Supplementary 5/5: 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

Tab.S14 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

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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)
```

Tab.S15 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

The ANOVA (**Tab.S15**) 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).

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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.S16 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 **Tab.S17**.

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

Tab.S17 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

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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.S18 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 **Tab.S19**. 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.S19 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

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