

STATISTICAL ANALYSES OF SINGLE GENOTYPES

In this additional file, ANOVA statistical analyses and Tukey test on nutraceutical and antioxidant values, performed separately for each year using the data of the single genotypes employed, are presented.

The genotypes employed were:

- a) 3 eggplant allied species (*S. integrifolium*, *S. aethiopicum*, *S. sodomaeum*);
- b) 3 eggplant recurrent genotypes (1F5(9), Tal 1/1 and CCR3);
- c) 3 groups of advanced introgression lines (ILs).

Traits analyzed over two subsequent years (2005 and 2006) were:

- 1) soluble refractometric residue (SRR, % on dw);
- 2) solasonine (mg/100g dw);
- 3) solamargine (mg/100g dw);
- 4) chlorogenic acid (CA, mmol/100g dw);
- 5) delphinidin 3-rutinoside (D3R, mg/100g peel dw);
- 6) polyphenoloxidase (PPO, U/100mg dw) activity;
- 7) total phenols (TP, mmol CA eq./100g dw);
- 8) superoxide anion (mmol CA eq./100g dw);
- 9) hydroxyl radical (mmol CA eq./100g dw).

For Tukey test values, single genotypes are evidenced as follows:

Solanum integrifolium (S.int.)

Solanum aethiopicum (S.aeth.)

Solanum sodomaeum (S.sod.)

Eggplant recurrent genotypes

ILs from *S. integrifolium*

ILs from *S. aethiopicum*

ILs from *S. sodomaeum*

1a) Soluble refractometric residue (SRR) - 2005

Summary of Fit

RSquare 0,986881
 RSquare Adj 0,980482
 Root Mean Square Error 0,816857
 Mean of Response 46,69634
 Observations (or Sum Wgts) 123

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	40	4116,0809	102,902	154,2167
Error	82	54,7150	0,667	Prob > F
C. Total	122	4170,7959		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	40	40	4116,0809	154,2167	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean
41 A	54,700000
187 A	54,150000
1F5(9) A B	53,800000
182 A B C	52,250000
54 B C D	51,100000
131 C D E	51,000000
214 C D E	50,950000
199 C D E	50,900000
255 C D E	50,850000
202 C D E	50,600000
219 C D E	50,550000
CCR3 C D E F	50,450000
99 C D E F G	50,300000
191 C D E F G	50,150000
21 C D E F G	50,150000
220 TO C D E F G	50,150000
Tal 1/1 D E F G H	49,350000
262 D E F G H I	48,900000
181 E F G H I J	48,350000
176 F G H I J K	47,750000
87 G H I J K L	47,600000
286 H I J K L M	47,350000
197 H I J K L M	47,150000
23 H I J K L M	47,150000
213 H I J K L M N	46,850000
209 I J K L M N O	46,200000
238 J K L M N O	46,050000
132 J K L M N O	45,800000
15 J K L M N O	45,700000
194 K L M N O	45,450000
190 L M N O P	45,000000
186 M N O P	44,600000
28 N O P	44,250000
19 O P	43,600000
192 P Q	42,650000
183 P Q	42,600000
S. aeth Q R	39,950000
84 R	39,250000
S. sod. S	31,250000
130 S	31,000000
S. int. S	28,700000

Levels not connected by same letter are significantly different

1b) Soluble refractometric residue (SRR) - 2006

Summary of Fit

RSquare	0,993632
RSquare Adj	0,990561
Root Mean Square Error	0,681844
Mean of Response	44,65179
Observations (or Sum Wgts)	84

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	27	4062,2772	150,455	323,6207
Error	56	26,0350	0,465	Prob > F
C. Total	83	4088,3122		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	27	27	4062,2772	323,6207	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean
393	53,000000
475	52,500000
214	52,450000
282	51,850000
352	51,350000
351	51,150000
1F5(9)	50,700000
237	50,400000
Tal1/1	50,350000
283	49,850000
183	48,350000
390	47,500000
212	46,850000
190	45,700000
169	45,550000
187	44,650000
238	44,400000
197	43,850000
CCR3	43,700000
215	43,600000
170	43,050000
167	40,750000
S. aeth.	37,650000
363	35,100000
494	32,900000
S. int	32,400000
248	32,050000
S. sod.	28,600000

Levels not connected by same letter are significantly different

2a) Solasonine - 2005

Summary of Fit

RSquare 0,998176
 RSquare Adj 0,997286
 Root Mean Square Error 5,049646
 Mean of Response 29,16886
 Observations (or Sum Wgts) 123

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	40	1144207,3	28605,2	1121,819
Error	82	2090,9	25,5	Prob > F
C. Total	122	1146298,2		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	40	40	1144207,3	1121,819	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean
S. sod. A	610,50000
S. aeth B	178,47000
S. int. C	68,05333
182 C	59,14333
84 D	33,66333
99 D E	28,60000
CCR3 E F	12,45000
Tal 1/1 F	10,96000
191 F	10,29000
219 F	10,23333
130 F	9,77000
23 F	9,73333
1F5(9) F	9,21000
199 F	8,65000
255 F	8,58333
19 F	8,20333
220 TO F	7,85000
28 F	7,68000
21 F	7,62333
214 F	7,57000
262 F	7,46000
181 F	6,92000
190 F	6,90000
209 F	6,59667
194 F	5,93000
213 F	5,16000
15 F	4,81000
186 F	4,33000
286 F	4,05333
54 F	3,90667
87 F	3,83000
197 F	3,80000
183 F	3,48000
176 F	3,26000
131 F	3,21333
192 F	3,12000
238 F	2,87000
202 F	2,71333
132 F	2,70000
41 F	1,89000
187 F	1,74333

Levels not connected by same letter are significantly different

2b) Solasonine - 2006

Summary of Fit

RSquare	0,999287
RSquare Adj	0,998943
Root Mean Square Error	4,184751
Mean of Response	42,56414
Observations (or Sum Wgts)	84

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	27	1373701,7	50877,8	2905,29
Error	56	980,7	17,5	Prob > F
C. Total	83	1374682,4		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	27	27	1373701,7	2905,29	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean
S. sod. A	690,4913
S. int B	96,1820
S. aeth. B	91,3333
352 B	85,8300
494 C	65,7000
167 D	26,4419
238 D E	23,8407
363 D E F	19,8320
214 D E F G	14,7773
237 E F G H	12,7713
1F5(9) E F G H	10,7133
475 F G H	9,6800
212 F G H	9,4600
197 F G H	8,3000
183 F G H	8,0800
283 F G H	6,7000
215 G H	5,6500
390 G H	4,5327
393 G H	1,4800
169 H	0,0000
170 H	0,0000
248 H	0,0000
282 H	0,0000
351 H	0,0000
187 H	0,0000
190 H	0,0000
Tal1/1 H	-0,0000
CCR3 H	-0,0000

Levels not connected by same letter are significantly different

3a) Solamargine - 2005

Summary of Fit

RSquare 0,999118
 RSquare Adj 0,998688
 Root Mean Square Error 4,269969
 Mean of Response 41,57301
 Observations (or Sum Wgts) 123

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	40	1693321,8	42333,0	2321,828
Error	82	1495,1	18,2	Prob > F
C. Total	122	1694816,8		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	40	40	1693321,8	2321,828	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean
S. sod. A	769,57000
S. aeth B	107,16333
182 C	92,31000
S. int. C	80,89000
191 D	57,69333
190 E	38,77333
197 E F	33,72000
99 E F	31,23000
194 E F G	31,17333
1F5(9) E F G H	29,94000
183 E F G H I	27,58333
54 E F G H I	27,41000
Tal 1/1 E F G H I	27,25000
132 F G H I J	23,07000
209 F G H I J	23,07000
CCR3 F G H I J	22,92333
181 F G H I J K	22,74333
23 F G H I J K L	20,91000
255 F G H I J K L	20,83333
84 G H I J K L M	17,10000
262 H I J K L M N	16,16000
219 H I J K L M N	16,03333
28 I J K L M N	14,36000
220 TO I J K L M N	14,14000
186 J K L M N	12,53000
87 J K L M N	12,44000
213 J K L M N	10,43000
15 J K L M N	10,17000
192 J K L M N	10,15000
286 J K L M N	10,09000
202 K L M N	8,72333
176 L M N	8,54000
238 L M N	8,40000
187 L M N	8,27000
19 L M N	7,33000
199 L M N	7,30000
21 L M N	6,95333
130 M N	6,04000
41 M N	5,09333
214 M N	3,43000
131 N	2,55333

Levels not connected by same letter are significantly different

3b) Solamargine - 2006

Summary of Fit

RSquare	0,997059
RSquare Adj	0,995641
Root Mean Square Error	2,733941
Mean of Response	30,10594
Observations (or Sum Wgts)	84

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	27	141887,17	5255,08	703,0739
Error	56	418,57	7,47	Prob > F
C. Total	83	142305,74		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	27	27	141887,17	703,0739	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean
S. sod.	A 185,0333
S. int	B 102,1227
494	B 99,6200
352	C 84,6133
167	D 54,7433
S. aeth.	E 44,7469
475	F 34,7200
187	F G 32,0100
237	F G 28,8700
190	G H 24,8327
1F5(9)	G H 23,4400
283	H I 18,8600
238	H I J 18,5127
Tal1/1	H I J 18,3773
170	I J K 14,4600
363	I J K L 11,5000
169	J K L M 10,0900
351	K L M 9,1107
197	K L M N 6,1100
390	K L M N 6,0000
214	L M N 5,2300
215	L M N 3,8133
183	L M N 3,2900
212	M N 2,6200
282	N 0,2400
393	N 0,0000
248	N 0,0000
CCR3	N -0,0000

Levels not connected by same letter are significantly different

4a) Chlorogenic acid (CA) - 2005

Summary of Fit

RSquare 0,998316
 RSquare Adj 0,997494
 Root Mean Square Error 0,069461
 Mean of Response 2,818088
 Observations (or Sum Wgts) 123

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	40	234,51272	5,86282	1215,129
Error	82	0,39564	0,00482	Prob > F
C. Total	122	234,90836		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	40	40	234,51272	1215,129	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean
CCR3 A	6,7621000
S. sod. B	6,2157900
197 C	5,7840133
186 D	4,5928633
192 D	4,5900100
190 D	4,5850333
187 E	4,1516733
84 F	3,9063333
15 G	3,5452633
176 G	3,5310733
182 H	3,2192300
1F5(9) H	3,1872200
183 H	3,1757500
Tal 1/1 H I	3,1565433
130 I J	2,9409233
262 J	2,8514000
54 J	2,8339600
132 J K	2,8056300
214 J K L	2,7930633
238 J K L	2,7569333
209 J K L	2,7376633
199 K L M	2,6015033
191 K L M	2,5816400
286 L M	2,5672533
181 M N	2,4110300
99 N	2,2874300
28 O	2,0201700
131 O	2,0154500
213 O	1,9894800
194 O	1,9435333
21 P	1,7088533
23 P	1,7024300
202 P	1,6932933
41 P	1,6794200
19 P	1,6415500
87 P	1,6215333
219 Q	1,3472100
S. int. Q	1,2842300
220 TO R	0,9023133
255 R	0,8263500
S. aeth S	0,5944833

Levels not connected by same letter are significantly different

4b) Chlorogenic acid (CA) - 2006

Summary of Fit

RSquare	0,99907
RSquare Adj	0,998622
Root Mean Square Error	0,071176
Mean of Response	3,377099
Observations (or Sum Wgts)	84

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	27	304,90647	11,2928	2229,158
Error	56	0,28369	0,0051	Prob > F
C. Total	83	305,19017		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	27	27	304,90647	2229,158	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean
S. sod	9,2183305
363	6,3395123
1F5(9)	5,9189802
351	5,7675121
390	5,0708587
248	4,7128883
Tal1/1	3,9456722
CCR3	3,8675885
282	3,8553549
169	3,7819739
170	3,7669221
212	3,7208230
393	3,4207116
215	3,0768525
183	3,0749714
187	3,0302831
214	2,9249141
283	2,8788183
197	2,8632929
475	2,4869789
352	2,4220626
237	2,3947806
238	2,3924293
190	1,2512505
167	1,1853936
494	0,5216687
S. aeth.	0,4520497
S. int	0,2159109

Levels not connected by same letter are significantly different

5a) Delphinidin 3-rutinoside (D3R) - 2005

Summary of Fit

RSquare 0,999932
 RSquare Adj 0,999898
 Root Mean Square Error 7,784698
 Mean of Response 503,5402
 Observations (or Sum Wgts) 123

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Model	40	72590403	1814760	29945,79	
Error	82	4969	61		
C. Total	122	72595372			<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	40	40	72590403	29945,79	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean
CCR3 A	406,6533
214 B	295,1600
Tal 1/1 C	113,2233
209 C	112,0823
220 TO D	103,7193
87 E	88,6643
1F5(9) F	81,6293
23 F	80,4203
286 G	74,7960
219 H	72,1590
130 I	64,7730
176 I	62,9423
28 J	51,0423
15 J	49,5293
182 K	44,9460
21 K	44,4520
262 L	40,8203
19 M	33,2563
199 M	31,7643
213 M	31,7370
190 N	30,0540
194 N	29,0263
255 O	19,2243
202 P	19,0140
192 P	16,7383
183 P	15,3283
99 Q	14,9853
238 Q	12,8193
181 S	7,6033
187 S	5,1453
132 T	4,2183
41 T	3,4683
197 T	3,1193
186 U	0,000
191 U	0,000
131 U	-0,000
S. int. U	-0,000
S. sod. U	-0,000
84 U	-0,000
S. aeth U	-0,000
54 U	-0,000

Levels not connected by same letter are significantly different

5b) Delphinidin 3-rutinoside (D3R) - 2006

Summary of Fit

RSquare	0,999983
RSquare Adj	0,999974
Root Mean Square Error	11,81656
Mean of Response	3001,956
Observations (or Sum Wgts)	84

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	27	447793383	16584940	118776,9
Error	56	7819	139,63105	Prob > F
C. Total	83	447801202		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	27	27	447793383	118776,9	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean
1F5(9) A	811,80200
363 B	752,76233
238 C	568,69900
283 D	553,04233
237 E	521,48933
214 F	509,22433
187 G	473,94733
Tal1/1 H	461,13500
190 I	457,06233
CCR3 J	394,21533
183 K	360,52700
282 L	335,88633
248 M	329,49200
197 N	313,30900
352 O	309,47300
212 P	300,16533
215 Q	257,11100
393 R	237,49000
351 S	212,56400
390 T	112,64500
167 T	110,47533
169 U	7,78833
494 U	7,54800
475 U	5,83100
170 V	1,79083
S. int V	0,0000
S. aeth. V	0,0000
S. sod. V	0,0000

Levels not connected by same letter are significantly different

6a) Polyphenoloxidase (PPO) - 2005

Summary of Fit

RSquare 0,983097
 RSquare Adj 0,974851
 Root Mean Square Error 2,755104
 Mean of Response 28,66732
 Observations (or Sum Wgts) 123

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	40	36200,795	905,020	119,2291
Error	82	622,429	7,591	Prob > F
C. Total	122	36823,224		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	40	40	36200,795	119,2291	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean									
Tal 1/1	A									76,060000
190	B									61,513333
176	B									57,990000
CCR3	B	C								55,490000
192	B	C	D							53,933333
262	B	C	D							52,840000
23		C	D	E						48,213333
130			D	E						45,533333
286			D	E						45,260000
132				E						42,220000
213				E	F					40,493333
182					F	G				32,783333
84					F	G	H			32,130000
181						G	H	I		30,983333
41						G	H	I	J	30,353333
183						G	H	I	J	29,903333
186						G	H	I	J	29,510000
202						G	H	I	J	27,873333
54						G	H	I	J	27,683333
194						G	H	I	J	26,823333
197						G	H	I	J	24,270000
87							H	I	J	23,263333
220 TO								I	J	22,950000
199									J	21,403333
214									K	20,710000
131									K	20,570000
21									K	20,533333
255									L	20,293333
187									L	20,173333
99									L	19,703333
1F5(9)									L	19,043333
238									L	18,873333
15									M	17,953333
191									N	14,203333
209									O	10,280000
28									P	9,403333
19									Q	6,980000
219									Q	6,480000
S. aeth									R	5,030000
S. sod.									R	3,040000
S. int.									R	2,613333

Levels not connected by same letter are significantly different

6b) Polyphenoloxidase (PPO) - 2006

Summary of Fit

RSquare	0,963391
RSquare Adj	0,94574
Root Mean Square Error	4,519315
Mean of Response	25,38857
Observations (or Sum Wgts)	84

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	27	30098,297	1114,75	54,5799
Error	56	1143,756	20,42	Prob > F
C. Total	83	31242,053		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	27	27	30098,297	54,5799	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean									
282	A									65,080000
Tal1/1	A	B								63,260000
1F5(9)	A	B								61,850000
214	A	B	C							50,873333
475		B	C							50,600000
283			C	D						43,303333
212			C	D	E					38,063333
197				D	E	F				33,500000
352				D	E	F				33,383333
351				D	E	F				31,723333
237				D	E	F				31,000000
238					E	F	G			24,640000
494					E	F	G			23,880000
183						F	G	H		21,120000
393							G	H	I	16,450000
215							G	H	I	14,960000
190							G	H	I	14,673333
CCR3							G	H	I	13,623333
169							G	H	I	13,323333
390							G	H	I	11,930000
363							G	H	I	11,860000
S. aeth.							G	H	I	11,226667
167							G	H	I	11,003333
187								H	I	8,080000
S. int									I	5,150000
170									I	4,710000
248									J	1,100000
S. sod.									K	0,513333

Levels not connected by same letter are significantly different

7a) Total Phenols (TP) - 2005

Summary of Fit

RSquare	0,990175
RSquare Adj	0,985382
Root Mean Square Error	0,236084
Mean of Response	5,293372
Observations (or Sum Wgts)	123

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	40	460,59419	11,5149	206,5968
Error	82	4,57034	0,0557	Prob > F
C. Total	122	465,16453		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	40	40	460,59419	206,5968	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean
S. sod. A	12,833333
190 B	9,101695
192 C	7,596045
187 C	7,522599
CCR3 C	7,416667
197 C D	7,264124
84 C D E	6,930791
183 D E F	6,528249
186 E F G	6,420904
262 E F G H	6,240113
238 E F G H I	6,216102
99 F G H I	6,141243
54 F G H I	6,128531
176 G H I J	5,718927
194 H I J K	5,522599
132 H I J K	5,518362
15 I J K L	5,418079
209 J K L M	5,268362
23 J K L M	5,254237
182 J K L M	5,180791
213 J K L M N	5,132768
286 K L M N O	4,908192
181 K L M N O P	4,841808
130 L M N O P Q	4,641243
28 M N O P Q	4,632768
1F5(9) M N O P Q	4,535311
191 M N O P Q R	4,511299
Tal 1/1 N O P Q R	4,395480
87 O P Q R	4,333333
199 O P Q R	4,274011
19 O P Q R S	4,155367
214 P Q R S	4,107345
41 Q R S	4,045198
202 Q R S T	3,959040
21 R S T U	3,745763
131 S T U	3,399718
219 T U	3,182203
255 U	3,173729
220 TO U	3,094633
S. aeth V	2,093220
S. int. V	1,644068

Levels not connected by same letter are significantly different

7b) Total Phenols (TP) - 2006

Summary of Fit

RSquare 0,975
 RSquare Adj 0,962947
 Root Mean Square Error 0,361728
 Mean of Response 5,741475
 Observations (or Sum Wgts) 84

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	27	285,77053	10,5841	80,8891
Error	56	7,32743	0,1308	Prob > F
C. Total	83	293,09797		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	27	27	285,77053	80,8891	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean									
S. sod.	A									11,860169
363	B									7,939266
1F5(9)	B									7,898305
214	B C									7,156780
238	B C D									6,871469
170	C D E									6,618644
351	C D E									6,580508
282	C D E F									6,351695
212	C D E F G									6,161017
393	C D E F G									6,155367
283	C D E F G									6,096045
187	D E F G H									5,926554
494	D E F G H I									5,871469
CCR3	D E F G H I									5,833333
183	E F G H I									5,661017
197	E F G H I									5,661017
Tal1/1	E F G H I J									5,559322
352	E F G H I J									5,505650
237	E F G H I J									5,495763
475	F G H I J									5,399718
169	G H I J									5,187853
390	H I J K									4,814972
215	I J K									4,741525
190	J K									4,468927
167	K L									3,872881
248	L M									3,062147
S. int	M N									2,107345
S. aeth.	N									1,902542

Levels not connected by same letter are significantly different

8a) Superoxide anion - 2005

Summary of Fit

RSquare 0,993695
 RSquare Adj 0,990619
 Root Mean Square Error 0,123562
 Mean of Response 3,258455
 Observations (or Sum Wgts) 123

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Model	40	197,31227	4,93281	323,0924	
Error	82	1,25193	0,01527		
C. Total	122	198,56421			<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	40	40	197,31227	323,0924	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean
186 A	6,3200000
262 B	5,4000000
194 B C	5,1300000
192 B C	5,0600000
187 C D	4,9533333
197 C D	4,9333333
190 D E	4,5533333
132 E	4,5233333
131 E F	4,2100000
191 E F G	4,1533333
183 F G	4,0533333
286 F G H	3,9533333
84 F G H	3,9500000
199 G H I	3,7800000
214 H I J	3,5900000
S. sod. I J K	3,5100000
176 I J K	3,4733333
181 I J K	3,4500000
130 I J K	3,4400000
182 I J K L	3,3900000
238 J K L M	3,3633333
209 J K L M	3,3133333
CCR3 K L M N	3,1700000
54 L M N O	3,0300000
Tal 1/1 M N O	2,9600000
213 N O P	2,7833333
87 N O P	2,7833333
99 O P Q	2,7200000
255 O P Q	2,6600000
1F5(9) P Q	2,5500000
219 P Q R	2,4400000
21 Q R	2,3733333
202 R S	2,1100000
23 R S	2,0433333
220 TO S T	1,8700000
15 T U	1,6200000
19 U	1,4500000
41 U	1,4233333
S. aeth U V	1,3233333
S. int. V W	0,9900000
28 W	0,7933333

Levels not connected by same letter are significantly different

8b) Superoxide anion - 2006

Summary of Fit

RSquare	0,958774
RSquare Adj	0,938898
Root Mean Square Error	0,115655
Mean of Response	2,303333
Observations (or Sum Wgts)	84

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	27	17,420800	0,645215	48,2361
Error	56	0,749067	0,013376	Prob > F
C. Total	83	18,169867		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	27	27	17,420800	48,2361	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level	Least Sq Mean									
238	A									2,9800000
S. sod.	A	B								2,8633333
494	A	B								2,8600000
214	A	B								2,8433333
CCR3	A	B	C							2,7533333
363	A	B	C	D						2,7433333
390		B	C	D	E					2,6033333
215		B	C	D	E	F				2,5700000
351		B	C	D	E	F	G			2,5400000
167		B	C	D	E	F	G	H		2,5300000
1F5(9)		B	C	D	E	F	G	H	I	2,5100000
197			C	D	E	F	G	H	I	2,4133333
212			C	D	E	F	G	H	I	2,3933333
282				D	E	F	G	H	I	2,3833333
283				D	E	F	G	H	I	2,3800000
475					E	F	G	H	I	2,3533333
Tal1/1						F	G	H	I	2,2300000
187							G	H	I	2,1933333
393								H	I	2,1700000
190								H	I	2,1633333
352									I	2,1533333
170									J	2,0500000
169									K	2,0000000
183									K	2,0000000
237									K	1,9900000
248									L	1,5100000
S. int									L	1,2233333
S. aeth.									M	1,0900000

Levels not connected by same letter are significantly different

9a) Hydroxyl radical - 2005

Summary of Fit

RSquare 0,98254
 RSquare Adj 0,974023
 Root Mean Square Error 0,747546
 Mean of Response 21,96081
 Observations (or Sum Wgts) 123

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	40	2578,6519	64,4663	115,3606
Error	82	45,8236	0,5588	Prob > F
C. Total	122	2624,4755		<.0001

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	40	40	2578,6519	115,3606	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level											Least Sq Mean															
1F5(9)	A										29,413333															
214	A										29,323333															
219	A										29,203333															
187	A	B									28,220000															
131	A	B	C								27,503333															
21	A	B	C	D							27,220000															
194		B	C	D	E						26,650000															
209		B	C	D	E	F					25,773333															
199			C	D	E	F					25,623333															
23			C	D	E	F	G				25,560000															
186			C	D	E	F	G				25,493333															
181			C	D	E	F	G	H			25,040000															
191				D	E	F	G	H	I		24,770000															
213					E	F	G	H	I	J		24,466667														
Tal 1/1					E	F	G	H	I	J	K		24,183333													
19						F	G	H	I	J	K	L		23,710000												
192						F	G	H	I	J	K	L		23,670000												
220 TO							G	H	I	J	K	L		23,090000												
286								H	I	J	K	L		22,690000												
190									I	J	K	L		22,483333												
41										I	J	K	L		22,483333											
182											J	K	L	M		22,243333										
197											J	K	L	M		22,120000										
238												K	L	M	N		21,830000									
176												K	L	M	N	O		21,730000								
S. aeth													L	M	N	O		21,253333								
202														M	N	O	P		20,000000							
28														M	N	O	P		19,970000							
183														M	N	O	P		19,823333							
130															N	O	P	Q		19,620000						
255																O	P	Q	R		19,330000					
54																	P	Q	R	S		18,473333				
132																		P	Q	R	S		17,773333			
CCR3																			Q	R	S	T		17,223333		
87																				R	S	T		16,973333		
262																					S	T		16,803333		
99																					S	T		16,073333		
15																						T	U		14,790000	
84																						T	U		14,753333	
S. sod.																							U	V		12,610000
S. int.																								V		10,430000

Levels not connected by same letter are significantly different

9b) Hydroxyl radical - 2006

Summary of Fit

RSquare	0,975636
RSquare Adj	0,963889
Root Mean Square Error	1,253723
Mean of Response	34,6106
Observations (or Sum Wgts)	84

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Ratio
Model	27	3524,7225	130,545	83,0536
Error	56	88,0219	1,572	Prob > F
C. Total	83	3612,7445		<.0001

Parameter Estimates

Effect Tests

Source	Nparm	DF	Sum of Squares	F Ratio	Prob > F
genotype	27	27	3524,7225	83,0536	<.0001

genotype

LSMeans Differences Tukey HSD

Alpha=0,050

Level																Least Sq Mean		
393	A															47,020000		
237	A	B														43,940000		
390	A	B														43,823333		
475		B	C													40,760000		
167		B	C	D												40,160000		
CCR3			C	D	E											39,773333		
282			C	D	E	F									39,083333			
190			C	D	E	F	G								37,953333			
1F5(9)			C	D	E	F	G	H							37,790000			
212			C	D	E	F	G	H							37,670000			
S. int			C	D	E	F	G	H							37,580000			
214				D	E	F	G	H							36,660000			
Tal1/1				D	E	F	G	H							36,410000			
170					E	F	G	H	I						36,110000			
283						F	G	H	I	J					35,293333			
S. aeth.						F	G	H	I	J					35,263333			
215							G	H	I	J	K				34,113333			
352								H	I	J	K				33,920000			
238									I	J	K	L			32,210000			
351										J	K	L			31,853333			
187											J	K	L			31,443333		
197												K	L			30,160000		
248													L			29,843333		
183														M			28,603333	
494															M	N	25,383333	
363															M	N	24,983333	
S. sod.																N	23,210000	
169																	O	18,083333

Levels not connected by same letter are significantly different