

Article

Pupation Substrate Type and Volume Affect Pupation, Quality Parameters and Production Costs of a Reproductive Colony of *Ceratitis capitata* (Diptera: Tephritidae) VIENNA 8 Genetic Sexing Strain

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Supplementary File S1

Linear predictors of the Generalized Linear Models fitted to the data of the different response variables of Experiment 1 (See the Materials and Methods and Results section of the main text for details). We present the output from the analyses computed in the R software (R Development Core Team 2017).

Pupation (YBIN = a binary vector with data of larvae that pupated and larvae that do not pupated)

Call:

```
glm(formula = YBIN ~ SubstrateType + SubstrateVolumemL, family = quasibinomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-3.1348	-0.8115	0.0089	0.6253	3.7821

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	2.82200	0.15180	18.591	< 2e-16 ***
SubstrateTypeBSawdust	0.23769	0.17351	1.370	0.1777
SubstrateTypeCCellulose	1.34021	0.25091	5.341	3.1e-06 ***
SubstrateTypeDCoconutFiber	-1.27371	0.13743	-9.268	6.6e-12 ***
SubstrateTypeEVermiculite	-0.13716	0.16594	-0.827	0.4129
SubstrateVolumemL	0.03586	0.01408	2.547	0.0144 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 1.617764)

Null deviance: 504.801 on 49 degrees of freedom

Residual deviance: 74.482 on 44 degrees of freedom

AIC: NA

Number of Fisher Scoring iterations: 4

Pupal sex ratio (YBIN = a binary vector with data of female pupae and male pupae)

Call:

```
glm(formula = YBIN ~ SubstrateType, family = quasibinomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-3.4923	-0.9731	0.1880	1.0014	5.2794

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.7162696	0.0702584	10.195	4.79e-13 ***
SubstrateTypeBSawdust	0.2437128	0.1018546	2.393	0.0212 *
SubstrateTypeCCellulose	-0.0007678	0.1027132	-0.007	0.9941

```
SubstrateTypeDCoconutFiber -0.1798137 0.1101688 -1.632 0.1099
SubstrateTypeEVermiculite -0.0817985 0.1040338 -0.786 0.4360
---
```

```
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(Dispersion parameter for quasibinomial family taken to be 2.835261)
```

```
Null deviance: 171.97 on 47 degrees of freedom
Residual deviance: 124.46 on 43 degrees of freedom
(2 observations deleted due to missingness)
AIC: NA
```

```
Number of Fisher Scoring iterations: 4
```

Female emergence (YBIN = a binary vector with data of females that emerged and females that did not emerged)

```
Call:
glm(formula = YBIN ~ 1, family = quasibinomial)
```

```
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-4.6951 -0.6311  0.3362  0.7451  2.3971
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.13245    0.04265   3.106 0.00321 **
---
```

```
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(Dispersion parameter for quasibinomial family taken to be 1.458164)
```

```
Null deviance: 69.474 on 47 degrees of freedom
Residual deviance: 69.474 on 47 degrees of freedom
(2 observations deleted due to missingness)
AIC: NA
```

```
Number of Fisher Scoring iterations: 3
```

Female fliers (YBIN = a binary vector with data of females fliers and females that did not fly)

```
Call:
glm(formula = YBIN ~ SubstrateType * SubstrateVolumemL, family = quasibinomial)
```

```
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.3653 -0.6650  0.1023  0.8286  2.1030
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)      0.098361  0.213536   0.461  0.6477
SubstrateTypeBSawdust -0.392161  0.292350  -1.341  0.1877
SubstrateTypeCCellulose -0.146776  0.328765  -0.446  0.6578
SubstrateTypeDCoconutFiber -0.536480  0.305119  -1.758  0.0868 .
SubstrateTypeEVermiculite  0.186829  0.303052   0.616  0.5412
SubstrateVolumemL -0.003939  0.025600  -0.154  0.8785
SubstrateTypeBSawdust: SubstrateVolumemL  0.053564  0.035396   1.513  0.1385
SubstrateTypeCCellulose: SubstrateVolumemL -0.029018  0.038726  -0.749  0.4583
SubstrateTypeDCoconutFiber: SubstrateVolumemL  0.058439  0.037032   1.578  0.1228
SubstrateTypeEVermiculite: SubstrateVolumemL -0.038669  0.036496  -1.060  0.2960
---
```

```
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(Dispersion parameter for quasibinomial family taken to be 1.361853)
```

```
Null deviance: 84.906 on 47 degrees of freedom
Residual deviance: 52.934 on 38 degrees of freedom
(2 observations deleted due to missingness)
AIC: NA
```

Number of Fisher Scoring iterations: 4

References

R Development Core Team. *R: A Language and Environment for Statistical Computing*; R Foundation for Statistical Computing: Vienna, Austria, 2017.

Supplementary File S2

This Supplementary File S2 presents the multiple comparisons of means performed after ANOVA tests detected significant effects of the predictor variable (i.e., substrate type) in the response variables (i.e., pupation, female emergence and female fliers) (See the Materials and Methods and Results section of the main text for details). We present the output of the Tukey contrasts computed in the R software (R Development Core Team 2017) using the *glht* function of the package *multcomp* (Hothorn et al. 2008).

Pupation

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: `lm(formula = logit(Pupation) ~ SubstrateType + Block)`

Linear Hypotheses:

	Estimate	Std. Error	t value	Pr(> t)
Cellulose1 - Sawdust == 0	0.43584	0.17761	2.454	0.1137
Cellulose2 - Sawdust == 0	0.38489	0.17761	2.167	0.2047
Cellulose3 - Sawdust == 0	0.37152	0.17761	2.092	0.2356
FineWheatBran - Sawdust == 0	-0.09877	0.17761	-0.556	0.9808
Cellulose2 - Cellulose1 == 0	-0.05095	0.17761	-0.287	0.9985
Cellulose3 - Cellulose1 == 0	-0.06432	0.17761	-0.362	0.9962
FineWheatBran - Cellulose1 == 0	-0.53461	0.17761	-3.010	0.0291 *
Cellulose3 - Cellulose2 == 0	-0.01337	0.17761	-0.075	1.0000
FineWheatBran - Cellulose2 == 0	-0.48366	0.17761	-2.723	0.0608 .
FineWheatBran - Cellulose3 == 0	-0.47029	0.17761	-2.648	0.0729 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Adjusted p values reported -- single-step method)

Female emergence

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

Fit: `lm(formula = logit(Emergence) ~ SubstrateType + Block)`

Linear Hypotheses:

	Estimate	Std. Error	t value	Pr(> t)
Cellulose1 - Sawdust == 0	-0.52254	0.17806	-2.935	0.0356 *
Cellulose2 - Sawdust == 0	-0.31129	0.17806	-1.748	0.4121
Cellulose3 - Sawdust == 0	-0.19470	0.17806	-1.093	0.8093
FineWheatBran - Sawdust == 0	-0.46414	0.17806	-2.607	0.0805 .
Cellulose2 - Cellulose1 == 0	0.21126	0.17806	1.186	0.7591
Cellulose3 - Cellulose1 == 0	0.32785	0.17806	1.841	0.3590
FineWheatBran - Cellulose1 == 0	0.05841	0.17806	0.328	0.9974

```
Cellulose3 - Cellulose2 == 0      0.11659      0.17806      0.655      0.9652
FineWheatBran - Celulosa2 == 0    -0.15285      0.17806     -0.858      0.9109
FineWheatBran - Celulosa3 == 0    -0.26944      0.17806     -1.513      0.5576
```

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)
```

Female fliers

Simultaneous Tests for General Linear Hypotheses

Multiple Comparisons of Means: Tukey Contrasts

```
Fit: lm(formula = logit(Voladoras...) ~ Sustrato + Block)
```

Linear Hypotheses:

	Estimate	Std. Error	t value	Pr(> t)	
Cellulose1 - Sawdust == 0	-0.44476	0.12312	-3.612	0.0051	**
Cellulose2 - Sawdust == 0	-0.27115	0.12312	-2.202	0.1913	
Cellulose3 - Sawdust == 0	-0.11537	0.12312	-0.937	0.8814	
FineWheatBran - Sawdust == 0	-0.34400	0.12312	-2.794	0.0510	.
Cellulose2 - Cellulose1 == 0	0.17361	0.12312	1.410	0.6234	
Cellulose3 - Cellulose1 == 0	0.32939	0.12312	2.675	0.0684	.
FineWheatBran - Cellulose1 == 0	0.10076	0.12312	0.818	0.9241	
Cellulose3 - Cellulose2 == 0	0.15578	0.12312	1.265	0.7131	
FineWheatBran - Cellulose2 == 0	-0.07285	0.12312	-0.592	0.9759	
FineWheatBran - Cellulose3 == 0	-0.22863	0.12312	-1.857	0.3502	

```
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```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Adjusted p values reported -- single-step method)
```

References

- Hothorn, T.; Bretz, F.; Westfall, P. Simultaneous inference in general parametric models. *Biom. J.* **2008**, *50*, 346–363.
- R Development Core Team. *R: A Language and Environment for Statistical Computing*; R Foundation for Statistical Computing: Vienna, Austria, 2017.