

ANEXO 3

Resultados estadísticos de cada uno de los modelos, entorno R 3.6.1.

A- COMPARACIONES SOBRE VARIABLES ESTOMÁTICAS

I- Análisis del efecto del NIVEL DE PLOIDÍA

NÚMERO DE CÉLULAS EPIDÉRMICAS ppdd.

```
Generalized linear mixed model fit by maximum likelihood (Laplace
Approximation) [glmerMod]
Family: poisson ( log )
Formula: N.cel.epid ~ ploidia + (1 | acc/plant/leaf)
Data: estomas
```

AIC	BIC	logLik	deviance	df.resid
3601.7	3628.3	-1794.8	3589.7	624

Scaled residuals:

Min	1Q	Median	3Q	Max
-0.59735	-0.14863	-0.02185	0.12252	0.87257

Random effects:

Groups	Name	Variance	Std.Dev.
leaf:(plant:acc)	(Intercept)	0.000000	0.00000
plant:acc	(Intercept)	0.000000	0.00000
acc	(Intercept)	0.001079	0.03285

Number of obs: 630, groups: leaf:(plant:acc), 127; plant:acc, 40; acc, 14

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.78354	0.01259	300.539	<2e-16 ***
ploidia4x	-0.05695	0.03107	-1.833	0.0668 .
ploidia6x	-0.03384	0.03097	-1.092	0.2746

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

Correlation of Fixed Effects:

(Intr) plod4x

```

ploidia4x -0.405
ploidia6x -0.406 0.165
convergence code: 0
boundary (singular) fit: see ?isSingular

> summary(glmer(N.cel.epid~ploidia2 + (1|acc/plant/leaf), estomas,
family=poisson))
boundary (singular) fit: see ?isSingular
Generalized linear mixed model fit by maximum likelihood (Laplace
Approximation) [glmerMod]
Family: poisson ( log )
Formula: N.cel.epid ~ ploidia2 + (1 | acc/plant/leaf)
Data: estomas

      AIC      BIC   logLik deviance df.resid
3601.7  3628.3 -1794.8  3589.7     624

Scaled residuals:
    Min       1Q   Median       3Q      Max
-0.59735 -0.14863 -0.02185  0.12252  0.87257

Random effects:
 Groups              Name          Variance Std.Dev.
leaf:(plant:acc) (Intercept) 0.000000 0.00000
plant:acc         (Intercept) 0.000000 0.00000
acc               (Intercept) 0.001079 0.03285
Number of obs: 630, groups: leaf:(plant:acc), 127; plant:acc, 40; acc, 14

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   3.78354    0.01259 300.539 <2e-16 ***
ploidia23_6x -0.03384    0.03097  -1.092  0.2746
ploidia24x   -0.05695    0.03107  -1.833  0.0668 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) pl23_6
ploidi23_6x -0.406
ploidia24x  -0.405 0.165
convergence code: 0
boundary (singular) fit: see ?isSingular

```

NÚMERO DE ESTOMAS

```

> summary(glmer(N.estomas~ploidia + (1|acc/plant/leaf), estomas,
family=poisson))

```

boundary (singular) fit: see ?isSingular
 Generalized linear mixed model fit by maximum likelihood (Laplace
 Approximation) [glmerMod]
 Family: poisson (log)
 Formula: N.estomas ~ ploidia + (1 | acc/plant/leaf)
 Data: estomas

AIC	BIC	logLik	deviance	df.resid
2707.0	2733.7	-1347.5	2695.0	624

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.04361	-0.19750	-0.02006	0.26009	1.26948

Random effects:

Groups	Name	Variance	Std.Dev.
leaf:(plant:acc)	(Intercept)	0.000e+00	0.000e+00
plant:acc	(Intercept)	1.625e-10	1.275e-05
acc	(Intercept)	5.966e-03	7.724e-02

Number of obs: 630, groups: leaf:(plant:acc), 127; plant:acc, 40; acc, 14

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.33795	0.02850	82.042	< 2e-16 ***
ploidia4x	-0.27349	0.07214	-3.791	0.00015 ***
ploidia6x	-0.15838	0.07107	-2.229	0.02584 *

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

Correlation of Fixed Effects:

	(Intr)	plod4x
ploidia4x	-0.395	
ploidia6x	-0.401	0.158

convergence code: 0
 boundary (singular) fit: see ?isSingular

> summary(glmer(N.estomas~ploidia2 + (1|acc/plant/leaf), estomas,
 family=poisson))
 boundary (singular) fit: see ?isSingular
 Generalized linear mixed model fit by maximum likelihood (Laplace
 Approximation) [glmerMod]
 Family: poisson (log)
 Formula: N.estomas ~ ploidia2 + (1 | acc/plant/leaf)
 Data: estomas

AIC	BIC	logLik	deviance	df.resid
2707.0	2733.7	-1347.5	2695.0	624

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-1.04361	-0.19750	-0.02006	0.26009	1.26948

Random effects:

Groups	Name	Variance	Std.Dev.
leaf:(plant:acc)	(Intercept)	0.000e+00	0.000e+00
plant:acc	(Intercept)	1.625e-10	1.275e-05
acc	(Intercept)	5.966e-03	7.724e-02

Number of obs: 630, groups: leaf:(plant:acc), 127; plant:acc, 40; acc, 14

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.33795	0.02850	82.042	< 2e-16 ***
ploidia23_6x	-0.15838	0.07107	-2.229	0.02584 *
ploidia24x	-0.27349	0.07214	-3.791	0.00015 ***

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

Correlation of Fixed Effects:

	(Intr)	p123_6
ploidi23_6x	-0.401	
ploidia24x	-0.395	0.158

convergence code: 0

boundary (singular) fit: see ?isSingular

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```
> summary(lmer(Indice.estoma~ploidia + (1|acc/plant/leaf), estomas))
```

Linear mixed model fit by REML ['lmerMod']

Formula: Indice.estoma ~ ploidia + (1 | acc/plant/leaf)

Data: estomas

REML criterion at convergence: 2200.1

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-2.97244	-0.64228	0.04843	0.65482	2.64510

Random effects:

Groups	Name	Variance	Std.Dev.
leaf:(plant:acc)	(Intercept)	0.1853	0.4304
plant:acc	(Intercept)	0.2694	0.5190
acc	(Intercept)	0.7755	0.8806
Residual		1.5966	1.2636

Number of obs: 630, groups: leaf:(plant:acc), 127; plant:acc, 40; acc, 14

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	19.0220	0.3051	62.339
Ploidia4x	-3.0809	0.7442	-4.140
Ploidia6x	-1.8654	0.7442	-2.507

Correlation of Fixed Effects:

```
(Intr) plod4x
ploidia4x -0.410
ploidia6x -0.410 0.168
> summary(lmer(Indice.estoma~ploidia2 + (1|acc/plant/leaf), estomas))
Linear mixed model fit by REML ['lmerMod']
Formula: Indice.estoma ~ ploidia2 + (1 | acc/plant/leaf)
Data: estomas
```

REML criterion at convergence: 2200.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.97244	-0.64228	0.04843	0.65482	2.64510

Random effects:

Groups	Name	Variance	Std.Dev.
leaf:(plant:acc)	(Intercept)	0.1853	0.4304
plant:acc	(Intercept)	0.2694	0.5190
acc	(Intercept)	0.7755	0.8806
Residual		1.5966	1.2636

Number of obs: 630, groups: leaf:(plant:acc), 127; plant:acc, 40; acc, 14

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	19.0220	0.3051	62.339
Ploidia23_6x	-1.8654	0.7442	-2.507
Ploidia24x	-3.0809	0.7442	-4.140

Correlation of Fixed Effects:

```
(Intr) pl23_6
ploidi23_6x -0.410
ploidia24x -0.410 0.168
```

Análisis del efecto de los LINAJES

NÚMERO DE CÉLULAS EPIDÉRMICAS ppdd.

```
Generalized linear mixed model fit by maximum likelihood (Laplace
Approximation) [glmerMod]
Family: poisson ( log )
Formula: N.cel.epid ~ Linaje + (1 | acc/plant/leaf)
Data: estomas22
```

AIC	BIC	logLik	deviance	df.resid
2834.5	2859.7	-1411.2	2822.5	489

Scaled residuals:

Min	1Q	Median	3Q	Max
-0.56758	-0.16324	-0.00905	0.13665	0.79303

Random effects:

Groups	Name	Variance	Std.Dev.
leaf:(plant:acc)	(Intercept)	0.000000	0.00000
plant:acc	(Intercept)	0.000000	0.00000
acc	(Intercept)	0.001363	0.03692

Number of obs: 495, groups: leaf:(plant:acc), 100; plant:acc, 31; acc, 11

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.76857	0.01937	194.532	<2e-16 ***
LinajeAzul	0.01813	0.03159	0.574	0.566
LinajeRojo	-0.02250	0.03170	-0.710	0.478

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

Correlation of Fixed Effects:

	(Intr)	LnjAzl
LinajeAzul	-0.613	
LinajeRojo	-0.611	0.375

convergence code: 0

boundary (singular) fit: see ?issingular

```
> summary(glmer(N.cel.epid~Linaje2 + (1|acc/plant/leaf), estomas22,
family=poisson))
```

boundary (singular) fit: see ?issingular

```
Generalized linear mixed model fit by maximum likelihood (Laplace
Approximation) [glmerMod]
Family: poisson ( log )
Formula: N.cel.epid ~ Linaje2 + (1 | acc/plant/leaf)
Data: estomas22
```

AIC	BIC	logLik	deviance	df.resid
2834.5	2859.7	-1411.2	2822.5	489

Scaled residuals:

Min	1Q	Median	3Q	Max
-0.56758	-0.16324	-0.00905	0.13665	0.79303

Random effects:

Groups	Name	Variance	Std.Dev.
leaf:(plant:acc)	(Intercept)	0.000000	0.00000
plant:acc	(Intercept)	0.000000	0.00000
acc	(Intercept)	0.001363	0.03692

Number of obs: 495, groups: leaf:(plant:acc), 100; plant:acc, 31; acc, 11

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	3.76857	0.01937	194.532	<2e-16 ***
Linaje2Rojo	-0.02250	0.03170	-0.710	0.478
Linaje2Zazu1	0.01813	0.03159	0.574	0.566

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

Correlation of Fixed Effects:

	(Intr)	Lnj2Rj
Linaje2Rojo	-0.611	
Linaje2Zazu1	-0.613	0.375

convergence code: 0

boundary (singular) fit: see ?issingular

Generalized linear mixed model fit by maximum likelihood (Laplace

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Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [glmerMod]

Family: poisson (log)

Formula: N.estomas ~ Linaje + (1 | acc/plant/leaf)

Data: estomas22

AIC	BIC	logLik	deviance	df.resid
2137.4	2162.6	-1062.7	2125.4	489

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.0999	-0.2311	0.0163	0.2463	1.1874

Random effects:

Groups	Name	Variance	Std.Dev.
leaf:(plant:acc)	(Intercept)	0.0000	0.0000

```

plant:acc      (Intercept) 0.0000  0.0000
acc            (Intercept) 0.0114  0.1068
Number of obs: 495, groups:  leaf:(plant:acc), 100; plant:acc, 31; acc, 11

```

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.28881	0.05227	43.787	<2e-16 ***
LinajeAzul	-0.01214	0.08540	-0.142	0.887
LinajeRojo	-0.06334	0.08562	-0.740	0.459

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

Correlation of Fixed Effects:

	(Intr)	LnjAzl
LinajeAzul	-0.612	
LinajeRojo	-0.610	0.374

convergence code: 0
boundary (singular) fit: see ?issingular

```

> summary(glmer(N.estomas~Linaje2 + (1|acc/plant/leaf), estomas22,
family=poisson))
boundary (singular) fit: see ?issingular
Generalized linear mixed model fit by maximum likelihood (Laplace
Approximation) [glmerMod]
Family: poisson ( log )
Formula: N.estomas ~ Linaje2 + (1 | acc/plant/leaf)
Data: estomas22

```

AIC	BIC	logLik	deviance	df.resid
2137.4	2162.6	-1062.7	2125.4	489

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.0999	-0.2311	0.0163	0.2463	1.1874

Random effects:

Groups	Name	Variance	Std.Dev.
leaf:(plant:acc)	(Intercept)	0.0000	0.0000
plant:acc	(Intercept)	0.0000	0.0000
acc	(Intercept)	0.0114	0.1068

Number of obs: 495, groups: leaf:(plant:acc), 100; plant:acc, 31; acc, 11

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.28881	0.05227	43.787	<2e-16 ***
Linaje2Rojo	-0.06334	0.08562	-0.740	0.459
Linaje2Zazul	-0.01214	0.08540	-0.142	0.887

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

Correlation of Fixed Effects:

(Intr) Lnj2Rj

Linaje2Rojo -0.610

Linaje2Zazl -0.612 0.374

convergence code: 0

boundary (singular) fit: see ?issingular

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Linear fixed model fit by REML. T-tests use Satterthwaite's method

[lmerModLmerTest]

Formula: Indice.estoma ~ Linaje + (1 | acc/plant/leaf)

Data: estomas22

REML criterion at convergence: 1792.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.78458	-0.66716	0.02386	0.67750	2.49809

Random effects:

Groups	Name	Variance	Std.Dev.
leaf:(plant:acc)	(Intercept)	0.2261	0.4755
plant:acc	(Intercept)	0.3305	0.5749
acc	(Intercept)	1.7067	1.3064
Residual		1.7915	1.3385

Number of obs: 495, groups: leaf:(plant:acc), 100; plant:acc, 31; acc, 11

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	18.5088	0.6155	7.9678	30.070	1.73e-09 ***
LinajeAzul	-0.4693	1.0064	8.0059	-0.466	0.653
LinajeRojo	-0.5956	1.0030	7.9016	-0.594	0.569

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

Correlation of Fixed Effects:

(Intr) LnjAZl

LinajeAzul -0.612

LinajeRojo -0.614 0.375

> summary(lmer(Indice.estoma~Linaje2 + (1|acc/plant/leaf), estomas22))

Linear mixed model fit by REML. t-tests use Satterthwaite's method [

lmerModLmerTest]

Formula: Indice.estoma ~ Linaje2 + (1 | acc/plant/leaf)

Data: estomas22

REML criterion at convergence: 1792.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.78458	-0.66716	0.02386	0.67750	2.49809

Random effects:

Groups	Name	Variance	Std.Dev.
leaf:(plant:acc)	(Intercept)	0.2261	0.4755
plant:acc	(Intercept)	0.3305	0.5749
acc	(Intercept)	1.7067	1.3064
Residual		1.7915	1.3385

Number of obs: 495, groups: leaf:(plant:acc), 100; plant:acc, 31; acc, 11

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	18.5088	0.6155	7.9678	30.070	1.73e-09 ***
Linaje2Rojo	-0.5956	1.0030	7.9016	-0.594	0.569
Linaje2Zazu1	-0.4693	1.0064	8.0059	-0.466	0.653

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

Correlation of Fixed Effects:

	(Intr)	Lnj2Rj
Linaje2Rojo	-0.614	
Linaje2Zazu1	-0.612	0.375

B- PERMANOVA

MASA SEMILLA

```
> summary(lmer(peso.de.semilla~Linaje2 + (1|Muestra),solanum))
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: peso.de.semilla ~ Linaje2 + (1 | Muestra)
Data: solanum
```

REML criterion at convergence: -4552.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-5.4711	-0.4410	-0.0103	0.4291	6.2972

Random effects:

Groups	Name	Variance	Std.Dev.
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Muestra (Intercept) 1.479e-04 0.012163
 Residual 8.495e-06 0.002915
 Number of obs: 561, groups: Muestra, 79

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.035713	0.001494	75.123507	23.912	<2e-16 ***
Linaje2Amarillo	0.008629	0.005662	74.836623	1.524	0.132
Linaje2Rojo	-0.005039	0.007227	75.643278	-0.697	0.488
Linaje2Zazul	0.001909	0.006287	74.896803	0.304	0.762

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

Correlation of Fixed Effects:

(Intr) Lnj2Am Lnj2Rj
 Linaj2Amrll -0.264
 Linaje2Rojo -0.207 0.055
 Linaje2Zazl -0.238 0.063 0.049

> summary(lmer(peso.de.semilla~Ploidia.1 + (1|Muestra), solanum))
 Linear mixed model fit by REML. t-tests use Satterthwaite's method [lmerModLmerTest]
 Formula: peso.de.semilla ~ Ploidia.1 + (1 | Muestra)
 Data: solanum

REML criterion at convergence: -4549.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-5.4655	-0.4324	-0.0096	0.4269	6.3023

Random effects:

Groups	Name	Variance	Std.Dev.
Muestra	(Intercept)	1.497e-04	0.012234
	Residual	8.496e-06	0.002915

Number of obs: 561, groups: Muestra, 79

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.036786	0.001721	74.984876	21.370	<2e-16 ***
Ploidia.12x	-0.002052	0.003610	74.916405	-0.568	0.571
Ploidia.13_6x	-0.005473	0.004955	74.992395	-1.105	0.273
Ploidia.14x	0.003386	0.005321	75.819718	0.636	0.526

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

Correlation of Fixed Effects:

(Intr) Pld.12 P.13_6

```
Ploidia.12x -0.477
Ploid.13_6x -0.347  0.166
Ploidia.14x -0.324  0.154  0.112
> summary(lmer(peso.de.semilla~Ploidia + (1|Muestra), solanum))
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: peso.de.semilla ~ Ploidia + (1 | Muestra)
Data: solanum
```

REML criterion at convergence: -4549.2

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-5.4655	-0.4324	-0.0096	0.4269	6.3023

Random effects:

Groups	Name	Variance	Std.Dev.
Muestra	(Intercept)	1.497e-04	0.012234
Residual		8.496e-06	0.002915

Number of obs: 561, groups: Muestra, 79

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.036786	0.001721	74.984875	21.370	<2e-16 ***
Ploidia2x	-0.002052	0.003610	74.916405	-0.568	0.571
Ploidia4x	0.003386	0.005321	75.819718	0.636	0.526
Ploidia6x	-0.005473	0.004955	74.992395	-1.105	0.273

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

Correlation of Fixed Effects:

	(Intr)	Plod2x	Plod4x
Ploidia2x	-0.477		
Ploidia4x	-0.324	0.154	
Ploidia6x	-0.347	0.166	0.112

TRICOMAS

ÁREA DE TRICOMAS

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method
['lmerModLmerTest']
Formula: area.tricomas ~ Linaje + (1 | Muestra)
Data: solanum
```

REML criterion at convergence: 8154.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.6918	-0.5304	-0.0559	0.4938	4.1419

Random effects:

Groups	Name	Variance	Std.Dev.
Muestra	(Intercept)	7034	83.87
	Residual	3372	58.07

Number of obs: 715, groups: Muestra, 141

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	209.702	7.668	138.098	27.347	<2e-16 ***
LinajeAmarillo	17.767	34.058	138.290	0.522	0.603
LinajeAzul	3.413	51.266	138.296	0.067	0.947

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

Correlation of Fixed Effects:

	(Intr)	LnjAmr
LinajeAmr11	-0.225	
LinajeAzul	-0.150	0.034

> summary(lmer(area.tricomas~Linaje2 + (1|Muestra), solanum))
 Linear mixed model fit by REML. t-tests use Satterthwaite's method
 ['lmerModLmerTest']
 Formula: area.tricomas ~ Linaje2 + (1 | Muestra)
 Data: solanum

REML criterion at convergence: 8154.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.6918	-0.5304	-0.0559	0.4938	4.1419

Random effects:

Groups	Name	Variance	Std.Dev.
Muestra	(Intercept)	7034	83.87
	Residual	3372	58.07

Number of obs: 715, groups: Muestra, 141

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	209.702	7.668	138.098	27.347	<2e-16 ***
Linaje2Amarillo	17.767	34.058	138.290	0.522	0.603
Linaje2Zazul	3.413	51.266	138.296	0.067	0.947

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

Correlation of Fixed Effects:

```
(Intr) Lnj2Am
Linaj2Amr1l -0.225
Linaje2Zazl -0.150 0.034
```

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method
['lmerModLmerTest']
Formula: area.tricomas ~ Ploidia + (1 | Muestra)
Data: solanum
```

REML criterion at convergence: 8146.5

Scaled residuals:

```
Min      1Q  Median      3Q      Max
-3.6931 -0.5331 -0.0554  0.4923  4.1405
```

Random effects:

```
Groups Name          Variance Std.Dev.
Muestra (Intercept) 7035      83.87
Residual          3372      58.07
Number of obs: 715, groups: Muestra, 141
```

Fixed effects:

```
Estimate Std. Error    df t value Pr(>|t|)
(Intercept) 210.572      8.447 137.123 24.929 <2e-16 ***
Ploidia2x   -18.144     24.193 137.229 -0.750 0.455
Ploidia4x    14.080     26.671 136.257 0.528 0.598
Ploidia6x    19.059     36.827 137.238 0.518 0.606
```

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

Correlation of Fixed Effects:

```
(Intr) Plod2x Plod4x
Ploidia2x -0.349
Ploidia4x -0.317 0.111
Ploidia6x -0.229 0.080 0.073
```

```
> summary(lmer(area.tricomas~Ploidia.1 + (1|Muestra), solanum))
Linear mixed model fit by REML. t-tests use Satterthwaite's method
['lmerModLmerTest']
Formula: area.tricomas ~ Ploidia.1 + (1 | Muestra)
Data: solanum
```

REML criterion at convergence: 8146.5

Scaled residuals:

```
Min      1Q  Median      3Q      Max
```

-3.6931 -0.5331 -0.0554 0.4923 4.1405

Random effects:

Groups	Name	Variance	Std.Dev.
Muestra	(Intercept)	7035	83.87
	Residual	3372	58.07

Number of obs: 715, groups: Muestra, 141

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	210.572	8.447	137.123	24.929	<2e-16 ***
Ploidia.12x	-18.144	24.193	137.229	-0.750	0.455
Ploidia.13_6x	19.059	36.827	137.238	0.518	0.606
Ploidia.14x	14.080	26.671	136.257	0.528	0.598

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

Correlation of Fixed Effects:

	(Intr)	Pld.12	P.13_6
Ploidia.12x	-0.349		
Ploid.13_6x	-0.229	0.080	
Ploidia.14x	-0.317	0.111	0.073

RAYOS DEL TRICOMA

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [
glmerMod]

Family: poisson (log)
Formula: N.rayos.tricoma ~ Linaje + (1 | Muestra)
Data: solanum

AIC	BIC	logLik	deviance	df.resid
3408.4	3426.7	-1700.2	3400.4	711

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.9138	-0.1384	0.1152	0.1152	2.6514

Random effects:

Groups	Name	Variance	Std.Dev.
Muestra	(Intercept)	0	0

Number of obs: 715, groups: Muestra, 141

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.743795	0.009835	278.978	<2e-16 ***
LinajeAmarillo	0.014405	0.043684	0.330	0.742

LinajeAzul 0.028794 0.065295 0.441 0.659

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

Correlation of Fixed Effects:

(Intr) LnjAmr

LinajeAmr11 -0.225

LinajeAzul -0.151 0.034

convergence code: 0

boundary (singular) fit: see ?issingular

```
> summary(glmer(N.rayos.tricoma~Linaje2 + (1|Muestra), solanum,
family=poisson))
```

boundary (singular) fit: see ?issingular

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [

glmerMod]

Family: poisson (log)

Formula: N.rayos.tricoma ~ Linaje2 + (1 | Muestra)

Data: solanum

AIC	BIC	logLik	deviance	df.resid
3408.4	3426.7	-1700.2	3400.4	711

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.9138	-0.1384	0.1152	0.1152	2.6514

Random effects:

Groups	Name	Variance	Std.Dev.
Muestra	(Intercept)	0	0

Number of obs: 715, groups: Muestra, 141

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.743795	0.009835	278.978	<2e-16 ***
Linaje2Amarillo	0.014405	0.043684	0.330	0.742
Linaje2Zazul	0.028794	0.065295	0.441	0.659

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

Correlation of Fixed Effects:

(Intr) Lnj2Am

Linaj2Amr11 -0.225

Linaje2Zaz1 -0.151 0.034

convergence code: 0

boundary (singular) fit: see ?issingular

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [

glmerMod]

Family: poisson (log)

Formula: N.rayos.tricoma ~ Ploidia + (1 | Muestra)

Data: solanum

AIC	BIC	logLik	deviance	df.resid
3410.2	3433.1	-1700.1	3400.2	710

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.9115	-0.1355	0.1182	0.1182	2.6555

Random effects:

Groups	Name	Variance	Std.Dev.
Muestra	(Intercept)	0	0

Number of obs: 715, groups: Muestra, 141

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.743028	0.010868	252.388	<2e-16 ***
Ploidia2x	-0.002618	0.031284	-0.084	0.933
Ploidia4x	0.022808	0.032957	0.692	0.489
Ploidia6x	0.006378	0.047438	0.134	0.893

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

Correlation of Fixed Effects:

	(Intr)	Plod2x	Plod4x
Ploidia2x	-0.347		
Ploidia4x	-0.330	0.115	
Ploidia6x	-0.229	0.080	0.076

convergence code: 0

boundary (singular) fit: see ?issingular

```
> summary(glmer(N.rayos.tricoma~Ploidia.1 + (1|Muestra), solanum, family=poisson))
```

boundary (singular) fit: see ?issingular

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [

glmerMod]

Family: poisson (log)

Formula: N.rayos.tricoma ~ Ploidia.1 + (1 | Muestra)

Data: solanum

AIC	BIC	logLik	deviance	df.resid
3410.2	3433.1	-1700.1	3400.2	710

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.9115	-0.1355	0.1182	0.1182	2.6555

Random effects:

Groups	Name	Variance	Std.Dev.
Muestra	(Intercept)	0	0

Number of obs: 715, groups: Muestra, 141

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	2.743028	0.010868	252.388	<2e-16 ***
Ploidia.12x	-0.002618	0.031284	-0.084	0.933
Ploidia.13_6x	0.006378	0.047438	0.134	0.893
Ploidia.14x	0.022808	0.032957	0.692	0.489

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

Correlation of Fixed Effects:

	(Intr)	Pld.12	P.13_6
Ploidia.12x	-0.347		
Ploid.13_6x	-0.229	0.080	
Ploidia.14x	-0.330	0.115	0.076

convergence code: 0
boundary (singular) fit: see ?isSingular

RASGOS FLORALES

LARGO DE LA COROLA

(No hay linaje ROJO)

Linear mixed model fit by REML. t-tests use Satterthwaite's method
['lmerModLmerTest']
Formula: largo.corola ~ Linaje + (1 | Muestra)
Data: solanum

REML criterion at convergence: 1661.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.8467	-0.4706	0.0116	0.5132	6.0664

Random effects:

Groups	Name	Variance	Std.Dev.
--------	------	----------	----------

Muestra (Intercept) 17.779 4.216
 Residual 0.497 0.705
 Number of obs: 511, groups: Muestra, 115

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	25.1626	0.4016	112.0444	62.659	<2e-16 ***
LinajeAmarillo	1.7142	3.0167	111.7718	0.568	0.5710
LinajeAzul	-6.5313	3.0167	111.7718	-2.165	0.0325 *

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

Correlation of Fixed Effects:

	(Intr)	LnjAmr
LinajeAmr11	-0.133	
LinajeAzul	-0.133	0.018

Linear mixed model fit by REML. t-tests use Satterthwaite's method
 ['lmerModLmerTest']

Formula: largo.corola ~ Ploidia + (1 | Muestra)
 Data: solanum

REML criterion at convergence: 1660.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.8475	-0.4708	0.0140	0.5089	6.0663

Random effects:

Groups	Name	Variance	Std.Dev.
Muestra	(Intercept)	18.069	4.251
Residual		0.497	0.705

Number of obs: 511, groups: Muestra, 115

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	25.17335	0.43304	111.01858	58.132	<2e-16 ***
Ploidia2x	-1.78947	1.35685	111.00681	-1.319	0.190
Ploidia4x	4.56798	3.04496	110.76377	1.500	0.136
Ploidia6x	-0.06828	1.95656	111.17081	-0.035	0.972

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

Correlation of Fixed Effects:

	(Intr)	Plod2x	Plod4x
Ploidia2x	-0.319		
Ploidia4x	-0.142	0.045	

```
Ploidia6x -0.221 0.071 0.031
> summary(lmer(largo.corola~Ploidia.1 + (1|Muestra), solanum))
Linear mixed model fit by REML. t-tests use Satterthwaite's method
['lmerModLmerTest']
Formula: largo.corola ~ Ploidia.1 + (1 | Muestra)
Data: solanum
```

REML criterion at convergence: 1660.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.8475	-0.4708	0.0140	0.5089	6.0663

Random effects:

Groups	Name	Variance	Std.Dev.
Muestra	(Intercept)	18.069	4.251
Residual		0.497	0.705

Number of obs: 511, groups: Muestra, 115

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	25.17335	0.43304	111.01858	58.132	<2e-16 ***
Ploidia.12x	-1.78947	1.35685	111.00681	-1.319	0.190
Ploidia.13_6x	-0.06828	1.95656	111.17081	-0.035	0.972
Ploidia.14x	4.56798	3.04496	110.76377	1.500	0.136

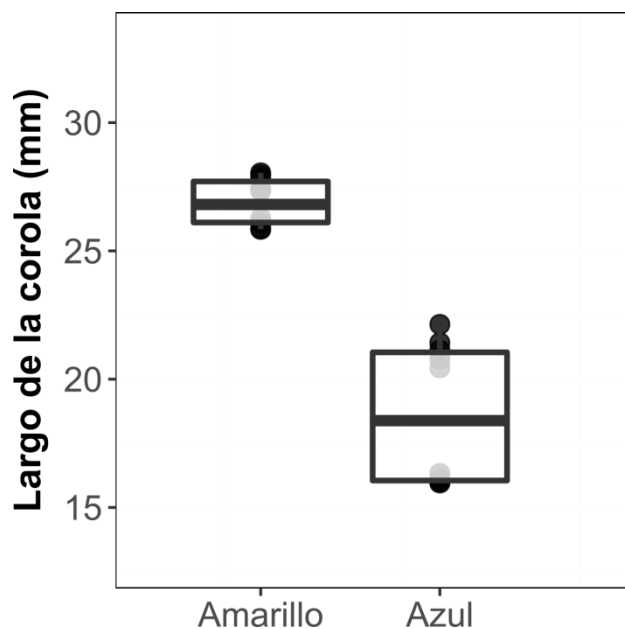
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)	Pld.12	P.13_6
Ploidia.12x	-0.319		
Ploid.13_6x	-0.221	0.071	
Ploidia.14x	-0.142	0.045	0.031

Los estadísticos para citar esta diferencia son: $z=-2.16$; $P= 0.03$).

No hay mediciones de Linaje Rojo



LARGO PROMEDIO DE LOS ESTAMBRES

Linear mixed model fit by REML. t-tests use Satterthwaite's method
['lmerModLmerTest']

Formula: largo.estambres ~ Linaje + (1 | Muestra)

Data: solanum

REML criterion at convergence: 2129.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.5374	-0.5549	-0.0228	0.6048	3.3790

Random effects:

Groups	Name	Variance	Std.Dev.
Muestra	(Intercept)	16.5357	4.0664
Residual		0.9581	0.9788

Number of obs: 577, groups: Muestra, 119

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	16.2899	0.3832	115.9341	42.513	<2e-16 ***
LinajeAmarillo	-2.9950	2.9173	115.7920	-1.027	0.307
LinajeAzul	-2.0029	2.3922	115.7933	-0.837	0.404

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

Correlation of Fixed Effects:

(Intr) LnJAmr

LinajeAmr11 -0.131

LinajeAzul -0.160 0.021

> summary(lmer(largo.estambres~Ploidia + (1|Muestra), solanum))

Linear mixed model fit by REML. t-tests use Satterthwaite's method

['lmerModLmerTest']

Formula: largo.estambres ~ Ploidia + (1 | Muestra)

Data: solanum

REML criterion at convergence: 2127.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.5365	-0.5577	-0.0281	0.6055	3.3788

Random effects:

Groups	Name	Variance	Std.Dev.
Muestra	(Intercept)	16.6877	4.0851
Residual		0.9581	0.9788

Number of obs: 577, groups: Muestra, 119

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	16.2408	0.4109	114.8816	39.521	<2e-16 ***
Ploidia2x	-1.3098	1.3053	114.8346	-1.003	0.318
Ploidia4x	1.5532	2.9361	115.0914	0.529	0.598
Ploidia6x	0.8597	1.7292	115.3751	0.497	0.620

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

Correlation of Fixed Effects:

(Intr) Plod2x Plod4x

Ploidia2x -0.315

Ploidia4x -0.140 0.044

Ploidia6x -0.238 0.075 0.033

> summary(lmer(largo.estambres~Ploidia.1 + (1|Muestra), solanum))

Linear mixed model fit by REML. t-tests use Satterthwaite's method

['lmerModLmerTest']

Formula: largo.estambres ~ Ploidia.1 + (1 | Muestra)

Data: solanum

REML criterion at convergence: 2127.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.5365	-0.5577	-0.0281	0.6055	3.3788

Random effects:

Groups	Name	Variance	Std.Dev.
Muestra	(Intercept)	16.6877	4.0851
	Residual	0.9581	0.9788

Number of obs: 577, groups: Muestra, 119

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	16.2408	0.4109	114.8816	39.521	<2e-16 ***
Ploidia.12x	-1.3098	1.3053	114.8346	-1.003	0.318
Ploidia.13_6x	0.8597	1.7292	115.3751	0.497	0.620
Ploidia.14x	1.5532	2.9361	115.0914	0.529	0.598

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

Correlation of Fixed Effects:

	(Intr)	Pld.12	P.13_6
Ploidia.12x	-0.315		
Ploid.13_6x	-0.238	0.075	
Ploidia.14x	-0.140	0.044	0.033

LARGO DEL PISTILO

Call:

glm(formula = largo.pistilo ~ Linaje, family = gaussian, data = solanum)

Deviance Residuals:

Min	1Q	Median	3Q	Max
-15.2522	-4.9985	0.8657	5.2498	14.3422

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	18.3585	0.6746	27.212	<2e-16 ***
LinajeAmarillo	6.3614	5.0260	1.266	0.208
LinajeAzul	-2.0856	4.1221	-0.506	0.614

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

(Dispersion parameter for gaussian family taken to be 49.61019)

Null deviance: 5600.3 on 113 degrees of freedom
 Residual deviance: 5506.7 on 111 degrees of freedom
 (1628 observations deleted due to missingness)

AIC: 773.56

Number of Fisher Scoring iterations: 2

Call:

```
glm(formula = largo.pistilo ~ Ploidia, family = gaussian, data = solanum)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-15.2872	-5.0335	0.9677	5.2147	14.3072

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	18.3935	0.7156	25.703	<2e-16 ***
Ploidia2x	-2.0894	2.3299	-0.897	0.3718
Ploidia4x	8.4185	5.0093	1.681	0.0957 .
Ploidia6x	1.0888	2.9506	0.369	0.7128

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

(Dispersion parameter for gaussian family taken to be 49.16264)

Null deviance: 5600.3 on 113 degrees of freedom

Residual deviance: 5407.9 on 110 degrees of freedom

(1628 observations deleted due to missingness)

AIC: 773.49

Number of Fisher Scoring iterations: 2

```
> summary(glm(largo.pistilo~Ploidia.1 , solanum, family=gaussian))
```

Call:

```
glm(formula = largo.pistilo ~ Ploidia.1, family = gaussian, data = solanum)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-15.2872	-5.0335	0.9677	5.2147	14.3072

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	18.3935	0.7156	25.703	<2e-16 ***
Ploidia.12x	-2.0894	2.3299	-0.897	0.3718
Ploidia.13_6x	1.0888	2.9506	0.369	0.7128
Ploidia.14x	8.4185	5.0093	1.681	0.0957 .

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

(Dispersion parameter for gaussian family taken to be 49.16264)

Null deviance: 5600.3 on 113 degrees of freedom

Residual deviance: 5407.9 on 110 degrees of freedom

(1628 observations deleted due to missingness)

AIC: 773.49

Number of Fisher scoring iterations: 2