

Estimates of Variance Components and Broad-Sense Heritability for Yield in Watermelon

Gabriele Gusmini and Todd C. Wehner

Department of Horticultural Science, North Carolina State University, Raleigh, NC 27695-7609

Watermelon breeders in the late 1800s were able to release many new cultivars of different types with good quality and early maturity for use in the U.S. By 1900 'Angelino', 'Chilean', 'Florida Favorite', 'Georgia Rattlesnake', 'Cole Early', 'Kleckley Sweet', and other open pollinated cultivars had been on the market many years (8). In the 20th century, development of high yielding cultivars (total weight per unit area) became a major goal for public and private watermelon breeders (4).

Overall, watermelon yield in the United States has been increasing during the last five years (7), from 24 Mg·ha⁻¹ in 1998 up to 29 Mg·ha⁻¹ in 2002. Part of the increase in yield might be due to more reliable production practices and to the availability of more efficient pesticides (3), but it is also due to genetic improvement of yield.

Currently, breeders evaluate breeding lines and new cultivars for yield and quality using 1- to 3-row plots, multiple locations, and multiple seasons (planting dates) for trialing. Usually, plots are harvested once by private breeders and several times by public breeders (5). It is important to have genetic variability for yield if progress is to be made in trialing. In addition, it is important to measure the effect of environment (year, location, etc.) on yield.

The objective of this study was to use a diverse set of watermelon cultivars to measure genetic variance for yield and the effect of year and location on broad-sense heritability.

Methods: The experiment was conducted in 2001 and 2002 at the Horticultural Crops Research Station at Clinton, North Carolina

and at the Cunningham Research Station at Kinston, North Carolina (2002 only). Rows were direct seeded on raised, shaped beds on 3.1 m centers. Plots were 3.7 m long, with 0.6 m between hills, and 2.5 m alleys at each end of the plot. In Kinston, rows were covered with black polyethylene mulch and drip irrigated. The experiment was conducted using horticultural practices recommended to the growers by the North Carolina Extension Service (6). A total of 80 cultivars were evaluated for fruit yield and quality. There were 72 obsolete cultivars obtained from seed companies, the Seed Savers Exchange, and the National Seed Storage Laboratory (Fort Collins, Colorado). Eight elite hybrid cultivars were included as checks ('Starbrite', 'Stars-N-Stripes', 'Legacy', 'Sangria', 'Fiesta', 'Sultan', 'Regency', and 'Royal Flush'). Plots were harvested twice (26 July and 9 August) in Clinton in 2001, once (25 July) in Clinton in 2002, and twice (23 July and 6 August) in Kinston in 2002 for fruit yield and quality measurements. Individual cull and marketable fruit were weighed to the nearest pound for each plot. Numbers of cull and marketable fruit were also recorded.

Variance components estimates for the experiment were obtained from two different datasets: 1) two years (2001 and 2002), four replications per year, and one location (Clinton), and 2) two locations (Clinton and Kinston), two replications per location, and one year (2002). The regression models used were, respectively:

- 1) $Y = \text{Year} + [\text{Replication}(\text{Year})] + \text{Cultivar} + (\text{Cultivar} * \text{Year}) + \text{Error}$
- 2) $Y = \text{Location} + [\text{Replication}(\text{Location})] + \text{Cultivar} + (\text{Cultivar} * \text{Location}) + \text{Error}$

We analyzed data for the yield traits using variance component analysis, and then calculated broad-sense heritability for each of the two both models as follows (2):

- 1) $H^2_B = \sigma^2(\text{Cultivar}) / [\sigma^2(\text{Error}) / (\# \text{rep.} \times \# \text{year}) + \sigma^2(\text{Year}) / \# \text{year} + \sigma^2(\text{Cultivar})]$
- 2) $H^2_B = \sigma^2(\text{Cultivar}) / [\sigma^2(\text{Error}) / (\# \text{rep.} \times \# \text{location}) + \sigma^2(\text{Location}) / \# \text{location} + \sigma^2(\text{Cultivar})]$

Data were analyzed using the MEANS, GLM, and VARCOMP procedures of SAS-STAT Statistical Software Package (SAS Institute, Cary, NC).

Results: Our estimates of variance components and broad-sense heritability are not definitive, since they are based only on measurements of a diverse set of cultivars of unknown and/or diverse genealogy. Additional research should make use of populations developed from known and divergent parents. Nevertheless, our estimates apply to this dataset, and the diversity of cultivars included in our study allows useful conclusions to be drawn.

The experiments had a large error variance (Table 1). That was probably due to 1) the wide range of fruit-types tested, which might have affected the precision and accuracy of harvest and weighing; 2) the unbalanced number of harvests among locations and years, due to different homogeneity of maturation of the different cultivars in the same field; and 3) the generally high weight of single fruit that, if not accurately measured, might greatly bias the calculation of total yield. The latter might account for the larger error, relative to the other variance components, recorded for total weight per hectare than for the other traits.

Besides error variance, most of the variation in yield traits (total weight and total number) was due to environmental factors (year or location) and to the genotype. A larger interaction variance (genotype x environment) was present in the analysis

among locations for total weight. The largest variance component for the percentage of marketable weight was due to the genotype (among locations) or to interaction of genotype and year of testing. The variation of average fruit size and soluble solids content were mostly genotypic in both analyses.

Broad-sense heritability was consistently high in both analyses only for average fruit size. For percentage of marketable weight, broad-sense heritability was very low in both cases, while for the other traits it was medium to high when year was in the model and medium to low when location was in the model. Yield components (total weight and total number) in our experiments had low heritability and, if confirmed in a larger experiment, would explain why yield improvement is so difficult. Watermelon breeders usually develop new cultivars using pedigree and backcross methods and few lines being tested in field trials. The identification of quantitative trait loci (QTL) for yield may improve the efficiency of selection for traits of low heritability relative to phenotypic selection (1).

Our experiments indicate low genotype by environment (year or location) interaction. Thus, trial location may not be a problem for obtaining data that reflects performance in the general region. Therefore, testing on bare ground with overhead irrigation in few locations and one year would be possible for the early stages of selection, where ranking among cultivars matters more than absolute estimates of yield. Furthermore, genetic variability for yield components in our varied set of cultivars was high and should allow progress in selection for increased yield. Nevertheless, more limits to progress might be present in certain fruit classes (fruit size, shape, rind pattern, etc.). The current market appears to be expanding away from certain types (i.e. 'Allsweet' types in the United States or 'Charleston Gray' types in the Middle-East) in favor of new types.

In conclusion, genetic variability for yield components is still present in watermelon and the new fruit types coming into the market might allow breeders to exploit new genetic sources for yield improvement.

Literature Cited

1. Dekkers, J. C. M., and R. Chakraborty. 2001. Potential gain from optimizing multigeneration selection on an identified quantitative trait locus. *Journal of Animal Science* 79:2975-2990.
2. Hallauer, A. R., and J. B. Miranda. 1988. *Quantitative genetics in maize breeding*. II ed. Ames, IO: Iowa State University Press. 468 pp.
3. Maynard, D. N., ed. *Watermelons. Characteristics, production, and marketing*. I ed. 2001, ASHS Press: Alexandria, Virginia. 227.
4. Mohr, H. C., *Watermelon breeding*, in *Breeding vegetable crops*, M.J. Basset, Editor. 1986, AVI Publishing Co. p. 37-66.
5. Nepl, G. P., and T. C. Wehner. 2001. Survey of watermelon trialing methods used by breeders in the United States. *Cucurbit Genetics Cooperative Report* 24:67-69.
6. Sanders, D. C., ed. *Vegetable crop guidelines for the Southeastern US 2001-2002*. 2001. 193.
7. USDA-ARS, *Agricultural statistics data base - QuickSTAT*. 2003, USDA-ARS.
8. Whitaker, T. W., and I. C. Jagger, *Breeding and improvements of Cucurbits*, in *Yearbook of Agriculture*, USDA-ARS, Editor. 1937. p. 207-232.

Table 1. Variance components and broad-sense heritability for yield and quality data of the 80 cultivars evaluated in two experiments.

Genetic Parameter	Total Yield		Percentage of marketable weight	Fruit size	Soluble solids
	Weight	Number			
Experiment 1: 2 years, 4 replications of data per year					
σ^2 (Year)	188.13	7.16	0.00	0.76	0.00
σ^2 (Rep. (Year))	52.37	1.33	11.04	0.15	0.15
σ^2 (Cultivar)	229.34	6.38	0.89	5.83	0.57
σ^2 (Cultivar * Year)	101.60	1.02	17.14	0.69	0.05
σ^2 (Error)	574.55	9.00	89.95	2.55	0.86
H^2_B ^a	0.58	0.57	0.07	0.89	0.84
Experiment 2: 2 locations, 2 replications of data per location					
σ^2 (Location)	1170.85	20.17	0.00	0.01	0.33
σ^2 (Rep. (Location))	40.54	0.92	6.56	0.12	0.01
σ^2 (Cultivar)	192.29	9.17	9.75	6.30	0.51
σ^2 (Cultivar * Location)	20.75	0.16	2.63	0.82	0.17
σ^2 (Error)	1070.31	12.69	99.73	2.37	0.73
H^2_B ^b	0.18	0.41	0.28	0.91	0.59

^a $H^2_B = \sigma^2(\text{Cultivar}) / [\sigma^2(\text{Error}) / (\#rep.*\#year)] + [\sigma^2(\text{Year}) / \#year] + [\sigma^2(\text{Cultivar})]$

^b $H^2_B = \sigma^2(\text{Cultivar}) / [\sigma^2(\text{Error}) / (\#rep.*\#location)] + [\sigma^2(\text{Location}) / \#location] + [\sigma^2(\text{Cultivar})]$