1 Supplementary 3/5: Field Trial Evaluation 1 (alate aphids)

2 Data

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

4 • *Var:* Different treatments
5 • *Plot:* Plots on the field
6 • *inpl:* Location of the lettuce plants in the plots (0: border, 1: centre)
7 • *aphids_sum:* sum of flying aphids per location in each plot
8 • *n:* Number of lettuce plants for each sum
9 • *scaled_sum:* scaled sums calculated as (aphids_sum+1)/n
10

11 **Tab.S2** 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

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12 Statistical analysis

13 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)
```

17 ANOVA
```
library(lmerTest)

anova(lmm_fit)
```

21 **Tab.S3** 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

22 The ANOVA (**Tab.S3**) revealed the significance ($\alpha = 0.05$) of the treatment (Var) since the
23 p-value is 0.002, but no location effect (inpl) nor a treatment-location interaction (Var:inpl).

2

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
```

Tab.S4 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 **Tab.S5**.

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

Tab.S5 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
```

Tab.S6 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 **Tab. S7**. 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
```

Tab.S7 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

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