**Appendix: Late life parental age effects**

Data selection

* For measures of adulthood traits (LRS and lifespan), chicks without a known death date (either due to being currently alive, or more commonly being unable to distinguish emigration from death) were excluded. Individuals that died before the start of their first breeding season (age one year) were also excluded. This resulted in sample sizes of 934 males and 303 females.

Statistical analysis

* *Lifespan:* Lifespan was measured in years, with individuals increasing in age at the start of each breeding season (September 1st) they survived beyond. Lifespan ranged from 1 to 13 years old. There was considerable differences in variance in lifespan between males and females and so the sexes were modelled separately, both using a negative binomial (log-link) model.
* *Lifetime reproductive success:* LRS was measured as the total number of offspring hatched (for females) and the total number of offspring sired that survived to 7 days old when blood sampled (for males). LRS was modelled separately in the two sexes using a zero-inflated quasi-Poisson (log link) model for females and a zero-inflated negative binomial (log link) model for males.

Results

Lifespan

* For males sired by within-pair fathers, lifespan improved with the lifespan of their father. There was no association between social father or genetic father lifespan and lifespan for extra-pair sired chicks (table 5). Number of helpers was not associated with male lifespan (supplementary).
* There were no parental age or parental lifespan effects on female lifespan (table 6). Number of helpers also had no association with female lifespan (supplementary).

**Table 5.** Effects of parental ages and lifespans on male lifespan from a negative binomial (log-link) generalized linear mixed-model (log-link function).

|  |  |  |  |
| --- | --- | --- | --- |
| Predictors | Log-Mean | CI | p |
| Intercept | 0.67 | 0.39 – 0.96 | **<0.001** |
| Mother Age | -0.00 | -0.04 – 0.04 | 0.987 |
| Mother Lifespan | 0.02 | -0.01 – 0.05 | 0.289 |
| Extra-pair Genetic Father Age | -0.02 | -0.06 – 0.03 | 0.462 |
| Extra-pair Genetic Father Lifespan | 0.01 | -0.03 – 0.05 | 0.692 |
| Extra-pair Social Father Age | 0.00 | -0.05 – 0.05 | 0.991 |
| Extra-pair Social Father Lifespan | 0.00 | -0.03 – 0.04 | 0.906 |
| Within-pair Father Age | -0.04 | -0.09 – 0.02 | 0.175 |
| Within-pair Father Lifespan | 0.05 | 0.01 – 0.09 | **0.017** |
| Extra-Group [yes] | 0.26 | -0.09 – 0.61 | 0.142 |
| Incubation Date | -0.19 | -0.52 – 0.14 | 0.268 |

Note: Sample size is 934 males. The model includes random effects of mother ID (n = 342, τ = 0.01), social father ID (n = 335, τ = 0.02), genetic father ID (n = 351, τ = 0.00), and cohort (n = 28, τ = 0.03). The residual variance is 0.46. A value of 1 for the binomial variable ‘extra-group’ indicates the chick was sired by a male outside the natal territory, while a value of 0 indicates the sire was the within-pair social mate. All extra-pair father terms are interaction terms between the effect and the extra-pair binomial variable. Both within-pair father terms are also interaction terms, with each effect interacting with a second dummy variable for within-pair sire (0/1).

**Table 6.** Effects of parental ages and lifespans on female lifespan from a negative binomial (log-link) generalized linear mixed-model (log-link function).

|  |  |  |  |
| --- | --- | --- | --- |
| Predictors | Log-Mean | CI | p |
| Intercept | 1.63 | 1.14 – 2.12 | **<0.001** |
| Mother Age | -0.02 | -0.09 – 0.05 | 0.548 |
| Mother Lifespan | 0.02 | -0.03 – 0.07 | 0.490 |
| Extra-pair Genetic Father Age | -0.05 | -0.12 – 0.03 | 0.223 |
| Extra-pair Genetic Father Lifespan | 0.02 | -0.04 – 0.09 | 0.486 |
| Extra-pair Social Father Age | 0.01 | -0.06 – 0.08 | 0.746 |
| Extra-pair Social Father Lifespan | 0.03 | -0.03 – 0.09 | 0.328 |
| Within-pair Father Age | -0.02 | -0.12 – 0.09 | 0.751 |
| Within-pair Father Lifespan | -0.05 | -0.14 – 0.03 | 0.197 |
| Extra-Group [yes] | -0.60 | -1.18 – -0.02 | **0.043** |
| Incubation Date | -1.03 | -1.63 – -0.43 | **0.001** |

Note: Sample size is 303 males. The model includes random effects of mother ID (n = 190, τ = 0.00), social father ID (n = 189, τ = 0.05), genetic father ID (n = 190, τ = 0.00), and cohort (n = 27, τ = 0.02). The residual variance is 0.40. A value of 1 for the binomial variable ‘extra-group’ indicates the chick was sired by a male outside the natal territory, while a value of 0 indicates the sire was the within-pair social mate. All extra-pair father terms are interaction terms between the effect and the extra-pair binomial variable. Both within-pair father terms are also interaction terms, with each effect interacting with a second dummy variable for within-pair sire (0/1).

Discussion

Sex differences

* Sex differences were mild or nonexistent in early life
* In late life males appear to only be affected by fathers (much of the literature demonstrates sex specific effects where fathers affect sons and mothers affect daughters)
* The smaller sample size of adult females may mean that weak parental effects are unable to be detected