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block	parental age	sex	develop. time	body size	PO immunity	wing morph	fecundity
A	7 days	female	99	97	35	96	40
A	7 days	male	142	142	42	140	–
A	14 days	female	82	80	28	80	32
A	14 days	male	125	126	33	123	–
A	21 days	female	78	73	30	72	34
A	21 days	male	137	134	37	131	–
B	7 days	female	90	88	30	87	37
B	7 days	male	139	138	35	140	–
B	14 days	female	81	82	27	82	36
B	14 days	male	101	100	26	102	–
B	21 days	female	81	75	24	75	30
B	21 days	male	115	112	19	118	–

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3 Table S1. Numbers of female and male samples collected for each variable within each  
4 block and parental age treatment.

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Path model	Test statistic	df	p	RMSEA	Comparative fit index
Female model 1	80.8	10	0.000*	0.123	0.472
Female model 2	15.0	4	0.005*	0.073	0.924
<b>Female model 3</b>	<b>33.1</b>	<b>2</b>	<b>0.217</b>	<b>0.030</b>	<b>0.994</b>
Male model 1	73.2	6	0.000*	1.123	0.396
Male model 2	21.8	3	0.000*	0.094	0.825
<b>Male model 3</b>	<b>1.37</b>	<b>1</b>	<b>0.242</b>	<b>0.024</b>	<b>0.996</b>

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7 Table S2. Tests of alternative path models. P-values with an asterisk indicate rejection of  
8 the path model at an alpha value of 0.05. We failed to reject the models in bold. These  
9 models also received good support based on RMSEA and comparative fit index (CFI)  
10 values. Values of RMSEA < 0.05 and CFI > 0.95 indicate a good fit between data and  
11 model.

12

	parental age	block	develop. time	body size	PO immunity	wing morph
parental age	–	-0.0288± N/A	-0.0499 ± 0.0358	<b>0.164 ± 0.0359 ***</b>	–	0.0496 ± 0.0343
block	0.0331 ± N/A	–	<b>-0.112 ± 0.0352 **</b>	<b>-0.0743 ± 0.0365 *</b>	<b>0.144 ± 0.0705 *</b>	<b>-0.149 ± 0.0348 ***</b>
develop. time	<b>-0.139 ± 0.0423 **</b>	<b>0.0884 ± 0.0435 *</b>	–	<b>0.120 ± 0.0393 **</b>	<b>0.271 ± 0.0542 ***</b>	<b>-0.210 ± 0.0348 ***</b>
body size	<b>0.149 ± 0.0462 **</b>	<b>-0.235 ± 0.0413***</b>	<b>0.112 ± 0.0486 *</b>	–	0.0175 ± 0.0612	<b>0.0896 ± 0.0381 *</b>
PO immunity	–	0.095 ± 0.0753	<b>0.243 ± 0.0764 **</b>	-0.105 ± 0.0795	–	-0.0323 ± 0.0649
wing morph	0.0545 ± 0.0424	<b>-0.172 ± 0.0411 ***</b>	<b>-0.357 ± 0.0469 ***</b>	0.0699 ± 0.0458	0.0210 ± 0.0785	–
fecundity	–	-0.0192 ± 0.0685	0.0308 ± 0.0553	<b>0.139 ± 0.0645*</b>	-0.0210 ± 0.0793	-0.0456 ± 0.0748

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14 Table S3. Regression and covariance coefficients ( $\pm 1$  standard error) from the path  
 15 analysis for Model 3. These correspond to “Female model 3” and “Male model 3” in  
 16 Figure 2 and Table S2. Here, females are below the diagonal and males are above the  
 17 diagonal. Bold values indicate that  $p < 0.05$ . \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\*  $p < 0.001$ .  
 18 Covariances are shaded. Standard error and p-values were not calculated for  
 19 correlations between categorical variables, as indicated by “N/A.”

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	parental age	block	develop. time	body size	PO immunity	wing morph
parental age	–	-0.0288 ± N/A	-0.0506 ± 0.0358	<b>0.165 ± 0.0359 ***</b>	0.0889 ± 0.0758	0.0487 ± 0.0339
block	0.0331 ± N/A	–	<b>-0.111 ± 0.0353 **</b>	<b>-0.0746 ± 0.0365 *</b>	<b>0.151 ± 0.0687 *</b>	<b>-0.153 ± 0.0347 ***</b>
develop. time	<b>-0.139 ± 0.0423 **</b>	<b>0.0882 ± 0.0435 *</b>	–	<b>0.120 ± 0.0393 **</b>	<b>0.274 ± 0.0543 ***</b>	<b>-0.221 ± 0.0343 ***</b>
body size	<b>0.149 ± 0.0462 **</b>	<b>-0.235 ± 0.0413 ***</b>	<b>0.112 ± 0.0486 *</b>	–	0.00934 ± 0.0617	<b>0.0944 ± 0.0378 *</b>
PO immunity	0.0832 ± 0.0687	0.093 ± 0.0754	<b>0.248 ± 0.0765 **</b>	-0.115 ± 0.0772	–	-0.0316 ± 0.0639
wing morph	0.0555 ± 0.0422	<b>-0.195 ± 0.0410 ***</b>	<b>-0.347 ± 0.0473 ***</b>	0.0783 ± 0.0456	-0.00856 ± 0.0780	–
fecundity	0.0796 ± 0.0658	-0.0199 ± 0.0691	0.0422 ± 0.0543	<b>0.132 ± 0.0636*</b>	-0.0302 ± 0.0793	-0.0351 ± 0.0756

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22 Table S4. Regression and covariance coefficients ( $\pm 1$  standard error) from the path  
 23 analysis for the full model. This corresponds to the path diagram in Fig 3a. This full  
 24 model was used to calculate direct and indirect effects of the paths in Fig 3a. Females  
 25 are below the diagonal and males are above the diagonal. Bold values indicate that  $p <$   
 26  $0.05$ . \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\*  $p < 0.001$ . Covariances are shaded. Standard error and  $p$ -  
 27 values were not calculated for correlations between categorical variables, as indicated  
 28 by “N/A.”

Type	Path	Estimates $\pm$ SE	
		Female model	Male model
Direct	parental age $\rightarrow$ body size	<b>0.1494 <math>\pm</math> 0.0462**</b>	<b>0.1647 <math>\pm</math> 0.0359***</b>
Direct	parental age $\rightarrow$ wing morph	0.0555 $\pm$ 0.0422	0.0487 $\pm$ 0.0339
Direct	parental age $\rightarrow$ PO immunity	0.0833 $\pm$ 0.0687	0.0888 $\pm$ 0.0758
Direct	development time $\rightarrow$ PO immunity	<b>0.2477 <math>\pm</math> 0.0765**</b>	<b>0.2735 <math>\pm</math> 0.0543***</b>
Direct	parental age $\rightarrow$ fecundity	0.0796 $\pm$ 0.0658	–
Direct	development time $\rightarrow$ fecundity	0.0422 $\pm$ 0.0543	–
Indirect	parental age $\rightarrow$ development time $\rightarrow$ body size	-0.0155 $\pm$ 0.0085	-0.0061 $\pm$ 0.0045
Indirect	parental age $\rightarrow$ development time $\rightarrow$ wing morph	<b>0.0481 <math>\pm</math> 0.016**</b>	0.0112 $\pm$ 0.008
Indirect	parental age $\rightarrow$ development time $\rightarrow$ PO immunity	<b>-0.0344 <math>\pm</math> 0.0148*</b>	-0.0138 $\pm$ 0.0103
Indirect	parental age $\rightarrow$ development time $\rightarrow$ wing morph $\rightarrow$ PO immunity	0.0004 $\pm$ 0.0037	-0.0004 $\pm$ 0.0008
Indirect	parental age $\rightarrow$ wing morph $\rightarrow$ PO immunity	0.0005 $\pm$ 0.0044	-0.0015 $\pm$ 0.0033
Indirect	parental age $\rightarrow$ development time $\rightarrow$ body size $\rightarrow$ PO immunity	0.0018 $\pm$ 0.0014	-0.0001 $\pm$ 0.0004
Indirect	parental age $\rightarrow$ body size $\rightarrow$ PO immunity	-0.0172 $\pm$ 0.0119	0.0015 $\pm$ 0.0102
Indirect	parental age $\rightarrow$ development time $\rightarrow$ fecundity	-0.0059 $\pm$ 0.0078	–
Indirect	parental age $\rightarrow$ development time $\rightarrow$ wing morph $\rightarrow$ fecundity	-0.0017 $\pm$ 0.0037	–
Indirect	parental age $\rightarrow$ wing morph $\rightarrow$ fecundity	-0.0019 $\pm$ 0.0045	–
Indirect	parental age $\rightarrow$ development time $\rightarrow$ body size $\rightarrow$ fecundity	-0.0021 $\pm$ 0.0016	–
Indirect	parental age $\rightarrow$ body size $\rightarrow$ fecundity	0.0198 $\pm$ 0.0116	–
Indirect	development time $\rightarrow$ wing morph $\rightarrow$ PO immunity	-0.003 $\pm$ 0.027	0.007 $\pm$ 0.0141
Indirect	development time $\rightarrow$ body size $\rightarrow$ PO immunity	-0.0129 $\pm$ 0.0095	0.0011 $\pm$ 0.0074
Indirect	development time $\rightarrow$ wing morph $\rightarrow$ fecundity	0.0122 $\pm$ 0.0263	–
Indirect	development time $\rightarrow$ body size $\rightarrow$ fecundity	0.0149 $\pm$ 0.01	–
Total	parental age $\rightarrow$ body size	<b>0.1339 <math>\pm</math> 0.0445**</b>	<b>0.1587 <math>\pm</math> 0.0359***</b>
Total	parental age $\rightarrow$ wing morph	<b>0.1036 <math>\pm</math> 0.0437*</b>	0.0599 $\pm$ 0.0346
Total	parental age $\rightarrow$ PO immunity	0.0344 $\pm$ 0.07	0.0746 $\pm$ 0.075
Total	parental age $\rightarrow$ fecundity	0.0879 $\pm$ 0.0671	–
Total	development time $\rightarrow$ PO immunity	<b>0.2319 <math>\pm</math> 0.0729**</b>	<b>0.2816 <math>\pm</math> 0.0521***</b>
Total	development time $\rightarrow$ fecundity	0.0692 $\pm$ 0.0504	–

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30 Table S5: Estimates ( $\pm$  1 standard error) for direct, indirect, and total effects of parental  
31 age on female and male offspring body size, PO immunity, wing morph, and female  
32 fecundity. Bold values indicate that  $p < 0.05$ . \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\*  $p < 0.001$ .

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Free Parameter	df	AIC	BIC	Chisq	Chisq diff	df diff	P
None	18	11328.35	11462.59	37.415	2.575469	1	0.109
Parental age to development time	17	11327.88	11467.29	34.945	2.575469	1	0.109
Parental age to body size	17	11330.25	11469.65	37.311	0.105455	1	0.745
Parental age to wing morph	17	11329.98	11469.39	37.043	0.372948	1	0.541
Parental age to PO immunity	17	11330.34	11469.75	37.408	0.007482	1	0.931
<b>Block to development time</b>	<b>17</b>	<b>11318.09</b>	<b>11457.5</b>	<b>25.156</b>	<b>12.3985</b>	<b>1</b>	<b>0.000430</b>
Block to body size	17	11323.23	11462.64	30.297	7.344824	1	0.00672
Block to wing morph	17	11329.52	11468.93	36.582	0.799629	1	0.371
Block to PO immunity	17	11330.15	11469.56	37.215	0.195415	1	0.658
Development time to body size	17	11330.34	11469.75	37.40612	0.008779	1	0.925
Development time to wing morph	17	11321.97	11461.37	29.03054	6.402211	1	0.0114
Development time to PO immunity	17	11330.04	11469.45	37.104	0.249828	1	0.617

36

37 Table S6: Likelihood ratio tests for model comparisons of male and female models. The  
 38 critical value for statistical significance with correction for multiple comparisons is  $p <$   
 39 0.00455. Bold values indicate that  $p < 0.00455$ .

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Supplementary text: Path analysis methods

Parental age was coded as an ordinal variable with values 0, 1 and 2 representing the first, second and third oviposition pads. The two replicate experimental blocks were coded as a binomial variable. Because wing length was bimodal, we categorized wing lengths as short (< 10.33 mm) or long (> 10.33 mm). The cutoff was based on inspection of histograms of wing length; for both males and females, this value represented the lowest frequency (zero) that lay between the two peaks in the distribution. PO values were log transformed as described earlier. All variables were zero-centered and z-normalized for all analyses.

Question 1: Which path model best describes the causative relationship between parental age, development time, adult body size, immunity, fecundity, and wing morph?

We used structural equation modeling to test three *a priori* models that differed in which life history variables were directly affected by parental age (Fig 2). We constructed separate models for males and females because fecundity was only included in the female models. All models include direct effects of block on all offspring traits (not shown on Fig 2).

Model 1: "Acquisition." Model 1 tests the hypothesis that offspring life history traits are causally independent of one another, but are causally dependent on parental age. In this model, parental age directly affects all offspring life history traits except the fecundity of female offspring. In female models, body size directly affects fecundity. The covariance terms among all offspring life history traits are constrained to zero. Therefore, if there is a trade-off among life history traits, then this model should be rejected.

Model 2: "Trade-off." Model 2 tests the hypothesis that offspring morphological traits are causally dependent on development time, and that parental age indirectly affects these traits through development time. In this model, parental age directly affects development time but not the morphological traits of offspring body size or wing morphology. Development time directly affects body size and wing morphology. Development time, body size and wing morphology directly affect the other offspring life history traits of immunity and, in female models, fecundity. Covariance terms between wing morphology and body size and between immunity and fecundity (in female models) are included. If there is a trade-off between development time and other traits, then we expect that faster development times of offspring result in smaller adult body size and lower PO activity. If parental age mediates an acquisition effect, for example, offspring of younger (or older) parents are able to both grow quickly and attain large size, then this model should be rejected. Variation in acquisition for other reasons would not necessarily result in rejection of this model.

84 Model 3: “Acquisition and trade-off.” Model 3 tests the hypothesis that offspring  
85 morphological traits are causally dependent on development time and parental age. In  
86 this model, parental age directly affects development time and the morphological traits  
87 of offspring body size or wing morphology. Development time directly affects body size  
88 and wing morphology. Development time, body size and wing morphology directly  
89 affect the other offspring life history traits of immunity and, in female models,  
90 fecundity. The covariance terms between wing morphology and body size and between  
91 immunity and fecundity (in female models) are included. If there is a trade-off between  
92 development time and other traits, then we expect that faster development times of  
93 offspring result in smaller adult body size and lower PO activity, controlling for the  
94 effects of other variables like parental age. If variation in parental age mediates an  
95 acquisition effect, then we expect that this model will not be rejected. The direct effects  
96 of age on life history traits should be such that younger (or older) parents are able to  
97 both grow quickly and attain large size.

98  
99 Our models necessarily make several assumptions. First, because parental age and block  
100 precede offspring development, offspring adult body size, offspring wing morphology,  
101 offspring immunity and the fecundity of female offspring, we assume that parental age  
102 and block cause the offspring variables, and not the reverse. Similarly, because offspring  
103 development from egg to adult precedes adulthood, we only test models in which  
104 development time causes variation in adult body size, wing morph, immunity, and  
105 female fecundity, and not the reverse. Finally, because adult body size and wing morph  
106 do not change after eclosion, whereas immunity and fecundity can be influenced by  
107 events after eclosion, we only test models in which morphological variables cause  
108 variation in immunity and female fecundity, and not the reverse. Finally, parental age  
109 and block were assumed to be causally independent variables; that is, a change in one  
110 would not cause a change in the other. However, we included a covariance term  
111 between age and block in all models to test for non-random association between these  
112 variables.

113  
114 Each model was fit with the *sem* procedure in the R-package *lavaan*, using the “MLR”  
115 estimator. Because there were missing values for some variables, we used full  
116 information maximum likelihood estimation (FIML) to fit the model to incomplete data.  
117 Some variables were only measured for a randomly selected subset of individuals in the  
118 study. Thus the missing data is analyzed as missing at random (MAR). The MLR  
119 estimator produces a scaled test statistic that is asymptotically equal to the Yuan-  
120 Bentler test statistic (Rosseel 2012). We used this test statistic to test whether the model  
121 could be rejected at an alpha value of 0.05. Therefore, we fail to reject a model if the p-  
122 value for this test statistic was  $> 0.05$ . We also assessed two measures of approximate  
123 fit for each model: Bentler’s comparative fit index (CFI) and root mean square error of  
124 approximation (RMSEA). In SEM, CFI values greater than 0.95 and RMSEA values less  
125 than 0.05 are typically considered reasonable levels of approximate fit between the  
126 model to the data (Shipley 2016).

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128 Question 2: How do parental age and development time affect offspring body size,  
129 immunity, fecundity, and wing morph?

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131 To explore the direct and indirect effects of parental age and development time on  
132 offspring life history variables, we constructed a ‘full’ model based on the general  
133 structure of Models 2 and 3. In this model, parental age and block are causal to  
134 development time, parental age, block and development time are causal to the  
135 morphological variables of body size and wing morph, and all of these are causal to  
136 immunity and, in females, fecundity. This model differs from models 2 and 3 above in  
137 that all possible direct causal pathways were included. For example, direct effects of  
138 parental age on female fecundity and immunity were included in this model. We  
139 included all direct effects in this model to be able to parameterize the total direct and  
140 indirect effects of parental age and development time on other offspring life history  
141 traits. As for question 1, female and male models were fit separately, as fecundity was  
142 only measured for females.

143

144 Models were fit with the *sem* procedure in the R-package *lavaan*, using the “MLR”  
145 estimator. Because there were missing values for some variables, we used full  
146 information maximum likelihood estimation (FIML) to fit the model to incomplete data.  
147 Direct effects of parental age on other model variables were the standardized  
148 regression coefficients of age on the target variables. Indirect effects were the product  
149 of the standardized regression coefficients along a pathway. For example, the indirect  
150 effect of age on a target variable, through its effect on development time is the product  
151 of the regression coefficient of age on development time and that of development time  
152 on the target variable. Total effects of age or development time on a target variable  
153 were the sums of all direct and indirect effects. Nonparametric bootstrap confidence  
154 intervals for standardized parameter estimates of direct and indirect effects were  
155 obtained using the *boot.ci* procedure with type “perc” (or bootstrap percentile interval)  
156 in the *boot* package in R. Significance of model parameters was assessed by inspecting  
157 whether the 95% confidence interval for each parameter overlapped 0.

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159 Question 3: Are male and female offspring life history traits affected similarly or  
160 differently by parental age and development time?

161

162 To test whether the direct and indirect effects of parental age and block on other model  
163 variables differed between male and female offspring. We constructed an acyclic  
164 directed graph as shown in Fig. 3, with the exception that fecundity was not included as  
165 it was not measured in males. The model was fit using data from male and female  
166 offspring, with sex included as a grouping variable. We initially constrained all model  
167 parameters to be equal for males and females (“fully constrained model”). We then  
168 allowed one path coefficient to vary freely between males and females (“free path  
169 model”). To test whether allowing paths to vary between males and females improved  
170 the fit of the model, we compared the goodness of fit of each free path model with that  
171 of the fully constrained model using a likelihood ratio tests (LRT). We performed eleven

172 separate LRTs, one for each regression parameter in the model. We adjust for multiple  
173 comparisons by using a Bonferroni adjusted  $\alpha$ -value of 0.00455.

174

175 Literature Cited

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