Lanphere supplementary material

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Finalized code for analyses

You can also embed plots, for example:

## Analysis of Variance Table of type III with Kenward-Roger   
## approximation for degrees of freedom  
## Sum Sq Mean Sq NumDF DenDF F.value Pr(>F)   
## Wind\_exposure 1.8369 1.83685 1 8.986 14.2905 0.004359 \*\*   
## Genotype 7.6537 0.85041 9 149.520 6.6161 6.251e-08 \*\*\*  
## Wind\_exposure:Genotype 1.3212 0.14680 9 149.520 1.1421 0.336809   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Response | Factor | num\_df | den\_df | F | P |
| log(Height) | Wind\_exposure | 1 | 9.0 | 14.29 | 0.004 |
|  | Genotype | 9 | 149.5 | 6.62 | 0.000 |
|  | Wind\_exposure:Genotype | 9 | 149.5 | 1.14 | 0.337 |
| (Height) | Wind\_exposure | 1 | 9.4 | 20.16 | 0.001 |
|  | Genotype | 9 | 128.6 | 3.66 | 0.000 |
|  | Wind\_exposure:Genotype | 9 | 128.6 | 1.94 | 0.052 |
| all.shoot.total.length | Wind\_exposure | 1 | 9.0 | 19.59 | 0.002 |
|  | Genotype | 9 | 149.5 | 4.29 | 0.000 |
|  | Wind\_exposure:Genotype | 9 | 149.5 | 2.04 | 0.039 |
| log(all.shoot.total.length) | Wind\_exposure | 1 | 9.3 | 3.85 | 0.080 |
|  | Genotype | 9 | 128.2 | 4.42 | 0.000 |
|  | Wind\_exposure:Genotype | 9 | 128.2 | 0.94 | 0.492 |
| all.shoot.count | Wind\_exposure | 1 | 8.9 | 7.39 | 0.024 |
|  | Genotype | 9 | 150.4 | 9.38 | 0.000 |
|  | Wind\_exposure:Genotype | 9 | 150.4 | 1.43 | 0.181 |
| all.shoot.count | Wind\_exposure | 1 | 9.4 | 9.63 | 0.012 |
|  | Genotype | 9 | 128.9 | 2.22 | 0.025 |
|  | Wind\_exposure:Genotype | 9 | 128.9 | 0.95 | 0.483 |
| leaf\_C\_N | Wind\_exposure | 1 | 9.6 | 0.49 | 0.500 |
|  | Genotype | 9 | 72.1 | 4.20 | 0.000 |
|  | Wind\_exposure:Genotype | 9 | 72.1 | 1.07 | 0.395 |
| SLA | Wind\_exposure | 1 | 9.5 | 0.44 | 0.523 |
|  | Genotype | 9 | 123.1 | 5.89 | 0.000 |
|  | Wind\_exposure:Genotype | 9 | 123.1 | 0.86 | 0.564 |
| log(leaf\_WC) | Wind\_exposure | 1 | 9.1 | 1.96 | 0.195 |
|  | Genotype | 9 | 116.8 | 3.24 | 0.001 |
|  | Wind\_exposure:Genotype | 9 | 116.7 | 1.19 | 0.310 |
| leaf\_WC | Wind\_exposure | 1 | 9.5 | 0.05 | 0.834 |
|  | Genotype | 9 | 124.5 | 3.15 | 0.002 |
|  | Wind\_exposure:Genotype | 9 | 124.5 | 2.00 | 0.045 |
| log(leaf\_trichome.density + 1) | Wind\_exposure | 1 | 9.1 | 0.07 | 0.792 |
|  | Genotype | 9 | 117.7 | 8.95 | 0.000 |
|  | Wind\_exposure:Genotype | 9 | 117.7 | 0.86 | 0.563 |
| larva.wet.wt.exp1 | Wind\_exposure | 1 | 8.8 | 1.10 | 0.322 |
|  | Genotype | 9 | 53.0 | 1.84 | 0.082 |
|  | Wind\_exposure:Genotype | 9 | 53.2 | 0.65 | 0.749 |
| log(larva.wet.wt.exp2 + 1) | Wind\_exposure | 1 | 9.5 | 0.20 | 0.668 |
|  | Genotype | 9 | 100.9 | 1.90 | 0.060 |
|  | Wind\_exposure:Genotype | 9 | 101.0 | 2.66 | 0.008 |

## Analysis of Variance Table of type III with Satterthwaite   
## approximation for degrees of freedom  
## Sum Sq Mean Sq NumDF DenDF F.value  
## Aphid.Treatment 0.0005 0.00048 1 213.722 0.0020  
## Ant.Mound.Dist 0.1185 0.11849 1 9.246 0.4835  
## Genotype 14.1546 1.57273 9 213.223 6.4178  
## Aphid.Treatment:Ant.Mound.Dist 0.0938 0.09376 1 213.375 0.3826  
## Aphid.Treatment:Genotype 2.2548 0.25053 9 213.610 1.0223  
## Ant.Mound.Dist:Genotype 3.2549 0.36166 9 213.421 1.4758  
## Pr(>F)   
## Aphid.Treatment 0.9646   
## Ant.Mound.Dist 0.5039   
## Genotype 4.655e-08 \*\*\*  
## Aphid.Treatment:Ant.Mound.Dist 0.5369   
## Aphid.Treatment:Genotype 0.4231   
## Ant.Mound.Dist:Genotype 0.1584   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Linear mixed model fit by REML t-tests use Satterthwaite approximations  
## to degrees of freedom [lmerMod]  
## Formula:   
## log(leaf\_trichome.density + 1) ~ (Aphid.Treatment + Ant.Mound.Dist +   
## Genotype)^2 + (1 | Block/Ant.Mound.Dist)  
## Data: filter(aa.df, Year == "2012")  
##   
## REML criterion at convergence: 366.3  
##   
## Scaled residuals:   
## Min 1Q Median 3Q Max   
## -2.6315 -0.5125 0.1518 0.5898 1.8133   
##   
## Random effects:  
## Groups Name Variance Std.Dev.   
## Ant.Mound.Dist:Block (Intercept) 4.829e-16 2.198e-08  
## Block (Intercept) 4.024e-02 2.006e-01  
## Residual 1.540e+00 1.241e+00  
## Number of obs: 114, groups: Ant.Mound.Dist:Block, 14; Block, 5  
##   
## Fixed effects:  
## Estimate Std. Error df t value  
## (Intercept) 1.48160 0.81526 81.57000 1.817  
## Aphid.Treatmentnone -0.34596 0.89182 83.62000 -0.388  
## Ant.Mound.Dist 0.03596 0.10141 82.56000 0.355  
## GenotypeG 1.23721 1.20049 81.61000 1.031  
## GenotypeI -0.29150 1.08074 83.90000 -0.270  
## GenotypeJ 0.14328 1.03755 82.88000 0.138  
## GenotypeL 0.58731 1.07546 83.98000 0.546  
## GenotypeS 1.44823 1.07525 83.44000 1.347  
## GenotypeT -1.22734 1.51254 81.26000 -0.811  
## GenotypeU 0.98715 1.38500 83.99000 0.713  
## GenotypeW 0.80045 0.92994 83.93000 0.861  
## GenotypeX 2.00531 0.99740 83.79000 2.011  
## Aphid.Treatmentnone:Ant.Mound.Dist -0.04547 0.05906 83.21000 -0.770  
## Aphid.Treatmentnone:GenotypeI 0.93409 1.15644 83.87000 0.808  
## Aphid.Treatmentnone:GenotypeJ 1.76025 1.05495 83.06000 1.669  
## Aphid.Treatmentnone:GenotypeL -0.88148 1.15383 83.98000 -0.764  
## Aphid.Treatmentnone:GenotypeS 1.86348 1.25478 83.12000 1.485  
## Aphid.Treatmentnone:GenotypeT 3.37213 1.53861 83.15000 2.192  
## Aphid.Treatmentnone:GenotypeU -0.32992 1.24704 83.49000 -0.265  
## Aphid.Treatmentnone:GenotypeW 1.07171 0.99378 82.84000 1.078  
## Aphid.Treatmentnone:GenotypeX -0.04541 1.04741 83.86000 -0.043  
## Ant.Mound.Dist:GenotypeG -0.17646 0.17082 82.61000 -1.033  
## Ant.Mound.Dist:GenotypeI 0.06983 0.13080 83.14000 0.534  
## Ant.Mound.Dist:GenotypeJ -0.02336 0.11898 81.31000 -0.196  
## Ant.Mound.Dist:GenotypeL 0.08140 0.13593 82.42000 0.599  
## Ant.Mound.Dist:GenotypeS -0.08856 0.13700 81.64000 -0.646  
## Ant.Mound.Dist:GenotypeT -0.01636 0.15796 82.65000 -0.104  
## Ant.Mound.Dist:GenotypeU -0.04022 0.15868 83.42000 -0.253  
## Ant.Mound.Dist:GenotypeW 0.08068 0.11343 82.35000 0.711  
## Ant.Mound.Dist:GenotypeX 0.05390 0.12171 83.41000 0.443  
## Pr(>|t|)   
## (Intercept) 0.0728 .  
## Aphid.Treatmentnone 0.6991   
## Ant.Mound.Dist 0.7238   
## GenotypeG 0.3058   
## GenotypeI 0.7880   
## GenotypeJ 0.8905   
## GenotypeL 0.5864   
## GenotypeS 0.1817   
## GenotypeT 0.4195   
## GenotypeU 0.4780   
## GenotypeW 0.3918   
## GenotypeX 0.0476 \*  
## Aphid.Treatmentnone:Ant.Mound.Dist 0.4435   
## Aphid.Treatmentnone:GenotypeI 0.4215   
## Aphid.Treatmentnone:GenotypeJ 0.0990 .  
## Aphid.Treatmentnone:GenotypeL 0.4470   
## Aphid.Treatmentnone:GenotypeS 0.1413   
## Aphid.Treatmentnone:GenotypeT 0.0312 \*  
## Aphid.Treatmentnone:GenotypeU 0.7920   
## Aphid.Treatmentnone:GenotypeW 0.2840   
## Aphid.Treatmentnone:GenotypeX 0.9655   
## Ant.Mound.Dist:GenotypeG 0.3046   
## Ant.Mound.Dist:GenotypeI 0.5949   
## Ant.Mound.Dist:GenotypeJ 0.8449   
## Ant.Mound.Dist:GenotypeL 0.5509   
## Ant.Mound.Dist:GenotypeS 0.5198   
## Ant.Mound.Dist:GenotypeT 0.9177   
## Ant.Mound.Dist:GenotypeU 0.8005   
## Ant.Mound.Dist:GenotypeW 0.4789   
## Ant.Mound.Dist:GenotypeX 0.6590   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
## fit warnings:  
## fixed-effect model matrix is rank deficient so dropping 1 column / coefficient

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Response | Factor | num\_df | den\_df | F | P |
| log(Height) | Aphid.Treatment | 1 | 213.8 | 0.00 | 0.965 |
|  | Ant.Mound.Dist | 1 | 9.2 | 0.48 | 0.504 |
|  | Genotype | 9 | 213.3 | 6.42 | 0.000 |
|  | Aphid.Treatment:Ant.Mound.Dist | 1 | 213.4 | 0.38 | 0.537 |
|  | Aphid.Treatment:Genotype | 9 | 213.7 | 1.02 | 0.423 |
|  | Ant.Mound.Dist:Genotype | 9 | 213.5 | 1.47 | 0.159 |
| all.shoot.count | Aphid.Treatment | 1 | 214.8 | 0.76 | 0.384 |
|  | Ant.Mound.Dist | 1 | 9.5 | 0.65 | 0.439 |
|  | Genotype | 9 | 213.7 | 2.70 | 0.005 |
|  | Aphid.Treatment:Ant.Mound.Dist | 1 | 213.9 | 3.85 | 0.051 |
|  | Aphid.Treatment:Genotype | 9 | 214.6 | 1.57 | 0.127 |
|  | Ant.Mound.Dist:Genotype | 9 | 214.1 | 0.75 | 0.662 |
| log(leaf\_WC) | Aphid.Treatment | 1 | 80.1 | 0.56 | 0.457 |
|  | Ant.Mound.Dist | 1 | 10.2 | 0.16 | 0.694 |
|  | Genotype | 9 | 77.3 | 1.31 | 0.247 |
|  | Aphid.Treatment:Ant.Mound.Dist | 1 | 77.3 | 0.36 | 0.550 |
|  | Aphid.Treatment:Genotype | 8 | 76.9 | 0.50 | 0.852 |
|  | Ant.Mound.Dist:Genotype | 9 | 76.2 | 0.79 | 0.623 |
| log(leaf\_trichome.density + 1) | Aphid.Treatment | 1 | 82.8 | 1.25 | 0.267 |
|  | Ant.Mound.Dist | 1 | 12.2 | 0.05 | 0.831 |
|  | Genotype | 9 | 79.4 | 1.43 | 0.188 |
|  | Aphid.Treatment:Ant.Mound.Dist | 1 | 80.1 | 0.57 | 0.452 |
|  | Aphid.Treatment:Genotype | 8 | 80.3 | 1.97 | 0.061 |
|  | Ant.Mound.Dist:Genotype | 9 | 78.7 | 0.60 | 0.796 |

No difference in soil nutrients among wind exposure treatments.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Response | Factor | num\_df | den\_df | F | P |
| Nutrient composition | Wind\_exposure | 1 | 18 | 1.03 | 0.383 |
| Moisture (VWC) | Wind\_exposure | 1 | 9 | 3.82 | 0.082 |