ABSTRACT

DIA, MAHENDRA. Genotype x Environment Interaction and Stability Analysis of Performance, and Mega-Environment Identification of Fruit Yield and Yield Components in Watermelon [*Citrullus lanatus* (Thumb.) Matsum & Nakai] Tested in Multiple US Locations. (Under the direction of Dr. Todd C. Wehner).

One of the major breeding objectives for watermelon [*Citrullus lanatus* (Thumb.) Matsum & Nakai] is improved fruit yield. High yielding genotypes have been identified, so our objective was to evaluate genotypes for stability of fruit yield and yield components over diverse environments. The success of any breeding program depends on several factors, including understanding and selection of suitable breeding and test locations. The objectives of this study were to (i) evaluate the influence of years and locations on yield of watermelon genotypes, (ii) identify genotypes with high stability for yield, (iii) determine whether locations belong to a single mega-environment, or a diverse set, and (iv) rank locations based on discriminating ability and representativeness. A set of 40 genotypes was tested over 3 years (2009, 2010, and 2011) and 8 locations across the southern United States in replicated, multi-harvest trials. The genotypes included new vs. old releases, small vs. large fruit size, round vs. elongate fruit shape, striped vs. solid rind pattern, resistant vs. susceptible to anthracnose, eastern vs. western adapted, and inbred vs. hybrid type. Yield traits were summed over harvests, and measured as marketable yield, fruit count, % cull fruit, % early fruit, and fruit size. There were strong effects of environment and genotype x environment interaction (GEI) on watermelon yield traits. There was a significant advantage of hybrids over inbreds for performance of yield components and responsiveness to favorable environments. Four genotypes, including 'Fiesta F1', 'Stars-N-Stripes F1', 'Stone Mountain' and 'Calhoun Gray' had high trait means and high stability: high marketable yield, high fruit count, low % cull fruit, above average % early yield, and medium fruit size. Inbreds 'Big

Crimson' and 'Legacy' would be good for development of cultivars having high yield and stability. Two locations including, Florida and Clinton, NC were consistently represented as key centers of two mega-environments for marketable yield, fruit count, and % early fruit. The entire southern US should be considered one mega-environment for breeding watermelon for fruit size. Identification of separate mega-environments in the watermelon production region of the US has several implications for future breeding objectives and genotype evaluation, including deployment of different genotypes in different areas for optimum performance.

Genotype x Environment Interaction and Stability Analysis of Performance, and Mega-Environment Identification of Fruit Yield and Yield Components in Watermelon [*Citrullus lanatus*(Thumb.) Matsum & Nakai] Tested in Multiple US Locations

by
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BIOGRAPHY

Mahendra Dia was born in small village Dewas, close to Ajmer (district headquarter), in Northern India. He spent his childhood in two little towns called Gulabpura and Hurda, both in Bhilwara district, with his parents Suraj Karan Dia and Kanta Dia. He grew up in joint family along with his sister, brother and cousins. Mahendra went to school at Vivekananda Kendra Vidyalaya in Hurda along with his siblings and cousins from kindergarten to high school. In his high school he studied physics, chemistry, mathematics and biology.

Mahendra spent his school vacations in his native village Dewas during summer and winter where his grandparents, uncle and aunt would live and do farming. Dewas is situated in semi-arid region of western India and foot of Aravali mountain range, which is worlds one of the oldest mountainous range. Living in Dewas, he was able to enjoy so many things the place has to offer including playing hiding and seeking in corn, sorghum, and pulses field; milking goats; herding cattle; climbing mountains; and harvesting fruits from trees.

Mahendra's love for nature and agriculture blossomed while living in his native village Dewas and with his father who would work as Agricultural Officer for state government. After finishing high school, he enrolled in the undergraduate program in Agricultural Sciences at Rajasthan Agricultural University in Ajmer and always interested in pursuing his higher studies to learn more about agriculture. In 2003, Mahendra passed All India Entrance Examination to pursue MS in agronomy at Acharya N.G. Ranga Agricultural University in Hyderabad, India and he was awarded by 'Junior Research Fellowship' by Indian Council of Agricultural Research. He did his research on improvement of yield and

quality of baby corn under the direction of Dr. D.S. Reddy. During his MS studies Mahendra enjoyed cultural diversity including food, language, and life style; and made lot of new friends there.

While working in corn field in MS degree, Mahendra had opportunity to get acquaint him to plant breeding experiments from his colleagues research work. He was always curious and wanted to expand his plant breeding and genetics knowledge from aboard, particularly from the United States of America (US). For spring 2006, Mahendra got admission from Cornel University in plant breeding program; however, he could not join because of financial obstruction. At the same time Mahendra decided continue his studies without break and he enrolled in fall 2006 at Tarleton State University in Texas for second Master degree in Agricultural Sciences with major emphasis on soil and environmental sciences. He did his research work on accumulation of carcinogenic metals in soils from gasoline exhaust under the direction of Dr. David C. Weindorf. His graduate school taught him so much about US education system, culture and food; and he cherished his experience at Tarleton State University.

As Mahendra was always aspirant to learn more about plant breeding and genetics and his professional goal was until still unfilled. From fall 2008 he started his doctoral study in Plant Breeding and Genetics at North Carolina State University (NCSU) in Raleigh under the direction of Dr. Todd C. Wehner. He has been working as graduate research assistant on various projects in cucurbit breeding program. His graduate school career at NCSU not only trained him as a plant breeder, but also helped him honing soft skills and making new friends. Currently, Mahendra is planning his future as a professional in plant breeding in the US.

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GENERAL INTRODUCTION

GENOTYPE STABILITY AND LOCATION VALUE FOR YIELD AND YIELD COMPONENTS IN WATERMELON FROM GENOTYPE X ENVIRONMENT STUDY IN THE SOUTHERN US

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History of watermelon breeding and genetics

Worldwide, the United States (US) is the fifth largest producer of watermelon [*Citrullus lanatus* (Thumb.) Matsum & Nakai], with 2 million Mg harvested on 21,450 ha in 2007, valued in excess of $476 million dollars (FAO, 2010; USDA, 2010). Watermelons are grown in most states of the United States (US). However, the major producers are in the South and West, including Florida, Texas, Oklahoma and California, where the long frost-free warm season lasts longer (Wehner, 2008).

Watermelon production in the US is highly seasonal, peaking from May through August and declining through December. Florida is the only domestic source of watermelons from December through April. Florida growers harvest watermelons during virtually every month. However, the peak harvest occurs during May, June, and early July. Watermelon production season in the US begins from Florida, followed by output from Arizona, Texas, California, and the southeastern and south-central states (USDA-Economic Research Service, 2011).

Although Florida, California, Texas, and Georgia are the leading watermelon-producing states, accounting for two-thirds of US output; watermelon is grown from south-eastern, south-central to western states across the US. In 2010, it was grown in at least 20 states of the US (USDA-Economic Research Service, 2011).

Watermelon breeding has been practiced during the last three centuries in the US. However, formal watermelon breeding in the US did not start until the late 1800s. By 1900, 'Angeleno', 'Chilean', 'Florida Favorite', 'Georgia Rattlesnake', 'Cole Early', 'Kleckley Sweet', and other open-pollinated cultivars were available (Whitaker and Jagger, 1937). In the late

1800s and early 1900s, the watermelon market became more established, and resistant cultivars were developed. In 1954, C.F. Andrus released 'Charleston Gray' with elongate fruit, gray rind, and red flesh. It was resistant to Fusarium wilt, anthracnose, and sunburn. The Fusarium wilt resistant cultivar 'Jubilee' (1963) was developed by J.M. Crall. In 1970, C.V. Hall developed 'Allsweet' with similar resistance to 'Charleston Gray', but higher fruit quality. 'Allsweet' had elongate fruit shape and rind with wide, dark green stripes. In addition to 'Allsweet', Hall developed 'Crimson Sweet', 'Super Sweet', and 'Petite Sweet'. During the late 1900s, 'Crimson Sweet' and 'Allsweet' gained popularity among commercial growers and captured a majority of the market in the US and 50 countries around the world (Gusmini and Wehner, 2005). In 1990, Crall released the improved Fusarium wilt resistant cultivar 'Jubilee II', and in 1995 along with a co-worker he released the small-seeded cultivar 'Dixielee', an alternative to 'Allsweet' for its different fruit type and superior quality. Cultivars that dominated the market in the mid 1900s were open-pollinated ones such as 'Charleston Gray', 'Jubilee', 'Crimson Sweet', and 'Sugar Baby'.

By the end of 1900s, hybrids had replaced open-pollinated cultivars for the commercial market. 'Sangria' was the first hybrid developed by T.V. Williams of Rogers NK (now Syngenta) in 1985. An important change in the watermelon industry was the production of seedless cultivars. O.J. Eigsti worked for twenty years with H. Kihara of Japan, first to work on seedless watermelon, to improve the systems of seedless watermelon. O.J. Eigsti released the first seedless watermelon, 'Tri-X-313', in 1962. However, seedless watermelon did not become commercially important until the 1990s due to poor fertility of tetraploid parents used in triploid hybrid seed production. In the early 21st century, X. Zhang of

Syngenta Inc. was first to introduce mini seedless watermelons, and were sold under the PureHeartTM brand in the US and SolindaTM brand in the Europe (Maynard et al., 2007). Mini seedless watermelons became popular, especially in the winter season. Although seedless watermelons are more difficult to produce than seeded types, they sell for a higher price and earn a larger return for growers (USDA-Economic Research Service, 2011). The National Watermelon Promotion Board, Orlando, Florida, reported that in the US, 53% of watermelons sold are seedless (TAMU-Vegetable Production and Marketing, 2011).

The last century of watermelon breeding has been focused on disease resistance and fruit quality traits, often controlled by single genes. Many genes of watermelon, have been used in cultivar improvement (Cucurbit Gene List Committee, 1979; Cucurbit Gene List Committee, 1982; Guner and Wehner, 2004; Henderson, 1991; Henderson, 1992; Rhodes and Dane, 1999; Rhodes and Zhang, 1995; Wehner and Guner, 2004).

Breeding for yield and stability

In the 20th century, high yielding watermelon cultivars became a major goal for breeders. Unlike corn (*Zea mays*), many researchers, mainly in the 1950s and 1960s, reported that heterosis was not a large influence on yield. However, hybrids provided growers with added value over open pollinated cultivars for uniform fruit yield and quality. Also, hybrids provided protection of intellectual property and novel traits such as blocky shape (Gusmini and Wehner, 2005). Seedless cultivars are in high demand and can only be produced as triploid hybrids (TAMU-Vegetable Production and Marketing, 2011). However, it might be possible to develop transgenic diploid seedless watermelon. In that case, the question of the

advantage in using heterotic hybrid vs. inbred cultivars will still be important (Gusmini and Wehner, 2005).

In the last five decades, watermelon yield in the US has increased approximately 200% (USDA, 2010). However, high yield is often associated with decreased yield stability (Calderini and Salfer, 1999; Padi, 2007). The terms 'stability' or 'adaptability' refer to consistent high performance of genotypes across diverse sets of environments (Romagosa and Fox, 1993). Yield is a complex quantitative trait, and such traits are often controlled by many genes, influenced by prevailing environmental conditions, with each gene having a small effect. In order to identify the most stable and high yielding genotypes, it is important to conduct multi-environment trials (Lu'quez et al., 2002). Although many yield trials of new watermelons cultivars are run every year in the US, information on stability of yield in watermelon is limited (Gusmini and Wehner, 2005).

Genotypes tested in different locations or years often have significant fluctuation in yield due to the response of genotypes to environmental factors such as soil fertility or the presence of disease pathogens (Kang, 2004). These fluctuations are often referred as genotype x environment interaction (GEI) and are common. Genotype x environment interactions have been studied in many crops, including common bean (*Phaseolus vulgaris* L.) (Mekbib, 2003), corn (*Zea mays* L.) (Fan et al., 2007), cowpea (*Vigna unguiculata* L.) (Padi, 2007), rice (*Oryza sativa*) (Haryanto et al., 2008), soybean (*Glycine max* L.) (Yan and Rajcan, 2002), tomato (*Lycopersicon esculentum* Mill.) (Ortiz and Izquierdo, 1994), and wheat (*Triticum aestivum* L.) (Vita et al., 2010).

GEI results from a change in the relative rank of genotype performance or a change in the magnitude of differences between genotype performance from one environment to another. GEI affects breeding progress because it complicates the demonstration of superiority of any genotype across environments and the selection of superior genotypes (Magari and Kang, 1993; Ebdon and Gauch, 2002). Another undesirable effect of GEI includes low correlation between phenotypic and genotypic values, thereby reducing progress from selection. This leads to bias in the estimation of heritability and in the prediction of genetic advance (Comstock and Moll, 1963; Alghamdi, 2004). Therefore, the magnitude and nature of GEI determine the features of a selection and testing program.

Mega-environment identification

Often, plant breeders want to develop broadly-adapted genotypes for a wide range of environments. However, it is often not possible to identify genotypes that are superior in yield and yield components in all environments. Furthermore, the same genetic system may not control yield over a diverse set of environments (Ceccarelli and Grando, 1993; Ceccarelli, 1989; Simmonds, 1991). Therefore, breeders often develop genotypes for a particular environment to take advantage of specific adaptations (Annicchiarico et al., 2005; Samonte et al., 2005). However, breeding for a specific adaptation is more efficient if production areas are divided into mega-environments, each representing a target environment for breeding. Mega-environment is a portion (not necessarily contiguous) of the growing region of a crop species having a fairly homogeneous environment that causes similar genotypes to perform best there (Gauch and Zobel, 1997).

The success of any plant breeding program depends on many factors; one of the most important factors is the understanding and selection of suitable test locations (Yan et al., 2011). An efficient test location is discriminating, so that differences among genotypes can be easily detected using few replications, and is representative of the target environments for the cultivars to be released. The representation of the location for the target environment should be repeatable so that genotypes selected in each year will have superior performance in future years (Yan et al., 2011). Therefore, knowledge of target environment for breeding for locally adapted genotype is important and, also, it requires a subdivision of the target locations into mega-environments.

Multiple-environment trials are routinely conducted as part of plant breeding programs. The trials serve to identify superior genotypes for target regions, and to subdivide the target region into different mega-environments. Subdivision of crop growing region into several mega-environments helps in allocation of resources in a breeding program (Peterson and Pfeiffer, 1989), target genotype distribution to appropriate production area, and information exchanges between breeding programs (Brown et al., 1983). Understanding and identification of mega-environment results in heritability increase within relatively well-defined and predictable environment (Abdalla et al., 1996). Therefore, it improves the efficiency of the testing and breeding program by focusing on the most promising material.

Stability methods

Various statistics have been proposed to measure the stability of genotypes over environments. However, no single method can adequately explain cultivar performance across environments (Dehghani et al., 2006). Becker and Leon (1988) suggested two

different concepts of stability: static (biological) and dynamic (agronomic). With the static concept, a stable genotype possesses an unchanged performance regardless of variation in the environmental conditions. Thus, genotypic variance among environments is zero. With the dynamic concept, response of a genotype to environments is predictable. Thus, a stable genotype has no deviation from response to environments. Both concepts of stability are useful, but their application depends on the trait considered. For qualitative traits such as resistance to diseases or stress, the static concept of stability is useful. For quantitative traits such as yield, the dynamic concept of stability is useful (Norden et al., 1986).

Statistical methods for measuring genotypic stability should partition the information from a genotype - environment data matrix into simpler components representing real responses vs. random variation (Gauch, 1992). These statistical methods can be classified into two groups: univariate and multivariate. Univariate models ranged from parametric, such as environmental variance (Roemer, 1917), ecovalence (Wricke, 1962), stability variance (Shukla, 1972), regression slope (Finlay and Wilkinson, 1963), deviation from regression (Eberhart and Russell, 1966) and coefficient of determination (Pinthus, 1973). Non-parametric models include Kang's yield stability statistic (Kang, 1993). Multivariate models includes a wide range of methods such as principal component analysis (PCA) (Gower, 1967), cluster analysis (Mungomery et al., 1974), genotype main effect plus genotype by environment interaction (GGE) biplot analysis (Yan, 2001), and additive main effects and multiplicative interaction models (AMMI) (Gauch and Zobel, 1988).

Univariate, nonparametric stability statistics define environments and phenotypes relative to biotic and abiotic factors. Nonparametric stability statistics are based on rank order

of genotypes and do not rely upon assumptions about distribution of observed values or of variance homogeneity. Univariate, parametric stability statistics involve relating observed genotypic responses to a sample of environmental conditions. With certain statistical assumptions, parametric stability methods exhibit beneficial properties, providing information about the normal distribution of error and of interaction effects (Huehn, 1990). For those reasons, parametric stability is more commonly used. Mut et al., (2009) reported that for many applications, including selection in breeding and testing programs, parametric stability statistics are useful but there is justification for the use of non-parametric measures for the assessment of the yield stability of crop genotypes.

The multivariate models, AMMI and GGE biplot, appeared to be able to extract a large part of the genotype - environment interaction and were efficient in analyzing interaction patterns (Zobel et al., 1988). Gauch (1992) reported that multivariate models captured a large portion of the genotype x environment interaction sum of squares clearly separating main and interaction effects, and the model often provided an agronomically meaningful interpretation of the data. Differences in genotype stability and adaptability to environment can be qualitatively assessed using the biplot graphical representation that scatters the genotypes according to their principal component values (Vita et al., 2010).

Objectives

The objectives of this research were to (i) evaluate the influence of years and locations on yield of watermelon genotypes, (ii) identify genotypes with high stability for yield, (iii) group test locations into mega-environments, and (iv) rank locations based on discriminating ability and representativeness.

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CHAPTER 1

GENOTYPE X ENVIRONMENT INTERACTION AND STABILITY ANALYSIS OF PERFORMANCE OF FRUIT YIELD AND YIELD COMPONENTS IN WATERMELON [*Citrullus lanatus* (Thunb.) Matsum. & Nakai] TESTED IN MULTIPLE US LOCATIONS

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Genotype x Environment Interaction and Stability Analysis of Performance of Fruit Yield and Yield Components in Watermelon [*Citrullus lanatus* (Thumb.) Matsum & Nakai] Tested in Multiple US Locations

Abstract

One of the major breeding objectives for watermelon [*Citrullus lanatus* (Thumb.) Matsum & Nakai] is improved fruit yield. High yielding genotypes have been identified, but we also were interested to evaluate genotypes for stability for fruit yield and yield components over diverse environments. The objectives of this study were to (i) evaluate the influence of years and locations on yield of watermelon genotypes, and (ii) identify genotypes with high stability for yield. A set of 40 genotypes was tested over 3 years (2009, 2010, and 2011) and 8 locations across the southern United States in replicated, multi-harvest trials. The genotypes included new vs. old releases, small vs. large fruit size, round vs. elongate fruit shape, striped vs. solid rind pattern, resistant vs. susceptible to anthracnose, eastern vs. western adapted, and inbred vs. hybrid type. Yield traits were summed over harvests, and measured as marketable yield, fruit count, % cull fruit, % early fruit, and fruit size. There were strong effects of environment as well as genotype x environment interaction (GEI) on watermelon yield traits. There was a significant advantage of hybrids over inbreds for yield components performance and responsiveness to favorable environments. Four genotypes including, 'Fiesta F1', 'Stars-N-Stripes F1', 'Stone Mountain' and 'Calhoun Gray' had a high trait mean performance and high phenotypic stability. The four stable genotypes identified in this study had high marketable yield, average fruit count, low % cull fruit, above average early yield, and medium fruit size. Inbreds 'Big Crimson' and 'Legacy' would be

good lines for breeding for high yield and stability. Hybrids can provide growers with added value expressed through a high probability of enhanced fruit yield and improved yield responsiveness and stability relative to conventional genotypes. A significantly (P<0.001) and positively correlation was found between trait mean and Kang's yield-stability statistics (YS_i), and Shukla's stability variance (σ_i^2) and deviation from regression (S^2_d) for all the traits evaluated in this study. None of the stability statistics (M, b_i, S^2_d, and σ_i^2) alone were useful for selecting high yield and stable genotypes except YS_i.

Introduction

Watermelon (*Citrullus lanatus* [Thumb.] Matsum & Nakai) is a valuable crop grown throughout the world. The United States is the fifth largest producer, with 2 million Mg harvested from 21,450 ha in 2007, valued in excess of $476 million (FAO, 2010; USDA, 2010). Watermelons are grown in almost all the states of the US. However, the major producers are in the South and West, including Florida, Texas, Oklahoma and California, where there is a long frost-free season (Wehner, 2008). During the past century, watermelon cultivars have been developed with high fruit yield, fruit quality, earliness, percentage marketable fruit, excellent shipping characteristics, and disease resistance. A century of breeding has produced uniform hybrids, seedless triploids, tough rind, high sugar content, dark red flesh, 9 kg picnic watermelons, and 3 kg mini watermelons (Gusmini and Wehner, 2008). Since 1960, yield has increased approximately 200% in the US (USDA, 2010). However, high yield is often associated with decreased yield stability (Calderini and Salfer, 1999; Padi, 2007). Yield stability is important, but has not been studied in watermelon.

By growing genotypes in different environments, the highest yielding and most stable genotypes can be identified (Lu'quez et al., 2002). Genotypes tested in different locations or years often have significant fluctuation in yield due to the response of genotypes to environmental factors such as soil fertility or the presence of disease pathogens (Kang, 2004). These fluctuations are often referred as genotype x environment interaction (GEI) and are a common, and have been studied in many crops (Bednarz et al., 2000; Mekbib, 2003; Riday and Brummer, 2006; Fan et al., 2007; Mulema et al., 2008; Vitta et al., 2010).

GEI results from a change in the relative rank of genotype performance or a change in the magnitude of differences between genotypes performance from one environment to another. Thus, GEI affects breeding progress because it complicates the demonstration of superiority of any genotype across environments and, thus, the selection of superior genotypes (Magari and Kang, 1993; Ebdon and Gauch, 2002). Another undesirable effect of GEI includes low correlation between phenotypic and genotypic values, thereby reducing progress from selection. This leads to bias in the estimation of heritability and in the prediction of genetic advance (Comstock and Moll, 1963; Alghamdi, 2004). Therefore, the magnitude and nature of GEI determine the features of a selection and testing program.

Many researchers use the terms 'stability' and 'adaptability' to refer to consistent high performance of genotypes across diverse sets of environments (Romagosa and Fox, 1993). Lin and Binns (1994) described two types of stable genotypes; those showing a stable average yield across environments, and those with high yield in specific environments, but poor yield in non-target environments (genotypes with specific adaptability).

Statistical methods have been proposed for the analysis of yield stability. The methods partition the information from a genotype - environment data matrix into simpler components representing real responses vs. random variation (Gauch, 1992). These statistical methods range from univariate models, such as regression slope, deviation from regression, environmental variance, and Kang's yield-stability; as well as multivariate models such as genotype main effect plus genotype by environment interaction (GGE) biplot (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Yan, 2001; Kang, 1993; Yan and Kang 2003).

Lin et al. (1986) classified stability analysis models into three groups: types 1, 2 and 3. Each model reflects different aspects of stability, and no single method adequately explained genotype performance across environments (Wachira et al., 2002). Type 1 stability parameters – genotype mean squares (S_i^2) and genotypic coefficient of variation (CV_i) – measure the variation within a genotype across environment. In type 1, a genotype is considered to be stable if its environmental variance is small (Roemer, 1917). This stability parameter is often related to homeostasis and has been associated with low yield. Therefore, it is less appealing and infrequently used by plant breeders (Mekbib, 2003).

The most widely used approach is based on linear regression of genotype yield on an environmental index derived from the average performance of all genotypes in each environment (Finlay & Wilkinson, 1963; Eberhart & Russell, 1966; Freeman, 1973; Chakroun et al., 1990). The regression model provides two stability parameters. The first estimate is the linear regression coefficient (b_i) of genotype mean on environmental index. The regression, or slope, is a type 3 stability measure. The second estimate obtained from regression is the mean square deviation from regression (S^2_d) for each genotype. The

deviation from regression is a type 3 stability measure. According to the Eberhart and Russell (1966), a b_i approximating unity along with a S^2_d near zero indicate average stability. When this is associated with high mean yield, genotypes have general adaptability and when associated with low mean yield, genotypes are poorly adapted to all environments. A b_i greater than unity describes genotypes with higher sensitivity to environmental change (below average stability), and greater specificity of adaptability to high yielding environments. A b_i less than unity provides a measure of greater resistance to environmental change (above average stability), and therefore increasing specificity of adaptability to low yielding environments. Despite the frequent use of the regression method, several researchers reported deficiencies of the method for determination of GEI patterns (Zobel et al., 1988; Nachit et al., 1992; Annicchiarico, 1997; Vita et al., 2010). The linear regression method captures a small part of sum of squares of GEI, and confuses GEI and main effects (Wright, 1971). Thus, regression technique is unable to predict non-linear genotypic response to environment (Nachit et al., 1992).

Shukla (1972) proposed an unbiased estimate of the variance of GEI plus an error term associated with genotype. This stability statistic is termed 'stability variance' (σ_i^2), and is a type 2 stability measure. The σ_i^2 partitions GEI and error term, and assigns it to individual genotypes. Shukla's stability statistic measures the contribution of a genotype to the GEIs and error term, therefore a genotype with low σ_i^2 is regarded as stable. Shukla's stability variance (σ_i^2) is a linear combination of Wricke's ecovalance (W_i^2), another type 2 stability measure which represents the proportion of GEI variance attributed to each genotype. W_i^2 and σ_i^2 are equivalent in ranking genotypes for stability (Kang et al., 1987). Significant positive

correlation between W_i^2 and σ_i^2 was observed in studies on yield stability of barley (*Hordeum vulgare* L.) (Bahrami, 2008), common beans (*Phaseolus vulgaris* L.) (Mekbib, 2003), and winter rapeseed (*Brassica napus* L.) (Marjanovic-Jeromela, 2008). Therefore, it is sufficient and justifiable to use just one of the two statistics (Ngeve and Bouwkamp, 1993).

Kang's stability statistics (YS_i) is nonparametric stability procedure in which both trait mean (*M*) and Shukla's (1972) stability variance (σ_i^2) of trait are used as selection criteria. This method assumed equal weight for *M* and σ_i^2. The genotype with the highest *M* was given the rank of 1 and the rank of *M* was adjusted based on LSD (Mekbib, 2003). Mean rank was adjusted by +1 if mean yield is greater than overall mean yield and their difference is less than 1LSD; +2 if mean yield is greater than or equal to 1LSD above overall mean yield; +3 if mean yield is greater than or equal to 2LSD above overall mean yield; -1 if mean yield is lesser than overall mean yield and their difference is less than 1LSD; -2 if mean yield is lesser than or equal to 1LSD above overall mean yield; and -3 if mean yield is lesser than or equal to 2LSD above overall mean yield (Mekbib, 2003). Stability variance (σ_i^2) was assigned rating of -8, -4, -2, and 0 based on *F* test. The rating of -8, -4, and -2 was assigned, if σ_i^2 was significant at $\alpha = 0.01$, 0.05, and 0.01, respectively; and 0 for non-significant σ_i^2 (Mekbib, 2003). The adjusted rank of *M* and rating of σ_i^2 were summed (YS_i) for each genotype. According to this method, genotypes with YS_i greater than the mean YS_i are considered stable (Kang, 1993; Mekbib, 2003, Fan et al., 2007).

Several models for evaluating stability have been proposed, reflecting different aspects of the concept. However, no single method adequately explains genotype performance across environments. The stability statistics (variation) are not informative and

useful in selection unless they are combined with performance (mean). Thus, stability must be used along with performance.

GEI for yield has been studied in several crops, including common bean (*Phaseolus vulgaris* L.) (Mekbib, 2003), corn (*Zea mays* L.) (Fan et al., 2007), cowpea (*Vigna unguiculata* L.) (Padi, 2007), rice (*Oryza sativa*) (Haryanto et al., 2008), soybean (*Glycine max* L.) (Yan and Rajcan, 2002), tomato (*Lycopersicon esculentum* Mill.) (Ortiz and Izquierdo, 1994), and wheat (*Triticum aestivum* L.) (Vita et al., 2010). GEI for oil production has been studied in winter rapeseed (*Brassica napus* L.) (Marjanovic-Jeromela et al., 2008). GEI for leaf yield has been studied in tea (*Camellia sinensis*) (Wachira et al., 2002). GEI for carotenoid content has been studied in potato (*Solanum tuberosum*) (Haynes et al., 2010).

However, information on stability of watermelon for yield in the US is limited. Therefore, we were interested to evaluate the stability for yield and yield components of watermelon, and to identify genotypes having high stability across locations or specific location adaptability. The objective of this study was to (i) evaluate the influence of years and locations on yield of watermelon genotypes, and (ii) identify genotypes with high stability for yield.

Materials and Methods

Germplasm and location

Forty genotypes of watermelon were evaluated for 3 years (2009, 2010, and 2011) and 8 locations across the southern United States. Locations were chosen to represent major watermelon production regions in the US. These locations ranged from North Carolina and South Carolina in the east to Georgia, Florida, Oklahoma, and Texas in the south to

California in the west. Data were not collected from Oklahoma in 2009, Georgia in 2010, and Florida location in 2011. Forty genotypes were chosen to represent new vs. old releases, small vs. large fruit size, round vs. elongate fruit shape, striped vs. solid rind pattern, anthracnose resistance vs. susceptibility, eastern vs. western adapted, and inbred vs. hybrid type (Tables 1, 2 and 3).

Plots work and Cultural systems

The experiment design was a randomized complete block with four replications in each location and year. For Kinston and Clinton locations of North Carolina, seeds of all 40 genotypes were sown in 72-cell polyethylene flats in the greenhouses at North Carolina State University. An artificial soilless growing medium 4P *Fafard* soilless *mix* (Conrad Fafard Incorporated, Massachusetts), was used. The flats were moistened to capacity after seeding, and held in the greenhouse at 25-30°C until full emergence. The transplants were moved to cold frames for acclimation one week before transplanting. The seedlings were transplanted by hand at the two-true-leaf stage. Missing or damaged transplants were replaced one week after the initial transplanting.

The crop was planted on raised, shaped beds in rows on 3.1-m centers with single-plant hills 1.2 m apart. The beds were made up with drip irrigation tubes and covered with black polyethylene mulch. Production practices were according to the North Carolina Extension Service and Southeastern US 2009 Vegetable Crops handbook (Sanders, 2004; Holmes and Kemble; 2009). The same protocols were followed at other locations in each year.

Data collection and Traits

At each location, the 40 watermelon genotypes were evaluated for traits including marketable yield (Mg ha^{-1}), fruit count (thousand fruit ha^{-1}), % cull fruit (100 x cull fruit yield/total fruit yield), % early fruit (100 x fruit weight of first harvest/fruit weight over all harvests), and fruit size (kg $fruit^{-1}$). Yield traits were the same as used by commercial growers and plant breeders.

Fruit were harvested using the guide of number of days to maturity, as well as the indicators of maturity: a brown and dry tendril at the node bearing the fruit, a dull waxy fruit surface, a light-colored groundspot on the fruit, and a dull sound of the fruit when thumped (Maynard, 2001). Fruit were weighed individually, and yield was calculated as total and marketable fruit weight (Mg ha^{-1}) and number (thousands ha^{-1}) by summing plot yields over harvests. Numbers of cull and marketable fruit were also recorded. Percent cull fruit was calculated as cull fruit weight divided by total fruit weight. All crooked, bottle-necked, and other deformed fruit were considered culls. Depending on location and year 1 to 4 harvests were done; however, most locations had 2-3 harvests (Table 3). Data were not collected on % cull fruit from South Carolina in 2009, 2010, and 2011; and Florida in 2009 and 2010. Only single harvest was done at California in 2009 and Georgia in 2011, therefore for % early fruit no data was collected from California in 2009 and Georgia in 2011.

Data analysis

Data were analyzed for genotype, environment and genotype - environment interactions (GEI) using the SAS (SAS Institute, Cary, NC) procedure for general linear models (PROC GLM). Years, locations, replications, and genotypes were analyzed as

random effects. ANOVA was used to determine the size and significance for genotype - environment interactions for the traits of interest. An *F* test was used to test the interaction effect. If GEIs were significant, additional statistics were calculated to determine the stability of each genotype over the 24 environments. The stability parameters used were b_i, S^2_d, and σ_i^2 (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Shukla, 1972). Least squared means or adjusted trait means (*M*) and their least significant difference (LSD) for each genotype were computed over the 24 environments for the traits of interest. Hereafter, 'mean' is used to indicate least squared mean or adjusted trait mean. Stability parameters b_i, S^2_d and σ_i^2 were used to identify the most stable genotypes. Additionally, the Kang's yield-stability statistic (YS_i) was computed (Kang, 1993; Mekbib, 2003; Fan et al., 2007) for simultaneous selection of high mean and high stability for yield and yield components.

Tests for significance were derived using a t-test for each b_i and an *F* test for each S^2_d for statistical differences from unity and zero, respectively, at 0.05, 0.01 and 0.001 levels of probability. Ranks were assigned to each genotype in an increasing order for each stability parameter, except % cull fruit (selected for low values). Simple correlation coefficients using Spearman's rank correlations were calculated on the ranks to measure the relationship between the parameters. When compared to Pearson correlation coefficients, spearman correlation coefficients may be more reliable since they use rank order and are therefore not as sensitive to extreme values as the Pearson coefficient (Masson et al., 2003).

Results and Discussion

ANOVA

The combined analysis of variance (ANOVA) indicated highly significant environment, genotype and genotype - environment interaction (GEI) effects for all traits evaluated (Table 4). Marketable yield was affected greatly by environment (48% of total sum of squares), moderately by GEI (18% of total sum of squares), and a small amount by genotype (8% of total sum of squares) (Table 4). Of the environmental (48%) variation for marketable yield, 75% was attributable to location, 21% to location - year interaction (LEI), and 3% to year (Table 4). However, fruit count was controlled largely by environment, genotype and GEI effects (35%, 20%, and 21% of total sum of squares, respectively) (Table 4). The E portion (35%) of fruit count was attributable to 68% to location, 27% to LEI, and 7% to year (Table 4).

ANOVA for % cull fruit indicated that environment, genotype and GEI effects accounted for 26% 10% and 23%, respectively, of the total sum of squares (Table 4). Percent cull fruit was affected moderately by environment (26% of total sum of squares) and GEI (23% of total sum of squares), and a small amount by genotype (10% of total sum of squares) (Table 4). Of the environmental (26%) variation for % cull fruit, 58% was attributable to location, 31% to LEI, and 12% to year (Table 4).

ANOVA for % early fruit indicated that environment, genotype and GEI effects accounted for 38%, 7% and 22%, respectively, of the total sum of squares (Table 4). Percent early fruit was affected greatly by environment (38% of total sum of squares), moderately by GEI (21% of total sum of squares), and a small amount by genotype (7% of total sum of

squares) (Table 4). Of the environmental (48%) variation for % early fruit, 58% was attributable to location, 6% to LEI, and 3% to year (Table 4).

ANOVA for fruit size indicated that environment, genotype and GEI effects accounted for 14%, 51% and 13%, respectively, of the total sum of squares (Table 4). Fruit size was affected largely by genotype (51% of total sum of squares), and small amount by environment (14% of total sum of squares) and GEI (13% of total sum of squares) (Table 4). Of the environmental (14%) variation for fruit size, 54% was attributable to location, 44% to LEI, and 1% to year (Table 4).

All yield traits except fruit size had a large sum of squares due to environment, with large differences among environments for genotype means causing most of the variation in genotype performance. Similarly, these results suggested that yield and yield components were influenced by GEI and, thus, required separate stability analysis for each trait.

Genotype means (M)

Marketable yield ranged from 80.44 to 27.43 Mg ha^{-1}. Highest marketable yield was for 'Big Crimson', but 'Stone Mountain', 'Stars-N-Stripes F1' and 'Starbrite F1' were not significantly different (Table 5). Other high yielding genotypes were 'Fiesta F1', 'Regency F1', 'Calhoun Gray', 'Legacy' and 'Mountain Hoosier'. 'Golden Midget' had the lowest marketable yield, significantly lower than the other genotypes tested (Table 5). A similar observation was made by Gusmini and Wehner (2005). They evaluated 80 watermelon genotypes for yield performance and found that highest yielders were the inbreds 'Mountain Hoosier', 'Hopi Red Flesh', 'Early Arizona', Stone Mountain', 'AU-Jubilant', 'Sweetheart', 'Calhoun Gray', 'Big Crimson', 'Moon & Stars', 'Cole Early', 'Yellow Crimson', 'Legacy', and

'Blacklee', and the F1 hybrids 'Starbrite F1', and 'Stars-N-Stripes'. Fruit count ranged from 3.94 to 15.59 thousand fruit ha^{-1} (Table 6). Highest fruit count was for 'Golden Midget', followed by 'Minilee' and 'King & Queen' (Table 6). Lowest fruit count was for 'Carolina Cross#183', significantly lower than all other genotypes (Table 6). Genotypes with high marketable yield had intermediate fruit count, confirming the results of Gusmini and Wehner (2005).

Large fruit size was correlated with high % cull fruit (Tables 7 and 9). 'NC Giant' and 'Congo' had large fruit and the highest % cull fruit (23.42% and 20.55%, respectively, Table 7). Lowest % cull fruit were for 'Minilee', which was similar to high yielding 'Starbrite F1' and 'Regency F1' (Table 7). 'Carolina Cross#183', 'NC Giant', 'Georgia Rattlesnake', 'AU-Jubilant', and 'Jubilee' had the largest fruit size; 'Golden Midget', 'Minilee', and 'Mickylee' had the smallest fruit size (Table 9).

'Golden Midget', 'Early Canada', 'Stone Mountain', and 'Regency F1' had the highest % early fruit (Table 8). Genotypes 'Navajo Sweet', 'Peacock WR-60', 'King & Queen', 'Minilee' and 'Tom Watson' produced the lowest % early fruit (Table 8).

Regression coefficient or slope (b_i)

For marketable yield, the b_i value of most of the genotypes was similar ($P>0.01$) to unity, except for 'Big Crimson', 'Carolina Cross#183', 'Charleston Gray', 'Congo', 'Early Canada' 'Golden Midget', 'Graybelle', 'King & Queen', 'Royal Flush F1', 'Starbrite F1' and 'Tom Watson' (Table 5). According to Eberhart and Russell (1966), large variation in b_i indicates large differences in genotype response to different environments. However, several high, medium and low yielders had a b_i close to unity (Table 5). Those included 'Stars-N-

Stripes F1', 'Georgia Rattlesnake', 'Sangria F1', 'Early Arizona', 'Navajo Sweet', 'Peacock WR60', and 'Mickylee'. Thus, these genotypes were the most stable for marketable yield using the regression coefficient method.

Similarly, b_i for fruit count was close to unity for 'Sugar Baby', ' Stars-N-Stripes F1', 'Tender Sweet OF', 'Crimson Sweet', 'Fiesta F1', 'Crimson Sweet', 'Mountain Hoosier', 'Legacy', and 'Peacock WR-60' (Table 6). With the exception of 'Black Diamond', 'Congo', and 'Starbrite F1' all genotypes had b_i of unity (Table 6). Genotypes 'Black Diamond' and 'Congo' had b_i of zero. High positive value of b_i indicates that fruit count increased as environmental index increased. Low b_i indicates that fruit count did not increase as environmental index increased (Table 6).

For % cull fruit, b_i ranged from -1.35 to 2.79 (Table 7). Interestingly, a positive association was observed for b_i and % cull fruit (Table 10). This suggests that genotypes such as 'Congo' and 'Hopi Red Flesh' with high % cull fruit also had high b_i, indicated that they produced more culls as environment improved. Conversely, genotypes such as 'Stars-N-Stripes F1', 'Fiesta F1', Peacock WR 60, and 'Yellow Crimson' with low % cull fruit had resistance to environment changes. 'Minilee', 'Navajo Sweet', and 'Calsweet' had low % cull fruit and negative b_i value, which suggested that these genotypes produced fewer culls as environment improved.

The b_i value for % early fruit for all the genotypes were positive and found to be significantly similar to 1.0, except 'Georgia Rattlesnake' (Table 8). These findings suggested that early yield of all the genotypes was more influenced by environment. These genotypes tended to have higher % early fruit as environment improved. Therefore, these genotypes

were the most desirable for yield performance over environments since their % early fruit improved directly as the environment improved.

Deviation from regression (S^2_d) and Shukla's stability variance (σ_i^2)

A significant positive rank correlation was found between S^2_d and σ_i^2 for the yield of marketable yield, fruit count, % cull fruit, and % early fruit; and fruit size (Table 10). The high correlation between S^2_d and σ_i^2 indicated overlap in the aspect of stability measured by the two statistics. Similar observation has been reported by Ngeve and Bouwkamp (1993) and Mekbib (2003) in sweet potato (*Ipomoea batatas* L.) and common bean (*Phaseolus vulgaris* L.), respectively. Therefore, it is sufficient to use just one of the two statistics.

The genotypes with the highest marketable yield in this study were 'Starbrite F1', 'Stars-N-Stripes F1', 'Fiesta F1', 'Regency F1', 'Big Crimson', 'Stone Mountain', 'Calhoun Gray', and 'Legacy'. Among these high yielding genotypes, two inbreds ('Big Crimson' and 'Legacy') and a hybrid ('Starbrite F1') had significant S^2_d and high σ_i^2 for marketable yield (Table 5). It suggested that marketable yield of 'Big Crimson', 'Legacy', and 'Starbrite F1' were more likely to change over environments. Two high yielding inbreds ('Big Crimson' and 'Legacy') had significant S^2_d and high σ_i^2 for yield components including, fruit count and % early fruit (Tables 6 and 8). According to Eberhart and Russell (1966) and Shukla (1972) an ideal genotype is the one that combines high yield with non-significant S^2_d and low σ_i^2. Therefore, the inbred genotypes 'Big Crimson' and 'Legacy' were unstable and non-ideal for marketable yield. For % early fruit, except two hybrids ('Fiesta F1' and 'Starbrite F1'), all high yielding genotypes had non-significant S^2_d and low σ_i^2 (Table 8). In contrast, for fruit size all high yielding genotypes had non-significant S^2_d and low σ_i^2, except inbred 'Calhoun

Gray' (Tables 9). It suggested that the performance of high yielding genotypes for % early fruit was more likely to change over environments and fruit size was less likely to change over environments.

With respect to inbreds with high marketable yield, hybrids with high marketable yield consistently had non-significant S^2_d and low σ_i^2 for fruit count and % early fruit (Tables 6 and 7). The top three high yielding hybrids ('Starbrite F1', 'Regency F1', and 'Stars-N-Stripes F1') had non-significant S^2_d and low σ_i^2 for fruit count and % cull fruit (Tables 6 and 7). Whereas, high yielding inbred *per se* did not have non-significant S^2_d and low σ_i^2 for both fruit count and % cull fruit (Tables 6 and 7). It is assumed that the presence of heterozygous loci in hybrids might have masked the effect of genes controlling trait for less fruit count and low % cull fruit. Similar to this study, Bruns and Peterson (1998) compared yield stability of hybrids and pure lines in Agitprop Standard Variety Trials and USDA-ARS Southern Regional Performance Nurseries from 1990 to 1995. They found strong evidence for substantial hybrid yield advantage and hybrid responsive to favorable environments. However, they did not find significant difference in deviation from regression line in hybrid. vs. inbreds.

Kang's stability statistics (YS_i)

Kang's stability statistics (YS_i) analysis used both trait mean (M) and Shukla's (1972) stability variance (σ_i^2) of the trait. This method assumed equal weight for M and σ_i^2; however, if F test value of σ_i^2 was non-significant then σ_i^2 gets rating of 0 which leads to equal rank of M and YS_i. In present study, these observations were confirmed by a strong correlation was found between YS_i and M for marketable yield, fruit count, % cull fruit, %

early fruit, and fruit size (Table 10). Hence it would lead to genotypes which ranked superior in marketable yield, fruit count, % cull fruit, % early fruit, and fruit size were stable in performance according to YS_i statistics. These observations support with earlier findings of Bachireddy et. al., (1992), Mekbib (2003), and Fan et al., (2007). They found that the genotypes which ranked superior in yield for sweet corn, common bean, and corn were stable in performance according to YS_i statistics. Therefore, in the present study we considered M instead of YS_i.

Genotype stability

The genotypes that recorded significantly high marketable yield in this study included four hybrids and inbreds: 'Starbrite F1'; 'Stars-N-Stripes F1'; 'Fiesta F1'; and 'Regency F1', and 'Big Crimson'; 'Stone Mountain'; 'Calhoun Gray'; and 'Legacy', respectively. The b_i value of these six genotypes with high marketable yield had b_i close to unity (Table 5). Thus based on b_i value alone, genotypes 'Fiesta F1', 'Stars-N-Stripes F1', 'Regency F1', 'Calhoun Gray', 'Legacy' and 'Stone Mountain' can be considered stable. Genotypes 'Big Crimson' and 'Starbrite F1' had b_i greater than unity, which described that these genotypes were sensitivity to environmental change (below average stability) and greater specificity of adaptability to high yielding environments.

Five genotypes with high marketable yield had non-significant S^2_d and low σ_i^2 (Table 5). Hence, according to non-significant S^2_d and low σ_i^2, genotypes 'Fiesta F1', 'Stars-N-Stripes F1', 'Regency F1', 'Calhoun Gray', and 'Stone Mountain' could be considered stable. However, Eberhart and Russell (1966) described as desirable and stable genotypes as one with a high mean yield, b_i close to unity, low and non-significant S^2_d, and low σ_i^2.

Considering this definition, the best genotypes were hybrids 'Fiesta F1', 'Stars-N-Stripes F1', and 'Regency F1'; and inbreds 'Calhoun Gray' and 'Stone Mountain'. They had high marketable yield, b_i close to unity, non-significant S^2_d, and low σ_i^2; hence, they had high adaptability across wide range of environments. Genotype 'Legacy' had high marketable yield and b_i close to unity, but a S^2_d value significantly higher than zero; as a result, it could be regarded as unstable for marketable yield.

Similarly, according to Eberhart and Russell (1966) model high yielding genotypes 'Stars-N-Stripes F1', 'Regency F1', 'Calhoun Gray', and 'Stone Mountain' were desirable for fruit count (Table 6). For % cull fruit and % early fruit genotypes 'Stars-N-Stripes F1' and 'Regency F1', and 'Fiesta F1' and 'Starbrite F1' were stable (Table 7 and 8). However, for fruit size all top eight high yielding genotypes were stable and desirable, except 'Calhoun Gray' (Table 9).

Correlation among trait mean, b_i, S^2_d, σ_i^2, and YS_i

Trait mean was significantly (P<0.001) and positively correlated (Spearman) with YS_i for all the traits evaluated in this study (Table 10). The high correlation between trait mean and YS_i is expected because during computation of YS_i F test value of σ_i^2 was non-significant for all the traits evaluated. Thus it captured large trait mean component; therefore, the rank of M and YS_i remain unchanged. Similarly, significant correlations was found between S^2_d and σ_i^2 for all the traits evaluated in this study, and among % cull fruit and stability statistics (b_i, S^2_d, σ_i^2, and YS_i) (Table 10). It suggested that all these statistics measure the same aspect of stability and provided same information (Wachira et al., 2002). Therefore, these stability

statistics could be used interchangeably to select stable genotypes, and it is sufficient to use just one of the statistics.

However, non-significant correlation was noticed between some of the pairs from stability statistics (b_i, S^2_d, σ_i^2, and YS_i) and trait mean for marketable yield, fruit count, % early and fruit size (Table 10). The non-significant correlation between trait mean and stability statistics suggested that these statistics provide information that cannot be obtained from trait mean (Mekbib, 2003).

The positive and significant correlation between b_i with marketable yield and YS_i suggested that genotypes that were responsive to environment also had high marketable yield. Similar correlation was found for fruit size (Table 10). The negative and non-significant correlation between marketable yield with S^2_d and σ_i^2 indicated that high yielding genotypes were normally associated with low S^2_d and σ_i^2. Similarly, negative and non-significant correlation between b_i, with S^2_d and σ_i^2; and YS_i and S^2_d for marketable yield suggested that genotypes with high b_i and YS_i values were associated with low σ_i^2 and S^2_d. The lack of significant or weak correlation among trait mean and stability statistics (b_i, S^2_d, σ_i^2, and YS_i) suggested the independence and possibility of using these statistics simultaneously (Kang and Pham, 1991; Kang and Gauch, 1996, Mekbib, 2003).

Conclusions

Several watermelon genotypes had strong environmental response as well as GEI on yield and yield components, and there was evidence for the advantage of hybrid over inbred for yield and responsiveness to favorable environments. Four genotypes including, two hybrids 'Fiesta F1' and 'Stars-N-Stripes F1', and two hybrids inbred 'Stone Mountain' and

'Calhoun Gray' had a high trait mean performance and high stability for yield. Interestingly, the highest performing inbred and hybrid genotype for watermelon fruit yield and yield components (e.g. 'Big Crimson' and 'Starbrite F1') were not the highest in yield stability. All four stable genotypes had high marketable yield, average fruit count, low % cull fruit, above average % early fruit, and medium sized fruit. These four genotypes can be recommended for planting over a wide range of environments of the southern US.

Neither of these two hybrids and inbred, *per se*, were stable for all the yield components. Therefore, there is opportunity to further improve both hybrids and inbred. However, hybrids 'Fiesta F1' and 'Stars-N-Stripes F1' were more stable for yield components evaluated in this study than inbreds 'Stone Mountain' and 'Calhoun Gray'. Inbreds 'Stone Mountain' and 'Calhoun Gray' were less appealing in appearance and quality than other two high yielding genotypes ('Legacy' and 'Big Crimson'). Although, 'Legacy' and 'Big Crimson' were unstable for marketable yield but they were stable in performance for some yield components, which were lacking in 'Stone Mountain' and 'Calhoun Gray'. With the current emphasis on hybrids in the global market, these inbreds can be utilized in a breeding program for transferring stability genes into inbreds for use in hybrid production. Hybrids provide growers with added value over inbreds through high fruit yield, improved yield responsiveness, and stability.

The strong correlation between YS_i and trait mean, and S^2_d and σ_i^2 (for all the traits evaluated in this study) suggested these statistics measure the same aspect of stability and provided same information (Wachira et al., 2002). Therefore, these stability statistics could be used interchangeably to select stable genotypes or use just one of the statistics. Overall,

the results presented in this study showed that GEI plays a significant role in the success of any breeding programs and there is a clear opportunity to continue to breed watermelon genotypes with high trait mean, wide adaptation, and stability.

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Table 1. The 40 watermelon genotypes tested.

Genotype	Year of release	Pedigree
AU-Jubilant	1985	Jubilee x PI 271778
Allsweet	1972	[(Miles x Peacock) x Charleston Gray]
Big Crimson	NA†	NA
Black Diamond	1949	Segregation within Cannonball or Black Diamond
Calhoun Gray	1965	Calhoun Sweet x Charleston Gray
Calsweet	NA	[(Miles x Peacock) x Charleston Gray]
Carolina Cross#183	NA	NA
Charleston Gray	1954	[{(Africa 8 x Iowa Belle) x Garrison} x Garrison] x [(Hawkesbury x Leesburg) x Garrison]
Congo	1949	(African x Iowa Belle) x Garrison
Crimson Sweet	1963	(Miles x Peacock) x Charleston Gray
Desert King	NA	NA
Early Arizona	NA	NA
Early Canada	NA	NA
Fiesta F1	1991	Unknown (Plant Variety Protection)
Georgia Rattlesnake	1870	
Golden Midget	1959	New Hampshire Midget x Pumpkin Rind
Graybelle	1963	Sugar Baby x Charleston Gray sister line
Hopi Red Flesh	NA	NA
Jubilee	1963	Africa 8, Iowa Belle, Garrison, Hawkesbury, and Leesburg
King & Queen	NA	NA
Legacy	1997	(Early Gray x Little Jubilee 4) x Verona
Mickylee	1986	Texas W5, Fairfax, Summit, and Graybelle
Minilee	1986	Texas W5, Fairfax, Summit, and Graybelle
Mountain Hoosier	NA	NA
NC Giant	NA	NA
Navajo Sweet	NA	NA
Peacock WR-60	1955	Klondike R7 x Peacock
Quetzali	1965	NA
Regency F1		Unknown (Plant Variety Protection)
Royal Flush F1	1995	Unknown (Plant Variety Protection)
Sangria F1	NA	Unknown (Plant Variety Protection)
Starbrite F1	NA	Unknown (Plant Variety Protection)
Stars-N-Stripes F1	NA	Unknown (Plant Variety Protection)
Stone Mountain	1924	NA
Sugar Baby	1955	Tough Sweets selection, inbred 13 years
Sugarlee	1981	Texas W5, Summit, Charleston Gray, Fairfax, Crimson Sweet, and Graybelle
Sweet Princess	1967	small-seeded Congo type x Charleston Gray
Tendersweet OF	NA	NA
Tom Watson	1906	NA
Yellow Crimson	NA	NA

† Not available

Table 2. Traits and pedigrees for the 40 watermelon genotypes evaluated.

	Fruit		Rind			Seed		Flesh
Genotype	Shape†	Size‡	Color§	Thickness¶	Pattern#	Size††	Color‡‡	color¶¶
AU-Jubilant	L	M	LG	S	M	L	R	R
Allsweet	L	M	LG	N	W	S	R	S
Big Crimson	R	M	MG	M	W	M	R	R
Black Diamond	R	S	DB	M	S	L	R	R
Calhoun Gray	L	M	G	M	S	M	R	R
Calsweet	L	M	LG	T	W	S	B	S
Carolina Cross#183	E	G	LG	T	N	L	W	R
Charleston Gray	L	L	G	T	R	M	R	R
Congo	L	M	DG	M	R	L	T	R
Crimson Sweet	R	M	LG	M	M	S	B	R
Desert King	O	S	SG	S	S	M	R	O
Early Arizona	O	S	SG	N	S	L	R	R
Early Canada	R	S	G	N	R	S	R	R
Fiesta F1	L	M	LG	M	W	S	B	R
Georgia Rattlesnake	L	G	LG	M	N	L	R	R
Golden Midget	O	C	Y	N	S	L	R	R
Graybelle	G	S	G	N	S	S	R	R
Hopi Red Flesh	O	M	SG	M	S	L	B	R
Jubilee	L	L	LG	T	N	L	R	R
King & Queen	O	M	LG	N	N	M	B	R
Legacy	L	M	LG	N	N	M	R	R
Mickylee	R	N	LG	N	R	M	R	S
Minilee	R	S	G	N	R	S	R	S
Mountain Hoosier	O	M	SG	T	S	L	W	R
NC Giant	L	G	LG	T	R	L	R	R
Navajo Sweet	R	S	LG	M	N	M	R	R
Peacock WR-60	L	S	SG	M	S	S	R	R
Quetzali	R	S	LG	N	S	M	R	R
Regency F1	O	S	MG	M	M	S	T	R
Royal Flush F1	L	M	MG	M	W	S	B	S
Sangria F1	O	M	MG	M	S	S	B	S
Starbrite F1	O	M	LG	L	S	S	R	R
Stars-N-Stripes F1	O	M	DG	T	W	L	B	S
Stone Mountain	O	M	SG	T	S	L	T	R
Sugar Baby	R	M	MB	S	S	S	R	S
Sugarlee	R	S	LG	M	N	M	R	R
Sweet Princess	O	M	G	M	R	T	R	R
Tendersweet OF	E	M	DG	M	W	L	W	O
Tom Watson	E	M	MG	T	S	L	T	R
Yellow Crimson	L	L	LG	N	S	L	B	C

†Fruit Shape: elongate (E), oval (O), round (R)
‡Fruit Size: micro (<3 lb.) (C), mini (3-8 lb.) (N), icebox (9-13 lb.) (B), small (S), sometimes called pee-wee (14-18 lb.), medium (19-24 lb.) (M), large (25-32 lb.) (L), and giant (>32 lb.) (G).
¶Rind Color: light green (LG), medium green (MG), dark green (DG), solid light black (LB), solid medium black (MB), solid dark black (DB) golden (G), solid green (SG), gray (R), Yellow (Y), mottled (M)
§Rind thickness: thick (>10mm) (T), medium (5-10mm) (M), thin (<5mm) (N)
#Rind Pattern: wide stripe (W), medium stripe (M), narrow stripe (N), gray (G), solid (S), Rattle Snake (R) [Dark green is dominant, stripe is decided by dark green]
††Seed Size: tomato size (T), small (S), medium (M), large (L)
‡‡Seed Color: black (B), brown (R), tan (T), dotted (D), white (W)
§§Flesh Color: scarlet red (S), coral red (R), orange (O), salmon yellow (Y), canary yellow (C), or white (W)

Table 3. Number of harvest done on 40 watermelon genotypes tested in 3 years and 8 locations.

Location		Co-ordinate		Harvests		
Abb rev.	Name	Latitude	Longitude	2009	2010	2011
KN	Kinston, NC	35° 15' 45" N	77° 34' 54" W	4	2	3
CI	Clinton, NC	35° 45' 25" N	80° 27’ 36" W	3	2	3
SC	Charleston, SC	32° 46' 35" N	79° 55' 52" W	3¶	2¶	3¶
GA	Cordele, GA	31° 57' 47" N	83° 46' 57" W	2	-	1
FL	Quincy, FL	30° 35' 13" N	84° 34' 59" W	2¶	2¶	-
TX	College Station, TX	30° 37' 40" N	96° 20' 3" W	3	4	3
WD	Woodland, CA	38° 40' 43" N	121° 46' 20" W	1	2	3
OK	Lane, OK	34° 17' 55" N	95° 59' 17" W	-†	4	4

† Data were not collected from this location
¶ Data were not collected on % cull fruit

Table 4. ANOVA for marketable yield (Mg ha^{-1}), fruit count, % cull fruit, % early fruit, and fruit size of 40 watermelon genotypes (kg $fruit^{-1}$) tested in 3 years and 8 locations.

	Marketable yield		Fruit count		% of total sum of squares	
Source	df	Mean square	df	Mean square	Fruit yield	Fruit count
Environment (E)	20	106825.19*	20	1554.37*	47.83	34.51
Location (L)	7	231712.42 *	7	3036.82*	75.92	68.38
Year (Y)	2	3240.24	2	107.95	3.00	6.90
L x Y	11	40726.21*	11	752.03*	20.97	26.61
Replication within E	63	2366.27*	63	30.36*	3.33	2.12
Genotype (G)	39	9227.34*	39	456.12*	8.05	19.75
G x E	780	1023.33*	779	24.27*	17.87	20.99
G x L	273	1322.62*	273	34.52*	45.23	49.84
G x Y	78	870.00	78	21.31	8.50	8.79
G x L x Y	429	850.71*	428	18.23*	45.72	41.26
Pooled Error	2442	419.77	2436	8.37	22.95	22.52
CV (%) for Fruit yield = 33.50; for fruit count = 32.78						
R^2 (%) for Fruit yield = 77.05; for fruit count = 77.48						

	% cull fruit		% early fruit		% of total sum of squares	
Source	df	Mean square	df	Mean square	% cull fruit	% early fruit
Environment (E)	18	10327.63*	19	40143.06*	25.52	37.67
Location (L)	6	17835.89	7	63207.46*	57.57	58.01
Year (Y)	2	10925.12	2	11355.56*	11.75	2.98
L x Y	10	5801.61*	10	4879.89*	31.21	6.40
Replication within E	57	359.93*	57	1301.27*	2.82	3.66
Genotype (G)	39	1792.39*	39	3498.84*	9.59	6.74
G x E	699	234.49*	661	648.49*	22.50	21.17
G x L	234	306.34*	273	743.35*	4.73	47.34
G x Y	78	293.43*	78	782.52*	13.96	14.24
G x L x Y	387	186.02*	310	542.10*	43.92	39.20
Pooled Error	2163	133.89	2019	305.96	39.75	30.51
CV (%) for % culls = 139.19; for % early = 56.01						
R^2 (%) for % cull = 60.24; % early = 69.49						

	Fruit size		% of total sum of squares
Source	df	Mean square	Fruit size
Environment (E)	20	226.17*	14.45
Location (L)	7	345.91	53.53
Year (Y)	2	21.28	0.94
L x Y	10	180.26*	43.84
Replication within E	63	9.70*	1.95
Genotype (G)	39	412.78*	51.46
G x E	776	5.42*	13.45
G x L	273	6.18*	40.10
G x Y	78	8.58*	15.91
G x L x Y	386	4.13*	41.74
Pooled Error	2374	2.21	16.77
CV (%) for size = 20.11			
R^2 (%) for size = 83.22			

* Significant at the 0.01 level of probability

Table 5. Means (corrected by least squares) (*M*) and stability parameters (regression coefficient [b_i], deviation from regression [S^2_d] and Shukla's stability variance [σ_i^2]) for marketable yield of 40 watermelon genotypes tested in 3 years and 8 locations.

	Marketable yield (Mg ha^{-1})			
Genotype	*M*‡	b_i,	S^2_d	σ_i^2
AU-Jubilant	67.01	0.51	729.93	627.02
Allsweet	55.23	1.20	529.91	461.84
Big Crimson	80.44	1.81*	1221.68**	1147.63
Black Diamond	66.92	0.47	975.78*	827.32
Calhoun Gray	69.36	1.06	357.14	328.05
Calsweet	63.59	0.50	826.28**	760.13
Carolina Cross#183	55.72	2.05**	958.57*	713.76
Charleston Gray	61.29	0.42*	2969.41***	2738.22
Congo	52.74	0.25*	489.92	390.70
Crimson Sweet	50.31	0.59	3441.21***	3328.37
Desert King	67.06	1.11	780.30	717.13
Early Arizona	55.76	0.94	578.07*	525.57
Early Canada	49.67	0.44*	539.23**	445.37
Fiesta F1	71.25	1.33	656.44	616.62
Georgia Rattlesnake	59.56	1.43	674.45	557.60
Golden Midget	27.43	0.47**	944.24***	1079.91
Graybelle	49.43	0.41*	509.83	433.72
Hopi Red Flesh	53.90	1.29	757.71*	690.31
Jubilee	58.10	1.18	535.55	782.96
King & Queen	62.65	-0.48**	1869.72**	1375.31
Legacy	68.28	1.09	1406.18***	1351.33
Mickylee	51.18	0.84	623.40***	572.04
Minilee	50.05	0.48*	461.80*	435.90
Mountain Hoosier	68.19	1.03	1195.74***	1126.19
NC Giant	63.11	1.24	1749.65***	1682.30
Navajo Sweet	59.14	1.12	1155.01***	1091.29
Peacock WR-60	54.03	0.72	584.19	528.58
Quetzali	51.58	1.07	312.54	273.09
Regency F1	70.13	0.56	614.90	566.88
Royal Flush F1	66.44	1.91**	713.50*	539.54
Sangria F1	66.62	1.32	461.87	442.03
Starbrite F1	80.40	2.21**	1365.50**	1221.86
Stars-N-Stripes F1	77.25	1.13	432.06	416.09
Stone Mountain	79.10	1.57	497.48	523.36
Sugar Baby	45.00	0.75	335.32**	322.94
Sugarlee	56.86	1.23	524.47	478.75
Sweet Princess	62.23	1.02	956.33***	882.04
Tendersweet OF	63.23	0.84	600.27*	564.54
Tom Watson	59.71	1.94*	1023.61	922.92
Yellow Crimson	67.31	1.00	1798.93***	1736.10

*, **, *** indicate significantly different from unity for the regression coefficients or slope (b_i) and from zero for the deviation from regression (S^2_d) at 0.05, 0.01 and 0.001 levels of probability, respectively

‡LSD = 7.56

Table 6. Means (corrected by least squares) (*M*) and stability parameters (regression coefficient [b_i], deviation from regression [S^2_d] and Shukla's stability variance [σ_i^2])for fruit count of 40 watermelon genotypes tested in 3 years and 8 locations.

	Fruit count (thousand fruit ha^{-1})			
Genotype	*M*‡	b_i,	S^2_d	σ_i^2
AU-Jubilant	7.02	0.53	6.81	6.20
Allsweet	6.25	1.25	5.70	4.91
Big Crimson	9.21	1.24	16.01**	15.06
Black Diamond	8.53	0.00**	15.34**	11.46
Calhoun Gray	8.32	1.19	4.94	4.12
Calsweet	7.93	0.37	9.77	9.26
Carolina Cross#183	3.94	0.64	6.94**	8.39
Charleston Gray	7.40	0.86	33.55***	31.91
Congo	6.59	-0.03**	5.21	3.73
Crimson Sweet	6.51	1.02	40.97***	39.10
Desert King	8.25	0.96	8.84	7.80
Early Arizona	11.91	1.20	26.68**	28.83
Early Canada	9.54	0.63	15.35	14.35
Fiesta F1	9.27	1.02	16.95**	15.79
Georgia Rattlesnake	6.20	1.39	10.20*	8.51
Golden Midget	15.59	2.18	89.64***	180.23
Graybelle	9.00	0.73	11.72	10.40
Hopi Red Flesh	9.56	1.39	31.56***	31.40
Jubilee	6.04	0.49	6.67	9.43
King & Queen	13.75	-0.35	94.25***	82.76
Legacy	7.62	0.99	16.30***	15.66
Mickylee	12.54	1.60	37.72**	36.12
Minilee	14.00	1.74	20.63	23.61
Mountain Hoosier	7.99	0.98	16.90***	15.35
NC Giant	5.45	0.78	13.24***	13.67
Navajo Sweet	11.69	1.74	42.97***	44.48
Peacock WR-60	8.22	0.96	14.56*	13.76
Quetzali	9.53	1.20	8.77	7.71
Regency F1	8.36	0.31	7.14	6.92
Royal Flush F1	8.72	1.67	8.99	7.05
Sangria F1	8.28	1.15	10.55	9.53
Starbrite F1	9.10	1.79*	8.51	6.54
Stars-N-Stripes F1	9.18	1.04	5.75	5.39
Stone Mountain	9.06	1.13	8.14	7.17
Sugar Baby	10.17	1.00	11.99*	11.31
Sugarlee	7.78	0.65	7.95	6.94
Sweet Princess	7.38	0.84	7.32	6.62
Tendersweet OF	7.56	1.10	6.51	5.94
Tom Watson	7.96	1.94	22.31*	21.57
Yellow Crimson	9.23	0.85	27.83***	26.37

*, **, *** indicate significantly different from unity for the regression coefficients or slope (b_i) and from zero for the deviation from regression (S^2_d) at 0.05, 0.01 and 0.001 levels of probability, respectively
‡LSD = 1.07

Table 7. Means (corrected by least squares) (*M*) and stability parameters (regression coefficient [b_i], deviation from regression [S^2_d] and Shukla's stability variance [σ_i^2]) for % cull fruit of 40 watermelon genotypes tested in 3 years and 8 locations.

	% cull fruit			
Genotype	*M*‡	b_i,	S^2_d	σ_i^2
AU-Jubilant	13.60	1.18	98.36	80.18
Allsweet	16.04	2.50*	191.10	155.26
Big Crimson	6.46	1.48	245.23***	194.91
Black Diamond	6.46	1.08	170.02	141.74
Calhoun Gray	11.28	2.21*	221.95*	156.39
Calsweet	5.33	-0.00**	57.22	36.93
Carolina Cross#183	15.86	1.32	532.23	379.76
Charleston Gray	9.39	1.92	91.49	72.11
Congo	21.35	3.11*	487.61	352.77
Crimson Sweet	3.59	0.59	40.52	24.00
Desert King	6.39	0.77	89.21	76.72
Early Arizona	7.83	1.66	162.98	147.63
Early Canada	5.02	0.38	83.34	58.97
Fiesta F1	6.93	0.08*	130.83*	74.58
Georgia Rattlesnake	11.41	1.12	387.48	338.16
Golden Midget	8.21	0.91	281.42***	235.78
Graybelle	5.53	-0.17***	115.96**	70.70
Hopi Red Flesh	16.28	2.55*	1099.50***	906.86
Jubilee	15.20	2.06	508.70*	327.92
King & Queen	2.86	0.10***	83.96***	67.26
Legacy	6.27	-0.36**	84.43	37.23
Mickylee	1.68	-0.15***	28.91***	18.76
Minilee	1.83	0.43***	22.77**	18.73
Mountain Hoosier	9.55	0.82	128.98*	94.15
NC Giant	24.91	1.89	833.35**	443.77
Navajo Sweet	5.82	-0.12**	253.53***	156.07
Peacock WR-60	5.49	0.03*	112.75	84.55
Quetzali	5.59	-1.35***	249.23	82.21
Regency F1	5.26	0.43	62.42	48.18
Royal Flush F1	6.16	2.25**	142.95*	57.25
Sangria F1	9.60	2.62**	224.73	143.48
Starbrite F1	5.82	0.11*	58.94	39.42
Stars-N-Stripes F1	6.28	0.66	45.43	44.41
Stone Mountain	7.07	2.79**	334.06**	154.14
Sugar Baby	4.59	0.10**	99.76**	66.45
Sugarlee	5.62	0.59	60.68	46.36
Sweet Princess	8.62	1.54	95.16	74.85
Tendersweet OF	10.47	2.12*	230.93	183.98
Tom Watson	7.72	1.12	150.39*	124.70
Yellow Crimson	5.75	0.04**	109.54**	64.26

*, **, *** indicate significantly different from unity for the regression coefficients or slope (b_i) and from zero for the deviation from regression (S^2_d) at 0.05, 0.01 and 0.001 levels of probability, respectively
‡LSD = 4.27

Table 8. Means (corrected by least squares) (*M*) and stability parameters (regression coefficient [b_i], deviation from regression [S^2_d] and Shukla's stability variance [σ_i^2]) for % early fruit of 40 watermelon genotypes tested in 3 years and 8 locations.

	% early fruit			
Genotype	*M*‡	b_i,	S^2_d	σ_i^2
AU-Jubilant	36.08	0.95	429.88	309.51
Allsweet	23.78	1.35	339.57	315.49
Big Crimson	23.24	0.85	348.66*	282.65
Black Diamond	36.23	0.85	789.02*	596.49
Calhoun Gray	35.58	1.37	615.01**	472.83
Calsweet	24.39	0.92	827.49*	652.68
Carolina Cross#183	10.12	0.62	615.29**	462.37
Charleston Gray	35.25	0.96	383.92	321.04
Congo	29.24	0.83	293.42	203.85
Crimson Sweet	35.99	0.45	611.13	620.50
Desert King	27.45	1.35	867.46**	713.43
Early Arizona	26.71	0.69	458.64	200.03
Early Canada	40.72	0.63	796.46	618.94
Fiesta F1	29.76	0.82	410.59	303.73
Georgia Rattlesnake	34.63	1.94*	475.12	326.56
Golden Midget	49.94	1.12	1459.36***	1354.65
Graybelle	36.77	0.51	381.10	280.04
Hopi Red Flesh	24.01	0.49	408.96	305.28
Jubilee	38.25	1.07	624.24	504.73
King & Queen	18.92	0.92	388.78*	320.57
Legacy	35.80	0.63	1071.41***	804.17
Mickylee	29.70	0.81	856.80**	521.90
Minilee	21.00	1.25	434.02**	148.06
Mountain Hoosier	23.09	0.90	225.63	168.69
NC Giant	31.36	1.13	425.26	552.71
Navajo Sweet	17.43	1.16	543.81*	411.79
Peacock WR-60	17.66	0.86	297.29	248.39
Quetzali	31.38	1.44	727.02**	580.39
Regency F1	39.10	1.42	573.47*	444.39
Royal Flush F1	28.57	0.94	434.25*	344.01
Sangria F1	28.53	1.16	501.74**	407.42
Starbrite F1	37.43	0.92	324.72	246.83
Stars-N-Stripes F1	35.16	0.37	700.04***	434.81
Stone Mountain	39.66	1.04	1030.07**	787.81
Sugar Baby	36.29	1.22	601.11	485.01
Sugarlee	30.53	1.45	283.69	198.99
Sweet Princess	36.81	0.41	561.52	415.38
Tendersweet OF	29.73	0.17	664.43	553.05
Tom Watson	21.41	1.49	467.95*	363.66
Yellow Crimson	30.15	1.00	196.83	137.34

*, **, *** indicate significantly different from unity for the regression coefficients or slope (b_i) and from zero for the deviation from regression (S^2_d) at 0.05, 0.01 and 0.001 levels of probability, respectively
‡LSD = 6.45

Table 9. Means (corrected by least squares) (*M*) and stability parameters (regression coefficient [b_i], deviation from regression [S^2_d] and Shukla's stability variance [σ_i^2]) for fruit size of 40 watermelon genotypes tested in 3 years and 8 locations.

	Fruit size (kg fruit^{-1})			
Genotype	*M*‡	b_i,	S^2_d	σ_i^2
AU-Jubilant	9.55	0.65	3.20	4.23
Allsweet	8.65	0.95	3.35	5.03
Big Crimson	8.60	1.05	2.41	2.42
Black Diamond	7.59	0.85	1.37	1.56
Calhoun Gray	8.31	0.69	3.08**	3.31
Calsweet	7.94	1.45	4.07***	3.34
Carolina Cross#183	14.56	4.18***	37.20***	66.74
Charleston Gray	8.39	1.18	3.54*	9.43
Congo	7.79	0.66	3.13	5.87
Crimson Sweet	8.10	-0.16**	2.69*	5.33
Desert King	7.98	1.43	3.62	6.61
Early Arizona	4.59	0.81	0.99*	3.44
Early Canada	5.08	0.49	4.12***	3.63
Fiesta F1	7.62	0.94	2.09	2.11
Georgia Rattlesnake	9.64	1.40	2.90	5.16
Golden Midget	1.72	0.32***	0.70	3.81
Graybelle	5.27	0.42*	1.65	1.90
Hopi Red Flesh	5.90	0.56	14.14***	15.41
Jubilee	9.54	2.03*	4.83	8.80
King & Queen	4.72	0.47*	2.62***	3.60
Legacy	8.81	1.19	3.21	3.77
Mickylee	4.10	0.12***	1.72**	2.37
Minilee	3.51	0.55*	1.04*	1.76
Mountain Hoosier	8.34	0.94	1.82	1.82
NC Giant	11.37	1.89	13.32**	21.71
Navajo Sweet	5.03	0.34*	1.88	2.39
Peacock WR-60	6.47	0.65	4.88*	5.56
Quetzali	5.25	0.73	1.78***	2.05
Regency F1	8.09	0.77	1.94	2.09
Royal Flush F1	7.55	0.72	1.57	2.08
Sangria F1	7.93	1.04	1.36	1.43
Starbrite F1	8.54	1.13	2.83	3.15
Stars-N-Stripes F1	8.30	1.00	1.11	1.02
Stone Mountain	8.52	1.11	2.93	4.03
Sugar Baby	4.25	0.44**	1.85***	2.66
Sugarlee	7.15	0.59	2.85*	3.04
Sweet Princess	8.47	0.88	2.34	3.05
Tendersweet OF	8.09	1.24	2.16	3.58
Tom Watson	7.42	1.09	5.63**	7.73
Yellow Crimson	7.31	1.71	3.95	4.65

*, **, *** indicate significantly different from unity for the regression coefficients or slope (b_i) and from zero for the deviation from regression (S^2_d) at 0.05, 0.01 and 0.001 levels of probability, respectively
‡LSD = 0.55

Table 10. Spearman rank correlation coefficients among trait mean (*M*) and stability parameters (regression coefficient [b_i], deviation from regression [S^2_d], Shukla's stability variance [σ_i^2], and Kang's stability statistics [YS_i] for watermelon based on 40 genotypes tested in 24 environments.

	Marketable yield				
	M	b_i	S^2_d	σ_i^2	YS_i
M	1.00				
b_i	0.41**	1.00			
S^2_d	-0.25	-0.04	1.00		
σ_i^2	-0.28	-0.05	0.96***	1.00	
YS_i	0.99***	0.41**	-0.25	-0.28	1.00
	Fruit count				
	M	b_i	S^2_d	σ_i^2	YS_i
M	1.00				
b_i	0.39	1.00			
S^2_d	-0.52***	-0.27	1.00		
σ_i^2	-0.47**	-0.21	0.97***	1.00	
YS_i	0.66***	0.23	-0.26	-0.22	1.00
	% cull fruit				
	M	b_i	S^2_d	σ_i^2	YS_i
M	1.00				
b_i	0.77***	1.00			
S^2_d	0.74***	0.55***	1.00		
σ_i^2	0.81***	0.62***	0.94***	1.00	
YS_i	0.99***	0.77***	0.73***	0.81***	1.00
	% early fruit				
	M	b_i	S^2_d	σ_i^2	YS_i
M	1.00				
b_i	-0.01	1.00			
S^2_d	-0.45**	-0.04	1.00		
σ_i^2	-0.47**	-0.04	0.91***	1.00	
YS_i	0.99***	-0.01	-0.45**	-0.47**	1.00
	Fruit size				
	M	b_i	S^2_d	σ_i^2	YS_i
M	1.00				
b_i	0.69***	1.00			
S^2_d	-0.45**	-0.45**	1.00		
σ_i^2	-0.35	-0.33	0.83***	1.00	
YS_i	0.96***	0.65***	-0.29	-0.13	1.00

** and *** indicate significance level at 0.01 and 0.001 levels of probability, respectively.

CHAPTER 2

VALUE OF LOCATIONS FOR REPRESENTING MEGA-ENVIRONMENTS AND FOR TESTING YIELD OF WATERMELON [*Citrullus lanatus* (Thunb.) Matsum. & Nakai] IN THE US

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Value of Locations for Representing Mega-Environments and for Testing Yield of Watermelon in the US

Abstract

In a crop breeding program, multiple-environment trials can be used to understand target regions. Understanding target regions and sub-division of mega-environments will help the breeder evaluate genotypes for release as cultivars. In addition, locations can be chosen that are efficient for distinguishing among genotypes and that are good representatives of target regions of interest. The objectives of this study were to study mega-environments, measure correlations among test locations, and identify test locations that were both discriminating and representative of target regions. Watermelon fruit yield and yield components were evaluated in three years and eight locations using replicated, multiple-harvest trials. Data were analyzed using genotype main effect and genotype x environment interaction and the GGE biplot model. Two key locations, Quincy FL and Clinton NC were efficient representatives of two mega-environments for marketable yield, fruit count, and % early fruit. College Station TX and Woodland CA represented one mega-environment, and Clinton NC represented a second for % cull fruit. The subdivision of major watermelon producing states for fruit size could not be justified. Identification of mega-environments for watermelon in the southern US has implications for future breeding and genotype evaluation in the US, including the use of specialized genotypes for the mega-environments identified to achieve optimum adaptation.

Introduction

Watermelon (*Citrullus lanatus* [Thumb.] Matsum & Nakai) is a valuable cash crop grown throughout the world. Worldwide, the United States (US) is the fifth largest watermelon producer, with 2 million Mg harvested on 21,450 ha in 2007, valued in excess of $476 million (FAO, 2010; USDA, 2010). It is widely adapted, with wild accessions growing in hot, dry environments, and can be found from Kalahari Desert of Africa to mountainous regions of China and Uzbekistan (Wehner, 2008). Watermelons are grown in almost all the states of the US. However, the major producers are in the South and West in states having a long frost-free season. Major producers include Florida, Texas, Oklahoma and California (Wehner, 2008).

During the past century, watermelon breeding activity in the US has been focused on development of new cultivars that are diploid or triploid (seedless) hybrids with high fruit yield, early maturity, high percentage marketable fruit, excellent shipping characteristics, disease resistance, uniformity, high sugar content, and bright red flesh (Gusmini and Wehner, 2008). Fruit size is available in 6 and 8 kg sizes, as well as mini (3 kg) size. The success of any crop breeding program depends on many factors; one of the most pivotal factors is the understanding and selection of suitable selection and test locations (Yan et al., 2011). An efficient test location is discriminating, so that differences among genotypes can be easily detected using few replications, and is representative of the target environments for the cultivars to be released. The representation of the location for the target environment should be repeatable so that genotypes selected in each year will have superior performance in future years (Yan et al., 2011). Therefore, knowledge of target environment for breeding for locally

adapted genotype is important and, also, it requires a subdivision of the target locations into mega-environments.

Often, plant breeders want to develop broadly-adapted genotypes for a wide range of environments. However, it is often not possible to identify genotypes that are superior in yield and yield components in all environments. Furthermore, the same genetic system does not control yield over a diverse set of environments (Ceccarelli and Grando, 1993; Ceccarelli, 1989; Simmonds, 1991). Therefore, breeders often develop genotypes for a particular environment to take advantage of specific adaptations (Annicchiarico et al., 2005; Samonte et al., 2005). However, breeding for a specific adaptation is more efficient if production areas are divided into mega-environments each representing a target environment for breeding.

Several definitions have been proposed for mega-environments. For example, CIMMYT (Centro Internacional de Mejoramiento de Maiz y Trigo) defined a mega-environment as "a broad, not necessarily contiguous area, occurring in more than one country and frequently transcontinental, defined by similar biotic and abiotic stresses, cropping system requirements, consumer preferences, and, for convenience, by volume of production" (Braun et al, 1996). Based on this definition, the CIMMYT wheat breeding program identified 12 mega-environments across the world (Braun et al., 1996). Yan (2006) defined mega-environment as a group of geographical locations that share the same (sets of) genotypes consistently across years. Gauch and Zobel (1997) defined mega-environment as a portion (not necessarily contiguous) of the growing region of a crop species having a fairly homogeneous environment that causes similar genotypes to perform best. Other researchers

defined mega-environment as a group of growing areas that are similar in terms of genotype response, and that show a repeatable relative performance of crop genotypes across years (Yan and Rajcan, 2002; Yan and Tinker, 2005).

Multiple-environment trials are routinely conducted as part of plant breeding programs. The trials serve to identify superior genotypes for target regions, and to subdivide the target region into different mega-environments. Gauch and Zobel (1997) suggested that it is important to understand and characterize mega-environments in research on genotype x environment interaction (GEI), clustering environments, yield stability and dependability, wide and narrow adaptation, and heritability. Subdivision of crop growing region into several mega-environments helps in allocation of resources in a breeding program (Peterson and Pfeiffer, 1989), target genotype distribution to appropriate production area and information exchanges between breeding programs (Brown et al., 1983). Understanding and identification of Mega-environment results in heritability increase within relatively well-defined and predictable environment (Abdalla et al., 1996). Therefore, it improves the efficiency of testing and breeding program by focusing on the most promising material. The disadvantage of subdivision of target region into mega-environments is that it results in more work for plant breeders and seed producers. However, the concept has useful predictive value for locations in the same mega-environment (Gauch and Zobel, 1997).

Mega-environments are generally identified through the analysis of multiple-environment trial data for a diverse set of genotypes. The purpose of mega-environment analysis is to understand the genotype × location interaction (GLI) patterns within a target region in order to explore the feasibility of dividing the target region into meaningful mega-

environments. That permits the GLI (which causes specific adaptation) to be exploited to maximize the response to selection within mega-environments, and increase the productivity of the target region (Yan et al., 2011). Several methods have been used to analyze multiple-environment trial data and to group the environments. Those include cluster analysis, correlation among environments, additive main effects and multiplicative interaction (AMMI) model, and genotype main effects plus GEI (GGE) model (Van Oosterom et al., 1993; Collaku et al., 2002, Gauch, 2006; Putto, 2008). Recently, the GGE model with a biplot display has gained in popularity for analyzing multiple-environment trial data (Casanoves et al., 2005; Dehghani et al., 2006). The GGE biplot method can also be used for determining mega-environments for crop breeding (Yan et al., 2000; Yan and Rajcan, 2002; Yan and Tinker, 2005; Dehghani et al., 2006). Proponents of the AMMI and the GGE biplot methods disagree on the superiority of one over the other for analyzing multi-environment trial data (Gauch, 2006; Yan et al., 2007). However, the two methods provide similar results (Gauch, 2006).

Yan et al., (2000) referred to biplots based on singular value decomposition of environment-centered or within-environment standardized two-way (genotype-by-environment) data matrix as 'GGE biplots'. GGE biplot was constructed from the first two principal components (PC1 and PC2), that explained maximum variability in the data, derived by singular value decomposition of two-way (genotype-by-environment) data matrix (Yan et al., 2000). The GGE biplot graphically displays the two-way (genotype-by-environment) data matrix and allows visualization of the interrelationship among environments and genotypes, and interactions (Yan and Kang, 2003). In GGE biplot

genotype effect and GEI effect are the two sources of variation that are relevant to genotype evaluation and mega-environment identification (Kang, 1993; Gauch and Zobel, 1996; and Yan and Kang, 2003).

The work reported here was undertaken to analyze multiple-environment trial data for yield and yield components of watermelon. The objectives of this research were to (i) identify mega-environments for the main watermelon production areas of the US; (ii) measure the correlation among locations and identify redundant test locations to improve trialing efficiency; (iii) identify locations having high discriminating ability; and (iv) identify locations having high representativeness.

Materials and Methods

Germplasm and location

Forty genotypes of watermelon were evaluated for three years (2009, 2010, and 2011) in eight locations across the United States (Table 1). Forty genotypes were chosen to represent new vs. old releases, small vs. large fruit size, round vs. elongate fruit shape, striped vs. solid rind pattern, resistant vs. susceptible to anthracnose, eastern vs. western adapted, and inbred vs. hybrid type (Table 2). Locations were Kinston NC, Clinton NC, Charleston SC, Cordele GA, Quincy FL, College Station TX, Lane OK and Woodland CA (Table 3). The locations were chosen to represent the key watermelon production regions in the US, and ranged from North Carolina and South Carolina in the east to Georgia, Florida, Oklahoma and Texas in the south to California in the west. Data were not collected from Oklahoma in 2009, Georgia in 2010, or Florida in 2011.

Field plots and cultural practices

The experiment design was a randomized complete block with four replications for each location and year. For Kinston NC and Clinton NC, seeds of the 40 genotypes were sown in 72-cell polyethylene flats in the greenhouses at North Carolina State University. An artificial soilless growing medium (4P Fafard soilless mix, Conrad Fafard Incorporated, Massachusetts), was used. The flats were moistened to capacity after seeding, and held in the greenhouse at 25-30°C until full emergence. The transplants were moved to cold frames for acclimation one week before transplanting. The seedlings were transplanted by hand at the two-true-leaf stage. Missing or damaged transplants were replaced one week after the initial transplanting.

The fields had raised and shaped beds (rows) on 3.1-m centers with single hills 1.2 m apart. The beds were made up with drip irrigation tubes and covered with black polyethylene mulch. The experiment was conducted using horticultural practices recommended by the North Carolina Extension Service and Southeastern US 2009 Vegetable Crops handbook (Sanders, 2004; Holmes and Kemble; 2009). At other locations, similar protocols were followed.

Traits evaluated

At each location, the 40 watermelon genotypes were evaluated for traits including marketable yield (Mg ha^{-1}), marketable fruit number or count (thousand fruit ha^{-1}), % cull fruit (= 100 x cull fruit weight/total fruit weight), % early fruit (100 x first harvest of marketable yield/total harvest weight) and fruit size (kg $fruit^{-1}$). Growers calculate their gross

returns based on yield, earliness, and % marketable fruit, so we chose those traits for evaluation. Percent cull fruit data were not recorded at Florida or South Carolina locations.

Fruit were determined to be ripe based on days from planting to harvest, and if there was a brown tendril nearest the fruit, a light-colored ground spot, and a dull sound of the fruit when thumped (Maynard, 2001). Fruit were graded into marketable and cull, and then counted and weighed for each plot. Yield was calculated as total and marketable fruit weight (Mg ha^{-1}) and number (thousands ha^{-1}) for first harvest, and for all harvested summed. All curved, bottle-necked, and deformed fruit were considered culls. Each trial had one to four harvests depending on year and location (Table 3). Data were not collected on % cull fruit from South Carolina in 2009, 2010, and 2011; and Florida in 2009 and 2010. Only single harvest was done at California in 2009 and Georgia in 2011, therefore for % early fruit no data was collected from California in 2009 and Georgia in 2011.

Data analysis

Data were analyzed for each trait over environments (E), and genotypes (G), and for GEIs using the GLM procedure (PROC GLM) of the SAS statistical package (SAS Institute, Cary, NC). Environment (year x location combinations), replications, and genotypes were considered random effects. This procedure was used initially to determine if GEI and location were significant for the traits of interest. An *F* test was used to test the interaction and main effect. If location effects were significant, within-year analysis was conducted using PROC GLM of SAS to determine the repeatability of locations. The PROC CORR of SAS was used to calculate correlation among pairs of locations. GGE biplot analysis was used through the 'GGEBiplotGUI' package of R statistical software, to visually assess the

presence of mega-environments, redundancy, discriminating ability and representativeness of the test locations (Yan et al, 2000; Yan and Kang, 2003; R Development Core Team 2007).

Results

ANOVA

The combined analysis of variance (ANOVA) revealed highly significant environment, Genotype, and GEI effects for all evaluated traits (Table 4). Marketable yield was controlled to a large extent by environment (48% of total sum of squares) and GEI (18% of total sum of squares), and small extent by genotype effects (8% of total sum of squares) (Table 4). Of the 48% environmental variation of marketable yield, 75% was attributable to locations, 21% to location x year interaction (LYI), and 3% to year (Table 4). However, yield of fruit count was controlled largely by environment, genotype and GEI effects (35%, 20%, and 21% of total sum of squares, respectively) (Table 4). The environment portion (35%) of yield of fruit count was attributable to 68% to location, 27% to LYI, and 0.70% to year (Table 4).

ANOVA for % cull fruit and % early fruit showed that environment, genotype, and GEI effects accounted for 26% and 38%; 10% and 7%; and 23% and 22%, respectively, of the total sum of squares (Table 4). On the contrary, for fruit size about 51% of total variance was due to genotype effects and a relative small effect of environment (14%) and GEI (13%) was observed (Table 4). Other than fruit size, all yield traits had large variance due to environment, which confirms that the experimental sites were different, with large differences among environmental means causing most of the variation in genotypic performance.

The significant LYI for all the traits evaluated in this study warranted separate ANOVA for each year (Tables 5, 6, 7, 8, and 9) (Fan et al., 2007). The results of ANOVA for the yearly data gave an overall picture of the relative magnitude of the location, genotype, and genotype x location interaction (GLI) variance term. Within each year, location effect was significant for all the traits evaluated in this study (Tables 5, 6, 7, 8, and 9). Except for fruit size, location was always the most important source of yield and yield components variation, accounting for 35 to 57%; 25 to 38%; 5 to 33%; and 27 to 38% of total sum of squares for marketable yield, fruit count, % cull fruit, and % early fruit, respectively (Tables 5, 6, 7, 8, and 9). The magnitude of the GLI relative to genotype suggested the existence of different mega-environments, and justified the choice of GGE biplot as the appropriate method for analyzing the multiple-environment data (Yan et al., 2000).

Mega-environment investigation

The visualization of "Which won where?" pattern is important for searching for the existence of different mega-environments in a region. That is important because evaluation of test locations and genotypes is most useful when conducted within mega-environments (Yan et al., 2007). The existence of mega-environment is justified by different genotypes performing best in different test locations, clear crossover GLI, and joint analysis of multiple-environment trial data (Gauch and Zobel, 1997; Yan and Kang, 2003). The two-dimensional GGE biplot of multiple-environment trial data of three years, 40 genotypes and eight locations was based on environment-standardized data and environment-focused singular value partition (Figure 1). The straight line originating from the biplot origin and being perpendicular to the each side of the polygon divides the biplot into sectors. These

sectors divide test locations into groups and indicate the existence of different mega-environments. The sectors were labeled from 1 to 4 for all the traits evaluated in this study (Figure 1).

There were two mega-environments for marketable yield (Figure 1A), fruit count (Figure 1B), % cull fruit (Figure 1C), and % early fruit (Figure 1D). For marketable yield, the biplot sectors between straight lines labeled 1 and 2; and 2 and 3 represented the first and second mega-environments, respectively (Figure 1A). The first mega-environment for marketable yield contained locations Woodland CA, College Station TX, and Clinton NC. Mega-environment 2 contained locations Cordele GA, Quincy FL, Kinston NC, Charleston SC, and Lane OK (Figure 1A). For fruit count, mega-environment 1 contained locations Cordele GA, College Station TX, Woodland CA, Clinton NC, and Kinston NC. Mega-environment 2 contained locations Quincy FL, Charleston SC, and Lane OK (Figure 1B).

For % cull fruit, mega-environment 1 contained locations Lane OK, Cordele GA, Woodland CA, and College Station TX; mega-environment 2 contained locations Kinston NC and Clinton NC (Figure 1C). For % early fruit, mega-environment 1 contained locations Cordele GA, Lane OK, Woodland CA, Quincy FL, Kinston NC and College Station TX; mega-environment 2 contained locations Charleston SC and Clinton NC (Figure 1D).

For fruit size, all eight locations formed one large mega-environment (Figure 1E). The mega-environment was considered simple because there was no major crossover GEI found, with Carolina Cross #183 being the top in all the locations (Figure 1E). Whereas for marketable yield, fruit count, % cull fruit, and % early fruit the mega-environment was considered to be complex because large, unpredictable, crossover GEI was present (Figures

1A, B, C, and D). For a simple mega-environment, one or a few test locations are sufficient to identify the best genotypes that can be recommended everywhere within the mega-environment. On the contrary, for a complex mega-environment, multiple-environment trials are essential and genotype recommendation must be based on both mean and stability (Yan and Kang, 2003). Also, classification of target locations into different mega-environments and deploying different genotypes in different mega-environments is the best way to deal with GEI (Gauch and Zobel, 1997).

Correlation among and redundancy of the test locations

Environment-focused scaling, also known as principal component (PC) analysis scaling, fully incorporates the singular values into environment scores. This scaling help determine interrelationships among environments. The GGE biplot based on environment-focused singular value partitioning has following advantages: 1) the cosine of the angle between the vectors of two locations approximates the correlation coefficient between them; and 2) the lengths of the location vectors are approximately proportional to their standard deviations (Rosenberg, 1995; DeLacy et al., 1996, Yan 2002; Yan and Tinker, 2006).

Since the biplot does not explain all of the variation in the dataset, the cosine of the angle does not precisely translate into correlation coefficients. Nevertheless, the angles are informative enough to show interrelationships among test locations (Yan et al., 2011). Studies conducted by Yan and Kang (2003) revealed high correspondence between location vector angle and correlation coefficients among locations. The smaller angle between location vectors and are, therefore, highly positively correlated, information on genotypes obtained from these locations must be similar (Yan, 2011). Thus, the vector view of biplot

helps identify redundant test locations. This permits the use of fewer test locations for obtaining trial information. This reduces costs and increases the efficiency of the breeding program.

The vector view of the GGE biplot, which is based on environment-focused scaling, for marketable yield, fruit count, % cull fruit, % early fruit, and fruit size was presented in Figure 2. For marketable yield, correlation coefficients among all the locations in their respective mega-environments were found to be significant ($P<0.01$). However, in mega-environment 1 for marketable yield, Woodland CA and College Station TX had a small angle between their vectors; and hence they had strong and significant ($P<0.001$) coefficient of correlation (Figure 2A and Table 10). Similarly, in mega-environment 2 of marketable yield, Quincy FL and Kinston NC had a small angle between their vectors; therefore they were highly correlated (Figure 2A and Table 10). These results indicated that in mega-environment 1 Clinton NC and College Station TX, and in mega-environment 2 Quincy FL and Kinston NC were closely related and provided similar information on genotypes for marketable yield. Therefore, a single location of the two locations in each mega-environment would suffice.

Similarly, for fruit count highly significant ($P<0.001$) correlations were found among the locations in their respective mega-environment (Table 10). The correlation coefficient among locations between two mega-environments for fruit count was either weak or non-significant ($P>0.001$) (Table 10). The angle between the location vectors of mega-environment 1 were small; therefore any single location among College Station TX, Woodland CA, Cordele GA, Clinton NC, and Kinston NC would be sufficient to provide

information on genotype performance for marketable yield (Figure 2B). On the other hand, among Quincy FL, Charleston SC, and Lane OK in mega-environment 2, a small angle was found only for the Quincy FL and Charleston SC vector (Figure 2B). Therefore, either Charleston SC or Quincy FL would suffice for genotype evaluation for fruit count.

In mega-environment 1 for % cull fruit, a small angle was found between Cordele GA and Lane OK, and Woodland CA and College Station TX vectors (Figure 2C). In contrast, correlation coefficients between Woodland CA and College Station TX suggested only a weak correlation (Table 10). In mega-environment 2 for % cull fruit, a small angle was found for the Kinston and Clinton vector (Figure 2C). These results indicated that two locations in mega-environment 1 and one location in mega-environment 2 were redundant for evaluating genotypes for % cull fruit. Between Cordele GA and Lane OK, Woodland CA and College Station TX, and Kinston NC and Clinton NC; any one location in each pair would be sufficient for evaluating watermelon genotypes for % cull fruit. For % early fruit, two locations in mega-environment 1 and one location in mega-environment 2 were redundant. A small angle was found between Cordele GA and Woodland CA vectors, and Kinston NC and College Station TX vectors in mega-environment 1 and Clinton NC and Charleston SC in mega-environment 2 (Figure 2D). Thus, these pairs were strongly correlated and gave similar information on % early fruit (Table 10).

For fruit size, the correlation coefficient among locations ranged from 83 to 97% (Table 10). All correlation coefficient values were strong and significant (P<0.001). Thus, all locations were strongly correlated to each other and provided the same information on genotypes for fruit size. The vector view of GGE biplot for fruit size displayed small angles

between three pairs: Charleston SC and Lane OK; Quincy FL and Clinton NC; and Woodland CA, Kinston NC and College Station TX (Figure 2E). Despite the larger angle between Charleston SC and Cordele GA vectors, the correlation coefficient between them was highly significant ($P<0.001$). Therefore, any one location among eight locations evaluated in this study would be sufficient in providing required information on genotype performance for fruit size.

Discriminating ability of the test locations

In the vector view of GGE biplot, the length of the location vectors approximates the standard deviation within each location, which is a measure of their discriminating ability (Yan and Kang, 2003). Discriminating ability is an important measure of test location. If test location lacks discriminating ability, then it provides less information about genotypes and is of little use. Therefore, a test location must be discriminating so that differences among genotypes can be detected. The vector view of GGE biplot for watermelon yield and yield components was presented in Figure 2. However in this study, the vector view of GGE biplot had the same length of location vectors. Therefore, the standard deviation within each test locations was used to determine discriminating ability of the test locations (Table 11).

For discriminating ability, Cordele GA had the highest standard deviation, followed by Quincy FL (Table 11). Therefore, they were the most discriminating locations for marketable yield. College Station TX and Woodland CA recorded the lowest standard deviation, so were the least discriminating for marketable yield. For fruit count, Kinston NC and Clinton NC had the highest discriminating ability; Lane OK and College Station TX had the lowest discriminating ability. For % cull fruit, Lane OK had the highest discriminating

ability; Cordele GA and Woodland CA had the lowest. Cordele GA had the highest discriminating ability; Charleston SC and College Station TX had the lowest for % early fruit and fruit size.

Representativeness of locations

Representativeness of the test location is another important measure of a test location. Representative locations test genotypes with the desired adaptation to a target region. If a test location is not representative of the target region, it may not be useful, and further, may provide misleading information for genotypes tested there. The representativeness of location is difficult to measure, since it is not possible to sample all locations within a mega-environment, and determine the representativeness of each individual location. According to Yan and Kang (2003) the biplot way of measuring representativeness of location is to define an average environment and use it as a benchmark. The average environment is defined by the mean ordinates or mean PC1 and PC2 scores of all environments in the biplot. The line passes through the biplot origin and the average environment is known as average environment axis. For watermelon fruit yield and yield components, the average environment is indicated by small circle in Figure 3. The angle between the vector of an environment (not drawn in Figure 3) and the average environment axis is a measure of the representativeness of the location. The smaller the angle between location vector and the average environment axis, the more representative the test location will be. Hence, for marketable yield, fruit count, % cull fruit, % early fruit and fruit size, Cordele GA; Kinston NC; Woodland CA; Quincy FL; and Quincy FL, respectively, were most representative (Figures 3A, B, C, D and E).

Locations with discriminating ability and representativeness

The ideal test location should be both discriminating and representative. The small circle surrounded by concentric circles on the average environment axis, with an arrow pointing to it represented the ideal location (Figure 3). An ideal location is both discriminating and representative of the target location. The ideal location is used as a reference point. For marketable yield, Cordele GA, Quincy FL and Kinston NC were closest to the ideal location, and therefore the most desirable of all eight locations (Figure 3A). Clinton NC and Charleston SC were next best, and Woodland CA, College Station TX, and Lane OK were the least desirable test environments for marketable yield.

Among other yield component traits, for fruit count Kinston NC and Clinton NC were most desirable test environments, and Cordele GA and Lane OK were the least desirable (Figure 3B). For % cull fruit Texas followed by Woodland CA and Clinton NC were the most desirable locations (Figure 3C). For % early fruit, Quincy FL followed by Kinston NC and College Station TX were the most desirable locations (Figure 3D). Lane OK and Cordele GA were the least desirable locations for both % cull fruit and % early fruit evaluation. For fruit size, Quincy FL and Clinton NC were the most discriminating and representative (Figure 3E).

Discussion

As expected, ANOVA confirmed the consistently presence of location and GLI for marketable yield, fruit count, % cull fruit and % early fruit (Table 4, 5, 6, 7, and 8). Despite a large number of test locations and a diverse set of genotypes, the relative contribution of GLI for watermelon fruit size was small compared with those of the location and genotype main

effects (Table 4 and 9). This suggests that breeding watermelon for location-adapted fruit size would not be much advantage, as pointed out by Annicchiarico (2002). However, for marketable yield, fruit count, % cull fruit and % early fruit, GLI must be exploited to identify mega-environments and watermelon genotypes that are high performing in specific locations, or over many locations. That is especially true where GLI was large relative to genotype main effects and genotype x year interactions (GYI).

The GGE biplot analysis showed that PC1 and PC2 together accounted for 60% to 95% of the total variation for watermelon fruit yield and yield components (Figure 1). GGE biplot analysis identified two mega-environments for marketable yield, fruit count, % cull fruit and % early fruit; and one mega-environment for fruit size (Figure 1). These mega-environments indicate the opportunity to exploit narrow adaptation for the yield component traits for watermelon. The results of this study show that all the key locations representing the mega-environments for watermelon yield and yield components were not uniformly distributed across the US. For marketable yield and fruit count, the three key locations representing two mega-environments were Quincy FL, Kinston NC and Clinton NC. Interestingly, these three locations not only showed high discriminating ability but they were also highly representative. However, unlike Quincy FL, Kinston NC and Clinton NC were low environments for marketable yield and fruit count. According to Yan and Kang (2003) and Putto (2008), location which has high discriminating ability and high representativeness tends to easily differentiate the performance among genotypes and suggested that the selected genotypes have the desired adaptation in that location, respectively. Also, we assumed that

the crew variation and within each genotype variation were constant from location to location and year to year.

For % cull fruit, analysis using GGE biplot revealed College Station TX and Woodland CA were the ideal locations for the mega-environment representing southwestern and western US, and Clinton NC was the ideal location for the mega-environment representing in south eastern or eastern US. Similarly, for % early fruit Quincy FL and Clinton NC were the two key locations that were representative of mega-environment 1 and mega-environment 2. The results of this study suggested that subdivision of major watermelon producing states for fruit size is unjustified and therefore the entire US should be considered as one mega-environment for breeding watermelon for fruit size. Except for % cull fruit, the two locations--Quincy FL and Clinton NC--were consistently represented as key locations for two mega-environments for marketable yield, count, and % early fruit. Therefore, Quincy FL and Clinton NC locations can be used for breeding high performing watermelon genotypes for marketable yield, fruit count, and % early fruit for two mega-environments.

Plant breeders often select in high performing locations and hope for good performance in low performing locations because the trial data for such locations are often not available. However, in our study, the locations representing mega-environments were not always those with the highest genotype yields. For example, Clinton NC and Kinston NC were key locations representing mega-environments, but were low or marginal for all the yield traits evaluated. Historically, high performing locations are used for trials more often than are marginal locations. However, selection in marginal or high stress mega-

environments is prone to large errors, with less discrimination, and less repeatability over years (Braun et al., 1992). Breeding in marginal environments may be helped using experimental techniques such as optimum replication number, and advanced analysis such as AMMI and GGE biplot to improve accuracy.

Conclusions

GLI was significant for watermelon yield traits, indicating that some locations were better for testing than the others. Except for fruit size, analysis using the GGE biplot method revealed two mega-environments in the US for watermelon fruit yield and yield components. The two key locations, Quincy FL and Clinton NC, were consistently represented as key locations for two mega-environments for marketable yield, fruit count, and % early fruit. College Station TX and Woodland CA, and Clinton NC were the ideal locations for two mega-environments, respectively, for % cull fruit.

Identification of mega-environments in the US watermelon production region has several implications for plant breeding. First, different genotypes should be grown in different mega-environments to achieve maximum yield. Second, crossover GLI can be minimized through genotype evaluation and selection focusing on genotype main effect or general adaptation. The finding that the some test locations were better than others for genotype evaluation suggested that the genotype may be evaluated at fewer locations, still obtaining good yield data. Evaluation of fruit size can be done equally well in any location of those tested. Finally, it was not always the key locations representing mega-environment where the highest yields were obtained.

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Table 1. The 40 watermelon genotypes tested.

Genotype	Year of release	Pedigree
AU-Jubilant	1985	Jubilee x PI 271778
Allsweet	1972	[(Miles x Peacock) x Charleston Gray]
Big Crimson	NA†	NA
Black Diamond	1949	Segregation within Cannonball or Black Diamond
Calhoun Gray	1965	Calhoun Sweet x Charleston Gray
Calsweet	NA	[(Miles x Peacock) x Charleston Gray]
Carolina Cross#183	NA	NA
Charleston Gray	1954	[{(Africa 8 x Iowa Belle) x Garrison} x Garrison] x [(Hawkesbury x Leesburg) x Garrison]
Congo	1949	(African x Iowa Belle) x Garrison
Crimson Sweet	1963	(Miles x Peacock) x Charleston Gray
Desert King	NA	NA
Early Arizona	NA	NA
Early Canada	NA	NA
Fiesta F1	1991	Unknown (Plant Variety Protection)
Georgia Rattlesnake	1870	
Golden Midget	1959	New Hampshire Midget x Pumpkin Rind
Graybelle	1963	Sugar Baby x Charleston Gray sister line
Hopi Red Flesh	NA	NA
Jubilee	1963	Africa 8, Iowa Belle, Garrison, Hawkesbury, and Leesburg
King & Queen	NA	NA
Legacy	1997	(Early Gray x Little Jubilee 4) x Verona
Mickylee	1986	Texas W5, Fairfax, Summit, and Graybelle
Minilee	1986	Texas W5, Fairfax, Summit, and Graybelle
Mountain Hoosier	NA	NA
NC Giant	NA	NA
Navajo Sweet	NA	NA
Peacock WR-60	1955	Klondike R7 x Peacock
Quetzali	1965	NA
Regency F1		Unknown (Plant Variety Protection)
Royal Flush F1	1995	Unknown (Plant Variety Protection)
Sangria F1	NA	Unknown (Plant Variety Protection)
Starbrite F1	NA	Unknown (Plant Variety Protection)
Stars-N-Stripes F1	NA	Unknown (Plant Variety Protection)
Stone Mountain	1924	NA
Sugar Baby	1955	Tough Sweets selection, inbred 13 years
Sugarlee	1981	Texas W5, Summit, Charleston Gray, Fairfax, Crimson Sweet, and Graybelle
Sweet Princess	1967	small-seeded Congo type x Charleston Gray
Tendersweet OF	NA	NA
Tom Watson	1906	NA
Yellow Crimson	NA	NA

† Not available

Table 2. Traits and pedigrees for the 40 watermelon genotypes evaluated.

	Fruit		Rind			Seed		Flesh
Genotype	Shape†	Size‡	Color§	Thickness¶	Pattern#	Size††	Color‡‡	color¶¶
AU-Jubilant	L	M	LG	S	M	L	R	R
Allsweet	L	M	LG	N	W	S	R	S
Big Crimson	R	M	MG	M	W	M	R	R
Black Diamond	R	S	DB	M	S	L	R	R
Calhoun Gray	L	M	G	M	S	M	R	R
Calsweet	L	M	LG	T	W	S	B	S
Carolina Cross#183	E	G	LG	T	N	L	W	R
Charleston Gray	L	L	G	T	R	M	R	R
Congo	L	M	DG	M	R	L	T	R
Crimson Sweet	R	M	LG	M	M	S	B	R
Desert King	O	S	SG	S	S	M	R	O
Early Arizona	O	S	SG	N	S	L	R	R
Early Canada	R	S	G	N	R	S	R	R
Fiesta F1	L	M	LG	M	W	S	B	R
Georgia Rattlesnake	L	G	LG	M	N	L	R	R
Golden Midget	O	C	Y	N	S	L	R	R
Graybelle	G	S	G	N	S	S	R	R
Hopi Red Flesh	O	M	SG	M	S	L	B	R
Jubilee	L	L	LG	T	N	L	R	R
King & Queen	O	M	LG	N	N	M	B	R
Legacy	L	M	LG	N	N	M	R	R
Mickylee	R	N	LG	N	R	M	R	S
Minilee	R	S	G	N	R	S	R	S
Mountain Hoosier	O	M	SG	T	S	L	W	R
NC Giant	L	G	LG	T	R	L	R	R
Navajo Sweet	R	S	LG	M	N	M	R	R
Peacock WR-60	L	S	SG	M	S	S	R	R
Quetzali	R	S	LG	N	S	M	R	R
Regency F1	O	S	MG	M	M	S	T	R
Royal Flush F1	L	M	MG	M	W	S	B	S
Sangria F1	O	M	MG	M	S	S	B	S
Starbrite F1	O	M	LG	L	S	S	R	R
Stars-N-Stripes F1	O	M	DG	T	W	L	B	S
Stone Mountain	O	M	SG	T	S	L	T	R
Sugar Baby	R	M	MB	S	S	S	R	S
Sugarlee	R	S	LG	M	N	M	R	R
Sweet Princess	O	M	G	M	R	T	R	R
Tendersweet OF	E	M	DG	M	W	L	W	O
Tom Watson	E	M	MG	T	S	L	T	R
Yellow Crimson	L	L	LG	N	S	L	B	C

†Fruit Shape: elongate (E), oval (O), round (R)
‡Fruit Size: micro (<3 lb.) (C), mini (3-8 lb.) (N), icebox (9-13 lb.) (B), small (S), sometimes called pee-wee (14-18 lb.), medium (19-24 lb.) (M), large (25-32 lb.) (L), and giant (>32 lb.) (G).
¶Rind Color: light green (LG), medium green (MG), dark green (DG), solid light black (LB), solid medium black (MB), solid dark black (DB) golden (G), solid green (SG), gray (R), Yellow (Y), mottled (M)
§Rind thickness: thick (>10mm) (T), medium (5-10mm) (M), thin (<5mm) (N)
#Rind Pattern: wide stripe (W), medium stripe (M), narrow stripe (N), gray (G), solid (S), Rattle Snake (R) [Dark green is dominant, stripe is decided by dark green]
††Seed Size: tomato size (T), small (S), medium (M), large (L)
‡‡Seed Color: black (B), brown (R), tan (T), dotted (D), white (W)
§§Flesh Color: scarlet red (S), coral red (R), orange (O), salmon yellow (Y), canary yellow (C), or white (W)

Table 3. Number of harvest done on 40 watermelon genotypes tested in 3 years and 8 locations.

Location		Co-ordinate		Harvests		
Abb rev.	Name	Latitude	Longitude	2009	2010	2011
KN	Kinston, NC	35° 15' 45" N	77° 34' 54" W	4	2	3
CI	Clinton, NC	35° 45' 25" N	80° 27’ 36" W	3	2	3
SC	Charleston, SC	32° 46' 35" N	79° 55' 52" W	3¶	2¶	3¶
GA	Cordele, GA	31° 57' 47" N	83° 46' 57" W	2	-	1
FL	Quincy, FL	30° 35' 13" N	84° 34' 59" W	2¶	2¶	-
TX	College Station, TX	30° 37' 40" N	96° 20' 3" W	3	4	3
WD	Woodland, CA	38° 40' 43" N	121° 46' 20" W	1	2	3
OK	Lane, OK	34° 17' 55" N	95° 59' 17" W	-†	4	4

† Data were not collected from this location
¶ Data were not collected on % cull fruit

Table 4. ANOVA for marketable yield (Mg ha^{-1}), fruit count, % cull fruit, % early fruit, and fruit size of 40 watermelon genotypes (kg $fruit^{-1}$) tested in 3 years and 8 locations.

	Marketable yield		Fruit count		% of total sum of squares	
Source	df	Mean square	df	Mean square	Fruit yield	Fruit count
Environment (E)	20	106825.19*	20	1554.37*	47.83	34.51
Location (L)	7	231712.42 *	7	3036.82*	75.92	68.38
Year (Y)	2	3240.24	2	107.95	3.00	6.90
L x Y	11	40726.21*	11	752.03*	20.97	26.61
Replication within E	63	2366.27*	63	30.36*	3.33	2.12
Genotype (G)	39	9227.34*	39	456.12*	8.05	19.75
G x E	780	1023.33*	779	24.27*	17.87	20.99
G x L	273	1322.62*	273	34.52*	45.23	49.84
G x Y	78	870.00	78	21.31	8.50	8.79
G x L x Y	429	850.71*	428	18.23*	45.72	41.26
Pooled Error	2442	419.77	2436	8.37	22.95	22.52
CV (%) for Fruit yield = 33.50; for fruit count = 32.78						
R^2 (%) for Fruit yield = 77.05; for fruit count = 77.48						

	% cull fruit		% early fruit		% of total sum of squares	
Source	df	Mean square	df	Mean square	% cull fruit	% early fruit
Environment (E)	18	10327.63*	19	40143.06*	25.52	37.67
Location (L)	6	17835.89	7	63207.46*	57.57	58.01
Year (Y)	2	10925.12	2	11355.56*	11.75	2.98
L x Y	10	5801.61*	10	4879.89*	31.21	6.40
Replication within E	57	359.93*	57	1301.27*	2.82	3.66
Genotype (G)	39	1792.39*	39	3498.84*	9.59	6.74
G x E	699	234.49*	661	648.49*	22.50	21.17
G x L	234	306.34*	273	743.35*	4.73	47.34
G x Y	78	293.43*	78	782.52*	13.96	14.24
G x L x Y	387	186.02*	310	542.10*	43.92	39.20
Pooled Error	2163	133.89	2019	305.96	39.75	30.51
CV (%) for % culls = 139.19; for % early = 56.01						
R^2 (%) for % cull = 60.24; % early = 69.49						

	Fruit size		% of total sum of squares
Source	df	Mean square	Fruit size
Environment (E)	20	226.17*	14.45
Location (L)	7	345.91	53.53
Year (Y)	2	21.28	0.94
L x Y	10	180.26*	43.84
Replication within E	63	9.70*	1.95
Genotype (G)	39	412.78*	51.46
G x E	776	5.42*	13.45
G x L	273	6.18*	40.10
G x Y	78	8.58*	15.91
G x L x Y	386	4.13*	41.74
Pooled Error	2374	2.21	16.77
CV (%) for size = 20.11			
R^2 (%) for size = 83.22			

* Significant at the 0.01 level of probability

Table 5. ANOVA by year for marketable yield (Mg ha^{-1}) of 40 watermelon genotypes tested in 3 years and 8 locations.

Source of variation	Marketable yield					
	Mean squares			% of total sum of squares		
	2009†	2010‡	2011¶	2009	2010	2011
Location (L)	64868.68*	129253.87*	151364.02*	35	57	47
Replication within L	1463.79*	2048.16*	3586.88*	3	3	4
Genotype (G)	3803.10*	3030.13*	4250.95*	13	9	9
G x L	742.81*	799.03*	1560.35*	16	14	19
Pooled Error	454.35	300.93	502.12	33	18	21
CV (%) for 2009 = 32; 2010 = 30; 2011 = 39						
R^2 (%) for 2009 = 66; 2010 = 82; 2011 = 79						

* Significant at the 0.01 level of probability

† Degrees of freedom (df) for L=6; Rep (L)=21; G=39; GxL=234; Pooled error=819.

‡ Degrees of freedom (df) for L=6; Rep (L)=21; G=39; GxL=234; Pooled error=805.

¶ Degrees of freedom (df) for L=6; Rep (L)=21; G=39; GxL=234; Pooled error=818.

Table 6. ANOVA by year for fruit count (thousand ha^{-1}) of 40 watermelon genotypes tested in 3 years and 8 locations.

Source of variation	Fruit count					
	Mean squares			% of total sum of squares		
	2009†	2010‡	2011¶	2009	2010	2011
Location (L)	1133.47*	1554.13*	2272.97*	25	38	37
Replication within L	19.73	26.42*	44.93*	2	2	3
Genotype (G)	204.48*	119.93*	174.74*	30	19	18
G x L	17.27*	21.85*	34.56*	15	21	22
Pooled Error	9.22	6.28	9.42	28	20	21
CV (%) for 2009 = 32; 2010 = 30; 2011 = 37						
R^2 (%) for 2009 = 72; 2010 = 80; 2011 = 79						

* Significant at the 0.01 level of probability
† Degrees of freedom (df) for L=6; Rep (L)=21; G=39; GxL=234; Pooled error=819.
‡ Degrees of freedom (df) for L=6; Rep (L)=21; G=39; GxL=233; Pooled error=799.
¶ Degrees of freedom (df) for L=6; Rep (L)=21; G=39; GxL=234; Pooled error=818.

Table 7. ANOVA by year for % cull fruit of 40 watermelon genotypes tested in 3 years and 8 locations.

Source of variation	% cull fruit					
	Mean squares			% of total sum of squares		
	2009†	2010‡	2011¶	2009	2010	2011
Location (L)	4900.62*	1809.37*	22520.81*	19	5	33
Replication within L	180.00	211.10	641.69	3	2	3
Genotype (G)	390.70*	1040.95*	937.92*	12	23	9
G x L	150.11*	251.78*	272.44*	23	28	16
Pooled Error	77.26	119.70	195.47	42	46	38
CV (%) for 2009 = 118; 2010 = 202; 2011 = 121						
R^2 (%) for 2009 = 58; 2010 = 54; 2011 = 62						

* Significant at the 0.01 level of probability
† Degrees of freedom (df) for L=5; Rep (L)=18; G=39; GxL=195; Pooled error=693.
‡ Degrees of freedom (df) for L=5; Rep (L)=18; G=39; GxL=194; Pooled error=677.
¶ Degrees of freedom (df) for L=6; Rep (L)=21; G=39; GxL=232; Pooled error=793.

Table 8. ANOVA by year for % early fruit of 40 watermelon genotypes tested in 3 years and 8 locations.

Source of variation	% early fruit					
	Mean squares			% of total sum of squares		
	2009†	2010‡	2011¶	2009	2010	2011
Location (L)	43343.60*	28996.69*	29643.91*	38	27	30
Replication within L	1285.27*	1540.35*	988.93*	4	5	3
Genotype (G)	1955.00*	1784.89*	1422.89*	11	11	11
G x L	535.38*	724.74*	652.81*	18	21	20
Pooled Error	239.69	386.12		28	37	36
CV (%) for 2009 = 63; 2010 = 46; 2011 = 64						
R^2 (%) for 2009 = 72; 2010 = 63; 2011 = 64						

* Significant at the 0.01 level of probability
† Degrees of freedom (df) for L=6; Rep (L)=21; G=39; GxL=234; Pooled error=810.
‡ Degrees of freedom (df) for L=6; Rep (L)=21; G=39; GxL=193; Pooled error=635.
¶ Degrees of freedom (df) for L=5; Rep (L)=15; G=39; GxL=156; Pooled error=574.

Table 9. ANOVA by year for fruit size (kg fruit^{-1}) of 40 watermelon genotypes tested in 3 years and 8 locations.

Source of variation	Fruit size					
	Mean squares			% of total sum of squares		
	2009†	2010‡	2011¶	2009	2010	2011
Location (L)	194.27*	439.51*	101.14*	12	26	5
Replication within L	8.80*	8.70*	11.59*	2	2	2
Genotype (G)	147.21*	115.49*	176.53*	59	44	62
G x L	3.73*	5.49*	5.55*	9	12	12
Pooled Error	2.31	1.93	2.38	20	15	17
CV (%) for 2009 = 20; 2010 = 20; 2011 = 20						
R^2 (%) for 2009 = 81; 2010 = 85; 2011 = 83						

* Significant at the 0.01 level of probability
† Degrees of freedom (df) for L=6; Rep (L)=21; G=39; GxL=234; Pooled error=810.
‡ Degrees of freedom (df) for L=6; Rep (L)=21; G=39; GxL=232; Pooled error=785.
¶ Degrees of freedom (df) for L=6; Rep (L)=21; G=39; GxL=232; Pooled error=779.

Table 10. Correlation among test locations for marketable yield (Mg ha^{-1}), fruit count (thousand ha^{-1}), % cull fruit, % early fruit, and fruit size (kg $fruit^{-1}$) of 40 watermelon genotypes tested in 3 years and 8 locations.

	Marketable yield							
Location	CA	CI	FL	GA	KN	OK	SC	TX
CA	1.00							
CI	0.53***	1.00						
FL	0.47**	0.55***	1.00					
GA	0.49**	0.42*	0.52***	1.00				
KN	0.40*	0.66***	0.70***	0.57***	1.00			
OK	0.24	0.30	0.50**	0.49**	0.56**	1.00		
SC	0.31	0.63***	0.63***	0.41**	0.63***	0.57***	1.00	
TX	0.72***	0.71***	0.47*	0.47*	0.57***	0.25	0.44*	1.00

	Fruit count							
Location	CA	CI	FL	GA	KN	OK	SC	TX
CA	1.00							
CI	0.84***	1.00						
FL	0.66***	0.66***	1.00					
GA	0.40*	0.40*	0.36*	1.00				
KN	0.89***	0.91***	0.68***	0.47**	1.00			
OK	0.23	0.27	0.45**	0.24	0.38*	1.00		
SC	0.66***	0.75***	0.80***	0.34*	0.75***	0.52***	1.00	
TX	0.90***	0.84***	0.62***	0.53***	0.88***	0.22	0.64***	1.00

	% cull fruit					
Location	CA	CI	GA	KN	OK	TX
CA	1.00					
CI	0.44**	1.00				
GA	0.21	0.49**	1.00			
KN	0.45**	0.82***	0.48**	1.00		
OK	0.47**	0.41*	0.60***	0.29	1.00	
TX	0.47**	0.80***	0.55**	0.61***	0.48**	1.00

	% early fruit							
Location	CA	CI	FL	GA	KN	OK	SC	TX
CA	1.00							
CI	0.16	1.00						
FL	0.56***	0.57***	1.00					
GA	0.49**	-0.02	0.37*	1.00				
KN	0.30	0.53***	0.36*	0.28	1.00			
OK	0.27	0.07	0.21	0.18	0.19	1.00		
SC	0.09	0.64***	0.48**	-0.01	0.65***	0.04	1.00	
TX	0.13	0.29	0.28	0.15	0.48**	0.05	0.34*	1.00

Table 10 Continued

	Fruit size							
Location	CA	CI	FL	GA	KN	OK	SC	TX
CA	1.00							
CI	0.95***	1.00						
FL	0.94***	0.96***	1.00					
GA	0.90***	0.93***	0.90***	1.00				
KN	0.96***	0.98***	0.95***	0.93***	1.00			
OK	0.87***	0.92***	0.89***	0.86***	0.89***	1.00		
SC	0.90***	0.94***	0.93***	0.83***	0.91***	0.91***	1.00	
TX	0.93***	0.94***	0.92***	0.93***	0.94***	0.88***	0.89***	1.00

***, **, * Significant at the 0.001, 0.01, and 0.05 level of probability, respectively

Table 11. Standard deviation within test location for marketable yield (Mg ha^{-1}), fruit count (thousand ha^{-1}), % cull fruit, % early fruit, and fruit size (kg $fruit^{-1}$) of 40 watermelon genotypes tested in 3 years and 8 locations.

Location	Marketable yield		Fruit count		% cull fruit	
	Mean	Standard deviation	Mean	Standard deviation	Mean	Standard deviation
CA	46.27	08.45	07.31	2.86	11.74	4.85
CI	74.58	14.86	10.77	3.73	06.37	6.75
FL	99.58	18.04	13.45	3.20	-‡	-
GA	81.19	28.89	09.63	3.15	4.83	4.31
KN	65.64	11.56	09.56	3.51	5.19	7.58
OK	28.33	11.97	04.64	1.89	21.09	10.62
SC	71.96	14.42	10.04	2.22	-	-
TX	29.17	07.83	5.24	1.91	12.50	9.56

Location	% early fruit		Fruit size	
	Mean	Standard deviation	Mean	Standard deviation
CA	-†	-	7.27	2.41
CI	45.80	12.59	7.59	2.30
FL	46.20	13.08	7.89	2.26
GA	13.27	14.60	9.25	3.48
KN	24.65	12.20	7.83	2.76
OK	24.71	12.06	6.67	2.17
SC	47.09	08.97	7.46	1.94
TX	16.36	08.83	5.80	1.95

‡ Missing location
† Not enough genotypes were harvested early

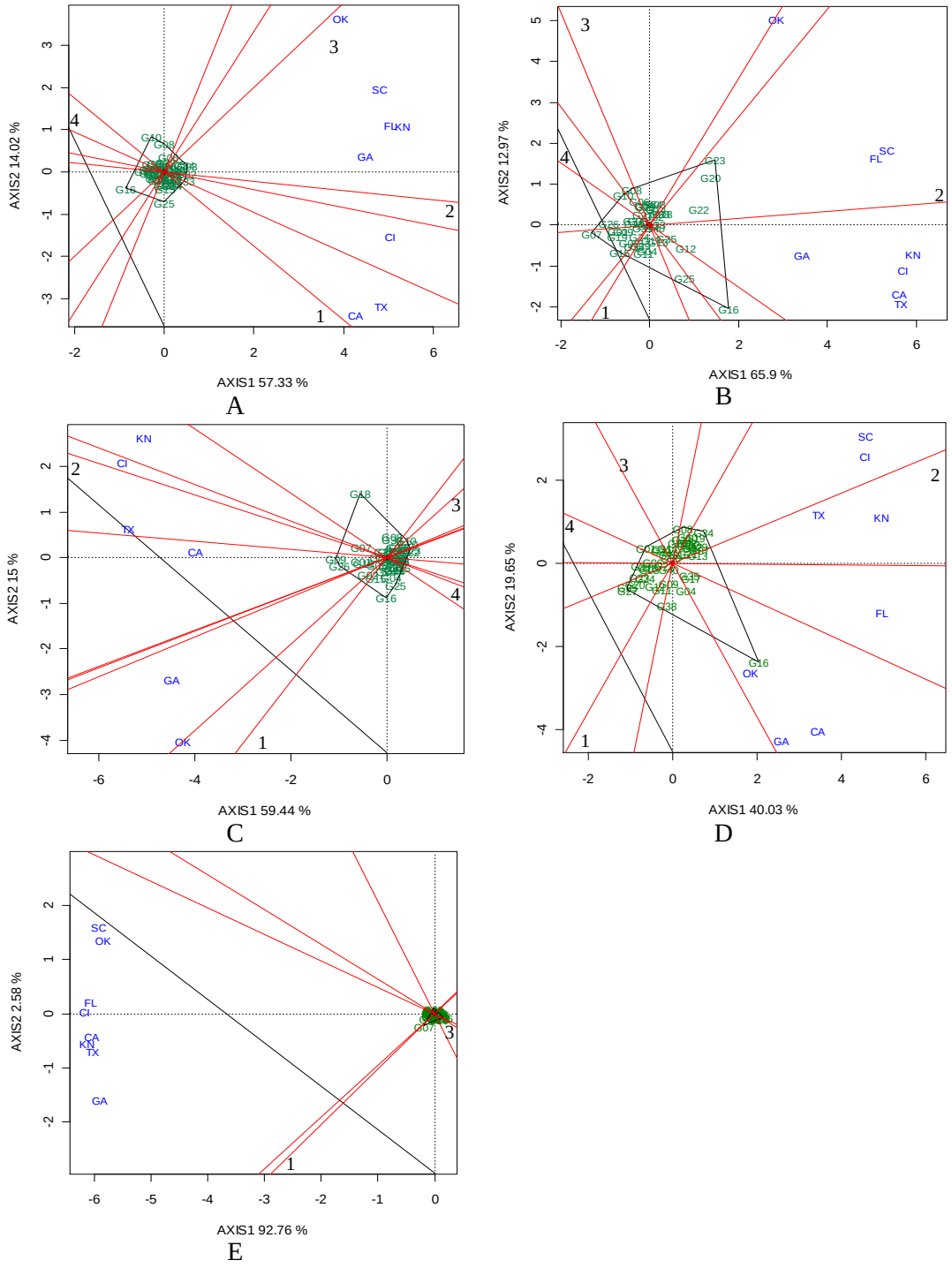

Figure 1. Polygon view of the GGE biplot based on watermelon (A) fruit yield (Mg ha^{-1}), (B) count (thousand ha^{-1}), (C) % culls, (D) % early, and (E) size (kg fruit^{-1}) of 40 genotypes tested in 3 years and 8 locations.

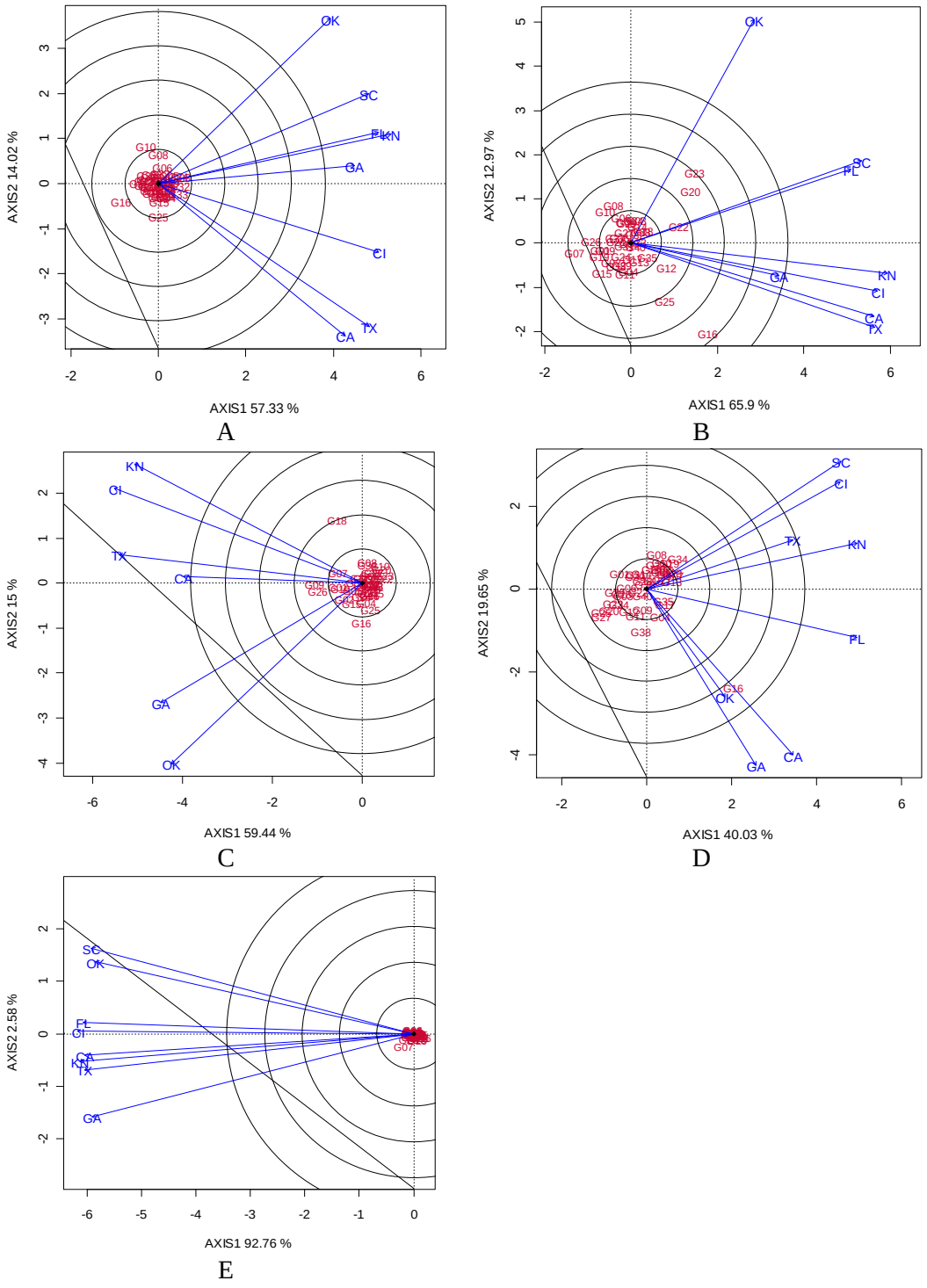

Figure 2. The vector view of the GGE biplot based on watermelon (A) fruit yield (Mg ha^{-1}), (B) count (thousand ha^{-1}), (C) % culls, (D) % early, and (E) size (kg fruit^{-1}) of 40 genotypes tested in 3 years and 8 locations.

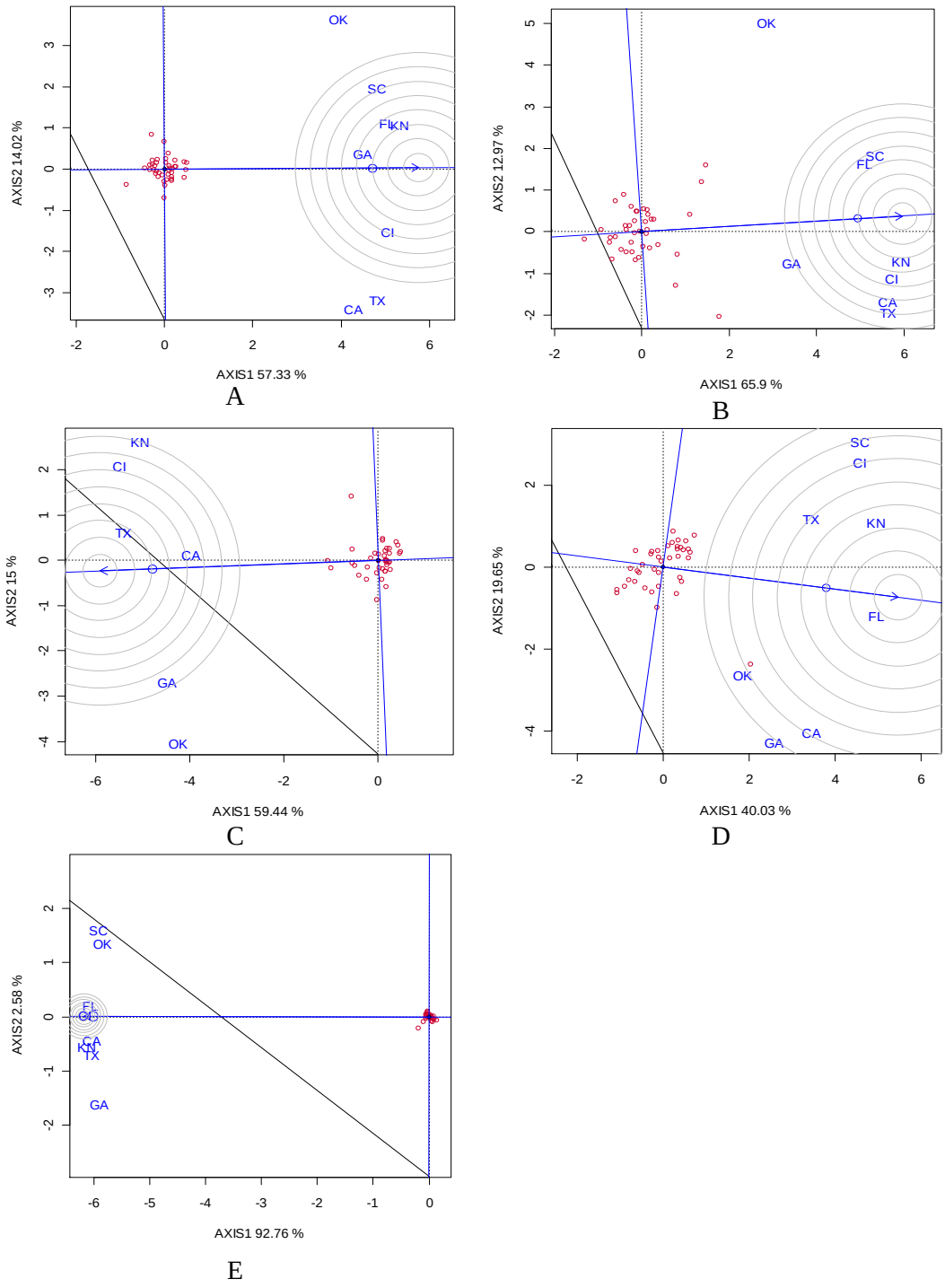

Figure 3. Comparison of all locations with the ideal location for watermelon (A) fruit yield (Mg ha^{-1}), (B) count (thousand ha^{-1}), (C) % culls, (D) % early, and (E) size (kg $fruit^{-1}$) of 40 genotypes tested in 3 years and 8 locations. The ideal location was represented by the smallest circle, and was the most discriminating and yet representative of other test locations.

GENERAL CONCLUSIONS

Watermelon production in the US is valued at $476 million, just below tomato and pepper (USDA, 2010). Traits of interest to watermelon breeders include yield and yield stability. The research literature available on these traits is limited.

This study will permit plant breeders working on watermelon [*Citrullus lanatus* (Thumb.) Matsum & Nakai] to identify high yielding, stable and adaptable watermelon genotypes for major watermelon producing regions of the US. It will also permit us to understand and select the best target and selection locations for yield and yield components of watermelon.

Yield stability

The results of genotype x environment interaction and stability analysis indicated that four genotypes including, two hybrids 'Fiesta F1' and 'Stars-N-Stripes F1', and two inbred 'Stone Mountain' and 'Calhoun Gray' had a high trait mean performance and high stability for yield. All four stable genotypes had high marketable yield, average fruit count, low % cull fruit, above average % early fruit, and medium fruit size. These four genotypes can be recommended for planting over a wide range of environments of the southern US.

It was interesting that the highest performing inbred genotype ('Big Crimson') and hybrid genotype ('Starbrite F1') for watermelon fruit yield and yield components were not the highest for yield stability. Hybrids 'Fiesta F1' and 'Stars-N-Stripes F1' and inbreds 'Stone Mountain' and 'Calhoun Gray' had high stability for fruit count, % early fruit, % cull fruit and fruit size. However, hybrids 'Fiesta F1' and 'Stars-N-Stripes F1' were more stable for fruit

count, % early fruit, % cull fruit and fruit size than inbreds 'Stone Mountain' and 'Calhoun Gray'.

Inbred 'Stone Mountain' was less appealing in appearance and quality than other two high yielding genotypes ('Legacy' and 'Big Crimson'). Although, 'Legacy' and 'Big Crimson' were unstable for marketable yield, they were stable for some yield components, which were lacking in 'Stone Mountain' and 'Calhoun Gray'. These inbreds can be used to develop cultivars with higher stability.

Location value

Two mega-environments were identified for marketable yield, fruit count, % cull fruit and % early fruit, and one mega-environment was identified for fruit size. Existence of mega-environments indicates the opportunity for the watermelon breeder to exploit narrow adaptation for the yield component traits. Two locations, Quincy FL and Clinton NC, were key locations for two mega-environments for marketable yield, fruit count, and % early fruit. College Station TX and Woodland CA, and Clinton NC were the ideal locations for two mega-environments, respectively, for % cull fruit. However, evaluation of fruit size can be done equally well in any location of those tested. The key locations representing the mega-environments for watermelon yield and yield components were not uniformly distributed across the US.

Some test locations were better than others for genotype evaluation, so watermelon breeders can evaluate genotypes at fewer locations, and obtain good yield data.

In our study, the locations representing mega-environments were not always those with the highest genotype yields. For example, Clinton NC and Kinston NC were key

locations representing mega-environments, but were low for all the yield traits evaluated. Historically, high-performing locations are used for trials more often than are low-performing locations. However, selection in marginal or high stress mega-environments is often associated with large errors, less discrimination, or less repeatability over years (Braun et al., 1992). Breeding in marginal environments may be improved using experimental techniques such as optimum replication number, and advanced analysis such as AMMI and GGE biplot to improve accuracy.

Implication for watermelon breeders

The two hybrids 'Fiesta F1' and 'Stars-N-Stripes F1', and two inbred 'Stone Mountain' and 'Calhoun Gray' identified for high trait mean and high stability for yield can be recommended for planting over a wide range of environments of the southern US. Watermelon breeders can use high yielding stable genotypes for developing stable hybrids. Hybrids will provide growers with added value over inbreds through high fruit yield, improved yield responsiveness, and stability. Hybrids provide additional advantage by protecting intellectual property and providing novel traits.

Crosses can be among high yielding stable inbreds 'Stone Mountain' and 'Calhoun Gray', and elite lines which watermelon breeder uses for developing commercial hybrids. These crosses will be comparable with test cross or combining ability used for hybrid evaluation. Stability evaluation for marketable yield of F_1 progeny obtained from these crosses can be evaluated simultaneously along with hybrid evaluation. Evaluation should be conducted at Clinton NC and Quincy FL. Clinton NC and Quincy FL have high

discriminating ability and representativeness. These two key locations represent two mega-environments for marketable yield for watermelon in southern US.

Otherwise, paired crosses can be made among four high marketable fruit yielder Inbreds 'Stone Mountain', 'Calhoun Gray', 'Big Crimson', and 'Legacy' for developing segregating populations. Seeds from early generation F_3 or F_4 can be evaluated for stability in replicated trials at four locations including Clinton NC, College Station TX, Quincy FL, and Cordele GA. Clinton NC and College Station TX; and Quincy FL, and Cordele GA represented two mega-environments, respectively. However, evaluation of stability for marketable yield in advanced generation F_5 or F_6 can be conducted at fewer locations. Clinton NC and Quincy FL will be sufficient to represent two mega-environments.

Similarly, identification of mega-environments in the US watermelon production region has several implications for watermelon breeders, as follows: (i) different genotypes should be grown in different mega-environments to achieve maximum yield, and (ii) crossover genotype x location interaction can be minimized through genotype evaluation and selection focusing on genotype main effect or general adaptation.

References

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