Supplementary information

Results

1st Evaluation (alate aphids only)

Figure S1 shows the intensity of initial infestation by alate aphids (*N. ribisnigri* and *M. euphorbiae* in relation 57% to 43%) for every evaluated plant by increasing colour hue. In all treatments, more alate aphids on outer plants than on plants in the centre of the plots were counted, (except for SFB, because there were no alate aphids at all), but the ANOVA (Table S2) did not show statistical significance (p-value = 0.55) for a location effect neither on average, nor within the plots (p-value=0.79). The mean ratios of counted aphids between inner and outer plants for each treatment are given in Table S6. As for the total number of aphids, only the treatment effect was significant (p-value=0.002, Table S2).

The total number of infested plants by alate aphids was 21 (23%, NF), 23 (26%, PEG), 20 (22%, SFG), 5 (6%, PEB), 0 (0%, SFB).

1st Evaluation (alate and apterous aphids)

For the total number of aphids (*N. ribisnigri* and *M. euphorbiae,* alate and apterous) the ANOVA (Table S8) revealed significant differences (α=0.05) between the treatments (p-value <0.001) but no significance for the location (inner or centre) nor the interaction between treatment and location. Therefore, only the differences between the treatments were statistically analysed in detail.

Figure S2 shows the total number of aphids (alate and apterous, scaled sums) found on the lettuce plants in the first evaluation (non-destructive) for each treatment, separated into outer (dots) and inner plants (triangles) and corresponding least square means (black dots) together with their 95% confidence interval (black line), over all repetitions. Due to the scaling (y + 1)/n, a sum that equals zero leads to a scaled sum of 0.083 (n=12), respective 0.056 (n=18*)*.

The control plots (NF) showed the highest number of aphids (least square mean 5.091) followed by the treatments SFG (3.134) and PEG (1.986), which were statistically different from the other two treatments PEB (0.139) and SFB (0.086. Least square means are shown in Table S9. The mean comparisons (contrasts) were run as differences on the log-scale. Therefore, back transformation results in the ratio between the means of the scaled sums. These ratios, their standard error and the corresponding p-values are given in Table S10.

Figure S3 shows the total number of aphids (alate and apterous) for every evaluation plant in the first evaluation by increasing colour hue. In all treatments, more alate aphids on outer plants than on plants in the centre of the plots were counted, but the ANOVA (Table S9) did not show statistical significance (p-value=0.19) for a location effect neither on average, nor within the plots (p-value=0.95). As for the total number of aphids, only the treatment effect was significant (p-value=<0.001). The mean ratios of counted aphids between inner and outer plants for each treatment are given
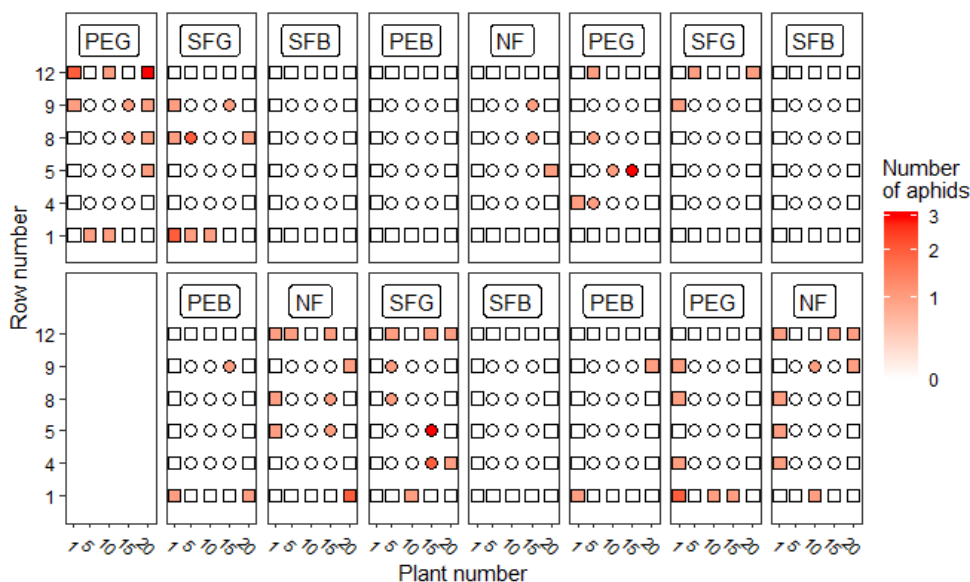

Fig. S1. Heatmap for the number of alate aphids (May 16, 2018) with overview over all evaluated lettuce plants (n=450). Five treatments with three replications each on 15 randomized plots (n=30 per plot). Number of alate aphids found in the 1st evaluation is represented by increasing colour hue. Evaluated plants are indicated by plant number (x-axis) and row number (y-axis). Outer plants at the edge to bare soil are shown as square dots, plants surrounded by other plants, as round dots. Orientation is north to south (from left to right).
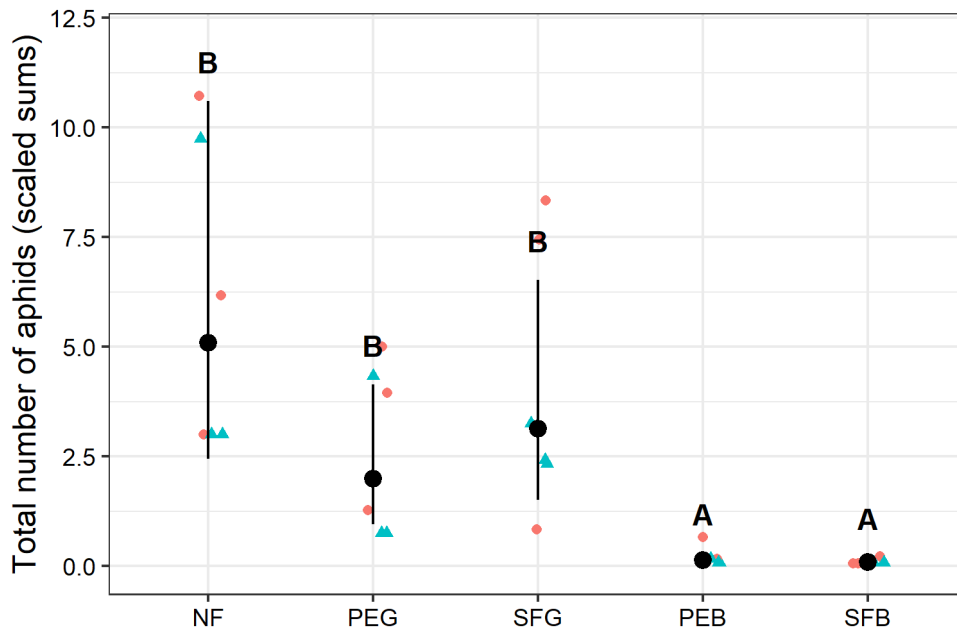
Fig. S2. Scaled sums of the total number of aphids per location in each plot (May 16, 2018). The sums were scaled to be (y + 1)/n. Dots indicate sums from the border plants, triangles indicate sums from the centre of a plot. The black dots are model based least square means of the scaled sums together with their 95% confidence intervals (black bars). Treatment means that have at least one letter in common do not differ significantly (α=0.05) from each other.
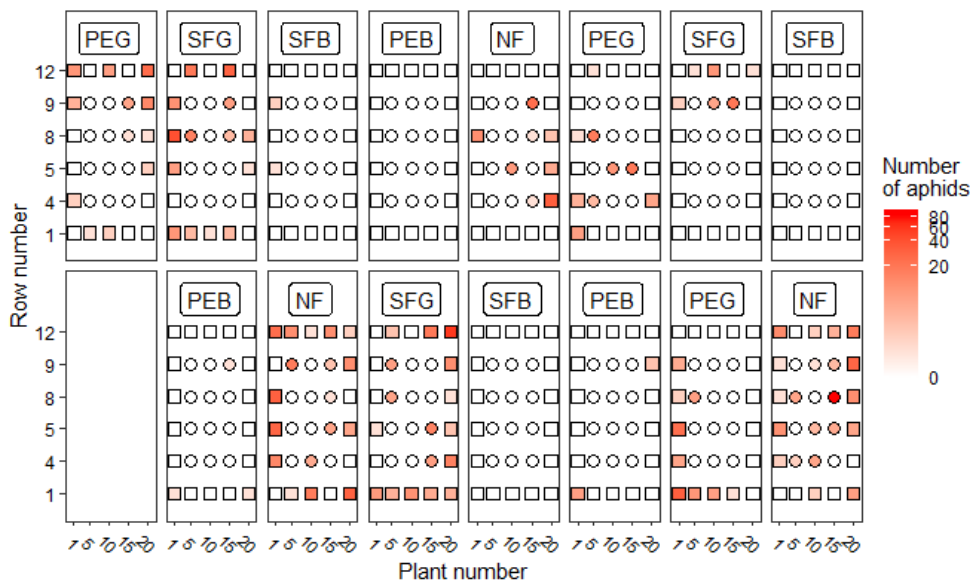
Fig. S3. Heatmap for the total number of aphids (alate and apterous) (May 16, 2018) with overview over all evaluated lettuce plants (n=450). Five treatments with three replications each on 15 randomized plots (n=30 per plot). Total number of aphids (alate and apterous) found in the 1st evaluation is represented by increasing colour hue. Evaluated plants are indicated by plant number (x-axis) and row number (y-axis). Outer plants at the edge to bare soil are shown as square dots, plants surrounded by other plants, as round dots. Orientation is north to south (from left to right).

in Table S13. Number of infested plants was 47 (52%, NF), 30 (33%, PEG), 37 (41%, SFG), 5 (6%, PEB), 2 (2%, SFB).

2nd Evaluation

The ANOVA (Table S13) revealed only significant differences between the treatments but no significance for the location (inner or centre) nor the interaction between treatment and location. Therefore, only the differences between the treatments were analysed in detail. Figure S4 shows the total number of aphids (*N. ribisnigri* only) found on the lettuce heads

in the second evaluation (destructive at harvest time) for each treatment, and location together with their corresponding least square means. Treatment PEG showed the highest least square mean (0.575), only statistically different to the treatment SFB (0.175) which showed the smallest mean value. Treatment NF (0.418), PEB (0.279) and SFG (0.237) were not statistically different from each other and the other two treatments (PEG, SFB). The mean comparisons (contrast tests) were run as differences on the log-scale. Therefore, back transformation results in the ratio between the means of the scaled sums. These ratios, their standard error and the corresponding p-values are given in Table S15.
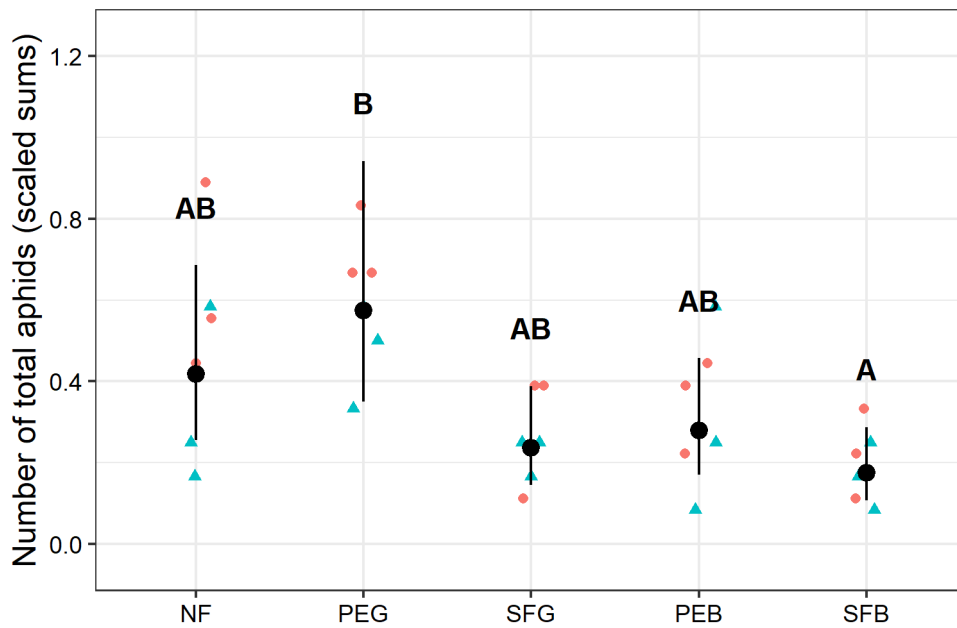
Fig. S4. Scaled sums of the total number of aphids per location in each plot (June 22, 2018). The sums were scaled to be $(y + 1)/n$. Dots indicate sums from the border plants, triangles indicate sums from the centre of a plot. The black dots are model based least square means of the scaled sums together with their 95% confidence intervals (black bars). Treatment means that have at least one letter in common do not differ significantly ($\alpha=0.05$) from each other.

Fig. S5. Overview over "sample-plots" in the field experiments. Plots are shown in different stages of lettuce growth: before planting (line1), short after planting (line2), two weeks after planting (line 3), and shortly before harvest (line4). Overview of one replicate plot per treatment, consisting of 3 dams with 4 rows of plants and 20 plants per row in each dam, thus totalling 240 plans per replicate.

Treatments (from left to right): SFB (Spray-Film Black-grey) – PEB (PE Black) – NF (No Foil/Film) – SFG (Spray-Film Green) – PEG (PE Green)

Field Trial Evaluation 1 (alate aphids)

Data

The statistical analysis was run on the following data set called datsum with the variables:

var: Different treatments

plot: Plots on the field

inpl: Location of the lettuce plants in the plots (0: border, 1: centre)

aphids_sum: sum of flying aphids per location in each plot

n: Number of lettuce plants for each sum

scaled_sum: scaled sums calculated as (aphids_sum + 1)/n

Table S1. Summed total number of alate aphids in first evaluation

var	plot	inpl	aphids_sum	n	scaled_sum
NF	5	0	8	18	0.500
NF	5	1	2	12	0.250
NF	8	0	1	18	0.111
NF	8	1	2	12	0.250
NF	12	0	8	18	0.500
NF	12	1	1	12	0.167
PEB	3	0	2	18	0.167
PEB	3	1	1	12	0.167
PEB	7	0	0	18	0.056
PEB	7	1	0	12	0.083
PEB	13	0	2	18	0.167
PEB	13	1	0	12	0.083
PEG	1	0	12	18	0.722
PEG	1	1	2	12	0.250
PEG	9	0	2	18	0.167
PEG	9	1	6	12	0.583
PEG	11	0	7	18	0.444
PEG	11	1	0	12	0.083
SFB	4	0	0	18	0.056
SFB	4	1	0	12	0.083
SFB	6	0	0	18	0.056
SFB	6	1	0	12	0.083
SFB	14	0	0	18	0.056
SFB	14	1	0	12	0.083
SFG	2	0	7	18	0.444
SFG	2	1	3	12	0.333
SFG	10	0	3	18	0.222
SFG	10	1	0	12	0.083
SFG	15	0	5	18	0.333
SFG	15	1	7	12	0.667

Statistical analysis

A linear mixed model was fit to the data as described in the text

```
library(lme4)

lmm_fit <- lmer(log(scaled_sum) ~ var * inpl + (1|plot), data=datsum)
```

ANOVA

```
library(lmerTest)

anova(lmm_fit)
```

Table S2. ANOVA table of alate aphids in first evaluation

Effect	SSQ	MSQ	NumDF	DenDF	F_value	p_Value
var	10.707	2.677	4	20	6.491	0.002
inpl	0.148	0.148	1	20	0.360	0.555
var:inpl	0.694	0.173	4	20	0.421	0.792

The ANOVA (Table S2) revealed the significance ($\alpha = 0.05$) of the treatment (Var) since the p-value is 0.002, but no location effect (inpl) nor a treatment-location interaction (Var:inpl).

Mean comparisons between the treatments

The mean comparisons were run on the logarithm of the scaled sums (as the model does), but are already back transformed to the original scale for easier interpretation. The least square means of the scaled sums for each treatment, their standard error and their 95% confidence intervals are given in Table 3.

```
# Model based least square means and ther comparisons
library(emmeans)
lmm_comp <- emmeans(lmm_fit, specs="var", contr="pairwise", type="response")

# LS-means for the treatments
lmm_comp$emmeans
```

Table S3. Least square means and their confidence intervals of alate aphids in first evaluation

var	mean	se	df	lower	upper
NF	0.257	0.067	10	0.143	0.461
PEB	0.110	0.029	10	0.061	0.198
PEG	0.294	0.077	10	0.164	0.528
SFB	0.068	0.018	10	0.038	0.122
SFG	0.291	0.076	10	0.162	0.522

The mean comparisons (contrasts) were run as differences on the log-scale. Therefore back transformation results in the ratio between the means of the scaled sums These ratios, their standard error and the corresponding p-values are given in Table S4.

```
# Contrast tests
lmm_comp$contrasts
```

Table S4. Contrasts and p-values of alate aphids in first evaluation

contrast	ratio	se	df	t_ratio	p_value
NF/PEB	2.335	0.866	10	2.287	0.226
NF/PEG	0.874	0.324	10	-0.364	0.996
NF/SFB	3.780	1.401	10	3.586	0.032
NF/SFG	0.883	0.327	10	-0.335	0.997
PEB/PEG	0.374	0.139	10	-2.651	0.133
PEB/SFB	1.619	0.600	10	1.299	0.698
PEB/SFG	0.378	0.140	10	-2.622	0.139
PEG/SFB	4.326	1.604	10	3.950	0.018
PEG/SFG	1.011	0.375	10	0.029	1.000
SFB/SFG	0.234	0.087	10	-3.921	0.019

Location effect

The model based average scaled sums for each location were compared on log-scale. Back-transformations results in a ratio between both sums (0: border plant, 1: inner plant). Please note that the ratio is not significantly different from zero.

```
# Model based least square means and ther comparisons for the location effect
lmm_comp_inpl <- emmeans(lmm_fit, specs="inpl",
                     contr="pairwise", type="response")

# Ratio between the mean scaled sums for each location
lmm_comp_inpl$contrasts
```

Table S5. Ratios of scaled sums between the locations of alate aphids in first evaluation

contrast	ratio	se	df	t_ratio	p_value
0/1	1.151	0.27	10	0.6	0.562

Location effect in each treatment

Ratios between the scaled sums of the border plants (0) and the inner plants (1) split by the treatments are given in Table S6. Please note, that none of these ratios is significantly different from zero.

```
# Model based least square means and ther comparisons for the location effect
# in each treatment
lmm_comp_inter <- emmeans(lmm_fit, specs="inpl", by="var",
                     contr="pairwise", type="response")

# Ratios
lmm_comp_inter$contrasts
```

Table S6. Ratios of scaled sums between the locations and p-values of alate aphids in first evaluation

contrast	var	ratio	se	df	t_ratio	p_value
0/1	NF	1.387	0.727	10	0.624	0.547
0/1	PEB	1.101	0.577	10	0.183	0.859
0/1	PEG	1.639	0.859	10	0.942	0.368
0/1	SFB	0.667	0.350	10	-0.773	0.457
0/1	SFG	1.211	0.635	10	0.366	0.722

References are given in the main reference list.

Field Trial Evaluation 1 (alate and apterous aphids)

Data

The statistical analysis was run on the following data set called datsum with the variables:

var: Different treatments

plot: Plots on the field

inpl: Location of the lettuce plants in the plots (0: border, 1: centre)

aphids_sum: sum of aphids per location in each plot

n: Number of lettuce plants for each sum

scaled_sum: scaled sums calculated as (aphids_sum + 1)/n

Table S7. Summed total number of alate and apterous aphids in first evaluation

var	plot	inpl	aphids_sum	n	scaled_sum
NF	5	0	192	18	10.722
NF	5	1	35	12	3.000
NF	8	0	53	18	3.000
NF	8	1	35	12	3.000
NF	12	0	110	18	6.167
NF	12	1	116	12	9.750
PEB	3	0	2	18	0.167
PEB	3	1	1	12	0.167
PEB	7	0	0	18	0.056
PEB	7	1	0	12	0.083
PEB	13	0	11	18	0.667
PEB	13	1	0	12	0.083
PEG	1	0	70	18	3.944
PEG	1	1	8	12	0.750
PEG	9	0	22	18	1.278
PEG	9	1	51	12	4.333
PEG	11	0	89	18	5.000
PEG	11	1	8	12	0.750
SFB	4	0	3	18	0.222
SFB	4	1	0	12	0.083
SFB	6	0	0	18	0.056
SFB	6	1	0	12	0.083
SFB	14	0	0	18	0.056
SFB	14	1	0	12	0.083
SFG	2	0	133	18	7.444
SFG	2	1	28	12	2.417
SFG	10	0	14	18	0.833
SFG	10	1	27	12	2.333
SFG	15	0	149	18	8.333
SFG	15	1	38	12	3.250

Statistical analysis

A linear mixed model was fit to the data as described in the text

```
library(lme4)

lmm_fit <- lmer(log(scaled_sum) ~ var * inpl + (1|plot), data=datsum)
```

ANOVA

```
library(lmerTest)

anova(lmm_fit)
```

Table S8. ANOVA table of alate and apterous aphids in first evaluation

Effect	SSQ	MSQ	NumDF	DenDF	F_value	p_Value
var	85.014	21.254	4	20	32.711	<0.001
inpl	1.213	1.213	1	20	1.867	0.187
var:inpl	0.458	0.115	4	20	0.176	0.948

The ANOVA (Table S8) revealed the significance ($\alpha = 0.05$) of the treatment (Var) since the p-value is far smaller than 0.05, but no location effect (inpl) nor a treatment-location interaction (Var:inpl).

Mean comparisons between the treatments

The mean comparisons were run on the logarithm of the scaled sums (as the model does), but are already back transformed to the original scale for easier interpretation. The least square means of the scaled sums for each treatment, their standard error and their 95% confidence intervals are given in Table 3.

```
# Model based least square means and ther comparisons
library(emmeans)
lmm_comp <- emmeans(lmm_fit, specs="var", contr="pairwise", type="response")

# LS-means for the treatments
lmm_comp$emmeans
```

Table S9. Least square means and their confidence intervals of alate and apterous aphids in first evaluation

var	mean	se	df	lower	upper
NF	5.091	1.675	10	2.445	10.598
PEB	0.139	0.046	10	0.067	0.289
PEG	1.986	0.654	10	0.954	4.135
SFB	0.086	0.028	10	0.041	0.178
SFG	3.134	1.031	10	1.505	6.524

The mean comparisons (contrasts) were run as differences on the log-scale. Therefore back transformation results in the ratio between the means of the scaled sums. These ratios, their standard error and the corresponding p-values are given in Table S10.

```
# Contrast tests
lmm_comp$contrasts
```

Table S10. Contrasts and p-values of alate and apterous aphids in first evaluation

contrast	ratio	se	df	t_ratio	p_value
NF/PEB	36.682	17.071	10	7.741	0.000
NF/PEG	2.563	1.193	10	2.022	0.322
NF/SFB	59.384	27.636	10	8.776	0.000
NF/SFG	1.624	0.756	10	1.042	0.830
PEB/PEG	0.070	0.033	10	-5.718	0.001
PEB/SFB	1.619	0.753	10	1.035	0.834
PEB/SFG	0.044	0.021	10	-6.698	0.000
PEG/SFB	23.171	10.783	10	6.753	0.000
PEG/SFG	0.634	0.295	10	-0.980	0.858
SFB/SFG	0.027	0.013	10	-7.733	0.000

Location effect

The model based average scaled sums for each location were compared on log-scale. Back-transformations results in a ratio between both sums (0: border plant, 1: inner plant). Please note that the ratio is not significantly different from zero.

```
# Model based least square means and ther comparisons for the location effect
lmm_comp_inpl <- emmeans(lmm_fit, specs="inpl",
                         contr="pairwise", type="response")

# Ratio between the mean scaled sums for each location
lmm_comp_inpl$contrasts
```

Table S11. Ratios of scaled sums between the locations of alate and apterous aphids in first evaluation

contrast	ratio	se	df	t_ratio	p_value
0/1	1.495	0.44	10	1.366	0.202

Location effect in each treatment

Ratios between the scaled sums of the border plants (0) and the inner plants (1) split by the treatments are given in Table S12. Please note, that none of these ratios is significantly different from zero.

```
# Model based least square means and ther comparisons for the location effect
# in each treatment
lmm_comp_inter <- emmeans(lmm_fit, specs="inpl", by="var",
                          contr="pairwise", type="response")

# Ratios
lmm_comp_inter$contrasts
```

Table S12. Ratios of scaled sums between the locations and p-values of alate and apterous aphids in first evaluation

contrast	var	ratio	se	df	t_ratio	p_value
0/1	NF	1.312	0.864	10	0.413	0.688
0/1	PEB	1.747	1.150	10	0.848	0.416
0/1	PEG	2.178	1.434	10	1.183	0.264
0/1	SFB	1.058	0.696	10	0.086	0.933
0/1	SFG	1.413	0.930	10	0.525	0.611

Field Trial Evaluation 2

Data

The statistical analysis was run on the following data set called datsum with the variables:

var: Different treatments

plot: Plots on the field

inpl: Location of the lettuce plants in the plots (0: border, 1: centre)

aphids_sum: sum of aphids per location in each plot

n: Number of lettuce plants for each sum

scaled_sum: scaled sums calculated as (aphids_sum + 1)/n

Table S13. Summed total number of alate and apterous aphids in second evaluation

var	plot	inpl	aphids_sum	n	scaled_sum
NF	5	0	7	18	0.444
NF	5	1	1	12	0.167
NF	8	0	9	18	0.556
NF	8	1	6	12	0.583
NF	12	0	15	18	0.889
NF	12	1	2	12	0.250
PEB	3	0	3	18	0.222
PEB	3	1	0	12	0.083
PEB	7	0	7	18	0.444
PEB	7	1	6	12	0.583
PEB	13	0	6	18	0.389
PEB	13	1	2	12	0.250
PEG	1	0	11	18	0.667
PEG	1	1	3	12	0.333
PEG	9	0	14	18	0.833
PEG	9	1	6	12	0.583
PEG	11	0	11	18	0.667
PEG	11	1	5	12	0.500
SFB	4	0	1	18	0.111
SFB	4	1	2	12	0.250
SFB	6	0	5	18	0.333
SFB	6	1	0	12	0.083
SFB	14	0	3	18	0.222
SFB	14	1	1	12	0.167
SFG	2	0	6	18	0.389
SFG	2	1	1	12	0.167
SFG	10	0	1	18	0.111
SFG	10	1	2	12	0.250
SFG	15	0	6	18	0.389
SFG	15	1	2	12	0.250

Statistical analysis

A linear mixed model was fit to the data as described in the text

```
library(lme4)

lmm_fit <- lmer(log(scaled_sum) ~ var * inpl + (1|plot), data=datsum)
```

ANOVA

```
library(lmerTest)

anova(lmm_fit)
```

The ANOVA (Table S14) revealed the significance ($\alpha = 0.05$) of the treatment (Var) since the p-value is 0.025, but no location effect (inpl) nor a treatment-location interaction (Var:inpl).

Table S14. ANOVA table of alate and apterous aphids in second evaluation

Effect	SSQ	MSQ	NumDF	DenDF	F_value	p_Value
var	5.151	1.288	4	10	4.478	0.025
inpl	1.212	1.212	1	10	4.215	0.067
var:inpl	0.276	0.069	4	10	0.240	0.909

Mean comparisons between the treatments

The mean comparisons were run on the logarithm of the scaled sums (as the model does), but are already back transformed to the original scale for easier interpretation. The least square means of the scaled sums for each treatment, their standard error and their 95% confidence intervals are given in Table 3.

```
# Model based least square means and ther comparisons
library(emmeans)
lmm_comp <- emmeans(lmm_fit, specs="var", contr="pairwise", type="response"
)

# LS-means for the treatments
lmm_comp$emmeans
```

Table S15. Least square means and their confidence intervals of alate and apterous aphids in first evaluation

var	mean	se	df	lower	upper
NF	0.418	0.093	10	0.255	0.685
PEB	0.279	0.062	10	0.170	0.457
PEG	0.575	0.128	10	0.350	0.942
SFB	0.175	0.039	10	0.107	0.287
SFG	0.237	0.053	10	0.144	0.388

The mean comparisons (contrasts) were run as differences on the log-scale. Therefore back transformation results in the ratio between the means of the scaled sums. These ratios, their standard error and the corresponding p-values are given in Table S16.

```
# Contrast tests
lmm_comp$contrasts
```

Table S16. Contrasts and p-values of alate and apterous aphids in second evaluation

contrast	ratio	se	df	t_ratio	p_value
NF/PEB	1.501	0.471	10	1.293	0.701
NF/PEG	0.727	0.228	10	-1.014	0.844
NF/SFB	2.391	0.751	10	2.776	0.110
NF/SFG	1.767	0.555	10	1.814	0.417
PEB/PEG	0.485	0.152	10	-2.307	0.219
PEB/SFB	1.593	0.500	10	1.483	0.594
PEB/SFG	1.178	0.370	10	0.521	0.983
PEG/SFB	3.286	1.032	10	3.790	0.023
PEG/SFG	2.430	0.763	10	2.828	0.102
SFB/SFG	0.739	0.232	10	-0.962	0.866

Location effect

The model based average scaled sums for each location were compared on log-scale. Back-transformations results in a ratio between both sums (0: border plant, 1: inner plant). Please note that the ratio is not significantly different from zero.

```
# Model based least square means and ther comparisons for the location effe
ct
lmm_comp_inpl <- emmeans(lmm_fit, specs="inpl",
                         contr="pairwise", type="response")

# Ratio between the mean scaled sums for each location
lmm_comp_inpl$contrasts
```

Table S17. Ratios of scaled sums between the locations of alate and apterous aphids in second evaluation

contrast	ratio	se	df	t_ratio	p_value
0/1	1.495	0.293	10	2.053	0.067

Location effect in each treatment

Ratios between the scaled sums of the border plants (0) and the inner plants (1) split by the treatments are given in Table S18. Please note, that none of these ratios is significantly different from zero.

```
# Model based least square means and ther comparisons for the location effe
ct
# in each treatment
lmm_comp_inter <- emmeans(lmm_fit, specs="inpl", by="var",
                          contr="pairwise", type="response")

# Ratios
lmm_comp_inter$contrasts
```

Table S18. Ratios of scaled sums between the locations and p-values of alate and apterous aphids in second evaluation

contrast	var	ratio	se	df	t_ratio	p_value
0/1	NF	2.082	0.912	10	1.675	0.125
0/1	PEB	1.468	0.643	10	0.876	0.402
0/1	PEG	1.562	0.684	10	1.018	0.333
0/1	SFB	1.333	0.584	10	0.657	0.526
0/1	SFG	1.173	0.514	10	0.364	0.723