

# Ergot and sterility in bahiagrass: genotypic and environmental effects on seed yield potential

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**Supplementary Table 2. Type III ANOVA tables, REML covariance parameter estimates with standard errors for the different traits measured in the experiment.**

Number of seed-heads per plant (square-root). Type 3 Analysis of Variance							Covariance Parameter Estimates REML		
Source	DF	Sum of Squares	Mean Square	Error DF	F Value	Pr > F	Cov Parm	Estimate	SE
loc	2	46.67839	23.339195	2.9658	0.2	0.8305	loc	0	.
block(loc)	6	157.128231	26.188039	96	5.19	0.0001	block(loc)	0.5661	0.3714
genotype	16	1243.856783	77.741049	17.073	3.92	0.0039	genotype	3.0352	1.4568
loc*genotype	32	159.241527	4.976298	25.161	1.05	0.4531	loc*genotype	0	.
block*genotype(loc)	96	484.213439	5.04389	102	1.22	0.162	block*genotype(loc)	0.1247	0.3549
year	1	2721.034332	2721.034332	2.6561	24.62	0.0208	year	17.7783	25.8484
loc*year	2	191.346886	95.673443	32	25.03	<.0001	loc*year	1.1559	0.9033
genotype*year	16	298.761717	18.672607	32	4.88	<.0001	genotype*year	1.439	0.6844
loc*genotype*year	32	122.333829	3.822932	102	0.92	0.5877	loc*genotype*year	0.143	0.2941
Residual	102	421.885338	4.136131	.	.	.	Residual	3.8058	0.5114

  

Seed-head weight (logarithm). Type 3 Analysis of Variance							Covariance Parameter Estimates REML		
Source	DF	Sum of Squares	Mean Square	Error DF	F Value	Pr > F	Cov Parm	Estimate	SE
loc	2	15.929748	7.964874	2.0853	0.36	0.7359	loc	0	.
block(loc)	6	3.383089	0.563848	98.319	4.64	0.0003	block(loc)	0.01422	0.01025
genotype	16	10.853781	0.678361	17.149	2.07	0.0729	genotype	0.02309	0.01526
loc*genotype	32	4.330622	0.135332	17.775	1.3	0.282	loc*genotype	0.001244	0.006218
block*genotype(loc)	94	11.427739	0.121572	94	1.03	0.4473	block*genotype(loc)	0.00301	0.01164
year	1	23.778797	23.778797	2.0348	1.09	0.4047	year	0.07982	0.2663
loc*year	2	43.49469	21.747345	35.127	214.54	<.0001	loc*year	0.2989	0.2146
genotype*year	16	4.688571	0.293036	33.43	2.9	0.0046	genotype*year	0.01881	0.01133
loc*genotype*year	32	3.22158	0.100674	94	0.85	0.6912	loc*genotype*year	0	.
Residual	94	11.118581	0.118283	.	.	.	Residual	0.1148	0.01445

Severity of infection (square-root). Type 3 Analysis of Variance							Covariance Parameter Estimates REML		
Source	DF	Sum of Squares	Mean Square	Error DF	F Value	Pr > F	Cov Parm	Estimate	SE
loc	2	153.421731	76.710866	1.9902	1.5	0.4006	loc	0.3228	0.9702
block(loc)	6	3.108828	0.518138	97.62	0.53	0.7875	block(loc)	0	.
genotype	16	427.950178	26.746886	15.3	6.85	0.0002	genotype	1.3449	0.56
loc*genotype	32	63.979229	1.999351	26.186	1.21	0.3114	loc*genotype	0.04353	0.1184
block*genotype(loc)	94	92.645454	0.98559	95	1.01	0.4894	block*genotype(loc)	0	.
year	1	47.109622	47.109622	2.1486	0.9	0.4378	year	0	.
loc*year	2	101.926826	50.963413	33.511	31.41	<.0001	loc*year	1.0378	0.8863
genotype*year	16	56.761035	3.547565	32.675	2.17	0.0299	genotype*year	0.2106	0.1545
loc*genotype*year	32	52.73048	1.647828	95	1.68	0.0282	loc*genotype*year	0.2739	0.1603
Residual	95	93.128245	0.980297	.	.	.	Residual	0.9715	0.09856

Total seed yield per plant (logarithm). Type 3 Analysis of Variance							Covariance Parameter Estimates REML		
Source	DF	Sum of Squares	Mean Square	Error DF	F Value	Pr > F	Cov Parm	Estimate	SE
year	1	72.840777	72.840777	1.9571	8.26	0.1054	loc	0.05552	0.1964
loc	2	29.241048	14.620524	2.4879	1.45	0.3826	block(loc)	0.03662	0.02777
block(loc)	6	8.844301	1.47405	98.933	4.14	0.0009	genotype	0.4298	0.1657
genotype	16	128.56679	8.035424	6.6487	15.43	0.0008	loc*genotype	0.011	0.03553
loc*genotype	32	19.894476	0.621702	22.85	1.06	0.449	block*genotype(loc)	0	.
block*genotype(loc)	94	33.382782	0.355136	94	0.9	0.6951	year	0.4689	0.7606
loc*year	2	17.908348	8.954174	33.67	14.54	<.0001	loc*year	0.1885	0.2007
genotype*year	16	8.373541	0.523346	32.766	0.84	0.632	genotype*year	0	.
loc*genotype*year	32	19.995121	0.624848	94	1.58	0.0461	loc*genotype*year	0.07699	0.04409
Residual	94	37.099712	0.394678	.	.	.	Residual	0.3754	0.03864

% Full seeds (arcsine-square-root). Type 3 Analysis of Variance							Covariance Parameter Estimates REML		
Source	DF	Sum of Squares	Mean Square	Error DF	F Value	Pr > F	Cov Parm	Estimate	SE
loc	1	4.030305	4.030305	9.8943	80.38	<.0001	loc	0.08208	0.1173
block(loc)	4	0.101144	0.025286	62	1.88	0.125	block(loc)	0.000663	0.001076
genotype	16	0.400187	0.025012	16	0.65	0.8	genotype	0	.
loc*genotype	16	0.614572	0.038411	62	2.86	0.0016	loc*genotype	0.005895	0.002825
Residual	62	0.833374	0.013442	.	.	.	Residual	0.01361	0.002468

% Empty seeds. Type 3 Analysis of Variance							Covariance Parameter Estimates REML		
Source	DF	Sum of Squares	Mean Square	Error DF	F Value	Pr > F	Cov Parm	Estimate	SE
loc	1	591.138636	591.138636	9.1468	1.52	0.2478	loc	4.0259	17.124
block(loc)	4	919.053556	229.763389	62	3.4	0.0142	block(loc)	9.7819	9.7562
genotype	16	4481.04556	280.065347	16	1.24	0.3382	genotype	8.7431	21.5382
loc*genotype	16	3624.222781	226.513924	62	3.35	0.0003	loc*genotype	54.216	27.5597
Residual	62	4195.969777	67.676932	.	.	.	Residual	67.4669	12.0814

% Ergot sclerotia. Type 3 Analysis of Variance						
Source	DF	Sum of Squares	Mean Square	Error DF	F Value	Pr > F
loc	1	18691	18691	6.8026	42.08	0.0004
block(loc)	4	1303.222378	325.805594	62	4.24	0.0042
genotype	16	5221.164918	326.322807	16	1.67	0.1584
loc*genotype	16	3131.796686	195.737293	62	2.55	0.0044
Residual	62	4762.467622	76.813994	.	.	.

Covariance Parameter Estimates REML		
Cov Parm	Estimate	SE
loc	376.65	545.74
block(loc)	15.95	14.6753
genotype	21.2132	22.4039
loc*genotype	39.7874	24.6968
Residual	77.6739	14.0948

Total seeds TSW. Type 3 Analysis of Variance						
Source	DF	Sum of Squares	Mean Square	Error DF	F Value	Pr > F
loc	1	34.67602	34.67602	9.3847	177.09	<.0001
block(loc)	4	0.420581	0.105145	62	2	0.1054
genotype	16	4.906089	0.306631	16	2.13	0.0699
loc*genotype	16	2.297941	0.143621	62	2.73	0.0024
Residual	62	3.257752	0.052544	.	.	.

Covariance Parameter Estimates REML		
Cov Parm	Estimate	SE
loc	0.6973	0.9916
block(loc)	0.003	0.004413
genotype	0.02744	0.02014
loc*genotype	0.03065	0.01741
Residual	0.05252	0.009425

Full seeds TSW. Type 3 Analysis of Variance						
Source	DF	Sum of Squares	Mean Square	Error DF	F Value	Pr > F
loc	1	16.853841	16.853841	9.0384	388.04	<.0001
block(loc)	4	0.047718	0.01193	62	0.59	0.6711
genotype	16	12.596863	0.787304	16	15.18	<.0001
loc*genotype	16	0.829811	0.051863	62	2.57	0.0042
Residual	62	1.253465	0.020217	.	.	.

Covariance Parameter Estimates REML		
Cov Parm	Estimate	SE
loc	0.3384	0.4799
block(loc)	0	.
genotype	0.1229	0.04663
loc*genotype	0.01084	0.006263
Residual	0.01968	0.003418

Empty seeds TSW. Type 3 Analysis of Variance						
Source	DF	Sum of Squares	Mean Square	Error DF	F Value	Pr > F
loc	1	3.115726	3.115726	6.2119	91.07	<.0001
block(loc)	4	0.097084	0.024271	62	1.65	0.1725
genotype	16	3.23469	0.202168	16	8.19	<.0001
loc*genotype	16	0.394839	0.024677	62	1.68	0.0749
Residual	62	0.910783	0.01469	.	.	.

Covariance Parameter Estimates REML		
Cov Parm	Estimate	SE
loc	0.06253	0.08942
block(loc)	0.000593	0.00104
genotype	0.02962	0.01204
loc*genotype	0.003468	0.003081
Residual	0.01462	0.002616

Ergot sclerotia TSW. Type 3 Analysis of Variance						
Source	DF	Sum of Squares	Mean Square	Error DF	F Value	Pr > F
loc	1	33.04617	33.04617	7.2223	64.11	<.0001
block(loc)	4	1.454217	0.363554	62	4.08	0.0053
genotype	16	10.381651	0.648853	16	2.68	0.0282
loc*genotype	16	3.867505	0.241719	62	2.71	0.0026
Residual	62	5.525683	0.089124	.	.	.

Covariance Parameter Estimates REML		
Cov Parm	Estimate	SE
loc	0.6547	0.9408
block(loc)	0.0172	0.01604
genotype	0.06994	0.04179
loc*genotype	0.05172	0.02934
Residual	0.08891	0.01593