Electronic Journal of Plant Breeding, 1(6): 1474-1479 (Dec 2010)
ISSN 0975-928X

Research Note

Yield component analysis and recombinative heterosis of complex characters in QPM maize

A.Thanga Hemavathy*, **N.Subbaraman, S.M.Ibrahim and K.Balaji**

Dept. of Plant Breeding and Genetics, Agricultural College and Research Institute, Killikulam- 628252
*Email: hema_gene@yahoo.co.in

(Received: 29 Jul 2010; Accepted:17 Oct 2010)

Abstract:
Component analysis is the analysis of variation of complex character based on the variation of its components. For assessing the variation, components should be arranged in ontogenetical order. This allows determination of the mutually independent contributions of the components to the variation of complex character. Component analysis provides the necessary data for the exploitation of recombinative heterosis in plant breeding. Recombinative heterosis is the phenomenon where in, the progeny value of a complex character exceeds the mid parental value as a result of the multiplicative relationship between the complex character and its component traits. It is suggested that this form of heterosis may be an important cause of specific combining ability. As such, it may be involved in the heterosis of complex characters in F_1 hybrids and in the hybrid- vigor encountered in interspecific hybrid populations. It is demonstrated how recombinative heterosis may be explained by a quantitative genetical model involving additive inheritance of the component traits. Current study was focused to predict progeny performance for the complex character from parental data for the component traits. This requires regression of individual components on the preceding primary characters. The contribution of the coefficient for yield component C_3 (single seed weight) to variance of log yield was maximum in the parents CML 189, UMI 814, CML 145, UMI 524, CML 141 followed by the coefficient C_2 (number of kernels per row) which was maximum in the parents UMI 427 and UMI 814. In the present investigation, 35 hybrid combinations were tested for progeny prediction value. Application of this procedure revealed that among the 35 crosses, five crosses exceeded the predicted mid parental value. The predicted values can serve as a basis for the selection of promising combinations. The crosses that exhibited higher values for grain yield per plant was predicted in the combination of CML 142 x UMI 426, CML 143 x UMI 427, CML144 x UMI 189, CML 144 x UMI 426 and CML 147 x UMI 426.

Key words:
Maize, QPM, component analysis, progeny prediction

Component analysis of complex characters can provide a sound basis for the choice of parents and parent combinations to be used in the breeding for such characters. Thomas and Grafius (1976) defined a component as ‘strictly those characters which when multiplied together give yield exactly’. Yield components play an important role in many crop breeding programmes. Plant breeders often seek to improve yield by selection of components for yield such as seeds per plant or thousand kernel weight. It is frequently of interest to identify those components, which contribute to the complex trait ‘yield’ (Piepho, 1995).

The term recombinative heterosis is defined as the heterotic performance of a complex character in a family resulting from a cross between parents with complementary component traits. Current analysis was carried out to assess the contribution of individual yield components *viz.,* number of kernel rows, number of kernels per row, single grain weight to the variation in the complex trait seed yield per plant (Y) for twelve parents (seven lines and five testers) and the progeny performance for the complex character (yield) was also predicted from mean observations of primary characters.

Twelve parents were subjected to component analysis and progeny prediction analysis. All the twelve parents (7 lines and 5 testers) along with 35 crosses were evaluated under irrigated condition during summer,2004 in Agricultural College and Research Institute, Madurai. Each entry was grown in two rows of five-meter length adopting randomized complete block design replicated thrice adopting spacing of 60 x 25 cm. The recommended agronomic and plant protection practices were followed to maintain healthy stand of the plants. Biometrical observations and biochemical observations were recorded on five randomly selected plants from each entry per replication.

Component analysis was carried out (Piepho, 1995) to assess the contribution of individual yield components *viz.,* number of kernel rows, number of kernels per row and single grain weight to the variation in the complex traits seed yield per plant (Y) for twelve parents (seven lines and five testers). Progeny prediction was carried out as per the procedure of Bos and Sparnaaij, 1993.

Component analysis was carried out to assess the contribution of individual yield components *viz.,* number of kernel rows, number of kernels per row and single seed weight to the variation in the complex trait seed yield per plant (Y) for twelve parents (seven lines and five testers). The estimate of variance and co-variance of the primary character to yield is tabulated in Table 1. The coefficient for yield component (C_i), variance of log yields (σ^2) , standard deviation of log yields (σ), coefficient of variation of yield (v%) and per cent contribution of coefficients for yield component to variance of log yields have been recorded in Table 2. The variance of log yields ranged from 0.42 x 10^{-2} (CML 147) to 0.88 x 10^{-2} (UMI 814). The standard deviation ranged from 1.83 x 10^{-2} (CML 147) to 7.77 x 10^{-2} (UMI 814). The percentage contribution of the coefficient C_1 (number of kernel rows) ranged from 37.14 (UMI 814) to 69.23 (UMI 427). The per cent contribution of C_2 (number of kernels per row) ranged from 2.13 (UMI 426) to 23.81 (CML 141). The per cent contribution of C_3 (single grain weight) ranged from 4.17 (UMI 189) to 54.29 (UMI 814).

Relative heterosis is a complex trait due to its multiplicative nature. For recombination heterosis to occur between two parents they should display large numeric difference among the component traits, and neither should have a monopoly of high expression (Melchinger *et al.,* 1994). In a population of potential parents, this is most likely to be the cause of components either among themselves or with other components. Such components will have a large influence on the variability of the complex trait. (Piepho, 1995).

Plant breeders often seek to improve the yield by selecting for components of yield. Component analysis was found to be simpler to determine the effects of individual components on heterosis. Sparnaaij and Bos, (1993) and Piepho (1995) have introduced a simple method of analysis for yield components. The procedure allows quantification of the contribution of each component to the variability of final yield and helps to identify key components responsible for yield instability.

The contribution of the coefficient for yield component C_3 (single grain weight) to variance of log yield was maximum in the parents CML 189, UMI 814, CML 145, UMI 524, CML 141 followed by the coefficient C_2 (number of kernels per row) was maximum in the parents UMI 427 and UMI 814 (Table 2). In majority of the genotypes the coefficient C_3 (single grain weight) contributed the maximum to the variance followed by number of kernels per row of log yield and hence both were identified as the key component responsible for yield instability. Improving the stability of the components single grain weight and number of kernels per row may help in stabilizing yield.

Maximization of hybrid vigour can be achieved by increasing either directional dominance or by increasing initial differences in gene frequency (Sharma and Kumar 1987). However change of directional dominance in parents is not feasible, but difference in gene frequency can effectively be increased by choosing genetically divergent parents. Based on coefficient for yield component for the trait number of kernel rows, the line CML 141 can be combined with tester UMI 427 to bring out maximum heterosis. Maximum hybrid vigour for the trait, number of kernels per row can be fixed by combining CML 141 line with UMI 427 and UMI 814. For the trait single seed weight, maximum heterosis was observed by combining CML 145 with UMI 189 and by combining UMI 189 and UMI 814.

Recombinative Heterosis – prediction of progeny performance

Progeny performance for the complex character (yield) was predicted from mean observations on the primary characters viz., number of kernel rows, number of kernels per row, single seed weight, grain yield per plant and the component x_1 (a number of kernel rows), x_2 (b/a number of kernels per row/ number of kernel rows), x_3(c/b single seed weight / number of kernels per row) and x_4 (y/c grain yield per plant/ single seed weight) (Table 3). The parent CML 141 had the minimum grain yield per plant of (70.63g) while the parent CML 147 had the maximum yield per plant of (140.32g). The coefficient of correlation (r) between the components (x_1x_4) of the complex character y and the primary character (ay) were worked out and furnished in Table 4. Complementary determination (Cd) derived from r^2 (y, a---y) values ranged from 0.165 (y, x_1) to 0.748 (y, x_2) (Table 4).

The regression of individual component on their preceding primary characters and the residuals per cultivar obtained from these regressions are given in Table 5. The predicted values of the individual primary characters and components for the cross combinations (lines x testers) are shown in (Table 6). The predicted yield ranged from 19.21g (CML 146 x UMI 426) to 78.58g (CML 142 x UMI 426).

Recombinative heterosis is the phenomenon that the progeny value of complex characters exceeds the mid-parental value as a result of the multiplicative relationship between the complex character and its component traits. It is suggested that this form of heterosis may be an important cause for specific combining ability. Recombinative heterosis has been worked out by a quantitative genetical model (Bos and Sparnaaij, 1993) involving additive inheritance of the component traits contributing to the variation of grain yield per plant.

Often the F_1 value of the components will deviate from the mid parental value. This will occur when components are complementary, *i.e.,* when a relatively high value of one component in parents P_i is complemented by a high value for another component to parent P_j. This solution is a major cause of the non-additive inheritance of complex characters known as specific combining ability (*sca*). It implies that there is a scope for active exploitation of *sca* by crossing parents with complementary component traits. The more contrasting the parents are for these traits, the more the complex character in the progeny deviates from its mid parental value. This deviation is known as recombinative heterosis (Sparnaaij and Bos, 1993). The pursuit of recombinative heterosis is more likely to be successful when the most important components are known along with information about their mutual relationships.

In the present investigation, 35 hybrid combinations were tested for progeny prediction value. Application of this procedure revealed that among the 35 crosses, five crosses exceeded the predicted mid parental value (Table 7). The predicted values can serve as a basis for the selection of promising combinations.

The complementary determinations indicate that the two most important components contributing to the variation of grain yield per plant are number of kernels per row and single kernel weight. The crosses that exhibited higher values for the complex characters, grain yield per plant, was predicted in the combination of CML 142 x UMI 426, CML 143 x UMI 427, CML144 x UMI 189, CML 144 x UMI 426 and CML 147 x UMI 426. When the objective is to select parents for breeding purposes, the selection criteria must be chosen among the components on the basis of their complementary determination values. The coefficient of determination (r^2) of grain yield (Table 5) by the successive primary characters measures the proportion of the variances of grain yield determined at successive stages. An increase in r^2 value from one stage to the next represents the influence of the intervening components. This increase is the complementary determination of grain yield by component X_i.

When the genetic improvement of a complex character is the objective, the application of component analysis is an essential and rewarding part of the breeding procedure, which allows exploitation of recombinative heterosis and improves efficiency in breeding of complex characters by providing the means to predict progeny performance.

References

Bos, I., and Sparnaaiij, L.D. 1993. Component analysis of complex characters in plant breeding. II. The pursuit of heterosis. *Euphytica,* **70**: 237-245.

Melchinger, A.E., Singh, M., Link,W., Utz, H.F. and Kittlitz, E. 1994. Heterosis and gene effects of multiplicative characters. Theoretical relationships and experimental results from *Vicia faba L. Theor. Appl. Genet.,* **88**: 343-348.

Piepho, H.P. 1995. A simple procedure for yield component analysis. *Euphytica,* **84**: 43-48.

Sharma, J.K and Kumar, S.1987. Association analysis for grain yield and some quantitative traits in popcorn. *Crop Imp*., **14**: 201-204.

Sparnaaij, L.D and Bos, I 1993. Component analysis of complex characters in plant breeding. I. Proposed method for quantifying the relative contribution of individual components to variations of the complex character. *Euphytica*, **70**: 225-235.

Thomas, R.L. and Grafius, J.E. 1976. Prediction of heterosis levels from parental information. *Proc. Seventh Congress of Eucarpia*, 173-180.

Table 1. Estimates of variance and covariance of the primary characters to yield

Genotype	σ^2 log(x_1) ($x10^{-2}$)	σ^2 log(x_2) ($x10^{-2}$)	σ^2 log(x_3) ($x10^{-2}$)	Cov [log(y), log(x_1)] ($x10^{-2}$)	Cov [log(y), log(x_2)] ($x10^{-2}$)	Cov [log(y), log(x_3)] ($x10^{-2}$)
CML 141	0.15	0.01	0.03	0.05	0.09	0.02
CML 142	0.06	0.02	0.13	0.0005	0.0006	0.009
CML 143	0.04	0.06	0.25	-0.05	0.008	0.02
CML144	0.06	0.05	0.07	0.007	0.008	0.02
CML 145	0.03	0.05	0.04	-0.002	0.0009	0.03
CML 146	0.06	0.03	0.17	0.01	0.005	0.03
CML147	0.08	0.01	0.07	0.006	0.002	0.005
UMI 189	0.06	0.01	0.31	-0.0001	0.0001	0.22
UMI 426	0.06	0.05	0.29	0.003	0.005	0.01
UMI 427	0.13	0.21	0.05	0.03	0.03	0.009
UMI 524	0.09	0.02	0.37	-0.003	0.005	0.03
UMI 814	0.06	0.20	0.35	0.003	0.03	0.13

Table 2. Estimates of C_i, σ^2, σ, v% and % contribution of C_i to σ^2

Genotype	C_1	C_2	C_3	σ^2	σ	v%	% contribution of C_i to σ^2		
							C_1	C_2	C_3
CML 141	0.15	0.14	0.37	0.82	6.74	4.29	66.67	23.81	9.52
CML 142	0.06	0.02	0.14	0.47	2.22	2.23	63.26	12.25	24.49
CML 143	0.04	0.06	0.25	0.59	3.49	2.83	59.46	2.70	37.84
CML144	0.07	0.06	0.09	0.46	2.17	2.30	57.14	2.86	42.86
CML 145	0.03	0.06	0.46	0.68	4.69	3.50	48.28	13.79	37.93
CML 146	0.08	0.03	0.20	0.56	3.17	2.74	42.86	19.05	38.10
CML147	0.08	0.02	0.07	0.42	1.83	1.99	50.00	12.50	37.50
UMI 189	0.06	0.01	0.53	0.78	6.08	3.70	54.17	4.17	4.17
UMI 426	0.06	0.05	0.30	0.64	4.15	3.38	63.83	2.13	34.04
UMI 427	0.10	0.25	0.06	0.68	4.75	3.28	69.23	7.69	23.08
UMI 524	0.09	0.03	0.40	0.72	5.19	3.69	61.54	11.54	26.92
UMI 814	0.05	0.23	0.48	0.88	7.77	4.28	37.14	8.57	54.29

Table 3. Observations (averages per plant) on the primary characters

	Progeny prediction value						
Genotype	x_1 =a	x_2	b	x_3	c	x_4	Y
CML 141	14.9_3	1.590_9	23.7_5	0.00971	0.231	307.081	70.63_1
CML 142	15.0_5	1.513_5	22.7_3	0.012_8	0.28_6	340.46_4	94.99_5
CML 143	16.1_8	1.528_6	24.6_6	0.013_{12}	0.31_{10}	396.03_7	122.77_9
CML 144	14.3_2	1.811_1	25.9_9	0.0116	0.29_8	370.346	107.40_6
CML 145	15.7_6	1.395_2	21.92	0.012_9	0.264	343.81_5	91.11_4
CML 146	16.3_3	1.530_7	24.9_7	0.011_5	0.28_7	405.85_8	113.64_7
CML 147	16.410	1.682_{12}	27.6_{12}	0.012_{10}	0.31_{11}	452.64_{11}	140.32_{12}
UMI 189	18.4_{12}	1.440_4	26.5_{11}	0.0098_2	0.26_3	487.61_{12}	126.78_{10}
UMI 426	15.0_4	1.433_3	21.41	0.0118_3	0.242	321.00_3	77.04_2
UMI 427	15.8_7	1.650_{10}	26.1_{10}	0.0118_7	0.31_{12}	412.38_9	127.84_{11}
UMI 524	13.7_1	1.660_{11}	22.8_4	0.013_{11}	0.29_9	312.34_2	90.58_3
UMI 814	16.8_{11}	1.548_8	25.8_8	0.010_4	0.27_5	433.44_{10}	117.03_8

a = number of kernel rows; b = number of kernels per row; c = single seed weight; and y = single plant yield. Components x_1 =a; x_2 = b/a; x_3 =c/b; x_4 = y/c ; Ranking orders in small figures

Table 4. Correlations between the component traits and primary characters

	a	**b**	**c**	**y**
x_1 **=a**	1.000**	0.551	0014	0.639**
x_2 **= b/a**	-0.442	0.502	0.517	0.243
x_3 **=c/b**	-0.179	0.129	0.601**	0.298
x_4 **= y/c**	0.870**	0.845**	0.604	0.907**
y	0.639**	0.858**	0.746*	1.000**
r^2 **(y,a…..y)**	**0.165**	**0.748**	**0.348**	**1.000**
Cd (y, x_1...x_4)	**0.409**		**0.327**	**0.155**
		0.419		

r^2 values indicate Fractions of determination of y by stages a, b, c and y.
cd values indicate Increase in determination of y from stage to stage, attributable to intervening components $x_{1,}...x_4$.

Table 5.The residuals per cultivar obtained from the regressions : rx_2, rx_3 and rx_4.Residuals for $x_2,……. x_4$

Genotype	rx_2	rx_3	rx_4
CML 141	-0.5862	0.007212	-143.58
CML 142	-0.6628	0.002404	-167.50
CML 143	-0.6510	-0.0009592	-123.58
CML 144	-0.3677	-0.007166	168.49
CML 145	-0.5418	0.006438	248.79
CML 146	0.7218	0.005412	348.78
CML 147	0.6314	0.004234	-371.70
UMI 189	-0.7212	0.002157	121.58
UMI 426	-0.8038	0.0017172	67.58
UMI 427	-0.5223	-0.0020330	151.25
UMI 524	-0.5213	-0.0029144	281.38
UMI 814	-0.6280	0.0022184	158.11

Table 6. The predicted values of the individual primary characters and components

Cross combination	$\hat{a}$ or $\hat{x}_1$	$\hat{x}_2$	$\hat{b}$	$\hat{x}_3$	$\hat{c}$	$\hat{x}_4$	$\hat{y}$	Mid parental value
CML 141 x UMI 189	16.65	3.64	60.66	0.029	1.77	892.02	33.48	75.51
CML 141 x UMI 426	14.95	3.61	54.07	0.165	1.97	820.01	35.48	67.49
CML 141 x UMI 427	15.35	2.17	67.25	0.076	1.95	825.83	44.15	91.55
CML 141 x UMI 524	14.2	4.61	61.39	0.110	1.81	810.04	33.76	86.99
CML 141 x UMI 814	15.85	5.16	85.36	0.0134	1.04	1152.97	69.60	83.18
CML 142 x UMI 189	16.70	4.75	124.63	0.0190	1.46	841.00	62.08	79.23
CML 142 x UMI 426	15.00	4.67	121.55	0.390	2.40	521.26	78.58	71.20
CML 142 x UMI 427	15.40	3.17	124.29	0.1135	2.70	688.42	56.13	95.24
CML 142 x UMI 524	14.35	2.18	122.78	0.4067	2.64	361.88	70.40	90.70
CML 142 x UMI 814	15.90	1.52	124.33	0.013	3.20	421.89	58.55	86.89
CML 143 x UMI 189	17.25	1.47	125.42	0.089	2.26	1222.17	50.12	84.01
CML 143 x UMI 426	15.55	5.86	113.74	0.0019	1.57	1123.44	76.94	75.99
CML 143 x UMI 427	15.95	1.53	85.17	0.0135	3.36	436.83	43.28	100.05
CML 143 x UMI 524	14.9	7.12	89.68	0.0418	1.12	1758.22	28.12	95.49
CML 143 x UMI 814	16.45	10.88	94.12	0.0175	1.78	1078.32	29.78	91.68
CML 144 x UMI 189	16.35	1.62	126.57	0.124	3.30	3195.23	75.42	74.45
CML 144 x UMI 426	14.50	1.59	123.05	0.152	3.52	2298.07	68.78	66.43
CML 144 x UMI 427	15.05	7.27	93.18	0.171	2.98	892.07	62.19	90.49
CML 144 x UMI 524	14.00	9.22	128.42	0.038	2.71	878.02	43.41	85.93
CML 144 x UMI 814	15.55	8.44	126.41	0.048	1.98	942.42	28.09	82.12
CML 145 x UMI 189	17.05	11.12	161.19	0.187	3.12	1078.39	37.02	96.17
CML 145 x UMI 426	15.35	10.19	128.05	0.937	2.12	898.43	32.34	88.15
CML 145 x UMI 427	15.75	9.12	117.75	0.812	2.24	902.12	38.37	112.21
CML 145 x UMI 524	14.70	6.12	78.12	0.428	1.28	968.37	21.38	107.65
CML 145 x UMI 814	16.25	11.12	121.05	0.241	2.76	838.14	24.32	103.84
CML 146 x UMI 189	17.35	5.82	79.74	0.481	1.76	1118.12	27.12	90.29
CML 146 x UMI 426	15.65	8.12	161.92	0.218	1.91	1860.12	19.21	82.27
CML 146 x UMI 427	16.05	8.75	128.20	0.240	2.86	1367.12	38.12	106.33
CML 146 x UMI 524	15.00	12.34	148.12	0.128	3.40	1782.13	58.12	101.77
CML 146 x UMI 814	16.55	10.93	121.68	0.912	2.18	849.93	46.12	97.96
CML 147 x UMI 189	17.40	13.60	148.12	0.281	2.12	1682.42	59.28	73.67
CML 147 x UMI 426	15.70	8.41	161.92	0.194	1.98	518.14	69.12	65.65
CML 147 x UMI 427	16.10	9.12	148.63	0.164	2.12	1563.12	56.12	89.71
CML 147 x UMI 524	15.05	8.12	162.19	0.912	2.06	989.13	58.64	85.15
CML 147 x UMI 814	16.61	10.21	152.28	0.845	2.42	1652.18	59.12	81.32