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Selection of Sweet Corn Inbred Lines by Agronomic Performance to Determining Hybrid Parents

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ABSTRACT

The development of hybrid sweet corn varieties involves the selection of parental lines with specific traits to ensure good yield potential. The selection of inbred lines of sweet corn is a critical aspect of breeding programs aimed at developing improved varieties. This research will provide useful information of sweet corn inbreed lines have the potential to be developed as parent lines in the development of hybrid varieties. The study utilized 24 inbred lines (G1-G24) of sweet corn and employed a Randomized Complete Block Design (RCBD). Data analysis involved the use of analysis of variance with a 5% significance level, path and dendrogram analysis. Based on the analysis of 24 inbreed line of sweet corn, the potential for selecting parents based on quantitative traits influencing the outcome is evident in inbreed line G18, G12, G4, G23, and G20. Identification of these potential parents is essential for the genetic improvement of the population. The correlation heatmap data indicates a 41% correlation between the number of rows and cob stag length, and correlation between number of rows and ear diameter by 48%. The path diagram indicates that fresh weight, a crucial measure of crop yield, is strongly influenced by several agronomic traits, including plant height, ear length, ear diameter, dry weight, number of plants, row length, brix, and ear stalk. G24 can indeed be used as one of the parents with other group in hybrid breeding programs.

keywords: sweet corn, selection, inbreed line

INTRODUCTION

The cultivation of sweet corn as a cross-pollinating plant is indeed generally directed towards producing hybrid varieties compared to non-hybrid varieties. Hybrid sweet corn varieties are developed through controlled cross-pollination of two genetically distinct parent lines. This process allows breeders to capitalize on the phenomenon of hybrid vigor, also known as heterosis, which results in the offspring (hybrid) exhibiting superior traits compared to the parents. This is due to the specific advantages that hybrid sweet corn varieties offer in terms of yield, uniformity, disease resistance, and overall quality.

The development of hybrid sweet corn varieties involves the selection of parental lines with specific traits to ensure good yield potential. Genetic variation plays a crucial role in the phenotypic response of sweet corn hybrids to factors such as population density (Shelton & Tracy, 2013). Significance of selecting parental lines with traits that confer tolerance to environmental stressors and agronomic management practices,

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ultimately contributing to the development of high-yielding hybrid sweet corn varieties.

The selection of inbred lines of sweet corn is a critical aspect of breeding programs aimed at developing improved varieties. The importance of selecting sweet corn inbred lines based on various traits, including consumer-oriented characteristics such as shape, size, flavor, and kernel row number (Hu et al., 2021). Additionally, the selection process involves considering traits related to carbohydrate components, tenderness, aroma, and overall eating quality to meet consumer preferences. Furthermore, the selection of inbred lines is influenced by the need to enhance specific nutritional attributes, such as provitamin A, lysine, and tryptophan content, through genomics-assisted breeding (Singh et al., 2023). The economic performance of specialized field crop farms producing sweet corn also underscores the significance of the selection process in ensuring profitability and market competitiveness (Nastić et al., 2022).

To select a sweet corn inbred line with high yield, it is essential to consider various traits and factors that contribute to the overall productivity of the crop. Several studies have highlighted the significance of genotype selection based on traits directly related to grain yield and the impact of genotypic effects on final stand and yield (Entringer et al., 2017). Additionally, the use of selection indexes based on characteristics with a direct effect on grain yield has been proposed to enhance the efficiency of genotype selection in segregating sweet corn populations (Silva et al., 2020). Furthermore, the development and selection of super-sweet corn genotypes through multivariate approaches have been investigated to improve the efficiency in the selection of superior genotypes (Gonçalves et al., 2018). To select inbred lines of sweet corn that have the potential for developing hybrid varieties, it is necessary to consider genetic factors that influence agronomic performance.

This research will provide useful information in selecting of sweet corn inbred lines which have the potential to be developed as parent lines in the development of hybrid varieties. By knowing the genetic factors that influence agronomic performance, researchers can select sweet corn varieties that have higher productivity and produce larger seeds, thereby increasing crop yields and economic profits..

MATERIALS AND METHODS

The research was conducted from November 2022 to February 2023 at the Experimental Field of Jatikerto, Brawijaya University, Malang, East Java, focusing on the cultivation of sweet corn. The study utilized 24 inbred lines (G1-G24) of sweet corn and employed a Randomized Complete Block Design (RCBD) with two replications for environmental analysis. Data analysis involved the use of analysis of variance with a 5% significance level and an honest significant difference (HSD) test at a 5% level. Additionally, the investigation incorporated correlation and path analysis techniques to ascertain the interrelationships among various traits in sweet corn. The utilization of dendrogram analysis, within the framework of genetic distance, was employed to visually depict and cluster genetic entities.

RESULTS AND DISCUSSIONS

Agronomic performance and some important characters are key to obtain inbreed line sweet corn. The agronomic performance of the sweet corn showed significant improvement compared to the previous generations. The plants were taller, with longer ears and larger cobs, indicating a successful breeding program. Additionally, the kernels exhibited vibrant colors, enhancing the visual appeal of the sweet corn variety.

Quantitative and qualitative character observations were made visually on all genotypes observed. Quantitative character observations are presented in Table 1 and qualitative character observations are presented in Table 2.

Table 1. Table of HSD further test results of quantitative characters in 24 inbred lines of sweet corn

Genotype	PH	CSL	EL	ED	NR	B	FW	DW
G1	184,85 ef	12,05 no	16,30 ghi	4,59 i	14,55 f	8,05 b	351,17l	101,40 h
G2	188,15 fg	11,70 mno	16,10 fgh	4,61 ij	15,20 hij	9,60 g	367,37 m	107,65 ijk
G3	202,00 kl	12,10 o	15,90 ef	4,04 d	14,30 ef	7,60 a	314,15 ij	90,02 efg
G4	211,40 m	10,75 kl	16,00 efg	4,92 o	16,05 o	9,20 f	371,00 m	100,75 hij
G5	203,80 l	9,50 f	14,20 a	4,38 e	14,55 f	8,60 d	289,27 efg	95,01 g
G6	193,40 ghi	10,60 jkl	15,15 bc	4,47 g	15,65 im	9,70 g	268,00 bcd	78,24 b
G7	179,55 cd	8,60 e	15,35 c	3,90 a	15,15 hi	11,20 m	309,87 hi	88,04 def
G8	160,50 b	6,65 a	14,50 a	4,84 n	15,95 no	8,90 e	299,47 gh	92,63 fg
G9	180,70 de	7,95 d	15,40 cd	4,62 jk	15,20 hij	10,80 l	331,95 k	94,33 g
G10	199,70 jkl	10,80 l	16,40 hi	4,53 h	14,95 gh	10,40 jk	352,27 l	91,97 fg
G11	189,05 fgh	7,35 b	15,95 ef	4,63 k	15,65 im	8,90 e	257,44 b	84,63 cde
G12	176,70 cd	8,10 d	15,90 ef	4,96 p	15,55 klm	8,40 cd	314,75 ij	110,19 jk
G13	197,15 ijk	7,40 bc	17,15 j	4,78 m	15,75 mn	9,75 gh	309,65 hi	131,20 m
G14	188,10 f	7,80 cd	15,35 c	3,98 c	14,05 e	10,15 ij	279,92 cde	95, 38 g
G15	193,55 hi	10,35 ijk	16,00 efg	4,83 n	15,30 ijk	9,60 g	282,51 def	104,58 hi
G16	164,65 b	10,95 l	15,10 bc	3,94 b	12,50 b	9,10 ef	265,59 bc	79,67 bc
G17	196,30 ij	11,65 mn	17,10 j	4,65 k	13,35 d	8,15 bc	290,79 efg	111,14 k
G18	199,60 jkl	8,90 e	18,25 k	4,55 h	14,85 g	10,50 k	325,92 jk	119,08 l
G19	160,85 b	9,55 f	15,20 bc	4,42 f	12,90 c	7,45 a	272,92 cd	90,09 efg
G20	159,60 b	9,80 fg	14,25 a	4,90 o	12,15 a	11,55 n	267,54 bc	74,50 b
G21	190,05 fgh	10,05 ghi	16,60 i	4,69 l	15,30 ijk	10,00 hi	279,04 cde	79,94 bc
G22	160,15 b	10,25 hij	15,70 de	4,47 g	15,70 lmn	10,35 jk	237,50 a	67,97 a
G23	175,30 c	9,90 fgh	15,25 bc	4,83 n	16,75 p	8,40 cd	292,88 efg	83,87 cd
G24	102,65 a	11,55 m	14,95 b	4,84 n	15,45 jkl	9,70 g	295,44 fgh	93,45 fg

Note: HSD significance is 5%, PH: plant height (cm), EL: Ear length (cm) ED: Ear diameter (cm), FW: fresh weight (g), DW: dry weight (g), NR: number of rows, B: brix (%), CSL: cob stag length (cm).

The hight maize inbreed line were observed in the G4 treatment, with an average height of 211.40 cm, while the shortest were in the G24 treatment, with an average height of 102.65 cm. Maize height is influenced by genetic factors and environmental conditions, significantly impacting maize yield. Maize plant height is a crucial agronomic trait that significantly influences maize yield. It is affected by genetic factors and environmental conditions, such as lodging stress, waterlogging, and drought (Esteban & Baldo, 2023; Olawuyi et al., 2015). Furthermore, the lodging of maize, which is influenced by plant height, is a major factor affecting maize yield (Hassaan, 2018). Environmental factors, such as sowing date and agroecological conditions, also significantly impact plant height and ultimately affect grain yield (Tabaković et al., 2020; Audu & Idris, 2020). In addition to genetic and environmental factors, physiological processes and hormonal interactions play a role in regulating plant height and ultimately impacting maize yield. For instance, gibberellins and brassinosteroids have been found to promote each other's action and increase heterosis for plant height in maize (Yu et al., 2023).

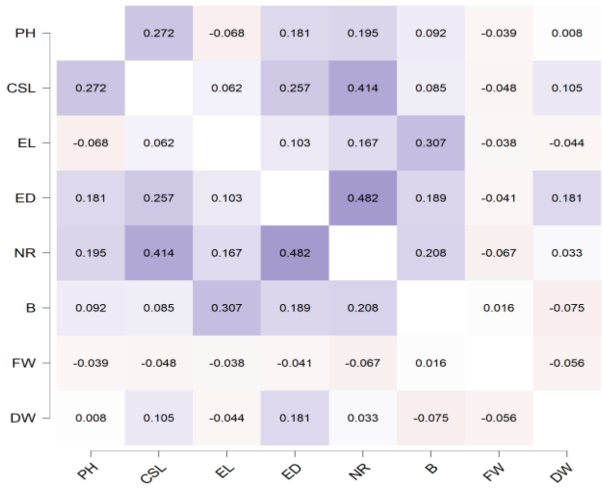
The study of maize inbred lines requires a comprehensive understanding of traits such as cob length, cob diameter, and cob stalk length. These traits play a pivotal role in determining the productivity and quality of maize. The data on maize cob length, cob diameter, and cob stalk length highlights the importance of these traits in the study of maize inbreed line. The highest cob length was observed in the G18 treatment, while the shortest was in the G9 treatment. Similarly, the largest cob diameter was recorded in the G12 treatment, and the lowest in the G7 treatment. Additionally, the longest cob stalk was found in the G1 treatment, with the shortest in the G8 treatment. These findings underscore the significance of these variables in characterizing maize inbreed line and their potential impact on hybrid production.

Research has shown that cob volume traits, including cob length and diameter, are crucial in assessing maize under different nitrogen management conditions, highlighting their significance in agronomic and genetic assessments Jansen et al. (2015). Furthermore, the genetic variability and path analysis studies have indicated the importance of cob diameter and length in influencing maize yield, emphasizing their role as key yield components (Matin et al., 2017).

The highest wet cob weight variable was in the G4 treatment with an average of 371 grams and the lowest was in the G22 treatment with an average of 237.50 grams. The highest dry weight variable in the G13 treatment with an average of 131.20 grams and the lowest in the G22 treatment with an average of 67.97 grams. Wet and dry cob weights are the main characters for consideration of determining superior elders for crosses. The data on wet and dry cob weights in different maize treatments underscores the importance of these traits in determining superior elders for crosses. These traits are crucial indicators of maize productivity and genetic potential. Studies have shown that genetic diversity plays a significant role in shaping these traits, as evidenced by the assessment of genetic variability and heritability in maize inbred lines (Maruthi & Rani, 2015). Based on the provided references, the wet weight and dry weight of maize cobs have been extensively studied as indicators for the selection of superior parent lines. The wet and dry shell weight per 10 cobs, as well as the wet stubble weight per 10 plants, have been identified as significant yield components Jauhari et al. (2021). Additionally, cob length, number of grains per cob, cob diameter, and 100-seed weight have been highlighted as important yield-contributing characters (Gul et al., 2015). Furthermore, harvested dry cobs weight per plant has shown a strong phenotypic correlation with yield, emphasizing its significance as a selection indicator (Sudika et al., 2022).

The highest number of rows in the G23 treatment with an average of 16.75 rows and the least in the G20 treatment with an average of 12.15 rows. Based on the provided references, the number of rows in maize cobs has been identified as a crucial indicator for inbred line selection in maize breeding programs. The earliest cobs appear to be robustly domesticated, having 10-14 rows, suggesting strong selection for increased yield Kennett et al. (2017). Additionally, the number of kernels per row was found to be more in specific maize varieties, indicating the importance of this trait in yield determination (Bastola et al., 2021). Increased kernel row number has been directly associated with increased grain yield, highlighting the importance of this trait in enhancing productivity (Mukri et al., 2022). The number of rows per cob has also been used to assess phenotypic variation in maize genebank accessions, further emphasizing its relevance in characterizing genetic diversity (Kienbaum et al., 2021).

The highest brix value variable was in the G20 treatment with an average of 11.55 and the lowest was in the G19 treatment with an average of 7.45. The sugar content in sweet corn, represented by the Brix value, is a crucial indicator for selecting maize elders. Studies have shown that the Brix values in sweet corn can vary significantly. For instance, in a study on sweet sorghum, Brix values ranged from 14.9% to 23% (Thao et al., 2015). Similarly, in another study, the Brix values in sweet corn kernels of different varieties ranged from 16.3% to 27.4% (Taş & Mutlu, 2021). Furthermore, it has been observed that different sweet corn genotypes possess peaks at different Days After Planting (DAP), with the majority recording the highest Brix value at 20-DAP (Mehta et al., 2017). This variability in Brix values underscores the importance of selecting the appropriate elders based on the specific Brix value suitable for the desired sweet corn variety.



Note: HSD significance is 5%, PH: plant height (cm), EL: Ear length (cm) ED: Ear diameter (cm), FW: fresh weight (g), DW: dry weight (g), NR: number of rows, B: brix (%), CSL: cob stag length (cm).

Figure 1. Heatmap data of correlation

Based on the correlation heatmap data, it shows that there is a correlation between number of rows and ear diameter by 48%. This relationship is due to the genetic and phenotypic factors influencing the development and growth of maize cobs. The correlation between dry weight and wet weight of the cob indicates the relationship between the moisture content and the overall weight of the cob, which is influenced by genetic and environmental factors affecting cob development. Similarly, the correlation between dry weight of the cob and cob length suggests that the size and length of the cob are important factors contributing to its overall dry weight. These relationships are indicative of the complex interplay between genetic and environmental factors in determining the physical characteristics and weight of maize cobs. Reference Lal et al. (2022): This reference discusses the character association and causation analysis of quantitative traits in maize, including the correlation between cob weight and cob length. It provides insights into the relationship between different quantitative traits in maize, which is directly relevant to the correlation between dry weight and wet weight of cob and their relationship with cob length.

The correlation heatmap data indicates a 41% correlation between the number of rows and cob stag length. The correlation coefficient of 0.41 between the number of rows and cob stag length suggests a moderate positive relationship, indicating that as the number of rows increases, the cob stag length also tends to increase. Based on the correlation heatmap data, there is a moderate positive relationship between the number of rows and cob stag length in sweet corn, with a correlation coefficient of 0.41. This suggests that as the number of rows increases, the cob stag length also tends to increase. This finding is consistent with the results of a study by (Rawal et al., 2023), which involved the agromorphological characterization of maize hybrids and estimation of genetic parameters. The experiment laid out in an alpha-lattice design revealed the performance of different maize hybrids, indicating the potential for variation in traits such as cob length based on the number of rows.

This reference by Begum et al. (2016) presents a study on genetic variability, character association, and path analysis in maize. It explores the relationship between various traits in maize, including cob weight, cob length, and the correlation between dry weight and wet weight of the cob. The findings from this study can provide additional evidence and support for understanding the relationship between cob weight, cob length, and the weight of the cob in different states.

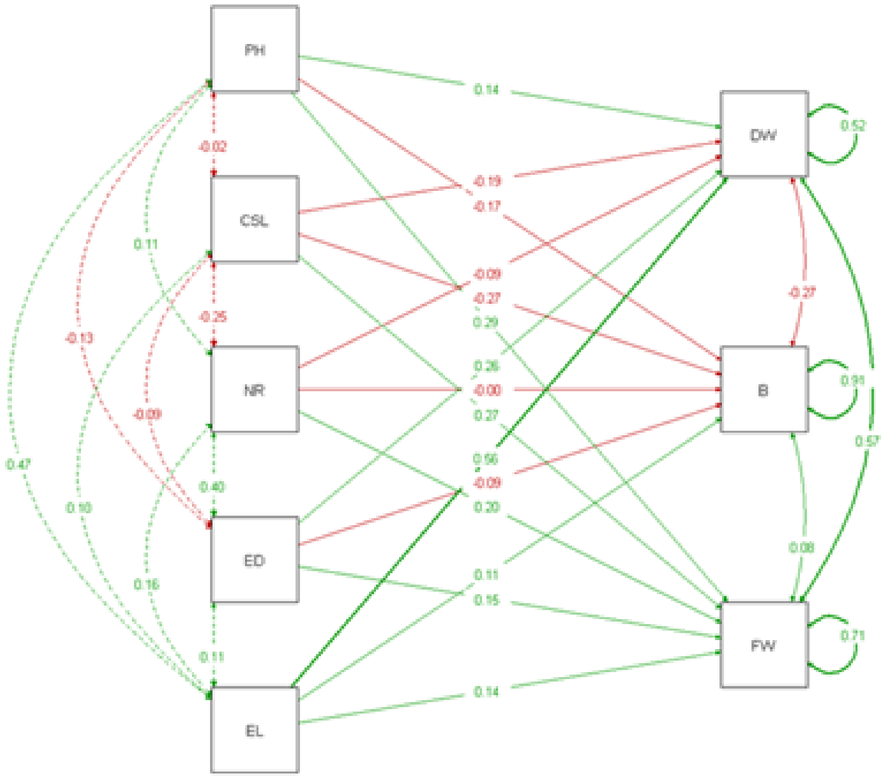


Figure 2. Path analysis diagram depicting the causal relationship of agronomic character

The agronomic character path diagram provides valuable insights into the complex relationships between various agronomic traits and their influence on crop yield. In the context of sweet corn production, the path diagram reveals important relationships between specific traits and the quality and yield of the crop. The path diagram (Figure 2.) indicates that fresh weight, a crucial measure of crop yield, is strongly influenced by several agronomic traits, including plant height, ear length, ear diameter, dry weight, number of plants, row length, brix, and ear stalk. This suggests that these traits play a significant role in determining the fresh weight of sweet corn (Schirrmann et al., 2016). Path analysis allows for the quantification of these relationships, highlighting the importance of considering all of these characteristics when selecting for fresh weight in breeding of sweet corn (Upadhyaya et al., 2019).

Furthermore, the path diagram also reveals that wet weight, another important measure of crop yield, is influenced by factors outside of the characteristics included in the diagram, with a coefficient of 0.71. This finding underscores the presence of external factors that impact wet weight and emphasizes the complexity of determining crop yield in sweet corn production. Moreover, the Brix character, which is essential for obtaining good quality sweet corn, is influenced by ear length and external factors, with a coefficient of 0.91. This highlights the critical role of ear length and external influences in determining the Brix content of sweet corn (Yang et al., 2019). Understanding these relationships is crucial for selecting sweet corn varieties with desirable Brix levels, which contribute to the overall quality of the crop (Upadhyaya et al., 2016).

By considering the influences of specific traits such as ear length, ear diameter, plant height, and external factors on fresh weight, wet weight, Brix content, and dry weight, breeders and agronomists can make informed decisions to improve sweet corn production. This information is essential for selecting sweet corn inbred lines with desirable traits and for optimizing agronomic practices to maximize yield and quality (Subaedah et al., 2021; Taş & Mutlu, 2021).

The path diagram provides valuable insights into the influence of specific agronomic traits on sweet corn production. Notably, the diagram reveals that dry weight is greatly influenced by ear length and ear diameter. The coefficient value for ear length in relation to dry weight is 0.56, indicating a substantial impact of ear length on dry weight. Additionally, the influence of external factors on dry weight is represented by a coefficient value of 0.52, further emphasizing the multifaceted nature of factors affecting dry weight in sweet corn (Sofyan et al. 2019; Fromme et al., 2019).

The influence of specific agronomic traits on sweet corn production, as revealed by the path diagram, underscores the importance of considering a range of factors in breeding and agronomic decision-making. By integrating insights from studies on nutrient uptake, genetic diversity, and environmental influences, breeders and agronomists can make informed decisions to optimize sweet corn production and enhance the performance of specific traits such as dry weight, ultimately contributing to the overall improvement of sweet corn varieties and agronomic practices (Sugiono, 2023; Filho & Toebe, 2020).

The following is a presentation of a cluster of 24 inbred sweet corn lines. This diagram will illustrate the relationship between sweet corn inbred lines based on qualitative and quantitative characters.

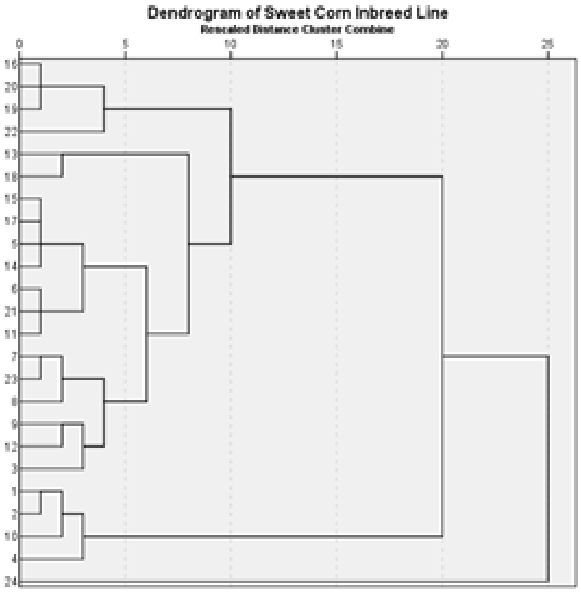


Figure 2. The dendogram of cluster analysis 24 inbred lines of sweet corn

According the dendogram (Figure 2.), it shows that there is a close relationship between the 24 inbred sweet corn lines, forming 2 groups or clusters. G4 shows the furthest genetic relationship from the other genotypes and stands as an independent entity making it suitable to be used as a parent representative. Cluster proximity can influence corn yields by influencing the genetic diversity and population structure of inbred lines of sweet corn. These different groups of inbred lines can then be used in breeding programs to develop new varieties with better yields.

The cluster analysis of 24 inbred lines of sweet corn, as illustrated in Figure 1, demonstrates the segregation of the inbred lines into two primary groups. One group, denoted as G24, is distinct from the second group, which comprises 23 inbred lines. Moreover, the second group is further divided into two subgroups, with the first subgroup encompassing 4 inbred lines (G4, G10, G2 andG1) and the second subgroup comprising 19 inbred lines. Notably, G24 exhibits a substantial genetic distance from the other inbred lines. The genetic diversity among sweet corn inbred lines has been extensively studied using various approaches such as microsatellite markers, agro-morphological traits, and population genomic analysis (Hu et al., 2021; Mehta et al., 2017; Mahato et al., 2018). These studies have provided insights into the genetic structure and diversity of sweet corn inbred lines, which is crucial for breeding programs aimed at developing superior genotypes. Agronomic characters in sweet corn encompass a range of qualitative and quantitative traits, including plant height, ear length, kernel row number, kernel weight, and days to silk, which are vital in determining the overall performance and adaptability of sweet corn in various environments (Hu et al., 2021).

The division of the inbred lines into distinct groups and subgroups based on agronomic characters suggests underlying genetic and phenotypic variations among the sweet corn lines. This has significant implications for breeding programs and the development of improved sweet corn varieties. Understanding the genetic distance between G24 and the other inbred lines is particularly important, as it may indicate unique genetic traits or characteristics that distinguish G24 from the rest of the lines. In the development of hybrid varieties, the selection of inbred lines with a long genetic distance is crucial for achieving heterosis and high yield potential. Research has shown that high-yielding hybrid varieties possess several superior alleles, indicating the importance of genetic distance between parental inbred lines (Huang et al., 2015). Furthermore, the genetic distance between inbred lines has been demonstrated to be predictive of heterosis and combining ability in maize, with more genetically distant inbred lines showing higher potential for heterosis (Perić et al., 2021). This is supported by the finding that hybrids derived from inbred lines with high genetic distance exhibit low seed yield, emphasizing the significance of genetic distance in hybrid performance (Fareghi et al., 2019).

CONCLUSION

The analysis of 24 inbreed lines of sweet corn identifies potential parent lines, including G18, G12, G4, G23, and G20, crucial for breeding programs aiming to enhance specific traits in subsequent generations. G24 is suggested as a viable parent in hybrid breeding programs, requiring a comprehensive understanding of genetic attributes and careful planning. The character of ear weight in sweet corn is intricately linked to other traits, necessitating a holistic selection approach. By integrating knowledge from various sources and considering genetic, morphological, and agronomic aspects, breeders can effectively select for superior cob weight while addressing a broader range of traits contributing to overall ear quality and performance.

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