

**S2 Table. Full models of life-history trait analyses.** Full models including non-significant terms that were removed during the model selection procedure of the life-history trait analyses (p-values in bold indicate significant terms).

<b>Trait</b>	<b>Estimate</b>	<b>Std. Error</b>	<b>t-value</b>	<b>P - value</b>
<b>Size at maturity of dispersers</b>				
Intercept	0.627	0.014	45.214	< <b>0.001</b>
Sex	-0.115	0.026	-4.378	< <b>0.001</b>
Deutonymph duration*	-0.001	0.001	-0.812	0.425
Deutonymph size*	0.709	0.539	1.314	0.199
Treatment*	0.003	0.015	0.233	0.817
Deut. Duration:Deut. Size*	-0.123	0.130	-0.943	0.355
<b>Size at maturity</b>				
Intercept	0.712	0.011	67.464	< <b>0.001</b>
Sex	-0.130	0.014	-9.114	< <b>0.001</b>
Deutonymph expression	-0.080	0.015	-5.376	< <b>0.001</b>
Treatment*	-0.005	0.004	-1.203	0.232
Sex:Deutonymph expression*	0.019	0.032	0.589	0.557
<b>Lifespan</b>				
Intercept	-1.263	1.538	-0.821	0.417
Lifespan	0.485	0.057	8.444	< <b>0.001</b>
Deutonymph	7.135	2.501	2.852	<b>0.007</b>
Lifespan:Deuto. expression	-0.276	0.081	-3.413	<b>0.002</b>
Treatment*	0.230	0.360	0.639	0.527

\* Values of terms that were not significant and removed (during model selection) are shown, however the p-value is an indication of the ANOVA comparison between the model including and the model excluding the term indicated.