

# Supporting Information

Rebke et al. 10.1073/pnas.1002645107

## SI Methods

**Supporting Equation.** Eq. 1 can be extended to account for new individuals entering the study at the second age. Kerr and Godfrey-Smith (1) previously incorporated an additional covariance term into the Price equation that illustrates the effect of immigration for change in an average trait value from one generation to the next. We instead use a difference to capture that term. The extended equation implies that the mean of the considered characteristic at the second age for all individuals  $V_{x+k}$  is no longer equal to the mean for the survivors  $v_{x+k}$ , unless the mean of the considered characteristic of the newly appearing individuals is not different from the average of this characteristic of the individuals that were in the study before. Therefore, the term

$$a = V_{x+k} - v_{x+k}, \quad [S1]$$

which represents the selective appearance of new individuals, has to be added to Eq. 1:

$$P = s + d + a. \quad [S2]$$

This extended equation is again exact if all living individuals are measured.

The mean of the characteristic for the newly entering individuals is a function of  $v_{x+k}$  and  $a$ , as well as the number of survivors and the number of newly entering individuals. If the mean for the newly entering individuals at the second age is higher than the mean for the individuals that were already in the study before (the survivors), then the aggregate mean  $V_{x+k}$  is higher than the mean for the survivors  $v_{x+k}$  and  $a$  is positive (Fig. S1A). In the opposite case the term  $a$  is negative (Fig. S1B).

**Mixed Models.** Our mixed models (2) all include individual identity as a random effect. Age, the number of past breeding events, the number of past successful breeding attempts, or the pair bond length is fitted as a linear fixed effect and/or quadratic.

We also modeled these factors by categorical groupings. The models are fitted to data on individual change in relative reproduction from one age  $r_{ixt}$  to the next  $r_{i(x+1)(t+1)}$ :

$$\Delta r_{ixt} = r_{ixt} - r_{i(x+1)(t+1)}. \quad [S3]$$

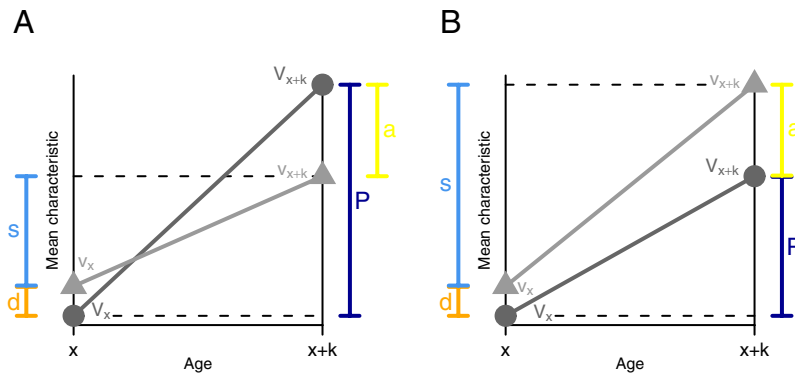
We only consider individuals for this analysis when we have information on age, the number of past breeding attempts, the number of past successful breeding events, and the length the bird bred together with its partner. We consider males and females separately. The mixed models are fitted via maximum likelihood (ML) in R version 2.7.0 by using the function `lmer` in package `lme4`.

## SI Discussion

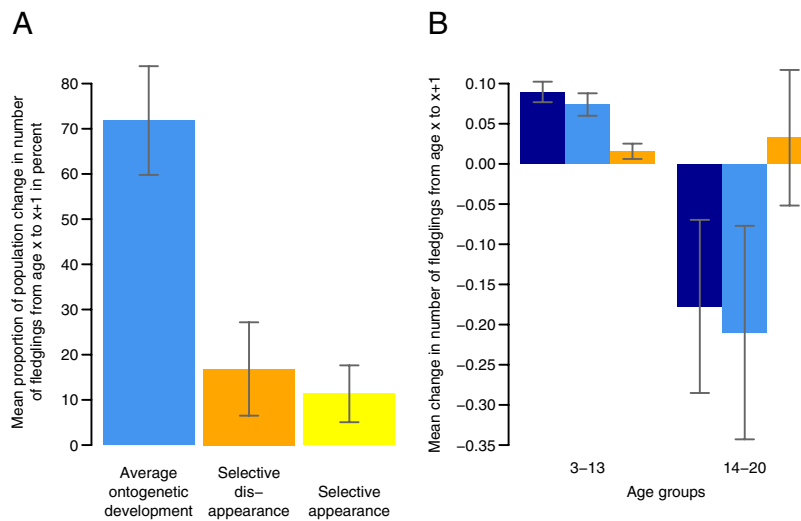
Analyses beyond population-level analyses to elucidate individual-level change include: a separate longitudinal analysis for a restricted sample of individuals that survive to old age (3, 4); examination of correlation in improvements in survival and breeding success (5); and a test for a relationship between breeding lifespan and reproductive performance (4).

Methods to correct for selective disappearance or selective appearance include: the arbitrary classification of individuals into groups (4) and inclusion of individual covariates in the model to capture observed heterogeneity (6); the construction of multistate models with states designed to account for the different qualities of individuals (7, 8); the joint modeling of survival and reproduction with individual identity included as a random effect (9); and correction for individual quality by including observed individual quality measures like longevity or age at first reproduction as fixed effects, and individual identity as a random effect (usually random intercept and no random slope) in linear, generalized linear mixed models (reference for model types, 2; references for applications, 10–20), and generalized additive mixed models (reference for model type, 21; reference for application, 22).

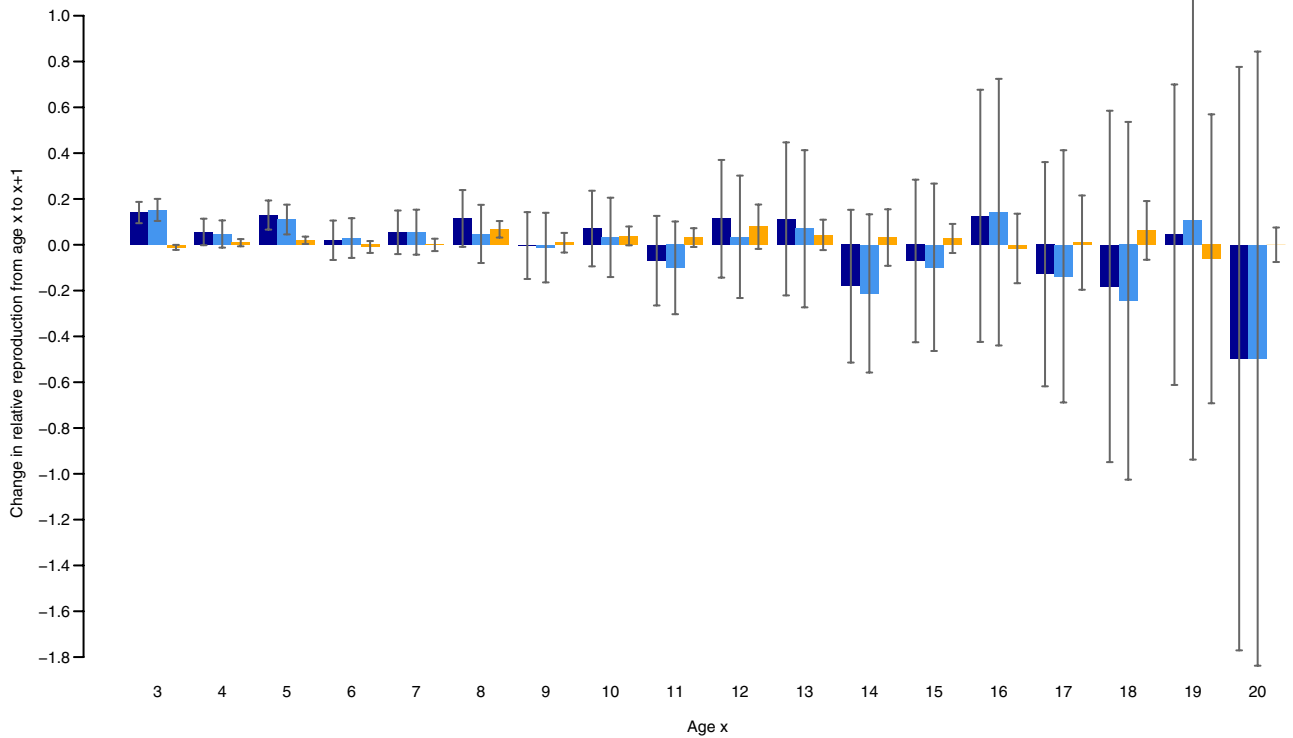
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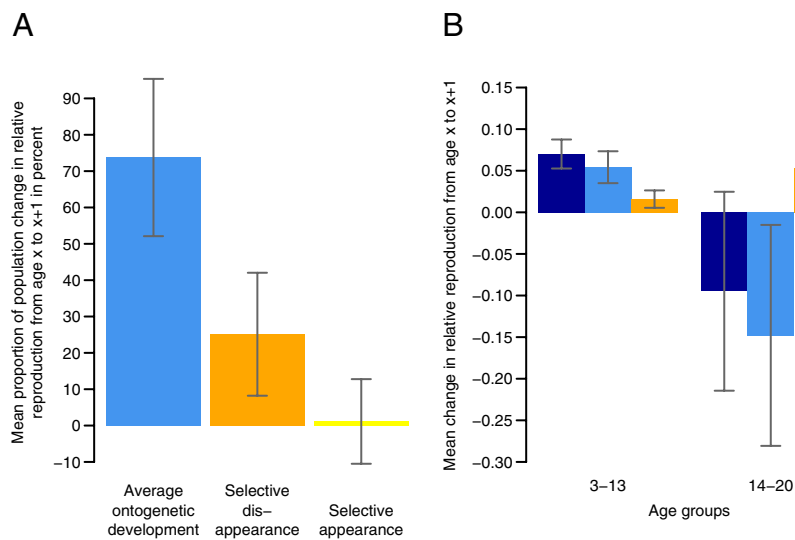
**Fig. S1.** Graphical representation of Eq. S2 to decompose the aggregate change at the population level into average ontogenetic development, change due to selective disappearance, and change due to selective appearance when newly entering individuals have a higher mean than the surviving individuals already in the study (A) and newly entering individuals have a lower mean than the surviving individuals (B).  $P$  is the aggregate change in the considered characteristic from age  $x$  to the age  $x + k$ ,  $s$  is the average ontogenetic development,  $d$  denotes the change due to selective disappearance, and  $a$  is the change due to selective appearance.  $V_x$  and  $V_{x+k}$  are the averages of the characteristic on the observed population level at age  $x$  and  $x + k$ , respectively, and  $v_x$  and  $v_{x+k}$  are the corresponding averages for the survivors.



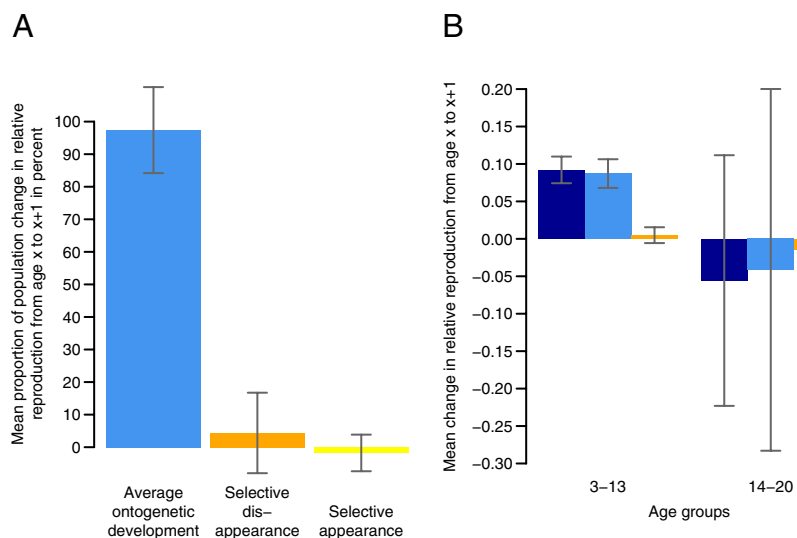
**Fig. S2.** Change in number of fledglings from age  $x$  to  $x + 1$  averaged over all individuals and all ages. (A) Decomposition of population change into average ontogenetic development, selective disappearance, and selective appearance in percent (959 individuals with 4,307 observations). The proportional change is equivalent to an absolute mean change from one age to the next of 0.091 fledglings at the population level, a positive average ontogenetic development of 0.065; a change of 0.015 is due to selective disappearance, and 0.01 to selective appearance. (B) Change in number of fledglings for the age groups 3–13 and 14–20, respectively, at the population level (dark blue bars), and the contributions to this change due to average ontogenetic development (light blue bars) and selective disappearance (orange bars; 955 individuals with 4,303 observations). The error bars represent 95% confidence intervals.



**Fig. S3.** Change in relative reproduction from age  $x$  to  $x + 1$  at the population level (dark blue bars), and the decomposition of this change into average ontogenetic development (light blue bars) and selective disappearance (orange bars; 955 individuals with 4,303 observations). The error bars represent 95% confidence intervals.



**Fig. S4.** Change in relative reproduction from age  $x$  to  $x + 1$  averaged over all females and all ages. (A) Decomposition of population change into average ontogenetic development, selective disappearance, and selective appearance in percent (411 individuals with 1,893 observations). (B) Change in relative reproduction for the age groups 3–13 and 14–20, respectively, at the population level (dark blue bars), and the contributions to this change due to average ontogenetic development (light blue bars) and selective disappearance (orange bars; 408 individuals with 1,890 observations). The error bars represent 95% confidence intervals.



**Fig. S5.** Change in relative reproduction from age  $x$  to  $x + 1$  averaged over all males and all ages. (A) Decomposition of population change into average ontogenetic development, selective disappearance, and selective appearance in percent (468 individuals with 2,123 observations). The average change among survivors contribution can be higher than 100% if the changes due to selective disappearance and/or selective appearance go in the opposite direction. (B) Change in relative reproduction for the age groups 3–13 and 14–20, respectively, at the population level (dark blue bars), and the contributions to this change due to average ontogenetic development (light blue bars) and selective disappearance (orange bars; 467 individuals with 2,122 observations). The error bars represent 95% confidence intervals.

**Table S1. Decomposition of population change in relative reproduction from event  $x$  to  $x + 1$  in percent**

Event	Average ontogenetic development	Selective disappearance	Sample size
Number of past breeding attempts	96.8% ( $\pm 11.6\%$ )*	3.2% ( $\pm 11.6\%$ )*	701 individuals (3,078 observations)
Number of past successful breeding attempts	88.8% ( $\pm 16.4\%$ )*	11.2% ( $\pm 16.4\%$ )*	489 individuals (1,454 observations)
Pair bond length in years	90.1% ( $\pm 36.9\%$ )*	9.9% ( $\pm 36.9\%$ )*	288 pairs (834 observations)

\*95% confidence intervals.

**Table S2. AIC for the linear mixed models to test which characteristic explains the change in breeding performance best**

Model	Females (207 individuals; 673 observations)	Males (250 individuals; 715 observations)
Intercept	1,669	1,750
Intercept and linear slope		
Age	1,671	1,752
(Age) <sup>2</sup>	1,671	1,751
Age: second-order polynomial	1,673	1,752
Number of past breeding attempts	1,670	1,749
(Number of past breeding attempts) <sup>2</sup>	1,671	1,750
Number of past breeding attempts: second-order polynomial	1,672	1,750
Number of past successful breeding attempts	1,664	1,736
(Number of past successful breeding attempts) <sup>2</sup>	1,670	1,746
Number of past successful breeding attempts: second-order polynomial	1,660	1,728
Pair bond length in years	1,671	1,751
(Pair bond length in years) <sup>2</sup>	1,671	1,751
Pair bond length in years: second-order polynomial	1,673	1,753
Factors		
Age	1,678	1,749
Age: 2 groups ( $x \leq 14$ , $x > 14$ )	1,671	1,751
Number of past breeding attempts	1,677	1,749
Number of past breeding attempts: 2 groups ( $x = 0$ , $x > 0$ )	1,667	1,744
Number of past successful breeding attempts	1,656	1,730
Number of past successful breeding attempts: 2 groups ( $x = 0$ , $x > 0$ )	<b>1,643</b>	<b>1,714</b>
Pair bond length in years	1,664	1,755
Pair bond length in years: 2 groups ( $x = 1$ , $x > 1$ )	1,671	1,750

The models are fitted to the change in relative reproduction. They all have random intercepts for the individuals and either age, the number of past breeding attempts, the number of past successful breeding events, or the pair bond length as fixed effect. The models are fitted via maximum likelihood (ML).