

Relationship between Genetic Distance and Heterosis in Cucumber

Jamal-Ali Olfati^{1*} • Habibollah Samizadeh² • Gholam-Ali Peyvast³ •
Babak Rabiei⁴ • S. Akbar Khodaparast⁵

¹ University of Guilan, Horticultural Department, Rasht, Iran

² University of Guilan, Department of Agronomy and Plant Breeding, Rasht, Iran

³ University of Guilan, Horticultural Department, Rasht, Iran

⁴ University of Guilan, Department of Agronomy and Plant Breeding, Rasht, Iran

⁵ University of Guilan, Department of Crop protection, Rasht, Iran

Corresponding author: *jamalaliolfati@gmail.com

ABSTRACT

In heterosis, hybrids perform better than the parents for a collection of characteristics. Heterosis has been utilized in many crops, including cucurbits, to exploit dominance variance through the production of hybrids. For determine the relationship between heterosis and genetic distance sample seeds of 6 cucumber (*Cucumis sativus* L.) lines were received from Europe and Asia. All lines were crossed with a partial diallel test. The experiment was a randomized complete block design with 15 F₁ hybrid and 6 parents and three replications. Factor analysis was performed using measured data. In related to the Eigen value we detected 8 factors and the specific combining ability (SCA) effects for the parents were estimated following Griffing's (1956) model 2 and 4 for these factors. Cluster analysis indicated three branches in Ward's tree. Using cluster analysis, information about the relationships among the investigated genotypes was obtained. Results showed that by increasing the genetic distance at first heterosis increased but when the genetic distance increased from special point by increasing of genetic distance heterosis decreased. So in hybrid seed production the breeders must be selected the lines with a moderate genetic distance.

Keywords: cluster, correlation, heterosis, regression, ward

Abbreviations: EF, early fruit; FSS, fruit shape score; GCA, general combining ability; MF, marketable fruit; SCA, specific combining ability; SWI, simple weight index; TFN, total fruit number

INTRODUCTION

Heterosis refers to the state in which hybrids achieve better than the parents in a collection of characteristics such as yield, biomass, stress tolerance, and reproducibility. Utilization of heterosis has become a major practice for increasing productivity of plants which has contributed significantly to the great increase of agricultural products worldwide in the last several decades (Stubber 1994; Yuan 1998; Huang *et al.* 2006). Heterosis has been utilized in many crops, including cucurbits, to exploit dominance variance through the production of hybrids. In cucumber (*Cucumis sativus* L.), Hayes and Jones (1916) first observed heterosis for fruit size and fruit number/plant. Others have reported heterosis for fruit yield in particular crosses of cucumbers (Hutchins 1938; Singh *et al.* 1970; Solanki *et al.* 1982a, 1982b; Rubino and Wehner 1986). Ghaderi and Lower (1979a, 1979b) reported heterosis for fruit number/plot, fruit weight/plot, and average fruit weight for several crosses of pickling cucumber (Rubino and Wehner 1986).

A large amount of hard work has been invested in separating the genetic basis of heterosis in crop plants. Two hypotheses, i.e., the dominance hypothesis (Davenport 1908) and the overdominance hypothesis (East 1908) were proposed early last century to detail the genetic basis of heterosis. The dominance hypothesis states that deleterious alleles at different loci in the parental genomes are complemented in the F₁ hybrid thus producing a better phenotype. The overdominance hypothesis asserts that the improved performance of an F₁ hybrid relative to its inbred parents is a consequence of favorable allelic interactions at heterozygous loci that outperform either homozygous state. Al-

though many investigators favored one hypothesis over the other (Allard 1960), data allowing for critical assessment of the hypotheses remained largely unavailable until very recently with the start of molecular marker technology and high-density molecular linkage maps.

Factor analysis or principle component analysis is a useful tool in the examination of multivariate data (Zitko 1994). In many crops, yield has been partitioned into its various components to better understand the factors which influence yield. However, the number of studies examining the correlation between yield components and heterosis for yield is limited. Hayes and Jones (1916) observed no heterosis when plants having similar fruit size and vine type were hybridized. This observation suggested that plants with large differences in their yield components were required for heterosis. Ghaderi and Lower (1978) suggested that heterosis in yield components such as number or weight of leaves, branches, and roots should have a direct effect on fruit yield. They hypothesized that more branches in F₁ hybrids than their parents might result in greater photosynthetic activity and, hence, higher yield. In another study, selection for a vigorous root system resulted in a 23% increase in fruit yield (Yurina and Lebedeva 1976).

Heterosis and combining ability of cucumber were reviewed by Peterson and Welgle (1958) for germplasm available in the US. The diallel mating design has been extensively used to estimate general combining ability (GCA) and specific combining ability (SCA) variances and their effects. Also, it is used to understand the nature of gene action involved in the expression of economically important quantitative traits. Thus, GCA and SCA estimates, which are useful in devising breeding strategies, were reported in

some cucurbits (Kanobdee *et al.* 1990; Cramer and wehner 1999; Wadid *et al.* 2003).

The objectives of this study were 1) to examine the amount of mid-parent and high-parent heterosis for fruit yield and yield components in pickling cucumber, and 2) to examine the amount of genetic distance between lines and 3) to examine the correlation and regression between genetic distance and heterosis in cucumber lines.

MATERIALS AND METHODS

Germplasm

Sample seeds of 6 cucumber lines were received from Czech Republic (BH 502, BH 504, BH 604, BH 605) and two (115 and 118) from the World Vegetable Center in Taiwan. All lines were crossed with a partial diallel test in which reciprocal crosses are

not used because previous research indicated that direct (Parent A as a female and parent B as a male) and reciprocal crosses (Parent B as a female and parent A as a male) do not affect many traits in cucumber (Kanobdee *et al.* 1990; Wadid *et al.* 2003).

Design

The experiment was a randomized complete block design with 15 F₁ hybrids and 6 parents and three replications. 40 seeds were planted in plots 3.1 m long as recommended by Swallow and Wehner (1986) on raised shaped beds. Plots were planted on the 8 July 2009. All research was conducted at the Agricultural research field in University of Guilan, Rasht, North of Iran I.R (37° 16' N) using standard cultural procedures for growing pickling cucumbers. Plots were thinned to 30 plants (64,500 plants/ha) on 22 July 2009. Plots were harvested when almost of the plots contained oversized fruit (> 51 mm in diameter) as recommended by Miller and

Table 1 Rotate (varimax) factor analysis of measured characteristics in cucumber lines.

Variables	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	Factor 6	Factor 7	Factor 8
Number of branches	-0.6	-0.32	0.34	0.17	0.009	-0.38	0.03	0.11
Non marketable yield	-0.81	0.14	0.29	-0.001	0.08	0.10	-0.11	0.01
Total yield	-0.24	0.005	0.92	-0.06	0.13	0.14	0.07	0.05
Early yield	-0.47	-0.14	0.03	-0.06	0.37	-0.40	-0.07	-0.24
Marketable yield	-0.04	-0.03	0.95	-0.07	0.11	0.13	0.08	0.03
plant length	0.07	-0.06	0.14	-0.08	0.18	0.80	-0.007	-0.04
Number of fruit on main branch	0.23	-0.10	0.25	0.21	0.29	0.15	0.70	0.15
Fruit end bitterness	0.03	0.01	0.10	0.05	0.05	-0.10	0.07	0.92
Days to harvest	0.70	0.17	-0.24	0.31	0.21	-0.007	-0.02	0.02
Number of nodes	0.05	-0.65	0.15	0.11	-0.1	0.47	0.25	0.02
Plant length	-0.18	-0.59	0.15	0.02	-0.24	0.62	0.09	0.04
Days to first male flower	0.03	-0.08	-0.06	-0.40	-0.17	-0.03	0.77	0.07
Days to first female flower	-0.07	-0.24	-0.54	-0.51	-0.02	0.16	0.16	0.09
Cotyledon bitterness	-0.03	0.95	0.07	0.09	-0.01	0.02	-0.002	0.03
5th leaf bitterness	-0.03	0.95	0.07	0.09	-0.01	0.02	-0.002	0.03
1st midrib length	-0.07	-0.07	0.11	0.42	0.70	0.14	-0.35	0.06
2nd midrib length	-0.37	0.12	-0.06	0.66	-0.007	0.25	-0.19	0.21
3rd midrib length	-0.08	0.25	-0.17	0.82	0.03	-0.08	0.12	-0.15
1st node length	-0.02	-0.34	0.06	0.76	0.20	-0.12	-0.13	0.003
Fruit shape	-0.85	0.02	-0.05	-0.22	-0.24	-0.01	-0.01	0.10
Marketable yield percent	0.83	-0.16	0.29	-0.04	-0.11	-0.05	0.02	-0.17
SWI	0.80	-0.04	0.50	-0.20	-0.15	0.04	-0.005	0.02
Overall performance	0.69	0.01	-0.30	-0.16	0.13	0.18	0.31	0.14
Fruit color	-0.21	0.16	0.18	0.04	0.82	0.01	0.22	0.19
Fruit seed cell size	-0.002	0.01	-0.17	-0.35	0.40	0.33	0.16	0.64
Eigen value	5.20	3.63	2.95	2.55	2.31	1.48	1.17	1.02
Proportion	0.21	0.15	0.12	0.10	0.09	0.06	0.05	0.04
Cumulative	0.21	0.36	0.48	0.58	0.67	0.73	0.78	0.82
Variance explained by each factor	4.58	3.09	2.98	2.74	1.91	1.89	1.58	1.54

Table 2 Estimated factors for each genotype.

Treatments	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	Factor 6	Factor 7	Factor 8
604	261.24	-70.17	-12.65	515.65	39.71	343.74	93.26	25.5
605	282.91	-40.03	-21.25	489.29	56.09	336.27	94.37	25.57
504	258.76	-107.2	-0.45	421.88	17.03	342.56	152.44	18.12
118	326.1	74.96	-26.24	495.63	105.06	211.68	66.01	2.98
502	299.88	-93.93	-3.94	373.21	31.2	353.31	143.64	27.34
115	115.06	-14.61	-46.92	531.29	107.53	250.71	71.65	36.1
604×115	182.14	-95.18	0.22	412.81	10.83	342.4	107.51	28.98
502×115	214.59	-111.28	20.45	391.09	44.66	373.94	103.37	42.21
118×115	112.09	-23.66	-71.64	490.02	74.93	349.91	100.39	66.21
504×605	205.31	-83.37	-21.6	473.31	70.09	379.65	94.73	49.68
502×605	275.68	-65.99	-35.6	306.26	28.14	324.72	156.14	34.21
502×504	166.54	-141.25	-8.23	508	34.93	411.9	128.49	38.43
604×605	212.54	-70.4	-32.69	573.84	43.14	342.76	109.64	31.63
504×118	270.97	-68.45	3.91	473.17	74.28	329.86	109.28	38.76
504×115	195.92	-97.9	11.22	441.15	26.26	362.53	111.82	30.74
118×605	276.38	91.78	-49.53	480.95	73.94	249.56	111.53	25.44
502×118	210.63	-103.33	10.43	658.36	99.12	377.68	74.39	36.66
502×604	177.09	-138.4	-19.87	420.14	28.12	370.36	111.02	40.14
118×604	256.31	17.4	-50.62	520.6	101.16	266.91	88.65	26.28
504×604	191.18	-140.79	17.73	581	62.15	392.38	92.06	32.67
605×115	219.49	22.18	-24.05	558.5	99	269.33	75.53	26.49

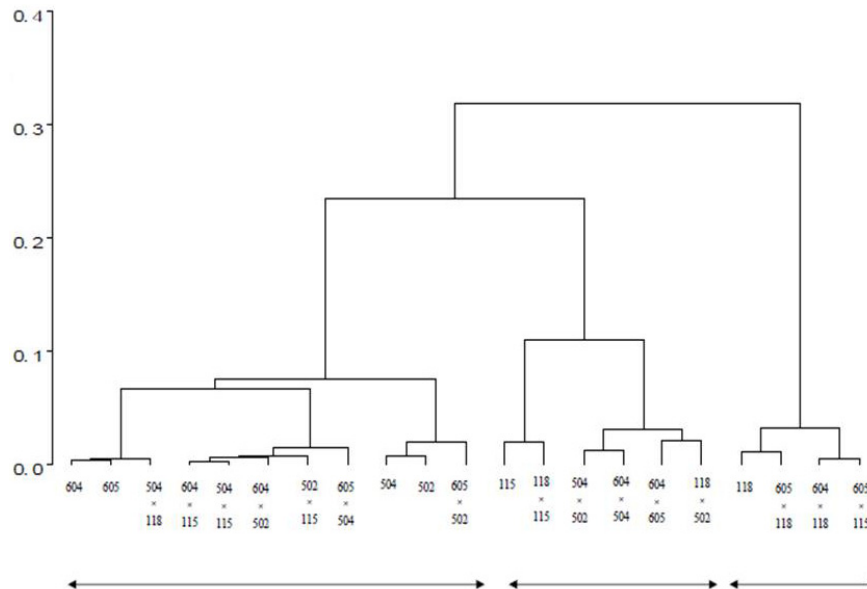


Fig. 1 Cluster analysis diagram.

Hughes (1969) for optimum fruit yield in once-over harvest of pickling cucumbers.

Data collection

Number of fruits/plant was counted to obtain early, marketable and total yield. Early fruit were the number of oversized fruit at harvest (>51 mm in diameter). The number of marketable fruit was calculated as total fruit minus culls. Cull fruits were misshapen (crooked or nubbin).

Days to harvest, day to first male flower appearance and day to first female flower appearance were recorded daily in the field for each plot.

Cotyledon bitterness, 5th leaf bitterness, 1st, 2nd and 3rd midrib length, first node length, plant length to first fruit were recorded during production season when each plot plants reach to measuring ability for each trait.

Number of nodes/plant, plant length, number of branches/plant, total yield, early yield, non-marketable yield, marketable yield, fruit shape, marketable yield percent, simple weight index (SWI), overall performance, fruit set percent, number of fruit in main branch, fruit bitterness, and fruit end bitterness were recorded in the field after harvesting.

SWI was calculated following Wehner and Cramer (1996):

$$\frac{TFN \times 0.2}{2} + \frac{(EF \times 0.3) + (MF \times 0.2)}{10} + FSS \times 0.3$$

where TFN = total fruit number, EF = early fruit, MF = marketable fruit and FSS = fruit shape score. For bitterness testing, 5 days after seeding, plants were examined by tasting one third of one cotyledon of each plant by 15 experts. Each taste-tester rinsed orally and ate a soda cracker after tasting a plant that had a bitter cotyledon to maintain accurate classification of bitter or non-bitter plants. In addition, fruit shape, color, seedcell size and overall performance were rated on a scale of 1 to 9, where 1–3 = poor, 4–6 = intermediate, 7–9 = excellent (Strefeler and Wehner 1986).

Data analysis

Factor analysis was performed using measured data. Data were rotated using varimax rotation. In related to the Eigen value, we detected 8 factors and the SCA effects for the parents were estimated following Griffing's 1956, model 2 (parents and one set of F_1 crosses) and 4 (one set of F_1 crosses) for these factors. Statistical analysis of the database includes cluster analysis, Pearson's correlation coefficient, and factor analysis introduced using SAS (version 9.1).

RESULTS AND DISCUSSION

Using rotated factor loading and commonalities varimax rotation analysis, information about the main factors (essential elements) in the cucumber was obtained (Table 1). The successive factors account for decreasing amounts of residual variance using 8 factors (varimax rotation) for the measured characteristics. Factor 1 makes up 21% of the total variance and contain days to harvest, marketable yield percent, SWI, and overall performance. Factor 2 makes up 15% of the total variance and contains cotyledon bitterness and 5th leaf bitterness. Factor 3 makes up 12% of the total variance and contains total yield and marketable yield. Factor 4 makes up 10% of the total variance and contains 1st, 2nd, and 3rd midrib length and first node length. Factor 5 makes up 9% of the total variance and only contain fruit color. Factor 6 makes up 6% of the total variance and contain plant length and number of nod. Factor 7 makes up 5% of the total variance and contain number of fruit in main branch, and days to first male flower appearance. Factor 8 makes up 4% of the total variance and contains fruit end bitterness and fruit seedcell size. Heterosis in yield components such as number or weight of leaves, branches, and roots should have a direct effect on fruit yield and are very important for breeders (Ghaderi and Lower 1978).

Cluster analysis indicated three branches in the WARD tree. Using cluster analysis information about the relationships among the investigated genotypes was obtained. This technique evaluated the relationships among the genotypes. The cluster diagram (Fig. 1) shows three main clusters: (A) includes 604, 605, 502, 504 while cluster (B) includes 115 and cluster (C) includes 118. According to this analysis we estimated genetic distance between lines.

In Table 2 we estimated factors for all genotypes and used these data for cluster analysis. Heterosis per midparent and high parent is represented in Tables 3–10. Tables 11 and 12 represented SCA estimated via Griffing's methods 2 and 4, respectively.

Orthogonal regression between genetic distance and other measured data showed that there is a correlation between genetic distance and some parameters. According to these results we found a sigmoid relationship between midparent heterosis and genetic distance for Factor 1 (containing days to harvest, marketable yield percent, SWI, overall performance) (Fig. 2), 4 (containing 1st, 2nd, and 3rd midrib length and first node length) (Fig. 3), 5 (containing fruit color) (Fig. 4) and 8 (containing fruit end bitterness and fruit seedcell size) (Fig. 5). There was a similar correlation between high parent heterosis and genetic distance for

Table 3 Heterosis by cross, relative to midparents or high parent for factor 1.

Parent 1	Parent 2	Het (Midparents)	Het (Maxparent)
604	605	-59.53	-70.37
604	504	-68.82	-70.06
604	118	-37.36	-69.79
604	502	-103.47	-122.79
604	115	-6.01	-79.1
605	504	-65.52	-77.6
605	118	-28.12	-49.72
605	502	-15.71	-24.2
605	115	20.5	-63.42
504	118	-21.46	-55.13
504	502	-112.78	-133.34
504	115	9.01	-62.84
118	502	-102.36	-115.47
118	115	-108.49	-214.01
502	115	7.12	-85.29

Table 5 Heterosis by cross, relative to midparents or high parent for factor 3.

Parent 1	Parent 2	Het (Midparents)	Het (Maxparent)
604	605	-15.74	-20.04
604	504	24.28	18.18
604	118	-31.17	-37.97
604	502	-11.57	-15.93
604	115	30	12.87
605	504	-10.75	-21.15
605	118	-25.78	-28.28
605	502	-23	-31.66
605	115	10.03	-2.8
504	118	17.25	4.36
504	502	-6.03	-7.78
504	115	34.9	11.67
118	502	25.52	14.37
118	115	-35.06	-45.4
502	115	45.88	24.39

Table 7 Heterosis by cross, relative to midparents or high parent for factor 5.

Parent 1	Parent 2	Het (Midparents)	Het (Maxparent)
604	605	-4.76	-12.95
604	504	33.78	22.44
604	118	28.77	-3.9
604	502	-7.33	-11.59
604	115	-62.79	-96.7
605	504	33.53	14
605	118	-6.63	-31.12
605	502	-15.5	-27.95
605	115	17.19	-8.53
504	118	13.23	-30.78
504	502	10.81	3.73
504	115	-36.02	-81.27
118	502	30.99	-5.94
118	115	-31.36	-32.6
502	115	-24.7	-62.87

factor 4 (containing 1st, 2nd, and 3rd midrib length and first node length) (Fig. 6), 5 (containing fruit color) (Fig. 7), and 8 (containing fruit end bitterness and fruit seedcell size) (Fig. 8). We found a correlation between SCA estimated via Griff-in's model 2 and genetic distance for factor 1 (containing days to harvest, marketable yield percent, SWI, overall performance) (Fig. 9), 4 (containing 1st, 2nd, and 3rd midrib length and first node length) (Fig. 10), 5 (containing fruit color) (Fig. 11), 6 (containing plant length and number of nodes) (Fig. 12) and 8 (containing fruit end bitterness and fruit seedcell size) (Fig. 13). The estimated SCA via model 4 produced different correlations with genetic distance. All other regressions were not significant.

The concept of combining ability is important in designing plant breeding programs. Cucumber breeders might

Table 4 Heterosis by cross, relative to midparents or high parent for factor 2.

Parent 1	Parent 2	Het (Midparents)	Het (Maxparent)
604	605	-15.3	-30.37
604	504	-52.1	-70.62
604	118	15	-57.56
604	502	-56.35	-68.23
604	115	-52.79	-80.57
605	504	-9.75	-43.34
605	118	74.31	16.82
605	502	0.99	-25.96
605	115	49.5	36.79
504	118	-52.33	-143.41
504	502	-40.68	-47.32
504	115	-36.99	-83.29
118	502	-93.84	-178.29
118	115	-53.83	-98.62
502	115	-57.01	-96.67

Table 6 Heterosis by cross, relative to midparents or high parent for factor 4.

Parent 1	Parent 2	Het (Midparents)	Het (Maxparent)
604	605	71.37	58.19
604	504	112.23	65.35
604	118	14.96	4.95
604	502	-24.29	-95.51
604	115	-110.66	-118.48
605	504	17.72	-15.98
605	118	-11.51	-14.68
605	502	-124.99	-183.03
605	115	48.21	27.21
504	118	14.41	-22.46
504	502	110.45	86.12
504	115	-35.43	-90.14
118	502	223.94	162.73
118	115	-23.44	-41.27
502	115	-61.16	-140.2

Table 8 Heterosis by cross, relative to midparents or high parent for factor 6.

Parent 1	Parent 2	Het (Midparents)	Het (Maxparent)
604	605	2.75	-0.98
604	504	49.23	48.64
604	118	-10.8	76.83
604	502	21.83	17.05
604	115	45.17	-1.34
605	504	40.23	37.09
605	118	-24.41	-86.71
605	502	-20.07	-28.59
605	115	-24.16	-66.94
504	118	52.74	-12.7
504	502	63.96	58.59
504	115	65.89	19.97
118	502	95.18	24.37
118	115	118.71	99.2
502	115	71.93	20.63

develop high yielding cultivars based on high general combining ability for their traits. Hayes and Jones (1916) observed no heterosis when plants having similar fruit size and vine type were hybridized; accordingly, the overdominance hypothesis asserts that the improved performance of an F₁ hybrid relative to its inbred parents is a consequence of favorable allelic interactions at heterozygous loci that outperform either homozygous state (Allard 1960). This observation suggests that plants with large differences in their yield components are required for heterosis.

Although yield heterosis is the primary target for increasing productivity, the biological complexity of yield as a trait frequently makes it difficult to draw meaningful conclusions of the data in order to track individual causal elements involved in heterosis. However, we are able with this

Table 9 Heterosis by cross, relative to midparents or high parent for factor 7.

Parent 1	Parent 2	Het (Midparents)	Het (Maxparent)
604	605	15.82	15.27
604	504	-30.79	-60.38
604	118	9.01	-4.61
604	502	-7.43	-32.62
604	115	25.05	14.25
605	504	-28.67	-57.71
605	118	31.34	17.16
605	502	37.13	12.5
605	115	-7.48	-18.84
504	118	0.05	-43.16
504	502	-19.55	-23.95
504	115	-0.22	-40.62
118	502	-30.43	-69.25
118	115	31.56	28.74
502	115	-4.27	-40.27

Table 10 Heterosis by cross, relative to midparents or high parent for factor 8.

Parent 1	Parent 2	Het (Midparents)	Het (Maxparent)
604	605	6.09	6.06
604	504	10.86	7.17
604	118	12.04	0.78
604	502	13.72	12.8
604	115	-1.82	-7.12
605	504	27.83	24.11
605	118	11.16	-0.13
605	502	7.75	6.87
605	115	-4.34	-9.61
504	118	28.21	20.64
504	502	15.7	11.09
504	115	3.63	-5.36
118	502	21.5	9.32
118	115	46.67	30.11
502	115	10.49	6.11

Table 11 SCA of factors estimated by Griffing's model 2.

Parent 1	Parent 2	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	Factor 6	Factor 7	Factor 8
604	605	-31.34	-21.19	-6.03	71.24	-6.94	12.02	9.1	2.4
604	504	-26.72	-21.54	18.38	84.78	27.66	21.28	-21.6	2.45
604	118	9.51	35.42	-23.47	-12.37	25.2	-33.67	3.12	-0.54
604	502	-52.92	-18.91	-13.87	-39.81	-5.82	-1.22	-5.07	7.44
604	115	13.37	-27.32	20.84	-87.88	-44.78	16.54	18.77	-6.28
605	504	-39.28	-11.85	-9.02	-1.88	22.89	29.01	-24.04	18.47
605	118	2.9	62.07	-10.45	-30.98	-14.73	-30.56	20.88	-2.36
605	502	18.98	5.77	-17.67	-132.66	-18.51	-26.39	34.94	0.53
605	115	24.04	42.31	8.5	78.84	30.68	-36.07	-18.32	-9.75
504	118	23.46	-28.12	16.98	-32.38	1.2	9.38	5.52	9.96
504	502	-64.18	0.55	-16.31	75.46	3.87	20.43	-5.83	3.76
504	115	26.44	-7.73	17.75	-32.13	-26.47	16.77	4.85	-6.5
118	502	-48.99	-62.76	28.85	189.07	26.59	56.73	-31.8	5.39
118	115	-86.28	-34.72	-38.6	-20	-19.27	74.67	21.54	32.38
502	115	33	-20.87	32.34	-45.92	-7.52	27.71	-6.03	2.5

Table 12 SCA of factors estimated by Griffing's model 4.

Parent 1	Parent 2	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	Factor 6	Factor 7	Factor 8
604	605	-22.94	-37.97	4.5	77.45	-9.71	36.94	2.98	4.7
604	504	-4.43	-1.87	13.29	63.66	20.95	8.99	-11.8	0.03
604	118	36.59	44.94	-14.94	-33.35	21.03	-40.88	-2.17	-7.13
604	502	-22.17	7.64	-15.34	-49	-4.9	-8.6	-2.1	7.16
604	115	12.95	-12.74	12.49	-58.76	-27.36	3.56	13.09	-4.75
605	504	-32.83	-24.84	-6.48	-15.14	11.66	33.45	-18.8	15.1
605	118	14.12	38.93	5.71	-44.12	-23.42	-21.04	11.03	-9.91
605	502	33.88	-0.34	-11.51	-134	-22.1	-17.05	33.35	-0.7
605	115	7.77	24.23	7.78	115.81	43.58	-32.31	-28.56	-9.18
504	118	48.58	-14.81	17.53	-72.84	-11.43	-18.31	11.58	-2.29
504	502	-35.39	30.89	-25.77	46.8	-3.66	-7.44	8.5	-2.2
504	115	24.07	10.64	1.43	-22.48	-17.51	-16.69	10.52	-10.63
118	502	-15.41	-42.57	33.01	160.54	21.59	33.94	-32.57	-4.74
118	115	-83.88	-26.5	-41.31	-10.23	-7.77	46.29	12.13	24.07
502	115	39.09	4.38	19.62	-24.34	9.07	-0.85	-7.18	0.49

result to explain the relationship between heterosis, SCA with genetic distance. By increasing the genetic distance at first heterosis and SCA (negative or positive) increased and in a specific point by more increasing of genetic distance heterosis and SCA decreased (Fig. 2-13).

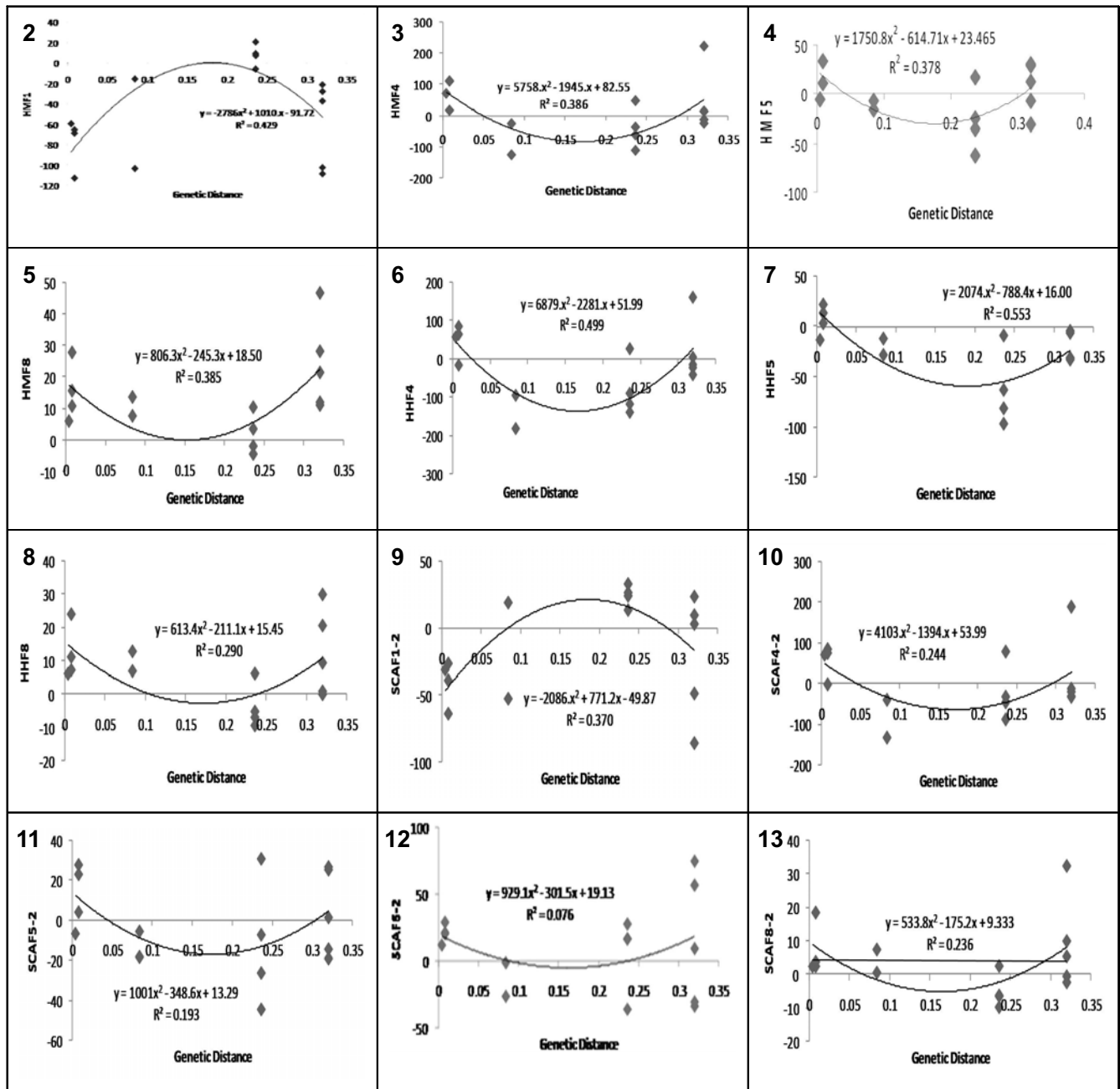
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Orthogonal regression between genetic distance and midparent heterosis for factor 1 (Fig. 2), factor 4 (Fig. 3), factor 5 (Fig. 4), factor 8 (Fig. 5). Orthogonal regression between genetic distance and high parent heterosis for factor 4 (Fig. 6), factor 5 (Fig. 7), factor 8 (Fig. 8). Orthogonal regression between genetic distance and factor 1 (Fig. 9), factor 4 (Fig. 10), factor 5 (Fig. 11), factor 6 (Fig. 12) and factor 8 (Fig. 13) SCA estimated in model 2.

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