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Supporting Information

This online Supporting Information accompanies the paper “A modelling exercise to show why population models should incorporate distinct life-histories of dispersers” by Jacques A. Deere, Ilona van den Berg, Gregory Roth and Isabel M. Smallegange.

The first section describes the methods used to parameterize the character demography functions and calculation of the mesh points used in the DPM. We also give the parameter estimates for all the character-demography functions for the DPM. This is followed by the DPM equations used in the model which can be found in table S1. Figure S1 highlights how population growth rate, when varying β and δ , is impacted when adult survival rate is altered.

Parameter estimation

Life-history data on female bulb mites taken from Deere et al. (2015) were used to parameterise the DPM. We estimated the parameters using statistical models for the five character-demography functions: the survival function (1), transition function (2), growth function (3), reproduction function (4) and the parent-offspring association function (5) (Fig. 2 in main text).

Non-dispersers

Parameters were estimated following the method used by Smallegange et al. (2014). Function parameters were estimated using the following statistical models (summarized in Table A1): (1) Survival - generalised linear mixed model (GLMMs) with binomial error

24 structure; (2) Transition rates – GLMM with binomial error structure; (3) Growth – GLMM with
 25 a Gaussian error structure; (4) Fertility rate (Reproduction) – GLMM with a Gaussian error
 26 structure; (5) Parent-offspring association kernel – generalised linear model (GLM) with a
 27 Gaussian error structure. In all cases body length and body length squared were linear
 28 predictors and, with the exception of the parent-offspring association function where we
 29 fitted a GLM, mite identity was included as a random factor. The response variables for the
 30 five functions were: (1) Survival – from time t to time $t+1$ (this is binary and set as 0 or 1), (2)
 31 Transition - probability of growing to the next stage at time $t+1$, $\gamma_{s,t+1}$ (see below), (3) Growth
 32 - mean and variance in body size at time $t+1$, (4) Fertility - the number of eggs produced at
 33 time $t+1$, and (5) Parent-offspring association - mean and variance in size of eggs produced at
 34 time $t+1$ by each individual at time t . In the case of eggs their size at time $t+1$ equalled their
 35 size at time t as eggs do not increase in size.

36 During data collection it was not always possible to locate each individual every day.
 37 As such, the days where an individual was not seen but was still alive (i.e. observed alive the
 38 next day), body length was estimated (not including these observations would result in an
 39 underestimation of the survival function). The missing values were filled in by using the
 40 Gompertz function to estimate female body length at age a (Smallegange et al. 2014):

41

$$42 \quad Z_a = Z_\infty e^{-e^{-k(a-a_0)}} \quad (\text{Eq. S1})$$

43

44 where Z_a is body length (mm) at age a (days), Z_∞ is the mean maximum length (mm, at $a = \infty$),
 45 k is the instantaneous growth rate at age a_0 , and a_0 is the inflection point of the curve and
 46 the age at which absolute growth rate begins to decline.

47 In the case of function (2), we used duration in the life stage as an indicator of the
 48 transitioning to the next stage (Smallegange et al. 2014); i.e. time spent in the current stage
 49 depends on the probability of growing to the next stage (Caswell 2001). Therefore, $\gamma_{s,t+1}$ is
 50 given by $\gamma_{s,t+1} = 1/d_{s,t}$, where $d_{s,t}$ is the number of days that an individual still has to spend in
 51 stage s . This means that d_s equals the total duration of stage s on the first day that a female is
 52 in stage s , and that when an individual develops from stage s into stage $s+1$ at time $t+1$, $d_s=1$
 53 so that $\gamma_{s,t+1} = 1$.

54 For function (3) and (5) the minimal model, which generated the predictors of mean
 55 size at time $t+1$, was utilised to generate the parameters for the variance around the mean
 56 size at $t+1$ by taking the squared residuals and fitting them against a statistical function of the
 57 same form as the mean size to estimate the variance in size at time $t+1$. The growth (3) and
 58 parent-offspring association functions (5) were then constructed using the equation following
 59 Easterling et al. (2000):

60

$$61 \quad y_i = \frac{1}{\sqrt{2\pi}\sigma_i} e^{-\frac{(z' - \mu_i)^2}{2\sigma_i^2}} \quad (\text{Eq. S2})$$

62

63 where y_i is either the growth or parent-offspring association function, μ_i describes the mean
 64 effect of the significant predictors on growth or parent-offspring association, and σ_i describes
 65 the squared residuals around μ_i .

66 For details on construction of the DPM from these parameters see main text. Note that
 67 mite identity was included in the statistical analyses (except in the parent-offspring
 68 association function) but was not modelled within the DPM.

69

71 In the case of dispersers the rates for eggs and larvae were the same as for the non-
72 dispersers (see Deere et al. (2015) and Fig. 2 in main text). However, protonymphs can also
73 develop into a deutonymph and we estimated the probability that a protonymph develops
74 into a deutonymph, tritonymph or stays as a protonymph using a multinomial logistic (which
75 generated the three transition probabilities). For the multinomial logistic the linear predictor
76 was body length at time t , the response variable was stage at time $t+1$ and the reference level
77 was set as the protonymph stage. This gives the probability of developing into a tritonymph,
78 a deutonymph or remaining as a protonymph as a function of individual size. As such, the
79 regression coefficients $\beta\mu$ are the log of the ratio of the two probabilities of developing into
80 a tritonymph or deutonymph over staying in the protonymph stage (the reference
81 level/choice). For example, if $\beta\mu$ represents the effect of μ (size), we expect that for one unit
82 change in μ , the relative risk of developing into a tritonymph over staying a protonymph will
83 increase by $\exp(\beta\mu)$. The multinomial logistic analyses were performed in R (version 3.0.2)
84 using the 'mlogit' package (R Development Core Team 2013). All other parameter estimates
85 were calculated in the same way, and using the same analyses, as those for non-dispersing
86 individuals.

87 In all statistical analyses a model simplification procedure was used. The full model was
88 fitted, after which the least significant term from the highest order interaction downwards
89 was identified and removed if the removal resulted in an insignificant increase in deviance.
90 The full and reduced models are shown in Table A1. Significance of simplified models was
91 assessed by performing a likelihood ratio test. The likelihood ratio (Λ) is calculated as $\Lambda = 2(LL_f$
92 $- LL_j)/(p_f - p_j)$; where LL_i is the log-likelihood of the full model and LL_j is the log-likelihood of
93 the reduced model ($j = r$) or constant-only model ($j = c$). p_i is the number of estimable

94 parameters in the full and p_j is the number of estimable parameters in the reduced and
95 constant-only model. The likelihood ratio is X_{ν}^2 distributed, where ν is the difference in
96 number of estimable parameters. The random factor was never removed during model
97 simplification. Model assumptions and homoscedacity were confirmed by inspection of
98 probability plots and error structures. All analyses were performed in R (version 3.0.2) with
99 models fitted by maximum likelihood in the 'lme4' package (R Development Core Team 2013).

100

101 ***Mesh point calculation***

102 Mesh points were created by dividing the size domain of each stage into very small-
103 width discrete bins. A number of different bin sizes were used and results compared, this was
104 done as an increase in the number of mesh points increases the numerical accuracy of the
105 approximation (Ellner and Rees 2006). The body size domain of each stage was eventually
106 divided into 50 size bins as a higher number of bins did not produce notably different results.
107 Transition rates for the midpoint of two adjacent mesh points were estimated for each stage
108 class. In the NM, the final matrix size was 250X250 (50 bins x 5 stages = 250 mesh points);
109 whereas in the DPM the final matrix size was 400X400 (50 bins x 8 stages = 400 mesh points).
110 The DPM takes into account the different number of life stages of dispersers and non-
111 dispersers as well two sets of tritonymph and adult life stages (tritonymphs and adults without
112 dispersal stage, and tritonymphs and adults with dispersal stage) into a single IPM, hence
113 there are eight stages in the final matrix and not five (Fig. 2 in main text).

114

115

Parameter values of character-demography functions

116 In the functions below, B denotes body length (mm) and sample size n is given in between
 117 brackets for each fitted function. E - egg; L – larva; P – protonymph; D – deutonymph; P/D –
 118 protonymph and deutonymph combined; T – tritonymph; TP – tritonymph from non-
 119 disperser; TD – tritonymph from disperser; A – adult; AP – Adult from non-disperser; AD –
 120 adult from disperser.

121

122 Survival rates for the DPM (fraction per day)123 E: $y = 0.956$ ($n = 297$); L: $y = 0.999$ ($n = 112$); P: $y = 0.910$ ($n = 166$); D: $y = 0.999$ ($n = 426$); TP:124 $y = 0.999$ ($n = 132$); $T_D: y = \frac{1}{1 + \frac{1}{e^{(-0.4175 + 6.9435B)}}}$ ($n = 119$); $A_P: y = 0.999$ ($n = 115$); $A_D: y = 0.933$ (n

125 = 60).

126

127 Life stage transition rates for the DPM (fraction per day)128 $E \rightarrow L: y = \frac{1}{1 + \frac{1}{e^{(-1.437 + 8.674B)}}}$ ($n = 97$); $L \rightarrow P: y = \frac{1}{1 + \frac{1}{e^{(-6.933 + 29.429B)}}}$ ($n = 47$);129 $P \rightarrow D: y = \frac{1}{1 + \frac{1}{e^{(-2.601 + (-5.673)B)}}}$ ($n = 137$); $P \rightarrow T: y = \frac{1}{1 + \frac{1}{e^{(-11.220 + 26.235B)}}}$ ($n = 137$); $D \rightarrow T:$ 130 $y = \frac{1}{1 + \frac{1}{e^{(55.05 - 385.54B + 654.02B^2)}}}$ ($n = 155$); $T_P \rightarrow A_P: y = \frac{1}{1 + \frac{1}{e^{(-6.703 + 13.100B)}}}$ ($n = 76$); $T_D \rightarrow A_D:$ 131 $y = \frac{1}{1 + \frac{1}{e^{(-6.275 + 14.933B)}}}$ ($n = 45$).

132

133 Reproduction rate for the DPM (no. per day)

134 $A_P: y = 0.5(-18.446 + 35.209B)$ ($n = 190$); $A_D: y = 0.5(-13.592 + 33.892B)$ ($n = 172$)

135

136 Mean growth rates for the DPM (when staying in the same life stage) (mm)

137 $E: y = L$ ($n = 65$); $L: y = 0.11739 + 0.64316B$ ($n = 29$); $P: y = 0.0772 + 0.904B$ ($n = 39$); $D: y = L$ ($n =$

138 153); $T_P: y = 0.0776 + 0.9538B$ ($n = 44$); $T_D: y = -0.0772 + 1.3570B$ ($n = 23$); $A_P:$

139 $y = 0.3977 + 0.5359B$ ($n = 215$); $A_D: y = 0.2816 + 0.6355B$ ($n = 238$)

140

141 Variance in growth rates for the DPM (when staying in the same life stage) (mm²)

142 $E: y = 0.0001$ ($n = 65$); $L: y = -0.0008 + 0.0050B$ ($n = 29$); $P: y = -0.0007 + 0.0040B$ ($n = 39$); $D:$

143 $y = 0.0001$ ($n = 153$); $T_P: y = 0.0039 - 0.0042B$ ($n = 44$); $T_D: y = -0.0044 - 0.0060B$ ($n = 23$); $A_P:$

144 $y = 0.0009 - 0.0004B$ ($n = 215$); $A_D: y = 0.0014 - 0.0016B$ ($n = 238$)

145

146 Parent-offspring association function (mean offspring-mother difference) for the DPM (mm)

147 $A_P: y = 0.1638$ ($n = 96$); $A_D: y = 0.1689$ ($n = 175$)

148

149 Variance around parent-offspring association function for the DPM (mm²)

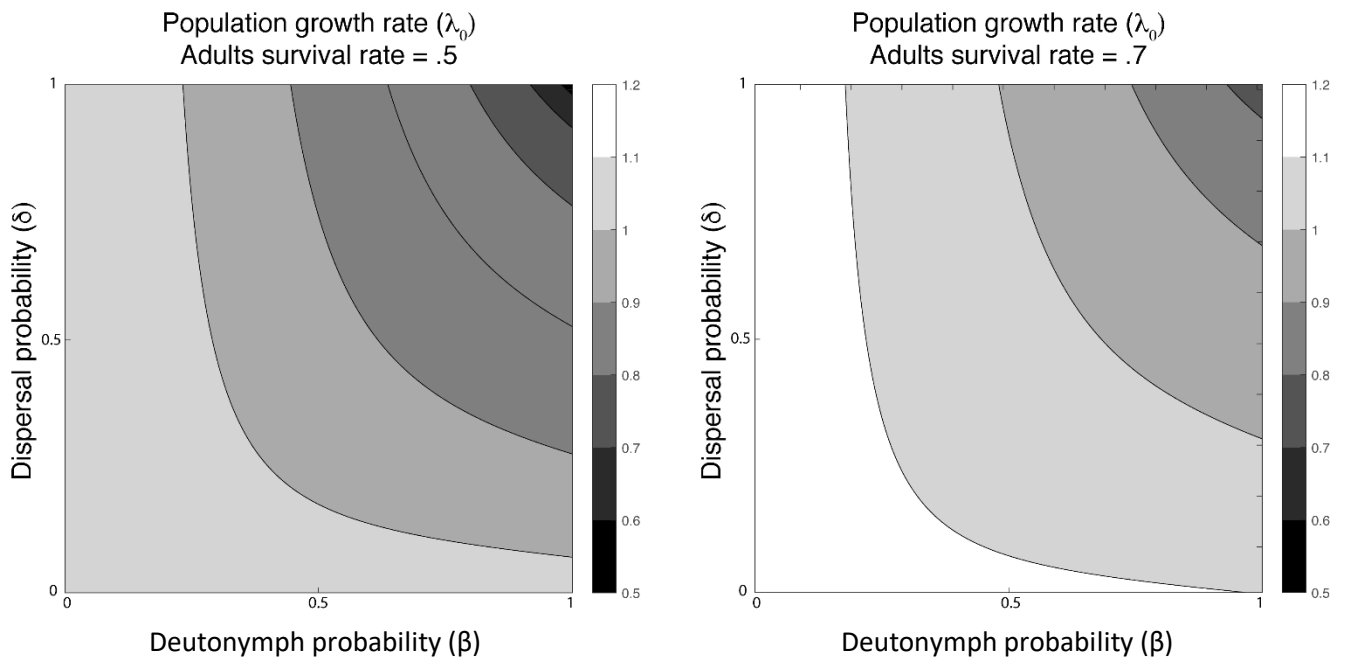
150 $A_P: y = 0.00008$ ($n = 96$); $A_D: y = 0.0001$ ($n = 175$)

152 **Table S1.** The DPM equations are constructed from the five statistical demography functions: Survival $S(\mathbf{z}, \mathbf{s}, t)$, Transition $T(\mathbf{s}' | \mathbf{z}, \mathbf{s}, t)$, Growth $G(\mathbf{z}' | \mathbf{z}, \mathbf{s}', t)$,
 153 Reproduction $R(\mathbf{z}, \mathbf{s}, t)$ and Offspring inheritance $O(\mathbf{z}' | \mathbf{z}, \mathbf{s}, t)$ and the dispersal matrix $D(t)$. The equations calculate the number of females in each stage s at time
 154 t which is described by $n(\mathbf{z}, \mathbf{s}, t)$ with the $R(\mathbf{z}, \mathbf{s}, t)$ and the $O(\mathbf{z}' | \mathbf{z}, \mathbf{s}, t)$ functions zero for all non-adult stages as only adults reproduce.

	Life stage Equation	Description
(3.1)	$n(\mathbf{z}', 1, t + 1) = \int O(\mathbf{z}' \mathbf{z}, 5, t) R(\mathbf{z}, 5, t) n(\mathbf{z}, 5, t) dz$ $+ \int O(\mathbf{z}' \mathbf{z}, 8, t) R(\mathbf{z}, 8, t) n(\mathbf{z}, 8, t) dz$	Egg production by non-dispersal and dispersal adults
(3.2)	$n(\mathbf{z}', s + 1, t + 1) = \int_{\Omega_s} G(\mathbf{z}' \mathbf{z}, s + 1, t) T(s + 1 \mathbf{z}, s, t) S(\mathbf{z}, s, t) n(\mathbf{z}, s, t) dz$ $n(\mathbf{z}', s, t + 1) = \int_{\Omega_s} G(\mathbf{z}' \mathbf{z}, s, t) T(s \mathbf{z}, s, t) S(\mathbf{z}, s, t) n(\mathbf{z}, s, t) dz$	Eggs and Larvae developing into the next stage and staying in the same stage
	} $1 \leq s \leq 2$	
(3.3)	$n(\mathbf{z}', 3, t + 1) = \int G(\mathbf{z}' \mathbf{z}, 3, t) T(3 \mathbf{z}, 3, t) S(\mathbf{z}, 3, t) n(\mathbf{z}, 3, t) dz$	Non-dispersal Protonymphs staying Protonymphs
(3.4)	$n(\mathbf{z}', 6, t + 1) = \int G(\mathbf{z}' \mathbf{z}, 6, t) T(6 \mathbf{z}, 3, t) S(\mathbf{z}, 6, t) n(\mathbf{z}, 3, t) dz$	Deutonymphs developing from Protonymphs
(3.5)	$n(\mathbf{z}', 4, t + 1) = \int G(\mathbf{z}' \mathbf{z}, 4, t) T(4 \mathbf{z}, 3, t) S(\mathbf{z}, 4, t) n(\mathbf{z}, 3, t) dz$	Non-dispersal Tritonymphs developing from Protonymphs
(3.6)	$n(\mathbf{z}', 4, t + 1) = \int G(\mathbf{z}' \mathbf{z}, 4, t) T(4 \mathbf{z}, 4, t) S(\mathbf{z}, 4, t) n(\mathbf{z}, 4, t) dz$	Non-dispersal Tritonymphs staying Tritonymphs

(Table 1 cont.)

	Life stage Equation	Description
(3.7)	$n(z', 6, t + 1) = \int G(z' z, 6, t)T(6 z, 6, t)D(6, t)S(z, 6, t)n(z, 6, t)dz$	Deutonymphs staying Deutonymphs
(3.8)	$n(z', 7, t + 1) = \int G(z' z, 7, t)T(7 z, 6, t)D(6, t)S(z, 7, t)n(z, 6, t)dz$	Dispersal Tritonymphs developing from Deutonymphs
(3.9)	$n(z', 8, t + 1) = \int G(z' z, 8, t)T(8 z, 7, t)S(z, 8, t)n(z, 7, t)dz$	Dispersal adults developing from dispersal Tritonymphs
(3.10)	$n(z', 7, t + 1) = \int G(z' z, 7, t)T(7 z, 7, t)S(z, 7, t)n(z, 7, t)dz$	Dispersal Tritonymph staying Tritonymphs
(3.11)	$n(z', 5, t + 1) = \int G(z' z, 5, t)T(5 z, 5 - 1, t)S(z, 5 - 1, t)n(z, 5 - 1, t)dz + \int G(z z, 5, t)S(z, 5, t)n(z, 5, t)dz$	Non-dispersal adults developing from non- dispersal Tritonymphs and surviving non-dispersal adults
(3.12)	$n(z', 8, t + 1) = \int G(z' z, 8, t)T(8 z, 8 - 1, t)S(z, 8 - 1, t)n(z, 8 - 1, t)dz + \int G(z z, 8, t)S(z, 8, t)n(z, 8, t)dz$	Dispersal adults developing from dispersal Tritonymphs and surviving dispersal adults



157

158 **Fig. S1.** Joint effect of increasing deutonymph probability (β) and increasing dispersal probability (δ)
 159 on population growth rate (λ_0). Dispersal probability and deutonymph probability increase from 0 to 1
 160 at 0.01 increments. Side bar indicates λ_0 , with λ_0 increasing from black to white. The two panels
 161 indicate the response of λ_0 when adult survival rate within the DPM is set at 0.5 (left panel) and 0.7
 162 (right panel).

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164

165 **Literature cited in the Supporting Information**

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