group identity), and a permanent environment effect (individual identity). Foster and peer group effects were always negligible and hence removed for practical reasons. Small but significant maternal effects were identified for three of the traits, and thus these were modeled for those traits in the subsequent multitrait model (mother identity has 321 levels). The model estimated variances and covariances at all possible levels: the additive-genetic matrix (five variances, 10 covariances), the maternal effect matrix (three variances, three covariances), the permanent environment matrix (five variances, four within-individual covariances; note that the six between-sex covariances are not defined), the residual variance matrix (five variances, covariances are not defined because measurements are from independent contexts), and the variance component of the identity of the courting extrapair male (one variance, for female extrapair response only).

All obtained matrices were confirmed to be positive-definite using the “corpcor” library in R 2.10.1 (1). To express genetic variances and covariances in the form of heritabilities and genetic correlations, we divided the variance components by the total phenotypic variances, and divided the covariances by the geometric mean of the corresponding trait variance components. The resulting relative components and correlations are given with their SEMs in Table S3. The fixed-effect estimates from this model are given in Table S2 (VCE estimate), and these are generally in close agreement with those obtained from simple mixed models in R (LMER estimate in Table S2). The model optimization finished with intermediate status 2 (“less than ideal”), indicating some problems with convergence. These convergence problems were not unexpected, given the large number of parameters to be estimated from this relatively small dataset. Hence, to seek confirmation we reduced the complexity of the model by fitting a series of two- and three-trait models. Reassuringly, these models mostly finished with status 1 and produced similar estimates in all parts of the G-matrix. However, the missing information on genetically correlated traits, as expected (2), led to larger SEs of estimates. Therefore, we only present the full five-trait models that make use of all of the information available. Another issue with Model I is that some of the dependent variables violated the assumption of normally distributed error structure. This problem is dealt with in Models III and IV.

Model II: Five-trait permanent environment model in MCMCglmm. We implemented the same model as above (same data and same parameters to be estimated) using MCMCglmm. We used a proper prior with all variances set to 0.02, covariances set to zero and a degree of belief parameter set to ν = (size of the matrix + 1) = 6. This prior should be uninformative for the genetic correlations. After a burn-in of 100,000 iterations, we ran 1,600,000 iterations from which a total of 200 samples were drawn (every 8,000 iterations). This high thinning interval was required to eliminate temporal autocorrelation, which indicates how demanding this model is in terms of the number of parameters to be estimated (the runtime was 4 wk). The fixed-effect estimates from this model are given in Table S2 (MCMC estimate), and the matrices obtained are shown in Table S4. These findings are qualitatively similar to those from the VCE model (Table S3), yet some of the critical between-sex genetic correlations were estimated to be less strong. The most extreme deviations from Model I concern maternal-effect correlations, which is understandable given the small size of the maternal-effect variance components. Hence, these estimates of maternal-effect correlations should be considered with great caution. Simplified versions of Model II with fewer parameters to be estimated (e.g., excluding maternal effects) showed less temporal autocorrelation and produced G-matrix estimates that were intermediate (less conservative than those shown in Table S4).

Model III: Five-trait model on individual estimates in VCE. The above Models I and II are of highly demanding complexity, in part because we used single observations as the unit of analysis rather than using mean trait values for each individual. Estimation of an individual’s average behavior, however, requires accounting for a range of confounding effects that tend to mask the intrinsic individual component. Hence, for each trait we fitted a separate mixed-effect models on the raw data using the lmer function in R [as described in *Methods*, with binomial error structure for female extrapair paternity (EPP), parameter estimates shown in Table S2], and extracted from these the random-effect estimates for each individual. We consider these the best available estimates for an individual’s average phenotype. Note that the recently made criticism of BLUPs (best linear unbiased predictions) obtained from animal models (3) does not apply to the kinds of random-effect estimates we use here. These (normally distributed; see Table S1) individual estimates were entered without further fixed effects into the animal model to extract the following variance-covariance matrices: additive genetic matrix (five variances, 10 covariances), maternal-effect matrix (three variances, three covariances), and residual matrix (five variances, four within-individual covariances). This model converged with status 1. As expected, the resulting heritability estimates (Table S5) tended to be higher than in the previous VCE model (Table S3), because the focus is on individual mean phenotypes rather than on single observations. Estimates of genetic correlations (Table S5) are hardly affected by this change in phenotypic variance, and were in close agreement with those from the permanent-environment VCE model (Table S3).

Model IV: Five-trait model on individual estimates in MCMCglmm. When implementing the above Model III in MCMCglmm, we encountered problems with model convergence (again because of the inclusion of maternal effects), so we reduced the model complexity to contain only the most essential variance components. We fitted a full additive genetic matrix (five variances, 10 covariances) and a residual matrix with only the variances modeled (five variances; the within-sex residual covariances are defined but were not modeled). We used a proper prior with variances set to 0.02, covariances set to zero and a degree of belief parameter set to ν = (size of the matrix + 1) = 6. After a burn-in of 100,000 iterations, we ran 3,000,000 iterations from which a total of 1,000 samples were drawn (every 3,000 iterations). Because of this high thinning interval, there were no problems with temporal autocorrelation. The resulting matrices are shown in Table S6. These findings are qualitatively similar to those from the previous three models (Tables S3–S5).

Model V: VCE model on within-pair vs. extrapair responsiveness. To examine the genetic correlation between within-pair and extrapair responsiveness, we fitted a two-trait permanent-environment model in VCE. The following matrices were estimated: the additive-genetic matrix (two variances, one covariance), the permanent environment matrix (two variances, one covariance), the residual variance matrix (two variances, covariances are not defined), and the matrix for the identity of the courting male (two variances, one covariance). We converted covariances to correlations as described above. The male-identity effect correlation was estimated as $r = 0.531 \pm 0.141$ (Table S7), indicating that males that received positive responses in extrapair courtships also tended to receive positive responses in within-pair courtships. This fact should make it easier to estimate the relative male and female contributions to within-pair responsiveness. However, even though the total female contribution was estimated as 10% (of the total phenotypic variance), most of this appeared to be nongenetic (7.6% permanent environment). Because of the low heritability of female within-pair response, it is difficult to estimate the genetic correlation between within- and extrapair responsiveness (see large SE in Table S7). Fixed-effect estimates in this permanent-environment model were in good agreement with estimates from separate mixed-effect models in R (Table S9).

Model VI: MCMC model on within-pair vs. extrapair responsiveness. The same permanent-environment model was also fitted in MCMCglmm. We used a proper prior with low variances (0.02), covariances of zero, and the degree of belief parameter was set to ν = (size of the matrix + 1) = 3. After a burn-in of 100,000 iterations, we ran 1,500,000 iterations from which a total of 1,000 samples were drawn (every 1,500 iterations). Because of the high thinning interval, there were no problems with temporal autocorrelation. The resulting matrices are shown in Table S8. These findings are qualitatively similar to those from Table S7. Fixed-effect estimates are shown in Table S9.

Analysis of evolutionary potential. To analyze the extent to which strong genetic correlations constrain the potential for evolutionary change, we calculate the effective number of dimensions (4) of the additive genetic variance-covariance matrix by means of principal component analysis (5) (using MAT-LAB). For this purpose, trait values of individuals were z-standardized. The above Model III was fitted to z-transformed trait values, and eigenvectors were extracted from the obtained five-trait variance-covariance matrix. The first eigenvector already explained 79% of all genetic variation, which means that the G-matrix contained only 1.27 effective dimensions. When excluding unpaired responsiveness (the trait that is only weakly linked to measures of extrapair paternity) from the matrix, the resulting four-trait matrix has only 1.12 effective dimensions, showing that the independent evolution of any one of those four traits would be greatly constrained by the genetic correlations with the other traits.

Description of Courtships in Aviaries. Video observations in aviaries yielded 4,601 within-pair courtships and 3,958 extrapair courtships. For clarity, we here briefly describe the outcome of these courtships in terms of copulations. Apparently successful copulations (cloacal contact) occurred in 1,071 of the within-pair courtships (23.3%; note that this percentage is biased upward by our focus on early morning observations and on this particular courtship tree). Of these courtships, 88.8% were because of solicited copulations (female tail-quivering before copulation), 11.1% because of nonsolicited but accepted copulations, and 0.1% (n = 1) because of a forced copulation that appeared successful despite signs of female resistance. Among all of the within-pair courtships, we also observed a total of 113 forced copulation attempts that were unsuccessful because of female resistance. Of all extrapair courtships only 283 (7.2%) resulted in successful copulation. Of these courtships, 69.3% were because of solicited copulations, 25.4% because of nonsolicited but accepted copulations, and 5.3% (n = 15) because of a situation where an extrapair male copulated with the female who actually appeared to solicit to her social partner. The female showed weak signs of resistance in 4 of these 15 cases, and no signs of resistance in the remaining 11 cases. A total of 323 unsuccessful forced copulation attempts occurred among the 3,958 extrapair courtships. For all extrapair courtships where female copulation solicitations occurred (n = 406), but did not lead to successful extrapair copulations (51%; n = 208), we examined the circumstances of "failure." This failure included the interruption of the copulation by other individuals, male loss of balance when perched on the female back during copulation, or premature female departure. In not a single case did we witness a clear lack of male interest as the reason for missed extrapair mating opportunities.

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3. Hadfield JD, Wilson AJ, Garant D, Sheldon BC, Kruuk LEB (2010) The misuse of BLUP in ecology and evolution. *Am Nat* 175:116–125.
4. Kirkpatrick M (2009) Patterns of quantitative genetic variation in multiple dimensions. *Genetica* 136:271–284.
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Table S1. Sample sizes and distributions

		Male courtship rate	Female unpaired response	Female extrapair response	Female within-pair response	Female EPP	Male EPP
N	Individuals	800	754	141	143	149	152
	Measurements	3,776	3,168	3,958	4,601	2,253[†]	202[‡]
Raw data	Mean	22.8[§]	−0.14	−0.16	0.47	0.29	4.28[¶]
	SD	20.5[§]	0.72	0.53	0.57		6.84[¶]
	# of levels	111	5	5	5	2	26
	Range	0–144[§]	−1 to +1	−1 to +1	−1 to +1	0, 1	0–40[¶]
Transformed	Transformation	Square root	—	—	—	logit	Square root
	Mean	4.05	−0.14	−0.16	0.47	−0.88	1.40
	SD	2.53	0.72	0.53	0.57		1.52
	Range	0–12	−1 to +1	−1 to +1	−1 to +1		0–6.3
	Assumed distribution	Normal	Normal	Normal	Normal	Binomial	Normal
	Normality of errors KS-test: D	0.037*	0.065*	0.095*	0.068*		0.074
BLUPs	Mean	0	0	0	0	0.20	0
	SD	1.57	0.42	0.12	0.10	1.88	0.35
	Range	−4.03 to 5.45	−0.89 to 1.16	−0.27 to 0.51	−0.26 to 0.21	−3.35 to 4.79	−0.60 to 1.27
	Normality of BLUPs KS-test: D	0.048	0.061*	0.091	0.042	0.086	0.080
	% phenotypic variance [‖]	57%	49%	9.5%	8.5%		22%

Sample sizes and distributions of the original measurements (raw data), the transformed values (square-root transformation for male courtship rate and male EPP; and logit transformation for female EPP), and of the male or female random effect estimates (BLUPs) extracted from the mixed models (shown in Tables S2 and S9). The D statistic of a Kolmogorov-Smirnov test for normality is given (small values indicate a good fit to normality), and significant deviation from normality is indicated by an asterisk. For BLUPs, the percentage of variance explained by the random effect (male or female identity) is given.

[†] Number of eggs.

[‡] Number of male breeding seasons.

[§] In seconds.

[¶] Number of extrapair young sired per male breeding season.

[‖] Of transformed values after controlling for fixed effects.

Table S2. Parameter estimates for fixed effects on five traits related to multiple mating

Dependent trait	Level or covariate	Reference level or scaling of the covariate	LMER estimate	SEM	VCE estimate	MCMC estimate
Male courtship rate	Intercept		6.125	0.302	5.840	6.121
	Test batch 2*	Test batch 1	−1.864	0.258	−1.756	−1.771
	Test batch 3	Test batch 1	−1.593	0.244	−1.597	−1.530
	Test batch 4	Test batch 1	−0.893	0.246	−0.851	−0.821
	Test batch 5	Test batch 1	−0.745	0.278	−0.903	−0.887
	Test batch 6	Test batch 1	−0.568	0.283	−0.725	−0.746
	Test batch 7	Test batch 1	−0.049	0.266	−0.203	−0.206
	Test batch 8	Test batch 1	0.095	0.411	−0.083	0.001
	Test batch 9	Test batch 1	−1.569	0.387	−1.753	−1.815
	Test batch 10	Test batch 1	−3.024	0.353	−2.999	−3.048
	Test batch 11	Test batch 1	−1.859	0.354	−1.834	−1.891
	Test day 2	Test day 1	−0.616	0.056	−0.616	−0.616
	Test day 3	Test day 1	−1.007	0.116	−1.007	−1.003
	Test day 4	Test day 1	−1.267	0.096	−1.267	−1.266
	Mixed-sex rearing[†]	Unisex rearing	0.569	0.241	0.606	0.655
	Male *F* (C)[‡]	Per 0.25 *F*	−1.112	0.394	−1.346	−1.381
	Daytime (C)	Per 1 h	−0.058	0.016	−0.057	−0.058
Female unpaired response	Intercept		−0.202	0.057	−0.183	−0.210
	Test batch 2*	Test batch 1	0.117	0.082	0.158	0.159
	Test batch 3	Test batch 1	0.121	0.074	0.198	0.169
	Test batch 4	Test batch 1	0.333	0.076	0.394	0.380
	Test batch 5	Test batch 1	0.242	0.083	0.169	0.221
	Test batch 6	Test batch 1	0.091	0.082	0.069	0.075
	Test batch 7	Test batch 1	0.098	0.077	0.050	0.083
	Test batch 8	Test batch 1	0.056	0.115	−0.050	0.014
	Test batch 9	Test batch 1	−0.199	0.113	−0.258	−0.219
	Test batch 10	Test batch 1	−0.312	0.104	−0.350	−0.332
	Test batch 11	Test batch 1	−0.178	0.103	−0.217	−0.197
	Test day 2	Test day 1	−0.134	0.020	−0.135	−0.134
	Test day 3	Test day 1	−0.106	0.044	−0.110	−0.111
	Test day 4	Test day 1	−0.129	0.035	−0.131	−0.127
	Mixed-sex rearing[†]	Unisex rearing	0.220	0.069	0.276	0.241
Female extrapair response	Intercept		0.320	0.060	0.289	0.296
	Author K.M.[§]	Author E.B.	−0.117	0.035	−0.106	−0.119
	Author W.F.	Author E.B.	−0.084	0.037	−0.076	−0.088
	Year 2007[¶]	Year 2006	−0.026	0.066	−0.028	−0.004
	Year 2008	Year 2006	−0.106	0.064	−0.102	−0.126
	Year 2009	Year 2006	−0.174	0.067	−0.183	−0.180
	Log time (C)	Per 9 min[‖]	−0.071	0.010	−0.066	−0.069
	Log days paired (C)	Per 9 d**	−0.115	0.018	−0.113	−0.108
	Days from day -3 (C)[††]	Per 1 d	−0.031	0.005	−0.032	−0.031
	Eggs in last 5 d (C)	Per 1 egg	−0.024	0.009	−0.024	−0.026
Female EPP	Intercept		−1.415[‡‡]	0.385[‡‡]	0.315	0.345
	Sex ratio 0.5	Sex ratio 0.4	0.319[‡‡]	0.237[‡‡]	0.031	0.020
	Sex ratio 0.6	Sex ratio 0.4	0.820[‡‡]	0.249[‡‡]	0.103	0.098
	Log days paired (C)	Per 9 d**	−0.394[‡‡]	0.158[‡‡]	−0.042	−0.051
	Partner *F* (C)[‡]	Per 0.25 *F*	1.912[‡‡]	0.768[‡‡]	0.255	0.235
Male EPP	Intercept		0.155	0.224	−0.102	0.067
	Mixed-sex rearing[†]	Uni-sex rearing	−0.237	0.224	−0.321	−0.257
	Days paired (C)	Per 100 d	1.704	0.265	1.882	1.823
	Male *F* (C)[‡]	Per 0.25 *F*	−0.687	0.373	−1.076	−0.884

For continuous predictors (covariates, marked by "C") we give slope estimates in relation to the units of change in the predictor. For factors we give estimates for each level relative to the first level (reference). Parameter estimates and SEM are from five univariate mixed-effect models performed in R (LMER estimate). For comparison, parameter estimates from five-trait permanent-environment animal models are given, one performed in VCE (Model I; VCE estimate) and one in MCMCglmm (Model II; MCMC estimate).

*Experimental tests were carried out in 11 separate batches taking place between July 2002 and May 2010.

[†] Birds were reared in either mixed-sex or unisex peer groups.

[‡] Inbreeding coefficient *F*, the parameter estimate is for a change in *F* of 0.25 units.

[§] Observer scoring responsiveness.

[¶] Year of study (i.e., experimental batch).

[‖] Log(x+1) transformed time in minutes; the first unit of time has passed 9 min after lights on, the second after 99 min.

**Log(x+1) transformed time paired in days; the first unit of time has passed 9 d after pair formation, the second after 99 d.

[††] The number of days between the courtship and the day 3 d before the start of egg laying (with values ≥5 coded as 5).

[‡‡] Parameter estimates are on the logit scale and hence not directly comparable to the VCE estimate.

Table S3. Variance components and correlations estimated from a five-trait permanent environment animal model performed in VCE (Model I)

		Male		Female		
Effects		Courtship	EPP	UP response	EP response	EPP
Genetic	Male courtship	0.198 ± 0.046	0.619 ± 0.203	**0.257 ± 0.139**	**0.832 ± 0.106**	**0.873 ± 0.239**
	Male EPP		0.173 ± 0.116	**0.432 ± 0.279**	**0.531 ± 0.335**	**0.867 ± 0.261**
	Female UP response			0.212 ± 0.044	0.695 ± 0.155	0.192 ± 0.293
	Female EP response				0.114 ± 0.023	0.603 ± 0.349
	Female EPP					0.061 ± 0.038
Maternal	Male courtship	0.056 ± 0.023	—	−0.609 ± 0.263	—	−0.044 ± 0.344
	Male EPP		—	—	—	—
	Female UP response			0.052 ± 0.022	—	0.819 ± 0.196
	Female EP response				—	—
	Female EPP					0.041 ± 0.021
Permanent environment	Male courtship	0.321 ± 0.042	0.244 ± 0.169	—	—	—
	Male EPP		0.280 ± 0.110	—	—	—
	Female UP response			0.238 ± 0.030	−0.612 ± 0.682	0.159 ± 0.108
	Female EP response				0.004 ± 0.008	0.555 ± 0.626
	Female EPP					0.340 ± 0.046
EP male ID	Male courtship	—	—	—	—	—
	Male EPP		—	—	—	—
	Female UP response			—	—	—
	Female EP response				0.130 ± 0.018	—
	Female EPP					—
Residual	Male courtship	0.425 ± 0.026	—	—	—	—
	Male EPP		0.548 ± 0.027	—	—	—
	Female UP response			0.498 ± 0.042	—	—
	Female EP response				0.752 ± 0.020	—
	Female EPP					0.559 ± 0.024

Variance components are standardized by the phenotypic variance (after controlling for fixed effects). Variance components ± SEM are shown on the diagonal (heritabilities are highlighted in gray), correlations ± SEM between pairs of traits are shown off the diagonal. Between-sex genetic correlations are highlighted in bold. The additive genetic, maternal, and permanent environment components together reflect the individual repeatability of single units of observation. EP male ID stands for the effect of the identity of the courting extrapair male on female extrapair responsiveness. EP, extrapair (aviary experiments); EPP, extrapair paternity; UP, unpaired (cage experiments). Parameters that were not or cannot be estimated (or in the case of EP male ID do not apply to most traits) are marked with "—."

Table S4. Variance components and correlations estimated from a five-trait permanent environment animal model performed in MCMCglmm (Model II)

		Male		Female		
Effects		Courtship	EPP	UP response	EP response	EPP
Genetic	Male courtship	0.200 ± 0.050	0.783 ± 0.269*	**0.170 ± 0.183**	**0.515 ± 0.188***	**0.420 ± 0.287†**
	Male EPP		0.164 ± 0.111	**0.323 ± 0.296**	**0.486 ± 0.229†**	**0.330 ± 0.315**
	Female UP response			0.253 ± 0.053	0.416 ± 0.172*	0.056 ± 0.336
	Female EP response				0.086 ± 0.024	0.276 ± 0.246
	Female EPP					0.146 ± 0.063
Maternal	Male courtship	0.021 ± 0.019	—	−0.014 ± 0.305	—	0.124 ± 0.362
	Male EPP		—	—	—	—
	Female UP response			0.036 ± 0.013	—	0.000 ± 0.121
	Female EP response				—	—
	Female EPP					0.068 ± 0.029
Permanent environment	Male courtship	0.351 ± 0.043	0.157 ± 0.547	—	—	—
	Male EPP		0.079 ± 0.105	—	—	—
	Female UP response			0.249 ± 0.045	0.102 ± 0.267	0.285 ± 0.234
	Female EP response				0.035 ± 0.012	0.240 ± 0.243
	Female EPP					0.265 ± 0.063
EP male ID	Male courtship	—	—	—	—	—
	Male EPP		—	—	—	—
	Female UP response			—	—	—
	Female EP response				0.126 ± 0.017	—
	Female EPP					—
Residual	Male courtship	0.428 ± 0.017	—	—	—	—
	Male EPP		0.758 ± 0.137	—	—	—
	Female UP response			0.497 ± 0.023	—	—
	Female EP response				0.717 ± 0.025	—
	Female EPP					0.521 ± 0.039

Variance components are standardized by the phenotypic variance (after controlling for fixed effects). Variance components ± SEM are shown on the diagonal (heritabilities are highlighted in gray), correlations ± SEM between pairs of traits are shown off the diagonal. Between-sex genetic correlations are highlighted in bold. The additive genetic, maternal, and permanent environment components together reflect the individual repeatability of single units of observation. EP male ID stands for the effect of the identity of the courting extrapair male on female extrapair responsiveness. EP, extrapair (aviary experiments); EPP, extrapair paternity; UP, unpaired (cage experiments). Parameters that were not or cannot be estimated are marked with "—."

*signifies that the 95% highest posterior density interval excludes zero.

†signifies that the 90% highest posterior density interval excludes zero.

Table S5. Variance components and correlations estimated from a five-trait animal model on individual random effect estimates (two-step model) performed in VCE (Model III)

		Male		Female		
Effects		Courtship	EPP	UP response	EP response	EPP
Genetic	Male courtship	0.277 ± 0.048	0.584 ± 0.389	**0.289 ± 0.128**	**0.857 ± 0.042**	**0.916 ± 0.202**
	Male EPP		0.060 ± 0.059	**0.636 ± 0.466**	**0.734 ± 0.445**	**0.782 ± 0.286**
	Female UP response			0.346 ± 0.071	0.740 ± 0.105	0.240 ± 0.405
	Female EP response				0.578 ± 0.117	0.761 ± 0.300
	Female EPP					0.147 ± 0.071
Maternal	Male courtship	0.084 ± 0.033	—	−0.621 ± 0.228	—	−0.155 ± 0.258
	Male EPP		—	—	—	—
	Female UP response			0.083 ± 0.032	—	0.871 ± 0.190
	Female EP response				—	—
	Female EPP					0.074 ± 0.050
Residual	Male courtship	0.639 ± 0.049	0.131 ± 0.077	—	—	—
	Male EPP		0.940 ± 0.066	—	—	—
	Female UP response			0.572 ± 0.080	−0.163 ± 0.133	0.136 ± 0.104
	Female EP response				0.422 ± 0.117	0.130 ± 0.108
	Female EPP					0.779 ± 0.069

Variance components are standardized by the phenotypic variance (after controlling for fixed effects). Variance components ± SEM are shown on the diagonal (heritabilities are highlighted in gray), correlations ± SEM between pairs of traits are shown off the diagonal. Between-sex genetic correlations are highlighted in bold. EP, extrapair (aviary experiments); EPP, extrapair paternity; UP, unpaired (cage experiments). Parameters that were not or cannot be estimated are marked with "—."

Table S6. Variance components and correlations estimated from a five-trait animal model on individual random effect estimates (two-step model) performed in MCMCglmm (Model IV)

		Male		Female		
Effects		Courtship	EPP	UP response	EP response	EPP
Genetic	Male courtship	0.296 ± 0.072	0.430 ± 0.250[†]	**0.237 ± 0.165**	**0.510 ± 0.148***	**0.851 ± 0.184***
	Male EPP		0.199 ± 0.073	**0.278 ± 0.258**	**0.277 ± 0.216**	**0.422 ± 0.262[†]**
	Female UP response			0.390 ± 0.072	0.419 ± 0.129*	0.391 ± 0.227[†]
	Female EP response				0.721 ± 0.086	0.529 ± 0.172*
	Female EPP					0.123 ± 0.084
Residual	Male courtship	0.704 ± 0.072	—	—	—	—
	Male EPP		0.801 ± 0.073	—	—	—
	Female UP response			0.610 ± 0.072	—	—
	Female EP response				0.279 ± 0.086	—
	Female EPP					0.877 ± 0.084

Variance components are standardized by the phenotypic variance (after controlling for fixed effects). Variance components ± SEM are shown on the diagonal (heritabilities are highlighted in gray); correlation means ± SEM between pairs of traits are shown off the diagonal. SEMs were calculated from the posterior distribution (the SD of all samples) for the sake of comparability with Table S3. Between-sex genetic correlations are highlighted in bold. EP, extrapair; EPP, extrapair paternity; UP, unpaired (cage experiments). Parameters that were not or cannot be estimated are marked with "—."

*signifies that the 95% highest posterior density interval excludes zero.

[†] signifies that the 90% highest posterior density interval excludes zero.

Table S7. Variance components and correlations estimated from a two-trait permanent environment animal model in VCE on extrapair (EP) and within-pair (WP) responsiveness (Model V)

Effects		Female EP response	Female WP response
Genetic	Female EP response	0.090 ± 0.027	−0.194 ± 0.513
	Female WP response		0.026 ± 0.023
Permanent environment	Female EP response	0.017 ± 0.017	1.000*
	Female WP response		0.076 ± 0.033
Male ID	Female EP response	0.133 ± 0.018	0.531 ± 0.141
	Female WP response		0.090 ± 0.028
Residual	Female EP response	0.759 ± 0.023	—
	Female WP response		0.808 ± 0.023

Variance components are standardized by the phenotypic variance (after controlling for fixed effects). Variance components ± SEM are shown on the diagonal (heritabilities are highlighted in gray), correlations ± SEM are shown off the diagonal. The additive genetic and permanent environment components together reflect the individual repeatability of behavior across single courtship observations. Male ID stands for the effect of the identity of the courting male on the responsiveness of the female.

*Correlation estimated larger than 1 is constrained to 1 and no meaningful SEM can be given.

Table S8. Variance components and correlations estimated from a two-trait permanent environment animal model in MCMCglmm on EP and WP responsiveness (Model VI)

Effects		Female EP response	Female WP response
Genetic	Female EP response	0.064 ± 0.022	0.073 ± 0.276*
	Female WP response		0.047 ± 0.021
Permanent environment	Female EP response	0.048 ± 0.017	0.355 ± 0.229
	Female WP response		0.067 ± 0.024
Male ID	Female EP response	0.134 ± 0.019	0.506 ± 0.136
	Female WP response		0.089 ± 0.024
Residual	Female EP response	0.753 ± 0.023	—
	Female WP response		0.797 ± 0.024

Variance components are standardized by the phenotypic variance (after controlling for fixed effects). Variance components means ± SEM are shown on the diagonal (heritabilities are highlighted in gray); correlation means ± SEM are shown off the diagonal. The additive genetic and permanent environment components together reflect the individual repeatability of behavior across single courtship observations. Male ID stands for the effect of the identity of the courting male on the responsiveness of the female.

*95% highest posterior density interval = −0.455 to +0.580.

Table S9. Parameter estimates for fixed effects on WP and EP responsiveness

Dependent trait	Level or covariate	Reference level or scaling of the covariate	LMER estimate	SEM	VCE estimate	MCMC estimate
Female WP response	Intercept		0.480	0.062	0.485	0.467
	Author K.M.*	Author E.B.	−0.115	0.034	−0.085	−0.115
	Author W.F.	Author E.B.	0.084	0.036	0.090	0.083
	Year 2007[†]	Year 2006	0.227	0.068	0.190	0.233
	Year 2008	Year 2006	0.207	0.065	0.217	0.216
	Year 2009	Year 2006	0.095	0.067	0.064	0.100
	Log time since dawn (C)	Per 9 min‡	−0.038	0.011	−0.039	−0.037
	Log days paired (C)	Per 9 d[§]	0.101	0.019	0.093	0.105
	Days from −3 (C)[¶]	Per 1 d	−0.055	0.005	−0.053	−0.055
	Eggs in last 5 d (C)	Per 1 egg	−0.081	0.011	−0.079	−0.082
Female EP response	Intercept		0.320	0.060	0.291	0.315
	Author K.M.*	Author E.B.	−0.117	0.035	−0.106	−0.118
	Author W.F.	Author E.B.	−0.084	0.037	−0.076	−0.082
	Year 2007[†]	Year 2006	−0.026	0.066	−0.014	−0.022
	Year 2008	Year 2006	−0.106	0.064	−0.075	−0.105
	Year 2009	Year 2006	−0.174	0.067	−0.163	−0.184
	Log time since dawn (C)	Per 9 min[‡]	−0.071	0.010	−0.066	−0.070
	Log days paired (C)	Per 9 d[§]	−0.115	0.018	−0.114	−0.114
	Days from −3 (C)[¶]	Per 1 d	−0.031	0.005	−0.032	−0.031
	Eggs in last 5 d (C)	Per 1 egg	−0.024	0.009	−0.024	−0.025

For continuous predictors (covariates, marked by "C") we give slope estimates in relation to the units of change in the predictor. For factors we give estimates for each level relative to the first level (reference). Parameter estimates and SEM are from two separate mixed-effect models performed in R (LMER estimate). For comparison, parameter estimates from two-trait permanent-environment animal models are given: one performed in VCE (Model V; VCE estimate) and one in MCMCglmm (Model VI; MCMC estimate).

*Observer scoring responsiveness.

[†] Year of study (i.e., experimental batch).

[‡] Log(x+1) transformed time in minutes; the first unit of time has passed 9 min after lights on, the second after 99 min.

[§] Log(x+1) transformed time paired in days; the first unit of time has passed 9 d after pair formation, the second after 99 d.

[¶] The number of days between the courtship and the day three days before the start of egg laying (with values ≥5 coded as 5).