

Comparison of genetic parameters among selfed lines of population A (PDM 53 x PDM 4441) and population B (HKI 1105 x HKI 323) and random mated population A (PDM 53 x PDM 4441) and random mated population B (HKI 1105 x HKI 323) and identification of transgressive segregants

Comment [R1]: Title seems to be lengthy; can it be precised?

ABSTRACT

The present study was conducted to estimate the genetic variability parameters among selfed lines of population A (PDM 53 x PDM 4441) and population B (HKI 1105 x HKI 323) and also random mated population A (PDM 53 x PDM 4441) and random mated population B (HKI 1105 x HKI 323) using original inbred parents and three commercial checks, HM-4 (National check), CPB 468 (Private check) and TENDER (Private check). The phenotypic variance was higher than the corresponding genotypic variance for all the traits studied. The difference between the GCV and PCV was less indicating less influence of the environment. High heritability coupled with high genetic advance was observed for number of cobs per plant, husked cob weight, dehusked cob weight, baby corn yield with and without husk per plant among selfed populations and a similar trend was observed in random mated populations except for ear length and days to 50 % silking. The most promising transgressive segregant identified can be used in the further breeding programmes.

Keywords: Baby corn, Variability, GCV, PCV, heritability, genetic advance, transgressive segregants

INTRODUCTION

Among the cereal crops over the world, maize ranks first in total production followed by wheat and rice. The Maize plant is a wonderful creation of God because it can be used at any stage of crop growth i.e., early-stage as succulent green fodder, very early cob stage as baby corn, little later stage as cob, and at fully matured stage as maize grain. So, it is called a "Contingent Crop". Baby corn (also known as young corn, mini corn, or candle corn) is the ear of maize (*Zea mays* L.) plant harvested young when the silks have either not emerged or just emerged and no fertilization has taken place. The export of fresh/canned baby corn and its processed foods for baby corn has a large potential for earning foreign exchange, aside from growing demand to meet local needs in the country (Paroda, 2001). Knowledge of genetic variation and accessions relationships is required for any improvement in economically important traits since it aids in understanding the extent of genetic variability, which forms

the basis for effective selection. However, the research on genetic variability studies conducted in baby corn is limited as the grain maize genotypes are grown for baby corn purposes due to the lack of availability of specific genotypes for baby corn production. Thus in the present study, an attempt has been made to measure the extent of genetic variability and heritability for yield and its attributing traits in segregating generations for grain yield in baby corn by using the 21 elite F₆ inbred lines of population A (PDM 53 x PDM 4441) and population B (HKI 1105 x HKI 323) and also random mated population A (PDM 53 x PDM 4441) and random mated population B (HKI 1105 x HKI 323) and to identify the transgressive segregants among the selfed lines and random mated populations.

MATERIALS AND METHODS:

During summer 2021, the experiment was carried out at the University of Agricultural Science Dharwad, India. The experimental material included 21 elite F₆ inbred lines from two different Populations: Population A (PDM 53 x PDM 4441) and Population B (HKI 1105 x HKI 323), as well as original inbred parents and three commercial checks, namely HM-4 (National check), CPB 468 (Private check), and TENDER (Private check). The sowing was done in a randomized complete block design with two replications, each of which had 21 inbred lines, 2 parents, and 3 checks, with each row measuring 3m in length. For random mated populations *viz.*, population A (PDM 53 x PDM 4441) and population B (HKI 1105 x HKI 323) unreplicated design was used. The distance between two rows was 60 centimeters, while the distance between plants was 20 centimeters with a population size of 500 plants. The crop was grown in accordance with the recommended set of cultivation practices. The observations on various baby corn traits such as days to 50% silking, number of cobs per plant, husked weight of baby corn, dehusked weight of baby corn, and baby corn yield without husk per plant were taken from 10 plants of each genotype selected randomly and observations in random mated plants was taken from 70 randomly selected plants. (Table 1)

STATISTICAL ANALYSIS

The data was analysed using INDOSTAT software version 9.2, with the analysis of variance (ANOVA) procedures described by Panse and Sukhatme (1985), and the mean, standard error, and range determined according to Singh and Chaudhary (1979). According to Sivasubramanian and Madhavamenon (1973), phenotypic and genotypic coefficients of variation (PCV and GCV) were classified as low (0-10%), moderate (10-20%), and large (>30%) and were as per Burton (1952). As indicated by Robinson *et al.*, (1949) heritability in

a broad sense was calculated as the ratio of genotypic variance to phenotypic variance and classified as low (0-30%), moderate (30-60%), and high (>60%).

The formulae provided by Robinson *et al.*, (1949) were used to determine genetic advance (GA) and genetic advance as a percent of mean (GAM) (1949). According to Robinson *et al.*, the GA as percent of mean was classified as low (0-10 percent), moderate (10-20 percent), and high (>20 percent) (1949).

For unreplicated design parental mean was used to calculate the GCV, PCV, heritability, genetic advance and genetic advance as percent of mean.

The transgressive segregants were identified both in selfed and random mated populations based on mean plus one standard deviation and mean plus two standard deviation. To estimate the transgressive segregants among selfed lines of Population A (PDM 53 x PDM 4441) and Population B (HKI 1105 x HKI 323), the comparison was made with respect to the mean of parents by a critical difference at 5 % and 1 % level.

Results and discussion

In crop breeding variability plays an important role. Analysis of variance (Table 2 and Table 3) was performed to test the significance of difference among the genotypes for the characters studied. The results obtained from variance analysis for all entries, including original inbred parents and checks for eight quantitative characters showed that the treatment variances were highly significant for all the characters and are shown in table 2. This indicates the presence of substantial variability among the inbred lines of Population A (PDM 53 x PDM 4441) and population B (HKI 1105 x HKI 323).

These results are consistent with the findings of Viola *et al.* (1999), Suvarna *et al.* (2008), and Rajesh *et al.* (2013), where major differences among the inbreds for all the characters were identified. However, when it comes to describing all of the intrinsic genetic variability, analysis of variance is unconvincing. To determine the genetic nature of a trait, it is important to calculate PCV, GCV, heritability, and genetic advance.

The range of variability in germplasm increases the potential for improvement through selection. The comparison of results revealed a higher range for yield and its components, implying that both populations, Population A (PDM 53 x PDM 4441) and Population B (PDM 53 x PDM 4441), have scope for improvement through selection (HKI 1105 x HKI 323).

One of the ways in which the variability of these characters can be assessed is through a simple approach of examining the range of variation. The Range of variation observed for all the traits indicated the presence of a sufficient amount of variation among the inbred lines for all the characters studied. The range in the values reflects the amount of phenotypic variability which is not very reliable since it includes genotypic, environmental, and genotype x environmental interaction components. Further, the phenotype of crop is influenced by additive gene effect (heritable), dominance (non-heritable) and epistatic (non-allelic interaction). Hence, it becomes necessary to split the observed variability into phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) which indicates the extent of variability existing for various traits.

For all traits, the magnitude of GCV was lower than that of PCV among 21 inbred lines of Population A (PDM 53 x PDM 4441). (Table 4) GCV and PCV (<10 percent) were shown to be lower for days to 50 percent silking, ear length, and ear diameter. Vaghela *et al.* (2009), Chauhan and Mohan (2010), Manigopa and Rameshwar (2012), and Ayodeji and Comfort (2019) all found similar results for these traits. GCV and PCV were found to be moderate (10-20%) for number of cobs per plant, cob weight with husk, and cob weight without husk. Vaghela *et al.* (2009), Chauhan and Mohan (2010), and Manigopa and Rameshwar (2011) also made similar observations (2012). Whereas baby corn yield with husk per plant and without husk per plant recorded high GCV and PCV (>20 %). These findings were in agreement with Vaghela *et al.* (2009), Reddy *et al.* (2010), Rajesh *et al.* (2013), Suhaisini *et al.* (2016), Niji *et al.* (2018).

In the case of 21 inbred lines of Population B (HKI 1105 x HKI 323), the magnitude of GCV was low as compared to that of PCV for all the traits. (Table 4). Lower values for GCV and PCV (<10 %) were noticed for days to 50 % silking, ear length, and ear diameter. Similar results were reported by Vaghela *et al.* (2009), Chauhan and Mohan (2010), Manigopa and Rameshwar (2012), Ghosh *et al.* (2014), Ayodeji and Comfort (2019) for these traits. For number of cobs per plant and cob weight without husk moderate (10-20 %) GCV and PCV were observed. Similar observations were made by Chauhan and Mohan (2010) and Manigopa and Rameshwar (2012). Whereas cob weight with husk, baby corn yield with husk per plant and without husk per plant recorded high GCV and PCV (>20 %). These findings were in agreement with Vaghela *et al.* (2009), Reddy *et al.* (2010), Rajesh *et al.* (2013), Suhaisini *et al.* (2016), Niji *et al.* (2018), Chavan *et al.* (2020).

When compared to selfed lines the magnitude of variability observed was more in random mated population A (PDM 53 x PDM 4441) and random mated population B (HKI 1105 x

HKI 323). (Table 5). The GCV and PCV (<10 %) were low for days to 50 % silking and ear length in both the random mated populations. These results were in accordance with Ghosh *et al.* (2014), Dagla *et al.* (2015), Meena *et al.* (2016). Moderate GCV and PCV values were observed for number of cobs per plant in random mated population A (PDM 53 x PDM 4441) and cob weight without husk in random mated population B (HKI 1105 x HKI 323). High GCV and PCV values were observed for ear diameter, cob weight without husk, baby corn yield with husk per plant and baby corn yield without husk per plant in random mated population A (PDM 53 x PDM 4441) and in random mated population B (HKI 1105 x HKI 323) number of cobs per plant, baby corn yield with husk per plant and baby corn yield without husk per plant had high GCV and PCV values.

Comment [R2]: I italic

Heritability in broad sense is not the true indicator of inheritance of traits. Since only additive component of genetic variance is efficiently transferred from generation to generation. Therefore, heritability in broad sense may mislead in judging the effectiveness of selection for the trait. Considering heritability in a broad sense along with genetic advance may reveal the presence of specific components (additive or non-additive) of genetic variance and thus, helps in judging the effectiveness of selection for the trait more accurately. High heritability accompanied with high genetic advance indicates the prevalence of additive gene effects and hence, selection would be effective for such traits.

Number of cobs per plant, cob weight with husk, cob weight without husk, and baby corn yield with husk and without husk per plant among 21 inbred lines of Population A (PDM 53 x PDM 4441) and Population B were found to have high heritability and genetic advance (HKI 1105 x HKI 323). This shows that additive gene action predominates and that phenotypic selection is possible. Results are in accordance with findings of Chauhan and Mohan (2010), Manigopa and Rameshwar (2012), Suhaisini *et al.* (2016). Ear length had high heritability and moderate genetic advance among 21 inbred lines of Population A (PDM 53 x PDM 4441), indicating that it is driven by non-additive gene action and might be exploited through heterosis breeding. The result was in accordance with findings of Begum *et al.* (2016), Sanjay *et al.* (2017), Niji *et al.* (2018).

Whereas in random mated population A (PDM 53 x PDM 4441) and random mated population B (HKI 1105 x HKI 323), number of cobs per plant, ear diameter, cob weight with husk and cob weight without husk, baby corn yield with husk and without husk per plant showed high heritability coupled with high genetic advance. The results were on par with Vaghela *et al.* (2009), Chauhan and Mohan (2010), and Manigopa and Rameshwar (2012).

Comparison of mean values among selfed lines of Population A (PDM 53 x PDM 4441) and Population B (HKI 1105 x HKI 323) and random mated population A (PDM 53 x PDM 4441) and population B (HKI 1105 x HKI 323) are presented in table 6 and 7 respectively.

Number of cobs per plant, cob weight with husk, cob weight without husk, baby corn yield without husk per plant, and baby corn yield with husk per plant all showed higher mean values among 21 inbred lines of Population A (PDM 53 x PDM 4441), while ear length and ear diameter showed higher mean values among 21 inbred lines of Population B. (HKI 1105 x HKI 323).

For days to 50% silking, number of cobs per plant, ear length, cob weight with husk, cob weight without husk, and baby corn yield per plant with husk and without husk random mated population A (PDM 53 x PDM 4441) had higher mean values than random mated population B (HKI 1105 x HKI 323) whereas for ear diameter, random mated population A (PDM 53 x PDM 4441) had lower mean value than random mated population B (HKI 1105 x HKI 323).

The comparison of variability in both selfed populations and random mated populations indicated that because allelic frequency differences occur in random mated populations and the pool of gametes originating from male and female is different when compared to the pollen source in selfed populations, the variability found was higher in random mated populations than in selfed populations.

The conventional view of hybridization is to recombine favorable traits in a new hybrid derivative that has already been detected in two parents. Because transgressive segregants are found in segregating generations, the concept of transgressive segregation can be employed as a positive tool in plant breeding. Due to the accumulation of favorable genes from both parents as a result of recombination, the performances of transgressive segregants fall outside the range of their parents. Complementary gene activity is thought to be the primary cause of quantitative character transgression, however, overdominance and epistasis also play a role (Rieseberg *et al.* 1999).

Genetic recombination between both linked and unlinked alleles is required to create the requisite transgressive segregants (Briggs and Allard, 1953). According to studies on transgressive segregation in the segregating generation, parents do not represent the extremes in terms of intended character intensities. If some genes for greater expression of a character are missing from the promising parent's genotype but present in the donor parent's, some hybrid descendants resulting from the cross of these parents may obtain a serendipitous gene combination with a larger influence than either of the parents (Gardner, 1968).

In this study, transgressants for the seven quantitative traits were recorded in a random mated Population A (PDM 53 x PDM 4441) in F₆ generation. When mean plus one standard deviation was taken into account, the trait husked yield (21.43 %) had the highest frequency percentage of transgressive segregants, followed by husked weight (21.42 %) and number of cobs per plant (18.57 %), whereas when mean plus two standard deviation was taken into account, the trait ear length (8.57 %) had the highest frequency percentage of transgressive segregants followed by husked weight (5.71 %), days to 50 % silking (4.29 %) and dehusked yield (4.29 %). (Table 8)

Comparably in random mated population B (HKI 1105 x HKI 323), the highest frequency of transgressive segregants were recorded for the husked weight (27.14 %) followed by days to 50 % silking (24.28 %) and dehusked weight and dehusked yield (21.43 %) upon consideration of mean plus one standard deviation whereas for mean plus two standard deviation ear length (8.57 %) recorded the highest frequency of transgressive segregants followed by husked weight (5.71 %) and days to 50 % silking (4.29 %) and dehusked weight (4.29 %). (See Table 9). Similar studies were reported by, Tagad *et al* (2020) in Soybean, Gibely R. H. (2021) in cotton.

Comment [R3]: *et al.*

Similarly, the frequency percentage of transgressive segregants was also worked out among 21 inbred lines of Population A (PDM 53 x PDM 4441) and Population B (HKI 1105 x HKI 323) and are presented in table 10 and table 11 respectively.

Based on mean plus one standard deviation, the highest frequency of transgressive segregants was found in dehusked yield (26.92%), followed by husked weight (23.07%), days to 50% silking (19.23%), number of cobs per plant (19.23%), and ear diameter (19.23%) among selfed lines of Population A (PDM 53 x PDM 4441), whereas for mean plus two standard deviation, the highest frequency of transgressive segregants were found for ear diameter (11.53 %) followed by ear length (7.69 %), days to 50 % silking (3.85 %) and number of cobs per plant (3.85 %).

On the basis of mean plus one standard deviation, the highest frequency of transgressive segregants were found in selfed lines of Population B (HKI 1105 x HKI 323) for ear length (23.07 %) and husked yield (23.07 %), followed by days to 50 percent silking (19.23 %) and ear diameter (19.23 %). Number of cobs per plant (3.85 %), ear length (3.85 %), and ear diameter (3.85 %) had the highest frequency percent of transgressive segregants for mean plus two standard deviation, while no transgressive segregants were found for the other traits.

Table 12 and 13, respectively shows the transgressive segregants among the 21 elite inbred lines (F_6) of population A (PDM 53 x PDM 4441) and population B (HKI 1105 x HKI 323) for economically important characters of baby corn that outraged both parents when critical differences at 1% and 5% significance were considered.

Table 12 shows the *per se* performance and percent improvement of F_6 inbreds of population A (PDM 53 x PDM 4441) over their parents for economically important baby corn traits. For days to 50% silking, 16 and 4 positive transgressive segregants were identified in the parents of Population A, namely PDM 53 and PDM 4441. For this trait, P-19, P-13, and P-36 were the top three positive transgressive segregants. 14 and 10 positive transgressive segregants were obtained over the parents PDM 53 and PDM 4441, respectively, for number of cobs per plant. For this characteristic, P-34, P-24, and P-38 were the top three positive transgressive segregants. 14 and 12 positive transgressive segregants for the trait dehusked weight of baby corn were found over PDM 53 and PDM 4441, respectively. The top three transgressive segregants for dehusked weight of baby corn were the inbred lines P-11, P-19, and P-48. Only three positive transgressive segregants were obtained over both parents for baby corn dehusked yield per plant, namely PDM 53 and PDM 4441.

The *per se* performance and percent improvement of F_6 inbreds of population A (PDM 53 x PDM 4441) over their respective parents for economically important traits of baby corn are presented in table 13. For the trait days to 50 % silking, 17 and 9 positive transgressive segregants were obtained over the parents *viz.*, HKI 1105 and HKI 323. The top three positive transgressive segregants for this trait were H-118, H-16, and H-19. For the trait number of cobs per plant, there were 16 positive transgressive segregants observed over the parent HKI 1105, while none were obtained over the parent HKI 323. The top three positive segregants for this trait were inbred lines H-35, H-91, and H-106. Over the parent HKI 1105 and HKI 323, there were 20 and 4 positive transgressive segregants for dehusked weight of baby corn, respectively. H-91, H-99, and H-29 were the top three transgressive segregants for this trait. whereas 17 positive transgressive segregants were found over both parents HKI 1105 and HKI 323 for dehusked yield of baby corn. H-06, H-32, and H-19 were the top three transgressive segregants found for this trait. Similar studies on the identification of transgressive segregants were reported by Alkuddsi *et al.* (2013), Ajay *et al.* (2014), Kenchareddi *et al.* (2014), Mohan *et al.* (2018), Anusha *et al.* (2019), Pattar and Deshpande (2019), Archana *et al.* (2021).

The findings revealed that the parents involved in the study differed for many genes which resulted in creating large amount of genetic variability for yield and yield related components

in segregating generations. The highest frequency of transgressive segregants were obtained for husked yield, dehusked yield, husked weight and days to 50 % silking revealing the contribution of favourable alleles from the parents. The promising transgressive segregants having a combination of desirable attributes must be included in breeding programs.

COMPETING INTERESTS DISCLAIMER:

Authors have declared that no competing interests exist. The products used for this research are commonly and predominantly use products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

References:

- Ajay BC, Byregowda M, Prashanth BH, Veera KGN. and Reena M. Variability and transgressive segregation for yield and yield contributing traits in pigeon pea crosses. *Electronic. J. Plant Breed.*, 2014; 5(4): 786-791.
- Alan O, Kinaci G, Kinaci E, Kutlu I, Basciftci Z B, Sonmez K. and Evrenosoglu Y. Genetic variability and association analysis of some quantitative characters in sweet corn. *Not. Bot. Horti Agrobot.*, 2013; 41(2): 404-413.
- Alkuddsi Y, Patil SS, Manjula SM, Patil BC, Nadaf HL and Nandihali BS. Studies of heterosis for exploitation of heterotic boxes in seed cotton yield and its attributing characters. *Cotton Genomics and Genetics*, 2013; 4:45-59.
- Anusha G, Rasal PN, Patil MR, Lavanya B, Nitya MB. and Shankaraiah K. Studies on transgressive segregation in F₂ generation in desi cotton (*Gossypium arboreum L.*). *Int. J. Pure App. Biosci.*, 2019; 7 (1): 172-176.
- Archana KA Deshpande S.K, Bhat JS, Kachapur RM, Mummigatti UV. and Hosamani J. Identification of transgressive segregants among newly derived F₄ inbred maize lines (*Zea mays L.*) for baby corn characteristics. *J. Pharmacogn. Phytochem.*, 2021; 10(2): 404-411.
- Ayodeji A. and Comfort AA. Genetic variability, heritability and genetic advance in shrunken-2 super-sweet corn (*Zea mays L. saccharata*) populations. *J. plant breed. crop sci.*, 2019; 11(4): 100-105.

- Begum S, Ahmed A, Omy S.H, Rohman M.M, and Amiruzzaman M. Genetic variability, character association and path analysis in maize (*Zea mays* L.). *Bangladesh J. Agril. Res.*, 2016; 41(1): 173-182.
- Briggs FN, Allard RW. The current status of the backcross method of plant breeding. *Agron. J.*, 1953; 45: 131-138.
- Burton GW. and Devane DE. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material [1](#). *Agronomy journal*, 1953; 45(10): 478-481.
- Chauhan SK. and Mohan J, Estimates of variability, heritability and genetic advance in baby corn. *Indian J. Hort.*, 2010; (67): 238-241.
- Chavan S, Bhadru D, Swarnalatha V. and Mallaiah B. Studies on genetic parameters, correlation and path analysis for yield and yield attributing traits in sweet corn (*Zea mays* L. *saccharata*). *Int.J.Curr.Microbiol.App.Sci.*, 2020; 9(7): 1725-1734.
- Gardner EJ. Principle of Genetics. John Wiley and sons, New York, 1968; pp. 405.
- Ghosh A, Subba V, Roy, A, Ghosh A. and Kundagrami S. Genetic variability and character association of grain yield components in some inbred lines of Maize (*Zea mays* L.). *J. Agric. Nat. Resour.*, 2014; 1: 34-39.
- Gibely RH, Estimation of genetic variance components and identification of transgressive segregants for two intraspecific extra-long staple cotton crosses. *Menoufia Journal of Plant Production*, 2021; 6(1): 53-70.
- Kencharaddi HG, Patil RS, Mohan NB, Praveenkumar B, Kumar KJY. and Chowkimath A. Identification of superior segregants in early segregating generations of upland cotton (*Gossypium hirsutum* L). *Plant Archives*, 2013; 13(1): 45-49.
- Manigopa C. and Rameswar PS, Genetic Component in Baby Corn (*Zea mays* L). *Plant Archives*, 2012; 12(1): 291-294.
- Mohan KNV, Katageri IS, Sunil KG and Anjan GS. Transgressive segregation for fibre quality, seed cotton yield and its component traits in *Gossypium barbadense* L. Cotton. *Int. J. Curr. Microbiol. App. Sci.*, 2018; 7(1): 1040-1051.
- Niji M S, Ravikesavan R, Ganesan KN. and Chitdeshwari T. Genetic variability, heritability and character association studies in sweet corn (*Zea mays* L. *saccharata*). *Electron. J. Plant Breed.*, 2018; 9 (3): 1038 – 1044.

Comment [R4]: 1

- Panse VG. and Sukhatme PV. 1954. Statistical methods for agricultural workers. Statistical methods for agricultural workers.
- Paroda RS. 2001. Bade Kuposhan ka Jawab Nahni Makka (Hindi). *Kheti*, 2(6): 33-34.
- Pattar VK, Deshpande SK. Combining ability studies for yield and quality traits in Baby Corn (*Zea mays* L.) *J. Pharmacogn. Phytochem.*, 2019; 8(4):1116-1119.
- Rajesh V, Kumar SS, Reddy VN. and Sankar AS. Studies on genetic variability, heritability and genetic advance estimates in newly developed maize genotypes (*Zea mays* L.). *Int. J. Appl. Biol. Pharm.*, 2013; 4(4): 00.
- Reddy VR, Jabeen F, Sudarshan MR. Rao AS, Studies on genetic variability, heritability, correlation and path analysis in maize (*Zea mays* L.) over locations. *Int. J. Appl. Biol. Pharm.*, 2012; 4(1): 00.
- Rieseberg LH, Archer MA and Wayne RK. Transgressive segregation, adaptation and speciation. *Heredity*, 1999, 83: 363-372.
- Robinson HF, Comstock RE. and Harvey PH. Estimates of heritability and the degree of dominance in corn. *Agron. J.*, 1949; 41: 353:359.
- Sanjay KR, Surya KG, Raju K, Chitra BK, Manoj S. and Ujjawal KSK. Study of Yield and Yield Attributing Traits of Maize. *American Journal of Food Science and Health.*, 2017; 3(6): 123-129.
- Singh RK. and Chaudhary BD. Variance and covariance analysis, biometrical methods in quantitative genetic analysis, 3rd Edn. Kalyani Publishers, New Delhi. 1979; 00:39-69.
- Sivasubramanian V. and Madhavamenon P. Path analysis for yield and yield components of rice. *Madras Ag. Journal.*, 1973; 60: 217-1221.
- Suhaisini B, Ravikesavan R. and Yuvaraja A. Genetic variability and correlation among yield and yield contributing traits in sweet corn. *Madras Ag. Journal.*, 2016; 103(10-12): 293-296.
- Suvarna, Nehru SD. and Manjunath A, Variability, correlation and path coefficient analysis in maize under dry land condition. *Env. Eco.*, 2008; 26(4): 2296-2299.
- Tagad BA, Girase VS, Rohini YP. and Barhate KK. Identification of desirable recombinants through transgressive segregation and association analysis in soybean, 2020, *Int.J. Curr. Microbiol. App.Sci.*, (2020) 9(12): 633-639.

Vaghela KP, Patel DB, Parmar D. and Macwana SS. Genetic variability studies for baby corn (*Zea mays* L). *Res. Crops*, 2009; 10(1): 132-134.

Table. 1 F₆ inbred lines used for evaluation programme:

Sl. No.	PDM population (Population A) (PDM 4441 x PDM 53)	Sl. No.	HM-4 population (Population B) (HKI 1105 x HKI 323)
1	P-34	1	H-95
2	P-45	2	H-91
3	P-19	3	H-59
4	P-15	4	H-08
5	P-48	5	H-16
6	P-27	6	H-35
7	P-24	7	H-118
8	P-32	8	H-05
9	P-38	9	H-49
10	P-10	10	H-13
11	P-11	11	H-28
12	P-13	12	H-61
13	P-47	13	H-57
14	P-50	14	H-99
15	P-39	15	H-19
16	P-14	16	H-32
17	P-04	17	H-106
18	P-37	18	H-46
19	P-17	19	H-22
20	P-12	20	H-06
21	P-36	21	H-29
Checks			
1	HM-4 (National check)		
2	CPB 468 (Private check)		
3	TENDER (Private check)		

21 F₅ families of population A (PDM 53 x PDM 4441) and 21 F₅ families of population B (HKI 1105 x HKI 323) during kharif 2020 were random mated in isolation; seeds representing population A and population B were harvested separately to derive new population A and new population B.

Table 2: Analysis of variance for 8 speciality traits of baby corn among 21 elite inbred lines (F₆) of Population A (PDM 53 x PDM 4441)

Source of variation	df	Days to 50% silking	Number of cobs per plant	Ear length (cm)	Ear diameter (cm)	Cob weight with husk (g)	Cob weight without husk (g)	Baby corn yield with husk per plant (g)	Baby corn yield without husk per plant (g)
Replication	1	0.69	0.03	0.08	0.05	0.52	0.01	26.38	24.38
Genotypes	25	7.48**	0.28**	0.62**	0.01**	49.96**	2.29**	1464.95**	83.88**
Error	25	0.37	0.01	0.04	0.02	1.82	0.22	175.97	14.12

** Significant at 1% level

* Significant at 5 % level

Table 3: Analysis of variance for 8 speciality traits of baby corn among 21 elite inbred lines (F₆) of Population B (HKI 1105 x HKI 323)

Source of variation	df	Days to 50% silking	Number of cobs per plant	Ear length (cm)	Ear diameter (cm)	Cob weight with husk (g)	Cob weight without husk (g)	Baby corn yield with husk per plant(g)	Baby corn yield without husk per plant(g)
Replication	1	0.17	0.01	0.09	0.03	1.28	0.06	55.89	0.53
Genotypes	25	9.28**	0.39**	0.53**	0.01**	306.65**	2.77**	2106.19**	52.79**
Error	25	0.49	0.03	0.11	0.02	6.69	0.12	176.25	3.29

** Significant at 1% level

* Significant at 5 % level

Table 4: Comparison of genetic parameters for different traits of baby corn among 21 selfed inbreds of population A (PDM 53 x PDM 4441) and population B (HKI 1105 x HKI 323) including original inbred parents and checks

Character	Selfed inbred lines of F ₆ population	Mean	Range		σ^2_g	σ^2_p	GCV	PCV	h^2_{bs}	GA	GAM
			Minimum	Maximum							
Days to 50% silking	Population A	54.46	51.00	59.00	3.55	3.92	3.46	3.63	90.51	3.69	6.78
	Population B	55.09	51.50	59.00	4.39	4.89	3.80	4.01	89.91	4.09	7.43
Number of cobs per plant	Population A	3.37	2.40	4.10	0.13	0.14	10.81	11.27	92.03	0.71	21.37
	Population B	3.36	2.45	4.40	0.18	0.21	12.76	13.80	85.44	0.82	24.30
Ear length (cm)	Population A	9.44	8.57	10.98	0.29	0.32	5.71	6.06	88.65	1.04	11.07
	Population B	9.57	8.18	10.53	0.21	0.32	4.81	5.95	65.34	0.78	8.01
Ear diameter (cm)	Population A	1.34	1.27	1.48	0.002	0.004	3.52	4.83	53.01	0.07	5.28
	Population B	1.36	1.25	1.50	0.002	0.004	3.97	4.67	72.32	0.09	6.96
Cob weight with husk (g)	Population A	49.01	35.25	55.03	24.07	25.89	10.01	10.39	92.96	9.74	19.88
	Population B	39.35	14.90	54.25	149.98	156.67	31.12	31.80	95.72	24.68	62.73
Cob weight without husk (g)	Population A	10.53	7.74	11.78	1.03	1.25	9.65	10.64	82.32	1.90	18.03
	Population B	9.30	10.74	6.40	1.32	1.44	12.37	12.93	91.58	2.26	24.40
Baby corn yield with husk per plant(g)	Population A	139.85	62.62	167.20	644.48	820.46	18.15	20.48	78.55	46.35	33.14
	Population B	111.58	39.54	161.07	964.96	1141.28	27.83	30.27	84.55	58.84	52.73
Baby corn yield without husk per plant(g)	Population A	25.99	12.75	33.89	34.88	48.99	22.71	26.92	71.18	10.26	39.48
	Population B	23.61	10.36	30.27	24.75	28.04	21.07	22.42	88.52	9.62	40.76

Table 5: Comparison of genetic parameters for different traits of baby corn in random mated population A (PDM 53 x PDM 4441) and random mated population B (HKI 1105 x HKI 323)

Character	Random mated F ₆ population	Mean	Range		σ^2_g	σ^2_p	GCV	PCV	h^2_{bs}	GA	GAM
			Minimum	Maximum							
Days to 50% silking	Population A	56.07	51.00	61.00	6.09	4.01	3.57	4.40	65.87	3.35	5.97
	Population B	54.37	50.00	60.00	3.57	5.86	3.42	4.45	60.99	3.04	5.59
Number of cobs per plant	Population A	3.14	1.25	4.10	0.27	0.31	16.53	17.76	86.68	1.00	31.71
	Population B	3.07	1.54	4.50	0.40	0.43	20.48	21.34	92.15	1.24	40.51
Ear length (cm)	Population A	9.75	8.55	11.63	0.49	0.27	5.38	7.21	55.51	0.80	8.25
	Population B	9.34	7.55	11.00	0.25	0.44	5.33	7.10	56.48	0.77	8.26
Ear diameter (cm)	Population A	1.3	1.15	1.55	0.02	0.03	5.28	6.85	59.19	0.11	8.36
	Population B	1.32	1.18	1.50	0.01	0.02	4.57	6.40	50.90	0.09	6.71
Cob weight with husk (g)	Population A	60.56	31.75	102.30	145.16	212.05	19.88	24.04	68.45	20.54	33.91
	Population B	56.36	26.80	82.80	71.36	138.97	14.98	20.91	51.34	12.47	22.12
Cob weight without husk (g)	Population A	13.01	7.70	24.50	11.70	10.52	24.95	26.33	89.58	6.32	48.60
	Population B	12.20	7.70	17.05	2.54	3.65	13.08	15.68	69.63	2.74	22.50
Baby corn yield with husk per plant(g)	Population A	191.72	95.25	332.48	2591.07	2324.66	26.54	25.15	89.71	94.08	49.06
	Population B	121.12	43.70	200.40	835.27	866.88	23.86	24.30	96.35	58.44	48.24
Baby corn yield without husk per plant(g)	Population A	41.14	23.85	87.80	140.17	114.71	26.03	28.77	81.83	19.96	48.51
	Population B	37.45	12.35	69.94	71.59	114.04	22.58	28.50	62.78	13.81	36.87

Table 6: Comparison of mean values of different traits of baby corn among 21 new inbred lines (F₆) of Population A (PDM 53 x PDM 4441) and among 21 new inbred lines (F₆) of Population B (HKI 1105 x HKI 323)

Sl. No.	Population	Days to 50% silking	Number of cobs per plant	Ear length (cm)	Ear diameter (cm)	Cob weight with husk (g)	Cob weight without husk (g)	Baby corn yield with husk per plant(g)	Baby corn yield without husk per plant(g)
1	Population A (PDM 53 x PDM 4441)	54.46	3.37	9.44	1.34	49.01	10.53	139.85	25.99
2	Population B (HKI 1105 x HKI 323)	55.09	3.36	9.58	1.36	39.35	9.26	111.58	23.62

Table 7: Comparison of mean values of different traits of baby corn in random mated Population A (PDM 53 x PDM 4441) and random mated Population B (HKI 1105 x HKI 323)

Sl. No.	Population	Days to 50% silking	Number of cobs per plant	Ear length (cm)	Ear diameter (cm)	Cob weight with husk (g)	Cob weight without husk (g)	Baby corn yield with husk per plant(g)	Baby corn yield without husk per plant(g)
1	Population A (PDM 53 x PDM 4441)	56.07	3.14	9.75	1.30	60.56	13.01	191.72	41.14
2	Population B (HKI 1105 x HKI 323)	54.37	3.07	9.34	1.32	56.36	12.20	121.12	37.45

Table 8: Transgressive segregants identified in the random mated Population A (PDM 53 x PDM 4441) for various baby corn traits

Sl. No.	Characters	Mean plus one standard deviation			Mean plus two standard deviation		
		Threshold value	Number of plants above threshold value	Frequency percentage of transgressive segregants	Threshold value	Number of plants above threshold value	Frequency percentage of transgressive segregants
1	Days to 50 % silking	58.08	12	17.14	60.08	3	4.29
2	Prolificacy	3.66	13	18.57	4.18	0	0
3	Husked weight	72.61	15	21.42	84.66	4	5.71
4	Dehusked weight	16.26	14	20.00	19.50	2	2.89
5	Length	10.27	14	20.00	10.80	6	8.57
6	Husked yield	239.94	12	21.43	288.15	1	1.43
7	Dehusked yield	51.85	13	18.57	62.56	3	4.29

Comment [R5]: Ear length

Table 9: Transgressive segregants identified in the random mated Population B (HKI 1105 x HKI 323) for various baby corn traits

Sl. No.	Characters	Mean plus one standard deviation			Mean plus two standard deviation		
		Threshold value	Number of plants above threshold value	Frequency percentage of transgressive segregants	Threshold value	Number of plants above threshold value	Frequency percentage of transgressive segregants
1	Days to 50 % silking	56.25	17	24.28	58.13	3	4.29
2	Prolificacy	3.70	13	18.57	4.32	1	1.43
3	Husked weight	64.81	19	27.14	73.26	4	5.71
4	Dehusked weight	13.78	15	21.43	15.37	3	4.29
5	Length	9.84	13	18.57	10.30	6	8.57
6	Husked yield	150.02	10	14.29	178.92	1	1.43
7	Dehusked yield	45.92	15	21.43	54.37	1	1.43

Comment [R6]: deviations

Comment [R7]: ear length

Table 10: Transgressive segregants identified among 21 elite inbreds of Population A (PDM 53 x PDM 4441) for various baby corn traits

Sl. No.	Characters	Mean plus one standard deviation			Mean plus two standard deviation		
		Threshold value	Number of inbreds above threshold value	Frequency percentage of transgressive segregants	Threshold value	Number of inbreds above threshold value	Frequency percentage of transgressive segregants
1	Days to 50 % silking	56.34	5	19.23	58.22	1	3.85
2	Prolificacy	3.73	5	19.23	4.09	1	3.85
3	Husked weight	53.91	6	23.07	58.81	0	0
4	Dehusked weight	11.55	3	11.53	12.57	0	0
5	Ear Length	9.98	3	11.53	10.52	2	7.69
6	Ear diameter	1.39	5	19.23	1.44	3	11.53
7	Husked yield	165.24	3	11.53	190.63	0	0
8	Dehusked yield	31.9	7	26.92	37.81	0	0

Comment [R8]: deviations

Comment [R9]: ear length

Table 11: Transgressive segregants identified among 21 elite inbreds of Population B (HKI 1105 x HKI 323) for various baby corn traits

Sl. No.	Characters	Mean plus one standard deviation			Mean plus two standard deviation		
		Threshold value	Number of inbreds above threshold value	Frequency percentage of transgressive segregants	Threshold value	Number of inbreds above threshold value	Frequency percentage of transgressive segregants
1	Days to 50 % silking	57.19	5	19.23	59.29	0	0
2	Prolificacy	3.79	3	11.53	4.22	1	3.85
3	Husked weight	51.60	3	11.53	63.85	0	0
4	Dehusked weight	10.45	3	11.53	11.60	0	0
5	Ear Length	10.03	6	23.07	10.49	1	3.85
6	Ear diameter	1.41	5	19.23	1.46	1	3.85
7	Husked yield	142.64	6	23.07	173.70	0	0
8	Dehusked yield	28.59	4	15.38	33.57	0	0

Comment [R10]: deviations

Comment [R11]: ear length

Table 12: Exploitation of recombinational variability and derivation of transgressive segregants for economically important traits of baby corn among selfed lines of population A (PDM 53 x PDM 4441)

Sl. No.	F ₆ lines of population A	Days to 50 % silking			F ₆ lines of population A	Number of cobs per plant			F ₆ lines of population A	Dehusked weight (g)			F ₆ lines of population A	Dehusked yield of baby corn per plant		
		Mean	% imp over inferior parent PDM 53	% imp over better parent PDM 4441		Mean	% imp over inferior parent PDM 53	% imp over better parent PDM 4441		Mean	% imp over inferior parent PDM 53	% imp over better parent PDM 4441		Mean	% imp over inferior parent PDM 53	% imp over better parent PDM 4441
1	P-19	51.00	-8.11**	-4.67**	P-34	3.90	25.81**	20.00**	P-11	11.80	10.34*	9.62*	P-34	33.90	4.61	2.46
2	P-13	52.00	-6.31**	-2.80*	P-24	3.90	25.81**	20.00**	P-19	11.72	9.64*	8.92	P-10	33.32	2.84	0.73
3	P-36	52.50	-5.41**	-1.87	P-38	3.80	22.58**	16.92**	P-48	11.61	8.56	7.85	P-37	33.12	2.23	0.13
4	P-14	53.00	-4.50**	-0.93	P-39	3.70	19.35**	13.85**	P-39	11.51	7.62	6.92	P-27	32.04	-1.11	-3.14
5	P-48	53.50	-3.60**	0	P-12	3.70	19.35**	13.85**	P-50	11.41	6.69	5.99	P-45	31.97	-1.32	-3.35
6	P-10	53.50	-3.60**	0	P-10	3.50	12.90**	7.69*	P-47	11.40	6.64	5.95	P-11	31.41	-3.06	-5.05
7	P-47	53.50	-3.60**	0	P-14	3.50	12.90**	7.69*	P-13	11.38	6.41	5.72	P-04	30.74	-5.12	-7.07
8	P-50	53.50	-3.60**	0	P-36	3.50	12.90**	7.69*	P-36	11.33	5.94	5.25	P-47	30.30	-6.5	-8.42
9	P-39	53.50	-3.60**	0	P-11	3.45	11.29**	6.15*	P-14	11.16	4.4	3.72	P-15	30.04	-7.28	-9.19
10	P-04	53.50	-3.60**	0	P-45	3.35	8.06*	3.08	P-38	11.08	3.65	2.97	P-39	26.55	-18.07	-19.76
11	P-45	54.00	-2.70*	0.93	P-04	3.20	3.23	-1.54	P-04	11.08	3.65	2.97	P-19	26.30	-18.84	-20.51
12	P-15	54.00	-2.70*	0.93	P-48	3.15	1.61	-3.08	P-17	10.79	0.94	0.28	P-17	25.93	-19.96	-21.61
13	P-17	54.00	-2.70*	0.93	P-47	3.15	1.61	-3.08	P-45	10.74	0.47	-0.19	P-32	23.99	-25.97	-27.49
14	P-12	54.00	-2.70*	0.93	P-50	3.15	1.61	-3.08	P-37	10.70	0.09	-0.56	P-48	22.40	-30.86	-32.29
15	P-34	54.50	-1.8	1.87	P-19	3.10	0	-4.62	P-27	10.68	-0.09	-0.74	P-12	22.25	-31.33	-32.74
16	P-37	54.50	-1.8	1.87	P-15	3.10	0	-4.62	P-12	10.46	-2.2	-2.83	P-24	21.32	-34.21	-35.57
17	P-27	55.50	0	3.74	P-32	3.10	0	-4.62	P-34	10.39	-2.85	-3.49	P-38	20.30	-37.36	-38.65
18	P-38	56.50	1.8	5.61	P-13	3.10	0	-4.62	P-15	9.70	-9.31	-9.9	P-50	17.36	-46.44	-47.54
19	P-24	57.00	2.7	6.54	P-37	3.10	0	-4.62	P-10	9.52	-10.94	-11.52	P-13	14.84	-54.2	-55.14
20	P-32	57.50	3.6	7.48	P-27	3.00	-3.23	-7.69	P-24	8.54	-20.11	-20.63	P-14	14.83	-54.24	-55.18
21	P-11	57.50	3.6	7.48	P-17	2.40		-26.15	P-32	7.74	-27.6	-28.07	P-36	12.75	-60.66	-61.47
	PDM 53	55.50			PDM 53	3.10			PDM 53	10.69			PDM 53	32.40		
	PDM 4441	53.50			PDM 4441	3.25			PDM 4441	10.76			PDM 4441	33.08		
	CD (5 %)	1.26			CD (5 %)	0.22			CD (5 %)	0.96			CD (5 %)	7.73		
	CD (1%)	1.70			CD (1%)	0.29			CD (1%)	1.31			CD (1%)	10.47		
	Significant positive over PDM 53	14.00			Significant positive over PDM 53	10			Significant positive over PDM 53	2			Significant positive over PDM 53	0		
	Non-significant Positive over PDM 53	2.00			Non-significant Positive over PDM 53	4			Non-significant Positive over PDM 53	12			Non-significant Positive over PDM 53	3		
	Significant positive over PDM 4441	2.00			Significant positive over PDM 4441	9			Significant positive over PDM 4441	1			Significant positive over PDM 4441	0		
	Non-significant Positive over PDM 4441	2.00			Non-significant Positive over PDM 4441	1			Non-significant Positive over PDM 4441	11			Non-significant Positive over PDM 4441	3		

Table 13: Exploitation of recombinational variability and derivation of transgressive segregants for economically important traits of baby corn among selfed lines of population B (HKI 1105 x HKI 323)

Sl. No.	F ₆ lines of population B	Days to 50 % silking			F ₆ lines of population B	Number of cobs per plant			F ₆ lines of population B	Dehusked weight (g)			F ₆ lines of population B	Dehusked yield of baby corn per plant		
		Mean	% imp over inferior parent HKI 1105	% imp over better parent HKI 323		Mean	% imp over inferior parent HKI 1105	% imp over better parent HKI 323		Mean	% imp over inferior parent HKI 1105	% imp over better parent HKI 323		Mean	% imp over better parent HKI 1105	% imp over inferior parent HKI 323
1	H-118	51.5	-10.43**	-5.50**	H-35	3.7	27.59**	0	H-91	10.74	58.88**	3.77	H-06	29.115	48.55**	59.19**
2	H-16	52.5	-8.70**	-3.67**	H-91	3.56	22.76**	-3.78	H-99	10.73	58.65**	3.62	H-32	29.09	48.42**	59.05**
3	H-19	52.5	-8.70**	-3.67**	H-106	3.55	22.41**	-4.05	H-29	10.6	56.73**	2.37	H-19	28.743	46.65**	57.15**
4	H-99	52.5	-8.70**	-3.67**	H-22	3.55	22.41**	-4.05	H-46	10.39	53.70**	0.39	H-49	28.367	44.73**	55.10**
5	H-57	52.5	-8.70**	-3.67**	H-61	3.55	22.41**	-4.05	H-57	10.35	53.11**	0	H-99	28.19	43.83**	54.13**
6	H-46	52.5	-8.70**	-3.67**	H-13	3.55	22.41**	-4.05	H-22	10.33	52.81**	-0.19	H-08	27.8995	42.34**	52.54**
7	H-35	53.5	-6.96**	-1.83	H-118	3.5	20.69**	-5.41	H-32	10.25	51.63**	-0.97	H-106	27.7775	41.72**	51.87**
8	H-05	53.5	-6.96**	-1.83	H-16	3.45	18.97**	-6.76	H-06	10.23	51.33**	-1.16	H-95	27.732	41.49**	51.62**
9	H-13	54	-6.09**	-0.92	H-08	3.45	18.97**	-6.76	H-35	10.18	50.52**	-1.69	H-57	27.3915	39.75**	49.76**
10	H-49	54.5	-5.22**	0	H-49	3.45	18.97**	-6.76	H-59	9.86	45.78**	-4.78	H-46	25.454	29.87**	39.17**
11	H-59	55.5	-3.48**	1.83	H-28	3.45	18.97**	-6.76	H-28	9.66	42.83**	-6.71	H-118	25.32	29.18**	38.44**
12	H-08	55.5	-3.48**	1.83	H-29	3.4	17.24**	-8.11	H-16	9.33	37.94**	-9.9	H-91	25.06	27.86**	37.01**
13	H-28	55.5	-3.48**	1.83	H-59	3.15	8.62	-14.86	H-19	9.27	37.13**	-10.43	H-35	24.86	26.84**	35.92**
14	H-95	56.5	-1.74	3.67	H-95	3.1	6.9	-16.22	H-95	8.97	32.62**	-13.38	H-61	24.0045	22.47	31.24**
15	H-32	56.5	-1.74	3.67	H-19	3.1	6.9	-16.22	H-13	8.96	32.54**	-13.43	H-16	22.05	12.5	20.56
16	H-106	56.5	-1.74	3.67	H-32	3.1	6.9	-16.22	H-118	8.83	30.55**	-14.73	H-22	21.42	9.29	17.11
17	H-06	56.5	-1.74	3.67	H-06	3.1	6.9	-16.22	H-49	8.78	29.81**	-15.22	H-13	18.66	-4.8	2.02
18	H-61	57	-0.87	4.59	H-99	3.1	6.9	-16.22	H-106	8.62	27.51**	-16.71	H-29	17.76	-9.39	-2.9
19	H-91	57.5	0	5.5	H-05	2.7	-6.9	-27.03	H-08	8.09	19.60**	-21.88	H-05	17.248	-12	-5.7
20	H-29	57.5	0	5.5	H-57	2.65	-8.62	-28.38	H-61	6.77	0.07	-34.64	H-28	14.795	-24.52	-19.11
21	H-22	58.5	1.74	7.34	H-46	2.45	-15.52	-33.78	H-05	6.4	-5.4	-38.21	H-59	10.355	-47.17	-43.38
	HKI 1105	57.5			HKI 1105	2.9			HKI 1105	6.76			HKI 1105	19.6		
	HKI 323	54.5			HKI 323	3.7			HKI 323	10.35			HKI 323	18.29		
	CD (5 %)	1.45			CD (5 %)	0.36			CD (5 %)	0.73			CD (5 %)	3.74		
	CD (1 %)	1.97			CD (1 %)	0.49			CD (1 %)	0.98			CD (1 %)	5.06		
	Significant positive over HKI 1105	13			Significant positive over HKI 1105	12			Significant positive over HKI 1105	19			Significant positive over HKI 1105	14		
	Non-significant positive over HKI 1105	4			Non-significant positive over HKI 1105	6			Non-significant positive over HKI 1105	1			Non-significant positive over HKI 1105	3		
	Significant positive over HKI 323	6			Significant positive over HKI 323	0			Significant positive over HKI 323	0			Significant positive over HKI 323	14		
	Non-significant positive over HKI 323	3			Non-significant positive over HKI 323	0			Non-significant positive over HKI 323	4			Non-significant positive over HKI 323	3		