

**COMPARATIVE BREEDING POTENTIAL OF  
SEGREGATING POPULATIONS DERIVED  
FROM VARYING NUMBER OF PARENTS IN  
SWEETCORN (*Zea mays* var. *saccharata*)**



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BANGALORE**

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Thesis submitted to the  
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BANGALORE

CERTIFICATE

This is to certify that the thesis entitled “Comparative breeding potential of segregating populations derived from varying number of parents in sweetcorn (*Zea mays* var. *saccharata*)” submitted in partial fulfilment of the requirements for the degree of **Master of Science (Agriculture) in Genetics and Plant Breeding** to the University of Agricultural Sciences, Bangalore is a record of *bona fide* research work carried out by **Ms. DANDE JYOSHNA, PAMB 0262**, during the period of her study in this University, under my guidance and supervision. The thesis has not previously formed the basis for the award of any degree, diploma, associateship, fellowship or other similar titles.

Bengaluru

January, 2023

  
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(Dande Jyoshna)

# Comparative breeding potential of segregating populations derived from varying number of parents in sweetcorn (*Zea mays*

**var.saccharata) \***

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## Introduction

- Sweetcorn (*Zea mays* var. *saccharata*), is a special type of maize with high sugar content.
- High sugar content is the result of recessive mutations in the genes which control conversion of sugar to starch inside the endosperm.
- Hybrid parental lines developed from segregating populations derived from biparental crosses have narrow genetic base.
- To address lack of substantial variability, development of hybrid parental lines from a population having broad genetic base offers a feasible solution.

## Objectives

- To identify potential segregating population derived from crosses involving varying number of parents.

## Material and Methods

- Six segregating populations derived from crosses involving varying number of parents were used in the study.
- Eight parental lines constituting working collections were used in developing the segregating populations.

### ❖ Six segregating populations derived from

**Single cross hybrids -** (BNG-3×40023),  
(40225×MAI-283)

**Three way cross hybrids -** (BNG-3×40023) × 40224,  
(40225×MAI-283) × 40224

**Double cross hybrids -** (BNG-3×40023) × (40225×MAI-283),  
(4085 × 1882) × (MAI-225 × 40224)

### ❖ Field evaluation and sampling of plants for data collection

Seeds of six segregating populations were sown separately in contiguous blocks. Eight parental lines were evaluated separately in randomized complete block design in three replications. Data were recorded on grain yield and its attributing traits on each plant from each of the six segregating populations and five randomly chosen plants from each of the three replications in each of the eight parental lines involved in developing segregating populations.

### ❖ Statistical analysis and criteria to identify potential population

Segregating populations having higher estimates of genetic advance (GA) + mean, frequency of transgressive segregants and transgressive index for grain yield and its attributing traits were considered as criteria for assessing breeding potential. Further, potential populations were identified following rank-sum method. Based on ten productivity traits and three statistical parameters, each population was ranked from 1 to 9. Further, ranks were summed across these traits (Kang, 1988) and the population with lower rank sum was identified as the potential population.

## Results and Discussion

- None of the segregating populations were superior across all the productivity traits and all three statistical parameters. Hence, rank sum method was followed to arrive at potential segregating population.
- Based on rank sum method, segregating populations derived from single cross hybrid (BNG-3 × 40023) was identified as most potential segregating population followed by segregating population derived from three way cross hybrid (40225 × MAI-283) × 40224 and then followed by segregating population derived from (BNG-3 × 40023) × 40224. (Table 1).
- The segregating population derived from three way cross hybrid [(40225 × MAI-283) × 40224] expressed higher frequency of transgressive segregants over better parent for grain yield plant<sup>-1</sup>.

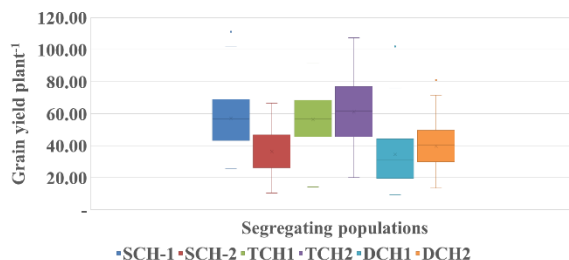


Figure 1. Box-Whisker plots depicting distribution of mean grain yield plant<sup>-1</sup> across six Segregating populations derived from varying number of parents.

| Segregating populations derived from | Parentage                       | Number of parents involved | Rank-sum based on trait GA + mean | Rank assigned to SPs | Rank-sum based on frequency of transgressive segregants | Rank assigned to SP | Rank-sum based on transgressive index | Rank assigned to SP | Cumulative rank-sum | Overall rank assigned to SPs |
|--------------------------------------|---------------------------------|----------------------------|-----------------------------------|----------------------|---------------------------------------------------------|---------------------|---------------------------------------|---------------------|---------------------|------------------------------|
| Single cross hybrids                 | BNG-3 × 40023                   | Two                        | 27                                | 1                    | 29                                                      | 2                   | 29                                    | 2                   | 5                   | 1                            |
|                                      | 40225 × MAI-283                 |                            | 38                                | 5                    | 33                                                      | 4                   | 25                                    | 1                   | 10                  | 4                            |
| Three-way cross hybrids              | (BNG-3×40023)×40224             | Three                      | 34                                | 2                    | 29                                                      | 3                   | 38                                    | 4                   | 9                   | 3                            |
|                                      | (40225 × MAI-283) × 40224       |                            | 34                                | 3                    | 26                                                      | 1                   | 29                                    | 2                   | 6                   | 2                            |
| Double cross hybrids                 | (BNG-3×40023)×(40225 × MAI-283) | Four                       | 35                                | 4                    | 43                                                      | 5                   | 45                                    | 6                   | 15                  | 5                            |
|                                      | (4085×1882)×(MAI-225 × 40224)   |                            | 42                                | 6                    | 46                                                      | 6                   | 43                                    | 5                   | 17                  | 6                            |

Table 1: Estimates of overall rank sum across grain yield and its attributing traits among segregating populations (SP) derived from crosses involving varying number of parents in sweetcorn

## Summary

- Selfing transgressive segregants with higher grain yield plant<sup>-1</sup> from the identified potential populations (BNG-3 × 40023) and (40225 × MAI-283) × 40224 could be stabilized to recover advanced breeding lines which could either be used as hybrid parental lines.

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# **COMPARATIVE BREEDING POTENTIAL OF SEGREGATING POPULATIONS DERIVED FROM VARYING NUMBER OF PARENTS IN SWEETCORN (*Zea mays var. saccharata*)**

**DANDE JYOSHNA**

## **ABSTRACT**

Cultivars derived from bi-parental crosses not only have narrow genetic base but also often lack desired combination of traits, leading to their genetic vulnerability. We hypothesized that cultivars derived from multi-parent populations are likely to have greater trait means, genetic variability and hence broader genetic base. To test this hypothesis, breeding potential of six segregating populations derived from crosses involving varying number of parents were field evaluated during Summer 2022 at the Experimental Plots of AICRP on Seed (Crops), University of Agricultural Sciences, Bangalore for ten quantitative traits. Breeding potential of six segregating populations was assessed based on three statistical parameters. Considering that different statistical parameters lead to identification of different population with good breeding potential, rank-sum method was employed as an objective criterion to identify populations with better breeding potential. Segregating populations derived from single cross hybrid; [BNG-3  $\times$  40023] with lower rank-sum was considered to possess higher breeding potential followed by segregating populations derived from three-way cross hybrid; [(40225  $\times$  MAI-283)  $\times$  40224]. Segregating population derived from three-way cross hybrid; [(40225  $\times$  MAI-283)  $\times$  40224] produced high frequency of transgressive segregants for grain yield plant<sup>-1</sup>. These segregating populations could preferentially be advanced to isolate advance breeding lines. Based on this study, optimum number of parental lines determined to be involved in generating potential segregating populations was not more than three.

**January, 2023**

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**T. M. Ramanappa**  
(Major Advisor)

**ಸಿಹಿ ಮೆಕ್ಕೆಜೋಳದಲ್ಲ ವಿವಿಧ ಪೋಷಕತಳಗಳಿಂದ ದೊರೆತ ಪೃಥಕ್ಪರಣ ಸಂತತಿಗಳ  
ತುಲನಾತ್ಮಕ ತಳವರ್ಧನೆಯ ಅಂತಸ್ತತ್ವದ ಮೌಲ್ಯಮಾಪನ**

**ದಂಡೆ ಜ್ಯೋಷ್ಣಾ**

**ಸಾರಾಂಶ**

ದ್ವಿ-ಪೋಷಕ ಸಂಕರಣಗಳಿಂದ ಪಡೆದ ತಳಗಳು ಕಿರಿದಾದ ಅನುವಂಶಿಕ ಮೂಲವನ್ನು (ತಳಹದಿ) ಹೊಂದಿರುವುದು ಮಾತ್ರವಲ್ಲದೆ ಸಾಮಾನ್ಯವಾಗಿ ಅಪೇಕ್ಷಿತ ಗುಣಲಕ್ಷಣಗಳ ಸಂಯೋಜನೆಯನ್ನು ಹೊಂದಿಲ್ಲದಿರುವುದು ಅವುಗಳ ಅನುವಂಶಿಕ ದುರ್ಬಲತೆಗೆ ಕಾರಣವಾಗಿವೆ. ಬಹು-ಪೋಷಕ ಸಂಕರಣಗಳಿಂದ ದೊರೆತ ತಳಗಳು ಹೆಚ್ಚಿನ ಗುಣಲಕ್ಷಣಗಳ ಸರಾಸರಿ, ಅನುವಂಶಿಕ ವ್ಯತ್ಯಯತೆಯನ್ನು ಹೊಂದಿರುವುದರಿಂದ ವಿಶಾಲವಾದ ಅನುವಂಶಿಕ ಮೂಲವನ್ನು ಹೊಂದಿರುವ ಸಾಧ್ಯತೆಯಿದೆ ಎಂದು ಊಹಿಸಲಾಯಿತು. ಈ ಊಹೆಯನ್ನು ಪರೀಕ್ಷಿಸಲು, ವಿವಿಧ ಪೋಷಕತಳಗಳನ್ನು ಒಳಗೊಂಡಿರುವ ಸಂಕರಣಗಳಿಂದ ದೊರೆತ ಆರು ಪೃಥಕ್ಪರಣ ಸಂತತಿಗಳ ತಳವರ್ಧನೆಯ ಅಂತಸ್ತತ್ವವನ್ನು ೨೦೨೨ರ ಬೇಸಿಗೆಯಲ್ಲಿ ಅಖಿಲ ಭಾರತ ಸುಸಂಘಟಿತ ಸಂಶೋಧನಾ ಪ್ರಾಯೋಜನೆಗಳು (ಎಐಸಿಆರ್‌ಪಿ), ಕೃಷಿ ವಿಶ್ವವಿದ್ಯಾಲಯ ಬೆಂಗಳೂರಿನ ಪ್ರಾಯೋಗಿಕ ತಾಕುಗಳಲ್ಲಿ ಹತ್ತು ಪರಿಮಾಣಾತ್ಮಕ ಗುಣಲಕ್ಷಣಗಳಿಗಾಗಿ ಮೌಲ್ಯಮಾಪನ ಮಾಡಲಾಯಿತು. ಆ ಆರು ಪೃಥಕ್ಪರಣ ಸಂತತಿಗಳ ತಳವರ್ಧನೆಯ ಅಂತಸ್ತತ್ವವನ್ನು ಮೂರು ಸಂಖ್ಯಾಶಾಸ್ತ್ರೀಯ ನಿಯತಾಂಕಗಳ ಆಧಾರದ ಮೇಲೆ ನಿರ್ಧರಿಸಲಾಯಿತು. ವಿಭಿನ್ನ ಸಂಖ್ಯಾಶಾಸ್ತ್ರೀಯ ನಿಯತಾಂಕಗಳು ವಿವಿಧ ಸಂತತಿಗಳನ್ನು ಉತ್ತಮ ತಳವರ್ಧನೆಯ ಅಂತಸ್ತತ್ವವನ್ನು ಹೊಂದಿರುವ ಸಂತತಿಗಳು ಎಂದು ಗುರುತಿಸುತ್ತಿರುವುದನ್ನು ಪರಿಗಣಿಸಿ, ಉತ್ತಮ ತಳವರ್ಧನೆಯ ಅಂತಸ್ತತ್ವವನ್ನು ಹೊಂದಿರುವ ಸಂತತಿಗಳನ್ನು ಗುರುತಿಸಲು ಶ್ರೇಣಿಯ ಮೊತ್ತದ ವಿಧಾನವನ್ನು ವಸ್ತುನಿಷ್ಠ ಮಾನದಂಡವಾಗಿ ಬಳಸಲಾಯಿತು. ಕಡಿಮೆ ಶ್ರೇಣಿಯ ಮೊತ್ತವನ್ನು ಹೊಂದಿರುವುದರಿಂದ ಜಿಎನ್‌ಜಿ-೩ × ೪೦೦೨೩ ಎಂಬ ಏಕಸಂಕರಣ ತದನಂತರ [(೪೦೨೨೫ × ಎಮ್‌ಎ೨೮೩) × ೪೦೨೨೪] ಎಂಬ ಮೂರು-ದಿಕ್ಕಿನ ಸಂಕರಣ ಮಿಶ್ರತಳಯಿಂದ ದೊರೆತ ಸಂತತಿಗಳನ್ನು ಉತ್ತಮ ತಳವರ್ಧನೆಯ ಅಂತಸ್ತತ್ವವನ್ನು ಹೊಂದಿರುವ ಸಂತತಿಗಳೆಂದು ಪರಿಗಣಿಸಲಾಯಿತು. [(೪೦೨೨೫ × ಎಮ್‌ಎ೨೮೩) × ೪೦೨೨೪] ಎಂಬ ಮೂರು-ದಿಕ್ಕಿನ ಸಂಕರಣ ಮಿಶ್ರತಳಯಿಂದ ದೊರೆತ ಸಂತತಿಗಳು ಪ್ರತಿ ಸಸ್ಯದ ಧಾನ್ಯ ಇಳುವರಿಗೆ ಹೆಚ್ಚಿನ ಅತಿಕ್ರಮೀ ಪೃಥಕ್ಪರಣ ಆವರ್ತನವನ್ನು ತೋರಿಸಿದವು. ಈ ಪೃಥಕ್ಪರಣ ಸಂತತಿಗಳನ್ನು ಸುಧಾರಿತ ತಳ ಅಭಿವರ್ಧನ ಸಾಲುಗಳನ್ನು ಗುರುತಿಸಿ ಬಳಸಲು ಆದ್ಯತೆಯೊಂದಿಗೆ ಮುಂದುವರಿಸಬಹುದು. ಈ ಅಧ್ಯಯನದ ಆಧಾರದ ಮೇಲೆ, ಸಂಭಾವ್ಯ ಪೃಥಕ್ಪರಣ ಸಂತತಿಗಳನ್ನು ಉತ್ಪಾದಿಸುವಲ್ಲಿ ತೊಡಗಿಸಿಕೊಳ್ಳಲು ನಿರ್ಧರಿಸಲಾದ ಪೋಷಕತಳಗಳ ಗರಿಷ್ಠ ಸಂಖ್ಯೆಯು ಮೂರಕ್ಕಿಂತ ಹೆಚ್ಚಿಲ್ಲ ಎಂದು ತಿಳಿದುಬಂದಿತು.

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ಕೃಷಿ ಮಹಾವಿದ್ಯಾಲಯ, ಗಾ. ಕೃ. ವಿ. ಕೇ., ಬೆಂಗಳೂರು-೫೬೦೦೬೫

**ಟಿ. ಎಮ್. ರಮಣಪ್ಪ**

(ಮುಖ್ಯ ಸಲಹೆಗಾರರು)

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# **INTRODUCTION**

## I INTRODUCTION

Maize (*Zea mays* L.), belonging to family Poaceae, is one of the most important cereal crops of the world. It contributes to food security in most of the developing countries. It is the fastest growing cash crop in the world with its largescale utilization as an important raw material in food processing, poultry, dairy and ethanol industry along with its traditional uses. Maize is emerging as third most important crop after rice and wheat. The primary centre of origin of maize is considered by most authorities to be the Central America and Mexico, where many diverse types of maize are found. Maize is a warm weather plant. It grows from sea level to 3000 meter altitudes. It is a seasonal crop, it can be harvested thrice, i.e., in *kharif*, *rabi* and summer seasons. Maize is usually grown as a sole crop; in some instances, it can be grown as an intercrop with different crop combinations like sugarcane, vegetables, legume crops etc.

In India, maize is grown on an area of 9.57 million hectares with annual production of 28.77 million tons. Productivity of maize is found to be 3006.13 kg hectare<sup>-1</sup>. In Karnataka, maize is grown on an area of about 1.42 million hectares with annual production of 4.26 million tonnes and productivity was found to be 2990.18 kg hectare<sup>-1</sup> (INDIASTAT, 2019-2020). It possesses highly diverse grain properties that provide the alteration of grain composition in relation to quantity and quality of certain components. Selection pressure by both humans and nature has resulted in evolution of various types of corn generally classified by characteristics of their kernel endosperm such as flint, dent, sweet, flour, waxy and popcorn (Knott *et al.*, 1995 and Zilic *et al.*, 2011).

Sweetcorn (*Zea mays* var. *saccharata*), more concisely field corn in its arrested state of development (Erwin, 1951). Sweetcorn consists of certain genes which differ from the normal corn genes, due to which normal starch synthesis is being reduced and one or more recessive alleles increases the amount of water-soluble polysaccharides (sugars) in the sweetcorn endosperm and hence the sugar content in sweetcorn is about 25-30 *per cent* at milky stage. There are about four most important mutants *shrunk-2* (*sh-2*), *brittle* (*bt*), *sugary* (*su*), and *sugary enhancer* (*se*) responsible for producing sugar enriched kernels. These mutant genes modify the flavour, tenderness and texture of kernels, seed viability

and appearance of plants and ears (Tracy 2000). The flavour of kernels is determined in part by sweetness, which is affected by the amounts of sugar and starch in the endosperm governed by different kinds of endosperm mutant genes.

The crop has achieved a major success as one of the important commercial cash crops in many tropical and sub-tropical countries, including the USA. It is one of the most popular vegetable in the US, Canada and many of the western countries. Brazil, as one of the world's largest corn producer, also has great potential for sweet corn production. Worldwide, sweet corn is being produced for three distinct markets: fresh, canning and freezing. The eating quality of fresh or processed whole kernels, canned or frozen is determined by its unique combination of flavour, texture and aroma. Sweetness is the most important factor in terms of consumer satisfaction which largely depends on kernel sucrose content. However, texture is primarily determined by pericarp tenderness, level of water-soluble polysaccharides and kernel moisture content (Lertrat and Pulam, 2007).

In India, although the widely cultivated type of maize belongs to flint and semi-flint type but sweet corn also occupies good coverage in the states like Andhra Pradesh, Karnataka and Maharashtra. Sweet corn in all its form fresh, frozen, canned etc. is exported throughout India and overseas from the growing hub on western Maharashtra where farmers choose this crop because of conducive weather, irrigation facility, short harvest duration, fodder creation, good and stable market facilities. It is grown round the year but bumper harvest is taken generally during the months of August, September, October and then February, March. It has huge market potential especially if the processing and packing needs for large scale production are taken care of.

The endosperm mutant seed used in sweet corn breeding has a higher sugar content, and at the same time, a lower starch content. The starch and sugar contents amount to 20-30 *per cent* and 15-35 *per cent*, respectively, at the milk stage when sweet corn is consumed, while these contents at the same stage in the grains of standard quality amount to 65 *per cent* and approximately 5 *per cent*, respectively (Hannah *et al.*, 1993).

In the milk stage, sweet corn has the best edible quality. Sweet corn has a relatively high oil content, which is primarily composed of linolenic acid (50%) and oleic acid (30%). Sugars, dietary fiber, vitamin C, beta-carotene, niacin, calcium and potassium are all abundant in this crop. The nutritional quality of sweet corn is determined by moisture (72.7%) and total solids (22.3%), which include carbohydrate (81%), protein (13%) and lipids (3.5%). Apart from that, fodder is really succulent, tasty and easy to digest for cattle (Brecht, 1990).

In breeding programs, it is a common practice to handle segregating populations generated from single crosses to derive potential hybrid parental lines. Such hybrid parental lines exhibit narrow genetic base and often lack all the desired combination of traits. This may lead to genetic vulnerability of cultivars and consequently result in disease epidemics. Creation of diversity and its subsequent utilization are the major goals of any crop improvement programme. To address lack of substantial variability, development of hybrid parental lines from a population having broad genetic base offers a feasible solution. Segregating generations derived from crosses involving more than two parents are expected to exhibit greater spectrum of variation due to enhanced and effective meiotic events in comparison to segregating populations derived from crosses involving just two parents. Assessing and examining spectrum of variability among segregating populations derived from crosses involving di, tri and tetra parents would help to determine optimum number of parents to be involved in generating base populations to be subjected to further cycles of selection to derive stabilized hybrid parental lines. Hence, use of multi-parent cross derived parental lines/segregants is likely to help realize hybrids with broad genetic base with a combination of desired traits.

Breeding potential of crosses can be assessed and is reflected in terms of variability and other statistical parameters viz., quantitative trait means, standardized range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), genetic advance as *per cent* of mean, frequency of transgressive segregants recovered and transgressive segregation index. Recovery of transgressive segregants is expected to be more when a greater number of alleles are dispersed among parents. Segregating populations derived from crosses involving more than two parental lines are expected to

harbour more allelic dispersion contributing to greater recovery of transgressive segregants.

Under this premise, the present investigation entitled “Comparative breeding potential of segregating populations derived from varying number of parents in Sweetcorn (*Zea mays* var. *saccharata*)” was taken up with the following objectives.

1. To compare genetic variability for grain yield and its attributing traits across di, tri and tetra parent derived segregating populations.
2. To compare the frequency of transgressive segregants for yield and its component traits across di, tri and tetra parent derived segregating populations.

# **REVIEW OF LITERATURE**

## II REVIEW OF LITERATURE

The literature related to the experiment is reviewed and presented under the following headings.

### 2.1 Genetic variability

### 2.2 Transgressive segregation

#### 2.1 Genetic variability

The success in any crop improvement programme depends mainly on the magnitude of genetic variability present for a character and an extent to which it is heritable. The knowledge on the estimates of variability in respect of yield and its heritable components in the material with which the breeder is working therefore, becomes prerequisite for any breeding programme. Hence, it became necessary to split the total variability into heritable and non- heritable components with the help of certain genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance.

In a study on genetic variability and heritability within sweetcorn breeding populations, Nigussie *et al.* (2007) observed significant differences among selfed progenies within BC<sub>1</sub>-10 x Syn-II for all traits, while differences among selfed progenies within BC<sub>2</sub>-10 were noted for fresh ear yield, ear length, ear diameter, number of kernels per row, ear height, days to tasseling and days to silking. Progenies developed from BC<sub>1</sub>-10 x Syn-II population had higher estimates of genotypic variance ( $\sigma^2 G$ ) than did progenies from BC<sub>2</sub>-10 population for number of kernel rows per ear, total soluble solids, plant height, days to tasselling and days to silking, showing that selection to improve these traits would be more effective in selfed progenies of BC<sub>1</sub>-10 x Syn-II than that in BC<sub>2</sub>-10. On the other hand, progenies developed from BC<sub>2</sub>-10 population had higher estimates of genotypic variance ( $\sigma^2 G$ ) for ear length, ear diameter and ear height, indicating that progenies from this population would have better genetic gain than BC<sub>1</sub>- 10 x Syn-II.

Turi *et al.* (2007) assessed the magnitude of genetic variability in maize genotypes for yield and yield components under agro climatic conditions of Peshawar valley and concluded that significant variability was observed for cob length, grains rows cob<sup>-1</sup>, fresh cob weight, grain moisture content, 300-grains weight and grain yield.

Analysed the genetic variability for quantitative characters in twenty-five sweetcorn genotypes and observed significant difference among the entries for almost all the studied characters. The characters 100-grains weight, number of seeds per row and grain yield per plot were the most important parameters to be considered in parents for effective selection before initiating actual crossing programme, since these attributes exhibited high variability, heritability combined with high genetic advance as per cent of mean. Eight superior sweetcorn lines with desirable characters were identified for future use in breeding programmes by Gautam *et al.* (2011).

Bello *et al.* (2012) evaluated ten open pollinated maize varieties and reported that high magnitude of phenotypic and genotypic coefficient of variations as well as high heritability along with genetic advance for grain yield, number of grains per ear, ear weight, plant and ear heights provides evidence that these parameters were under the control of additive gene effects and effective selection could be possible for improvement for these characters.

Lal and Singh, (2014) assessed the magnitude of genetic variability in quality protein maize (QPM) for morphological and quality traits. Seed yield per plot followed by plant height, ear girth, ear height, ear length, 1000 grain weight and number of grains per row had high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Heritability and genetic advance were low for days to 50 *per cent* silking, protein concentration, tryptophan concentration, lysine concentration, number of rows per cob and number of grains per row indicating the predominant role of non-additive gene action. Hence environment plays major role in governing these characters and improvement of these characters is complicated.

Sharma *et al.* (2014) estimated the genetic variability, heritability, genetic advance for yield and kernel quality traits in twenty diverse maize genotypes. Genetic variability parameters showed that phenotypic coefficient of variation (PCV) was higher than the respective genotypic coefficient of variation (GCV) and heritability was high for most of the traits under study. Test weight, grain yield per plant, grains per cob, cob length, grains per row and harvest index were found important in selection programmes aiming to maize yield improvement.

Ali *et al.* (2015) reported high heritability and genetic advance for plant height, stem diameter, leaves weight, stem weight, green fodder yield, leaves/stem weight ratio, leaf length, leaf area, photosynthetic rate, stomata conductance, transpiration rate and sub-stomata CO<sub>2</sub> concentration.

Ghimire and Timsina, (2015) evaluated fourteen maize genotypes to explore genetic variability and investigate yield and yield attributing traits. The genetic study revealed that days to silking, days to tasseling and grain yield *per* hectare were highly heritable (>0.6). Higher GCV and high GAM indicated efficient indirect selection for higher grain yield *per* hectare based on these traits. Thus, high GAM and GCV was observed for ear weight, grain yield *per* hectare and ear height.

Kapoor and Batra, (2015) revealed that genotypes were significantly different for all the characters, which indicated scope for further genetic studies. The phenotypic coefficients of variation (PCV) estimates were invariably higher than their corresponding genotypic coefficient of variation (GCV) values thereby suggesting the environmental influence. High estimates of GCV and PCV were observed for plant height, leaf length, stem girth, number of cobs, number of seeds, dry matter yield and green fodder yield suggesting that selection based on these characters would facilitate successful isolation of desirable types. High heritability along with high genetic advance was recorded for plant height, leaf length, leaf width, stem girth, number of leaves, crude protein, acid detergent fiber, dry matter yield and green fodder yield indicating the predominance of additive effects in the inheritance of these characters.

Rahman *et al.* (2015) assessed genetic diversity among nine maize genotypes using data on seven morphological traits. Statistical analysis showed significant variation among maize genotypes. Among all the traits higher phenotypic coefficient of variation and genotypic coefficient of variation were observed for yield/plant. Genetic advance was highest for 1000-kernel weight followed by number of kernels *per* ear.

Ashakina *et al.* (2016) studied the performance of single, double and three-way cross hybrids in tomato and found that the three categories of hybrids exhibited significant differences among the genotypes and exhibited high variation for the majority of characters studied. The single cross hybrids depicted stronger performance for days to 50 *per cent* flowering, number of fruits/plant (133.8) and yield/plant (4.03 kg). As expected, three-way cross hybrids were most uniform followed by double cross hybrids.

Patil *et al.* (2016) reported significant treatment differences for all the characters and also the magnitude of genotypic and phenotypic coefficient of variation indicated the presence of good amount of variability. Grain yield *per* plant showed the highest heritability (98.00 %) followed by the plant height, number of kernels *per* row and 100 grain weight. Grain yield *per* plant exhibited highest genetic advance followed by plant height and ear head height.

In a study on genetic variability and correlation among yield and yield contributing traits in sweetcorn, Suhaisini *et al.* (2016) evaluated 50 hybrids generated by Line  $\times$  Tester mating design using ten lines and five testers and concluded that genotypes differ significantly for all the traits under study.

Bhusal *et al.* (2017) estimated the extent of genetic variability in fifty-five maize genotypes. Analysis of variance revealed significant differences for 18 characters studied among the genotypes. High genotypic and phenotypic coefficient of variation was recorded for grain yield *per* plant, biological yield *per* plant and cob weight coupled with high heritability and genetic advance.

Kapoor (2017) evaluated twenty maize hybrids for variability and character association study during kharif 2012 and results revealed that the genotypes were

significantly different for all the characters, which indicated scope for further genetic studies. High heritability along with high genetic advance was recorded for all the traits except number of leaves *per* plant indicating the predominance of additive effects in the inheritance of these characters. The phenotypic coefficients of variation (PCV) estimates were invariably higher than their corresponding genotypic coefficient of variation (GCV) values thereby suggesting the environmental influence. High estimates of GCV and PCV were observed for plant height, leaf to stem ratio, dry matter yield and green fodder yield, suggesting that selection based on these characters would facilitate successful isolation of desirable types.

Kharel *et al.* (2017) evaluated the maize genotypes for their genetic parameters and association among yield parameters. Genotypic coefficient of variation was estimated high for number of kernels row<sup>-1</sup> and ear height, moderate for plant height, 100-kernel weight, days to 50 *per cent* silking, ear length, SPAD chlorophyll and leaf angle. Genetic advance as percentage of mean had high value for number of kernels row<sup>-1</sup>, ear height, plant height, days to 50 *per cent* silking, SPAD chlorophyll and 100-kernel weight and moderate value for ear length, leaf angle, days to 50 *per cent* tasseling and ear girth. High heritability was estimated for days to 50 *per cent* tasseling, plant height, SPAD chlorophyll, days to 50 *per cent* silking, number of kernels row<sup>-1</sup>, leaf angle and ear length while, ear girth while, 100-kernel weight, leaf number and number of kernel rows ear<sup>-1</sup> showed moderate heritability.

Sravanti *et al.* (2017) carried out an investigation to assess the variability, heritability and genetic advance in forty-two maize genotypes for twelve yield and its contributing traits. The analysis of variance revealed the presence of significant variability among the maize genotypes under study. Among all the characters under study, ear height exhibited highest PCV and GCV, whereas lowest PCV and GCV were recorded for days to maturity. Ear height and grain yield *per* plant expressed high heritability coupled with high genetic advance, which indicated the preponderance of additive gene action in controlling the traits. Hence direct selection of such characters would be effective in improving the yield. Emphasis should be given on these characters, while selection to improve yield potential of crop.

Ahalawat *et al.* (2018) evaluated thirty genotypes of forage sorghum for genetic variability and diversity. Analysis of variance revealed a substantial amount of variability among the genotypes for all the characters under study, indicated a wide spectrum of variability among the genotypes. Highest estimates of phenotypic coefficient of variation and genotypic coefficient of variation were observed for plant height, leaf breadth, leaves *per* plant, leaf to stem ratio and green fodder yield. High heritability coupled with high genetic advance was observed for plant height, leaf area, stem girth, leaves *per* plant, leaf to stem ratio and green fodder yield.

Najar *et al.* (2018) reported significant variability with high estimates of heritability (broad sense) for all the traits under study revealing that these traits are amenable to genetic improvement. Grain yield *per* plant exhibited positive and significant correlation with plant height, ear height, ear width, number of kernels *per* row, number of kernel rows and 100 seed weight at both the levels which exhibit a strong possibility for improvement of grain yield *per* plant by selection for these traits.

Niji (2018) studies on genetic variability, heritability and character association in sweetcorn revealed that high heritability coupled with high genetic advance as *per cent* of mean for the traits viz., green cob yield, green cob weight, 100 seed weight, total sugar, reducing sugar, non-reducing sugar, iron content and zinc content, indicating the importance of these traits for selection. Correlation studies revealed significant positive association of green cob yield with green cob weight, cob breadth, tassel length, plant height, cob length, total chlorophyll content, tassel branches, cob placement height, 100 seed weight and number of kernel rows *per* cob.

Shikha *et al.* (2018) revealed presence of a wide range of variability between the hybrids for cob yield with husk, cob yield without husk, cob weight, green fodder weight, number of cobs *per* plot, TSS(%), seedling emergence(%), ear height, plant height, kernels *per* row, ear width, ear length, kernel rows *per* cob, husk weight and 100 seed weight indicating the scope for selection of suitable hybrid for cultivation. The high heritability with high to moderate estimates of genetic advance were obtained from grain yield, plant

height, ear height, number of kernels *per* row, 100-kernel weight indicating additive gene action for which selection would be effective.

Tadesse *et al.* (2018) found high significance differences among genotypes for all traits studied except tassel size. The genotypic coefficient of variation (GCV) for all traits studied was smaller than the phenotypic coefficient of variation (PCV), indicating the significant role of environment in the expression of the traits. The estimates of PCV and GCV were high for grain yield, thousand kernel weight, ear height, ear diameter, anthesis and silking interval and plant aspect. High heritability along with high genetic advance were obtained for plant height, ear length and 1000-kernel weight, indicating the predominance of additive gene effects in controlling the traits and effective selection on the basis of these traits would be absolutely useful for the improvement of inbred lines.

Ayodeji and Comfort, (2019) evaluated twelve shrunken-2 super-sweetcorn populations and reported that genotypic variance was significant for number of marketable cobs, yield of cobs, number of cobs, number of kernel rows, husk cover, ear height and days to anthesis, while environmental variance was significant for all the traits. Phenotypic coefficients of variation were higher than the corresponding genotypic coefficients of variation for all traits. Broad sense heritability ranged from 22.2 *per cent* for anthesis-silking interval to 85.1 *per cent* for husk cover. The genetic advance was high (32.7%) for husk cover, medium (12%) for yield of cobs and low for other traits.

Bartaula *et al.* (2019) evaluated ten maize genotypes to assess the magnitude of genetic variability, heritability and genetic advance for growth, yield and yield contributing traits. Analysis of variance revealed significant differences for all traits. The phenotypic coefficient of variation (PCV) higher than genotypic coefficient of variation (GCV) was recorded for all traits. The grain yield showed the highest PCV and GCV whereas the lowest PCV and GCV were recorded for test weight; test weight showed high heritability with low genetic advance as a *per cent* of mean. Traits namely grain yield, number of kernels *per* cob and kernel rows *per* cob showed high GCV and PCV. Therefore, these traits can be used further in crop improvement program.

Rahim *et al.* (2019) assessed variability in 18 open-pollinated maize accessions for morpho-biochemical traits and observed significant results of variance and covariance for all morpho-biochemical traits, which revealed significant variation among the maize accessions.

Roy (2019) assessed the genetic variability in F<sub>2</sub> populations of interspecific cotton hybrids concluded that all the characters showed greater PCV values than GCV values, implying influence of environment on the expression of these traits. High PCV and GCV values indicated the extent of variability existing for these characters. High heritability coupled with high genetic advance was observed for seed cotton yield, number of bolls *per* plant and boll weight indicating a good selection approach. Transgressive segregants were identified based on mean ( $\pm 2$ ) standard deviation in four F<sub>2</sub> populations. The cross FQT-37 X SB-YF-425 10 showed highest number of transgressive segregants followed by HBS-1 X Suvin and FQT-26 X Suvin for the trait, seed cotton yield. These selected transgressive segregant plants can be used for further evaluation to identify superior genotypes.

Vanipraveena *et al.* (2022) studies on genetic variability, heritability and genetic advance in sweetcorn for green ear yield and yield related traits revealed a significant difference among the genotypes for traits studied indicating the presence of abundant genetic variability. The phenotypic co-efficient of variation ranged from 4.57 (DFS) to 36.41 (GEWH) while the genotypic co-efficient of variation ranged from 3.72 (DFT) to 25.35 (GEWH). Green ear yield without husk (25.35, 36.41); green fodder weight (22.47, 29.20) and green ear yield (24.63, 33.31) recorded high PCV and GCV values. High genetic advance over mean was observed for the traits green ear weight without husk, and green fodder weight. Moderate heritability coupled with high genetic advance was observed for the traits green ear weight without husk, green fodder weight and green ear yield.

## **2.2 Transgressive segregation**

Wallwork and Johnson, (1984) studied the transgressive segregation for resistance to yellow rust in wheat and obtained the lines with greater resistance than in both parents were obtained from each cross, those with greatest resistance being obtained from the cross between the moderately resistant parents. The selected lines also displayed race-specific

resistance. It is suggested that such transgressive resistance is more likely to be durable if it is derived from parents that have shown durable resistance.

In a study on the transgressive segregation of tiller angle in rice caused by complementary gene action, Xu *et al.* (1998), with four *indica* cultivars. As a result of selection, two types of true-breeding phenotypic extremes were obtained, one with larger tiller angle and the other with smaller tiller angle. When the extreme phenotypes were crossed with each other, strains with the largest tiller angle represented recombinants containing all increasing alleles from the four original parents.

In a study on genetics of transgressive segregation for yield and yield components in wheat, Yadav *et al.* (1998) indicated that both additive and non-additive components were significant for all the characters. Additive component was more pronounced than non-additive components for all the characters in all the crosses except for tillers/ plant in WH 377  $\times$  HD 2329. Predictions for transgressive segregants from F<sub>3</sub> was more accurate than that from generation mean analysis.

Rieseberg *et al.* (1999) studied transgressive segregation, adaptation and speciation. The production of extreme or 'transgressive' phenotypes in segregating hybrid populations has been speculated to contribute to niche divergence of hybrid lineages. Quantitative genetic studies of plant hybrids consistently point to the action of complementary genes as the primary cause of transgression, with the possible exception of those with a history of disruptive selection, although overdominance and epistasis also contribute.

Fasoula and Fasoula, (2002) reported in soybean that the heterotic crosses involving good general combining parents in desired direction are likely to result in higher frequency of transgressive segregants in advanced generations.

Sadat and Harati, (2005) studied F<sub>3</sub> populations derived from cross between four moderate salt resistant spring wheat (*Triticum aestivum* L.) were assessed for transgressive segregation of salt-tolerant genotypes. Root length of transgressive plants were longer than parents (except Tobari 66) showing more tolerance to NaCl. It may be assumed that the

character is quantitative trait based, and the parents of such hybrids may contain different genes for salt tolerance.

Rodriguez *et al.* (2005) studied the transgressive segregation for fruit quality traits in a cross between exotic and mutant genotypes of *Lycopersicon*. Transgressive inheritance was present for relevant traits such as shape, colour, firmness, and shelf life. The broad sense heritability values were highly significant for all traits and the shelf life was not associated with any other fruit quality trait.

In a study on variability and transgressive segregation for yield and yield contributing traits in pigeon pea crosses, Ajay *et al.* (2014) stated that high variance, high heritability and high genetic advance were recorded for secondary branches *per* plant, number of pods *per* plant and seed yield in F<sub>2</sub> and F<sub>3</sub> generations. Among the three crosses transgressive segregants were high in the cross TTB 7 × ICPL87119 indicating the superiority of this cross over the other crosses.

In a study on MAGIC population of tomato, Pascual *et al.* (2015) described its breeding potential at higher value upon crossing within different species and deciphered the genetics of quantitative traits. The MAGIC population developed using eight founder lines which covered wide range of genetic diversity.

Branch and Culbreath, (2018) studied transgressive segregation and long-term consistency for high TSWV field resistance in the ‘Georgia-06G’ peanut Cultivar. Both Georgia-06G and Georgia Greener have greater TSWV general field resistance with higher yields, total sound mature kernels grade, and dollar values than the parents (‘Georgia Green’ and ‘C-99R’), which shows transgressive segregation for these desirable quantitative traits.

In a study on Breeding potential of three-way and double cross hybrids in chilli, Lakshmipathy *et al.* (2018) described multi-parent derived hybrids have greater potential as they could carry three or four alleles from different parents at different loci in population, provided parents differ for alleles under consideration. The DC hybrid had higher mean

and variance compared to TWC hybrid since former is derived from four parents and latter from three.

Guindon *et al.* (2019) reported that in a cross between two pea varieties, namely DDR14 and Explorer high frequency of transgressive segregation was observed for characters viz., number of pods and number of seeds in F<sub>3</sub> generation (15.5% and 13.6%, respectively). There were 12.73 *per cent* families had transgressive for two or more characters, with genotypic values of 49.82–64.41 for number of pods and 153.75–189.59 for seed number. The crossing between Explorer and DDR14 provided a base for the selection of superior progeny.

In a study on performance prediction and validation of three way and double cross hybrids for fruit yield in chilli, Pathy *et al.* (2019) validated two models of prediction, including mean of non-parental single crosses and mean of all possible single crosses among the parents involved in that cross. They observed a perfect agreement between the observed and expected values in both prediction methods for all the traits under consideration, except green fruit yield plant<sup>-1</sup> suggesting that epistatic interaction might be involved in inheritance of this trait.

Koide *et al.* (2019) studied the genetic properties responsible for the transgressive segregation of days to heading in rice, examined transgressive phenotypes of flowering time in rice, and revealed transgressive segregation in F<sub>2</sub> populations derived from a cross between parents with similar days to heading (DTH). The DTH phenotypes of the A58 × Kitaake F<sub>2</sub> progenies were frequently more extreme than those of either parent. Among the four known loci required for a short DTH, three loci had common alleles in A58 and Kitaake, implying there is a similar genetic basis for DTH between the two varieties.

Reddyamini *et al.* (2019) studied the transgressive segregation for yield and its component traits in rice (*Oryza sativa* L.). High frequency of favourable transgressive segregants were observed for plant height and number of grains *per* panicle in the cross BPT5204 x NLR33892. Polygenic inheritance and high frequencies of favourable transgressive segregants for yield and its component traits indicates there is a lot of scope

to bring in beneficial alleles into a single genotype through careful selection in later generations.

Yamazaki *et al.* (2020) studied the transgressive segregation and gene regions controlling thermotolerance of fruit set and pollen germination in *Capsicum chinense*. F<sub>1</sub> hybrid of the *Capsicum chinense* cultivars 'Sy-2' and 'No. 3686', both of which yield poorly at high temperatures. Analysis of the F<sub>2</sub> population shows that the percentage of fruit set under high temperature is strongly associated to single nucleotide polymorphisms (SNPs) in a certain gene region of chromosome 6 and weakly associated to a gene region on the chromosome 3.

## **MATERIAL AND METHODS**

### III MATERIAL AND METHODS

The material used and methods followed to address the objectives stated in the introduction chapter are presented here under the following heads.

#### **3.1 To compare genetic variability for yield and traits related to yield across di, tri and tetra parent derived segregating populations**

##### **3.1.1 Experimental Location**

The present study was carried out for three seasons (*kharif* 2021, *rabi* 2021 and summer 2022) at AICRP on Seed (Crops), UAS, GKVK, Bengaluru located at 930 m above MSL and 13°08' N and 77°57' E latitude and longitude respectively. This region corresponds to the Eastern Dry Agro-climatic Zone (Zone V) of Karnataka.

##### **3.1.2 Experimental material**

The material for the present investigation composed of six segregating populations derived from crosses involving varying number of parents in sweetcorn. Eight sweetcorn inbred lines were procured from AICRP on Maize, ZARS, VC farm, Mandya and used in developing the segregating populations. Segregating populations were developed and maintained during 2021 - 2022 at AICRP on Seed (Crops), UAS, GKVK Bengaluru. Parents and crosses involved in generating the segregating populations are detailed in table 1 and 2 respectively.

##### **3.1.3 Layout of experiment**

Seeds of eight parental lines have been sown in plots of AICRP on Seed (Crops), UAS, GKVK, Bengaluru during *kharif* 2021 and single cross hybrids were developed and the same parental lines were also selfed. The single cross hybrids developed from the parental lines in *kharif* 2021 were sown in *rabi* 2021 to develop F<sub>2</sub> (selfing of single cross hybrids), three-way cross hybrids (crossing single cross hybrids with an inbred line) and double cross hybrids (crossing of two single cross hybrids). The actual parental lines were sown and evaluated in RCBD with three replications. While, six segregating populations derived from di, tri and tetra parental crosses were planted with a spacing of 60 cm between

rows and 20 cm between plants within a row during summer 2022. Recommended package of practices were followed to raise a healthy crop.

**Table 1: Inbred lines of Sweetcorn used in generating segregating populations derived from di, tri and tetra parent crosses**

| S. No                 | 1     | 2       | 3    | 4     | 5       | 6    | 7     | 8     |
|-----------------------|-------|---------|------|-------|---------|------|-------|-------|
| <b>Parental lines</b> | 40023 | MAI-283 | 1882 | 40225 | MAI-225 | 4085 | 40224 | BNG-3 |

**Table 2: Parentage of segregating populations derived from di, tri and tetra parent crosses**

| Segregating populations derived from      |                                                |                                            |
|-------------------------------------------|------------------------------------------------|--------------------------------------------|
| Single crosses<br>(involving two parents) | Three-way crosses<br>(involving three parents) | Double crosses<br>(involving four parents) |
| BNG-3 x 40023                             | (BNG-3 x 40023) x 40224                        | (BNG-3 x 40023) x (40225 x MAI-283)        |
| 40225 x MAI-283                           | (40225 x MAI-283) x 40224                      | (4085 x 1882) x (MAI-225 x 40224)          |

### 3.1.4 Observations recorded for grain yield and its attributing traits

Five random plants from each of the parental line and each of three replications were selected to record observations. Observations were recorded on each individual plant in the six segregating populations on the following ten quantitative traits.

- i. **Plant height (cm):** Height of the plant in cm was measured from the base of a plant at ground level to the top of tassel at dry silk stage with the help of a meter scale.
- ii. **Days to silking:** Days to silking was calculated as the period taken from date of seeding to silk emergence.
- iii. **Days to tasselling:** Days to tasselling was calculated as the period taken from date of seeding to anther emergence.

- iv. **Cob length (cm):** Length of the primary ear will be measured in cm, after harvest, from base to tip after removing the husk with the help of a centimetre scale.
- v. **Cob girth (cm):** Cob girth was measured in cm from the middle part of cob after removing the husk.
- vi. **Number of kernel rows per cob:** Number of kernel rows per cob was recorded by counting the number of rows in the middle of the primary ear after removing the dry husk at maturity.
- vii. **Number of kernels per row:** Number of kernels was counted in a randomly selected row in each ear and averaged.
- viii. **100-kernel weight (g):** Kernels from the primary ears of each plant were bulked and weight of 100 randomly selected kernels was recorded.
- ix. **Shelling percentage:** Shelling percentage is the ratio of seed weight to cob weight and expressed in percentage.
- x. **Grain yield plant<sup>-1</sup> (g):** The matured cobs harvested from each plant were sun dried and the seeds were separated and weighed. The weight was expressed as grain yield plant<sup>-1</sup> in grams.

### **Statistical analysis**

Mean of the five plants across ten quantitative traits from each of the three replications of the parental lines and observations recorded on individual plants of each of the six segregating populations were used for statistical analysis. Trait means were calculated for both parental lines and the six segregating populations whereas variability parameters like standardized range, PCV, GCV and genetic parameters were calculated only for the six segregating populations.

The following descriptive statistics and genetic parameters were estimated.

### 3.1.5 Estimation of mean and range

Mean and range for the observed traits was calculated using the following formula.

#### 3.1.5.1 The general mean was estimated as:

$$\text{General Mean } (\bar{X}) = \frac{\text{Sum of observations of five plants of parental lines or all plants in segregating population}}{\text{Number of plants in each population}}$$

#### 3.1.5.2 Absolute range (AR) was estimated as,

$$\text{AR} = \text{highest trait value} - \text{lowest trait value}$$

#### 3.1.5.3 Standardized range (SR) was estimated as,

$$\text{SR} = \frac{(\text{Highest trait value} - \text{lowest trait value})}{(\text{General mean})}$$

### 3.1.6 Estimation of components of variance and expected genetic advance

Genetic parameters namely GCV, PCV,  $h^2_{(bs)}$ , GA and GAM were estimated using the following formulae for ten quantitative traits under consideration.

#### 3.1.6.1 Estimation of phenotypic (PCV) and genotypic coefficient of variability (GCV)

Coefficients of variability at both phenotypic and genotypic levels were estimated for ten quantitative characters using the following formula given by Burton and Devane (1953).

##### □ Phenotypic Co-efficient of Variation (PCV)

$$\text{PCV} = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,

$\sigma_p$  = Phenotypic standard deviation

$\bar{X}$  = General mean

□ **Genotypic Co-efficient of Variation (GCV)**

$$GCV = \frac{\sigma_g}{\bar{X}} \times 100$$

Where,

$\sigma_g$  = Genotypic standard deviation

$\bar{X}$  = General mean

Estimated PCV and GCV were classified as suggested by Robinson *et al.* (1949)

5-10 % - Low;

10 -20 % - Moderate;

>20 % - High

**3.1.6.2 Levene's test for homogeneity of variances**

Levene's test ( Levene 1960) is used to examine if segregating populations derived from crosses involving varying number of parents have equal variances.

**The Levene test is defined as:**

$$H_0: \sigma_1^2 = \sigma_2^2 = \dots = \sigma_k^2$$

$$H_a: \sigma_i^2 \neq \sigma_j^2 \text{ for at least one pair (i,j).}$$

Where, k represent segregating populations.

**3.1.6.3 Estimation of broad sense heritability ( $h^2$ )**

Broad sense heritability estimates for ten quantitative traits under consideration were estimated according to the formula suggested by Lush (1945).

$$h^2 = \frac{V_g}{V_p} \times 100$$

Where,

$h^2$  = Broad sense heritability expressed in *per cent*

$V_g$  = Genotypic variance

$V_p$  = Phenotypic variance

Estimated heritability values were categorized following Robinson *et al.* (1949)

5-10 % = Low;

10-30 % = Moderate;

>30 % = High

#### **3.1.6.4 Estimation of expected genetic advance (GA)**

The extent of expected genetic advance of each trait at 5 *per cent* selection intensity was computed using the formula suggested by Johnson *et al.* (1955)

$$GA = k \times h^2 \times \sqrt{V_p}$$

Where,

$k$  = Selection differential which is equal to 2.06 at 5 per cent selection intensity, respectively.

$h^2$  = Broad sense heritability

$\sqrt{V_p}$  = Phenotypic standard deviation

Another important parameter for identifying the potential population from among the segregating populations derived from crosses involving varying number of parents is the sum of genetic advance and mean which is an usefulness criterion ( $U_c$ ) for identification of superior population.

$$U_c = \text{Trait Grand mean} + \text{Genetic advance}$$

#### **□ Expected Genetic Advance as *per cent* mean (GAM)**

The GAM was calculated as per Johnson *et al.* (1955)

$$GAM (\%) = (\text{Genetic advance (GA)}) / (\text{Trait grand mean } (\bar{X})) \times 100$$

GAM was categorized following Johnson *et al.* (1955)

0 -10 % = Low;

10 – 20 % = Moderate;

>20 % = High.

### 3.1.7 Coefficients of skewness and kurtosis

Genetic expectations of Skewness ( $-3/4 d^2 h$ ) indicates the nature of genetic control of the traits (Fisher *et al.*, 1932). Kurtosis reveals the relative number of genes controlling the traits (Robson, 1956). Coefficients of skewness and kurtosis were estimated (Snedecor and Cochran, 1994) to understand the nature of genetic control of ten quantitative traits using R software version 3.6.3 using libraries Performance Analytics. Further, results obtained for kurtosis and skewness were interpreted as indicated in Table 3 and Table 4, respectively.

**Table 3: Quantitative genetic interpretation of skewness**

| Type of skewness  | Interpretation                                                                 |
|-------------------|--------------------------------------------------------------------------------|
| Positive skewness | Complementary type of digenic epistasis between genes with decreasing effects. |
| Negative skewness | Duplicate type of digenic epistasis between genes with increasing effects.     |

**Table 4: Quantitative genetic interpretation of coefficients of kurtosis**

| Coefficients of kurtosis | Type of distribution | Interpretation                             |
|--------------------------|----------------------|--------------------------------------------|
| > 3                      | Leptokurtic          | Fewer number of genes control the trait    |
| 3                        | Mesokurtic           | Moderate number of genes control the trait |
| < 3                      | Platykurtic          | Large number of genes control the trait.   |

## 3.2 Comparison of frequency of transgressive segregants for productive traits across di, tri, tetra and multi parent derived segregating populations.

### 3.2.1 Frequency of transgressive segregants was estimated as

The number of plants in each of the segregating populations derived from di, tri and tetra parent crosses registering trait values lower than lower scoring parent and higher than higher scoring parent involved in the generation of the respective segregating populations derived from di, tri and tetra parent crosses were counted and designated as transgressive segregants in each of the two categories. Further, the frequency of transgressive segregants were worked out considering the total number of individuals in each of the segregating population using the formula

$$\text{Frequency of transgressive segregants} = \frac{\text{Number of transgressive segregants}}{\text{Total number of individuals in each population}} \times 100$$

Frequency of transgressive segregants recovered is an indicative of potential population.

### 3.2.2 Transgressive segregation index

Transgressive segregation index was estimated using the following formula (Koide *et al.*, 2019).

$$\text{TSI} = \frac{\text{Absolute range of a trait in F}_2 \text{ population}}{\text{Absolute parental range of a trait}}$$

Interpretation of TSI: Greater the value of the TSI, greater would be the chance of recovering transgressive segregants in the F<sub>2</sub> population.

### 3.2.3 Criteria for inference to assess breeding potential

The criteria used to draw inference is detailed in table 5. Potential segregating population(s) derived from di, tri and tetra parent crosses were identified following rank-sum method. Considering all the ten productivity traits viz., plant height, days to tasselling, days to silking, cob length, cob girth, number of kernel rows *per* cob, number of kernels *per* row, 100 kernel weight, shelling percentage, grain yield plant<sup>-1</sup>, each population was ranked from 1 to 6 (rank 1 for the population that expressed higher estimate under each of the statistical parameter and through 6 for population that expressed lower estimate under

each of the statistical parameter). Further, ranks were summed across these traits (Kang, 1988) and the population with lower rank sum was identified as the potential population.

**Table 5: Criteria for drawing inferences to assess breeding potential**

| <b>Statistical parameter</b>          | <b>Criteria</b> | <b>Inference</b>        |
|---------------------------------------|-----------------|-------------------------|
| Mean                                  | High            | High breeding potential |
| Standardized range                    | High            | High breeding potential |
| PCV and GCV                           | High            | High breeding potential |
| Genetic advance over mean             | High            | High breeding potential |
| Frequency of transgressive segregants | High            | High breeding potential |
| Transgressive segregation index       | High            | High breeding potential |



**Plate 1: General field view of segregating populations**

## **RESULTS AND DISCUSSION**

## IV RESULTS AND DISCUSSION

The results obtained are presented and discussed in this chapter under the following heads.

- 4.1 Comparison of mean performance among parental lines involved in developing segregating populations derived from crosses involving varying number of parents
  - 4.1.1 Descriptive statistics, genetic variability and their derived parameters for grain yield and its attributing traits among segregating populations derived from single cross, three way cross and double cross hybrids
  - 4.1.2 Frequency distribution of productivity traits among segregating populations derived from single cross, three way cross and double cross hybrids
- 4.2 Frequency of transgressive segregants and transgressive segregation index for grain yield and its attributing traits among segregating populations derived from single cross, three way cross and double cross hybrids
- 4.3 Breeding potential of segregating populations derived from single cross, three way cross and double cross derived hybrids

### **4.1 Comparison of mean performance among parental lines involved in developing segregating populations derived from crosses involving varying number of parents**

Mean performance among parental lines for grain yield and its attributing traits involved in developing segregating populations derived from single cross, three way cross and double cross hybrids are presented in Table 6. Mean plant height among parents ranged from 157.8 (40023) to 201.9 cm (BNG-3). Days to 50 *per cent* tasselling ranged from 54 days (1882) to 60 days (BNG-3). Days to 50 *per cent* silking ranged from 57 days (1882) to 62 days (BNG-3 and 4085). Cob length was greater for cobs produced by the parental line BNG-3 (16.3 cm) while 4085 (10.8 cm) parental line produced cobs of shorter length. Cob girth among parents ranged from 11.9 cm (40225) to 14.8 cm (BNG-3). Mean number of kernel rows *per* cob were more for the cobs produced by the parental line 1882 (17) while, the cobs produced by the parental line MAI-283 (12) contain less kernel rows.

**Table 6: Estimates of quantitative trait means among parents used in deriving segregating populations in sweetcorn**

| Parents | Plant height (cm) | Days to 50% tasselling | Days to 50% silking | Cob length (cm) | Cob girth (cm) | Number of kernel rows <i>per cob</i> | Number of kernels <i>per row</i> | 100 - kernel weight (g) | Shelling percentage | Grain yield plant <sup>-1</sup> (g) |
|---------|-------------------|------------------------|---------------------|-----------------|----------------|--------------------------------------|----------------------------------|-------------------------|---------------------|-------------------------------------|
| MAI-225 | 170.8±2.94        | 55.6±1.20              | 58.17±1.58          | 15.06±0.40      | 13.60±0.23     | 15.40±0.45                           | 26.6±0.62                        | 11.4±0.72               | 67.3±1.36           | 44.80±1.92                          |
| 40224   | 182.8±3.65        | 57.6±0.88              | 59.67±1.45          | 13.76±0.16      | 12.60±0.20     | 14.60±0.37                           | 23.8±0.83                        | 12.5±1.84               | 65.7±2.73           | 52.95±1.73                          |
| 1882    | 166.2±2.67        | 54.3±1.20              | 57.00±1.15          | 15.20±0.48      | 14.19±0.34     | 17.00±0.50                           | 29.2±1.17                        | 14.6±1.46               | 74.7±2.47           | 58.21±4.48                          |
| 4085    | 159.6±2.21        | 59.0±1.01              | 62.16±0.83          | 10.80±0.27      | 13.70±0.22     | 16.10±0.36                           | 18.8±0.67                        | 10.2±1.03               | 74.2±0.95           | 23.31±1.07                          |
| MAI-283 | 162.1±2.2         | 59.3±1.76              | 61.67±2.40          | 14.20±0.29      | 12.10±0.73     | 11.60±0.61                           | 19.8±0.47                        | 16.6±0.26               | 61.9±5.07           | 23.67±4.68                          |
| 40225   | 172.1±3.76        | 56.3±1.45              | 59.33±0.88          | 15.70±0.35      | 11.90±0.30     | 17.00±0.41                           | 25.0±0.73                        | 12.4±0.61               | 42.4±4.09           | 29.00±1.69                          |
| 40023   | 157.8±3.70        | 55.5±1.32              | 58.33±0.72          | 14.60±0.30      | 13.40±0.21     | 14.00±0.73                           | 21.3±0.89                        | 11.2±0.48               | 42.7±0.98           | 40.43±2.15                          |
| BNG-3   | 201.9±2.50        | 59.8±1.09              | 62.33±1.01          | 16.30±0.25      | 14.80±0.27     | 15.80±0.31                           | 26.2±1.06                        | 14.3±1.14               | 69.6±1.93           | 53.80±2.83                          |

Number of kernels *per* row ranged from 20 (MAI- 283) to 29 (1882). Mean of 100 kernel weight among parents ranged from 10.2 g (4085) to 16.6 g (MAI-283). Shelling percentage ranged from 42.4 *per cent* (40225) to 74.7 *per cent* (1882). For grain yield plant<sup>-1</sup>, 1882 showed higher yield (58.2 g) and 4085 showed lower yield (23.31g). Large differences in means across quantitative traits among parental lines suitably substantiate their usefulness in deriving segregating populations used in the present investigation.

#### **4.1.1 Estimation of descriptive statistics, genetic variability and their derived parameters for grain yield and its attributing traits among segregating populations derived from single cross, three way cross and double cross hybrids**

In any crop breeding programme, information on mean performance and genetic variability parameters is essential for improvement of productivity traits. To accomplish any breeding strategies, genetic variability available or created in the breeding material is very important, as it helps in selection of desired genotypes.

In the present study, variability present in the population is divided into genotypic and phenotypic variance. When absolute range is used as a criterion to assess the degree of variability, comparison of traits cannot be made, as these traits have different units of measurement. Hence, estimates of standardized range that provides reliable information could be used as a criterion to compare segregating populations across traits. However, standardized range does not reflect variability in the expression of traits as such. Thus, variability present in population expressed as PCV (phenotypic coefficient of variability), GCV (genotypic coefficient of variability) and heritability ( $h^2_{bs}$ ) and GAM (genetic advance as *per cent* of mean) were considered as criterion for identifying promising population.

Mean performance, genetic variability and their derived parameters for grain yield and its attributing traits among segregating populations derived from single cross, three way cross, double cross hybrids are presented in tables 7 - 17. Box-Whisker plots depicting distribution of quantitative trait means for these populations are presented in Figures 1-3.

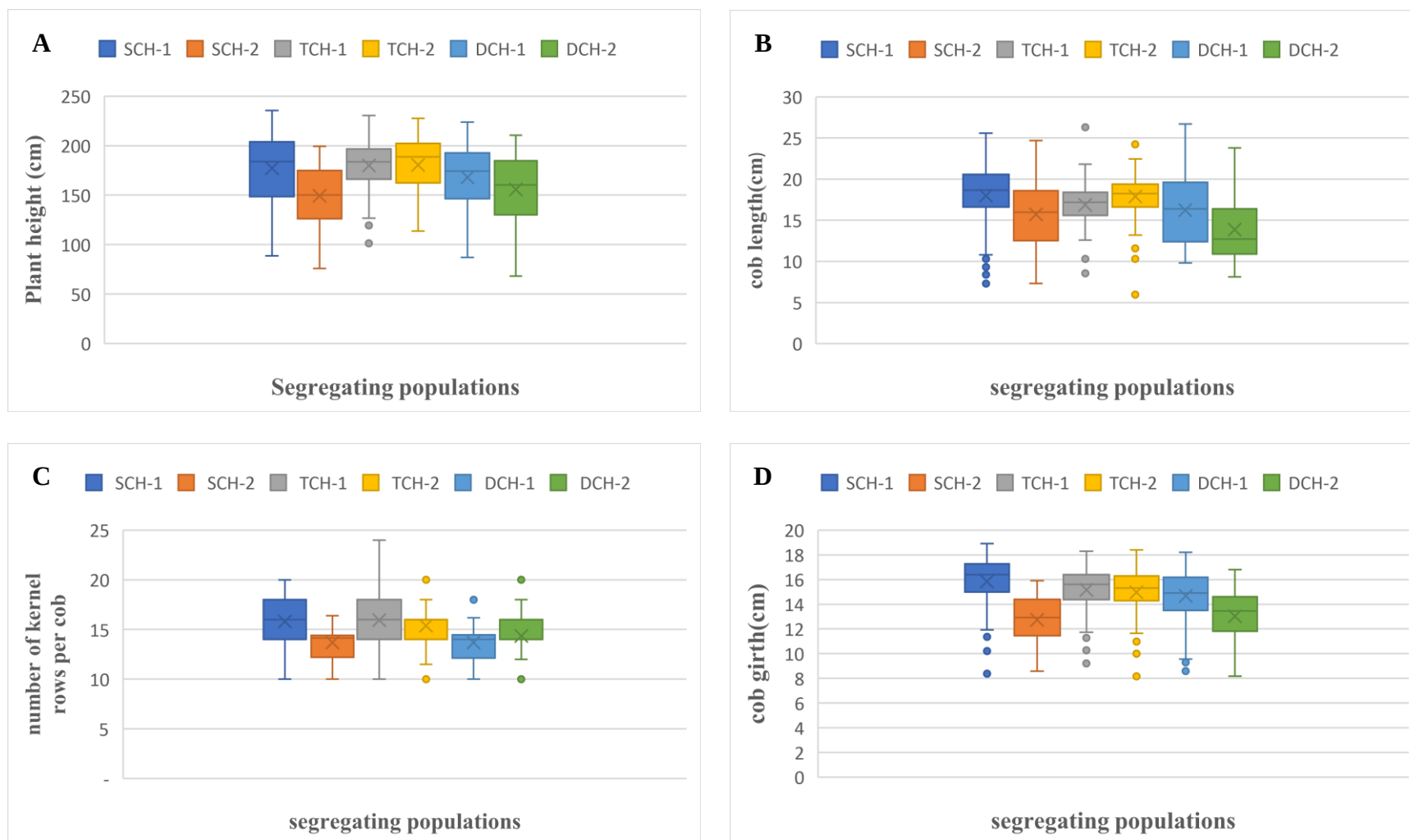


**Fig. 1: Box-Whisker plots depicting distribution of quantitative traits A. Plant height B. Cob length C. Cob girth D. Number of kernel rows per cob across six segregating populations in sweetcorn**

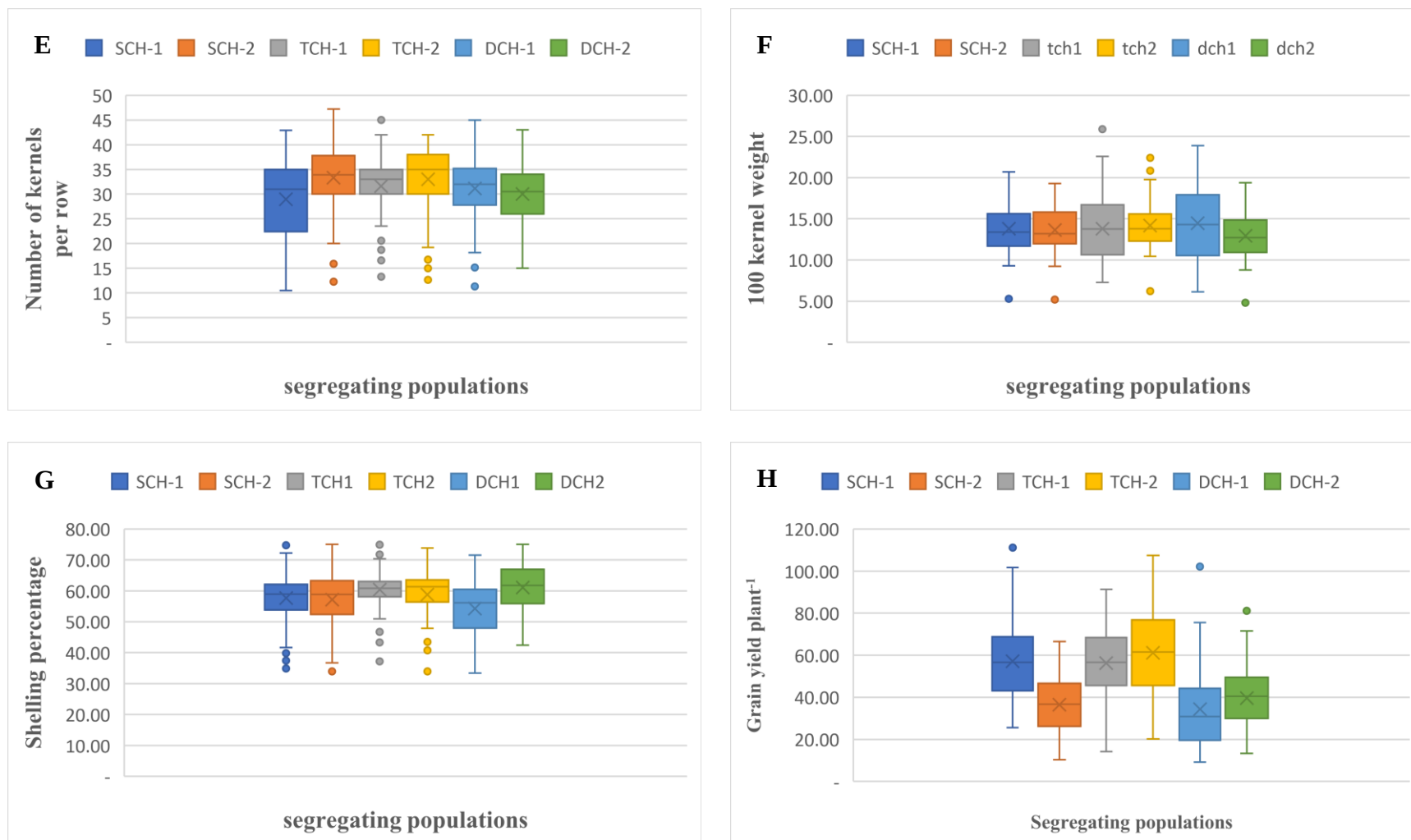


**Fig. 2: Box-Whisker plots depicting distribution of quantitative traits E. Number of kernels *per row* F. 100 kernel weight G. Shelling percentage H. Grain yield plant<sup>-1</sup> across six segregating populations in sweetcorn**

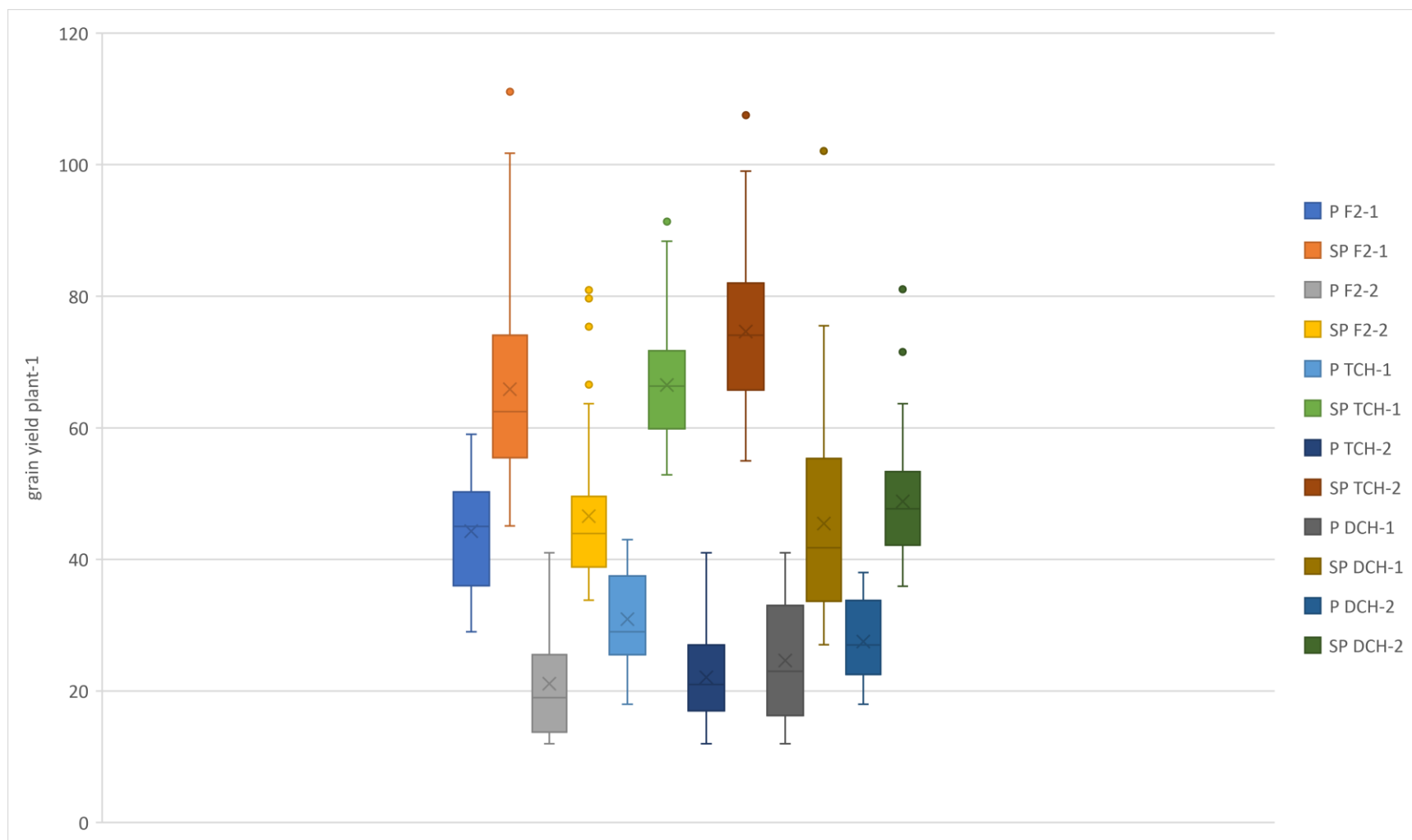


**Fig. 3: Box-Whisker plots depicting distribution of grain yield plant<sup>-1</sup> across six segregating populations in sweetcorn tandemly presented with their respective parents. P – Parents SP- Segregating Population**

#### **4.1.1.1 Estimates of quantitative trait means for grain yield and its attributing traits among segregating populations derived from crosses involving varying number of parents in sweetcorn**

Arithmetic mean is a measure of central tendency and often used in summarizing the data points. It picturizes the tendency of individuals in the populations to congregate in the distribution. The estimates of quantitative trait means among segregating populations derived from crosses involving varying number of parents in sweetcorn are depicted in Table 7 & 8. Estimates of mean plant height among six segregating populations varied from 151.6 cm in single cross hybrid [40225 × MAI-283] to 181.4 cm in three-way cross hybrid [(BNG-3 × 40023) × 40224]. Large differences observed for plant height between populations could be due to the fact that one of the parents involved in the cross [40225 × MAI-283] is MAI-283 which produced lower plant height (162.1 cm) while in the cross [(BNG-3 × 40023) × 40224] BNG-3 as a parent had higher mean plant height (201.9 cm). Days to tasseling ranged from 59.39 days in double cross hybrid [(BNG-3 × 40023) × (40225 × MAI-283)] to 61.21 days in three-way cross hybrid [(BNG-3 × 40023) × 40224]. Days to silking ranged from 61.05 days in single cross hybrid [40225 × MAI-283] to 63.46 days in single cross hybrid [BNG-3 × 40023]. The mean cob length ranged from 13.85 cm in double cross hybrid [(4085 × 1882) × (MAI-225 × 40224)] to 17.98 cm in single cross hybrid [BNG-3 × 40023]. The differences observed could be due to the fact that one of the parent involved in [(4085 × 1882) × (MAI-225 × 40224)] is 4085 which has shorter cob length (10.8 cm) and in [BNG-3 × 40023] BNG-3 has longer cob length (16.3 cm). The cob girth ranged from 12.72 cm in single cross hybrid [40225 × MAI-283] to 15.83 cm in single cross hybrid [BNG-3 × 40023] (Table 7). The number of kernel rows *per* cob ranged from 13.68 in single cross hybrid [40225 × MAI-283] to 15.93 in three-way cross hybrid [(BNG-3 × 40023) × 40224]. The differences observed could be due to the fact that one of the parent involved in [40225 × MAI-283] is MAI-283 which has less number of kernel rows *per* cob (11.6) and in [(BNG-3 × 40023) × 40224] BNG-3 has more number of kernel rows *per* cob (15.8). The number of kernels *per* row ranged from 28.96 in single cross hybrid [BNG-3 × 40023] to 33.34 in single cross hybrid [40225 × MAI-283].

**Table 7: Estimates of quantitative trait means among segregating populations derived from crosses involving varying number of parents in sweetcorn**

| Segregating populations derived from | Trait<br>Parentage                    | Number of parents involved | Plant height (cm) | Days to tasselling | Days to silking | Cob length (cm) | Cob girth (cm) |
|--------------------------------------|---------------------------------------|----------------------------|-------------------|--------------------|-----------------|-----------------|----------------|
| Single cross Hybrids                 | [BNG-3 × 40023]                       | <b>Two</b>                 | 177.5±3.74        | 60.98±1.08         | 63.46±0.38      | 17.98±0.45      | 15.83±0.21     |
|                                      | [40225 × MAI-283]                     |                            | 151.6±3.39        | 60.23±1.14         | 61.05±0.39      | 15.70±0.41      | 12.72±0.19     |
| Three-way cross Hybrids              | [(BNG-3 × 40023) × 40224]             | <b>Three</b>               | 181.4±2.79        | 61.21±1.07         | 63.15±0.31      | 16.85±0.26      | 15.15±0.17     |
|                                      | [(40225 × MAI-283) × 40224]           |                            | 178.6±3.41        | 60.98±1.20         | 62.94±0.44      | 17.89±0.28      | 14.96±0.19     |
| Double cross Hybrids                 | [(BNG-3 × 40023) × (40225 × MAI-283)] | <b>Four</b>                | 172.31±3.27       | 59.39±1.13         | 61.43±0.45      | 16.22±0.39      | 14.67±0.18     |
|                                      | [(4085×1882) × (MAI-225×40224)]       |                            | 155.7±3.52        | 59.52±0.99         | 61.18±0.37      | 13.85±0.36      | 13.03±0.21     |

The differences observed could be due to the fact that one of the parent involved in [BNG-3  $\times$  40023] is 40023 which has less number of kernels *per row* (21.3) and in [40225  $\times$  MAI-283] 40225 has more number of kernels *per row*. The 100-kernel weight among the segregating populations ranged from 12.97 gm in double cross hybrid [(4085 $\times$  1882)  $\times$  (MAI-225  $\times$  40224)] to 14.46 in double cross hybrid [(BNG-3  $\times$  40023)  $\times$  (40225  $\times$  MAI-283)]. The differences observed could be due to the fact that one of the parent involved in [(4085 $\times$  1882)  $\times$  (MAI-225  $\times$  40224)] is 4085 which has low 100 kernel weight (10.2 gm) and in [(BNG-3  $\times$  40023)  $\times$  (40225  $\times$  MAI-283)] 40225 has high 100 kernel weight (16.6gm). Shelling percentage ranged from 54.28 *per cent* in double cross hybrid [(BNG-3  $\times$  40023)  $\times$  (40225  $\times$  MAI-283)] to 61.07 *per cent* in [(4085 $\times$  1882)  $\times$  (MAI-225  $\times$  40224)]. The differences observed could be due to the fact that one of the parent involved in [(BNG-3  $\times$  40023)  $\times$  (40225  $\times$  MAI-283)] is 40225 which has low shelling percentage (42.4%) and in [(4085 $\times$  1882)  $\times$  (MAI-225  $\times$  40224)] 1882 has high shelling percentage (74.7%). Grain yield plant<sup>-1</sup> ranged from 38.38 gm in single cross hybrid [40225  $\times$  MAI-283] to 63.27 gm in three-way cross hybrid [(BNG-3  $\times$  40023)  $\times$  40224]. The differences observed could be due to the fact that one of the parent involved in [40225  $\times$  MAI-283] is MAI-283 has less grain yield (23.67gm) and in [(BNG-3  $\times$  40023)  $\times$  40224] BNG-3 has higher grain yield (53.8 gm). (Table 8). Higher trait's mean indicates the presence of genes that enhances traits phenotype (Dudley 1982, 1984; Melchinger 1987; Bernardo 2002) and hence maximizing the chances of recovering superior advanced breeding lines.

#### **4.1.1.2 Estimates of Standardized range for grain yield and its attributing traits among segregating populations derived from single cross, three way cross, and double cross hybrids**

Standardized range being yet another measures of dispersion, denotes variability present in the population. The merit of standardized range used as a measure of variability is helpful when traits with different units of measurement are to be compared within and among segregating populations. Thus, apart from absolute range, standardized range was also considered for assessing breeding potential of the populations. The estimates of unit-dependent absolute range and unit-independent standardized range are the reflections of occurrence of extreme phenotypes.

**Table 8: Estimates of quantitative trait means among segregating populations derived from crosses involving varying number of parents in sweetcorn**

| Segregating populations derived from | Trait<br>Parentage                    | Number of parents involved | Number of kernel rows <i>per cob</i> | Number of kernels <i>per row</i> | 100 kernel weight (g) | Shelling percentage | Grain yield plant <sup>-1</sup> (g) |
|--------------------------------------|---------------------------------------|----------------------------|--------------------------------------|----------------------------------|-----------------------|---------------------|-------------------------------------|
| Single cross Hybrids                 | [BNG-3×40023]                         | <b>Two</b>                 | 15.79±0.27                           | 29.07±0.87                       | 13.80±0.28            | 57.67±0.82          | 61.91±1.81                          |
|                                      | [40225×MAI-283]                       |                            | 13.68±0.18                           | 33.42±0.72                       | 13.65±0.25            | 57.11±0.86          | 38.38±1.73                          |
| Three-way cross Hybrids              | [(BNG-3×40023) × 40224]               | <b>Three</b>               | 15.93±0.25                           | 31.70±0.72                       | 13.80±0.38            | 60.38±0.60          | 56.27±1.99                          |
|                                      | [(40225×MAI-283) × 40224]             |                            | 15.39±0.22                           | 33.11±0.79                       | 14.19±0.28            | 58.74±0.87          | 59.18±1.77                          |
| Double cross Hybrids                 | [(BNG-3 × 40023) × (40225 × MAI-283)] | <b>Four</b>                | 13.69±0.17                           | 31.26±0.78                       | 14.46±0.49            | 54.28±0.91          | 40.28±2.10                          |
|                                      | [(4085 × 1882) × (MAI-225 × 40224)]   |                            | 14.36±0.18                           | 30.07±0.71                       | 12.94±0.26            | 61.07±0.73          | 39.55±1.63                          |

Standardized range provides the means of assessing the potentiality of the cross across quantitative traits as the estimated values are unit independent. Further these estimates across traits are relative. Accordingly, based on the standardized range values across traits, the same was classified as lower, moderate and higher magnitudes of standardized range. All the populations exhibited lower magnitudes of standardized range for days to tasselling, days to silking, cob girth, number of kernel rows *per* cob and shelling percentage. Lower magnitudes of standardized range for days to tasselling, days to silking, cob girth (cm), number of kernel rows *per* cob and shelling percentage might be attributed to fewer number of genes governing the trait and lack of substantial variability among parental lines. All the populations exhibited moderate magnitude of standardized range for plant height, cob length and 100 kernel weight. Moderate magnitude might be due to absence of substantial variability for plant height among the parental lines used in developing segregating populations under investigation. Further, number of kernels *per* row and grain yield plant<sup>-1</sup> manifested higher standardized range indicating probable governance of these traits by polygenes which in turn shuffled among the segregants to give rise to observed variation. Segregating population derived from single cross hybrid (40225 × MAI-283) expressed higher estimate of standardized range for the most economical trait, grain yield plant<sup>-1</sup> (3.26) (Table 9).

#### **4.1.1.3 Genetic variability parameters for ten quantitative traits among six segregating populations derived from single cross, three way cross and double cross hybrids**

The PCV estimates represent an unbiased and true reflection of variability unlike absolute range and standardize range which are biased by extreme values. Phenotypic coefficient of variation as a measure of dispersion confounds the genetic and environmental variability. Thus, narrow difference between PCV and GCV indicates little influence of environment on the expression of a trait. Such differences can be observed to be reflecting another genetic variability parameter, broad sense heritability which is a measure of the extent of phenotypic variation due to genotypic factors. An estimate of high heritability coupled with high GAM in any population drives effective selection of target traits.

**Table 9: Estimates of Standardized range for grain yield and its attributing traits among segregating populations derived from crosses involving varying number of parents in sweetcorn**

| Segregating populations derived from | Trait<br>Parentage                    | Number of parents involved | Plant height (cm) | Days to tasselling | Days to silking | Cob length (cm) | Cob girth (cm) | Number of kernel rows <i>per</i> cob | Number of kernels <i>per</i> row | 100 - kernel weight (g) | Shelling percentage | Grain yield plant <sup>-1</sup> (g) |
|--------------------------------------|---------------------------------------|----------------------------|-------------------|--------------------|-----------------|-----------------|----------------|--------------------------------------|----------------------------------|-------------------------|---------------------|-------------------------------------|
| Single cross hybrids                 | [BNG-3 × 40023]                       | Two                        | 1.22              | 0.26               | 0.21            | 1.01            | 0.66           | 0.63                                 | 2.12                             | 1.12                    | 0.69                | 2.17                                |
|                                      | [40225 × MAI-283]                     |                            | 1.18              | 0.24               | 0.31            | 1.11            | 0.57           | 0.46                                 | 1.98                             | 1.03                    | 0.72                | 3.26                                |
| Three-way cross hybrids              | [(BNG-3 × 40023) × 40224]             | Three                      | 1.21              | 0.22               | 0.16            | 1.05            | 0.60           | 0.87                                 | 2.01                             | 1.34                    | 0.62                | 2.12                                |
|                                      | [(40225 × MAI-283) × 40224]           |                            | 1.08              | 0.33               | 0.29            | 1.02            | 0.68           | 0.64                                 | 1.84                             | 1.14                    | 0.68                | 2.30                                |
| Double cross hybrids                 | [(BNG-3 × 40023) × (40225 × MAI-283)] | Four                       | 1.14              | 0.22               | 0.33            | 1.04            | 0.65           | 0.58                                 | 2.04                             | 1.22                    | 0.70                | 3.05                                |
|                                      | [(4085 × 1882) × (MAI-225 × 40224)]   |                            | 1.23              | 0.18               | 0.23            | 1.13            | 0.66           | 0.69                                 | 2.06                             | 1.12                    | 0.53                | 3.23                                |

For plant height, high magnitude of PCV and GCV was observed for segregating populations of single cross hybrid [BNG-3  $\times$  40023], single cross hybrid [40225  $\times$  MAI-283] and double cross hybrid [(4085 $\times$ 1882)  $\times$  (MAI-225 $\times$ 40224)] while moderate values of PCV and GCV was observed in remaining segregating populations. Low magnitude of PCV and GCV was observed among all the populations for days to tasselling and days to silking indicating less amount of variability for this trait and these traits also manifested less heritability and low GAM (Table 12-13). Moderate magnitude of PCV and GCV was observed for number of kernel rows *per* cob, shelling percentage and cob girth. For cob length, high magnitude of PCV and GCV was observed in segregating populations of single cross hybrid [BNG-3  $\times$  40023], single cross hybrid [40225  $\times$  MAI-283], double cross hybrid [(4085 $\times$ 1882)  $\times$  (MAI-225 $\times$ 40224)] and double cross hybrid [(BNG-3 $\times$ 40023)  $\times$  (40225 $\times$ MAI-283)] and in the remaining segregating populations moderate magnitudes of PCV and GCV were observed. For 100 kernel weight, high magnitude of PCV and GCV were observed for single cross hybrid [BNG-3  $\times$  40023], three-way cross hybrid [(BNG-3 $\times$ 40023)  $\times$  40224] and double cross hybrid [(BNG-3 $\times$ 40023)  $\times$  (40225 $\times$ MAI-283)] and moderate magnitude was observed in remaining populations. High magnitude of PCV and GCV was observed among all the segregating populations for number of kernels *per* row and grain yield plant<sup>-1</sup>. Similar results were reported by Rahman *et al.* (2015) for grain yield plant<sup>-1</sup>. The amount of variation was observed considerably more in segregating populations derived from double cross hybrids and single cross hybrids compared to segregating populations derived from three way cross hybrids. Similar results were reported by Ashakina *et al.* (2016) in tomato. High heritability and high GAM was observed for traits i.e., plant height, cob length, number of kernels *per* row and grain yield plant<sup>-1</sup> among all the segregating populations and for days to tasselling in [BNG-3  $\times$  40023] and [(BNG-3 $\times$ 40023)  $\times$  40224], cob girth in [BNG-3  $\times$  40023], [(BNG-3 $\times$ 40023)  $\times$  40224], [(4085 $\times$ 1882)  $\times$  (MAI-225 $\times$ 40224)], for number of kernel rows *per* cob in [BNG-3  $\times$  40023], [(BNG-3 $\times$ 40023)  $\times$  40224] and for 100 kernel weight in [BNG-3  $\times$  40023], [40225 $\times$ MAI-283], [(BNG-3 $\times$ 40023)  $\times$  40224], [(BNG-3 $\times$ 40023)  $\times$  (40225 $\times$ MAI-283)] and for shelling percentage in [BNG-3  $\times$  40023], [(BNG-3 $\times$ 40023)  $\times$  40224], [(4085 $\times$ 1882)  $\times$  (MAI-225 $\times$ 40224)] indicating comparable PCV and GCV values and less environmental influence and the variation among the segregating populations for these traits might be due to genetic factors (Table 11).

**Table 10: Estimates of Phenotypic and genotypic coefficients of variation (PCV and GCV) for grain yield and its attributing traits among segregating population derived from crosses involving varying number of parents in sweetcorn**

| Segregating populations derived from | Trait<br>Parentage                    | Number of parents involved | Plant height (cm) |       | Days to tasselling |      | Days to silking |      | Cob length (cm) |       | Cob girth (cm) |       |
|--------------------------------------|---------------------------------------|----------------------------|-------------------|-------|--------------------|------|-----------------|------|-----------------|-------|----------------|-------|
|                                      |                                       |                            | PCV               | GCV   | PCV                | GCV  | PCV             | GCV  | PCV             | GCV   | PCV            | GCV   |
| Single cross hybrids                 | [BNG-3 × 40023]                       | <b>Two</b>                 | 21.09             | 19.92 | 5.03               | 4.36 | 5.32            | 4.17 | 25.17           | 24.27 | 13.44          | 12.10 |
|                                      | [40225 × MAI-283]                     |                            | 22.41             | 20.97 | 5.37               | 1.30 | 5.62            | 3.25 | 26.17           | 25.13 | 15.29          | 10.79 |
| Three-way cross hybrids              | [(BNG-3 × 40023) × 40224]             | <b>Three</b>               | 15.40             | 13.65 | 4.95               | 3.84 | 4.31            | 3.04 | 15.39           | 14.09 | 11.10          | 9.54  |
|                                      | [(40225 × MAI-283) × 40224]           |                            | 19.08             | 17.69 | 5.61               | 2.85 | 6.30            | 4.96 | 15.91           | 14.88 | 12.54          | 9.65  |
| Double cross hybrids                 | [(BNG-3 × 40023) × (40225 × MAI-283)] | <b>Four</b>                | 19.03             | 17.68 | 5.41               | 3.46 | 6.59            | 5.22 | 23.92           | 22.79 | 12.42          | 5.06  |
|                                      | [(4085 × 1882) × (MAI-225 × 40224)]   |                            | 22.61             | 21.41 | 4.73               | 2.87 | 5.46            | 4.53 | 26.25           | 24.27 | 15.97          | 14.14 |

**Table 11: Estimates of Phenotypic and genotypic coefficients of variation (PCV and GCV) for grain yield and its attributing traits among segregating population derived from crosses involving varying number of parents in sweetcorn**

| Segregating populations derived from | Trait<br>Parentage                    | Number of parents involved | Number of kernel rows per cob |       | Number of kernels per row |       | 100 kernel weight (g) |       | Shelling percentage |       | Grain yield plant <sup>-1</sup> (g) |       |
|--------------------------------------|---------------------------------------|----------------------------|-------------------------------|-------|---------------------------|-------|-----------------------|-------|---------------------|-------|-------------------------------------|-------|
|                                      |                                       |                            | PCV                           | GCV   | PCV                       | GCV   | PCV                   | GCV   | PCV                 | GCV   | PCV                                 | GCV   |
| Single cross hybrids                 | [BNG-3 × 40023]                       | <b>Two</b>                 | 17.12                         | 14.86 | 30.13                     | 27.75 | 20.73                 | 17.23 | 14.14               | 13.36 | 31.54                               | 27.08 |
|                                      | [40225 × MAI-283]                     |                            | 13.50                         | 7.08  | 21.59                     | 20.94 | 18.45                 | 17.79 | 14.93               | 5.24  | 44.60                               | 39.60 |
| Three way cross hybrids              | [(BNG-3 × 40023) × 40224]             | <b>Three</b>               | 15.80                         | 13.41 | 22.90                     | 20.47 | 27.36                 | 21.93 | 9.85                | 7.98  | 31.14                               | 28.21 |
|                                      | [(40225 × MAI-283) × 40224]           |                            | 14.48                         | 10.79 | 24.06                     | 23.11 | 19.76                 | 14.34 | 14.58               | 8.23  | 31.17                               | 28.27 |
| Double cross hybrids                 | [(BNG-3 × 40023) × (40225 × MAI-283)] | <b>Four</b>                | 12.63                         | 6.77  | 24.92                     | 23.36 | 33.65                 | 32.57 | 16.59               | 12.46 | 51.52                               | 46.93 |
|                                      | [(4085 × 1882) × (MAI-225 × 40224)]   |                            | 12.73                         | 5.97  | 23.72                     | 21.23 | 19.75                 | 8.32  | 11.99               | 10.53 | 40.71                               | 32.13 |

Similar results were reported by Patil *et al.* (2016) for grain yield plant<sup>-1</sup>, plant height and number of kernels *per* row. Moderate magnitude of heritability and low GAM was observed for days to silking. Low magnitude of heritability and low GAM was observed in segregating populations for days to tasselling in [40225×MAI-283], [(40225 × MAI-283) × 40224], for cob girth in [BNG-3 × 40023], [(BNG-3×40023) × 40224], [(4085×1882) × (MAI-225×40224)], for number of kernel rows *per* cob in [BNG-3 × 40023], [40225×MAI-283], [(BNG-3×40023) × (40225×MAI-283)], [(4085×1882) × (MAI-225×40224)] and for 100 kernel weight in [(40225 × MAI-283) × 40224], [(4085×1882) × (MAI-225×40224)] and for shelling percentage in [40225 × MAI-283] indicating effect on environment on these traits. (Table 12-13).

#### **4.1.1.4 Levene's test for homogeneity of variances for grain yield and its attributing traits among segregating populations derived from varying number of parents**

Levene's test for homogeneity of variances is used when comparison is to be made among populations based on trait variances and when number of individuals among population being compared are not same. The variances among segregating populations derived from crosses involving varying number of parents significantly differed for all the quantitative traits except days to tasselling, days to silking and cob girth (Table 14).

#### **4.1.1.5 Estimates of absolute phenotypic variances among segregating populations derived from crosses involving varying number of parents across ten quantitative traits in sweetcorn**

Segregating population derived from double cross hybrid [(BNG-3×40023) × (40225×MAI-283)] registered high absolute variance for 100 kernel weight and grain yield plant<sup>-1</sup> indicating the population to be promising. There by suggesting to advance individuals of this segregating population to stabilize and isolate superior breeding lines with high grain yield plant<sup>-1</sup> and 100 kernel weight in advanced generations (Table 15).

**Table 12: Estimates of heritability for grain yield and its attributing traits among segregating population derived from crosses involving varying number of parents in sweetcorn**

| Statistic                           | Segregating populations derived from | Trait<br>Parentage                    | Number of parents involved | Plant height (cm) | Days to tasselling | Days to silking | Cob length (cm) | Cob girth (cm) | Number of kernel rows <i>per</i> cob | Number of kernels <i>per</i> row | 100 - kernel weight (g) | Shelling percentage | Grain yield plant <sup>-1</sup> (g) |
|-------------------------------------|--------------------------------------|---------------------------------------|----------------------------|-------------------|--------------------|-----------------|-----------------|----------------|--------------------------------------|----------------------------------|-------------------------|---------------------|-------------------------------------|
| <b>h<sup>2</sup><sub>(bs)</sub></b> | Single cross hybrids                 | [BNG-3 × 40023]                       | <b>Two</b>                 | 88.22             | 75.19              | 61.29           | 93.02           | 81.03          | 75.36                                | 81.41                            | 66.93                   | 89.38               | 68.61                               |
|                                     |                                      | [40225 × MAI-283]                     |                            | 85.91             | 5.89               | 33.46           | 92.18           | 49.85          | 27.52                                | 91.53                            | 92.26                   | 12.32               | 66.32                               |
|                                     | Three-way cross hybrids              | [(BNG-3 × 40023) × 40224]             | <b>Three</b>               | 74.72             | 60.07              | 49.83           | 83.81           | 73.88          | 72.04                                | 71.56                            | 64.24                   | 65.59               | 70.61                               |
|                                     |                                      | [(40225 × MAI-283) × 40224]           |                            | 80.25             | 25.84              | 61.81           | 87.43           | 59.11          | 55.48                                | 90.18                            | 49.52                   | 31.84               | 87.06                               |
|                                     | Double cross hybrids                 | [(BNG-3 × 40023) × (40225 × MAI-283)] | <b>Four</b>                | 83.72             | 41.03              | 62.64           | 90.83           | 16.64          | 28.76                                | 83.95                            | 93.70                   | 56.36               | 77.73                               |
|                                     |                                      | [(4085 × 1882) × (MAI-225 × 40224)]   |                            | 88.97             | 36.83              | 68.67           | 85.50           | 78.32          | 21.94                                | 71.31                            | 12.28                   | 77.08               | 46.64                               |

**Table 13: Estimates of genetic advance as *per cent* of mean for grain yield and its attributing traits among segregating population derived from crosses involving varying number of parents in sweetcorn**

| Statistic      | Segregating populations derived from | Trait<br>Parentage                    | Number of parents involved | Plant height (cm) | Days to tasselling | Days to silking | Cob length (cm) | Cob girth (cm) | Number of kernel rows <i>per</i> cob | Number of kernels <i>per</i> row | 100 - kernel weight (g) | Shelling percentage | Grain yield plant <sup>-1</sup> (g) |
|----------------|--------------------------------------|---------------------------------------|----------------------------|-------------------|--------------------|-----------------|-----------------|----------------|--------------------------------------|----------------------------------|-------------------------|---------------------|-------------------------------------|
| <b>GAM (%)</b> | Single cross hybrids                 | [BNG-3 × 40023]                       | <b>Two</b>                 | 36.66             | 7.78               | 6.72            | 48.23           | 22.44          | 26.58                                | 45.82                            | 27.56                   | 26.03               | 40.87                               |
|                |                                      | [40225 × MAI-283]                     |                            | 37.89             | 0.65               | 3.87            | 49.71           | 15.71          | 7.65                                 | 34.11                            | 33.48                   | 3.79                | 50.88                               |
|                | Three way cross hybrids              | [(BNG-3 × 40023) × 40224]             | <b>Three</b>               | 21.97             | 6.13               | 4.43            | 26.58           | 16.91          | 23.44                                | 28.43                            | 36.20                   | 13.32               | 39.73                               |
|                |                                      | [(40225 × MAI-283) × 40224]           |                            | 26.28             | 2.99               | 8.03            | 28.66           | 15.27          | 16.55                                | 39.62                            | 19.47                   | 9.56                | 59.78                               |
|                | Double cross hybrids                 | [(BNG-3 × 40023) × (40225 × MAI-283)] | <b>Four</b>                | 30.88             | 4.57               | 8.51            | 44.76           | 4.25           | 7.48                                 | 37.58                            | 64.95                   | 19.27               | 84.58                               |
|                |                                      | [(4085 × 1882) × (MAI-225 × 40224)]   |                            | 40.07             | 3.59               | 7.73            | 46.24           | 25.78          | 5.76                                 | 29.12                            | 4.83                    | 19.04               | 32.81                               |

**Table 14: ANOVA using levene's test for homogeneity of variance of quantitative trait phenotypic variances of segregating populations derived from crosses involving varying number of parents**

| <b>Traits</b>                        | <b>Degrees of Freedom</b> | <b>F value</b>        |
|--------------------------------------|---------------------------|-----------------------|
| Plant height                         | 5                         | 3.1893 <sup>**</sup>  |
| Days to tasselling                   | 5                         | 0.3883 <sup>NS</sup>  |
| Days to silking                      | 5                         | 1.1216 <sup>NS</sup>  |
| Cob length                           | 5                         | 8.9528 <sup>***</sup> |
| Cob girth                            | 5                         | 1.4397 <sup>NS</sup>  |
| Number of kernel rows <i>per</i> cob | 5                         | 4.2194 <sup>***</sup> |
| Kernels <i>per</i> row               | 5                         | 2.6534 <sup>***</sup> |
| 100 kernel weight                    | 5                         | 17.753 <sup>***</sup> |
| Shelling percentage                  | 5                         | 4.2943 <sup>***</sup> |
| Grain yield plant <sup>-1</sup>      | 5                         | 5.3146 <sup>***</sup> |

**Table 15: Estimates of absolute phenotypic variances among segregating populations derived from crosses involving varying number of parents across ten quantitative traits in sweetcorn**

| Segregating populations derived from | Trait<br>Parentage                    | Number of parents involved | Plant height (cm) | Days to tasselling | Days to silking | Cob length (cm) | Cob girth (cm) | Number of kernel rows <i>per</i> cob | Number of kernels <i>per</i> row | 100 - kernel weight (g) | Shelling percentage | Grain yield plant <sup>-1</sup> (g) |
|--------------------------------------|---------------------------------------|----------------------------|-------------------|--------------------|-----------------|-----------------|----------------|--------------------------------------|----------------------------------|-------------------------|---------------------|-------------------------------------|
| Single cross hybrids                 | [BNG-3 × 40023]                       | Two                        | 1401.27           | 9.39               | 11.41           | 20.50           | 4.53           | 7.31                                 | 76.72                            | 7.65                    | 66.43               | 322.23                              |
|                                      | [40225 × MAI-283]                     |                            | 1155.53           | 10.44              | 11.76           | 16.89           | 3.78           | 3.41                                 | 52.06                            | 5.81                    | 72.69               | 293.03                              |
| Three way cross hybrids              | [(BNG-3 × 40023) × 40224]             | Three                      | 780.72            | 9.19               | 7.42            | 6.73            | 2.83           | 6.33                                 | 52.71                            | 14.26                   | 35.40               | 388.08                              |
|                                      | [(40225 × MAI-283) × 40224]           |                            | 1161.37           | 11.69              | 15.74           | 8.11            | 3.52           | 4.96                                 | 63.43                            | 7.37                    | 73.31               | 306.67                              |
| Double cross hybrids                 | [(BNG-3 × 40023) × (40225 × MAI-283)] | Four                       | 1075.39           | 10.31              | 16.41           | 15.05           | 3.32           | 2.99                                 | 60.69                            | 23.65                   | 81.11               | 430.73                              |
|                                      | [(4085 × 1882) × (MAI-225 × 40224)]   |                            | 1239.95           | 7.91               | 11.17           | 13.24           | 4.33           | 3.34                                 | 50.89                            | 6.12                    | 53.62               | 259.29                              |

#### **4.1.2. Frequency distribution of productivity traits among six segregating populations derived crosses involving varying number of parents**

Skewness and kurtosis belong to third- and fourth-degree statistics, respectively. Genetic expectation of coefficient of skewness is a function of number of genes and parameters that specify their additive main genetic and digenic additive  $\times$  additive epistatic interaction effects (Pooni *et al.*, 1977). Kurtosis numerically indicates number of genes controlling trait(s) under investigation (Robson, 1956). Fisher *et al.* (1932) outlined theoretical basis employing skewness for explaining genetic causes for variation in quantitative traits. Skewed distribution of a trait in general suggests that the trait is governed by non-additive gene action, especially epistasis and influenced by environmental variables considerably (Pooni *et al.* 1977; Roy, 2000 and Kimbeng and Bingham, 1999). Positive skewness is caused by duplicate gene action predominantly in the same direction (Snape and Riggs, 1975). In contrast negatively skewed distribution indicates that the character is governed by duplicate gene action irrespective of either increasing or decreasing effect on expression of the character under study.

If the distribution is leptokurtic, mesokurtic and platykurtic it signifies that the character is governed by fewer, optimum and large number of genes, respectively. If the value of kurtosis is positive, it signifies the presence of gene interaction while negative or nearer to zero indicates the absence of gene interaction.

Negatively skewed and platykurtic distribution was observed across all the segregating populations derived from varying number of parents for plant height, cob girth, number of kernel rows *per* cob, number of kernels *per* row and shelling percentage suggesting the involvement of large number of genes with majority of them displaying duplicate epistasis with increasing effects in the expression of these traits. Positively skewed and platykurtic distribution was observed across all the segregating populations derived from varying number of parents for 100 kernel weight, days to tasseling and days to silking suggesting the involvement of large number of genes with majority of them displaying complementary epistasis with decreasing effects in the expression of these traits. Positively skewed and platykurtic distribution was observed for grain yield plant<sup>-1</sup> among all

populations except in segregating populations derived from three-way cross hybrid [(BNG-3  $\times$  40023)  $\times$  40224] which showed negatively skewed and platykurtic distribution. Positively skewed and platykurtic distribution was observed across all the segregating populations derived from varying number of parents for cob length whereas segregating populations derived from single cross hybrid [BNG-3  $\times$  40023] and three-way cross hybrid [(BNG-3  $\times$  40023)  $\times$  40224] showed negatively skewed platykurtic distribution and three way cross hybrid [(40225  $\times$  MAI-283)  $\times$  40224] showed negatively skewed leptokurtic distribution. Negatively skewed leptokurtic distribution indicated the role of fewer number of genes with majority of them exerting increasing effects on the expression of cob length in [(40225  $\times$  MAI-283)  $\times$  40224]. (Table 16 & 17). The frequency distribution of all the six segregating populations for grain yield plant<sup>-1</sup> is depicted in figure 4.

#### **4.2 Frequency of transgressive segregants for grain yield and its attributing traits among segregating populations derived from single cross, three way cross and double cross hybrids**

The frequency of plants transgressing the parental trait expression in terms of number of plants registering lesser value than the lower parent and higher trait value than the higher parent was computed and indicated in table 18-21. Among populations, frequency of plants that surpassed the high performing parent was higher for cob length, cob girth, number of kernels *per* row and grain yield plant<sup>-1</sup>. A very low frequency of transgressive segregants were observed for shelling percentage and number of kernel rows *per* cob.

Recovery of higher percentage of transgressive segregants that surpassed the higher parent was observed in all the six segregating populations for cob length, cob girth, number of kernels *per* row and grain yield plant<sup>-1</sup> suggesting possibility of producing inbred lines with more cob length, cob girth, number of kernels *per* row and grain yield plant<sup>-1</sup> exceeding the parental limits. Occurrence of transgressive segregants could be attributed to constellation of complete or incomplete dominant genes that are dispersed among their parents (Chahal and Gosal, 2002). Genetic studies conducted by Risenberg *et al.*, (1999) suggest that combination of alleles from both or multiple parents that have complementary gene effects result in recovery of transgressive segregants with desirable combinations of genes.

**Table 16: Estimates of Skewness and Kurtosis for grain yield and its attributing traits among segregating population derived from crosses involving varying number of parents in sweetcorn**

| Segregating populations derived from | Trait<br>Parentage                    | Number of parents involved | Plant height (cm) |          | Days to tasselling |          | Days to silking |          | Cob length (cm) |          | Cob girth (cm) |          |
|--------------------------------------|---------------------------------------|----------------------------|-------------------|----------|--------------------|----------|-----------------|----------|-----------------|----------|----------------|----------|
|                                      |                                       |                            | skewness          | kurtosis | skewness           | kurtosis | skewness        | kurtosis | skewness        | kurtosis | skewness       | kurtosis |
| Single cross hybrids                 | [BNG-3 × 40023]                       | <b>Two</b>                 | -0.49             | -0.64    | 0.16               | -0.23    | -0.01           | -0.93    | -0.85           | 0.27     | -1.55          | 2.30     |
|                                      | [40225 × MAI-283]                     |                            | -0.34             | -0.67    | 0.10               | -0.32    | 0.82            | 2.05     | 0.005           | -0.90    | -0.47          | -0.72    |
| Three way cross hybrids              | [(BNG-3 × 40023) × 40224]             | <b>Three</b>               | -0.63             | 0.54     | 0.16               | -0.47    | 0.05            | -0.81    | -0.43           | 2.65     | -1.10          | 1.28     |
|                                      | [(40225 × MAI-283) × 40224]           |                            | -0.78             | -0.39    | 0.70               | 1.52     | 0.85            | 0.21     | -1.14           | 3.03     | -1.24          | 2.23     |
| Double cross hybrids                 | [(BNG-3 × 40023) × (40225 × MAI-283)] | <b>Four</b>                | -0.66             | -0.36    | 0.54               | -0.30    | 1.07            | 1.72     | 0.12            | -0.99    | -0.81          | 0.88     |
|                                      | [(4085 × 1882) × (MAI-225 × 40224)]   |                            | -0.53             | -0.45    | 0.09               | -0.47    | 0.40            | -0.37    | 0.71            | -0.27    | -0.61          | -0.46    |

**Table 17: Estimates of Skewness and Kurtosis for grain yield and its attributing traits among segregating population derived from crosses involving varying number of parents in sweetcorn**

| Segregating populations derived from | Trait<br>Parentage                    | Number of parents involved | Number of kernel rows <i>per</i> cob |          | Number of kernels <i>per</i> row |          | 100 kernel weight (g) |          | Shelling percentage |          | Grain yield plant <sup>-1</sup> (g) |          |
|--------------------------------------|---------------------------------------|----------------------------|--------------------------------------|----------|----------------------------------|----------|-----------------------|----------|---------------------|----------|-------------------------------------|----------|
|                                      |                                       |                            | skewness                             | kurtosis | skewness                         | kurtosis | skewness              | kurtosis | skewness            | kurtosis | skewness                            | kurtosis |
| Single cross hybrids                 | [BNG-3 × 40023]                       | Two                        | -0.37                                | -0.49    | -0.59                            | -0.56    | 0.60                  | -0.27    | -0.77               | 1.03     | 0.35                                | -0.18    |
|                                      | [40225 × MAI-283]                     |                            | -0.34                                | -0.72    | -0.71                            | 1.14     | 0.28                  | -0.62    | -0.69               | -0.05    | 0.01                                | -0.64    |
| Three way cross hybrids              | [(BNG-3 × 40023) × 40224]             | Three                      | -0.03                                | 0.41     | -1.31                            | 1.93     | 0.48                  | -0.09    | -0.84               | 2.65     | -0.20                               | -0.09    |
|                                      | [(40225 × MAI-283) × 40224]           |                            | -0.21                                | -0.14    | -1.26                            | 0.84     | 0.92                  | 0.57     | -1.23               | 1.34     | 0.14                                | -0.54    |
| Double cross hybrids                 | [(BNG-3 × 40023) × (40225 × MAI-283)] | Four                       | -0.03                                | -0.51    | -0.65                            | 0.77     | 0.22                  | -0.86    | -0.22               | -0.65    | 0.97                                | 0.97     |
|                                      | [(4085 × 1882) × (MAI-225 × 40224)]   |                            | 0.27                                 | -0.03    | -0.21                            | -0.40    | 0.29                  | -0.37    | -0.37               | -0.48    | 0.15                                | -0.15    |

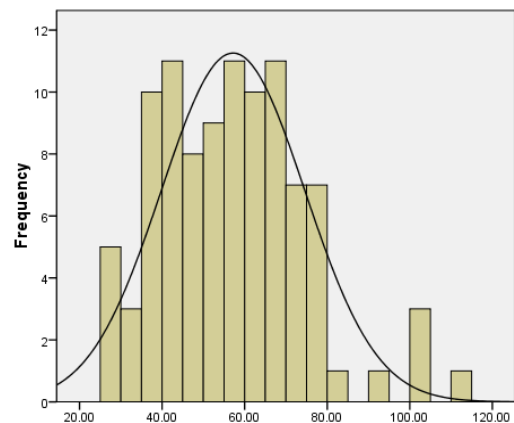
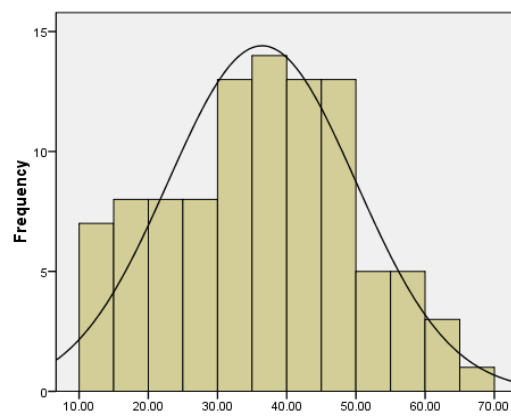
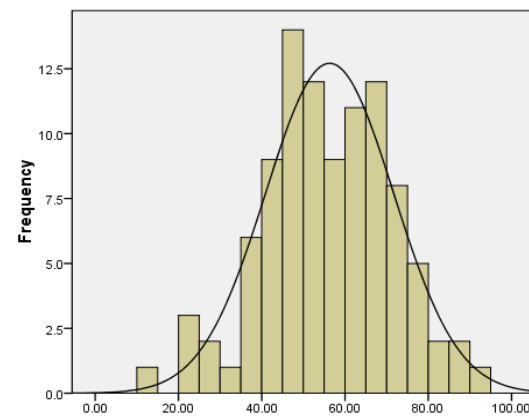
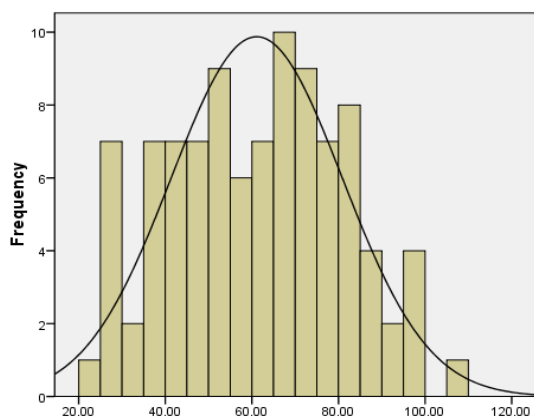
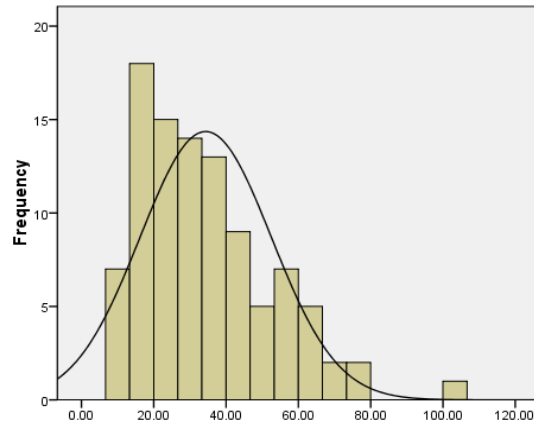
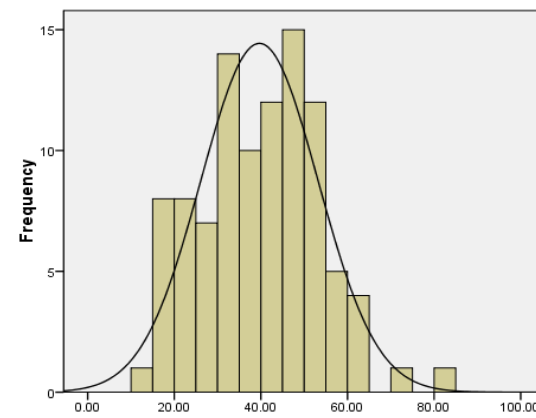
**SCH-1****SCH-2****TCH-1****TCH-2****DCH-1****DCH-2**

**Fig. 4: Frequency distribution of the six segregating populations derived from single, three-way and double cross hybrids for grain yield plant<sup>-1</sup>**

On the receipt of positive alleles (or) negative alleles from both the parents, segregants are likely to result in obtaining extreme phenotypes. Higher frequency of transgressive segregants in segregating populations could be attributed to parental dispersion of linked (repulsion phase) genes these traits (Kearsey and Pooni 2020; Bernardo 2002).

Among the six segregating populations, the segregating population derived from single cross hybrid [BNG-3  $\times$  40023] manifested higher frequency of transgressive segregants for number of kernel rows *per* cob, days to silking, cob length and grain yield plant<sup>-1</sup>. Three way cross hybrid [(40225  $\times$  MAI-283)  $\times$  40224] accounted for higher frequency of transgressive segregants for plant height, days to tasselling and cob girth. Higher frequency of transgressive segregants were observed in single cross hybrid [40225  $\times$  MAI-283] for number of kernels *per* row, in double cross hybrid [(4085 $\times$ 1882)  $\times$  (MAI-225 $\times$ 40224)] for shelling percentage and in three-way cross hybrid [(BNG-3  $\times$  40023)  $\times$  40224] for 100 kernel weight.

Non recovery or less frequency of transgressive segregants observed for some traits indicates that these traits maintain their originality despite experiencing meiotic events and recombination cycles. This could probably be due to the fact that these traits are under the influence of those genes that are commonly shared among parental lines used in developing segregating populations. (Table 18-21).

#### **4.2.1 Estimates of transgressive segregation index for grain yield and its attributing traits among segregating populations derived from crosses involving varying number of parents in sweetcorn**

Transgressive segregation index calculated as the ratio of absolute range of a population derived from cross for a trait and absolute range of parents involved in that cross for a trait. If the estimated value of transgressive segregation index is high it indicates higher absolute range among segregating population for the corresponding trait of that cross compared to parents involved in deriving the segregating population indicating the potentiality of the segregating population or otherwise.

**Table 18: Frequency of transgressive segregants for grain yield and its attributing traits among segregating population derived from crosses involving varying number of parents in sweetcorn**

| Segregating populations derived from | Trait<br>Parentage                    | Number of parents involved | Plant height (cm) |           |                |           | Days to tasselling |           |                |           | Days to silking |           |                |           |
|--------------------------------------|---------------------------------------|----------------------------|-------------------|-----------|----------------|-----------|--------------------|-----------|----------------|-----------|-----------------|-----------|----------------|-----------|
|                                      |                                       |                            | >Higher Parent    |           | < Lower parent |           | >Higher Parent     |           | < Lower parent |           | >Higher Parent  |           | < Lower parent |           |
|                                      |                                       |                            | No. of plants     | Frequency | No. of plants  | Frequency | No. of plants      | Frequency | No. of plants  | Frequency | No. of plants   | Frequency | No. of plants  | Frequency |
| Single cross Hybrids                 | [BNG-3 × 40023]                       | 2                          | 27                | 18.00     | 31             | 20.67     | 50                 | 33.33     | 3              | 2.00      | 39              | 26.00     | 3              | 2.00      |
|                                      | [40225 × MAI-283]                     |                            | 19                | 12.67     | 48             | 32.00     | 42                 | 28.00     | 7              | 4.67      | 25              | 16.67     | 18             | 12.00     |
| Three-way cross Hybrids              | [(BNG-3 × 40023) × 40224]             | 3                          | 29                | 12.67     | 18             | 12.00     | 51                 | 34.00     | 2              | 1.33      | 35              | 23.33     | 4              | 2.67      |
|                                      | [(40225 × MAI-283) × 40224]           |                            | 61                | 40.67     | 24             | 16.00     | 59                 | 39.33     | 4              | 2.67      | 34              | 22.67     | 7              | 4.67      |
| Double cross Hybrids                 | [(BNG-3 × 40023) × (40225 × MAI-283)] | 4                          | 8                 | 05.33     | 31             | 20.67     | 28                 | 18.67     | 2              | 1.33      | 18              | 12.00     | 11             | 7.33      |
|                                      | [(4085 × 1882) × (MAI-225 × 40224)]   |                            | 26                | 17.33     | 46             | 30.67     | 43                 | 28.67     | 3              | 2.00      | 28              | 18.67     | 5              | 3.33      |

**Table 19: Frequency of transgressive segregants for grain yield and its attributing traits among segregating population derived from crosses involving varying number of parents in sweetcorn**

| Segregating populations derived from | Trait<br>Parentage                    | Number of parents involved | Cob length (cm) |           |                |           | Cob girth (cm) |           |                |           | Number of kernel rows <i>per</i> cob |           |                |           |
|--------------------------------------|---------------------------------------|----------------------------|-----------------|-----------|----------------|-----------|----------------|-----------|----------------|-----------|--------------------------------------|-----------|----------------|-----------|
|                                      |                                       |                            | >Higher Parent  |           | < Lower parent |           | >Higher Parent |           | < Lower parent |           | >Higher Parent                       |           | < Lower parent |           |
|                                      |                                       |                            | No. of plants   | Frequency | No. of plants  | Frequency | No. of plants  | Frequency | No. of plants  | Frequency | No. of plants                        | Frequency | No. of plants  | Frequency |
| Single cross Hybrids                 | [BNG-3 × 40023]                       | 2                          | 79              | 52.67     | 16             | 10.67     | 76             | 50.67     | 8              | 5.33      | 36                                   | 24.00     | 16             | 10.67     |
|                                      | [40225 × MAI-283]                     |                            | 51              | 34.00     | 38             | 25.33     | 41             | 27.33     | 34             | 22.67     | 0                                    | 0.00      | 11             | 7.33      |
| Three-way cross Hybrids              | [(BNG-3 × 40023) × 40224]             | 3                          | 65              | 43.33     | 10             | 6.67      | 65             | 43.33     | 5              | 3.33      | 33                                   | 22.00     | 13             | 8.67      |
|                                      | [(40225 × MAI-283) × 40224]           |                            | 81              | 0.54      | 6              | 4.00      | 80             | 53.33     | 8              | 5.33      | 23                                   | 15.33     | 3              | 2.00      |
| Double cross Hybrids                 | [(BNG-3 × 40023) × (40225 × MAI-283)] | 4                          | 51              | 34.00     | 37             | 24.67     | 51             | 34.00     | 6              | 4.00      | 1                                    | 0.67      | 5              | 3.33      |
|                                      | [(4085 × 1882) × (MAI-225 × 40224)]   |                            | 31              | 20.67     | 23             | 15.33     | 39             | 26.00     | 38             | 25.33     | 6                                    | 6.00      | 24             | 16.00     |

**Table 20: Frequency of transgressive segregants for grain yield and its attributing traits among segregating population derived from crosses involving varying number of parents in sweetcorn**

| Segregating populations derived from | Parentage \ Trait                     | Number of parents involved | Number of kernels <i>per row</i> |           |                |           | 100 kernel weight (g) |           |                |           |
|--------------------------------------|---------------------------------------|----------------------------|----------------------------------|-----------|----------------|-----------|-----------------------|-----------|----------------|-----------|
|                                      |                                       |                            | >Higher Parent                   |           | < Lower parent |           | >Higher Parent        |           | < Lower parent |           |
|                                      |                                       |                            | No. of plants                    | Frequency | No. of plants  | Frequency | No. of plants         | Frequency | No. of plants  | Frequency |
| Single cross Hybrids                 | [BNG-3 × 40023]                       | 2                          | 68                               | 45.33     | 20             | 13.33     | 33                    | 22.00     | 17             | 11.33     |
|                                      | [40225 × MAI-283]                     |                            | 89                               | 59.33     | 2              | 1.33      | 13                    | 8.67      | 29             | 9.33      |
| Three-way cross Hybrids              | [(BNG-3 × 40023) × 40224]             | 3                          | 85                               | 56.67     | 10             | 6.67      | 39                    | 26.00     | 29             | 19.33     |
|                                      | [(40225 × MAI-283) × 40224]           |                            | 86                               | 57.33     | 6              | 4.00      | 15                    | 10.00     | 28             | 18.67     |
| Double cross Hybrids                 | [(BNG-3 × 40023) × (40225 × MAI-283)] | 4                          | 81                               | 54.00     | 5              | 3.33      | 31                    | 20.67     | 30             | 20.00     |
|                                      | [(4085 × 1882) × (MAI-225 × 40224)]   |                            | 53                               | 35.33     | 2              | 1.33      | 29                    | 19.33     | 14             | 9.33      |

**Table 21: Frequency of transgressive segregants for grain yield and its attributing traits among segregating population derived from crosses involving varying number of parents in sweetcorn**

| Segregating populations derived from | Trait<br>Parentage                    | Number of parents involved | Shelling percentage |           |                |           | Grain yield plant <sup>-1</sup> (g) |           |                |           |
|--------------------------------------|---------------------------------------|----------------------------|---------------------|-----------|----------------|-----------|-------------------------------------|-----------|----------------|-----------|
|                                      |                                       |                            | >Higher Parent      |           | < Lower parent |           | >Higher Parent                      |           | < Lower parent |           |
|                                      |                                       |                            | No. of plants       | Frequency | No. of plants  | Frequency | No. of plants                       | Frequency | No. of plants  | Frequency |
| Single cross Hybrids                 | [BNG-3 × 40023]                       | 2                          | 6                   | 4.00      | 9              | 6.00      | 54                                  | 36.00     | 20             | 13.33     |
|                                      | [40225 × MAI-283]                     |                            | 33                  | 22.00     | 8              | 5.33      | 39                                  | 26.00     | 31             | 20.67     |
| Three-way cross Hybrids              | [(BNG-3 × 40023) × 40224]             | 3                          | 3                   | 2.00      | 4              | 2.67      | 55                                  | 36.67     | 15             | 10.00     |
|                                      | [(40225 × MAI-283) × 40224]           |                            | 12                  | 8.00      | 9              | 6.00      | 64                                  | 42.67     | 3              | 2.00      |
| Double cross Hybrids                 | [(BNG-3 × 40023) × (40225 × MAI-283)] | 4                          | 2                   | 1.33      | 15             | 10.00     | 16                                  | 10.67     | 31             | 20.67     |
|                                      | [(4085 × 1882) × (MAI-225 × 40224)]   |                            | 3                   | 2.00      | 65             | 43.33     | 6                                   | 4.00      | 15             | 10.00     |

Segregating population derived from single cross hybrid [40225 × MAI-283] manifested higher absolute range for plant height, days to silking, cob length and number of kernels *per* row thus registering greater value of transgressive segregation index from among all the six segregating populations for these traits. Segregating population derived from three way cross hybrid [(BNG-3 × 40023) × 40224] expressed higher absolute range for number of kernel rows *per* cob, 100 kernel weight and grain yield plant<sup>-1</sup> and registering greater value of transgressive segregation index. Segregating population derived from three way cross hybrid [(40225 × MAI-283) × 40224] expressed higher absolute range for days to tasselling and cob girth and double cross hybrid [(4085×1882) × (MAI-225×40224)] for shelling percentage expressed higher absolute range than the absolute range of parents and thus estimated higher transgressive segregation index. (Table 22).

#### **4.3 Breeding potential of segregating populations derived from crosses involving varying number of parents for grain yield and its attributing traits in sweetcorn**

Breeders often encounter with limited resources while handling large number of crosses of bi-parent or multiparent derived populations. However, limited resources can be effectively utilized by identifying potential breeding populations among a set of crosses in terms of higher economic yield and greater recovery of transgressive segregants. Hence, seven parameters including quantitative trait means, standardized range, phenotypic coefficient of variation, genotypic coefficient of variation, genetic advance as *per cent* of mean, frequency of transgressive segregants and transgressive segregation index across ten traits, plant height, days to tasseling, days to silking, cob length, cob girth, number of kernel rows *per* cob, number of kernels *per* row, 100 kernel weight, shelling percentage and grain yield plant<sup>-1</sup> were considered to arrive at breeding potential of segregating populations derived from crosses involving varying number of parents. The differences in the estimates of quantitative trait means, absolute range, standardized range and PCV in generations derived from the six crosses could be attributed to differences in the number of genes dispersed between their parents (Kearsey and Pooni 2020; Bernardo 2002). The crosses whose parents differ for a larger number of dispersed genes is expected to exhibit higher traits means and variances than those whose parents differ for fewer genes (Kearsey and Pooni 2020; Bernardo 2002).

**Table 22: Estimates of transgressive segregation index for grain yield and its attributing traits among segregating population derived from crosses involving varying number of parents in sweetcorn**

| Segregating populations derived from | Trait<br>Parentage                    | Number of parents involved | Plant height (cm) | Days to tasselling | Days to silking | Cob length (cm) | Cob girth (cm) | Number of kernel rows <i>per</i> cob | Number of kernels <i>per</i> row | 100 - kernel weight (g) | Shelling percentage | Grain yield plant <sup>-1</sup> (g) |
|--------------------------------------|---------------------------------------|----------------------------|-------------------|--------------------|-----------------|-----------------|----------------|--------------------------------------|----------------------------------|-------------------------|---------------------|-------------------------------------|
| <b>Single cross hybrids</b>          | [BNG-3×40023]                         | <b>Two</b>                 | 3.33              | 3.67               | 3.36            | 10.76           | 3.62           | 5.56                                 | 6.62                             | 3.68                    | 1.46                | 5.48                                |
|                                      | [40225×MAI-283]                       |                            | 12.35             | 4.74               | 8.03            | 11.60           | 5.63           | 1.19                                 | 6.72                             | 2.40                    | 2.11                | 4.92                                |
| <b>Three-way cross hybrids</b>       | [(BNG-3 × 40023) × 40224]             | <b>Three</b>               | 2.93              | 3.18               | 2.64            | 6.99            | 3.13           | 7.78                                 | 6.48                             | 6.00                    | 1.40                | 5.77                                |
|                                      | [(40225 × MAI-283) × 40224]           |                            | 5.51              | 6.74               | 7.79            | 9.41            | 7.86           | 1.85                                 | 5.65                             | 2.90                    | 1.71                | 3.11                                |
| <b>Double cross hybrids</b>          | [(BNG-3 × 40023) × (40225 × MAI-283)] | <b>Four</b>                | 3.09              | 2.95               | 5.14            | 8.04            | 3.31           | 1.48                                 | 5.27                             | 3.29                    | 1.40                | 3.08                                |
|                                      | [(4085 × 1882) × (MAI-225×40224)]     |                            | 6.14              | 2.34               | 2.69            | 3.56            | 5.42           | 4.17                                 | 2.69                             | 2.64                    | 3.62                | 1.94                                |

None of the six segregating populations registered higher estimates for all the traits and criteria defined (mean, standardized range, PCV, GCV, genetic advance as *per cent* of mean, frequency of transgressive segregants recovered across productivity traits and transgressive segregation index). Hence, an objective criteria rank-sum method across traits and statistical parameters was employed to assess breeding potential of segregating populations derived from crosses involving varying number of parents. Segregating population having a higher estimate of a statistical parameter across traits was assigned with rank 1. While, segregating population that expressed lower estimate for statistical parameter across traits received rank 6. Similar method of assigning ranks to each of the segregating population was followed for each of the criteria. Further, ranks were summed across the traits (Kang, 1988). The segregating population having lower rank sum was considered as potential population. While arriving at the estimated rank sum instead of using six parameters only three parameters; genetic advance + mean, frequency of transgressive segregants and transgressive segregation index were considered under the assumption that genetic advance + mean would take into consideration trait mean and variability parameter like PCV (Bernardo, 2002). Transgressive segregation index is expected to take into consideration range of the traits across populations (Koide *et.al.*, 2019). While assigning ranks for days to tasseling and days to silking, segregating population having a lower estimate of a statistical parameter genetic advance + mean across traits was assigned with rank 1. While, segregating population that expressed higher estimate for statistical parameter genetic advance + mean across traits received rank 6 (Table 23). While assigning ranks for frequency of transgressive segregants, the frequency of plants higher than higher parent were considered for all the traits except days to tasseling and days to silking for which the frequency of plants lower than lower parent were considered (Table 24). Considering the rank-sum criteria obtained by each segregating population across ten productivity traits and three statistical parameters, segregating populations derived from crosses involving two parents, single cross hybrid (BNG-3×40023) was identified as first best potential population (with lowest rank-sums 5) (Table 26). Single cross [BNG-3×40023] derived population was ranked first for genetic advance + mean which is a usefulness criterion for identifying potential population.

**Table 23: Estimates of rank sums for genetic advance + mean across grain yield and its attributing traits among segregating populations derived from crosses involving varying number of parents to evaluate potentiality of the populations in sweetcorn**

| Genetic advance + Mean               |                   |          |                    |          |                 |          |                 |          |                   |          |                               |          |                           |          |                       |          |                     |          |                                     |          |              |
|--------------------------------------|-------------------|----------|--------------------|----------|-----------------|----------|-----------------|----------|-------------------|----------|-------------------------------|----------|---------------------------|----------|-----------------------|----------|---------------------|----------|-------------------------------------|----------|--------------|
| Segregating populations derived from | Plant height (cm) | Rank (a) | Days to tasselling | Rank (b) | Days to silking | Rank (c) | Cob length (cm) | Rank (d) | Cob diameter (cm) | Rank (e) | Number of kernel rows per cob | Rank (f) | Number of kernels per row | Rank (g) | 100 kernel weight (g) | Rank (h) | Shelling percentage | Rank (i) | Grain yield plant <sup>-1</sup> (g) | Rank (j) | Rank sum (l) |
| SCH1                                 | 242.12            | 1        | 65.72              | 6        | 67.73           | 5        | 26.67           | 1        | 19.38             | 1        | 19.98                         | 1        | 42.23                     | 4        | 17.65                 | 4        | 72.67               | 2        | 80.02                               | 2        | 27           |
| SCH2                                 | 205.76            | 6        | 60.61              | 1        | 63.41           | 1        | 23.51           | 2        | 14.72             | 6        | 14.72                         | 6        | 44.71                     | 2        | 18.28                 | 3        | 59.27               | 6        | 54.97                               | 5        | 38           |
| TCH1                                 | 219.51            | 4        | 64.95              | 5        | 65.98           | 3        | 21.33           | 5        | 17.71             | 2        | 19.66                         | 2        | 40.61                     | 5        | 18.80                 | 2        | 68.42               | 3        | 78.67                               | 3        | 34           |
| TCH2                                 | 227.91            | 2        | 62.79              | 4        | 67.99           | 6        | 23.03           | 4        | 17.24             | 3        | 17.93                         | 3        | 46.11                     | 1        | 17.00                 | 5        | 64.35               | 5        | 98.25                               | 1        | 34           |
| DCH1                                 | 219.76            | 3        | 62.10              | 3        | 66.65           | 4        | 23.48           | 3        | 15.29             | 5        | 14.71                         | 5        | 42.87                     | 3        | 23.84                 | 1        | 64.74               | 4        | 63.43                               | 4        | 35           |
| DCH2                                 | 218.01            | 5        | 61.65              | 2        | 65.91           | 2        | 20.26           | 6        | 16.39             | 4        | 15.18                         | 4        | 38.74                     | 6        | 13.60                 | 6        | 72.69               | 1        | 52.66                               | 6        | 42           |

$$\text{SCH1} = [\text{BNG-3} \times 40023]$$

$$\text{SCH2} = [40225 \times \text{MAI-283}]$$

$$\text{TCH1} = [(\text{BNG-3} \times 40023) \times 40224]$$

$$\text{TCH2} = [(40225 \times \text{MAI-283}) \times 40224]$$

$$\text{DCH1} = [(\text{BNG-3} \times 40023) \times (40225 \times \text{MAI-283})]$$

$$\text{DCH2} = [(4085 \times 1882) \times (\text{MAI-225} \times 40224)]$$

**Table 24: Estimates of rank sums for frequency of transgressive segregants across grain yield and its attributing traits among segregating populations derived from crosses involving varying number of parents to evaluate potentiality of the populations in sweetcorn**

| Frequency of transgressive segregants |                   |          |                    |          |                 |          |                 |          |                   |         |                                      |         |                                  |         |                       |         |                     |         |                                     |         |              |
|---------------------------------------|-------------------|----------|--------------------|----------|-----------------|----------|-----------------|----------|-------------------|---------|--------------------------------------|---------|----------------------------------|---------|-----------------------|---------|---------------------|---------|-------------------------------------|---------|--------------|
| Segregating populations derived from  | Plant height (cm) | Rank (a) | Days to tasselling | Rank (b) | Days to silking | Rank (c) | Cob length (cm) | Rank (d) | Cob diameter (cm) | Rank(e) | Number of kernel rows <i>per</i> cob | Rank(f) | Number of kernels <i>per</i> row | Rank(g) | 100 kernel weight (g) | Rank(h) | Shelling percentage | Rank(i) | Grain yield plant <sup>-1</sup> (g) | Rank(j) | Rank sum (1) |
| SCH1                                  | 18.00             | 3        | 2.00               | 3        | 2.00            | 6        | 52.67           | 1        | 50.67             | 2       | 24.00                                | 1       | 45.33                            | 5       | 22.00                 | 2       | 4.00                | 3       | 36.00                               | 3       | 29           |
| SCH2                                  | 12.67             | 5        | 4.67               | 1        | 12.00           | 1        | 34.00           | 3        | 27.33             | 5       | 0.00                                 | 6       | 59.33                            | 1       | 8.67                  | 6       | 22.00               | 1       | 26.00                               | 4       | 33           |
| TCH1                                  | 19.33             | 2        | 1.33               | 5        | 2.67            | 5        | 43.33           | 2        | 43.33             | 3       | 22.00                                | 2       | 56.67                            | 3       | 26.00                 | 1       | 2.00                | 4       | 36.67                               | 2       | 29           |
| TCH2                                  | 40.67             | 1        | 2.67               | 2        | 4.67            | 3        | 0.54            | 6        | 53.33             | 1       | 15.30                                | 3       | 57.33                            | 2       | 10.00                 | 5       | 8.00                | 2       | 42.67                               | 1       | 26           |
| DCH1                                  | 05.33             | 6        | 1.33               | 5        | 7.33            | 2        | 34.00           | 3        | 34.00             | 4       | 0.67                                 | 5       | 54.00                            | 4       | 20.67                 | 3       | 1.33                | 6       | 10.67                               | 5       | 43           |
| DCH2                                  | 17.33             | 4        | 2.00               | 3        | 3.33            | 4        | 20.67           | 5        | 26.00             | 6       | 6.00                                 | 4       | 35.33                            | 6       | 19.33                 | 4       | 2.00                | 4       | 4.00                                | 6       | 46           |

SCH1 = [BNG-3 × 40023]

TCH1 = [(BNG-3 × 40023) × 40224]

DCH1 = [(BNG-3 × 40023) × (40225 × MAI-283)]

SCH2 = [40225 × MAI-283]

TCH2 = [(40225 × MAI-283) × 40224]

DCH2 = [(4085 × 1882) × (MAI-225 × 40224)]

**Table 25: Estimates of rank sums for transgressive segregation index across grain yield and its attributing traits among segregating populations derived from crosses involving varying number of parents to evaluate potentiality of the populations in sweetcorn**

| Transgressive segregation index      |                   |          |                    |          |                 |          |                 |          |                   |         |                                      |         |                                  |         |                       |         |                     |         |                                     |         |              |
|--------------------------------------|-------------------|----------|--------------------|----------|-----------------|----------|-----------------|----------|-------------------|---------|--------------------------------------|---------|----------------------------------|---------|-----------------------|---------|---------------------|---------|-------------------------------------|---------|--------------|
| Segregating populations derived from | Plant height (cm) | Rank (a) | Days to tasselling | Rank (b) | Days to silking | Rank (c) | Cob length (cm) | Rank (d) | Cob diameter (cm) | Rank(e) | Number of kernel rows <i>per</i> cob | Rank(f) | Number of kernels <i>per</i> row | Rank(g) | 100 kernel weight (g) | Rank(h) | Shelling percentage | Rank(i) | Grain yield plant <sup>-1</sup> (g) | Rank(j) | Rank sum (1) |
| SCH1                                 | 3.33              | 4        | 3.66               | 3        | 3.36            | 4        | 10.76           | 2        | 3.62              | 4       | 5.56                                 | 2       | 6.62                             | 2       | 3.68                  | 2       | 1.46                | 4       | 5.48                                | 2       | 29           |
| SCH2                                 | 12.35             | 1        | 4.74               | 2        | 8.02            | 1        | 11.60           | 1        | 5.63              | 2       | 1.19                                 | 6       | 6.72                             | 1       | 2.40                  | 6       | 2.11                | 2       | 4.92                                | 3       | 25           |
| TCH1                                 | 2.93              | 6        | 3.17               | 4        | 2.63            | 6        | 6.99            | 5        | 3.13              | 6       | 7.78                                 | 1       | 6.48                             | 3       | 6.00                  | 1       | 1.40                | 5       | 5.77                                | 1       | 38           |
| TCH2                                 | 5.51              | 3        | 6.74               | 1        | 7.78            | 2        | 9.41            | 3        | 7.86              | 1       | 1.85                                 | 4       | 5.65                             | 4       | 2.90                  | 4       | 1.71                | 3       | 3.11                                | 4       | 29           |
| DCH1                                 | 3.10              | 5        | 2.95               | 5        | 5.14            | 3        | 8.04            | 4        | 3.31              | 5       | 1.48                                 | 5       | 5.27                             | 5       | 3.29                  | 3       | 1.40                | 5       | 3.08                                | 5       | 45           |
| DCH2                                 | 6.14              | 2        | 2.34               | 6        | 2.69            | 5        | 3.56            | 6        | 5.42              | 3       | 4.17                                 | 3       | 2.69                             | 6       | 2.64                  | 5       | 3.62                | 1       | 1.94                                | 6       | 43           |

SCH1 = [BNG-3 × 40023]

TCH1 = [(BNG-3 × 40023) × 40224]

DCH1 = [(BNG-3 × 40023) × (40225 × MAI-283)]

SCH2 = [40225 × MAI-283]

TCH2 = [(40225 × MAI-283) × 40224]

DCH2 = [(4085 × 1882) × (MAI-225 × 40224)]

**Table 26: Estimates of overall rank sum across grain yield and its attributing traits and three statistical parameters among segregating populations (SP) derived from crosses involving varying number of parents to evaluate potentiality of the populations in sweetcorn**

| Segregating populations derived from | Parentage \ Trait                     | Number of parents involved | Rank-sum based on trait GA + mean | Rank assigned to SPs | Rank-sum based on frequency of | Rank assigned to SP | Rank-sum based on transgressive | Rank assigned to SP | Cumulative rank-sum | Overall rank assigned to SPs |
|--------------------------------------|---------------------------------------|----------------------------|-----------------------------------|----------------------|--------------------------------|---------------------|---------------------------------|---------------------|---------------------|------------------------------|
| Single cross Hybrids                 | [BNG-3 × 40023]                       | Two                        | 27                                | 1                    | 29                             | 2                   | 29                              | 2                   | 5                   | 1                            |
|                                      | [40225 × MAI-283]                     |                            | 38                                | 5                    | 33                             | 4                   | 25                              | 1                   | 10                  | 4                            |
| Three-way cross Hybrids              | [(BNG-3 × 40023) × 40224]             | Three                      | 34                                | 2                    | 29                             | 3                   | 38                              | 4                   | 9                   | 3                            |
|                                      | [(40225 × MAI-283) × 40224]           |                            | 34                                | 3                    | 26                             | 1                   | 29                              | 2                   | 6                   | 2                            |
| Double cross Hybrids                 | [(BNG-3 × 40023) × (40225 × MAI-283)] | Four                       | 35                                | 4                    | 43                             | 5                   | 45                              | 6                   | 15                  | 5                            |
|                                      | [(4085 × 1882) × (MAI-225 × 40224)]   |                            | 42                                | 6                    | 46                             | 6                   | 43                              | 5                   | 17                  | 6                            |

Forwarding such biparental derived and double cross derived superior segregating populations could provide opportunities in isolation of elite advance breeding lines with desirable traits. Next most potential population was three way cross derived [(40225×MAI-283) ×40224] (with rank-sum 6) which had higher trait means and was also ranked first for frequency of transgressive segregants. Next most potential population was three way cross derived (BNG-3×40023) ×40224 (with rank-sum 9). According to rank sum method segregating populations derived from single cross hybrid (BNG-3×40023) ranked first and three way cross hybrids as next best populations indicating it is not worthwhile to generate segregating populations having more than three parental lines. Single cross hybrids are considered most desirable because breeding and seed production is much easier in such hybrids than in multi-parent hybrids (Khan and Dubey 2015). Summarized view of potentiality of the best identified segregating populations derived from varying number of parents in terms of recovery of transgressive segregants for grain yield plant<sup>-1</sup> is depicted in Table 27.

**Table 27: Transgressive segregants identified from potential single and multi-parent derived crosses for grain yield in sweetcorn**

| Segregating populations derived from               | Plant Identity        | Grain yield plant <sup>-1</sup>       |
|----------------------------------------------------|-----------------------|---------------------------------------|
| Single cross hybrid<br>[BNG-3×40023]               | P (66)                | 111.10                                |
|                                                    | P (29)                | 107.50                                |
|                                                    | P (48)                | 101.74                                |
|                                                    | P (72)                | 101.34                                |
|                                                    | P (12)                | 101.03                                |
|                                                    | Population Mean       | 61.91±1.81                            |
|                                                    | <b>Plant Identity</b> | <b>Grain yield plant<sup>-1</sup></b> |
| Three-way cross hybrid<br>[(40225×MAI-283) ×40224] | P (86)                | 98.99                                 |
|                                                    | P (65)                | 98.54                                 |
|                                                    | P (34)                | 95.50                                 |
|                                                    | P (114)               | 95.32                                 |
|                                                    | P (40)                | 84.44                                 |
|                                                    | Population Mean       | 59.18±1.77                            |
|                                                    | <b>Plant Identity</b> | <b>Grain yield plant<sup>-1</sup></b> |
| Three way cross Hybrid<br>[(BNG-3×40023) ×40224]   | P (91)                | 91.36                                 |
|                                                    | P (77)                | 88.37                                 |
|                                                    | P (53)                | 86.39                                 |
|                                                    | P (68)                | 83.14                                 |
|                                                    | P (94)                | 81.19                                 |
|                                                    | Population Mean       | 56.27±1.99                            |

# **SUMMARY**

## V SUMMARY

**Preamble:** Genetic variation among economically important traits is a must for improvement of any crop and sweetcorn is no exception. Commercial cultivars of sweetcorn are mostly  $F_1$  hybrids. These parental lines of  $F_1$  hybrid cultivars have been developed following hybridization and selection involving only two parents, leading to largely restricted scope for recombination, manifest reduced variability. Such hybrid parents not only have narrow genetic base but also often lack all the desired combination of traits. This may lead to genetic vulnerability of cultivars, consequently result in disease epidemic. To address lack of substantial variability, development of hybrid parental lines from a population having broad genetic base offers a feasible solution. Hence, there is a need to increase and quantify variability by providing opportunity for higher number of recombination events in relatively larger genomic backgrounds. Segregating generations derived from crosses involving more than two parents are expected to exhibit greater spectrum of variation due to enhanced and effective meiotic events in comparison to segregating populations derived from crosses involving just two parents. Assessing the spectrum of variability among segregating populations derived from crosses involving di, tri, tetra parents would help determine optimum number of parents to be involved in generating base population to be subjected to further cycles of selection to derive stabilized parental lines. Hence, present study was conducted to compare the breeding potential of segregating populations derived from crosses involving varying number of parents for grain yield and its component traits in sweetcorn.

### **Objectives:**

1. To compare genetic variability for grain yield and its attributing traits across di, tri and tetra parent derived segregating populations.
2. To compare the frequency of transgressive segregants for yield and its component traits across di, tri and tetra parent derived segregating populations.

**Material and methods:** Six segregating populations derived from crosses involving varying number of parents were used in the study. Six segregating populations were planted

separately in contiguous blocks in the Experimental plots of AICRP on Seed (Crops), UAS, GKVK, Bengaluru. While the parental lines were evaluated separately in randomized complete block design in three replications. Data were recorded on grain yield and its attributing traits on each plant from each of the segregating population and five randomly chosen plants in each of the 8 parental lines involved in developing segregating populations.

**Statistical analysis:** Descriptive statistics (trait means, standard deviation, standardized range) and genetic parameters (PCV, GCV, heritability and GAM) were estimated. Segregating populations having higher estimates of mean, PCV, GCV with high recovery frequency of transgressive segregants for grain yield and its attributing traits were considered as criteria to identify potential segregating population. In order to arrive at a potential segregating population across traits and statistical parameters rank-sum method was followed. The population with lowest rank-sum was considered to possess high breeding potential. Third- and fourth-degree statistics were used to determine the interaction effect and number of genes governing the traits under investigation.

#### **Salient findings of the study are summarized as under**

- Segregating population derived from single cross hybrid [40225 × MAI-283] expressed higher estimate of standardized range for the most economical trait, grain yield plant<sup>-1</sup>.
- Segregating population derived from single cross hybrid [BNG-3×40023] had a higher estimate of the sum of genetic advance and mean which is a usefulness criterion.
- Segregating population derived from single cross hybrid [BNG-3×40023] had a higher estimate of trait mean and frequency of transgressive segregants for grain yield plant<sup>-1</sup>.
- Based on magnitude of rank-sum across productivity traits, segregating population derived from single cross hybrid [BNG-3 × 40023] was identified as the most potential segregating populations. Next best potential population identified was derived from three way cross hybrid (40225 × MAI-283) × 40224] and segregating population derived from three way cross hybrid [(BNG-3 × 40023) × 40224] was identified as next best segregating population.

- Higher proportion of plants that surpassed the better parent for grain yield were recovered from the segregating population derived from three-way cross hybrid [(40225 × MAI-283) × 40224]. Stabilizing such transgressive segregants by selfing could possibly result in recovery of superior individuals with desired combination of traits contributing to grain yield.
- From among ten productivity *per se* traits, a high frequency of transgressive segregants were recovered in all the segregating populations for cob length, cob girth, number of kernels per row and grain yield plant<sup>-1</sup>.
- Based on this study, optimum number of parental lines to be involved in generating segregating populations is not more than three.

#### **Future line of work**

- The segregating populations derived from single cross hybrid [BNG-3 × 40023], three-way cross hybrid [(40225 × MAI-283) × 40224] that exhibited high breeding potential, may be forwarded to isolate superior stabilized recombinants in advance segregating generations for use in further breeding programs.
- Transgressive segregants with higher grain yield plant<sup>-1</sup> identified in each of segregating populations may be forwarded and stabilized for use as advanced breeding lines which could either be used as hybrid parental lines
- The dispersion of alleles among the parents is responsible for the difference in breeding potential. If there is no dispersion among the parents then there will be no variance in the segregating populations.
- As the populations size I have taken for my research is comparatively less the segregating populations derived from two parents was identified a s best compared to other segregating populations.

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## VI REFERENCES

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