The quantitative genetics of fitness in a wild bird population

—Online Supplementary Material—

SUPPLEMENTARY TEXT S1. PRIOR SPECIFICATION

We used different prior specifications for the different quantitative genetic parameters reported in the main text (see below). We also ran a prior sensitivity analysis and found that the reported parameters were not substantially influenced by the prior chosen, since posterior modes, means and 95% CI were similar (Results not shown). We therefore concluded that our results and interpretations were robust to reasonable alternative priors.

Prior used in the analysis for lifetime fitness:

G_A: V = diag(2)/2, nu = 2, alpha.mu = c(0,0), alpha.V = diag(2)*1000)

G_C: V = diag(2)/2, nu = 2, alpha.mu = c(0,0), alpha.V = diag(2)*1000)

R: V = diag(2)/2, nu = 1, fix = 2

Prior used in the analysis for Adult Reproductive Success:

G_A: V = 1, nu = 1, alpha.mu =0, alpha.V = 1000

G_{PE}: V = 1, nu = 1, alpha.mu =0, alpha.V = 1000

G_{YEAR}: V = 1, nu = 1, alpha.mu =0, alpha.V = 1000

R: V = 1, nu= 1

Prior used in the analysis for Adult Annual Survival:

G_A: V = 1, nu = 2, alpha.mu =0, alpha.V = 100

G_{PE}: V = 1, nu = 2, alpha.mu =0, alpha.V = 100

G_{YEAR}: V = 1, nu = 2, alpha.mu =0, alpha.V = 100

R: V = 1, fix= 1

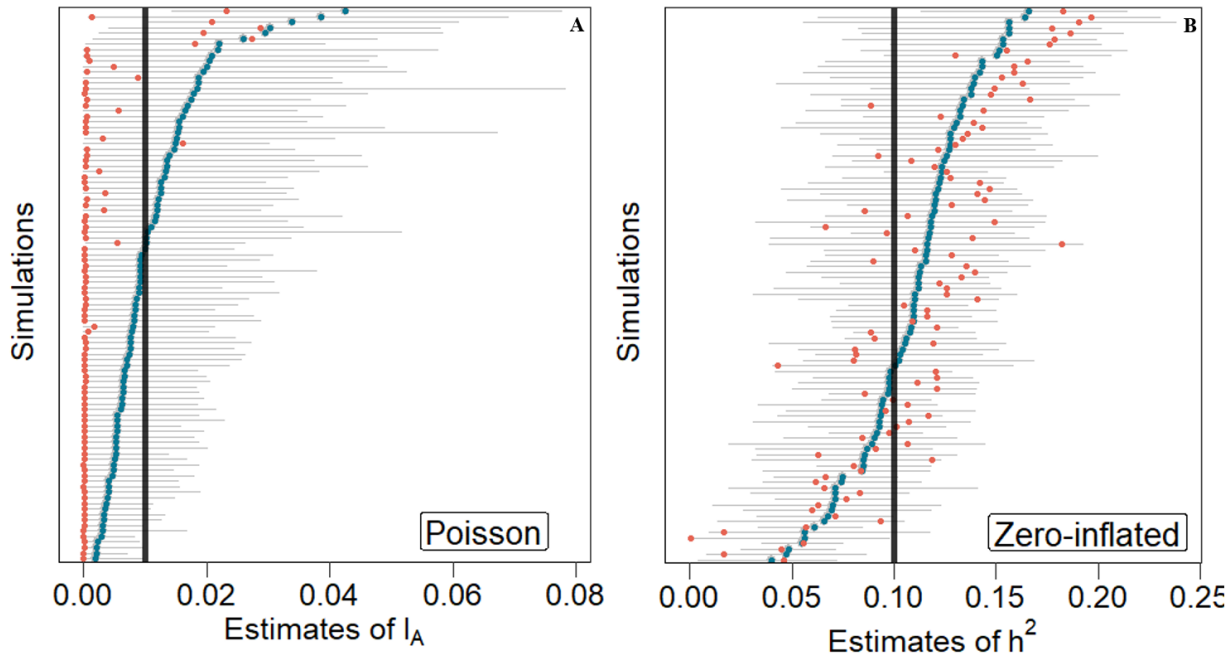
SUPPLEMENTARY TEXT S2. DATA SIMULATIONS

We performed a data simulation analysis to investigate whether we can effectively detect *small, but substantial* heritabilities and evolvabilities (*sensu* de Villemereuil et al. 2019) in lifetime fitness given our sample size and pedigree structure.

Methods: We used the pedigree and data structure of the common tern population at the Banter See to simulate a zero-inflated Poisson lifetime fitness trait, and compare the results of the quantitative genetic model with those from our empirical data. Following de Villemereuil et al. (2019), we used an evolvability (or additive genetic variance of relative fitness) of 0.01 for the Poisson component, and a heritability of 0.1 for the Zero-inflated component. We chose these metrics because (i) back-transformed heritabilities modeled with a Poisson error distribution are not appropriate metrics for the adaptive potential of a population (de Villemereuil et al. 2016; Bonnet et al. 2019; Morrissey and Bonnet 2019), and (ii) evolvabilities for binomial traits do not have a strong biological meaning, as the trait mean is arbitrary. We chose an evolvability of 0.01 and heritability of 0.1 because values below that arbitrary threshold would be considered inconsequential (de Villemereuil et al. 2019). Besides generating additive genetic variances, we simulated the effects of hatch-year (i.e., cohort) by adding it as a random effect. Residual variance for the Zero-inflated part of the simulated fitness trait was fixed to 1. This way, we followed the structure of our fitted Zero-inflated Poisson model and accounted for the precision lost by adding random effects. The simulation analysis consisted of 100 replicates, fitted to the same model structure as our main analyses in the R-package *MCMCglmm* (Hadfield 2010). The R-code for the data simulations was adapted from that of de Villemereuil et al. (2019) and is available in GitHub.

Results: Our data simulation indicated that, given our data structure and pedigree, we were able to detect *small but substantial* additive genetic variance for the Zero-inflated component of fitness (i.e., $h^2 = 0.1$, Fig S1B). The average value of h^2 across the 100 simulations for both posterior mode and mean was 0.109 and 0.113, respectively. Oppositely, the analysis of our data simulations revealed that we were not able to effectively detect a *small but substantial* additive genetic variance for the Poisson component of fitness (i.e., $I_A = 0.01$, Fig S1A). We found that posterior means estimated an I_A of similar magnitude to that of the simulated value (average of 0.011 across the 100 simulations), while posterior modes underestimated I_A (average of 0.002 across simulations). Additionally, the 95% CI showed important border effects (the lower 95% limit was effectively zero in 95% of the replicates). Given that a scenario where there was no simulated additive genetic variance for the Poisson component ($I_A = 0.00$) could give rise to a similar pattern, we ran the same data simulation as described above, but modifying the values of I_A so that instead of simulating a value of $I_A = 0.01$ for the Poisson component, we now simulated a nominally zero value. As expected, we found a similar pattern, namely that posterior means estimated an I_A larger than 0.00 (average of 0.008 across the 100 simulations), while posterior modes were close to zero (average of 0.001 across simulations). Again, the 95% CI showed important border effects. As a final step, we simulated a value of additive genetic variance in the Poisson component of fitness substantially larger (i.e., we arbitrarily chose $I_A = 0.1$) than in the two previous cases. The data simulation analysis showed that we did have sufficient power to detect larger values of I_A. We found that posterior means and modes estimated an I_A of the similar magnitude to that of the simulated value (average of 0.106 and 0.154 across the 100 simulations for the posterior mode and mean, respectively).

Figure S1. Data simulation analysis of lifetime fitness. Panels A and B show the posterior estimates for all 100 replicates of evolvability (I_A) of the Poisson component (A), and heritability (h^2) of the Zero-inflated component of simulated lifetime fitness (B). Posterior modes are represented as red dots, posterior means as blue dots and 95% credible intervals as grey horizontal lines. The black vertical line is the simulated value (i.e., an evolvability of 0.01 for the Poisson component and heritability of 0.1 for the Zero-inflated component).



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