Appendix A: Statistical model description and estimates

All models were run in R using brms and Hamiltonian Monte Carlo with two chains with each 5000 iteration from which 2000 were warmup

Model 1.1: Tomato preference during the ten rounds of artificial selection.

a) Model representation

$$P \sim Betabinomial(n, prop, \theta)$$

$$logit(prop) = a_{rep[i]} + aC * treatC + aT * treatT + round * (b_{rep[i]} + bC * treatC + bT * treatT)$$

$$\begin{bmatrix} a_{rep[i]} \\ b_{rep[i]} \end{bmatrix} \sim MVNormal\left(\begin{bmatrix} a_0 \\ b_0 \end{bmatrix}, S\right)$$

$$S = \begin{pmatrix} \sigma_a & 0 \\ 0 & \sigma_b \end{pmatrix} R \begin{pmatrix} \sigma_a & 0 \\ 0 & \sigma_b \end{pmatrix}$$

$$a_0 \sim Normal(0, 2)$$

$$b_0 \sim Normal(0, 2)$$

$$aC \sim Normal(0, 2)$$

$$aT \sim Normal(0, 2)$$

$$bC \sim Normal(0, 2)$$

$$bT \sim Normal(0, 2)$$

$$\sigma_a \sim Cauchy(0, 1)$$

$$\sigma_b \sim Cauchy(0, 1)$$

$$R \sim LKJCorr(2)$$

$$\theta \sim Exp(1)$$

With *P* the proportion of mites preferring tomato, *n* the sample size, *rep[i]* the ith replicate, *treatC* indicating the cucumber choice selection treatment, *treatT* indicating the tomato choice selection treatment and *round* the round or generation number. Betabinomial, MVNormal, Normal, Cauchy, LKJCorr, Exp and GammaPoisson, respectively, indicate a beta-bionomial, multivariate normal, normal, cauchy, Lewandowski Kurowicka Joe correlation matrix, exponential and gamma-Poisson distributions in this and following models. The LKJ correlation distribution is a prior for the correlation matrix for varying intercepts and varying slopes.

We choose relatively strong regularizing priors that make sense when modelling habitat preferences. The prior for intercepts, slopes and their deviations represents log-odds for preference that are mostly between -4 and 4 (two standard deviations, or almost 96% of that distribution) and roughly transform to a preference between 2% and 98%. We do not expect extremer preferences or changes in preference from the fact that the mites have no (known) evolutionary history on these hosts and from previous experience with mites on these hosts.

b) Model parameter estimates

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
b_Intercept	-0.58	0.01	0.32	-1.23	0.05	3482	1
b_treatmentR	0.72	0.01	0.45	-0.17	1.63	3880	1
b_treatmentT	0.62	0.01	0.46	-0.28	1.51	4076	1
b_selection	0.04	0.00	0.05	-0.06	0.14	3419	1
b_treatmentR:selection	-0.11	0.00	0.07	-0.24	0.02	3816	1
b_treatmentT:selection	-0.09	0.00	0.07	-0.23	0.05	3899	1
sd_code__Intercept	0.14	0.00	0.11	0.01	0.42	3558	1
sd_code__selection	0.02	0.00	0.02	0.00	0.06	3962	1
cor_code_Interc_selection	-0.13	0.01	0.46	-0.88	0.76	8061	1
phi	8.51	0.01	1.33	6.17	11.37	10273	1
r_code[1,Intercept]	-0.04	0.00	0.15	-0.41	0.25	6877	1
r_code[2,Intercept]	-0.06	0.00	0.16	-0.46	0.20	6028	1
r_code[3,Intercept]	0.03	0.00	0.15	-0.26	0.39	5673	1

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r_code[4,Intercept]        0.01    0.00 0.15    -0.30    0.33 6830    1
r_code[5,Intercept]        0.02    0.00 0.15    -0.27    0.37 6477    1
r_code[6,Intercept]       -0.04    0.00 0.15    -0.41    0.23 5547    1
r_code[7,Intercept]       -0.02    0.00 0.15    -0.36    0.29 5917    1
r_code[8,Intercept]        0.05    0.00 0.15    -0.21    0.45 5784    1
r_code[9,Intercept]       -0.05    0.00 0.15    -0.42    0.21 6052    1
r_code[10,Intercept]       0.02    0.00 0.15    -0.28    0.37 6235    1
r_code[11,Intercept]       0.04    0.00 0.15    -0.25    0.39 6116    1
r_code[12,Intercept]       0.03    0.00 0.15    -0.26    0.42 5871    1
r_code[1,selection]        0.00    0.00 0.02    -0.05    0.04 6080    1
r_code[2,selection]        0.00    0.00 0.02    -0.05    0.04 5943    1
r_code[3,selection]        0.00    0.00 0.02    -0.05    0.04 5551    1
r_code[4,selection]        0.00    0.00 0.02    -0.04    0.05 6170    1
r_code[5,selection]        0.00    0.00 0.02    -0.05    0.04 5517    1
r_code[6,selection]        0.00    0.00 0.02    -0.05    0.04 5347    1
r_code[7,selection]        0.00    0.00 0.02    -0.05    0.04 5637    1
r_code[8,selection]        0.00    0.00 0.02    -0.04    0.05 5572    1
r_code[9,selection]        0.00    0.00 0.02    -0.05    0.03 5108    1
r_code[10,selection]       0.00    0.00 0.02    -0.03    0.05 6200    1
r_code[11,selection]       0.01    0.00 0.02    -0.03    0.06 5349    1
r_code[12,selection]       0.00    0.00 0.02    -0.03    0.06 5892    1
```

Model 1.2: Alternative model for tomato preference during the ten rounds of artificial selection without the temporal effect.

a) Model representation

$$P \sim Betabinomial(n, prop, \theta)$$

$$logit(prop) = a_{rep[i]} + aC * treatC + aT * treatT$$

$$a_{rep[i]} \sim Normal(a_0, \sigma_a)$$

$$a_0 \sim Normal(0, 2)$$

$$aC \sim Normal(0, 2)$$

$$aT \sim Normal(0, 2)$$

$$\sigma_a \sim HalfCauchy(0, 1)$$

$$\theta \sim Exp(1)$$

b) Model parameter estimates

```
                      mean se_mean   sd    2.5%   97.5% n_eff Rhat
b_Intercept          -0.35    0.00 0.14   -0.62   -0.07 3929    1
b_treatmentR          0.07    0.00 0.20   -0.32    0.45 4476    1
b_treatmentT          0.07    0.00 0.20   -0.31    0.47 4006    1
sd_code__Intercept    0.11    0.00 0.09    0.00    0.32 2544    1
phi                   8.32    0.02 1.25    6.10   10.98 6710    1
r_code[1,Intercept]  -0.04    0.00 0.12   -0.33    0.17 3517    1
r_code[2,Intercept]  -0.05    0.00 0.13   -0.38    0.16 4407    1
r_code[3,Intercept]   0.01    0.00 0.11   -0.22    0.28 5935    1
r_code[4,Intercept]   0.01    0.00 0.11   -0.23    0.26 5998    1
r_code[5,Intercept]   0.01    0.00 0.11   -0.22    0.27 5216    1
r_code[6,Intercept]  -0.03    0.00 0.12   -0.34    0.20 5495    1
r_code[7,Intercept]  -0.02    0.00 0.12   -0.29    0.22 4374    1
r_code[8,Intercept]   0.05    0.00 0.12   -0.16    0.35 3971    1
r_code[9,Intercept]  -0.04    0.00 0.12   -0.34    0.16 5655    1
r_code[10,Intercept]  0.03    0.00 0.11   -0.19    0.30 5081    1
r_code[11,Intercept]  0.04    0.00 0.12   -0.17    0.33 4201    1
r_code[12,Intercept]  0.04    0.00 0.12   -0.18    0.32 4336    1
```

Model 2.1: reproductive success test before experiment

a) Model representation

$$R \sim Gammapoisson(\lambda, \theta)$$

$$log(\lambda) = a + bC * treatC + bT * treatT$$

$$a \sim Normal(0, 4)$$

$$bC \sim Normal(0, 4)$$

$$bT \sim Normal(0, 4)$$

$$\theta \sim Exp(1)$$

With *R* the amount of deutonymphs produced by a female in twelve days, *treatC* indicates whether reproductive success was tested on cucumber, *treatT* indicates reproductive success tested on tomato (third host tested was bean). All priors are not very regularizing when considering them estimating log values of fertility.

We choose relatively uninformative priors when modelling the life-history traits that for the intercept and the deviations are mostly situated between -8 and 8, which transforms to 0.003 and 2980.

b) Model estimates

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
b_Intercept	2.82	0.00	0.30	2.27	3.44	4167	1
b_patchC	-0.27	0.01	0.45	-1.16	0.63	4330	1
b_patchT	-0.41	0.01	0.43	-1.27	0.46	4219	1
shape	1.64	0.01	0.56	0.79	2.95	4148	1

Model 2.2: reproductive success test after experiment

a) Model representation

$$R \sim Gammapoisson(\lambda, \theta)$$
$$log(\lambda) = a_{trep[i]} + bC * treatC + bT * treatT$$
$$a_{trep[i]} \sim Normal(a, \sigma_{trep})$$
$$a \sim Normal(0, 10)$$
$$bC \sim Normal(0, 5)$$
$$bT \sim Normal(0, 5)$$
$$\sigma_{trep} \sim Cauchy(0, 2)$$
$$\theta \sim Exp(1)$$

With *R* the amount of deutonymphs produced by a female in twelve days, *rep[i]* the ith replicated treatment, *treatC* indicates whether reproductive success was tested on cucumber and *treatT* indicates whether reproductive success was tested on tomato (third host tested was bean).

b) Model estimates

	mean	se_mean	sd	2.5%	97.5%	n_eff	Rhat
b_Intercept	2.73	0.00	0.17	2.38	3.06	2878	1
b_patchC	-0.97	0.00	0.17	-1.30	-0.65	6005	1
b_patchT	-0.42	0.00	0.16	-0.75	-0.10	6299	1
sd_trep__Intercept	0.43	0.00	0.15	0.19	0.79	1666	1
shape	2.51	0.01	0.49	1.69	3.59	4114	1
r_trep[C1,Intercept]	0.09	0.00	0.24	-0.37	0.61	5216	1
r_trep[C2,Intercept]	0.04	0.00	0.24	-0.40	0.52	4913	1
r_trep[C3,Intercept]	0.39	0.00	0.27	-0.08	0.98	4016	1
r_trep[C4,Intercept]	0.11	0.00	0.24	-0.34	0.59	4906	1
r_trep[R1,Intercept]	0.21	0.00	0.26	-0.27	0.76	4864	1
r_trep[R2,Intercept]	-0.67	0.01	0.38	-1.50	0.00	3359	1
r_trep[R3,Intercept]	-0.39	0.00	0.27	-0.94	0.10	4055	1
r_trep[R4,Intercept]	0.11	0.00	0.23	-0.33	0.62	4416	1
r_trep[S13,Intercept]	0.49	0.00	0.20	0.11	0.90	3131	1
r_trep[T1,Intercept]	0.16	0.00	0.24	-0.31	0.66	4045	1
r_trep[T2,Intercept]	0.06	0.00	0.23	-0.38	0.55	4747	1
r_trep[T3,Intercept]	-0.25	0.00	0.25	-0.74	0.23	5154	1
r_trep[T4,Intercept]	-0.29	0.00	0.25	-0.79	0.19	5069	1

Model 3.1: habitat imprinting test before experiment

a) Model representation

$$P \sim Betabinomial(total, prop, \theta)$$
$$logit(prop) = a + b1 * devT$$

$$a \sim Normal(0, 2)$$

$$bT \sim Normal(0, 2)$$

$$\theta \sim Exp(1)$$

With *P* the proportion of mites preferring tomato, *total* the sample size and *devT* indicating whether the preference was tested on mites developed on tomato (as opposed to cucumber). The same regularizing prior for the intercept and deviation on it is chosen as in the intercept in model 1 for the same reasons.

b) Model estimates

```
      mean se_mean   sd    2.5%   97.5% n_eff Rhat
a    -1.08    0.01 0.53   -2.15   -0.06  4252    1
bT    0.73    0.01 0.66   -0.55    2.01  4450    1
θ     3.71    0.02 1.55    1.44    7.39  4425    1
```

Model 3.2: habitat imprinting test after experiment

a) Model representation

$$P \sim Betabinomial(total, prop, \theta)$$

$$logit(prop) = a + b_{treatment[i]} + bC * devC$$

$$a \sim Normal(0, 2)$$

$$b_{treatment[i]} \sim Normal(b, \sigma)$$

$$b \sim Normal(0, 2)$$

$$\sigma \sim Normal(0, 2)$$

$$bT \sim Normal(0, 2)$$

$$\theta \sim Exp(1)$$

With *P* the proportion of mites preferring tomato, *total* the sample size, *devT* indicating whether the preference was tested on mites developed on cucumber (as opposed to tomato) and $b_{treatment[i]}$ the variable intercept of treatment i.

b) Model estimates

```
                       mean se_mean   sd    2.5%  97.5% n_eff Rhat
a                     -1.40    0.01 0.43   -2.26  -0.53  1775    1
bT                     1.00    0.01 0.45    0.13   1.91  3704    1
sd_treatment__Intercept 0.46   0.01 0.40    0.01   1.51  1424    1
θ                      4.59    0.03 1.52    2.23   8.12  3691    1
b                     -0.92    0.01 0.36   -1.63  -0.16  1433    1
b[C,Intercept]        -0.01    0.01 0.36   -0.81   0.76  2041    1
b[R,Intercept]         0.16    0.01 0.39   -0.55   1.09  1789    1
b[T,Intercept]        -0.21    0.01 0.40   -1.23   0.48  1693    1
```

Appendix B: fertility

In parallel with reproductive success, fertility at the start did not suggest adaptation to tomato. The distributions of posterior predicted fertility on cucumber and tomato overlap notably (fig. B1, top left) and their posterior predicted differences in fertility overlap 0 very convincingly (fig. B1, bottom left). Additionally, fertility at the end also demonstrated mites to be tomato adapted by laying on average more eggs on tomato compared to cucumber (fig. B1, top right) as their differential response is convincingly different from 0 (fig. B1, bottom right).
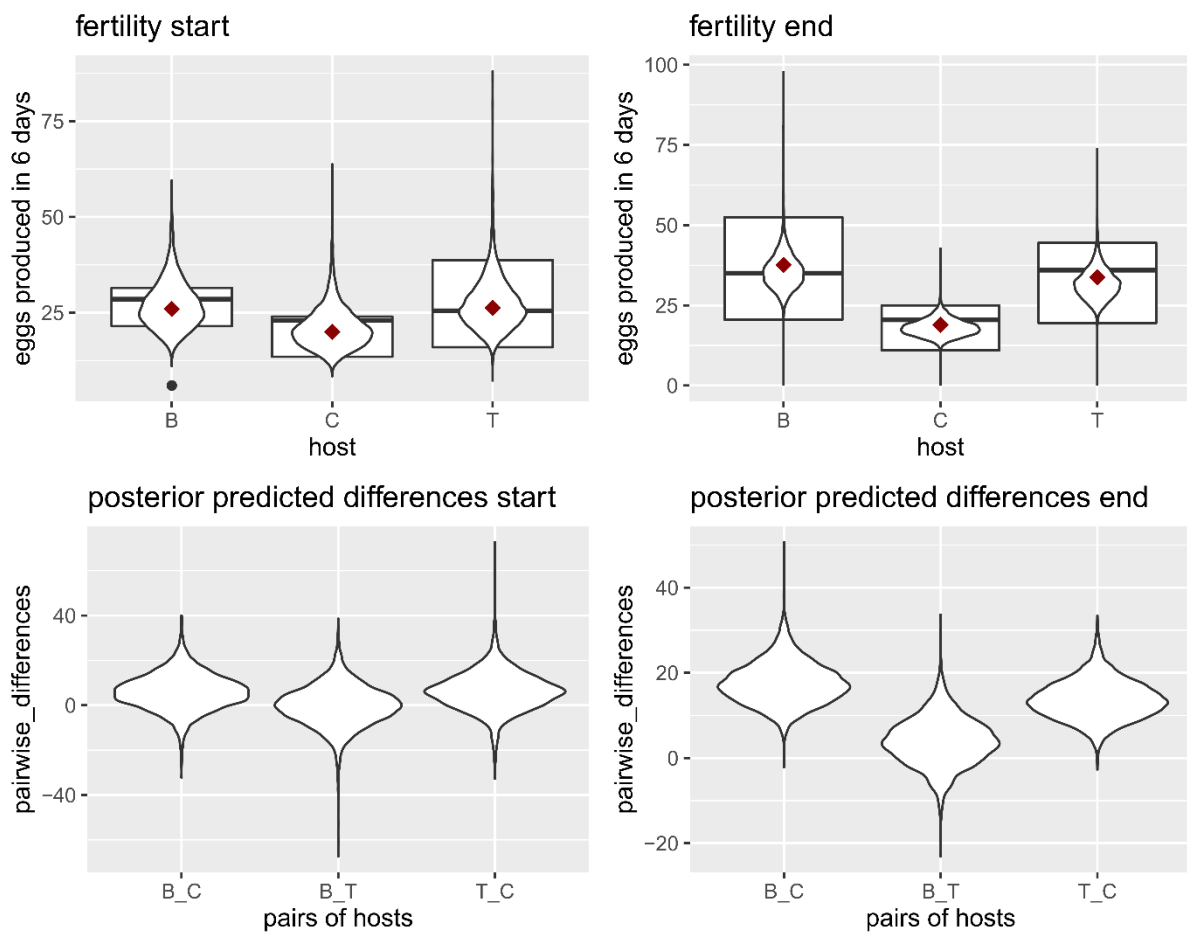
Figure B1. Top: fertility estimated as eggs produced by one female in six days on bean (B), cucumber (C) and tomato (T). The boxplot plots the data, the red dot the arithmetic mean of the data and the violin plots the posterior predicted fertility by the HMC model. Bottom: the posterior predicted pairwise differences in fertility. This was tested in the population used at the start of the experiment (left) and in all experimental and stock populations at the end of the experiment (right).

Appendix C: effect selection regime on life-history traits

Fertility or reproductive success on a host plant did not differ between experimental populations. This suggests that the different habitat choice selection regimes did not select for different levels of local adaptation on any of the host plants. However, we observed that fertility and reproductive success on all host plants is higher for the stock population compared to any of the experimental treatment (fig. C1, C2). This points at the importance of drift in the evolution of adaptation to the different host plants within our experimental setup due to relatively low population sizes and frequent bottlenecking.
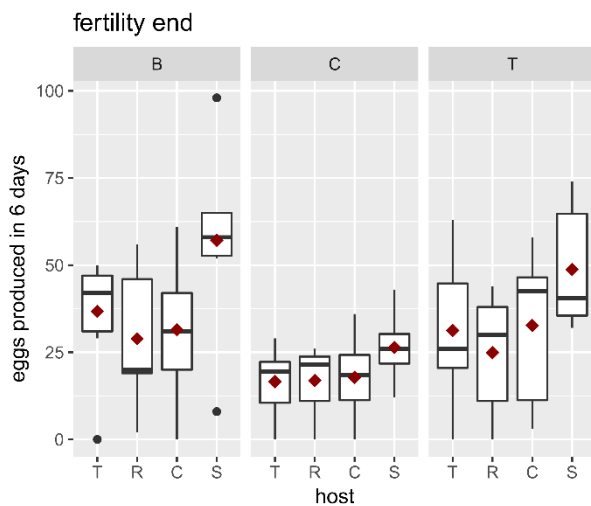

Figure C1. Fertility estimated as eggs produced in six days on bean (left), cucumber (middle) and tomato (right) of the different experimental treatments: tomato choice (T), random choice (R), cucumber choice (C) and control (S) at the end of the experiment. The red dot indicates the arithmetic mean of the data.
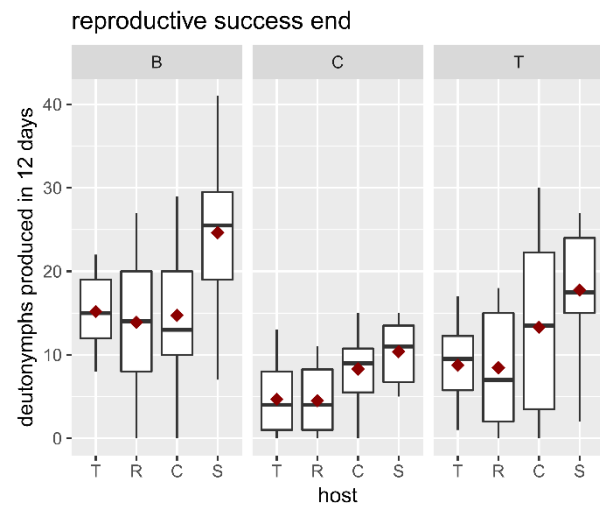
Figure C2. Reproductive success estimated as deutonymphs produced in twelve days on bean (left), cucumber (middle) and tomato (right) of the different experimental treatments: tomato choice (T), random choice (R), cucumber choice (C) and control (S) at the end of the experiment. The red dot indicates the arithmetic mean of the data.

Appendix D: effect selection regime on induced habitat choice

We tested the effect of the experimental treatment in concert with the developmental habitat and their interaction on tomato choice in the induced habitat choice test. We anticipated that the experimental treatment would affect the induced habitat choice because mites in our experimental populations were always induced for tomato habitat. Therefore, tomato choice populations would be selected for an increased induced effect and cucumber choice populations would be selected for a decreased induced effect. However, we observed no noteworthy differences in habitat choice induction between mites from different experimental populations (fig. D1). Choice slightly more induced in the random choice populations and slightly less in the tomato choice populations but the relatively small differences and large spread of the likelihood distributions does not indicated a meaningful treatment effect. Moreover, when comparing this model (WAIC = 102.2 ± 4.9 SE) to the one with only the developmental habitat as explaining variable (WAIC = 99.3 ± 4.9 SE) the latter is preferred completely (weight of 1) over the model discussed here.
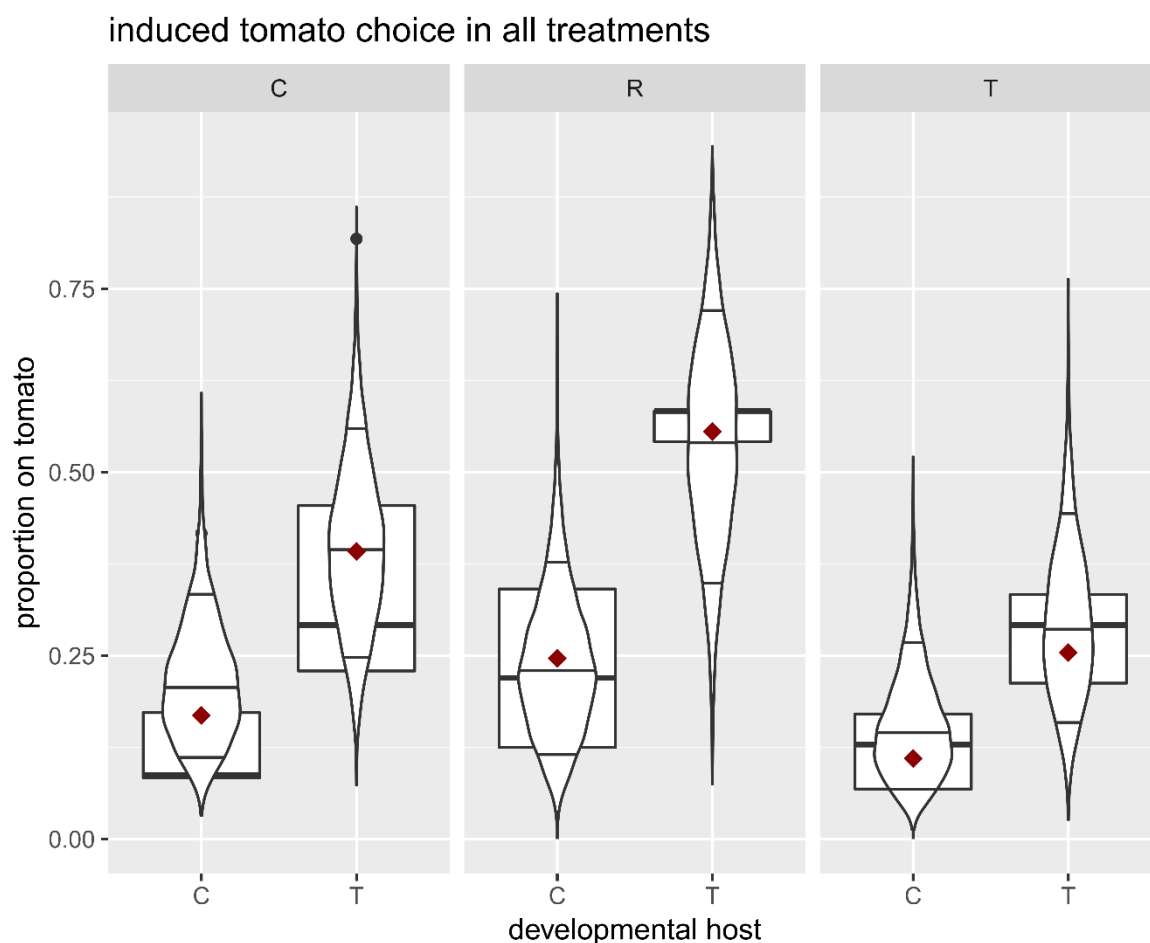

Figure D1. Tomato choice during induced habitat choice tests for mites originating from the cucumber choice treatment (left), random choice treatment (middle) and tomato choice treatment (right). Mites developed on cucumber (C) and tomato (T). The boxplot plots the data, the diamond the arithmetic mean of the data and the violin plots the posterior predicted tomato choice by the HMC model with the 0.09, 0.5 and 0.91 quantile indicated.