

Generation Mean Analysis for C:\INDOSTAT\DATA\DGW ( DAYS TO FLOWERING )

	Parent 1	Parent 2	F1 Cross	F2 Cross	BC1	BC2	Parameter	Value	F Ratio
Frequency	10.0000	10.0000	25.0000	100.0000	50.0000	50.0000	sl <sup>2</sup> e	5.8795	
Mean	60.7000	61.7000	63.4600	67.0480	74.2080	74.1680	Genetic Variation Test		
Variance	4.4380	8.2157	4.9849	21.5849	21.4959	26.2336	F2	3.6712	0.0012 **
Var.of Mean	0.4438	0.8216	0.1994	0.2158	0.4299	0.5247	BC1	3.6561	0.0001 ***
Std.Error	0.6662	0.9064	0.4465	0.4646	0.6557	0.7243	BC2	4.4619	0.0000 ***

Parameter	Parent 1	Parent 2	Mid-Parent	Inbreeding Depression
Heterosis over	4.547**	2.853**	3.693**	-5.654 %

Scaling Test

	Parameter	Variance	S.E.mean	t value	Probability
A	24.256	2.363	1.537	15.780	0.000
B	23.176	3.120	1.766	13.122	0.000
C	18.872	5.517	2.349	8.035	0.000
D	-14.280	1.818	1.348	-10.591	0.000

Non-allelic linteractions are present

Additive/Dominance model is inadequate

6 PARAMETER MODEL

	Parameter	Variance	S.E.mean	t value	Probability	Description	Value
m ( Hayman )	67.048	0.216	0.465	144.315	0.000	sl <sup>2</sup> G:	15.705
d ( Hayman )	0.040	0.955	0.977	0.041	0.967	sl <sup>2</sup> A	-4.560
h ( Hayman )	30.820	7.788	2.791	11.044	0.000	sl <sup>2</sup> D	20.265
m ( j & j )	32.640	7.588	2.755	11.849	0.000	sl <sup>2</sup> P	21.585
d ( j & j )	-0.500	0.316	0.562	-0.889	0.386	h <sup>2</sup> (Broad Sense)	0.728
h ( j & j )	106.812	51.226	7.157	14.924	0.000	h <sup>2</sup> (Narrow Sense)	17.025
L ( Dom * Dom )	-75.992	20.790	4.560	-16.666	0.000		
I ( Add * Add )	28.560	7.272	2.697	10.591	0.000		
J ( Add * Dom )	0.540	1.271	1.127	0.479	1.000		
Dominance Degree	27.7549						

Joint scaling test

	Parameter	Variance	S.E.mean	t value	Probability
M mean	66.352	0.211	0.460	144.395	
d Add	-1.201	0.234	0.483	-2.486	
h Dom	0.528	0.497	0.705	0.750	
Dominance Degree	-0.6631				

Joint scaling test

	Parameter	Variance	S.E.mean	t value	Probability
M mean	66.645	0.059	0.242	274.843	
d Add	-1.270	0.225	0.475	-2.675	
Dominance Degree	0.0000				

Test of Goodness of fit

Generation	Weight	Observed	Expected	$\chi^2$
P1	2.25	60.7000	65.3748	49.2439
P2	1.22	61.7000	67.9142	47.0025
F1	5.02	63.4600	66.6445	50.8590
F2	4.63	67.0480	66.6445	0.7543
BC1	2.33	74.2080	66.0097	156.3381
BC2	1.91	74.1680	67.2793	90.4441
			$\Sigma \chi^2$	394.642
			Probability	0.000

### Joint scaling test

	Parameter	Variance	S.E.mean	t value	Probability
M mean	32.640	7.588	2.755	11.849	
d Add	-0.500	0.316	0.562	-0.889	
h Dom	106.812	51.226	7.157	14.924	
i Add * Add	28.560	7.272	2.697	10.591	
j Add * Domt	1.080	5.084	2.255	0.479	
l Dom * Dom	-75.992	20.790	4.560	-16.666	
Dominance Degree	-14.6159				

### Joint scaling test

	Parameter	Variance	S.E.mean	t value	Probability
M mean	32.519	7.525	2.743	11.855	
d Add	-0.366	0.238	0.487	-0.750	
h Dom	107.174	50.655	7.117	15.058	
i Add * Add	28.640	7.244	2.691	10.641	
l Dom * Dom	-76.233	20.536	4.532	-16.822	
Dominance Degree	-17.1217				

### Joint scaling test

	Parameter	Variance	S.E.mean	t value	Probability
M mean	32.483	7.522	2.743	11.843	
h Dom	107.284	50.634	7.116	15.077	
i Add * Add	28.568	7.234	2.690	10.621	
l Dom * Dom	-76.306	20.527	4.531	-16.842	

### Test of Goodness of fit

Generation	Weight	Observed	Expected	$\chi^2$
P1	2.25	60.7000	61.0507	0.2772
P2	1.22	61.7000	61.0507	0.5131
F1	5.02	63.4600	63.4600	0.0000
F2	4.63	67.0480	67.0480	0.0000
BC1	2.33	74.2080	74.1900	0.0008
BC2	1.91	74.1680	74.1900	0.0009
			$\Sigma\chi^2$	0.792
			Probability	0.673

P1 = Parent 1

P2 = Parent 2