

Research paper

General and specific combining ability for yield-related traits in watermelon

Siavash Ghorbanian¹, Jamal-Ali Olfati¹, and Babak Rabiei²

Received: July 26, 2022 Accepted: February 13, 2023

¹Department of Horticultural Sciences, Faculty of Agriculture, University of Guilan, Rasht, Iran

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

*Corresponding author; Email: jamalaliolfati@gmail.com

Abstract

Estimates of combining ability are useful in determining the value of watermelon (*Citrullus lanatus* (Thunb.) Matsum. & Nakai) lines in producing new hybrids with high yield and better quality. This research was conducted to estimate the general combining ability (GCA), specific combining ability (SCA), and heterosis for five inbred lines chosen for watermelon breeding at the University of Guilan, Iran. Analysis of variance indicated significant differences among hybrids for fruit weight and the number of lateral branches per plant. The GCA and SCA effects were significant for fruit weight and the number of lateral branches, which indicates the existence of both additive and dominance effects in controlling these two traits. The low narrow sense heritability indicated the smaller impact of additive gene action on fruit weight and the number of lateral branches in watermelon. However, broad sense heritability was high for fruit weight (0.69) and the number of lateral branches (8.88). The large gap between the broad sense heritability and narrow sense heritability indicated the importance of dominance effects in controlling the fruit weight and the number of lateral branches compared to additive effects. These results justify the development of hybrid varieties to exploit the dominance genetic effects in watermelon. The highest fruit weight and the number of lateral branches belonged to the S × Red cross. The highest SCA for the fruit weight was associated with the cross An × S. The cross S × Red had the highest SCA for the number of lateral branches. The high-parent heterosis was also higher in the cross S × Red for these traits. In conclusion, the hybrid S × Red may be proposed for the production of a hybrid variety in watermelon. However, crossing among various genotypes to produce new inbred lines seems necessary for the hybrid breeding program of watermelons in Iran.

Keywords: additive effects, diallel, dominant effects, fruit weight, heritability, number of lateral branches

How to cite: Ghorbanian S, Olfati JA, Rabiei B. 2023. General and specific combining ability for yield-related traits in watermelon. J Plant Physiol Breed. 13(2): 161-168.

Introduction

Watermelon (*Citrullus lanatus* (Thunb.) Matsum. & Nakai) is used as fresh fruit and is an important vegetable crop in the world. Estimates of combining ability are used in determining the genetic worth of watermelon lines. To measure the combining ability, one of the popular methods is the diallel design. The concepts of general combining ability

(GCA) and specific combining ability (SCA) were first stated by Sprague and Tatum (1942). The GCA measures additive gene action and SCA measures non-additive gene action. GCA is determined by the deviation of the mean of a line in all crosses from the grand mean. SCA is the deviation of a cross from the sum of the GCA of two parental lines (Griffing 1956). When SCA is

significant, it shows the existence of non-additive gene action. In statistical terms, the GCAs are regarded as the main effects and the SCAs are the interactions (Griffing 1956).

GCA and SCA can be measured by a diallel-cross design (Griffing 1956; Kempthorne 1969; Mayo 1980). Complete diallel-cross design involves p inbred lines, their F1 crosses, and reciprocal F1s. When p is large, or maternal effects don't exist, it is impractical and inefficient to conduct a complete diallel-cross design. In such cases, other diallel crosses such as half-diallel or partial-diallel crosses are used (Griffing 1956).

Heterosis has been utilized to exploit the dominant gene action through the production of hybrid varieties (Baker 1978; Olfati *et al.* 2012). Both positive and negative heterosis have been reported in watermelon (Gvozdanovic *et al.* 2011; Bahari *et al.* 2012; Sapovadiya *et al.* 2013). Although GCA and SCA help breeders in the breeding programs of watermelons (Gvozdanovic *et al.* 2011; Rakesh 2011; Bahari *et al.* 2012), however, depending on the genotypes and experimental conditions, the estimates differ among the experiments. Therefore, the GCA and SCA values should be estimated in each case. This research was conducted to estimate the GCA, SCA, and heterosis for important traits of watermelon using a diallel-cross of five inbred lines.

Material and Methods

Five watermelon inbred lines were selected for crossing in a 5×5 half-diallel design to produce 10 F1 hybrids during spring and summer 2020 (Table 1). Seeds of all lines were obtained through several inbreeding and single-seed selection cycles from the progeny of commercial hybrids.

The soil of the experimental site (research field of the University of Guilan, Iran) was loamy sand and was prepared by plowing and disking. There was a pre-planting application of nitrogen (Urea) and phosphorus at the rates of 50 kg·ha⁻¹ and 100 kg·ha⁻¹, respectively. The plots were formed as raised beds with a between-rows distance of 1.2 m. Seedlings were transplanted in rows by hand at a distance of 100 cm. Irrigation was begun at flowering with 500 m³·ha⁻¹ of water done thrice a week. About 25 kg·ha⁻¹ of KNO₃ was applied by irrigation water during the growing season weekly. No pesticide was used during the growing season. The planting date was May 20, 2021.

Parental lines and their 10 F1 families were arranged in a randomized complete block design with three replications. Each plot consisted of six individual plants. Data were collected from all plants in each plot and fruit weight, fruit length, fruit width, pulp diameter, rind diameter, total soluble solids (TSS), seed width, seed length, the number of

lateral branches, the number of fruits, and fruit yield were measured.

Analyses of variance of the data were carried out on a plot mean basis. Means were compared by Duncan's multiple range test. For testing and comparing the GCA and SCA, measurements within plots were averaged and analyzed by the Diallel computer program of Burrow and Coors (1994). The parents were considered fixed because they were specifically selected and were of a limited number. The model used (Griffing 1956) assumed that epistasis was not present (Kupper and Staub 1988).

Results and Discussion

Four of the parental lines (An, G, S, and red) were small seeded and one parent (Gu) had large seeds. However, all possible hybrids among these lines had small seeds. Seed size in watermelon is controlled by genes (*s*) and (*l*) for short and long seed length, respectively, and are epistatic to each other (Poole *et al.* 1941). The genotypes LLSS, llSS, and LLss or llss govern medium size, long, and short seeds, respectively (Wehner 2012). Later, another gene (*Ti*) for small seeds was reported by Tanaka *et al.* (1995). They stated that the *Ti* gene was not similar to *s* and *l* genes. Guner and Wehner (2004) have summarized the research on seed length in their article.

Analysis of variance indicated significant

differences among the watermelon genotypes for fruit weight and the number of branches per plant (Table 1). There were no significant differences between watermelon genotypes for other traits. The highest fruit weight was associated with the S × Red cross followed by the An line, and An × Red and G × Gu crosses (Table 2). The highest number of lateral branches was also recorded for the S × Red cross but followed by S × Gu and An × S (Table 2). The S × Red cross also had the highest number of fruits per plant (data not shown), however, its value was not significantly different from the An line, and the An × Red and G × Gu crosses. The low genetic diversity among watermelon genotypes in this study, almost similar to some other previous reports, emphasizes the necessity to broaden the genetic base of cultivated watermelon (Levi *et al.* 2001).

Four dwarf genes affect stem length and plant habit in watermelon. The *dw-1s* gene is recessive to the normal type. The *dw-2* gene governs short internodes. The leaves in the plants with the *dw-3* gene have fewer lobes than the regular leaves (Guner and Wehner 2004). By reducing the terminal dominance, more lateral branches are produced. Hence, increasing the number of lateral branches reduces the longitudinal growth of the plant. This is important because of the possibility of increasing the plant density per unit area and the number of marketable fruits.

Estimates of GCA and SCA are useful for the selection of parental lines in a hybrid breeding program (Fasahat *et al.* 2016). In our experiment, the mean squares due to GCA and SCA effects were significant for fruit weight and the number of lateral branches (Table 1). This indicates the existence of both additive and dominance genetic effects in governing fruit weight and the number of lateral branches. However, the significance of dominance variance for both fruit weight and the number of lateral branches, justifies the development of hybrid varieties to exploit the dominance genetic effects in the watermelon.

Estimates of GCA, SCA, additive and dominance variances, and narrow sense heritability indicated the lower influence of

additive gene action on fruit weight and the number of lateral branches per plant (Table 3). Broad sense heritability was high for both fruit weight (0.69) and the number of lateral branches (8.88), however, these values may have been biased upward due to the effect of the genotype by environment interaction. The large difference between the broad sense heritability and narrow sense heritability again shows the importance of dominance effects compared to additive effects in governing fruit weight (0.69) and the number of lateral branches. When non-additive gene action is present, selection may be postponed to the later generations of crosses (Fasahat *et al.* 2016).

Table 1. Analysis of variance of yield, TSS, and some yield components of watermelon genotypes.

SOV	df	Fruit weight	Fruit length	Fruit width	Pulp diameter	Rind diameter
Block	2	0.25	48.63	13.29	12.02	0.10
Genotype	14	0.78**	49.31	8.07	8.09	0.21
GCA	4	1.18				
SCA	10	0.62*				
Error	28	0.27	31.74	6.50	6.77	0.15
CV (%)		12.13	15.65	12.89	14.21	27.92

** : Significant at the 5% and 1% probability levels, respectively; TSS: Total soluble solids

Table 1 Continued

SOV	df	TSS	Seed width	Seed length	Number of lateral branches	Number of fruits	Total yield per plant
Block	2	0.03	0.02	0.09*	0.03	0.67*	22.96
Genotype	14	2.06	0.02	0.04	1.26**	0.30	13.56
GCA	4				0.72		
SCA	10				1.47**		
Error	20	1.51	0.01	0.02	0.20	0.15	7.10
C.V (%)		13.06	13.88	14.47	5.07	12.79	20.75

** : Significant at 5% and 1% probability levels, respectively; TSS: Total soluble solids.

Table 2. Fruit weight and number of lateral branches of watermelon genotypes.

Genotype	Fruit weight (Kg)	Number of side branches
An × An	4.75a	8.48 b-d
An × G	4.08ab	8.81 abc
An × S	3.96ab	9.07 ab
An × Gu	4.44 ab	8.36 b-d
An × Red	4.70 a	8.17 cd
G × G	4.64 ab	7.37 e
G × S	4.16 ab	8.22 b-d
G × Gu	4.69 a	8.27 b-d
G × Red	4.34 ab	8.71 a-d
S × S	4.0 ab	7.33 e
S × Gu	4.11 ab	9.34 a
S × Red	4.79 a	9.45 a
Gu × Gu	2.89 c	8.98 a-c
Gu × Red	3.65 bc	8.62 a-d
Red × Red	4.37 ab	7.87 de

Means with letters in each column are significantly different at the 5% probability level based on Duncan's multiple range test.

Table 3. Estimates of general combining ability and specific combining ability variances and narrow sense heritability (h^2_n) from the diallel analysis for fruit weight and the number of lateral branches of watermelon (Griffing's mixed model 2 Method 2).

Parameter	Fruit weight	Number of lateral branches
GCA variance	0.043	0.025
SCA variance	0.117	0.423
Additive variance	0.086	0.050
Dominance variance	0.117	0.423
Narrow sense heritability (entry mean basis)	0.29	0.09
Broad sense heritability (entry mean basis)	0.69	0.88

Hybrid An × S had the highest positive SCA for fruit weight followed by G × S, An × G, S × Gu, S × Red, and An × Gu hybrids (Table 4). Hybrid S × Red had the highest positive SCA for the number of lateral branches. The magnitude of SCA for this trait was much higher than other crosses (Table 5).

Also, the highest high parent heterosis was obtained in the S × Red cross for fruit weight and the number of lateral branches (Table 6). Watermelon breeders might develop high-yielding cultivars supported by high SCA (Olfati *et al.* 2011).

Table 4. General and specific combining ability of lines (on diagonal) and hybrids (off-diagonal) for fruit weight according to Griffing's method 2.

Parent	An	G	S	Gu	Red
An	0.18	0.39	0.46*	0.31	0.16
G		0.17	0.40	-0.21	-0.17
S			0.06	0.38	0.35
Gu				-0.39	-0.07
Red					0.11

*: Significant at $p \leq 0.05$.

Table 5. General and specific combining ability of lines (on diagonal) and hybrids (off-diagonal) for the number of side branches according to Griffing's method 2.

Parent	An	G	S	Gu	Red
An	-13.62	29.39	-31.08	10.34	-13.84
G		-13.95	-31.45	10.17	-12.44
S			20.59	-23.20	219.92 **
Gu				-21.07	-32.16
Red					28.05

** : Significant at $p \leq 0.01$.

Table 6. High parent heterosis for fruit weight and the number of lateral branches in the watermelon hybrids.

Hybrid	Fruit weight (Kg)	Number of lateral branches
An \times G	-0.66	26.47
An \times S	0.8	0.53
An \times Gu	-0.72	0.3
An \times Red	-0.04	25.23
G \times S	0.15	0.93
G \times Gu	-1.06	-0.13
G \times Red	-0.3	26.3
S \times Gu	0.11	1.03
S \times Red	0.43	293.2
Gu \times Red	-0.44	-0.53

Conclusion

In our study, the hybrid S \times Red showed the highest mean and high parent heterosis for fruit weight and the number of lateral branches. It also had the highest SCA for the number of lateral branches. Therefore, S \times Red cross may be regarded as a potential

watermelon hybrid, however, before any recommendation, it should be evaluated in multi-environmental trials. Furthermore, crossing among various genotypes is needed to produce new inbred lines for the hybrid breeding of watermelons in Iran.

Acknowledgments

We are gratefully thankful to the Guilan Science and Technology Park for the financial support of this research project.

Conflict of interest

The authors declare that they have no conflict of interest with any organization concerning the subject of the manuscript.

References

Bahari M, Rafii MY, Saleh GB, Latif MA. 2012. Combining ability analysis in complete diallel cross of watermelon (*Citrullus lanatus* (Thunb.) Matsum. & Nakai). *Sci World J.* 1: 1-6.

- Baker RJ, 1978. Issues in diallel analysis. *Crop Sci.* 18: 533-536.
- Burrow MD, Coors JG. 1994. Diallel: a microcomputer program for the simulation and analysis of diallel crosses. *Agron J.* 86: 154-158.
- Fasahat P, Rajabi A, Rad JM Derera J. 2016. Principles and utilization of combining ability in plant breeding. *Biom Biostat Int J.* 4(1): 1-22.
- Griffing B, 1956. Concept of general and specific ability in relation to diallel crossing systems. *Aust J Biol Sci.* 9: 463-493.
- Guner N, Wehner TC. 2004. The genes of watermelon. *HortScience.* 39(6): 1175-1182.
- Gvozdanovic-Varga J, Vasic M, Milic D, Cervenski J. 2011. Diallel cross analysis for fruit traits in watermelon. *Genetika.* 43(1): 163-174.
- Kempthorne O. 1969. An introduction to genetic statistics. Ames, Iowa: Iowa State University Press.
- Kupper RS, Staub JE. 1988. Combining ability between lines of *Cucumis sativus* L. and *Cucumis sativus* var. *Hardwickii* (R.) Alef. *Euphytica.* 38: 197-220.
- Levi A, Thomas CE, Wehner TC, Zhang X. 2001. Low genetic diversity indicates the need to broaden the genetic base of cultivated watermelon. *HortScience.* 36(6): 1096-1101.
- Mayo O. 1980. The theory of plant breeding, Oxford, UK: Clarendon Press.
- Olfati JA, Samizadeh H, Peyvast Gh, Rabiei B, Khodaparast SA. 2011. Relationship between genetic distance and heterosis in cucumber. *Int J Plant Breed.* 6(1): 14-20.
- Olfati JA, Samizadeh H, Rabiei B. 2012. Griffing's methods comparison for general and specific combining ability in cucumber. *Sci World J.* 2(4): 1-4.
- Olfati JA, Peyvast Gh, Samizadeh Lahiji H, Rabie B, Khodaparast SA. 2013. General and specific combining ability and heterosis estimation of some cucumber lines for qualitative traits in partial diallel design. *J Hort Sci.* 26(4): 350-357.
- Poole CF, Grimball PC, Porter DR. 1941. Inheritance of seed characters in watermelon. *J Agron Res.* 63: 433-456.
- Rakesh K. 2011. Inheritance of fruit yield and other horticulturally important traits in watermelon [*Citrullus lanatus* (Thunb.) Matsum. & Nakai]. *HortScience.* 182(2): 141-144.
- Sapovadiya MH, Dhaduk HL, Mehta DR, Patel NB. 2013. Heterosis in watermelon [*Citrullus lanatus* (Thunb.) Mansf.]. *Progress Res.* 8(2): 217-220.
- Sprague GF, Tatum LA. 1942. General vs specific combining ability in single crosses of corn. *Agronom J.* 34: 923-932.
- Tanaka T, Wimol S, Mizutani T. 1995. Inheritance of fruit shape and seed size of watermelon. *J Japan Soc Hort Sci.* 64(3): 543-548.
- Wehner TC. 2012. Gene list for watermelon 2012. Cucurbit Genetics Cooperative. Vegetable Research: Charleston, SC, USA. Available online at: [https://www.ars.usda.gov/southeast-area/charleston-sc/vegetable-research/docs/cgc/gene-list-for-watermelon-2012/#:~:text=The%20genes%20\(s\)%20and%20,\(1995\).](https://www.ars.usda.gov/southeast-area/charleston-sc/vegetable-research/docs/cgc/gene-list-for-watermelon-2012/#:~:text=The%20genes%20(s)%20and%20,(1995).)

ترکیب پذیری عمومی و خصوصی صفات مرتبط با عملکرد در هندوانه

سیاوش قربانیان^۱، جمالعلی الفتی^{۱*} و بابک ربیعی^۲

۱- گروه علوم باغبانی، دانشکده علوم کشاورزی، دانشگاه گیلان، رشت

۲- گروه زراعت و اصلاح نباتات، دانشکده علوم کشاورزی، دانشگاه گیلان، رشت

*مسئول مکاتبه؛ Email: jamalaliolfati@gmail.com

چکیده

برآورد ترکیب‌پذیری در تعیین ارزش لاین‌های هندوانه (*Citrullus lanatus* (Thunb.) Matsum. & Nakai) برای تولید هیبریدهای جدید با عملکرد بالا و کیفیت بهتر مفید است. این تحقیق به منظور برآورد ترکیب‌پذیری عمومی (GCA)، ترکیب‌پذیری خصوصی (SCA) و هتروزیس در پنج لاین اینبرد انتخابی برای اصلاح هندوانه در دانشگاه گیلان انجام شد. تجزیه واریانس داده‌ها اختلاف معنی‌داری را بین ژنوتیپ‌های هندوانه برای وزن میوه و تعداد شاخه‌های جانبی در بوته نشان داد. اثرات GCA و SCA برای وزن میوه و تعداد شاخه‌های جانبی معنی‌دار بود که نشان دهنده وجود هر دو اثر افزایشی و غالبیت در کنترل این دو صفت است. وراثت پذیری خصوصی پایین بیانگر تأثیر کمتر عمل ژن افزایشی بر وزن میوه و تعداد شاخه‌های جانبی در هر بوته در هندوانه بود. با وجود این، وراثت پذیری عمومی برای وزن میوه (۰٫۶۹) و تعداد شاخه‌های جانبی (۰٫۸۸) بالا بود. اختلاف زیاد بین وراثت‌پذیری عمومی و وراثت‌پذیری خصوصی نشان دهنده اهمیت اثرات غالبیت در کنترل وزن میوه و تعداد شاخه‌های جانبی در مقایسه با اثرات افزایشی است. این نتایج، تولید واریته‌های هیبرید را برای بهره‌برداری از اثرات ژنتیکی غالبیت در هندوانه توجیه می‌کند. بیشترین وزن میوه و تعداد شاخه‌های جانبی به تلاقی $S \times Red$ مربوط بود. بیشترین SCA برای وزن میوه به تلاقی $An \times S$ تعلق داشت. تلاقی $S \times Red$ دارای بیشترین SCA برای تعداد شاخه‌های جانبی بود. بالاترین هتروزیس والد برتر برای وزن میوه و تعداد شاخه‌های جانبی نیز به تلاقی $S \times Red$ تعلق داشت. به طور کلی تلاقی $S \times Red$ برای تولید رقم هیبرید در هندوانه پیشنهاد می‌شود. با وجود این، انجام تلاقی بین ژنوتیپ‌های مختلف برای تولید لاین‌های نوترکیب جدید در برنامه‌های اصلاح هیبرید هندوانه در ایران لازم به نظر می‌رسد.

واژه‌های کلیدی: اثرهای افزایشی، اثرهای غالبیت، تعداد شاخه‌های جانبی، دیالل، وراثت‌پذیری، وزن میوه