

CORRELATION AND BOXPLOT ANALYSIS FOR FIELD EVALUATION OF MUSKMELON (*Cucumis melo* L.) GENOTYPES**M. Khatun¹ and M. A. R. Taohidi^{2*}**¹Dept. of Genetics and Plant Breeding, Gazipur Agricultural University, Gazipur-1706²Dept. of Cytogenetics, Bangladesh Jute Research Institute (BJRI), Dhaka-1207

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ABSTRACT

Muskmelon (*Cucumis melo* L) is a very important summer crop cultivating at large scale in Bangladesh. The goal of this study was to determine the degree of character relationship between the quantity of fruits per plant and other growth characteristics of the studied 22 genotypes of muskmelon. The genotypes in this investigation differed significantly. A strongly positive correlation was recorded between two vigor indices, two foliar disease resistance (FDR) values, first flowering and 50% flowering days. The yield trait (fruit quantity per plant) was positively correlated with vigor indices and negatively correlated with FDR values. G17, G6, G21, and G10 were the most superior genotypes in comparison to other genotypes based on the vigor index and FDR value at 56 DAT including the fruit number per plant. Such genotypes can be used as breeding materials for subsequent genetic improvement in the purpose of developing high yielding stable variety.

Key words: Fruit yield, box plot analysis, muskmelon.

Introduction

In carrot cultivation, fertilizer is the single most important factor that plays a crucial role in increasing growth and yield. The soil of Bangladesh is deficient in nitrogen, potassium and for which farmers are Muskmelon (*Cucumis melo* L) is thought to have originated on the African continent, particularly in the eastern part of the south Sahara Desert, although India has been identified as a significant secondary center of variation. However, recent research revealed that both muskmelon and cucumber are Asian in origin, and Sebastian *et al.* (2010) discovered that a large variety of wild species of *Cucumis melo* L. occur in China and India. Genetic improvement requires knowledge of the kind and extent of genetic variation controlling the transmission of quantitative traits like yield and its constituent parts. Superior variety is being developed in an attempt to boost its output. Yield is a complicated quantitative characteristic that depends on several contributing factors. Therefore, only the links between the characteristics are shown by the knowledge of the association of various components and their respective proportions; effect and cause information are not provided. This would help create an effective breeding program (Bhimappa *et al.*, 2017). Therefore, in order to increase the productivity of a new variety, yield as well as its relevant attributes must be taken into account. In order to provide information on the value of the correlation coefficient in muskmelon genotypes, that eventually aids in the development of improved varieties, the current study was conducted. The purpose of the study was to determine the distribution of data of eleven traits and to choose the best genotype for future breeding endeavors.

Materials and Methods

The following Table 1 shows the 22 genotypes of muskmelon that made up the experimental materials. During the summer (kharif 1) of 2024, this experiment was carried out using a randomized complete block design with three replications in the field of Genetics and Plant Breeding department of Gazipur

Agricultural University (GAU), Gazipur-1706. Silty clay loam, silt loam, clay loam, silty clay, and clay are the textural classes found in the majority of soils in Gazipur. The pH varied slightly depending on the kind of terrain, ranging from extremely acidic to mildly acidic. In the soils under study, the amount of organic matter increased from high land to low land in this experimental site (Begum *et al.*, 2009).

Table 1. Experimental materials (22 genotypes) used in this study

Coding	Genotype	Coding	Genotype
G1	M 14480	G12	Melon NF self
G2	M 14418 G1	G13	Chinal NR seeds
G3	M 16720	G14	Bangi ashgourd
G4	Rockmelon G1	G15	Bangi ashgourd G1
G5	Mouchak	G16	Bangi PK
G6	Local kapasia	G17	Bangi AM
G7	Melon SL 2M3	G18	Demo
G8	Bangi long	G19	Bangi small round
G9	Bangi self-green	G20	Melon NF
G10	Bangi self-0.05%	G21	Bangi round small self
G11	Ashgourd self	G22	Melon big self

In each replication, 20 plants of each genotype were cultivated. In raised beds, the seeds were planted at a distance of 0.5 m between plants within a row and 1.5 m between rows. To protect the genotypes, the required plant safeguarding procedures were implemented consistently. The plant was well-maintained until the most recent harvest, and 5 plants selected at random were observed for growth, yield, and yield-related traits. Data was collected on five random plants per replication for quantitative characters viz., vigor index at 14 days after transplanting (vig_14DAT), vig_28DAT, vig_42DAT, vig_56DAT, foliar disease resistance at 14 days after transplanting (FDR_14DAT), FDR_28DAT, FDR_42DAT, FDR_56DAT, first flowering, fifty percent flowering and quantity of fruit per plant.

Results and Discussion

Correlation Analysis

Strong positive correlations between vig_14DAT and vig_28DAT ($r=0.92$) and between vig_28DAT and vig_42DAT ($r=0.92$) were found among the vigor characteristics, suggesting that crop vigor is consistent across stages of growth. Similarly, vigor at 42 DAT and vigor at 56 DAT had a favorable connection ($r=0.69$) as shown in Fig. 1. Investigation on muskmelon genotypes revealed a significant association between vine length and branching amount per plant, indicating that healthy plants maintain higher vegetative proliferation throughout their whole life cycle (Chhonkar *et al.*, 1981). These relationships suggest that leafy growth markers are physiologically connected and may be used collectively to evaluate plant health.

Additionally, foliar disease resistance (FDR) attributes shown extremely significant positive associations, especially between FDR_28DAT and FDR_56DAT ($r=0.96$) and between FDR_28DAT and FDR_42DAT ($r=0.97$), indicating that disease reaction remained comparatively consistent during several development phases. Plant health attributes have been shown to impact production, even though limited research specifically look at FDR relationships. In muskmelon plants, robust plants that are more resistant to disease often sustain greater vegetative vigor and more fruit set, which improves productivity (Akter, 2022). As a whole, the correlation study shows that while foliar disease intensity has a negative impact on production, plant vigor attributes have a positive impact on fruit quantity. This emphasizes the significance of choosing genotypes with greater vigor and superior disease resistance for increased fruit output. Fruit output is

strongly positively impacted by the quantity of fruits per vine, according to research, and this is a key screening criterion in the breeding endeavors of muskmelon (Prajapati *et al.*, 2022).

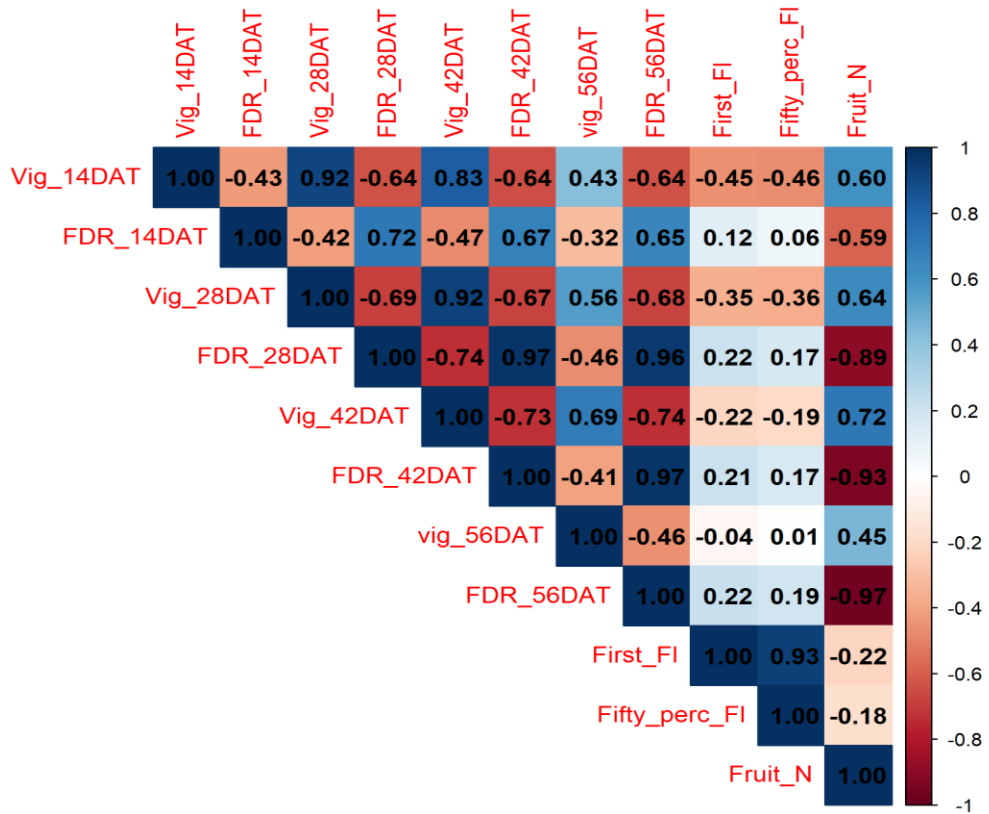


Fig. 1. Correlation coefficient for studied 11 traits in 22 genotypes of muskmelon

Boxplot analysis

For numerical data analysis, box and whisker plot is widely used. Tukey (1977) described the box and whisker method for displaying numerical data. The boxplot comprises a rectangle box having first quartile (Q1), median (second quartile, Q2) and third quartile (Q3). It also contains whiskers, Q1 to the minimum value and Q3 to maximum value. The Q1, Q2 and Q3, all together form interquartile range (IQR). Normally, it contains significantly longer whiskers than the box and small whiskers represents uniform distribution with sharp cutoff. Sometimes, the boxplot outlier indicates contamination of sample data in a population (Dawson, 2011).

Foliar disease resistance at different days after transplanting (DAT)

At 14 DAT: At 14 DAT, the FDR scores revealed early variation in foliar disease response among the evaluated genotypes (Fig. 2). Several genotypes recorded FDR scores close to zero, indicating strong resistance and minimal disease symptoms at the early vegetative stage. In contrast, a few genotypes exhibited relatively higher FDR scores, suggesting early susceptibility to foliar pathogens. Most genotypes displayed low to moderate scores, indicating partial resistance during the initial growth phase. Overall, disease pressure appeared relatively low at this stage, but differences in resistance levels among genotypes were already noticeable.

At 28 DAT: The differences in FDR scores across genotypes were more noticeable at 28 DAT. At increased burden of disease, certain genotypes showed persistent resistance by maintaining extremely low ratings. In addition, as the crop canopy grew and the surroundings remained more conducive to the emergence of disease, a number of genotypes displayed greater FDR ratings, suggesting greater vulnerability. The wider range of ratings at this point indicates that resistant and susceptible genotypes may be distinguished more clearly.

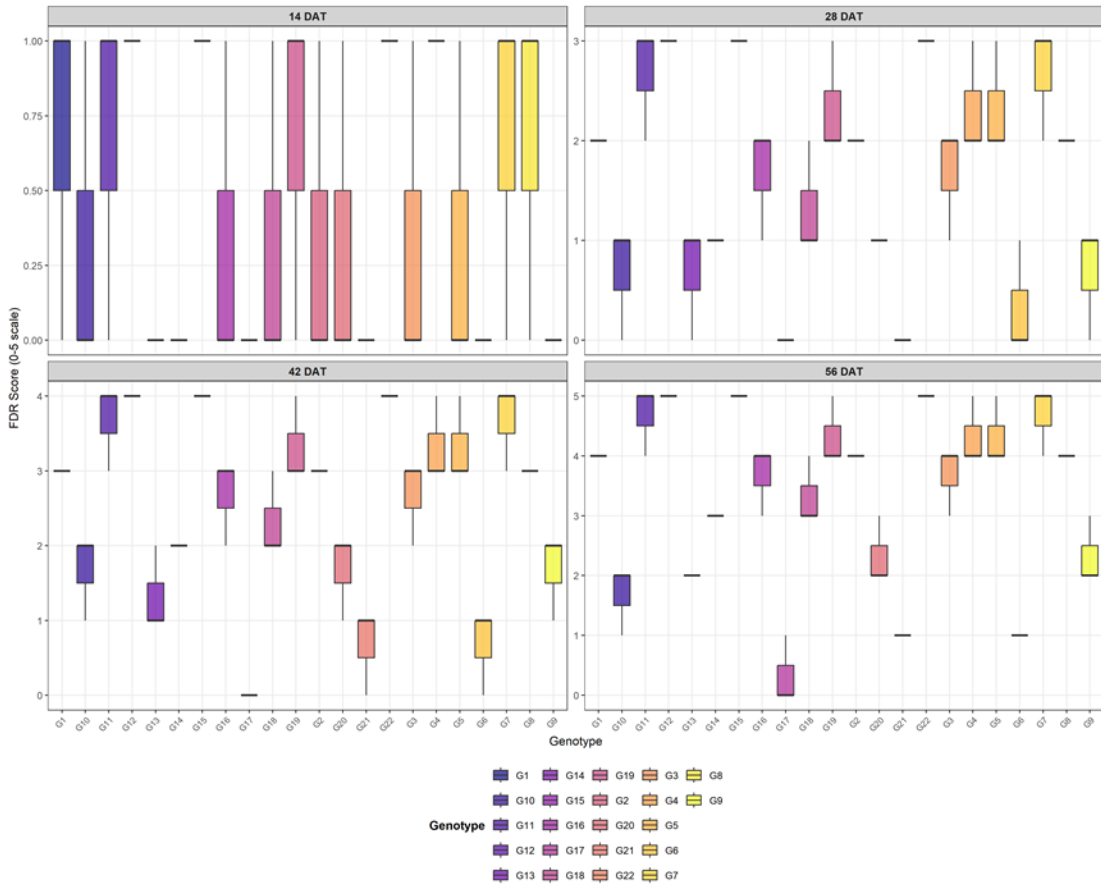


Fig. 2. Data distribution of foliar disease resistance (FDR) at different times after transplanting (14, 28, 42, and 56 DAT) using box plot.

At 42 DAT: The advancement of the disease was more noticeable in all genotypes at 42 DAT. The several genotypes showed significantly greater ratings, indicating a greater vulnerability and severity of the condition. The greater spectrum of FDR scores shown at this point emphasizes how crucial mid-growing assessment is for finding genotypes with long-lasting resistance against foliar pathogens.

At 56 DAT: The consequences of extended exposure to the illness were evident in the FDR ratings at 56 DAT. At this point, the genotypes that are resistant and susceptible may be clearly distinguished, which offers important information on the long-term durability of foliage pathogen resistance.

The allocation of foliage resistance to disease (FDR) ratings obtained at various times following transplanting is shown in the box plot. The FDR ratings for each of the 4 assessment phases showed that as plants became older, disease prevalence increased and genotype heterogeneity increased as well. While genotypes having greater ratings were at greater risk to pathogen infection, those that consistently had lower FDR values during all test periods showed stable and lasting foliage immunity to disease. In order to precisely select genotypes with dependable resilience for breeding and agricultural development initiatives, our results emphasize the significance of multi-stage assessment. The significance of host immunity in lowering disease prevalence and enhancing crop production was demonstrated by the fact that genotypes displaying lower disease ratings were thought to be more resistant (Dhiman *et al.*, 1995).

Vigor index at different days after transplanting (DAT)

Vigor index at 14 DAT: When genotypes were evaluated 14 days after transplanting, the vigor index showed significant phenotypic variance, varying between 1.8 to 4.1, suggesting a broad genetic capacity for rapid seedling establishment (Fig. 3). The simultaneous evaluation of efficacy and stability was made easier by box plot assessment in 3 replications per genotype. With the greatest median vigor (>3.6) and little variance, G3 and G21 genotypes were shown to be excellent performers. Therefore, they are ideal choices for breeding efforts aimed at enhancing the development of crops. Conversely, a unique genotype with scores as little as 1.8 indicated a very low performance, demonstrating the trial's discriminating potential. While the variation seen in other genotypes implies varying susceptibility to micro-environmental influences, stable, mid-range genotypes like G1 and G22 (medians ~3.0) provide constancy. The discovery of highly vigorous, durable genotypes (G3 and G21) offers useful genetic material for upcoming biological assessment and breeding initiatives targeted at improving muskmelon early-season productivity and resource usage efficacy. The genetic variation in seedling strength shown in this study is identical with observations in muskmelon genetic materials. Pal *et al.* (2017) found that treating *Pseudomonas fluorescens* and *Trichoderma harzianum* combined produced the greatest seedling length (20.12 cm) and vigor index (1745.10). *T. harzianum* alone (1705) and a combination of *T. viride* and *T. harzianum* (1680.60) followed this. The results confirm that appropriate seed treatments may considerably raise the vigor index and that these treatments are associated with a high degree of variation (Pal *et al.*, 2017).

Vigor index at 28 DAT: The vigor index box plot analysis of studied genotypes at 28 DAT successfully distinguished genotypes based on effectiveness and stability. G13 and G21 were determined to be the most suitable donors for breeding projects intended to increase initial vigor due to their high median score and exceptional stability. Furthermore, G3 is a remarkable genotype with nearly total uniformity. The discovery that G7 consistently performs poorly validates the trial's discriminating power. Genotypes that are prone to variability, such as G18, could be suitable for hybrid combinations as heterosis might increase output or necessitate further study. With vigor index scores that varied from 3.9 to 8.5, the evaluated genotypes at 28 DAT demonstrated significant morphological variability.

Vigor index at 42 DAT: 22 muskmelon genotypes were effectively distinguished according to both efficiency levels and durability using the box plot assessment of the vigor index at 42 DAT. With a median of 12.2 and outstanding steadiness, G13 was unquestionably the best performer, promptly followed by G6, G9, and G10 (medians 11.2-11.4). Remarkable growth patterns were found by temporal assessment; certain genotypes (G6, G9, G10) demonstrated faster mid-season advancement, whereas some (G3, G21) continued to perform well. The finding that G7 regularly performs poorly justifies the experimental setup and offers a useful negative control for further research.

Vigor index at 56 DAT: Genotypes were effectively distinguished in accordance with both efficiency levels and durability at a higher vegetative phase using the box plot assessment of a vigor index at 56 DAT. G13 is the best genetic material for muskmelon enhancement efforts aiming at improved vegetative progress across the development process since it reliably performed at the highest level throughout all

testing phases (28, 42, and 56 DAT) having a median score of 14.5 and outstanding stability. Many genotypes, namely G6, G9, G10, G14, G17, and G20 (medians 13.9-14.5), attained elite status by 56 DAT, suggesting excellent late-season growth potential. Such genotypes are valuable resources for breeding initiatives that seek to sustain vigor during advanced developmental stages. The stability evaluation indicates that most of the best performers (G6, G9, G10, G13, G14, G17, and G20) integrate exceptional talents via consistent manifestation and exhibit excellent stability. This combination makes them appropriate parental lines for hybrid development and population augmentation activities. More study is necessary since G15 continues to show great variability. G7 serves as a reliable negative control and validates the trial's discriminating capacity at all levels.

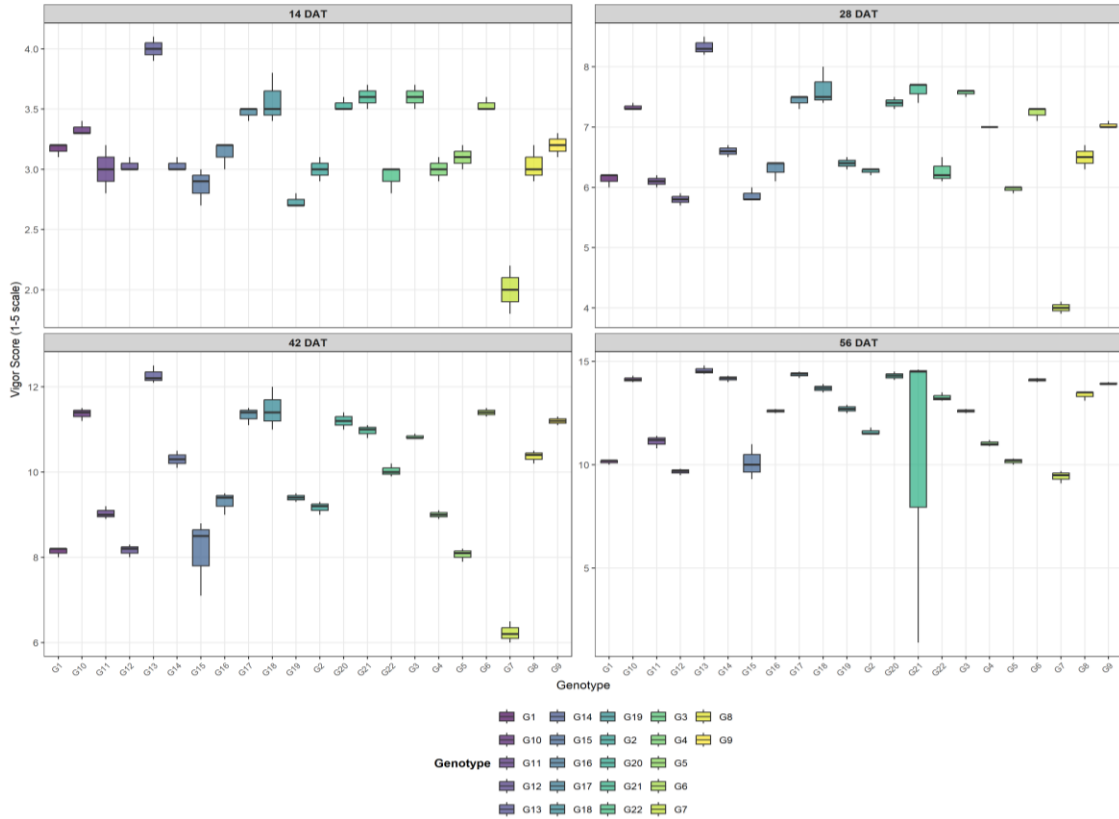


Fig. 3. Vigor index data distribution using box plot at 14, 28, 42, and 56 DAT (days after transplanting)

The temporal evaluation revealed that several genotypes had varied development pathways: some (G13) continuously operated at the peak tier, whereas others (G6, G9, G10, G14, G17, G20) progressively progressed to elite rankings, while some (G3, G12) deteriorated in advanced stages. With this knowledge, breeders may select genotypes that fulfill specific developmental goals. Compared to entries that lost vigor at later phases (G3, G12), outstanding entries that retained significant vigor at 56 DAT (G13, G6, G9, G10, G14, G17, G20) most likely had superior root architecture, slower senescence procedures, or stronger defense enzymatic pathways.

First flowering days

Using the box plot evaluation of initial flowering days based on both biological integrity and earlier flowering habit, genotypes were successfully differentiated (Fig. 4). The earliest-floral genotypes were G12

(median 21 days) and G10 (median 25 days), with G12 serving as a remarkable genetic asset for extremely early reproduction. G3, G4, and G13 provide more excellent-stability early blooming alternatives. The most desired ideotype, G10, exhibits exceptional vigor with extremely early blooming (25 days). G13 has early-medium blooming (28 days) and exceptional vitality. Superior vigour and moderate blooming (28-30 days) are combined in G6, G9, G14, G17, and G20. Such genotypes are important genetic assets for standard breeding initiatives that aim to achieve both early maturity and high production. The trustworthiness of biological data along with the genetic regulation of the period of blooming in such genetic material are confirmed by the extremely steady blooming behavior shown in the majority of genotypes (20 of 22 exhibiting minimum spread). Several investigations in muskmelon populations have shown considerable genetic heterogeneity in days to first blooming. In their evaluation of 48 muskmelon species, Ansari *et al.* (2020) found that in well-watered circumstances, the maximum time frames for first male flowering were 41.5 days, whereas in drought-like stress, blossoming took place sooner, alongside for the initial male blossoming 37.2 days and for first female floral development 47 days.

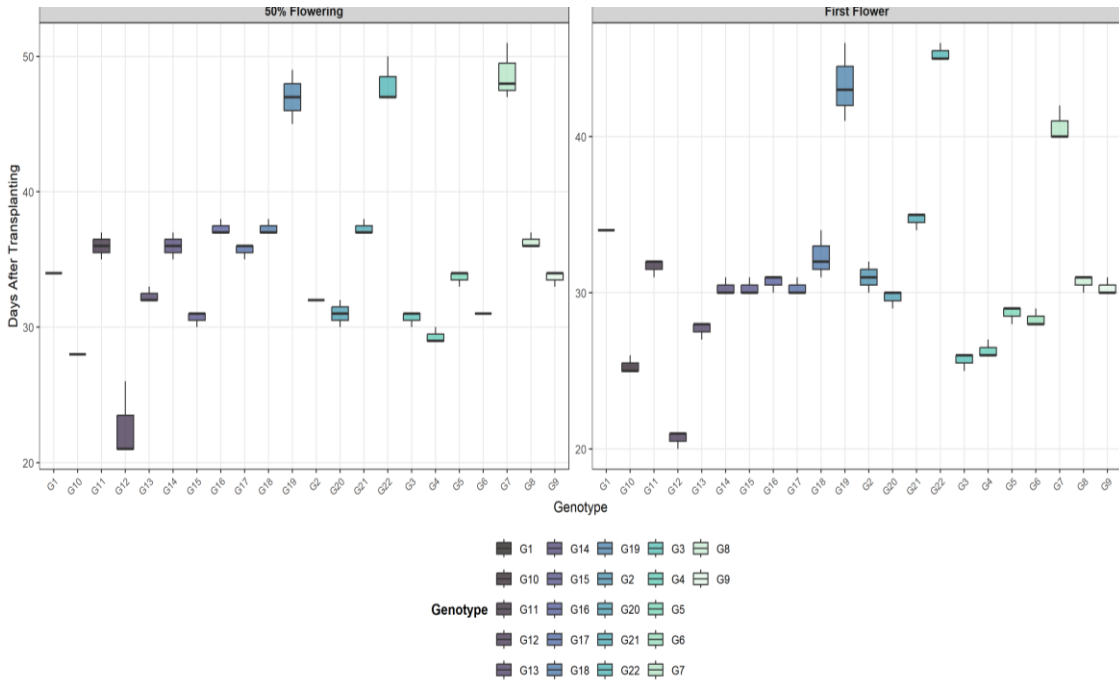


Fig. 4. Data distribution of first and 50 % flowering days of 22 muskmelon genotypes using box plot

50% flowering days

Genotypes were effectively distinguished through stable phenology and earliness using a box plot assessment of 50% blooming days (Fig. 4). The most useful genotype for early breeding is G10 (median 28 days, complete stability), which combines extremely early 50% blooming with outstanding vigor at 56 DAT-the optimal ideotype. The initial median (21 days) is displayed in G12, however there is considerable variation (21-26 days) and possible outlier problems. This genotype gives exceptional earliness if confirmed, although stability breeding is necessary. Other early blooming possibilities (29-31 days) with good to outstanding stability are offered by G3, G4, G6, and G15. The greatest amount of biological stability is represented by completely stable genotypes (G1, G2, G6, and G10) with no fluctuation among replications. For some late-maturity sectors or genetic research, late-blooming genotypes (G7, G19, G22) exhibit medium to extreme diversity.

The G10, G4, G6, and G22 are genotypes having focused blooming durations, which are important characteristics for consistent fruit setting and harvesting, according to the blooming synchronization assessment (a gap between initial and fifty percent blooming). Several investigations on muskmelon genetic materials have shown considerable genetic heterogeneity in 50% blooming days. Highest readings for 50% male blooming of 44 days and for 50% female flowering of 45 days at adequate hydration circumstances were reported by Ansari *et al.* (2020), who assessed 48 muskmelon populations in both adequate hydration and deficient hydration environments.

Fruit number per plant

Genotypes were effectively distinguished according to production and stability using a box plot evaluation of the fruit quantity per plant (Fig. 5). The best-performing genotype for fruit quantity, G17 (median 16 fruits), has exceptional stability and superior vigor at 56 DAT, making it the optimal donor for breeding schemes aimed at increasing production. Extraordinary secondary donors G6 (median 13 fruits) and G21 (median 11 fruits) combine an elevated level fruit quantity with exceptional vigor and adequate to outstanding stability. For breeding efforts, G10 (median 9 fruits) is an exceptional ideotype targeting at both production and earliness because of its high fruit amount, exceptional vigor, and very early flowering (28 days). G9, G13, and G20 (median 7 fruits per plant) produce robust, reliable fruit with remarkable vigor and optimal blossoming timing.

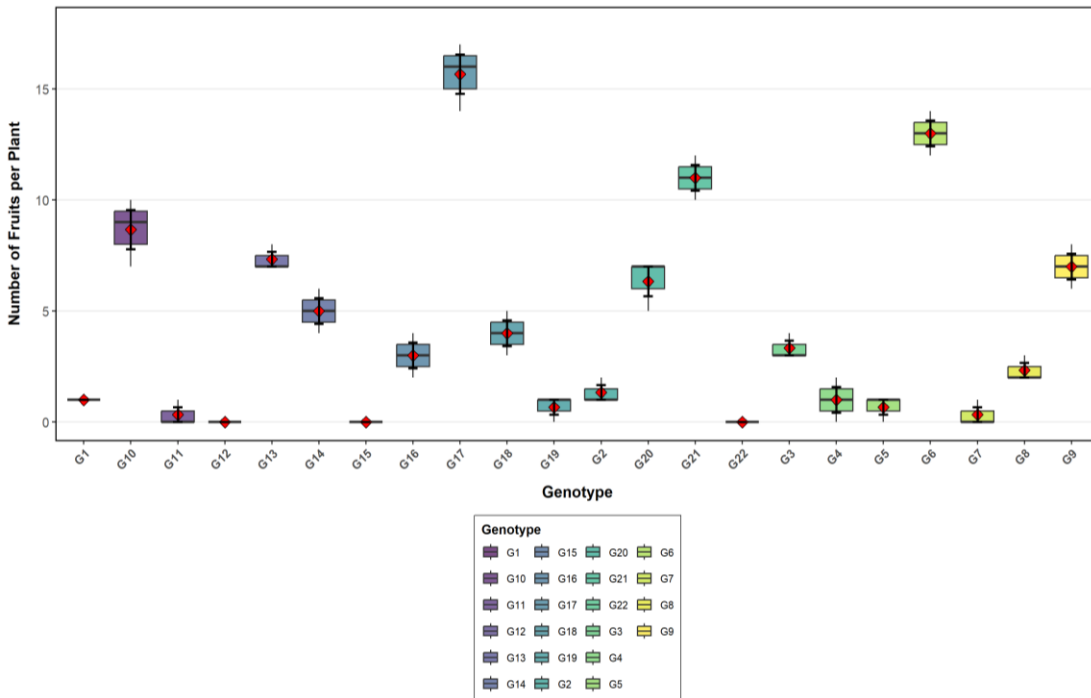


Fig. 5. Data distribution of the quantity of fruit per plant of 22 muskmelon genotypes using box plot

Three genotypes (G12, G15, and G22) did not produce any fruit in their replications, which called for more investigation into possible sterility, pollination issues, or data collecting issues. Five genotypes (G4, G5, G7, G11, and G19) showed uneven fruit set that affected no fruit at all in each replication, indicating issues with biological susceptibility or fertility. Genotypes that combine outstanding fruit quantity, superior vigor, earlier blooming, and excellent stability—such as G6, G10, G17, G21, G9, G13, and G20—are highly useful for breeding endeavors.

Numerous studies using muskmelon genotypes have shown considerable genetic heterogeneity in fruit quantity per plant. Bhimappa and Choudhary (2017) assessed 67 different muskmelon variants and found that yield and yield related traits varied significantly amongst genotypes and surprisingly, discovered that the quantity of fruits per plant had the minimum phenotypic and genotypic coefficient of variation, following the main branches quantity, initial female flowering days, and early fruit harvest days. This result is consistent with the current study, which found that genotypes ranged widely ranging 0 to 17 fruits per plant, having different categories from zero-fruited genotypes (G12, G15, G22) to exceptional performance (G17 with 16 fruits). In contrast to other qualities, fruit quantity variation is quite modest, indicating that this attribute may be more tightly controlled by genetics or more impacted by certain physical limitations.

Conclusion

The yield trait (fruit quantity per plant) was positively correlated with vigor indices and negatively correlated with FDR values. G17, G6, G21, and G10 were the most superior genotypes in comparison to other genotypes based on the vigor index and FDR value at 56 DAT including the fruit number per plant. Such genotypes can be used as breeding materials for subsequent genetic improvement in the purpose of developing high yielding stable variety.

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Author's contribution

The concept and methodology of the study were done by M. Khatun and M. A. R. Taohidi. The execution of the study in the field was mainly done by M. Khatun. The statistical analysis, initial draft of the manuscript, final reviewing and approval of the final manuscript were done by both M. Khatun and M. A. R. Taohidi.

Conflict of interest: Authors declare that there is no conflict of interest.

References

- Akter, A. 2022. Genetic variability studies in muskmelon (*Cucumis melo* L.)
- Ansari, W. A., Atri, N., Yang, L., Singh, B. and Pandey, S. 2020. Genetic diversity in muskmelon based on SSR markers and morphological traits under well-watered and water-deficit condition. *Biocatalysis Agric. Biotechnol.* 26:101630.
- Begum, K., Jahan, I., Rahman, M. H., Chowdhury, M. S. and Elahi, S. F. 2009. Status of some micronutrients in different soils of Gazipur district as related to soil properties and land type. *Bangladesh J. Sci. Industrial Res.*, 44(4):425-430.
- Bhimappa, B. B. and Choudhary, H. 2017. Genetic variability, heritability and genetic advance in muskmelon (*Cucumis melo* L.). *Annals Agric. Res.*, 38(2):212-217.
- Bhimappa, B. B., Choudhary, H., Behera, T. K. and Sharma, V. K. 2017. Correlation and path analysis study for yield and its contributing traits in different horticultural groups of muskmelons (*Cucumis melo* L.). *Vegetable Sci.*, 44(01):54-59.

- Chhonkar, V. S., Singh, D. N. and Singh, R. L. 1981. Genetic variability and correlation studies in muskmelon.
- Dawson, R. 2011. How significant is a boxplot outlier? *J. Sta. Education*, 19(2).
- Dhiman, J. S., Lal, T. and Bajaj, K. L. 1995. Evaluation of muskmelon (*Cucumis melo* L.) genotypes for multiple disease resistance, yield, and quality characteristics. *Tropical Agric.*
- Pal, N., Singh, N. and Buttar, D. S. 2017. Management of Fusarium wilt with the use of potential bioagents in muskmelon. *Plant Disease Res.*, 32(1), 50-57.
- Prajapati, P. J., Acharya, R. R., Patel, N. D., Pandya, M. M. and Patel, N. A. 2022. Character association and path analysis for fruit yield and its contributing traits in muskmelon (*Cucumis melo* L.). *The Pharma Inno. J.*, 11(1):670-674.
- Sebastian, P., Schaefer, H., Telford, I. R. and Renner, S. S. 2010. Cucumber (*Cucumis sativus*) and melon (*C. melo*) have numerous wild relatives in Asia and Australia, and the sister species of melon is from Australia. *Proceedings Nat. Aca. Sci.*, 107(32):14269-14273.