

RELATIVE FITNESS Model A: mixed model w/PHS structure -variance constrained**The Mixed Procedure**

Model Information	
Data Set	WORK.RELATIVE
Dependent Variable	relfit
Covariance Structure	Variance Components
Subject Effect	Sire(Population)
Estimation Method	REML
Residual Variance Method	Profile
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Satterthwaite

Class Level Information		
Class	Levels	Values
Population	3	Dales Mather pixley
Treatment	3	Nina Nino Normal
Sire	45	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 38 39 40 41 42 43 44 45 47
Dam	3	A B C

Dimensions	
Covariance Parameters	4
Columns in X	4
Columns in Z per Subject	595
Subjects	1
Max Obs per Subject	2959

Number of Observations	
Number of Observations Read	2959
Number of Observations Used	2959
Number of Observations Not Used	0

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
0	1	7841.11474319	
1	2	7774.24056933	0.01094238
2	1	7774.23994564	0.00000114
3	1	7774.23994557	0.00000000

Convergence criteria met but final Hessian is not positive definite.

RELATIVE FITNESS Model A: mixed model w/PHS structure -variance constrained**The Mixed Procedure**

Covariance Parameter Estimates					
Cov Parm	Subject	Estimate	Standard Error	Z Value	Pr > Z
Intercept	Sire(Population)	0.04725	0.01120	4.22	<.0001
Dam	Sire(Population)	0.005098	0.009560	0.53	0.2969
Sire(Population)		0.000920	0	.	.
Residual		0.7738	0.02149	36.01	<.0001

Asymptotic Covariance Matrix of Estimates					
Row	Cov Parm	CovP1	CovP2	CovP3	CovP4
1	Intercept	0.000125	-0.00003		-8.21E-7
2	Dam	-0.00003	0.000091		-0.00006
3	Sire(Population)				
4	Residual	-8.21E-7	-0.00006		0.000462

Fit Statistics	
-2 Res Log Likelihood	7774.2
AIC (Smaller is Better)	7782.2
AICC (Smaller is Better)	7782.3
BIC (Smaller is Better)	7774.2

Type 3 Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
Population	2	114	30.96	<.0001

GLM testing for differences among Populations and Treatments in RELATIVE FITNESS**The GLM Procedure**

Class Level Information		
Class	Levels	Values
Population	3	Dales Mather pixley
Treatment	3	Nina Nino Normal

Number of Observations Read	2959
Number of Observations Used	2959

GLM testing for differences among Populations and Treatments in RELATIVE FITNESS

The GLM Procedure

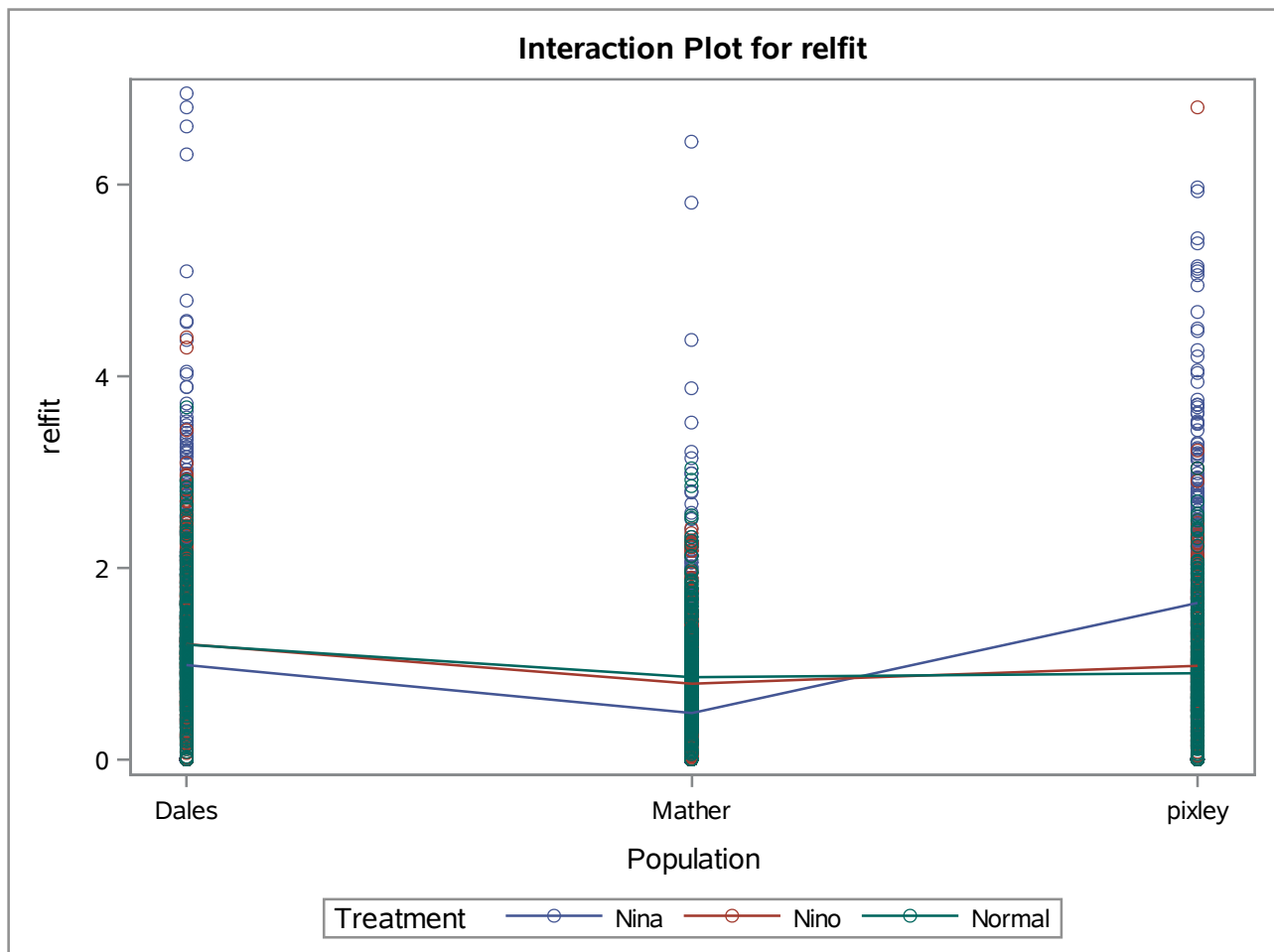
Dependent Variable: relfit

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	263.680182	32.960023	42.11	<.0001
Error	2950	2309.209575	0.782783		
Corrected Total	2958	2572.889757			

R-Square	Coeff Var	Root MSE	relfit Mean
0.102484	88.56481	0.884750	0.998986

Source	DF	Type I SS	Mean Square	F Value	Pr > F
Population	2	133.9020528	66.9510264	85.53	<.0001
Treatment	2	0.0273609	0.0136805	0.02	0.9827
Population*Treatment	4	129.7507684	32.4376921	41.44	<.0001

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Population	2	128.5634987	64.2817493	82.12	<.0001
Treatment	2	1.4290044	0.7145022	0.91	0.4015
Population*Treatment	4	129.7507684	32.4376921	41.44	<.0001

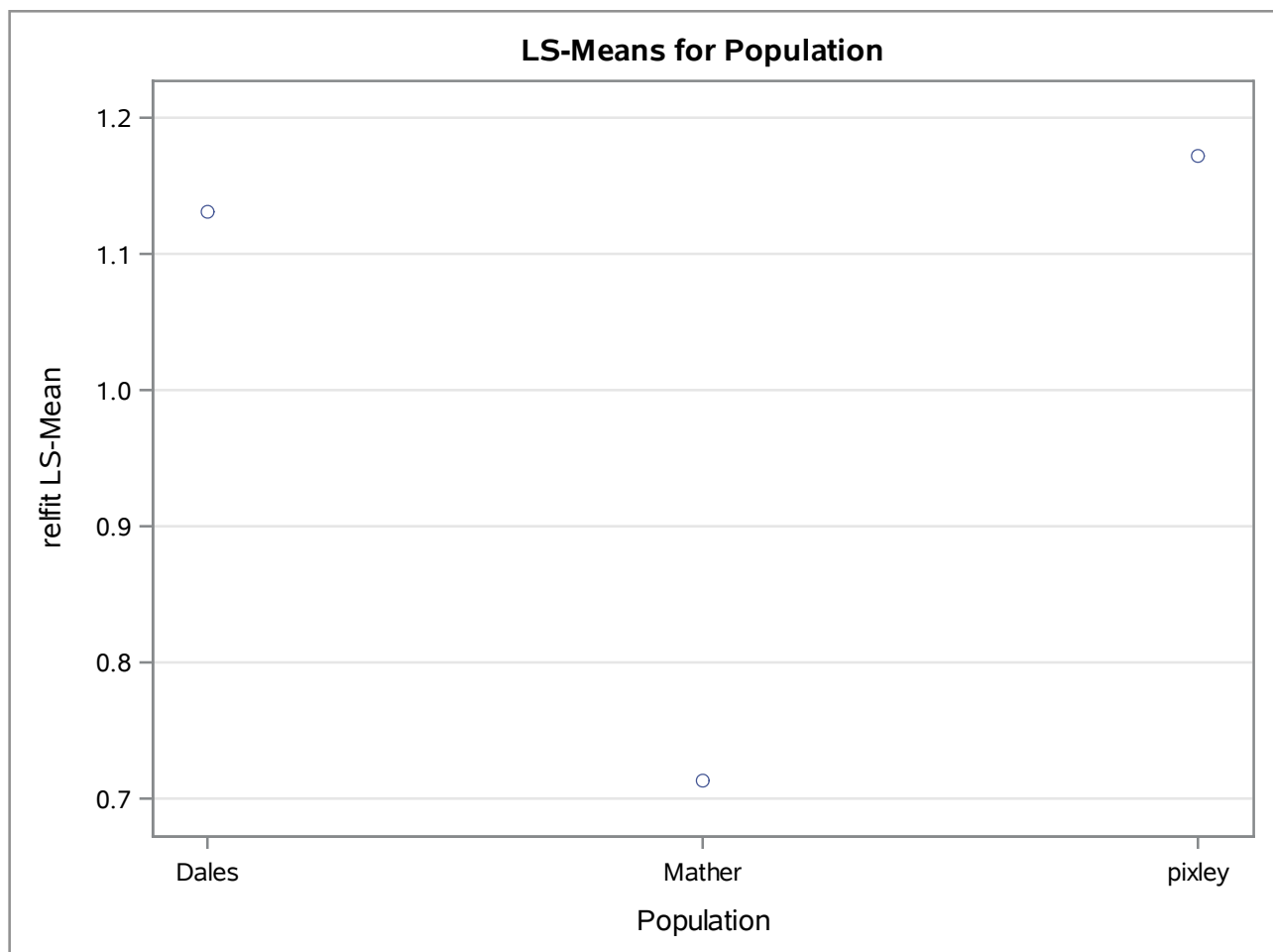


GLM testing for differences among Populations and Treatments in RELATIVE FITNESS

The GLM Procedure
Least Squares Means
Adjustment for Multiple Comparisons: Tukey-Kramer

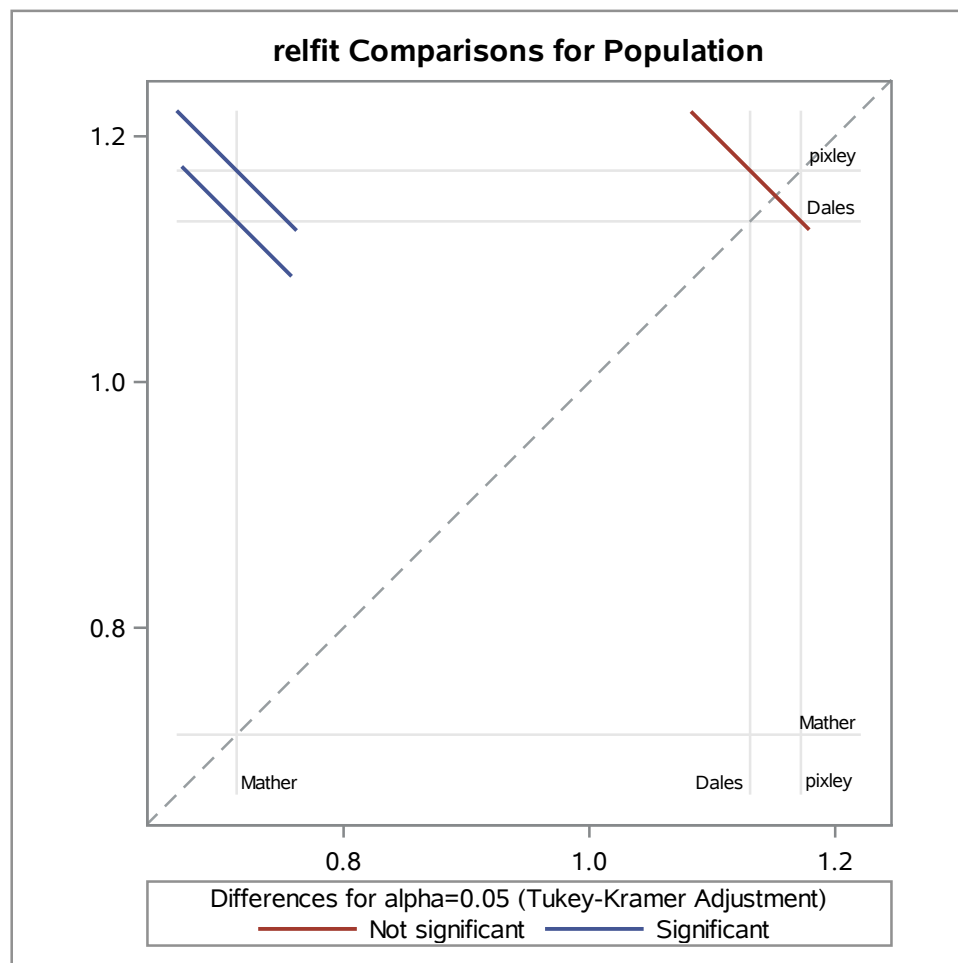
Population	relfit LSMEAN	LSMEAN Number
Dales	1.13076871	1
Mather	0.71298391	2
pixley	1.17209066	3

Least Squares Means for effect Population Pr > t for H0: LSMean(i)=LSMean(j)			
Dependent Variable: relfit			
i/j	1	2	3
1		<.0001	0.5725
2	<.0001		<.0001
3	0.5725	<.0001	



GLM testing for differences among Populations and Treatments in RELATIVE FITNESS

The GLM Procedure
Least Squares Means
Adjustment for Multiple Comparisons: Tukey-Kramer

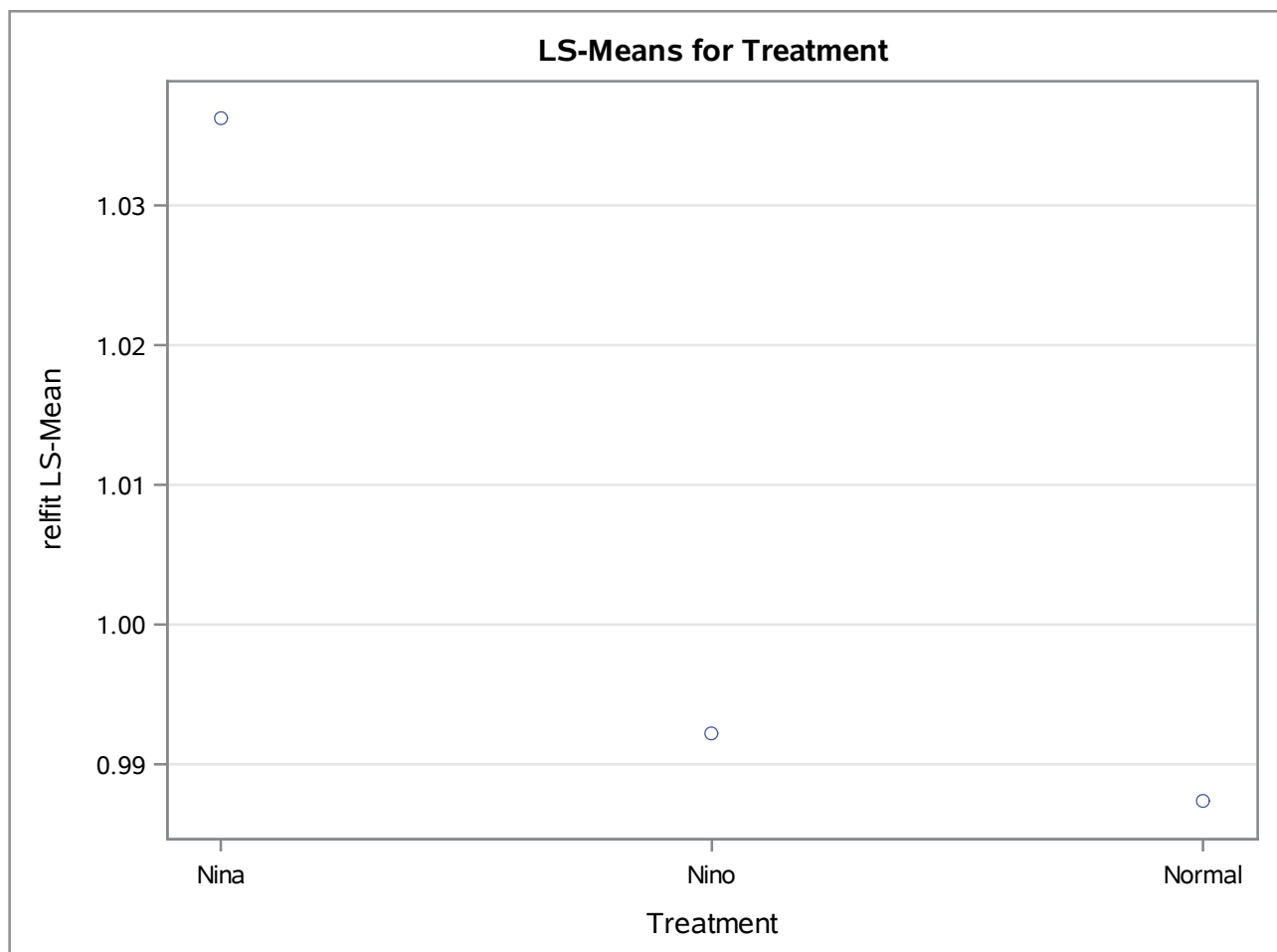


GLM testing for differences among Populations and Treatments in RELATIVE FITNESS

The GLM Procedure Least Squares Means Adjustment for Multiple Comparisons: Tukey-Kramer

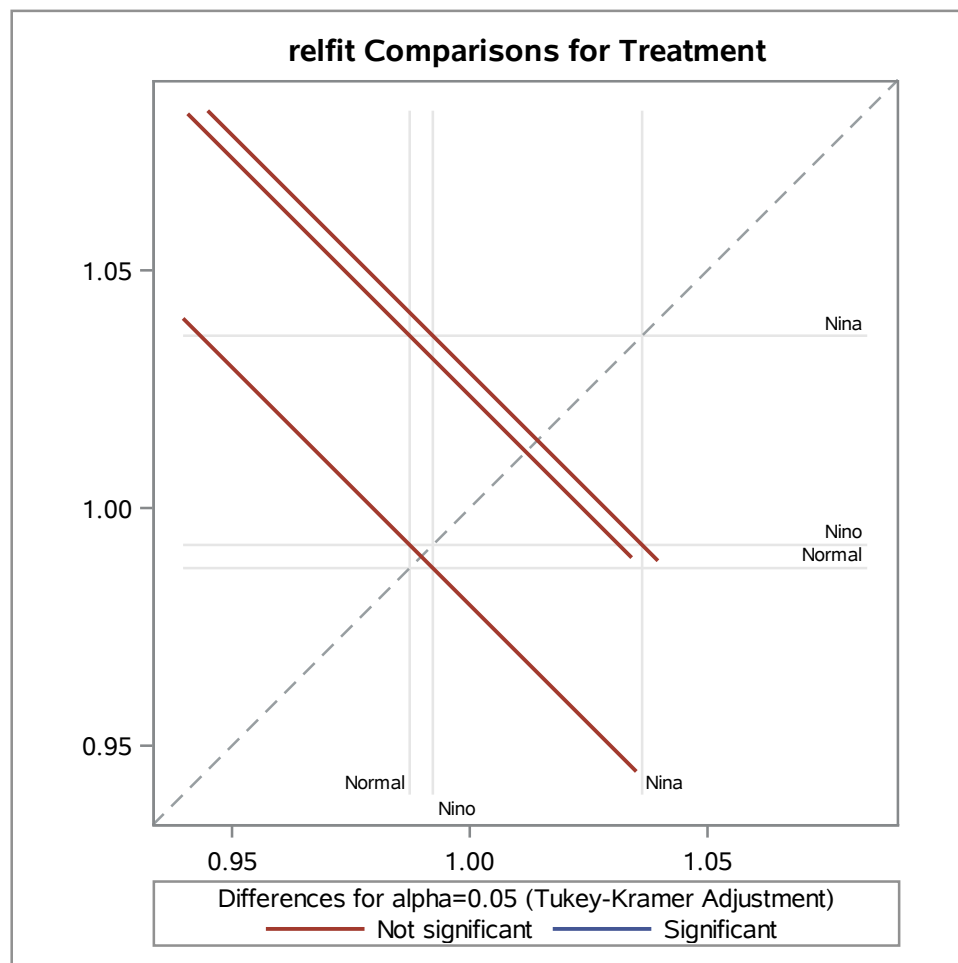
Treatment	relfit LSMEAN	LSMEAN Number
Nina	1.03624864	1
Nino	0.99223125	2
Normal	0.98736339	3

Least Squares Means for effect Treatment Pr > t for H0: LSMean(i)=LSMean(j)			
Dependent Variable: relfit			
i/j	1	2	3
1		0.5203	0.4369
2	0.5203		0.9921
3	0.4369	0.9921	



GLM testing for differences among Populations and Treatments in RELATIVE FITNESS

The GLM Procedure
Least Squares Means
Adjustment for Multiple Comparisons: Tukey-Kramer



GLM testing for differences among Populations and Treatments in RELATIVE FITNESS

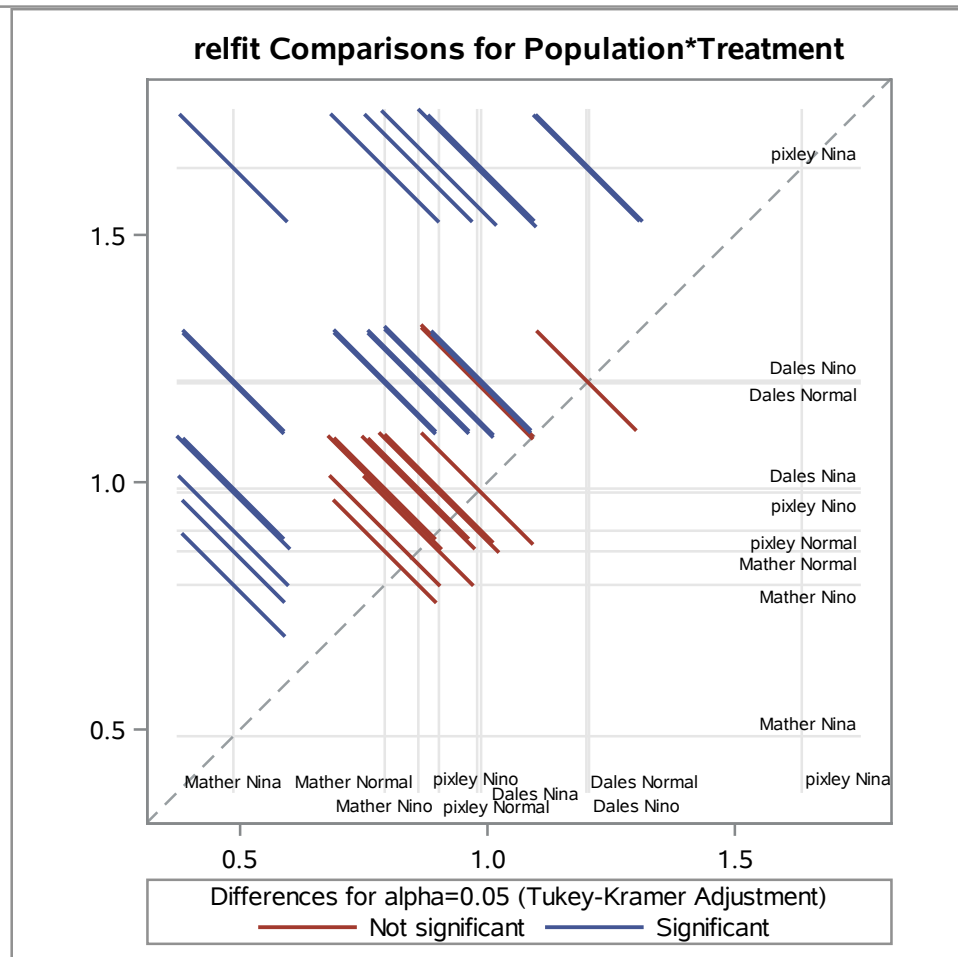
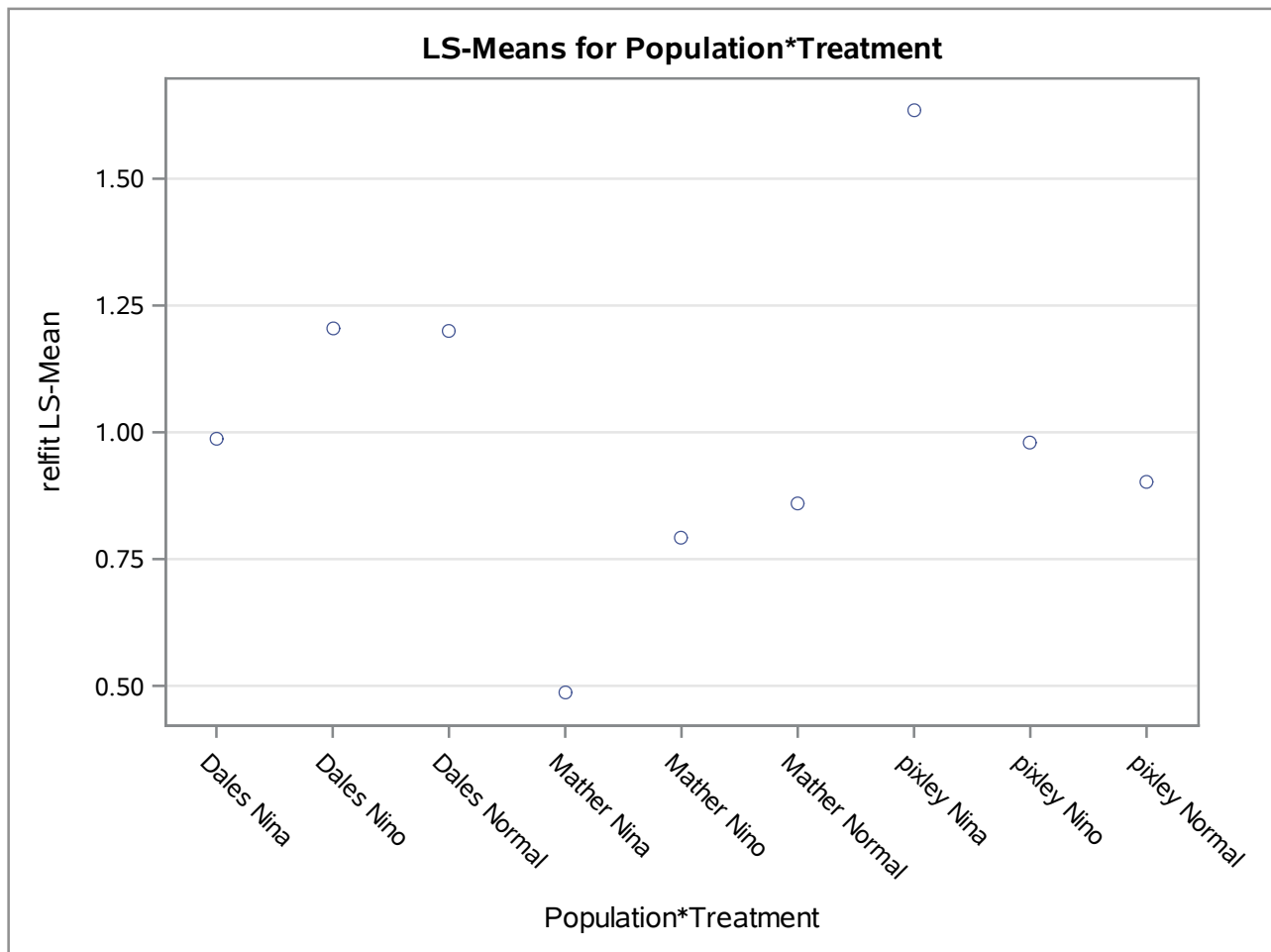
The GLM Procedure
Least Squares Means
Adjustment for Multiple Comparisons: Tukey-Kramer

Population	Treatment	relfit LSMEAN	LSMEAN Number
Dales	Nina	0.98710823	1
Dales	Nino	1.20523703	2
Dales	Normal	1.19996089	3
Mather	Nina	0.48636436	4
Mather	Nino	0.79232454	5
Mather	Normal	0.86026282	6
pixley	Nina	1.63527333	7
pixley	Nino	0.97913219	8
pixley	Normal	0.90186646	9

Least Squares Means for effect Population*Treatment Pr > t for H0: LSMean(i)=LSMean(j) Dependent Variable: relfit									
i/j	1	2	3	4	5	6	7	8	9
1		0.0229	0.0284	<.0001	0.0793	0.5924	<.0001	1.0000	0.9556
2	0.0229		1.0000	<.0001	<.0001	<.0001	<.0001	0.0518	0.0007
3	0.0284	1.0000		<.0001	<.0001	<.0001	<.0001	0.0618	0.0009
4	<.0001	<.0001	<.0001		0.0002	<.0001	<.0001	<.0001	<.0001
5	0.0793	<.0001	<.0001	0.0002		0.9849	<.0001	0.2228	0.8468
6	0.5924	<.0001	<.0001	<.0001	0.9849		<.0001	0.7980	0.9997
7	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001		<.0001	<.0001
8	1.0000	0.0518	0.0618	<.0001	0.2228	0.7980	<.0001		0.9870
9	0.9556	0.0007	0.0009	<.0001	0.8468	0.9997	<.0001	0.9870	

GLM testing for differences among Populations and Treatments in RELATIVE FITNESS

The GLM Procedure
Least Squares Means
Adjustment for Multiple Comparisons: Tukey-Kramer



GLM testing for differences among Populations and Treatments in RELATIVE FITNESS**The MEANS Procedure**

Population=Dales Treatment=Nina

Analysis Variable : inflorwt inflorwt				
N	Mean	Std Dev	Minimum	Maximum
169	6.9090651	3.9045788	0.4630000	21.9890000

Population=Mather Treatment=Nina

Analysis Variable : inflorwt inflorwt				
N	Mean	Std Dev	Minimum	Maximum
102	5.2783627	3.3062763	0.6380000	20.3770000

Model A: mixed model w/PHS structure - variance constrained**The Mixed Procedure**

Model Information	
Data Set	WORK.ONE
Dependent Variable	log_fitness
Covariance Structure	Variance Components
Subject Effect	Sire(Population)
Estimation Method	REML
Residual Variance Method	Profile
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Satterthwaite

Class Level Information		
Class	Levels	Values
Population	3	Dales Mather pixley
Treatment	3	Nina Nino Normal
Sire	45	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 38 39 40 41 42 43 44 45 47
Dam	3	A B C

Dimensions	
Covariance Parameters	4
Columns in X	16
Columns in Z per Subject	9
Subjects	119
Max Obs per Subject	27

Number of Observations	
Number of Observations Read	2959
Number of Observations Used	2959
Number of Observations Not Used	0

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
0	1	10641.02638592	
1	2	10558.60861828	0.00000542
2	1	10558.59448384	0.00000000

Convergence criteria met.

Model A: mixed model w/PHS structure - variance constrained**The Mixed Procedure**

Covariance Parameter Estimates					
Cov Parm	Subject	Estimate	Standard Error	Z Value	Pr > Z
Dam	Sire(Population)	0.07702	0.03018	2.55	0.0054
Treatment	Sire(Population)	0.09094	0.03026	3.01	0.0013
Population	Sire(Population)	0.07850	0.03191	2.46	0.0069
Residual		1.8854	0.05507	34.24	<.0001

Asymptotic Covariance Matrix of Estimates					
Row	Cov Parm	CovP1	CovP2	CovP3	CovP4
1	Dam	0.000911	0.000039	-0.00028	-0.00041
2	Treatment	0.000039	0.000916	-0.00031	-0.00035
3	Population	-0.00028	-0.00031	0.001018	0.000101
4	Residual	-0.00041	-0.00035	0.000101	0.003033

Fit Statistics	
-2 Res Log Likelihood	10558.6
AIC (Smaller is Better)	10566.6
AICC (Smaller is Better)	10566.6
BIC (Smaller is Better)	10577.7

Type 3 Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
Population	2	108	23.11	<.0001
Treatment	2	233	518.05	<.0001
Population*Treatment	4	231	45.77	<.0001

GLM testing for differences among Populations and Treatments in ABSOLUTE FITNESS**The GLM Procedure**

Class Level Information		
Class	Levels	Values
Population	3	Dales Mather pixley
Treatment	3	Nina Nino Normal

Number of Observations Read	2959
Number of Observations Used	2959

GLM testing for differences among Populations and Treatments in ABSOLUTE FITNESS

The GLM Procedure

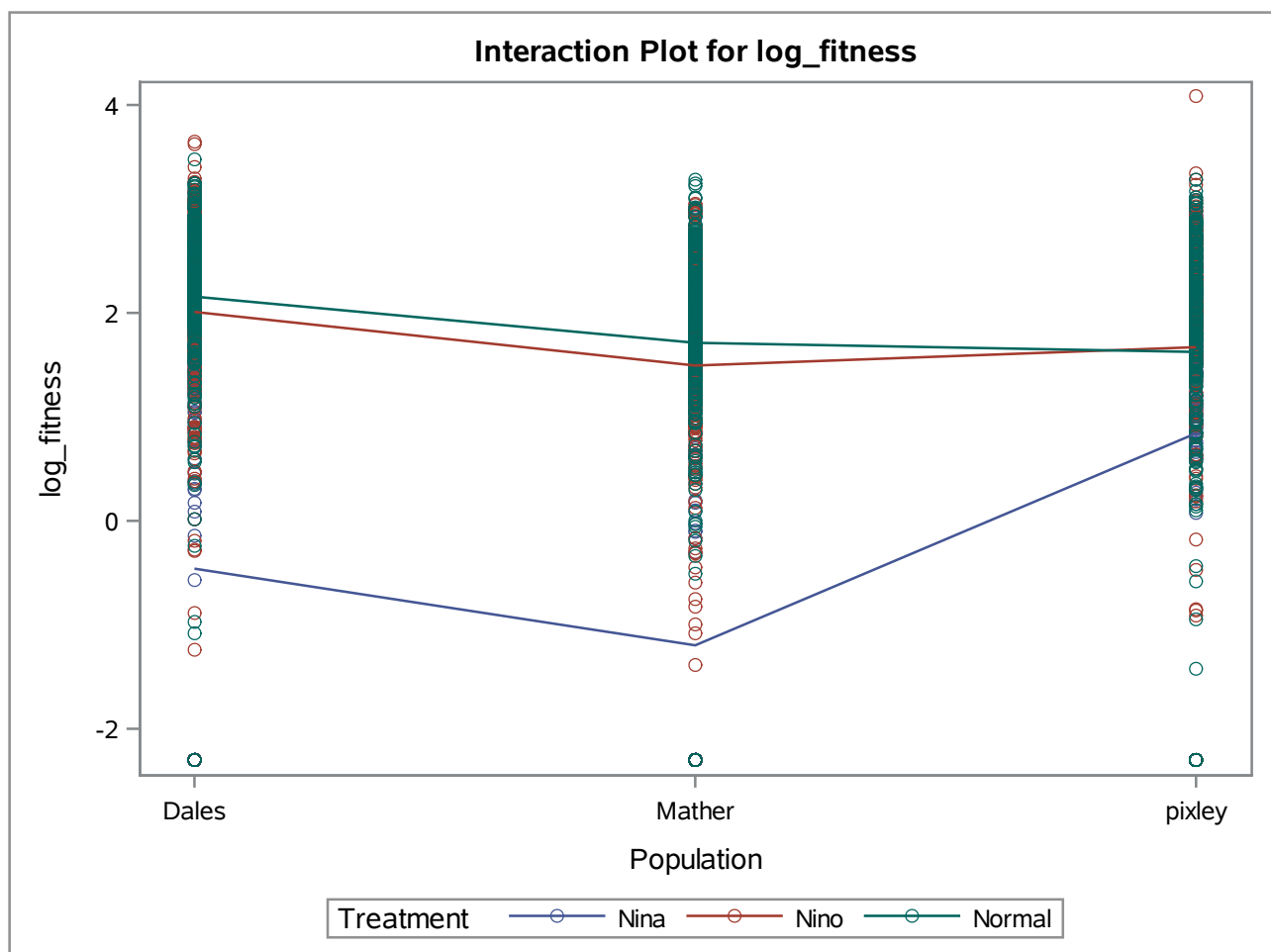
Dependent Variable: log_fitness

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	3830.02537	478.75317	225.78	<.0001
Error	2950	6255.16278	2.12039		
Corrected Total	2958	10085.18815			

R-Square	Coeff Var	Root MSE	log_fitness Mean
0.379767	136.7573	1.456157	1.064775

Source	DF	Type I SS	Mean Square	F Value	Pr > F
Population	2	264.913042	132.456521	62.47	<.0001
Treatment	2	3086.642787	1543.321393	727.85	<.0001
Population*Treatment	4	478.469541	119.617385	56.41	<.0001

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Population	2	273.957766	136.978883	64.60	<.0001
Treatment	2	2761.380869	1380.690434	651.15	<.0001
Population*Treatment	4	478.469541	119.617385	56.41	<.0001

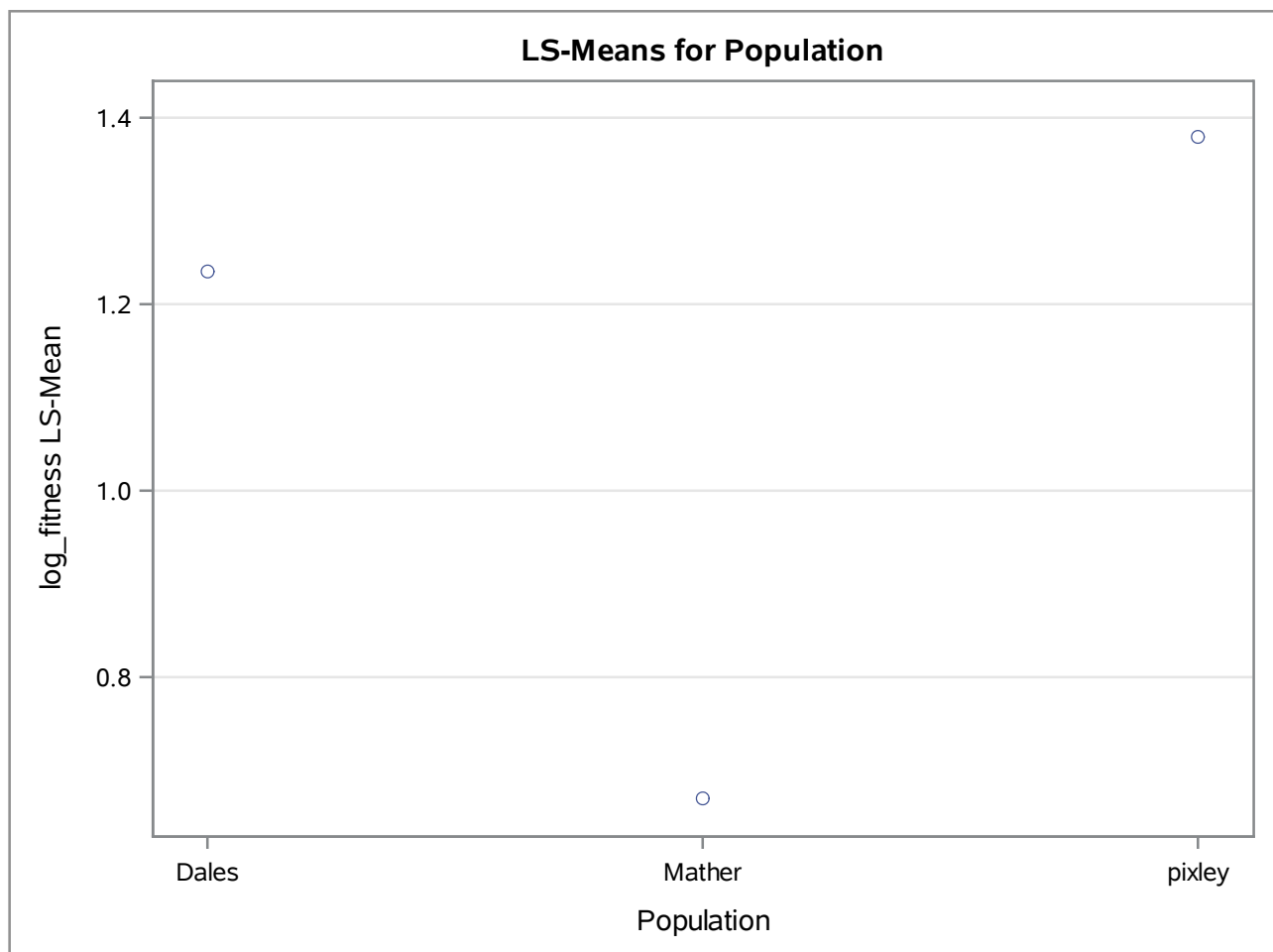


GLM testing for differences among Populations and Treatments in ABSOLUTE FITNESS

The GLM Procedure Least Squares Means Adjustment for Multiple Comparisons: Tukey-Kramer

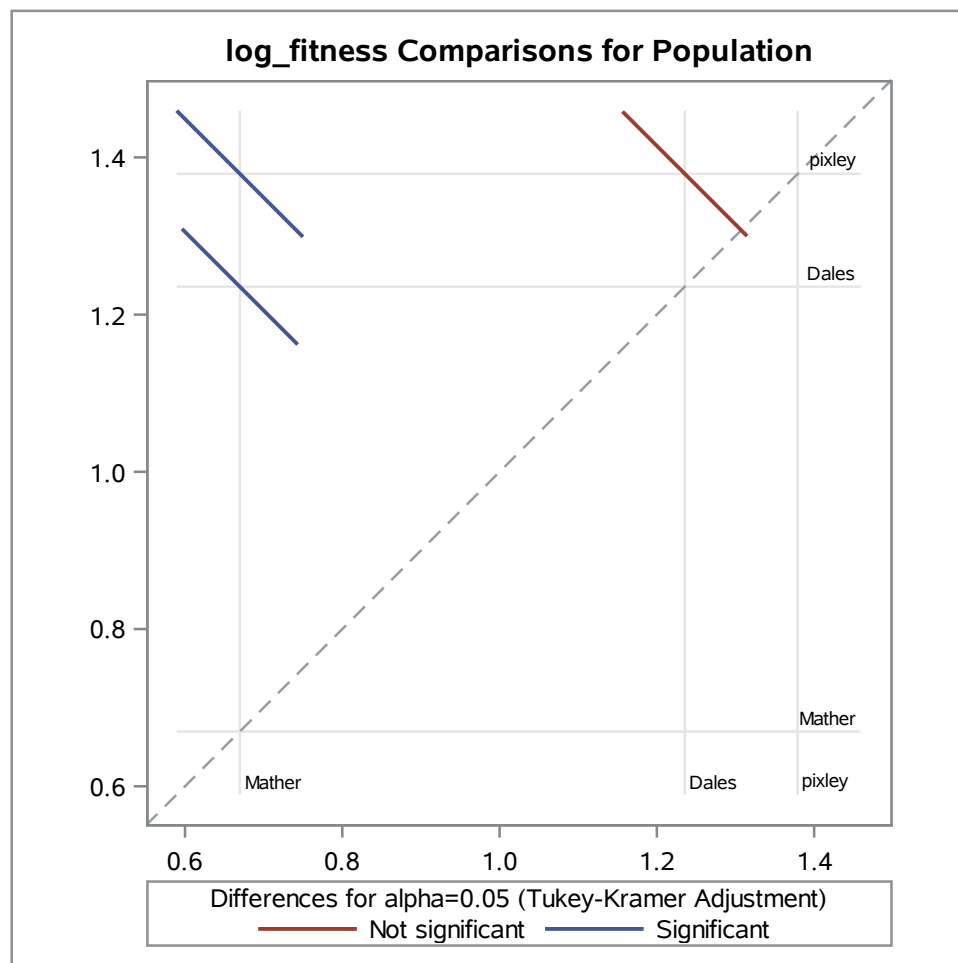
Population	log_fitness LSMEAN	LSMEAN Number
Dales	1.23550688	1
Mather	0.66968979	2
pixley	1.37909862	3

Least Squares Means for effect Population Pr > t for H0: LSMean(i)=LSMean(j)			
Dependent Variable: log_fitness			
i/j	1	2	3
1		<.0001	0.0848
2	<.0001		<.0001
3	0.0848	<.0001	



GLM testing for differences among Populations and Treatments in ABSOLUTE FITNESS

The GLM Procedure
Least Squares Means
Adjustment for Multiple Comparisons: Tukey-Kramer

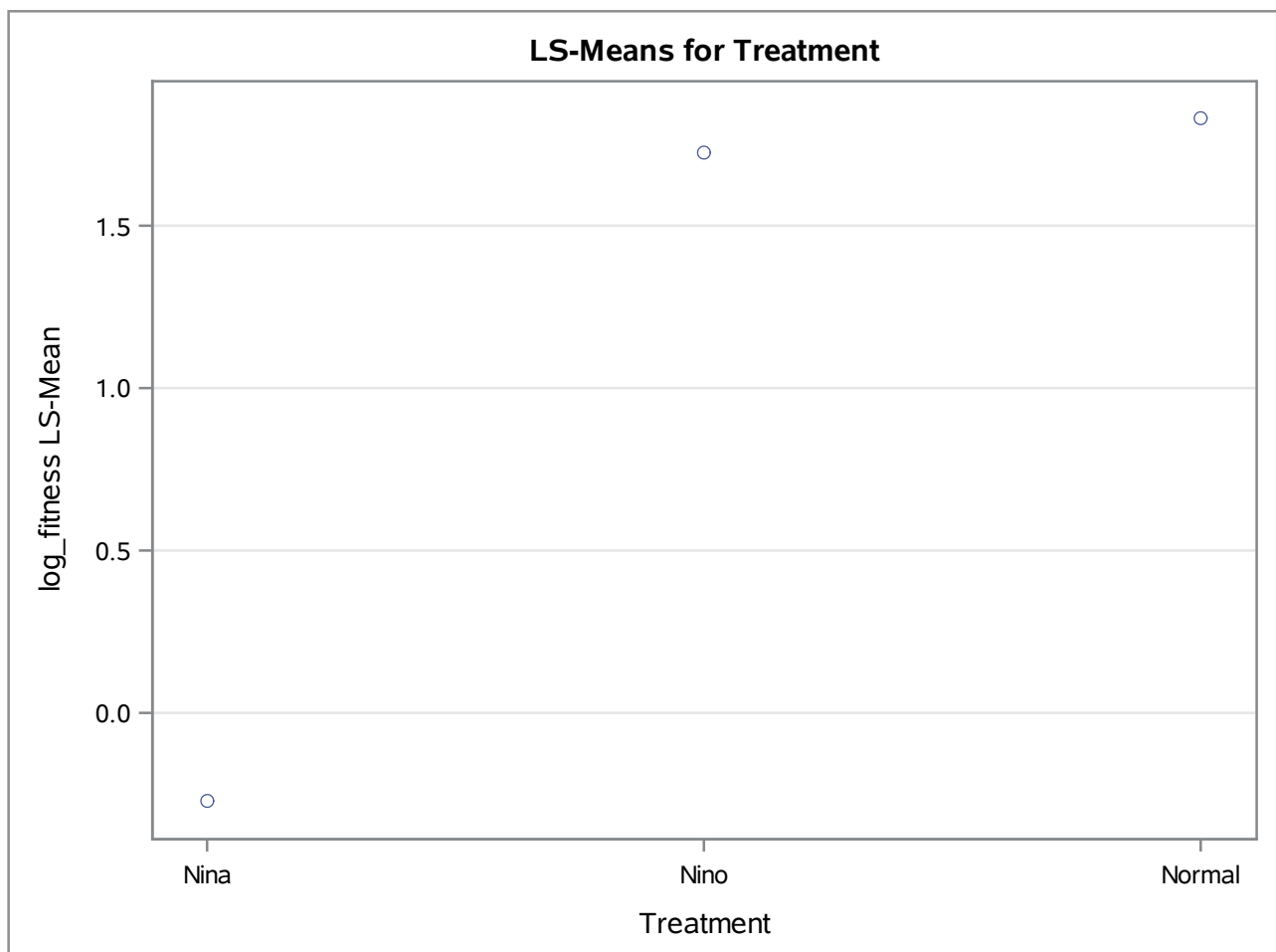


GLM testing for differences among Populations and Treatments in ABSOLUTE FITNESS

The GLM Procedure Least Squares Means Adjustment for Multiple Comparisons: Tukey-Kramer

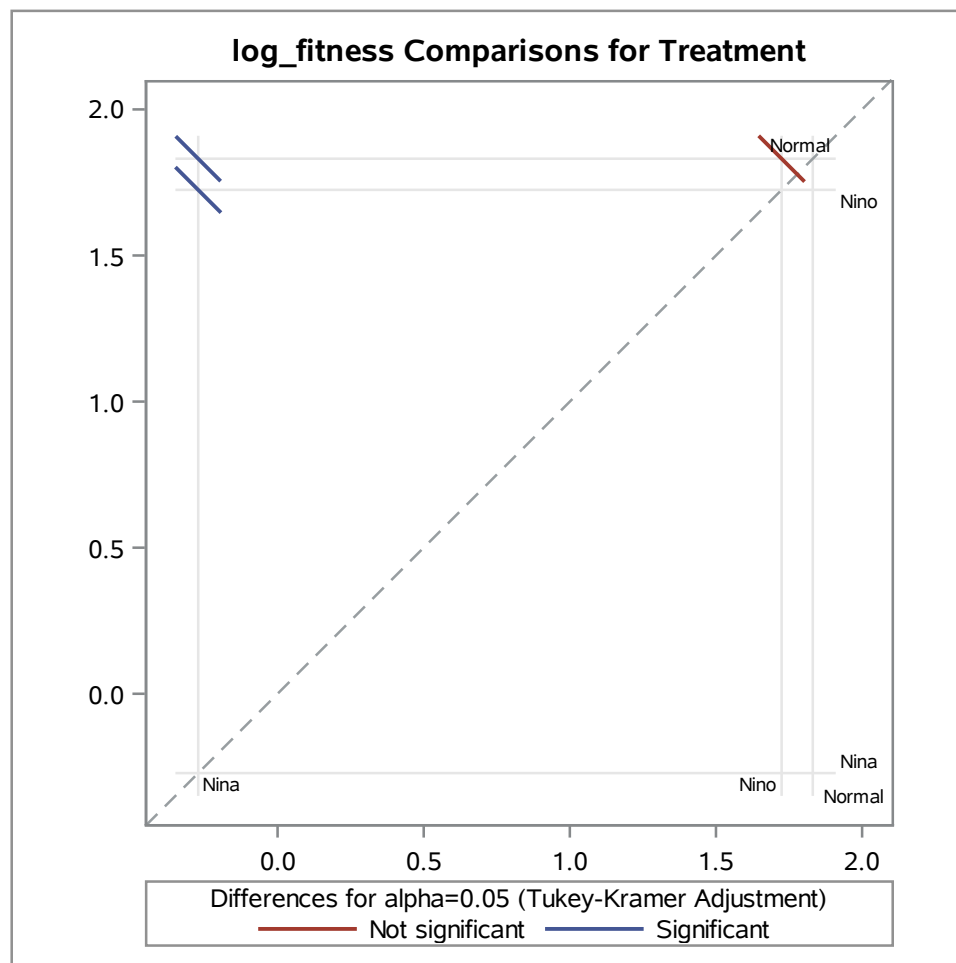
Treatment	log_fitness LSMEAN	LSMEAN Number
Nina	-0.27155336	1
Nino	1.72458412	2
Normal	1.83126452	3

Least Squares Means for effect Treatment Pr > t for H0: LSMean(i)=LSMean(j)			
Dependent Variable: log_fitness			
i/j	1	2	3
1		<.0001	<.0001
2	<.0001		0.2480
3	<.0001	0.2480	



GLM testing for differences among Populations and Treatments in ABSOLUTE FITNESS

The GLM Procedure
Least Squares Means
Adjustment for Multiple Comparisons: Tukey-Kramer



GLM testing for differences among Populations and Treatments in ABSOLUTE FITNESS

The GLM Procedure Least Squares Means Adjustment for Multiple Comparisons: Tukey-Kramer

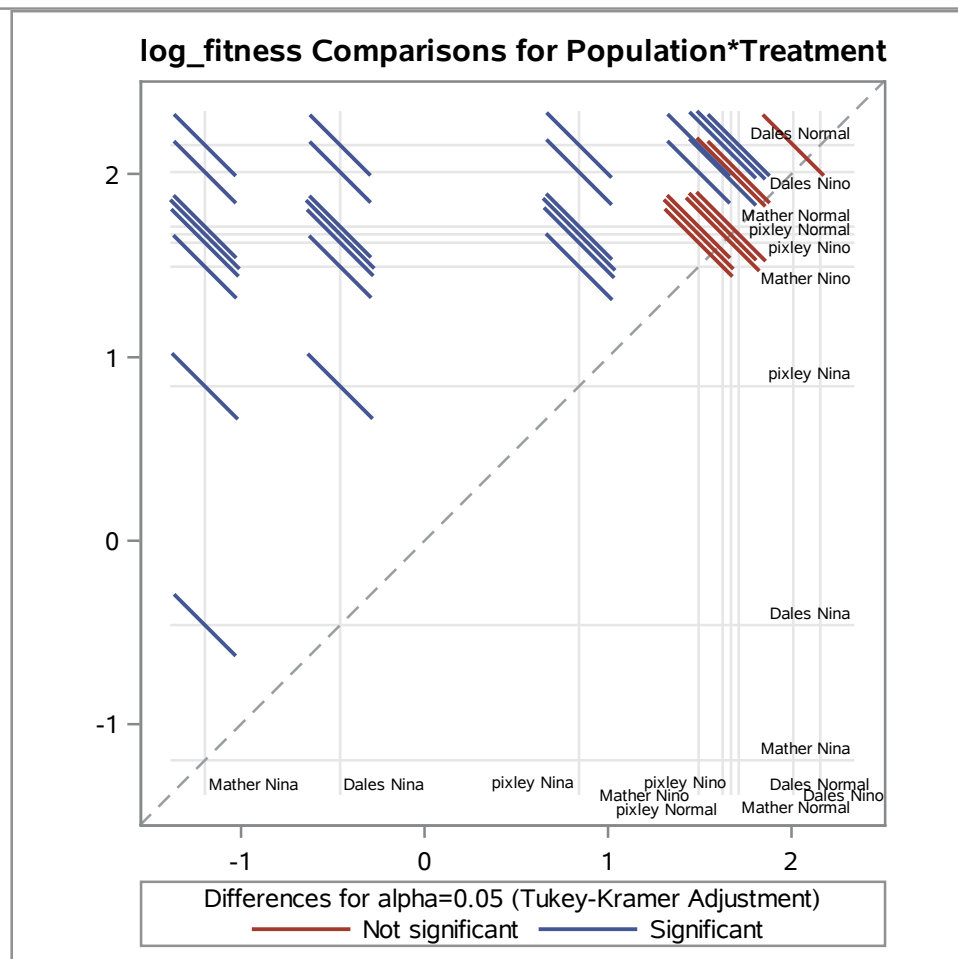
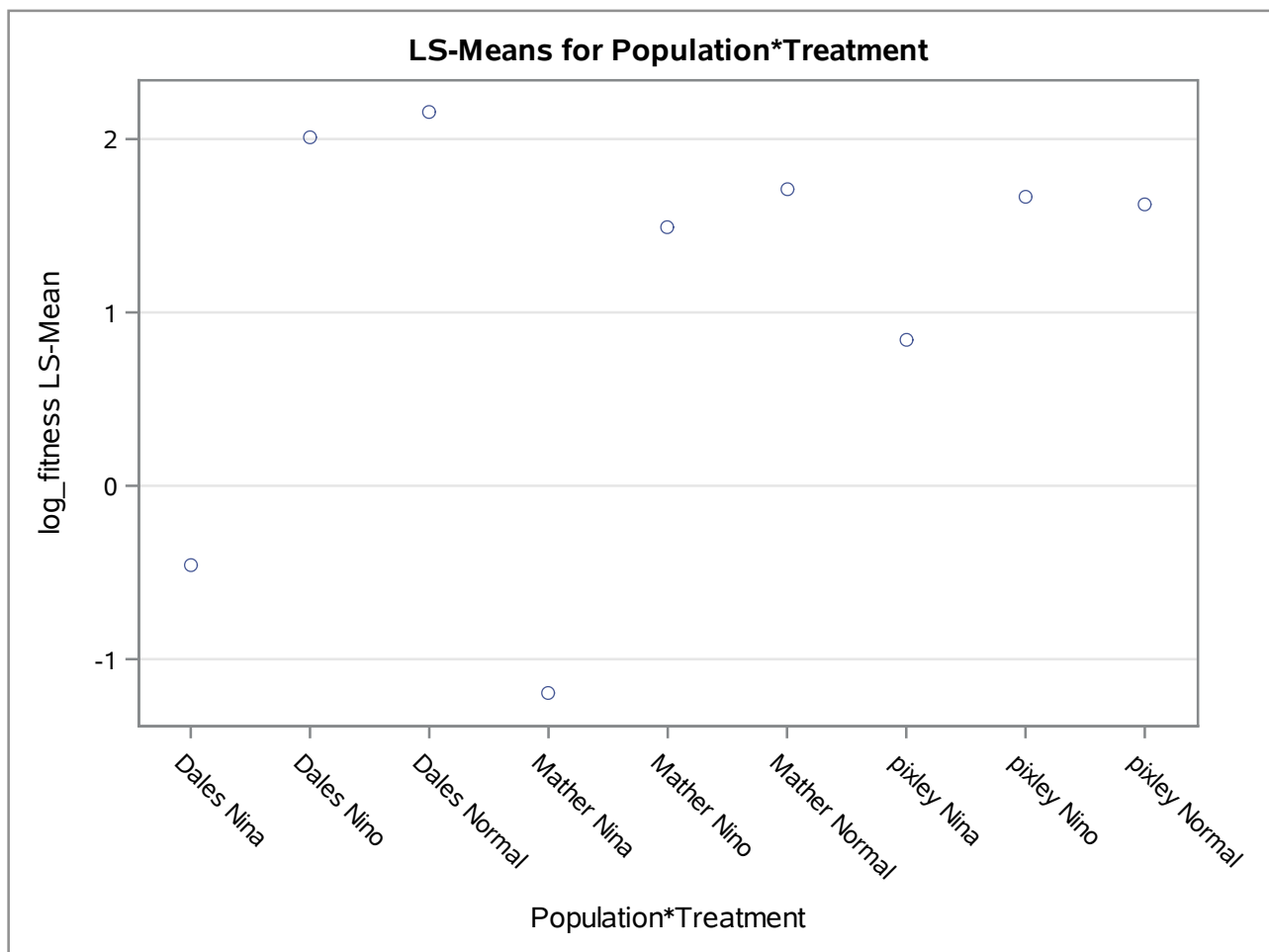
Population	Treatment	log_fitness LSMEAN	LSMEAN Number
Dales	Nina	-0.45985538	1
Dales	Nino	2.00958306	2
Dales	Normal	2.15679295	3
Mather	Nina	-1.19699287	4
Mather	Nino	1.49371052	5
Mather	Normal	1.71235171	6
pixley	Nina	0.84218818	7
pixley	Nino	1.67045878	8
pixley	Normal	1.62464889	9

Least Squares Means for effect Population*Treatment Pr > t for H0: LSMean(i)=LSMean(j) Dependent Variable: log_fitness									
i/j	1	2	3	4	5	6	7	8	9
1		<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
2	<.0001		0.9077	<.0001	<.0001	0.1363	<.0001	0.1105	0.0280
3	<.0001	0.9077		<.0001	<.0001	0.0014	<.0001	0.0017	0.0002
4	<.0001	<.0001	<.0001		<.0001	<.0001	<.0001	<.0001	<.0001
5	<.0001	<.0001	<.0001	<.0001		0.5593	<.0001	0.8788	0.9739
6	<.0001	0.1363	0.0014	<.0001	0.5593		<.0001	1.0000	0.9981
7	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001		<.0001	<.0001
8	<.0001	0.1105	0.0017	<.0001	0.8788	1.0000	<.0001		1.0000
9	<.0001	0.0280	0.0002	<.0001	0.9739	0.9981	<.0001	1.0000	

The GLM Procedure

Least Squares Means

Adjustment for Multiple Comparisons: Tukey-Kramer



GLM testing for differences among Populations and Treatments in ABSOLUTE FITNESS**The MEANS Procedure**

Population=Dales Treatment=Nina

Analysis Variable : log_fitness				
N	Mean	Std Dev	Minimum	Maximum
374	-0.4598554	2.0769471	-2.3025851	3.0950797

Population=Mather Treatment=Nina

Analysis Variable : log_fitness				
N	Mean	Std Dev	Minimum	Maximum
350	-1.1969929	1.7630758	-2.3025851	3.0193023

Model B: residual error allowed to vary among Treatments, among-sire variance constrained to be equal

The Mixed Procedure

Model Information	
Data Set	WORK.ONE
Dependent Variable	log_fitness
Covariance Structure	Variance Components
Subject Effect	Sire(Population)
Group Effect	Treatment
Estimation Method	REML
Residual Variance Method	None
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Satterthwaite

Class Level Information		
Class	Levels	Values
Population	3	Dales Mather pixley
Treatment	3	Nina Nino Normal
Sire	45	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 38 39 40 41 42 43 44 45 47
Dam	3	A B C

Dimensions	
Covariance Parameters	6
Columns in X	16
Columns in Z per Subject	9
Subjects	119
Max Obs per Subject	27

Number of Observations	
Number of Observations Read	2959
Number of Observations Used	2959
Number of Observations Not Used	0

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
0	1	10641.02638592	
1	4	10248.55944323	.
2	2	10242.61186180	0.00011650
3	2	10242.32338774	0.00000022
4	1	10242.32286698	0.00000000

Convergence criteria met.

Model B: residual error allowed to vary among Treatments, among-sire variance constrained to be equal

The Mixed Procedure

Covariance Parameter Estimates						
Cov Parm	Subject	Group	Estimate	Standard Error	Z Value	Pr > Z
Dam	Sire(Population)		0.01658	0.02115	0.78	0.2166
Population	Sire(Population)		0.07461	0.02157	3.46	0.0003
Treatment	Sire(Population)		0.003140	0.02085	0.15	0.4401
Residual		Treatment Nina	3.3947	0.1623	20.92	<.0001
Residual		Treatment Nino	1.4911	0.07416	20.11	<.0001
Residual		Treatment Normal	1.0927	0.05175	21.11	<.0001

Asymptotic Covariance Matrix of Estimates							
Row	Cov Parm	CovP1	CovP2	CovP3	CovP4	CovP5	CovP6
1	Dam	0.000447	-0.00013	0.000042	-0.00058	-0.00029	-0.00022
2	Population	-0.00013	0.000465	-0.00010	0.000051	0.000027	0.000084
3	Treatment	0.000042	-0.00010	0.000435	-0.00088	-0.00037	-0.00010
4	Residual	-0.00058	0.000051	-0.00088	0.02634	0.001108	0.000419
5	Residual	-0.00029	0.000027	-0.00037	0.001108	0.005500	0.000190
6	Residual	-0.00022	0.000084	-0.00010	0.000419	0.000190	0.002679

Fit Statistics	
-2 Res Log Likelihood	10242.3
AIC (Smaller is Better)	10254.3
AICC (Smaller is Better)	10254.4
BIC (Smaller is Better)	10271.0

Type 3 Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
Population	2	128	31.58	<.0001
Treatment	2	228	516.06	<.0001
Population*Treatment	4	226	46.85	<.0001

Model B vs. Model A: Chi-square test for significant differences in residual error among treatments

Obs	chiprob
1	0

Model C: residual error AND AMONG-SIRE VARIANCE allowed to vary among Treatments**The Mixed Procedure**

Model Information	
Data Set	WORK.ONE
Dependent Variable	log_fitness
Covariance Structures	Variance Components, Unstructured using Correlations
Subject Effects	Sire(Population), Sire(Population)
Group Effect	Treatment
Estimation Method	REML
Residual Variance Method	None
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Satterthwaite

Class Level Information		
Class	Levels	Values
Population	3	Dales Mather pixley
Treatment	3	Nina Nino Normal
Sire	45	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 38 39 40 41 42 43 44 45 47
Dam	3	A B C

Dimensions	
Covariance Parameters	11
Columns in X	16
Columns in Z per Subject	9
Subjects	119
Max Obs per Subject	27

Number of Observations	
Number of Observations Read	2959
Number of Observations Used	2959
Number of Observations Not Used	0

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
0	1	10641.02638592	
1	4	10386.87711012	.
2	3	10223.15012579	.
3	1	10223.15008103	21355803867
4	1	10223.15004828	7120750886.5
5	1	10223.14999154	2373602484.0
6	1	10223.14989313	791170944.95

Model C: residual error AND AMONG-SIRE VARIANCE allowed to vary among Treatments**The Mixed Procedure**

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
7	1	10223.14971538	263704818.06
8	1	10223.14902732	87886838.514
9	1	10223.12824976	29220862.937
10	1	10222.39017787	8891915.4617
11	2	10220.13501328	1993254.4339
12	2	10219.21685713	515675.00664
13	2	10219.04179152	188286.53750
14	2	10219.03131316	92891.054041
15	3	10218.92277382	82463.239206
16	3	10218.87607315	0.00003475
17	1	10218.75437773	0.00005878
18	1	10218.54866788	0.00009815
19	1	10218.20604041	0.00015956
20	1	10217.65150132	0.00024759
21	3	10215.48126435	.
22	2	10213.21384789	0.00037221
23	3	10212.66293949	.
24	2	10212.10889255	.
25	1	10212.02406024	0.00000086
26	1	10212.02199528	0.00000000

Convergence criteria met.

Covariance Parameter Estimates						
Cov Parm	Subject	Group	Estimate	Standard Error	Z Value	Pr Z
Dam	Sire(Population)		0.01860	0.02053	0.91	0.1825
Population	Sire(Population)		0	.	.	.
Var(1)	Sire(Population)		0.4328	0.1099	3.94	<.0001
Var(2)	Sire(Population)		0.1254	0.04230	2.97	0.0015
Var(3)	Sire(Population)		0.02367	0.01515	1.56	0.0591
Corr(2,1)	Sire(Population)		0.5028	0.1880	2.67	0.0075
Corr(3,1)	Sire(Population)		0.9346	0.3608	2.59	0.0096
Corr(3,2)	Sire(Population)		1.0000	0	.	.
Residual		Treatment Nina	3.1339	0.1512	20.73	<.0001
Residual		Treatment Nino	1.4615	0.07244	20.17	<.0001
Residual		Treatment Normal	1.1035	0.05184	21.29	<.0001

Model C: residual error AND AMONG-SIRE VARIANCE allowed to vary among Treatments**The Mixed Procedure**

Asymptotic Covariance Matrix of Estimates												
Row	Cov Parm	CovP1	CovP2	CovP3	CovP4	CovP5	CovP6	CovP7	CovP8	CovP9	CovP10	CovP11
1	Dam	0.000421		-0.00008	-0.00011	-0.00007	-0.00022	0.000453		-0.00052	-0.00025	-0.00021
2	Population											
3	Var(1)	-0.00008		0.01207	0.000310	0.000155	-0.00008	0.000508		-0.00262	0.000031	0.000076
4	Var(2)	-0.00011		0.000310	0.001789	0.000088	-0.00027	-0.00020		0.000132	-0.00049	0.000061
5	Var(3)	-0.00007		0.000155	0.000088	0.000229	0.000528	-0.00252		0.000087	0.000057	-0.00004
6	Corr(2,1)	-0.00022		-0.00008	-0.00027	0.000528	0.03535	-0.00331		0.001685	0.001041	-0.00015
7	Corr(3,1)	0.000453		0.000508	-0.00020	-0.00252	-0.00331	0.1302		0.001856	-0.00072	0.002070
8	Corr(3,2)											
9	Residual	-0.00052		-0.00262	0.000132	0.000087	0.001685	0.001856		0.02286	0.000326	0.000264
10	Residual	-0.00025		0.000031	-0.00049	0.000057	0.001041	-0.00072		0.000326	0.005248	0.000106
11	Residual	-0.00021		0.000076	0.000061	-0.00004	-0.00015	0.002070		0.000264	0.000106	0.002687

Fit Statistics	
-2 Res Log Likelihood	10212.0
AIC (Smaller is Better)	10230.0
AICC (Smaller is Better)	10230.1
BIC (Smaller is Better)	10255.0

Type 3 Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
Population	2	110	24.17	<.0001
Treatment	2	135	352.05	<.0001
Population*Treatment	4	134	30.56	<.0001

Model C vs. Model B: Chi-square test for significant differences in among-sire variance among treatments

Obs	chiprob
1	.000004252

Model D: residual error allowed to vary among Populations**The Mixed Procedure**

Model Information	
Data Set	WORK.ONE
Dependent Variable	log_fitness
Covariance Structure	Variance Components
Subject Effect	Sire(Population)
Group Effect	Population
Estimation Method	REML
Residual Variance Method	None
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Satterthwaite

Class Level Information		
Class	Levels	Values
Population	3	Dales Mather pixley
Treatment	3	Nina Nino Normal
Sire	45	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 38 39 40 41 42 43 44 45 47
Dam	3	A B C

Dimensions	
Covariance Parameters	6
Columns in X	16
Columns in Z per Subject	9
Subjects	119
Max Obs per Subject	27

Number of Observations	
Number of Observations Read	2959
Number of Observations Used	2959
Number of Observations Not Used	0

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
0	1	10641.02638592	
1	2	10557.45114428	0.00000636
2	1	10557.43467006	0.00000000

Convergence criteria met.

Model D: residual error allowed to vary among Populations**The Mixed Procedure**

Covariance Parameter Estimates						
Cov Parm	Subject	Group	Estimate	Standard Error	Z Value	Pr > Z
Dam	Sire(Population)		0.07391	0.03024	2.44	0.0073
Treatment	Sire(Population)		0.09149	0.03025	3.02	0.0012
Population	Sire(Population)		0.07750	0.03175	2.44	0.0073
Residual		Population Dales	1.9154	0.08692	22.04	<.0001
Residual		Population Mather	1.8132	0.08505	21.32	<.0001
Residual		Population pixley	1.9454	0.1091	17.83	<.0001

Asymptotic Covariance Matrix of Estimates							
Row	Cov Parm	CovP1	CovP2	CovP3	CovP4	CovP5	CovP6
1	Dam	0.000915	0.000037	-0.00027	-0.00029	-0.00027	-0.00084
2	Treatment	0.000037	0.000915	-0.00031	-0.00034	-0.00037	-0.00032
3	Population	-0.00027	-0.00031	0.001008	0.000085	0.000160	0.000023
4	Residual	-0.00029	-0.00034	0.000085	0.007556	0.000218	0.000407
5	Residual	-0.00027	-0.00037	0.000160	0.000218	0.007233	0.000378
6	Residual	-0.00084	-0.00032	0.000023	0.000407	0.000378	0.01190

Fit Statistics	
-2 Res Log Likelihood	10557.4
AIC (Smaller is Better)	10569.4
AICC (Smaller is Better)	10569.5
BIC (Smaller is Better)	10586.1

Type 3 Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
Population	2	107	23.52	<.0001
Treatment	2	233	515.38	<.0001
Population*Treatment	4	224	45.17	<.0001

Model D vs. Model A: Chi-square test for significant differences in residual error among populations

Obs	chiprob
1	0.54881

Model E: residual error AND AMONG-SIRE VARIANCE allowed to vary among populations**The Mixed Procedure**

Model Information	
Data Set	WORK.ONE
Dependent Variable	log_fitness
Covariance Structures	Variance Components, Unstructured using Correlations
Subject Effects	Sire(Population), Sire(Population)
Group Effect	Population
Estimation Method	REML
Residual Variance Method	None
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Satterthwaite

Class Level Information		
Class	Levels	Values
Population	3	Dales Mather pixley
Treatment	3	Nina Nino Normal
Sire	45	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 38 39 40 41 42 43 44 45 47
Dam	3	A B C

Dimensions	
Covariance Parameters	11
Columns in X	16
Columns in Z per Subject	9
Subjects	119
Max Obs per Subject	27

Number of Observations	
Number of Observations Read	2959
Number of Observations Used	2959
Number of Observations Not Used	0

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
0	1	10641.02638592	
1	3	10551.93810551	0.02505056
2	1	10551.80800224	0.00037393
3	1	10551.80520947	0.00000023
4	1	10551.80520764	0.00000000

Convergence criteria met but final Hessian is not positive definite.

Model E: residual error AND AMONG-SIRE VARIANCE allowed to vary among populations**The Mixed Procedure**

Covariance Parameter Estimates						
Cov Parm	Subject	Group	Estimate	Standard Error	Z Value	Pr Z
Dam	Sire(Population)		0.07720	0.03062	2.52	0.0058
Treatment	Sire(Population)		0.09063	0.03013	3.01	0.0013
Var(1)	Sire(Population)		0.07011	0.04595	1.53	0.0635
Var(2)	Sire(Population)		0.01172	0.03426	0.34	0.3661
Var(3)	Sire(Population)		0.1931	0.08694	2.22	0.0132
Corr(2,1)	Sire(Population)		0	.	.	.
Corr(3,1)	Sire(Population)		0	.	.	.
Corr(3,2)	Sire(Population)		0	.	.	.
Residual		Population Dales	1.9157	0.08709	22.00	<.0001
Residual		Population Mather	1.8211	0.08585	21.21	<.0001
Residual		Population pixley	1.9193	0.1074	17.88	<.0001

Asymptotic Covariance Matrix of Estimates												
Row	Cov Parm	CovP1	CovP2	CovP3	CovP4	CovP5	CovP6	CovP7	CovP8	CovP9	CovP10	CovP11
1	Dam	0.000938	0.000036	-0.00031	-0.00031	-0.00017				-0.00027	-0.00026	-0.00085
2	Treatment	0.000036	0.000908	-0.00031	-0.00030	-0.00033				-0.00034	-0.00038	-0.00032
3	Var(1)	-0.00031	-0.00031	0.002111	0.000197	0.000164				-0.00008	0.000207	0.000377
4	Var(2)	-0.00031	-0.00030	0.000197	0.001174	0.000160				0.000194	-0.00007	0.000373
5	Var(3)	-0.00017	-0.00033	0.000164	0.000160	0.007558				0.000169	0.000180	-0.00047
6	Corr(2,1)											
7	Corr(3,1)											
8	Corr(3,2)											
9	Residual	-0.00027	-0.00034	-0.00008	0.000194	0.000169				0.007584	0.000209	0.000352
10	Residual	-0.00026	-0.00038	0.000207	-0.00007	0.000180				0.000209	0.007369	0.000353
11	Residual	-0.00085	-0.00032	0.000377	0.000373	-0.00047				0.000352	0.000353	0.01153

Fit Statistics	
-2 Res Log Likelihood	10551.8
AIC (Smaller is Better)	10573.8
AICC (Smaller is Better)	10573.9
BIC (Smaller is Better)	10604.4

Model E: residual error AND AMONG-SIRE VARIANCE allowed to vary among populations**The Mixed Procedure**

Type 3 Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
Population	2	58.2	26.28	<.0001
Treatment	2	233	516.69	<.0001
Population*Treatment	4	224	45.93	<.0001

Model E vs. Model D: Chi-square test for significant differences in among-sire variance among populations

Obs	chiprob
1	0.060810

Model F: RESIDUAL variance allowed to vary with Population x Treatment**The Mixed Procedure**

Model Information	
Data Set	WORK.ONE
Dependent Variable	log_fitness
Covariance Structure	Variance Components
Subject Effect	Sire(Population)
Group Effect	Population*Treatment
Estimation Method	REML
Residual Variance Method	None
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Satterthwaite

Class Level Information		
Class	Levels	Values
Population	3	Dales Mather pixley
Treatment	3	Nina Nino Normal
Sire	45	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 38 39 40 41 42 43 44 45 47
Dam	3	A B C

Dimensions	
Covariance Parameters	12
Columns in X	16
Columns in Z per Subject	9
Subjects	119
Max Obs per Subject	27

Number of Observations	
Number of Observations Read	2959
Number of Observations Used	2959
Number of Observations Not Used	0

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
0	1	10641.02638592	
1	4	10176.22947790	.
2	2	10167.53309177	0.00019392
3	1	10167.04921199	0.00000140
4	1	10167.04587855	0.00000000

Convergence criteria met.

Model F: RESIDUAL variance allowed to vary with Population x Treatment**The Mixed Procedure**

Covariance Parameter Estimates						
Cov Parm	Subject	Group	Estimate	Standard Error	Z Value	Pr > Z
Dam	Sire(Population)		0.01552	0.01964	0.79	0.2147
Treatment	Sire(Population)		0.01469	0.02003	0.73	0.2317
Population	Sire(Population)		0.06710	0.02083	3.22	0.0006
Residual		Population*Treatment Dales Nina	4.1295	0.3093	13.35	<.0001
Residual		Population*Treatment Dales Nino	1.2316	0.09790	12.58	<.0001
Residual		Population*Treatment Dales Normal	0.6877	0.05343	12.87	<.0001
Residual		Population*Treatment Mather Nina	2.9727	0.2361	12.59	<.0001
Residual		Population*Treatment Mather Nino	1.6258	0.1291	12.59	<.0001
Residual		Population*Treatment Mather Normal	1.1245	0.08811	12.76	<.0001
Residual		Population*Treatment pixley Nina	2.9035	0.2582	11.25	<.0001
Residual		Population*Treatment pixley Nino	1.6764	0.1598	10.49	<.0001
Residual		Population*Treatment pixley Normal	1.6057	0.1425	11.27	<.0001

Model F: RESIDUAL variance allowed to vary with Population x Treatment**The Mixed Procedure****Asymptotic Covariance Matrix of Estimates**

Row	Cov Parm	CovP1	CovP2	CovP3	CovP4	CovP5	CovP6	CovP7	CovP8	CovP9	CovP10	CovP11
1	Dam	0.000386	0.000036	-0.00011	-0.00012	-0.00024	-0.00016	-0.00042	-0.00017	-0.00022	-0.00090	-0.00044
2	Treatment	0.000036	0.000401	-0.00008	-0.00060	-0.00042	-0.00009	-0.00087	-0.00026	-0.00006	-0.00075	-0.00025
3	Population	-0.00011	-0.00008	0.000434	-0.00011	0.000041	0.000084	0.000127	0.000045	0.000079	-0.00019	-0.00009
4	Residual	-0.00012	-0.00060	-0.00011	0.09568	0.000776	0.000067	0.001468	0.000445	0.000116	0.001648	0.000630
5	Residual	-0.00024	-0.00042	0.000041	0.000776	0.009585	0.000122	0.001128	0.000361	0.000168	0.001372	0.000556
6	Residual	-0.00016	-0.00009	0.000084	0.000067	0.000122	0.002854	0.000329	0.000116	0.000096	0.000466	0.000206
7	Residual	-0.00042	-0.00087	0.000127	0.001468	0.001128	0.000329	0.05577	0.000446	0.000236	0.002580	0.001023
8	Residual	-0.00017	-0.00026	0.000045	0.000445	0.000361	0.000116	0.000446	0.01668	0.000092	0.000877	0.000359
9	Residual	-0.00022	-0.00006	0.000079	0.000116	0.000168	0.000096	0.000236	0.000092	0.007763	0.000548	0.000257
10	Residual	-0.00090	-0.00075	-0.00019	0.001648	0.001372	0.000466	0.002580	0.000877	0.000548	0.06667	0.002030
11	Residual	-0.00044	-0.00025	-0.00009	0.000630	0.000556	0.000206	0.001023	0.000359	0.000257	0.002030	0.02553
12	Residual	-0.00025	-0.00005	4.553E-6	0.000171	0.000205	0.000104	0.000360	0.000139	0.000140	0.000860	0.000417

**Asymptotic
Covariance
Matrix of
Estimates**

Row	CovP12
1	-0.00025
2	-0.00005
3	4.553E-6
4	0.000171
5	0.000205
6	0.000104
7	0.000360
8	0.000139
9	0.000140
10	0.000860
11	0.000417
12	0.02030

Fit Statistics

-2 Res Log Likelihood	10167.0
AIC (Smaller is Better)	10191.0
AICC (Smaller is Better)	10191.2
BIC (Smaller is Better)	10224.4

Model F: RESIDUAL variance allowed to vary with Population x Treatment**The Mixed Procedure**

Type 3 Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
Population	2	128	32.71	<.0001
Treatment	2	277	504.51	<.0001
Population*Treatment	4	242	47.05	<.0001

Model F vs. Model B: Chi-square test for significant differences in residual error with Population x Treatment

Obs	chiprob
1	3.3307E-14

Model F vs. Model D: Chi-square test for significant differences in residual error with Population x Treatment

Obs	chiprob
1	0

Model G: residual error AND among-sire variance allowed to vary with Population x Treatment**The Mixed Procedure**

Model Information	
Data Set	WORK.ONE
Dependent Variable	log_fitness
Covariance Structures	Variance Components, Unstructured using Correlations
Subject Effects	Sire(Population), Sire(Population)
Group Effect	Population*Treatment
Estimation Method	REML
Residual Variance Method	None
Fixed Effects SE Method	Model-Based
Degrees of Freedom Method	Satterthwaite

Class Level Information		
Class	Levels	Values
Population	3	Dales Mather pixley
Treatment	3	Nina Nino Normal
Sire	45	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 38 39 40 41 42 43 44 45 47
Dam	3	A B C

Dimensions	
Covariance Parameters	55
Columns in X	16
Columns in Z per Subject	12
Subjects	119
Max Obs per Subject	27

Number of Observations	
Number of Observations Read	2959
Number of Observations Used	2959
Number of Observations Not Used	0

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
0	1	10641.02638592	
1	4	10341.15452806	.
2	3	10201.80411764	.
3	1	10201.80409323	6323722251.5
4	1	10201.80407536	2107949473.9
5	1	10201.80404439	702658591.87
6	1	10201.80398964	234224044.77

Model G: residual error AND among-sire variance allowed to vary with Population x Treatment**The Mixed Procedure**

Iteration History			
Iteration	Evaluations	-2 Res Log Like	Criterion
7	1	10201.80383802	78076733.969
8	1	10201.80063143	26017480.924
9	1	10201.65886163	8526909.4467
10	1	10198.54517266	2515091.1504
11	3	10165.88956505	.
12	1	10165.88770079	1778544119.5
13	1	10165.88445885	592649276.75
14	1	10165.87318882	197220360.35
15	1	10165.82835012	65222314.925
16	1	10165.67985972	21124235.491
17	1	10165.30085309	6653166.0724
18	3	10155.56247331	.
19	1	10155.49174877	8983354.2346
20	1	10155.37439355	2997758.4551
21	1	10155.12912338	988842.74386
22	1	10154.57267013	314328.69315
23	3	10148.66738544	.
24	2	10142.00231597	4065.5895309
25	2	10136.13034763	3078.6722202
26	3	10132.56776251	2289.6525712
27	3	10129.01564507	1197.8113122
28	3	10128.77932616	856.27135226
29	3	10128.66595952	3578.1855354
30	3	10128.65757596	3484.3772033
31	2	10128.61932836	1285.6834977
32	1	10128.58391921	442.41116405
33	1	10128.52741002	146.09333168
34	1	10128.43594346	47.14602596
35	1	10128.29653956	14.55213337
36	1	10128.11041924	4.02001309
37	1	10127.92336706	.
38	2	10127.48799052	.
39	4	10127.17127688	0.79607957
40	2	10126.34132162	0.10877698
41	2	10126.06393177	0.00840164
42	2	10125.91828512	0.00011393
43	1	10125.91720632	0.00000002
44	1	10125.91720619	0.00000000

Model G: residual error AND among-sire variance allowed to vary with Population x Treatment**The Mixed Procedure**

Convergence criteria met but final Hessian is not positive definite.
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Covariance Parameter Estimates						
Cov Parm	Subject	Group	Estimate	Standard Error	Z Value	Pr Z
Dam	Sire(Population)		0.01954	0.01946	1.00	0.1577
Var(1)	Sire(Population)		0.3858	0.1838	2.10	0.0179
Var(2)	Sire(Population)		0.1346	0.06365	2.11	0.0172
Var(3)	Sire(Population)		0.01531	0.01576	0.97	0.1656
Var(4)	Sire(Population)		0.3648	0.1582	2.31	0.0105
Var(5)	Sire(Population)		0.06727	0.05831	1.15	0.1243
Var(6)	Sire(Population)		0.01425	0.02076	0.69	0.2462
Var(7)	Sire(Population)		0.6047	0.2384	2.54	0.0056
Var(8)	Sire(Population)		0.2026	0.1073	1.89	0.0295
Var(9)	Sire(Population)		0.06582	0.05438	1.21	0.1131
Corr(2,1)	Sire(Population)		0.6700	0.2875	2.33	0.0198
Corr(3,1)	Sire(Population)		1.0000	0	.	.
Corr(3,2)	Sire(Population)		0.7979	0.5581	1.43	0.1528
Corr(4,1)	Sire(Population)		0	.	.	.
Corr(4,2)	Sire(Population)		0	.	.	.
Corr(4,3)	Sire(Population)		0	.	.	.
Corr(5,1)	Sire(Population)		0	.	.	.
Corr(5,2)	Sire(Population)		0	.	.	.
Corr(5,3)	Sire(Population)		0	.	.	.
Corr(5,4)	Sire(Population)		-0.1323	0.4485	-0.30	0.7680
Corr(6,1)	Sire(Population)		0	.	.	.
Corr(6,2)	Sire(Population)		0	.	.	.
Corr(6,3)	Sire(Population)		0	.	.	.
Corr(6,4)	Sire(Population)		0.6233	0.8578	0.73	0.4675
Corr(6,5)	Sire(Population)		1.0000	0	.	.
Corr(7,1)	Sire(Population)		0	.	.	.
Corr(7,2)	Sire(Population)		0	.	.	.
Corr(7,3)	Sire(Population)		0	.	.	.
Corr(7,4)	Sire(Population)		0	.	.	.
Corr(7,5)	Sire(Population)		0	.	.	.
Corr(7,6)	Sire(Population)		0	.	.	.
Corr(8,1)	Sire(Population)		0	.	.	.
Corr(8,2)	Sire(Population)		0	.	.	.
Corr(8,3)	Sire(Population)		0	.	.	.
Corr(8,4)	Sire(Population)		0	.	.	.

Model G: residual error AND among-sire variance allowed to vary with Population x Treatment**The Mixed Procedure**

Covariance Parameter Estimates						
Cov Parm	Subject	Group	Estimate	Standard Error	Z Value	Pr Z
Corr(8,5)	Sire(Population)		0	.	.	.
Corr(8,6)	Sire(Population)		0	.	.	.
Corr(8,7)	Sire(Population)		0.7472	0.2536	2.95	0.0032
Corr(9,1)	Sire(Population)		0	.	.	.
Corr(9,2)	Sire(Population)		0	.	.	.
Corr(9,3)	Sire(Population)		0	.	.	.
Corr(9,4)	Sire(Population)		0	.	.	.
Corr(9,5)	Sire(Population)		0	.	.	.
Corr(9,6)	Sire(Population)		0	.	.	.
Corr(9,7)	Sire(Population)		0.9326	0.4107	2.27	0.0232
Corr(9,8)	Sire(Population)		1.0000	0	.	.
Residual		Population*Treatment Dales Nina	3.9192	0.3045	12.87	<.0001
Residual		Population*Treatment Dales Nino	1.1977	0.09596	12.48	<.0001
Residual		Population*Treatment Dales Normal	0.6978	0.05370	12.99	<.0001
Residual		Population*Treatment Mather Nina	2.7299	0.2210	12.35	<.0001
Residual		Population*Treatment Mather Nino	1.6131	0.1306	12.35	<.0001
Residual		Population*Treatment Mather Normal	1.1326	0.08828	12.83	<.0001
Residual		Population*Treatment pixley Nina	2.5945	0.2378	10.91	<.0001
Residual		Population*Treatment pixley Nino	1.6339	0.1585	10.31	<.0001
Residual		Population*Treatment pixley Normal	1.6082	0.1427	11.27	<.0001

Model G: residual error AND among-sire variance allowed to vary with Population x Treatment**The Mixed Procedure****Asymptotic Covariance Matrix of Estimates**

Row	Cov Parm	CovP1	CovP2	CovP3	CovP4	CovP5	CovP6	CovP7	CovP8	CovP9	CovP10	CovP11
1	Dam	0.000379	-0.00011	-0.00009	-0.00006	-0.00011	-0.00015	-0.00006	5.668E-6	-0.00004	-0.00006	-0.00029
2	Var(1)	-0.00011	0.03379	0.001237	0.000153	0.000031	0.000043	0.000018	-1.66E-6	0.000011	0.000017	-0.00465
3	Var(2)	-0.00009	0.001237	0.004051	0.000094	0.000025	0.000034	0.000014	-1.31E-6	8.361E-6	0.000013	-0.00179
4	Var(3)	-0.00006	0.000153	0.000094	0.000248	0.000016	0.000022	9.488E-6	-8.67E-7	5.539E-6	8.631E-6	0.000615
5	Var(4)	-0.00011	0.000031	0.000025	0.000016	0.02503	0.000015	0.000034	-1.59E-6	0.000010	0.000016	0.000081
6	Var(5)	-0.00015	0.000043	0.000034	0.000022	0.000015	0.003400	0.000149	-2.17E-6	0.000014	0.000022	0.000111
7	Var(6)	-0.00006	0.000018	0.000014	9.488E-6	0.000034	0.000149	0.000431	-9.28E-7	5.932E-6	9.244E-6	0.000047
8	Var(7)	5.668E-6	-1.66E-6	-1.31E-6	-8.67E-7	-1.59E-6	-2.17E-6	-9.28E-7	0.05681	0.004284	0.002160	-4.32E-6
9	Var(8)	-0.00004	0.000011	8.361E-6	5.539E-6	0.000010	0.000014	5.932E-6	0.004284	0.01151	0.001131	0.000028
10	Var(9)	-0.00006	0.000017	0.000013	8.631E-6	0.000016	0.000022	9.244E-6	0.002160	0.001131	0.002958	0.000043
11	Corr(2,1)	-0.00029	-0.00465	-0.00179	0.000615	0.000081	0.000111	0.000047	-4.32E-6	0.000028	0.000043	0.08268
12	Corr(3,1)											
13	Corr(3,2)	-0.00086	0.007359	-0.00049	-0.00264	0.000242	0.000332	0.000142	-0.00001	0.000083	0.000129	0.01517
14	Corr(4,1)											
15	Corr(4,2)											
16	Corr(4,3)											
17	Corr(5,1)											
18	Corr(5,2)											
19	Corr(5,3)											
20	Corr(5,4)	-0.00080	0.000234	0.000184	0.000122	-0.00075	0.003781	0.001338	-0.00001	0.000076	0.000119	0.000609
21	Corr(6,1)											
22	Corr(6,2)											
23	Corr(6,3)											
24	Corr(6,4)	-0.00025	0.000073	0.000057	0.000038	0.01009	-0.00360	-0.00798	-3.7E-6	0.000024	0.000037	0.000189
25	Corr(6,5)											
26	Corr(7,1)											
27	Corr(7,2)											
28	Corr(7,3)											
29	Corr(7,4)											
30	Corr(7,5)											
31	Corr(7,6)											
32	Corr(8,1)											
33	Corr(8,2)											
34	Corr(8,3)											
35	Corr(8,4)											
36	Corr(8,5)											
37	Corr(8,6)											
38	Corr(8,7)	-0.00006	0.000018	0.000014	9.567E-6	0.000018	0.000024	0.000010	0.000026	-0.00025	0.002027	0.000048

Model G: residual error AND among-sire variance allowed to vary with Population x Treatment**The Mixed Procedure****Asymptotic Covariance Matrix of Estimates**

Row	CovP12	CovP13	CovP14	CovP15	CovP16	CovP17	CovP18	CovP19	CovP20	CovP21	CovP22	CovP23	CovP24
1		-0.00086							-0.00080				-0.00025
2		0.007359							0.000234				0.000073
3		-0.00049							0.000184				0.000057
4		-0.00264							0.000122				0.000038
5		0.000242							-0.00075				0.01009
6		0.000332							0.003781				-0.00360
7		0.000142							0.001338				-0.00798
8		-0.00001							-0.00001				-3.7E-6
9		0.000083							0.000076				0.000024
10		0.000129							0.000119				0.000037
11		0.01517							0.000609				0.000189
12													
13		0.3115							0.001823				0.000565
14													
15													
16													
17													
18													
19													
20		0.001823							0.2011				-0.00033
21													
22													
23													
24		0.000565							-0.00033				0.7358
25													
26													
27													
28													
29													
30													
31													
32													
33													
34													
35													
36													
37													
38		0.000143							0.000132				0.000041

Model G: residual error AND among-sire variance allowed to vary with Population x Treatment

The Mixed Procedure

[illegible]

Model G: residual error AND among-sire variance allowed to vary with Population x Treatment**The Mixed Procedure**

Asymptotic Covariance Matrix of Estimates													
Row	CovP38	CovP39	CovP40	CovP41	CovP42	CovP43	CovP44	CovP45	CovP46	CovP47	CovP48	CovP49	CovP50
1	-0.00006							2.382E-7		-0.00010	-0.00021	-0.00017	-0.00035
2	0.000018							-6.98E-8		-0.00969	0.000064	0.000240	0.000103
3	0.000014							-5.5E-8		0.000012	-0.00108	0.000045	0.000081
4	9.567E-6							-3.64E-8		0.000239	0.000032	-0.00006	0.000054
5	0.000018							-6.68E-8		0.000029	0.000059	0.000049	-0.00541
6	0.000024							-9.13E-8		0.000039	0.000080	0.000067	0.000132
7	0.000010							-3.9E-8		0.000017	0.000034	0.000028	0.000058
8	0.000026							0.005007		-1.52E-6	-3.14E-6	-2.6E-6	-5.25E-6
9	-0.00025							-0.00036		9.732E-6	0.000020	0.000017	0.000034
10	0.002027							-0.00607		0.000015	0.000031	0.000026	0.000052
11	0.000048							-1.82E-7		0.008740	0.003065	-0.00017	0.000267
12													
13	0.000143							-5.44E-7		-0.00588	0.003664	0.003387	0.000800
14													
15													
16													
17													
18													
19													
20	0.000132							-5.02E-7		0.000215	0.000442	0.000366	-0.00033
21													
22													
23													
24	0.000041							-1.56E-7		0.000067	0.000137	0.000113	0.005368
25													
26													
27													
28													
29													
30													
31													
32													
33													
34													
35													
36													
37													
38	0.06431							-0.01886		0.000017	0.000035	0.000029	0.000058

Model G: residual error AND among-sire variance allowed to vary with Population x Treatment**The Mixed Procedure**

Asymptotic Covariance Matrix of Estimates					
Row	CovP51	CovP52	CovP53	CovP54	CovP55
1	-0.00012	-0.00021	-0.00091	-0.00042	-0.00025
2	0.000036	0.000063	0.000266	0.000124	0.000073
3	0.000029	0.000049	0.000210	0.000098	0.000057
4	0.000019	0.000033	0.000139	0.000065	0.000038
5	0.000073	0.000171	0.000255	0.000119	0.000070
6	-0.00154	0.000061	0.000348	0.000163	0.000095
7	-0.00001	-0.00014	0.000149	0.000069	0.000041
8	-1.86E-6	-3.2E-6	-0.00821	-0.00010	0.000099
9	0.000012	0.000020	-5.87E-6	-0.00234	-0.00015
10	0.000018	0.000032	0.000055	0.000018	-0.00061
11	0.000095	0.000163	0.000692	0.000323	0.000189
12					
13	0.000283	0.000488	0.002073	0.000968	0.000567
14					
15					
16					
17					
18					
19					
20	-0.00267	-0.00002	0.001914	0.000894	0.000523
21					
22					
23					
24	0.001432	0.007886	0.000593	0.000277	0.000162
25					
26					
27					
28					
29					
30					
31					
32					
33					
34					
35					
36					
37					
38	0.000020	0.000035	0.004146	0.004017	-0.00116

Model G: residual error AND among-sire variance allowed to vary with Population x Treatment**The Mixed Procedure****Asymptotic Covariance Matrix of Estimates**

Row	Cov Parm	CovP1	CovP2	CovP3	CovP4	CovP5	CovP6	CovP7	CovP8	CovP9	CovP10	CovP11
39	Corr(9,1)											
40	Corr(9,2)											
41	Corr(9,3)											
42	Corr(9,4)											
43	Corr(9,5)											
44	Corr(9,6)											
45	Corr(9,7)	2.382E-7	-6.98E-8	-5.5E-8	-3.64E-8	-6.68E-8	-9.13E-8	-3.9E-8	0.005007	-0.00036	-0.00607	-1.82E-7
46	Corr(9,8)											
47	Residual	-0.00010	-0.00969	0.000012	0.000239	0.000029	0.000039	0.000017	-1.52E-6	9.732E-6	0.000015	0.008740
48	Residual	-0.00021	0.000064	-0.00108	0.000032	0.000059	0.000080	0.000034	-3.14E-6	0.000020	0.000031	0.003065
49	Residual	-0.00017	0.000240	0.000045	-0.00006	0.000049	0.000067	0.000028	-2.6E-6	0.000017	0.000026	-0.00017
50	Residual	-0.00035	0.000103	0.000081	0.000054	-0.00541	0.000132	0.000058	-5.25E-6	0.000034	0.000052	0.000267
51	Residual	-0.00012	0.000036	0.000029	0.000019	0.000073	-0.00154	-0.00001	-1.86E-6	0.000012	0.000018	0.000095
52	Residual	-0.00021	0.000063	0.000049	0.000033	0.000171	0.000061	-0.00014	-3.2E-6	0.000020	0.000032	0.000163
53	Residual	-0.00091	0.000266	0.000210	0.000139	0.000255	0.000348	0.000149	-0.00821	-5.87E-6	0.000055	0.000692
54	Residual	-0.00042	0.000124	0.000098	0.000065	0.000119	0.000163	0.000069	-0.00010	-0.00234	0.000018	0.000323
55	Residual	-0.00025	0.000073	0.000057	0.000038	0.000070	0.000095	0.000041	0.000099	-0.00015	-0.00061	0.000189

Model G: residual error AND among-sire variance allowed to vary with Population x Treatment**The Mixed Procedure****Asymptotic Covariance Matrix of Estimates**

Row	CovP12	CovP13	CovP14	CovP15	CovP16	CovP17	CovP18	CovP19	CovP20	CovP21	CovP22	CovP23	CovP24
39													
40													
41													
42													
43													
44													
45		-5.44E-7							-5.02E-7				-1.56E-7
46													
47		-0.00588							0.000215				0.000067
48		0.003664							0.000442				0.000137
49		0.003387							0.000366				0.000113
50		0.000800							-0.00033				0.005368
51		0.000283							-0.00267				0.001432
52		0.000488							-0.00002				0.007886
53		0.002073							0.001914				0.000593
54		0.000968							0.000894				0.000277
55		0.000567							0.000523				0.000162

Model G: residual error AND among-sire variance allowed to vary with Population x Treatment

The Mixed Procedure

[illegible]

Model G: residual error AND among-sire variance allowed to vary with Population x Treatment**The Mixed Procedure**

Asymptotic Covariance Matrix of Estimates													
Row	CovP38	CovP39	CovP40	CovP41	CovP42	CovP43	CovP44	CovP45	CovP46	CovP47	CovP48	CovP49	CovP50
39													
40													
41													
42													
43													
44													
45	-0.01886							0.1687		-6.4E-8	-1.32E-7	-1.09E-7	-2.2E-7
46													
47	0.000017							-6.4E-8		0.09274	0.000037	-0.00022	0.000094
48	0.000035							-1.32E-7		0.000037	0.009208	0.000102	0.000194
49	0.000029							-1.09E-7		-0.00022	0.000102	0.002884	0.000161
50	0.000058							-2.2E-7		0.000094	0.000194	0.000161	0.04883
51	0.000020							-7.8E-8		0.000033	0.000069	0.000057	0.000139
52	0.000035							-1.34E-7		0.000057	0.000118	0.000098	0.000225
53	0.004146							0.003503		0.000244	0.000503	0.000416	0.000840
54	0.004017							-0.00117		0.000114	0.000235	0.000194	0.000393
55	-0.00116							0.006917		0.000067	0.000137	0.000114	0.000230

Model G: residual error AND among-sire variance allowed to vary with Population x Treatment**The Mixed Procedure**

Asymptotic Covariance Matrix of Estimates					
Row	CovP51	CovP52	CovP53	CovP54	CovP55
39					
40					
41					
42					
43					
44					
45	-7.8E-8	-1.34E-7	0.003503	-0.00117	0.006917
46					
47	0.000033	0.000057	0.000244	0.000114	0.000067
48	0.000069	0.000118	0.000503	0.000235	0.000137
49	0.000057	0.000098	0.000416	0.000194	0.000114
50	0.000139	0.000225	0.000840	0.000393	0.000230
51	0.01705	0.000049	0.000297	0.000139	0.000081
52	0.000049	0.007793	0.000512	0.000239	0.000140
53	0.000297	0.000512	0.05654	0.001145	0.000720
54	0.000139	0.000239	0.001145	0.02512	0.000287
55	0.000081	0.000140	0.000720	0.000287	0.02035

Fit Statistics	
-2 Res Log Likelihood	10125.9
AIC (Smaller is Better)	10229.9
AICC (Smaller is Better)	10231.8
BIC (Smaller is Better)	10374.4

Type 3 Tests of Fixed Effects				
Effect	Num DF	Den DF	F Value	Pr > F
Population	2	59.5	27.14	<.0001
Treatment	2	118	350.33	<.0001
Population*Treatment	4	72.3	30.87	<.0001

Model F vs. Model G: Chi-square test for the among-sire variance AND residual variance to vary with Population x Treatment

Obs	chiprob
1	0