**Supporting Information**

**Strong habitat and weak genetic effects shape the lifetime reproductive success in a wild clownfish population**

Océane C. Salles, Glenn R. Almany, Michael L. Berumen, Geoffrey P. Jones, Pablo Saenz-Agudelo, Maya Srinivasan, Simon R. Thorrold, Benoit Pujol\*,and Serge Planes\*

*\*Both authors share senior authorship of this article*

**Correspondence:** Océane Salles andBenoit Pujol; Emails: oceane.salles@gmail.com and benoit.pujol@univ-perp.fr

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* **Table S1.** Previous estimates of fitness heritability and maternal effects on fitness in 15 wild populations.
* **Figure S1.** Pedigree data and power analysis for the Kimbe Island orange clownfish population.
* **Supplementary methods, results and discussion** on De-lifing measures.

**Table S1. Previous estimates of fitness heritability and maternal effects on fitness in wild populations.** Different fitness measures are denoted as lifetime reproductive success (LRS), De-lifing or relative RS (LRS/mean of LRS in the population). ♀ corresponds to female, ♂ corresponds to male and ⚥ corresponds to female and male confounded. NA indicates that maternal effects were not estimated or dropped from the quantitative genetic models.

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| **Study organism** | **Location** | **Years****of monitoring** | **Heritability estimate**± **SE or 95%SI** | **Maternal effects estimate** | **Fitness measure** | **Reference** |
| Collared flycatcher | Gotland Is. | 1980 to 1984 | ♀ 0.01 ± 0.16♂ 0.01 ± 0.13 | NANA | LRS | (Gustafsson 1986) |
| Red deer | Isle of Rum | 1971 to 1999 | ♀ 0.00 ± 0.05 | 0.16 ± 0.041 | LRS | (Kruuk *et al.* 2000) |
| ♂ 0.02 ± 0.06 | NA |  |
|  |  | 1971 to 2005 | ♀ 0.21 ± 0.06♂ 0.07 ± 0.06 | 0.00210.0045 | De-lifing | (Foerster *et al.* 2007) |
| Collared flycatcher | Gotland Is. | 1980 to 1997 | ♀ 0.21 ± 0.06 | NA | LRS | (Merila & Sheldon 2000) |
| ♂ 0.07 ± 0.06 | NA |
| Bighorn sheep | Ram MountainSheep River | 1973 to 19981981 to 1998 | ♀ 0.66 ± 0.32♀ 0.19 ± (0.50) | NANA | LRSLRS | (Réale & Festa-Bianchet 2000) |
| Cheetahs | Serengeti park | 1970 to 1994 | ♀ 0.88 ± ? | NA | LRS | (Kelly 2001) |
| Great tit | Wytham Wood | 1960 to 1998 | ♀ 0.00 ± 0.04♂ 0.02 ± 0.04 | NANA | LRS | (McCleery *et al.* 2004) |
| Bighorn sheep | Ram Mountain | 1971 to 2003 | ♀ 0.00 ± 0.00♂ 0.00 ± 0.00 | NANA | LRS | (Coltman *et al.* 2005) |
| Red billed gulls | Kaikoura | 1958 to 2004 | ♀ 0.36 ± 0.29♂ 0.00 ± 0.00 | NANA | LRS | (Teplitsky *et al.* 2009) |
| Rhesus macaques | Cayo Is. | 1959 to 1990 | ♀ 0.36 ± 0.081 | NA | LRS | (Blomquist 2010) |
| House sparrow | Lundy Is. | 2000 to 2011 | ⚥ 0.09 (0.03 to 0.18) | 0.33 (0.14 to 0.51) | De-lifing | (Schroeder *et al.* 2012) |
| Soay sheep | St Kilda | 1985 to 2002 | ⚥ 0.03 ± 0.01 | NA | Relative RS | (Morrissey *et al.* 2012) |
| Red squirrels | Yukon | 1987 to 2011 | ⚥ 4.90x10-04 (3.0x10-08 to 0.07)♀ 6.80 x10-04 (8.5x10-11 to 0.10)♂ 4.90 x10-04 (1.1x10-03 to 0.39) | 0.07 (0.02 to 0.14)0.08 (0.01 to 0.14)0.10 (0.10 to 0.37) | LRS | (McFarlane *et al.* 2014) |
| Savannah sparrow | Kent Is. | 1987 to 2005 | ♀ 0.002 ± 0.036♂ 0.000 ± 0.036 | NANA | LRSLRS | (Wheelwright *et al.* 2014) |
| Brown anole lizard | Kidd Cay | 2005 to 2008 | ⚥ 1.40 (8.0x10-10 to 0.023) | NA | RS | (Calsbeek *et al.* 2015) |
| Song sparrow | Mandarte Island | 1993-2015 | ♀ 0.5 ± 0.21♂ 0.44 ± 0.74 | NANA | LRS | (Wolak *et al.* 2018) |



**Figure S1.** Pedigree data of the Kimbe Island orange clownfish population. **(A)** Pedigree representation of the orange clownfish *Amphiprion percula* in Kimbe Island (n= 1735, excluding new-recruits). Each line connects a parent with one of its offspring (blue and red lines represent respectively paternal and maternal links). It is important to note that an individual can be father then mother. The generation is indicated on the left from first generation (F0, n=502) to fifth generation (F4). **(B)** Power analysis of the pedigree.

**SUPPLEMENTARY METHODS**

**Individual's contribution to biennial population growth rate**

We estimated the De-lifing (DL), which is the individual's contribution to the biennial population growth rate. DL was calculated following Coulson *et al.* (2006). This index can be considered as the realized fitness of an individual over the given period of time (here two years) by including survival and success to local recruitment. This index offers great opportunities to empirically study ecological and evolutionary changes in stochastic environments (Dupont *et al.* 2017).

According to Coulson *et al.* (2006), an individual's biennial fitness is measured by its contribution $DL\_{ti}$ to the growth rate of the population between $t$ and $t+1$.

$DL\_{ti}=\frac{s\_{ti}-\overbar{s}\_{t} }{N\_{t}-1 }$ + $\frac{F\_{ti}-\overbar{F}\_{t} }{N\_{t}-1 }$ (1)

where $N\_{t} $is the population size at time$ t$; $s\_{ti} $is the survival of individual $i$ between $t$ and $t+1$ (1 if it survived and 0 otherwise);$ \overbar{S}\_{t} $is the mean survival rate in the population between $t$ and $t+1$; $F\_{ti}$ is the fecundity of the individual $i$ defined as the number of offspring born between $t$ and $t+1$ and still alive at $t+1$ and $\overbar{F}\_{t} $is the mean individual fecundity in the population. A negative value of DL represents an individual that performed worse than the population mean while a positive value represents one that performed better. (Coulson *et al.* 2006)

**Quantitative genetic generalized linear model approach**

As for the IIRS variance, the DL variance was partitioned into six random effects: Additive genetic (*V*A), Maternal (*V*M), Natal Habitat (*V*NH), Resident Habitat (*V*RH), Permanent Environment (*V*PE) and Residual (*V*R) variances by using the ‘animal model’ quantitative genetic approach (Kruuk 2004).

The DL variance is the sum of six variance components:

*V*DL = $V\_{A\_{DL}}$+ $V\_{M\_{DL}}$+ $V\_{NH\_{DL}}$+ $V\_{RH\_{DL}}$+ $V\_{PE\_{DL}}$ + $V\_{R\_{DL}}$ (2)

We used a quantitative genetics model as univariate GLMMs using the 'MCMCglmm' package (Hadfield 2010) in R version 3.5.1 (R Core Team 2018), with DL as a Gaussian response variable. We used parameter expanded priors for all analyses (*V*=1, *nu*=0.02), which are often referred to as ‘non informative’ priors although such denomination can be debated, as we wanted posterior estimates to be determined from the data and not from the priors (Morrissey *et al.* 2014). We ran model MCMC chains over 1,000,000 iterations with initial burning of 10,000 iterations and a thinning of 1,000 iterations.

Variance components were estimated as the mean of the posterior distributions (the mean of the MCMC sample). and we reported the lower and the upper limits of the 95% credible interval. For the six variance components, we calculated their relative contribution to the sum of all variance components, thereby expressing their effects as percentages of the total phenotypic variance (*V*DL). As a result, we obtained standard heritability estimates for DL (*h*²DL) by applying the basic formula (*h*² =$V\_{A}$ / $V\_{P}$, see Falconer & McKay 1996), and similarly maternal effects by estimating the proportion of total phenotypic variance explained by the maternal variance (*m²*= $V\_{M}$ / $V\_{P}$). Because DL is Gaussian variable, we reported a standard heritability and a standard maternal effects. We calculated the 95% credibility intervals from the posterior distributions of observed parameters for all the variance components and other estimates expressed on their basis by using the ‘HDInterval’ package (Meredith & Kruschke 2016).

**SUPPLEMENTARY RESULTS**

**Habitats dominantly shape the De-lifing in the clownfish population.**

De-lifing (DL) varied from -2.56 ×10-3 to 1.81 ×10-2 (Figure S2, histogram), which illustrates that there is variation in the individual contribution to the population demographic growth through reproduction and survival. Its average value at the population level was 2.16×10-5 ± 8.04×10-5 units. When considering DL, 43.1% of its variance was explained by Natal Habitat (Figure S2, pie chart) and 55.3% by Resident Habitat, again with minor contributions from Additive genetic effects (0.3%) and Maternal effects (1.0%).



**Figure S2.** Sources of variation in De-lifing (DL) variance of the the Kimbe Island orange clownfish. Distribution (histograms) and variance components on standard data-scale (pie chart) for biennial DL explained by Additive genetic (VA), Maternal (VM), Natal Habitat (VNH), Resident Habitat (VRH), Permanent Environment (VPE) and Residual (VR) variances. These proportions were calculated from the values of the posterior mode of a quantitative genetics generalized linear mixed model analysis.

We found that Additive genetic variance was extremely low: *V*A,DL=3.151 × 10-5 (CI95% 2.897×10-5 to 3.470×10-5, Table S2). Consequently, heritability estimates expressed on the standard data-scale was *h*²DL *=*0.003 (CI95% 2.432 × 10-3 to 0.0261, Table S2) for DL. We also found that maternal was extremely small, to the extent that it might be considered as null: *V*M,DL=1.190×10-4 (CI95% 9.974×10-5 to 1.434×10-4, Table S2). While our analysis detected maternal variance, it made very little contribution to the total variance in DL estimate (*m*²DL=1.0%, Figure S2). The relative contribution of individuals to the population replenishment was indeed influenced by the Natal Habitat to an extent of 43.1% for DL.

**Table S2. Sources of variation in De-lifing (DL) for the Kimbe Island orange clownfish.** Here wereportedvariance component estimates quantified by using the animal model approach: Additive genetic effect(*V*A), Maternal effect (*V*M), Natal Habitat (*V*NH) and Resident Habitat (*V*RH) effects, Permanent Environmental (*V*PE) effect and Residual Variance (*V*R) and heritability (*h*²) and maternal effects (*m*²) for biennial DL. 95% credible intervals (CI) are reported for each estimate.

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| **Components** | **DL****Standard scale** |
| ***V*A****(CI)** | 3.151×10-5(2.897×10-5 to 3.470×10-5) |
| ***V*M****(CI)** | 1.190×10-4(9.974×10-5 to 1.434×10-4) |
| ***V*NH****(CI)** | 5.022×10-3(9.972×10-4 to 0.012) |
| ***V*RH****(CI)** | 6.443×10-3(1.13×10-3 to 0.017) |
| ***V*PE****(CI)** | 3.016×10-5(2.72× 10-5 to 3.25×10-5) |
| ***V*R****(CI)** | 2.978×10-5(1.15×10-5 to 1.29×10-5) |
| ***h²*****(CI)** | 0.003(6.506×10-4 to 6.712×10-3) |
| ***m²*****(CI)** | 0.010(2.432×10-3 to 0.0261) |

**SUPPLEMENTARY DISCUSSION**

Because of the different proprieties of the two measures of individual reproductive success (i.e., IIRS, which is the Intra-population Individual Reproductive Success, and DL), the results obtained on the DL highlights that the residual variance of SLR can be implicitly explained by annual environmental variation. The model decomposing the variance in DL measured a larger effect of the habitat, which is likely due to the fact that DL has different statistical properties. DL accounts for reproductive success, survival and population size. DL is expected to smooth out changes in demographic population growth and to account for the individuals that did not produce offspring but contributed to the population stability or growth by their own survival. Recruitment and population size vary through time in this population (Salles *et al.* 2015), which might explain why more variance in DL was explained by the model. This difference in outcomes among these two estimators of the individual contribution to the local replenishment of the population supports the hypothesis that a part of the self-recruitment variation explained by the habitat is confounded with temporal heterogeneity in population growth and survival.

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