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Supplementary material

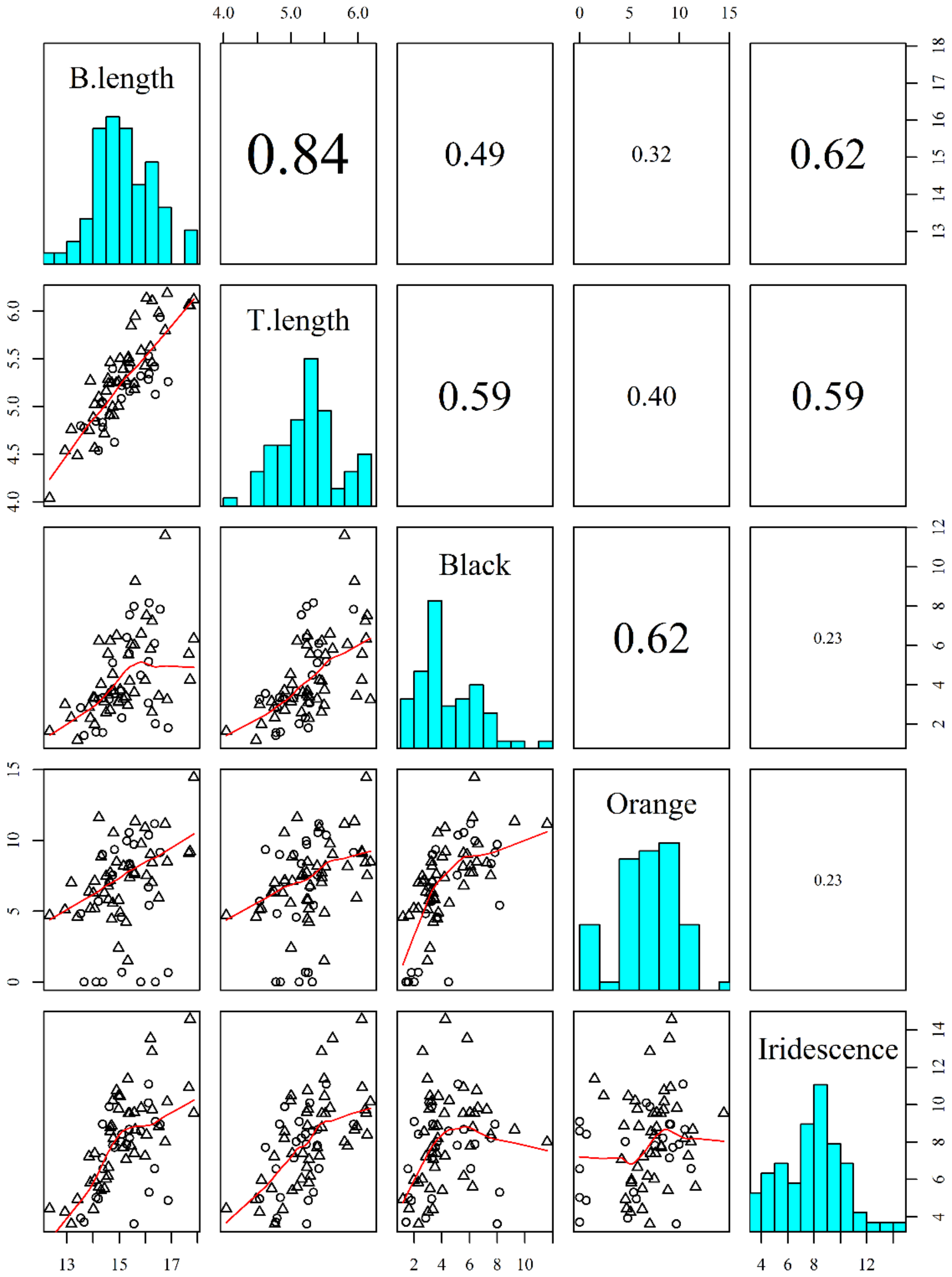

Fig. S1 Intercorrelations among male guppy morphometrics and measurements of colour. Each square depicts the correlation between the indicated trait of row and column. With; B.length = average body length (mm), T.length = average caudal fin length (mm), and the three colours whose surfaces were quantified (mm^2). Averages were taken from only two measurements (left and right side photograph) for each guppy (in mm for lengths and mm^2 for surfaces). The upper panel shows absolute correlations for each pair of traits, with size being proportionate to the strength of correlation.

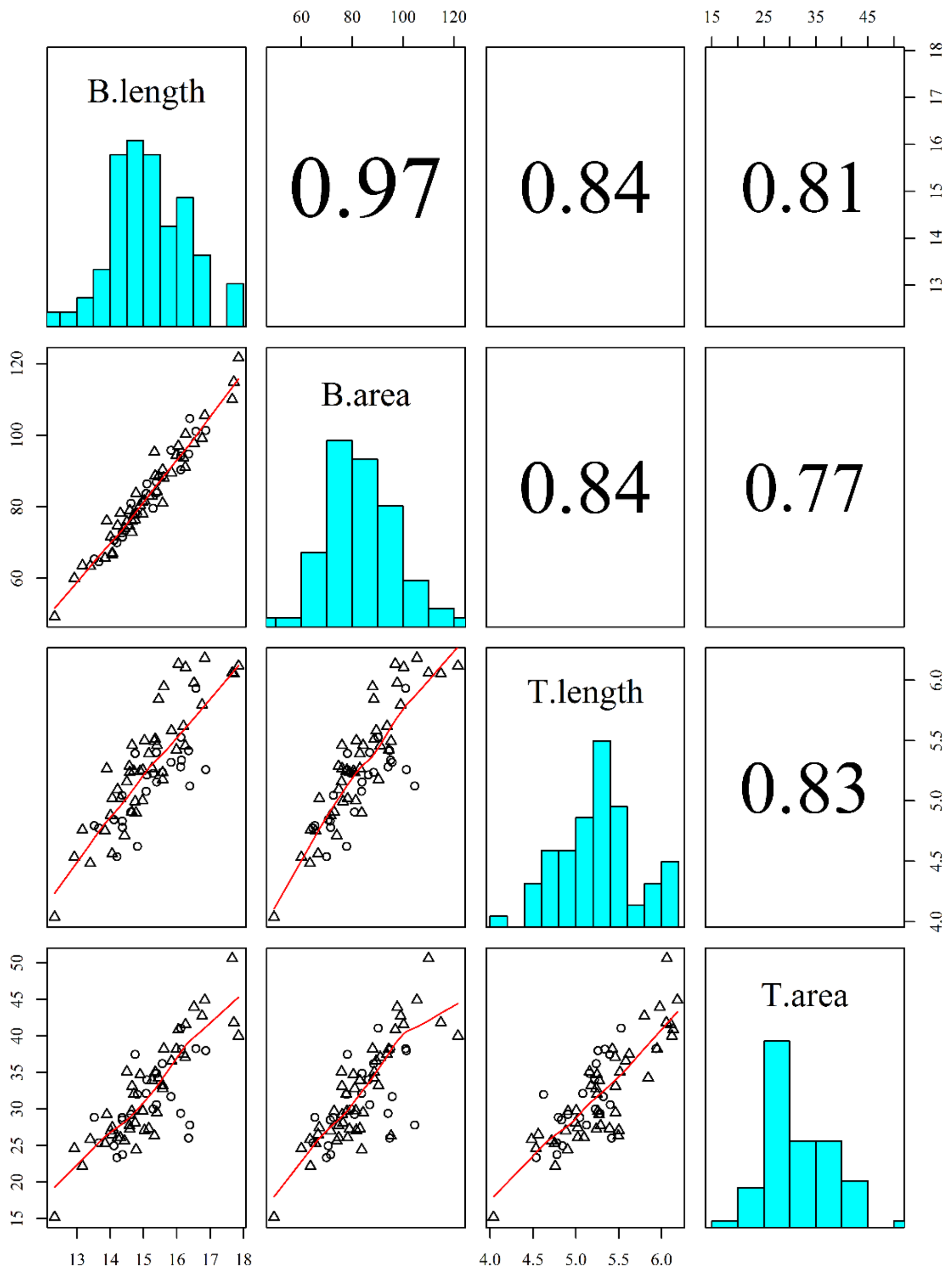

Fig. S2 Intercorrelations among male guppy morphometrics, each square depicts a correlation between the indicated trait of row and column. With; B.length = average body length, B.area = average body area, T.length = average caudal fin length and T.area = average caudal fin area. Averages were taken from only two measurements (left and right side photograph) for each guppy (in mm for lengths and mm^2 for surfaces). The upper panel shows absolute correlations for each pair of traits, with size being proportionate to the strength of correlation.

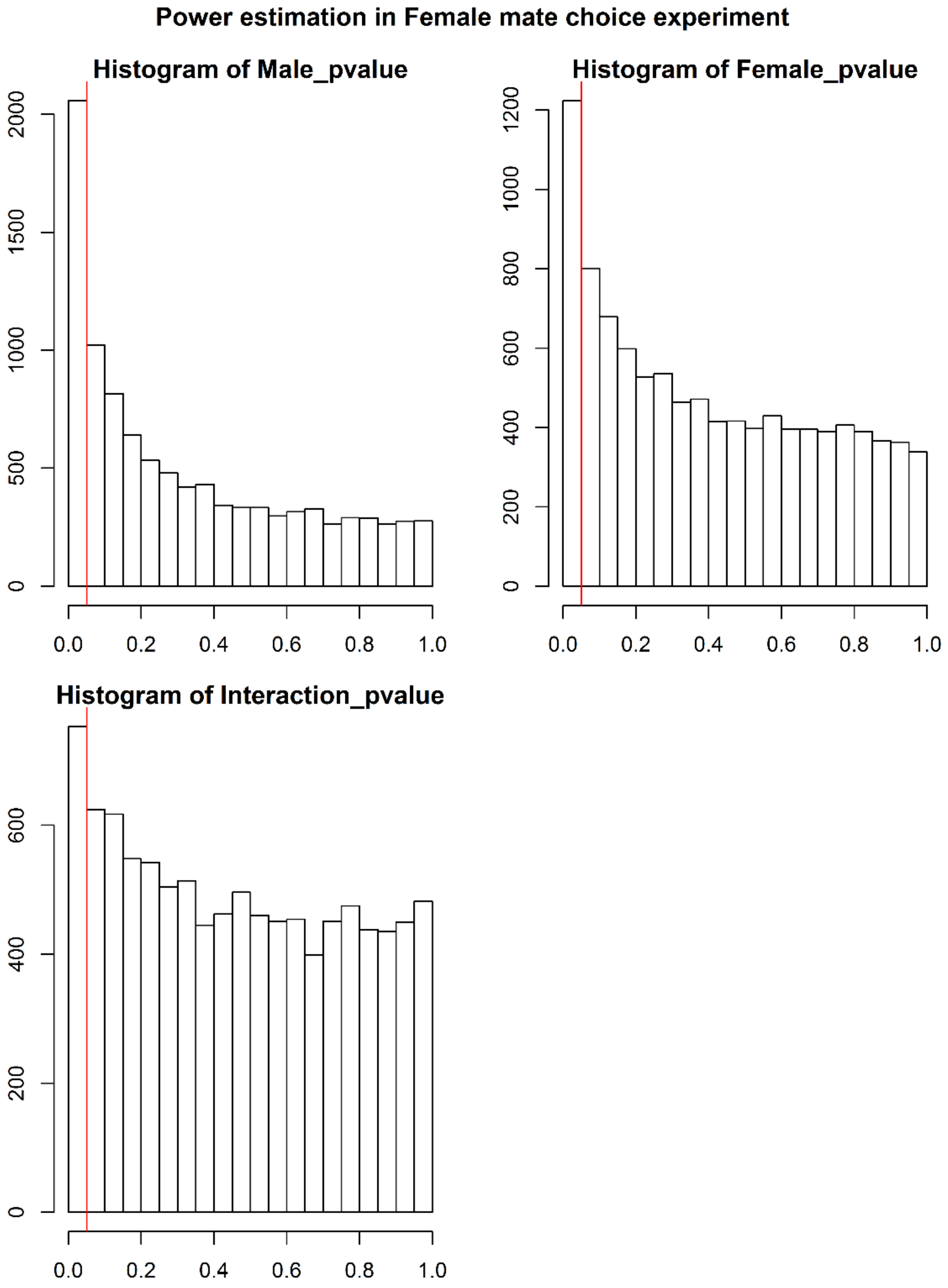

Fig. S3 A power estimation for the female choice experiment (set-up 1). A naive power analysis would, for instance, consist of: two groups with a size of 7 females each (independent level), a between group variance of 0.3152 and an averaged within group variance of 0.3331001. At an α-level of 0.05 this would yield a power of 66%. But this would not take into account repeated measures, nor multiple levels of testing. Hence, using the same paradigm; the same model parameters for set-up 1 were used to generate random distributions. These generated distributions were fitted back to the model and ANOVA-tested. *P*-values were extracted for both factors and their interaction, and this was simulated 10,000 times in total. The respective *p*-values were then plotted in the histograms above. The percentage of significant *p*-values (left of the red line) are then an estimation of power (1-β), i.e. given our model parameters (variance and effect size) how often would we detect a significant effect. For the male treatment effect a power of approximately 21% was attained. For code, see 'PowerEstimation.R'

Table S1 Measurement error on male morphometry following Sokal and Rohlf (1981). $\%\mathrm{ME} = \frac{s^2_{\mathrm{within}}}{s^2_{\mathrm{within}} + s^2_{\mathrm{among}}} * 100$; with $s^2_{\mathrm{within}} = \mathrm{MS}_{\mathrm{within}}$ and $s^2_{\mathrm{among}} = \frac{\mathrm{MS}_{\mathrm{among}} - \mathrm{MS}_{\mathrm{within}}}{\mathrm{m}}$ (with $\mathrm{m} = \#\ \mathrm{of\ repeated\ measurements}$)]. The considerably higher ME found for caudal fin area (27.5%) can be attributed to the spread of the caudal fin. While photographing, the males' caudal fins were spread out to their maximum extent by the observer.

Trait	Measurement error
Body length (mm)	3.3 %
Body area (mm²)	4.5 %
Caudal fin length (mm)	9.0 %
Caudal fin area (mm²)	27.5 %

Table S2: Tests for correlated response among replicates (A and B) in variables studied, within each male treatment (Inter and Intra). With Treat. = treatment, Dis. = probability distribution used (G = Gaussian; P = Poisson; QP = ‘Quasipoisson’, i.e. quasi-likelihood approach), link = link function used (I = Identity; L = Log), value = test value (F-value for F-tests; χ^2-value for Chi-square likelihood ratio tests), Df = nominal and denominator degrees of freedom, Test = model test used, and Sig. = significance levels (*p*<0.001=***; *p*<0.01=**; and *p*<0.05=*). Variables in red showed a significant uncorrelated response between replicates in one or both treatments and were hence not considered further (see main text). No post hoc correction was applied, since there is a reverse in paradigm. I.e. type I errors (or incorrect rejections of the null hypothesis) are less important than type II errors when one is interested in ‘retaining’ the null hypothesis.

	Variable	Treat.	Dis.	Link	Df	Value	Test	*p*-value	Sig.
Morphology	Orange area	Inter	G	I	1,22	NA	NA	NA	
		Intra	G	I	1,43	NA	NA	NA	
	Orange spots	Inter	QP	L	1,22	16.17	X^2	0.807	
		Intra	P	L	1,43	30.72	X^2	0.920	
	Black area	Inter	G	I	1,22	1.317	F	0.263	
		Intra	G	I	1,43	2.461	F	0.124	
	Black spots	Inter	P	L	1,22	18.21	X^2	0.693	
		Intra	QP	L	1,43	66.24	X^2	0.013	*
	Iridescence area	Inter	G	I	1,22	1.561	F	0.225	
		Intra	G	I	1,43	0.029	F	0.866	
	Iridescence spots	Inter	QP	L	1,22	2.082	X^2	1.000	
		Intra	QP	L	1,43	60.73	X^2	0.038	*
	Body length	Inter	G	I	1,22	13.53	F	0.001	**
		Intra	G	I	1,43	38.73	F	<0.001	***
	Tail length	Inter	G	I	1,22	7.270	F	0.013	*
		Intra	G	I	1,43	41.80	F	<0.001	***
	Total length	Inter	G	I	1,22	13.37	F	0.001	**
		Intra	G	I	1,43	43.38	F	<0.001	***
Mirror test	Aggression index	Inter	G	I	1,22	18.98	F	<0.001	***
		Intra	G	I	1,43	0.255	F	0.616	
Reproductive behaviour	Sigmoid display	Inter	QP	L	1,8	7.128	X^2	0.523	
		Intra	QP	L	1,14	16.41	X^2	0.289	
	Gonopodial flip	Inter	P	L	1,8	23.05	X^2	0.003	**
		Intra	QP	L	1,14	36.83	X^2	<0.001	***
	Nips	Inter	QP	L	1,8	18.76	X^2	0.016	*
		Intra	QP	L	1,14	13.50	X^2	0.487	
	Follow	Inter	G	I	1,8	1.940	F	0.201	
		Intra	G	I	1,14	0.683	F	0.422	
	Parallel	Inter	G	I	1,8	2.357	F	0.163	
		Intra	G	I	1,14	9.253	F	0.009	**
	Other	Inter	G	I	1,8	<0.001	F	0.977	
		Intra	G	I	1,14	14.03	F	0.002	**

Table S3: Tests for correlated response among replicates (A and B), within each female treatment (Inter and Intra). With Treat. = treatment, Dis. = probability distribution used (G = Gaussian and P = Poisson), link = link function used (I = Identity and L = Log), value = test value (Fvalue for F-tests and |z-value| for Wald tests), Df = nominal and denominator degrees of freedom, Test = model test used, and Sig. = significance levels (p<0.001=***; p<0.01=**; and p<0.05=*). Statistical models constituted linear mixed effects models (Gaussian) and generalised mixed effect models (Poisson) due to the repeated measures design in female experiments (Df estimated via Satterthwaite approximation). Variables in red showed a significant uncorrelated response between replicates in one or both treatments and were hence not considered further (see main text). No post hoc correction was applied, since there is a reverse in paradigm. I.e. type I errors (or incorrect rejections of the null hypothesis) are less important than type II errors (failing to reject an incorrect null hypothesis) when one is interested in 'retaining' the null hypothesis.

	Variable	Treat.	Dis.	Link	Df	Value	Test	*p*-value	Sig.
Preference	Association[a]	Inter	G	I	1,26	0.140	F	0.711	
		Intra	G	I	1,26	0.208	F	0.652	
Reproductive behaviour	Follow[a]	Inter	G	I	1,54	0.218	F	0.642	
		Intra	G	I	1,5	0.399	F	0.555	
	Hover[a]	Inter	G	I	1,5	3.219	F	0.133	
		Intra	G	I	1,5	0.054	F	0.826	
	Other[a]	Inter	G	I	1,5	0.146	F	0.718	
		Intra	G	I	1,5	0.188	F	0.683	
	Up & down motion	Inter	P	L	7,54	1.643	W	0.100	
		Intra	P	L	7,54	1.628	W	0.104	
	Zig zag motion	Inter	P	L	7,54	0.009	W	0.993	
		Intra	P	L	7,54	1.779	W	0.075	
	Away and return	Inter	P	L	7,54	2.373	W	0.018	*
		Intra	P	L	7,54	0.996	W	0.319	

[a] Arcsine transformed data to attain normality.