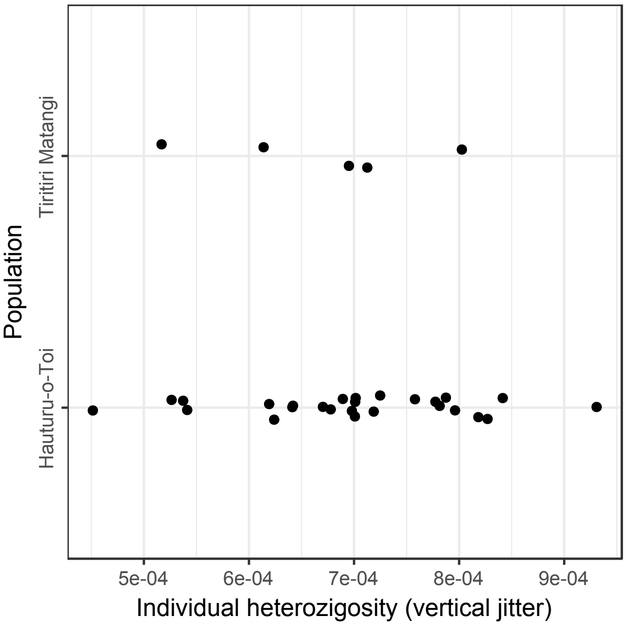


Figure S1: Individual heterozygosity. Individual heterozygosity (average number of heterozygote sites) computed from all sites (including monomorphic ones) for the 26 individuals from Te Hauturu-o-Toi and 5 individuals from Tiritiri Matangi. Vertical jitter was added to ease differentiating individual points. Tiritiri Matangi individuals fall well within the range of the individuals from Te Hauturu-o-Toi. **Related to Figure 1.**

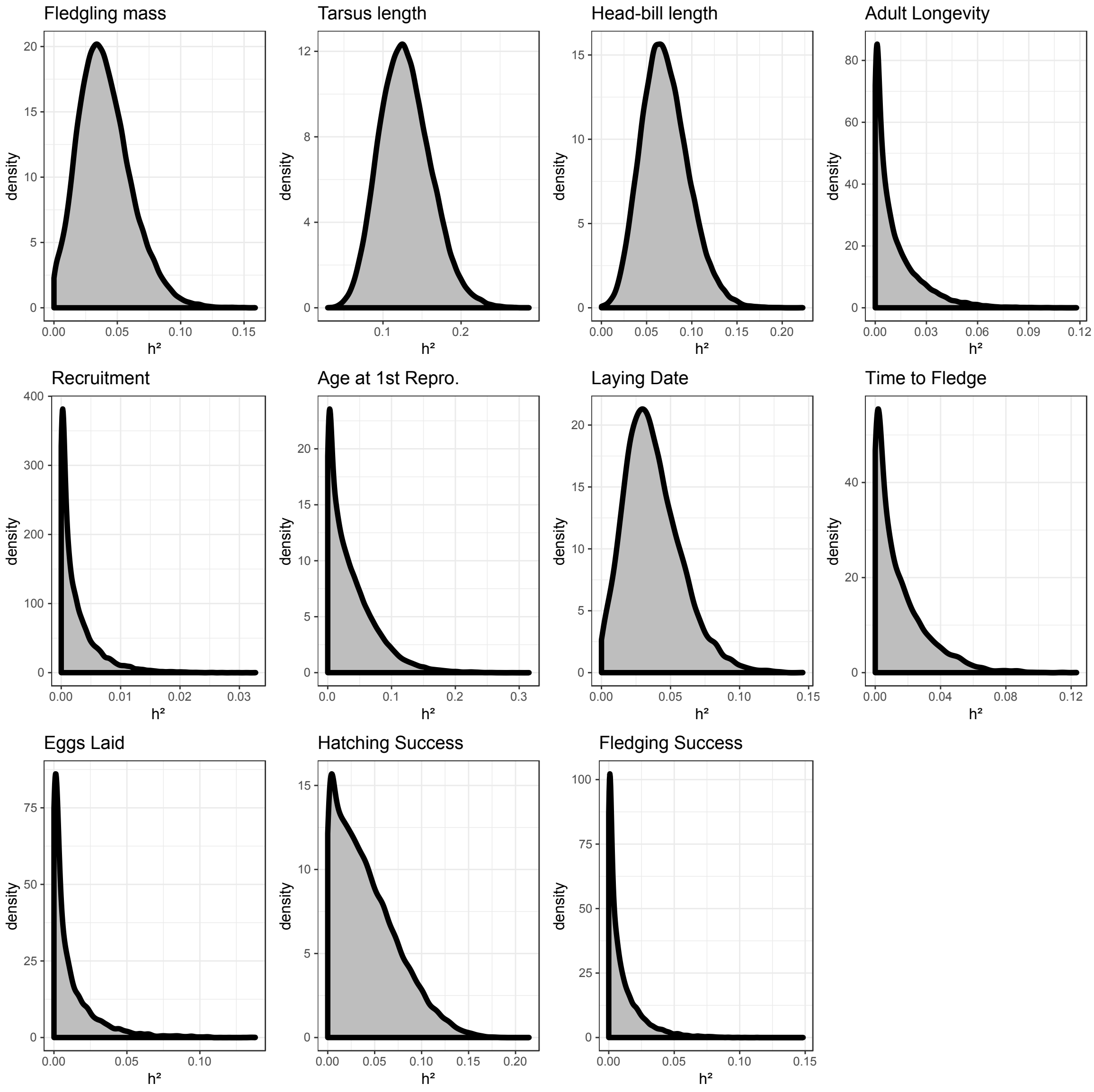
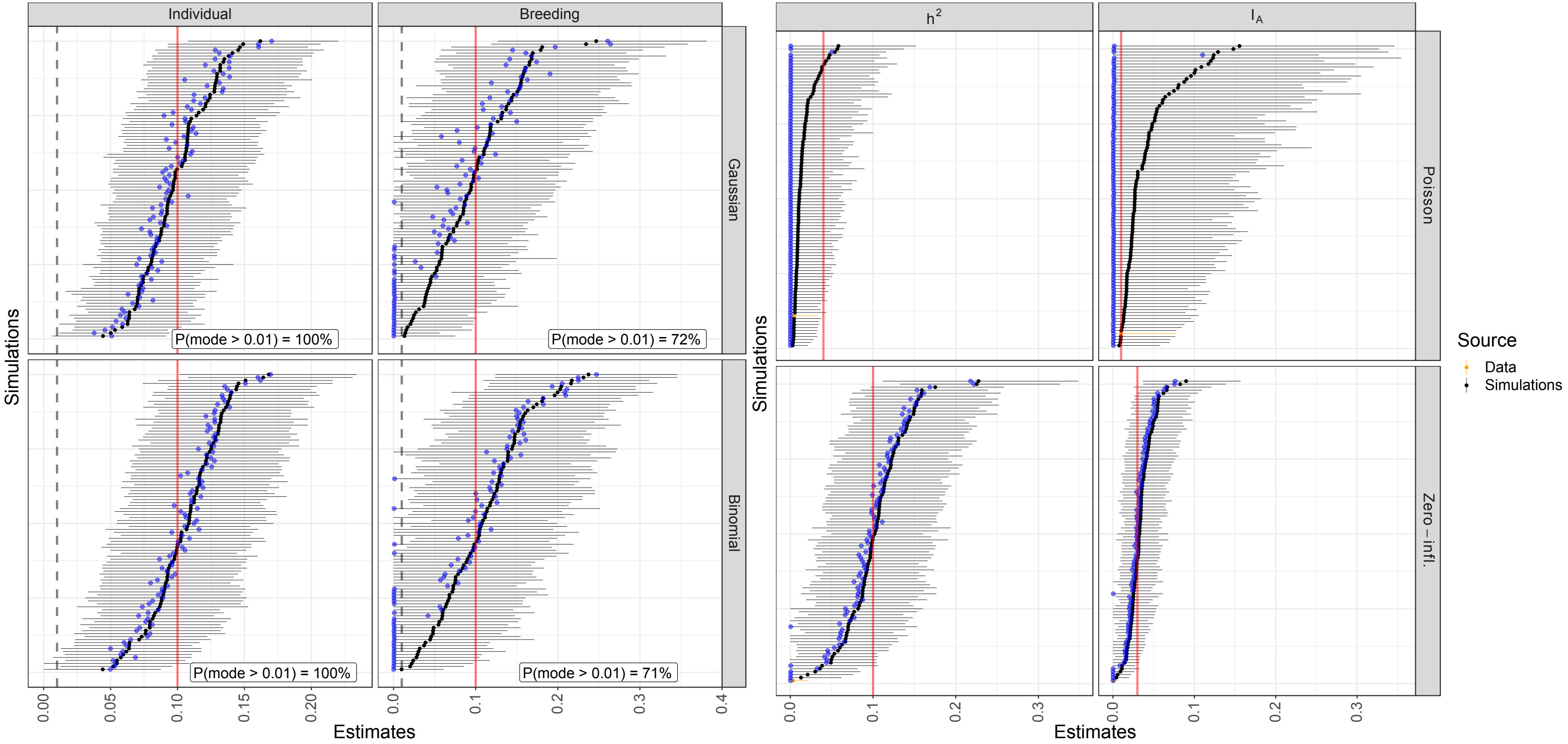


Figure S2: Posterior densities of the heritability estimates from the MCMCglmm output. **Related to Figure 2.**



(a) Scenarios *(i)-(iv)*

(b) Scenario *(v)*

Figure S3: Simulation analysis. Posterior mode (light blue point), median (black point) and 95% credible interval (black line) for all 100 replicates of the simulation analysis for scenarios *(i)-(iv)* (a) and *(v)* (b). The light red vertical line is the true simulated heritability and for (a), the dashed gray vertical line is the threshold used to consider the mode of the posterior distribution to be "at zero". Panel (b) shows estimates for heritability (h^2) and evolvability (I_A) of the Poisson and Zero-inflated part of the simulated fitness traits. The simulations in **Panel (a)** indicate that the size and structure of our pedigree is expected to be able to detect moderate to high heritabilities. For the simulation using the individual trait, heritability estimates were different from zero in all 100 replicates and in 98 of the 100 replicates, for the Gaussian and the binomial distributions, respectively. Posterior modes and medians were in good agreement (left panels). As a result, the proportion of posterior modes above an arbitrary threshold of 0.01 was 100% for the individual traits. For breeding trait scenarios (right panels), a larger number of credible intervals of heritabilities near zero is observed, with respectively 72% and 71% of the simulations with a posterior mode inferred not close to zero (i.e. above 0.01). Given the lower assumed additive genetic variance in the scenario of **Panel (b)**, border effects are more important, especially with little concordance between the posterior mode and median for the Poisson part of the trait (top panels). While the posterior mode systematically underestimates the evolvability (average of 0.0018 across simulations), the posterior median systematically overestimates it (average of 0.0415 across simulations). As a consequence, our estimates (in red) lie in at the bottom of the simulated estimates. The results for the zero-inflated part are easier to interpret, with more consistency between posterior modes and medians, reflecting a better power to detect small, but substantial heritabilities (and evolvabilities). For the zero-inflated part, our estimations (in red) were even clearer outliers from the simulations. **Related to Figure 2.**

Trait	Select. Diff.	Select. grad. (linear)	Select. grad. (non-linear)
Mass (Fledg.)	0.139	$\mathbf{0.117} \pm 0.0158$	$\mathbf{-0.19} \pm 0.0209$
Tarsus length	0.0631	$\mathbf{0.0425} \pm 0.0159$	$\mathbf{-0.21} \pm 0.0197$
Head-bill length	0.134	$\mathbf{0.128} \pm 0.0179$	-0.035 ± 0.0236
Adult Longevity	3.61	$\mathbf{0.68} \pm 0.0127$	$\mathbf{0.26} \pm 0.0201$
Recruit	1.82	—	—
Laying Date	-0.412	$\mathbf{-0.349} \pm 0.0185$	$\mathbf{-0.19} \pm 0.0293$
Age at 1st Repro.	-0.29	-0.0333 ± 0.032	-0.047 ± 0.0379
Time to Fledge	0.0163	0.00616 ± 0.0239	-0.0031 ± 0.00803
Eggs Laid	0.372	$\mathbf{0.395} \pm 0.0206$	-0.031 ± 0.032
Hatching Success	0.433	$\mathbf{0.324} \pm 0.0218$	$\mathbf{-0.35} \pm 0.0347$
Fledging Success	0.794	$\mathbf{0.505} \pm 0.0146$	$\mathbf{-0.43} \pm 0.0212$

Table S1: Selection estimates. Estimates for the selection differential and (linear and non-linear) gradients. Approximate standard-errors are given for the gradients. Bold estimates are significantly different from zero at the 5% threshold. The selection gradients for the probability of recruitment are not calculated, as the fact that all non-recruits have a fitness of 0 creates numerical complications. For age at first reproduction, non-significance might be due to a lack of power to test a small effect of the linear selection gradient, because when the non-linear selection gradient was set to zero, the linear gradient became significant ($\beta = -0.07 \pm 0.018$, $z = -3.85$, $p = 0.00012$). In contrast, the linear gradient of time to fledge was still non-significant when tested alone ($\beta = 0.01 \pm 0.021$, $z = 0.471$, $p = 0.638$). Overall, all traits except for time to fledge displayed a significant signal of selection, and can thus be considered adaptive. **Related to Figure 2.**

Trait	Sample Size	Nb. Ind.	Error	Fixed Effects	Pop. Mean	V_P	V_A	CV_A	h^2	h^2 (POreg)	h^2 (FSreg)	h^2 (MDreg)
Fledgling mass	2098	2098	Gaussian	Sex + ClutchSize	37.2 (37.1) [35.6 – 38.5]	44.8 (46.7) [40.3 – 54.4]	1.6 (1.9) [6.1E-7 – 3.6]	3.5 (3.6) [1.5 – 5.5]	0.0329 (0.04) [1.4E-8 – 0.078]	**0.205**	**0.147**	**0.264**
Tarsus length	2098	2098	Gaussian	Sex + ClutchSize	27.6 (27.7) [27.4 – 28]	1.6 (1.7) [1.4 – 1.9]	0.206 (0.21) [0.11 – 0.32]	1.7 (1.7) [1.2 – 2.1]	0.123 (0.13) [0.066 – 0.19]	**0.226**	**0.202**	**0.305**
Head-bill length	2098	2098	Gaussian	Sex + ClutchSize	38.8 (38.8) [38.4 – 39.2]	2.9 (3) [2.6 – 3.4]	0.181 (0.21) [0.069 – 0.36]	1.2 (1.2) [0.71 – 1.6]	0.0581 (0.071) [0.021 – 0.12]	**0.159**	**0.105**	**0.22**
Adult Longevity	2288	2288	Poisson	—	2.1 (2.3) [1.5 – 3.3]	2.5 (31.8) [3.4 – 28.2]	−0.00398 (0.13) [4E-10 – 0.42]	—	2.8E-4 (0.012) [6E-11 – 0.04]	0.0221	0.0574	0.0309
Recruitment	2183	2183	binomial	Mass	0.398 (0.4) [0.34 – 0.45]	0.24 (0.24) [0.23 – 0.25]	3.42E-6 (6.2E-4 [8.2E-13 – 0.002	—	2.36E-5 (0.0026) [3.4E-12 – 0.0095]	—	—	—
Age at 1st Repro.	581	581	binomial	Sex + ClutchNumber	0.261 (0.26) [0.19 – 0.34]	0.193 (0.19) [0.15 – 0.23]	7.12E-5 (0.0072) [4.2E-11 – 0.022]	—	1.5E-4 (0.037) [2.1E-10 – 0.11]	−0.00986	−0.146	0.189
Laying Date	1371	350	Gaussian	ClutchNumber	83.8 (83.9) [78.8 – 88.9]	913.4 (909.3) [829.6 – 994]	26.1 (34) [1.1E-5 – 69.1]	—	0.0309 (0.037) [1.2E-8 – 0.075]	—	—	0.0103
Time to Fledge	1259	311	Gaussian	ClutchNumber	47.6 (47.6) [47 – 48.2]	14.9 (15.1) [13.4 – 17]	0.00475 (0.22) [1.7E-8 – 0.72]	0.47 (0.83) [2.8E-4 – 1.8]	2.67E-4 (0.015) [1.1E-9 – 0.048]	—	—	0.166
Eggs Laid	1383	348	Gaussian	LD	4 (4) [3.9 – 4.1]	0.637 (0.64) [0.59 – 0.7]	1.95E-4 (0.0076) [1.7E-11 – 0.03]	0.271 (1.7) [0.0023 – 4.3]	2.79E-4 (0.012) [2.8E-11 – 0.046]	—	—	−0.354
Hatching Success	1358	345	binomial	Age	0.771 (0.76) [0.7 – 0.82]	0.181 (0.18) [0.15 – 0.21]	4.81E-5 (0.0078) [4.7E-11 – 0.021]	—	5.14E-4 (0.041) [2.5E-10 – 0.11]	—	—	—
Fledging Success	1244	318	binomial	LD + LD^2	0.601 (0.6) [0.54 – 0.66]	0.24 (0.24) [0.23 – 0.25]	6E-5 (0.0026) [7.8E-14 – 0.009	—	2.23E-4 (0.011) [3.3E-13 – 0.039]	—	—	—

Table S2: Quantitative genetics of the phenotypic traits. Estimates from the animal model for each phenotypic trait giving the total sample size, the number of individuals used, the error used for the model, and the fixed effects included as covariates (LD: Laying date). Estimates shown are the population mean, the population phenotypic variance (V_P), the additive genetic variance (V_A) and, when relevant, its associated coefficient of variance (CV_A) and the heritability h^2. For each estimate, the posterior mode is given, with the posterior median between parentheses and the 95% credible interval between brackets. Also provided when available are the heritabilities computed from parent-offspring (POreg), father-son (FSreg) and mother-daughter (MDreg) regression. Bold estimates are significantly different from zero. For non-Gaussian traits, all estimates are computed on the observed data scale. Regarding the fixed effects, sex was a significant effect for all almost all individual traits, reflecting the strong sexual dimorphism of this species. The only individual trait for which sex was not a significant covariate (probability of recruitment) included fledgling mass as a covariate which is partly linked with sex (sex effect on fledgling mass, $t_{2181} = 22.89$, $p < 10^{15}$, $R^2 = 0.194$). Clutch size had a significant negative effect on the three morphological traits (slope[95% CI], mass: $-0.895[-1.167, -0.608]$, tarsus: $-0.108[-0.161, -0.0547]$, head-bill: $-0.102[-0.178, -0.0271]$). For all breeding traits but one (hatching success), either clutch number or laying date were of significant influence. Hatching success, on the contrary, was influenced only by the age of the female. **Related to Figure 2.**

Type	Parameter	Post. mode	Post. median	Low. CI	High. CI	pMCMC
Fledgling mass						
Fixed	Intercept	38	38	36	39	0
	Sex	5.6	5.6	5.2	6	0
	ClutchSize	-0.88	-0.89	-1.2	-0.61	0
Random	V_{A}	1.6	1.8	6.1E-7	3.6	—
	V_{Mat}	4	4.3	2.5	6.3	—
	V_{Pat}	2.4	2.4	1.2	3.9	—
	V_{Month}	4.3	4.7	2.3	7.9	—
	V_{Year}	2.9	4.4	0.39	12	—
	V_{R}	20	20	18	22	—
Tarsus length						
Fixed	Intercept	28	28	27	28	0
	Sex	1	1	0.95	1.1	0
	ClutchSize	-0.11	-0.11	-0.16	-0.055	0
Random	V_{A}	0.21	0.21	0.11	0.32	—
	V_{Mat}	4.4E-4	0.04	3.8E-12	0.091	—
	V_{Pat}	0.072	0.079	0.033	0.13	—
	V_{Month}	0.099	0.12	0.044	0.23	—
	V_{Year}	0.16	0.2	0.037	0.47	—
	V_{R}	0.7	0.7	0.62	0.78	—
Head-bill length						
Fixed	Intercept	39	39	38	39	0
	Sex	1.2	1.2	1.1	1.3	0
	ClutchSize	-0.1	-0.1	-0.18	-0.027	0.0074
Random	V_{A}	0.18	0.2	0.069	0.36	—
	V_{Mat}	0.18	0.18	0.06	0.31	—
	V_{Pat}	0.14	0.15	0.063	0.25	—
	V_{Month}	0.24	0.28	0.13	0.49	—
	V_{Year}	0.19	0.25	1.5E-8	0.69	—
	V_{R}	1.5	1.5	1.3	1.6	—
Adult Longevity						
Fixed	Intercept	0.38	0.38	0.018	0.69	0.04
Random	V_{A}	3E-4	0.012	8.6E-11	0.079	—
	V_{Mat}	1.8E-4	3E-3	3.6E-13	0.024	—
	V_{Pat}	2.2E-4	0.0039	8.7E-11	0.031	—
	V_{Month}	4.4E-4	0.0078	2.2E-10	0.06	—
	V_{Year}	0.32	0.38	0.096	0.92	—
	V_{R}	0.38	0.39	0.27	0.52	—
Recruitment						
Fixed	Intercept	-0.85	-0.87	-1.3	-0.42	2E-4
	FldgMass	0.013	0.013	0.0028	0.023	0.014
Random	V_{A}	1.4E-4	0.0049	1.2E-11	0.036	—
	V_{Mat}	3.2E-4	0.021	5.4E-10	0.068	—
	V_{Pat}	3.4E-4	0.0084	6.4E-10	0.042	—
	V_{Month}	2.2E-4	0.012	4.6E-10	0.07	—
	V_{Year}	0.15	0.17	0.049	0.4	—
	V_{R}	1	1	1	1	—

Type	Parameter	Post. mode	Post. median	Low. CI	High. CI	pMCMC
Age at 1st Repro.						
Fixed	Intercept	-1.4	-1.5	-2.1	-0.97	0
	Sex	0.52	0.55	0.17	0.94	0.0042
	ClutchNumber2	0.37	0.33	-0.21	0.85	0.23
	ClutchNumber3	75	110	0.26	304	0.0021
Random	V_{A}	0.0016	0.15	1.2E-9	0.8	—
	V_{Mat}	0.0025	0.041	3.8E-11	0.3	—
	V_{Pat}	0.0024	0.22	4.7E-10	0.69	—
	V_{Month}	0.0013	0.081	2.9E-10	0.46	—
	V_{Year}	0.23	0.32	3.9E-11	0.94	—
	V_{R}	1	1	1	1	—
Laying Date						
Fixed	Intercept	22	23	18	28	0
	ClutchNumber	44	44	43	46	0
Random	V_{A}	26	31	1.1E-5	69	—
	V_{PE}	47	43	9.1	75	—
	V_{Mate}	18	18	5.8	31	—
	V_{Year}	64	74	30	149	—
	V_{R}	163	162	147	179	—
Time to Fledge						
Fixed	Intercept	48	48	47	49	0
	ClutchNumber2	-1.7	-1.6	-2.3	-0.83	0
	ClutchNumber3	-1.8	-1.8	-6.3	2.5	0.44
Random	V_{A}	0.0047	0.13	1.7E-8	0.72	—
	V_{PE}	0.0045	0.26	2.3E-11	1.1	—
	V_{Mate}	0.0047	0.17	8.5E-8	0.79	—
	V_{Year}	0.39	0.57	1.2E-4	1.7	—
	V_{R}	13	13	12	14	—
Eggs Laid						
Fixed	Intercept	4	4	3.9	4.1	0
	LD	-0.088	-0.084	-0.16	-0.011	0.019
Random	V_{A}	2E-4	0.0032	1.7E-11	0.03	—
	V_{PE}	0.037	0.042	9.9E-4	0.075	—
	V_{Mate}	1E-4	0.0043	1.2E-9	0.022	—
	V_{Year}	0.0093	0.013	0.0011	0.036	—
	V_{Site}	5.1E-5	0.0014	1.7E-10	0.012	—
	V_{R}	0.56	0.56	0.51	0.6	—
Hatching Success						
Fixed	Intercept	1.5	1.5	1.1	1.8	0
	Age	-0.1	-0.11	-0.17	-0.052	0
Random	V_{A}	3E-3	0.19	1.2E-9	0.56	—
	V_{PE}	0.4	0.37	4.7E-8	0.67	—
	V_{Mate}	1E-3	0.041	1.7E-10	0.16	—
	V_{Site}	0.0012	0.042	1.5E-8	0.16	—
	V_{Year}	0.046	0.065	4.1E-7	0.17	—
	V_{R}	1	1	1	1	—

Type	Parameter	Post. mode	Post. median	Low. CI	High. CI	pMCMC
Fledging Success						
Fixed	Intercept	0.72	0.69	0.34	1.1	1.6E-4
	LD	-0.44	-0.48	-0.77	-0.23	8E-5
	LD^2	-0.26	-0.27	-0.48	-0.076	0.0034
Random	V_{A}	0.0017	0.027	1.7E-12	0.2	—
	V_{PE}	0.4	0.42	0.14	0.72	—
	V_{Mate}	0.21	0.21	3.7E-11	0.44	—
	V_{Site}	2.3E-4	0.013	1.1E-10	0.092	—
	V_{Year}	0.082	0.12	1.5E-6	0.35	—
	V_{R}	1	1	1	1	—

Table S3: Estimates of the animal models. Point estimates (posterior mode and median) and credible interval (lower and higher 95% CI bounds) for the fixed and random parameters for each analysed trait (on the latent scale for non-Gaussian traits). The pMCMC (testing significance away from zero) are also displayed for the fixed effects. V_{A}: additive genetic variance, V_{Mat}: variance from maternal effect, V_{Pat}: variance from paternal effect, V_{Month}: variance from month effect, V_{Year}: variance from year effect, V_{R}: residual (or overdispersion for non-Gaussian traits) variance. **Related to Figure 2.**