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# Genetic studies on morpho-physiological traits in newly developed inbred lines of maize (*Zea mays* L.)

**Ayyanna, Bhat JS, Rakshith P and P Kariyannanavar**

## Abstract

This research investigates the genetic exploration of morpho-physiological traits in 47 newly developed elite inbred lines of maize (*Zea mays* L.) sourced from CIMMYT, IIMR, and IARI Regional Research Centre, Dharwad. The study, conducted during rabi-2016, employed a Randomized Complete Block Design with two replications, assessing 11 quantitative traits. The findings reveal substantial genetic variability across traits such as plant height, ear height, cob length, cob girth, number of kernel rows per cob, number of kernels per row, hundred-seed weight, shelling percentage, and grain yield per hectare. Traits like grain yield per hectare and hundred-seed weight displayed high heritability, genetic advance, and potential for improvement through selection. Conversely, days to 50 percent tasseling, days to 50 percent silking, and shelling percentage showed lower genetic advance, suggesting the need for nuanced breeding strategies. These results contribute useful insights for maize breeding programs, emphasizing the importance of considering multiple traits with high heritability and genetic advance for comprehensive crop improvement.

**Keywords:** Analysis of variance, genetic variability, heritability and genetic advance

## Introduction

Maize (*Zea mays* L.) stands as one of the most economically significant cereal crops globally, contributing substantially to food, fodder, and industrial applications. The continuous demand for increased productivity, coupled with changing climatic conditions, necessitates the development of maize varieties with enhanced adaptability and yield potential. In this context, the exploration of genetic variability, heritability, and genetic advance in newly developed inbred lines of maize emerges as a crucial avenue for crop improvement.

Genetic variability, the raw material for evolutionary processes and crop improvement, underlies the observed differences among individual plants within a population. Understanding the extent and nature of genetic variability in morpho-physiological traits is fundamental for targeted breeding efforts. Heritability, a key concept in genetics, delineates the proportion of phenotypic variation attributable to genetic factors. The differentiation between broad and narrow-sense heritability, as elucidated by Lush (1940) [7] and Hanson *et al*. (1956) [4], provides valuable insights into the genetic control of traits.

While the availability of genetic variability is crucial, it is equally important to comprehend the heritability of traits. This knowledge aids in distinguishing genetic and environmental influences, thereby guiding effective selection strategies for trait improvement. Furthermore, the genetic advance, a measure of the potential gain achievable through selection, is integral in devising strategies for crop enhancement. In light of the aforementioned considerations, a comprehensive genetic study on morpho-physiological traits in newly developed inbred lines of maize is proposed. This study aims to evaluate the extent of genetic variability, estimate heritability in both broad and narrow senses, and assess genetic advance for key traits in the context of diverse environmental conditions.

## Materials and Methods

### Location and Weather Conditions

The present investigation entitled "Genetic studies on morpho-physiological traits in newly developed inbred lines of maize" was carried out at, IARI Regional Research Centre, Dharwad during rabi-2016. The field experiments to assess genetic variability was conducted at IARI Regional Research Centre, Dharwad. It is located in transitional tract of Karnataka State at 15°27' north latitude, 75°13' east longitude and at an altitude of 678 m above mean sea level. The average rainfall of the IARI Regional Research Centre Dharwad, is 546 mm.

The soils are sandy loam type with pH of 7.2. Source of irrigation water is from Tube well. Crop was raised irrigated situation during Rabi.

### Experimental Material

The experimental material included 47 newly developed elite inbred lines of maize from diverse sources such as CIMMYT, IIMR and IARI Regional Research Centre, Dharwad with three testers DC-13 (MS heterotic pool) DC-14 (tuxpeno pool) and DC-17 (MS heterotic pool) (the list of genetic materials are provided in Supplementary file 1).

### Experimental Design

The experimental design employed for the field plots was a Randomized Complete Block Design (RCBD) with two replications. In each replication, there were a total of 50 entries. The rows in each plot spanned a length of 4 meters, and there were two rows per plot. The spacing between rows was set at 60 centimeters, and within each row, plants were spaced 20 centimeters apart. Consequently, the total plot size was calculated as 4.0 meters in length and 1.2 meters in width, resulting in a plot area of 4.8 square meters.

### Observations Recorded

In the observation phase, data were collected on 11 distinct quantitative traits from ten randomly chosen competitive plants. The average was then calculated, representing the mean for each treatment. The specific methodologies for recording observations on various traits are outlined as follows. Days to 50 percent tasseling was measured as the number of days from sowing to the point at which 50 percent of plants exhibited pollen shedding. Similarly, Days to 50 percent silking denoted the duration from sowing to the emergence of full silk in 50 percent of plants in a treatment. Plant height was recorded as the length from ground level to the tassel base when the plants reached maturity. Ear height represented the height from ground level to the uppermost ear-bearing internodes, measured in centimeters (cm). Ear length was measured from the ear's bottom to its tip in centimeters, while ear girth was recorded as the thickness of the ear, specifically at its middle, in centimeters. The number of kernel rows per ear was counted, and the mean was recorded as the number of kernel rows per cob. Additionally, the number of kernels per row was counted, and the average was recorded. The weight of 100 seeds was measured in grams, drawn from a randomly selected sun-dried sample in each plot. The shelling percentage is determined by dividing the weight of the grains by the total weight, which includes both the grain weight and the pith weight. This ratio is then multiplied by 100 to express the result as a percentage. Finally, grain yield was recorded by measuring the fresh ear weight per plot at harvest. Grain yield per hectare was then calculated based on specific formulas, taking into account factors such as moisture content and correction for zero percent moisture. This detailed process involved dehusking, air-drying, shelling, cleaning, and weighing the harvested cobs to compute the grain yield per hectare in tons (Supplementary file 2).

### Statistical analysis

In order to identify and ascertain the genetic variability among the genotypes and also to confirm the presence of environmental effect on various characteristics of genotypes, different genetic parameters were estimated by adopting appropriate formulae.

### Estimation of variance component

Genotypic and phenotypic components of variance were estimated by the following formulae.

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{MSS (treatment)} - \text{MSS (error)}}{\text{Number of replications}}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \text{MSS (error)}$$

### Co-efficient of variation

The genotypic and phenotypic coefficients of variation were calculated using the formula by Burton (1952) [1].

Genotypic coefficient of variation: $GCV\% = (\sigma^2_g)/X \times 100$

Genotypic coefficient of variation: $PCV\% = (\sigma^2_p)/X \times 100$

Genotypic coefficient of variation: $ECV\% = (\sigma^2_e)/X \times 100$

Where,

$\sigma_g$ = Genotypic standard deviation
$\sigma_p$ = Phenotypic standard deviation
X = General mean of character

GCV and PCV values were categorized as low, moderate and high values as suggested by Sivasubramanian and Menon (1973), which is as below.

1-10 percent: Low
10.1 - 20 percent: Moderate
20.1 percent and above: High

### Heritability in broad sense ($h^2_{bs}$)

Heritability in broad sense was computed as the ratio of genetic variance to the total phenotypic variance and narrow sense heritability was the ratio of additive genetic variance to the total phenotypic variance as suggested by Hanson *et al.* (1956) [4] and expressed as percentage.

$$\text{Heritability } (h^2_{bs}) = \frac{\sigma^2_g}{\sigma^2_p}$$

Where,

$\sigma^2_g$ = Genotypic variance
$\sigma^2_p$ = Phenotypic variance

Heritability in broad sense was categorized as per the classification given by Johnson *et al.* (1955) [6].

0 - 30 percent: Low
30.1 - 60 percent: Moderate
60.1 percent and above: High

### Genetic advance (GA)

Improvement in the mean genotype value of selected plants over the parental population is known as genetic advance or expected genetic advance (GA) was calculated as per the method suggested by Johnson *et al.* (1955) [6] using the formula:

$$GA = h^2_{bs} \times k \times \sigma p$$

Where,

$h^2_{bs}$ = Heritability in broad sense, $\sigma p$ = Phenotypic standard deviation

k = Selection deferential which is equal to 2.06 at 5% intensity of selection

### Genetic advance as percent of mean (GAM)

$$\text{GA \% over mean} = \frac{\text{GA}}{\overline{\text{X}}} \times 100$$

Where,
GA = Genetic advance an
X = General mean of the character

Genetic advance as percent mean was categorized as low, moderate and high as given by Johnson *et al.* (1955) [6].
0 - 10 percent: Low
10.1 - 20 percent: Moderate
20.1 percent and above: High

## Results and Discussion

### Analysis of variance (ANOVA) for yield and yield related traits in newly developed inbred lines of maize

The mean sum of squares due to eleven characters in newly developed inbred lines of maize *viz.*, Days to 50 percent tasseling, Days to 50 percent silking, plant height, ear height, cob length, cob girth, number of kernel rows per ear, number of kernels per row, 100-seed weight, shelling percentage and grain yield per hectare are presented in Table 1. The ANOVA revealed highly significant mean sum of squares for all the traits.

The analysis of variance for all the 11 characters revealed significant mean sum of squares due to genotypes indicating the existence of substantial variability among the newly developed inbred lines of maize for all the characters studied. Earlier workers like Suvarna *et al.* (2008) [15], Rajesh *et al.* (2013) [17], Gazal *et al.* (2017) [18], Rajwade *et al.* (2017) [13], Grace *et al.* (2018) [2] and Dar *et al.* (2018) [19] have reported the significant differences among the genotypes for all the characters considered. However, the analysis of variance by itself is inconclusive in explaining all the inherent genetic variability in the collection as the phenotypic variance is the function of genetic variance and environmental variance. Hence, it is necessary to work out PCV, GCV, heritability and genetic advance for understanding the genetic nature of a trait.

**Table 1:** Analysis of variance for yield and yield related traits in newly developed inbred lines of maize during *rabi*-2016

| Source of variation | d. f. | Days to 50 percent tasseling | Days to 50 percent silking | Plant height (cm) | Ear height (cm) | Ear length (cm) | Ear girth (cm) | Number of kernel rows per cob | Number of kernels per row | Hundred seed weight (g) | Shelling percentage (%) | Grain yield per hectare (t) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Replication | 1 | 2.25 | 5.29 | 36.08 | 13.74 | 11.15 | 0.05 | 5.95 | 60.37* | 0.81 | 1.05 | 0.55 |
| Treatments | 49 | 13.09** | 14.37** | 917.99** | 378.53** | 5.44** | 0.31** | 6.78** | 57.29** | 76.13** | 32.80** | 1.54** |
| Error | 49 | 1.47 | 2.53 | 134.02 | 65.99 | 0.66 | 0.01 | 0.46 | 8.63 | 5.28 | 1.70 | 0.21 |
| SE | | 0.85 | 1.12 | 8.18 | 5.74 | 0.57 | 0.08 | 0.48 | 2.07 | 1.62 | 0.92 | 0.32 |
| CV | | 2.03 | 2.61 | 7.91 | 11.35 | 6.15 | 3.35 | 5.32 | 11.13 | 9.02 | 1.59 | 14.40 |
| CD @ 5% | | 2.44 | 3.19 | 23.26 | 16.32 | 1.63 | 0.24 | 1.36 | 5.90 | 4.61 | 2.62 | 0.92 |
| CD @ 1% | | 3.25 | 4.27 | 31.02 | 21.77 | 2.19 | 0.33 | 1.83 | 7.87 | 6.16 | 3.50 | 1.23 |

*, ** - Significant at 5% and 1% level of probability

### Analysis of Means, Range, Genetic variability, Heritability and Genetic advance

The success of any breeding programme depends upon the quantum of genetic variability present in the population. Wide range of genetic variability helps in selecting desired genotypes. In addition to the genetic variability, knowledge on heritability and genetic advance helps the breeder to employ the suitable breeding strategy. Therefore, it is necessary to have information on these parameters. To understand the extent to which the observed variations are due to genetic factors, analysis of means, range, genetic variability estimates including genotypic and phenotypic coefficient of variations, heritability in broad sense and genetic advance as percent mean in respect of these characters are presented in Table 2.

In the investigation of various morpho-physiological traits among newly developed maize inbred lines, notable variations were observed. The duration for "Days to 50 percent tasseling" exhibited a broad range, spanning from 55 to 65 days among the inbred lines, with an average of 60 days. These lines showed low Genotypic Coefficient of Variation (GCV) at 4.03%, Phenotypic Coefficient of Variation (PCV) at 4.52%, along with elevated heritability estimates at 79.80%, and a relatively low genetic advance as a percentage of the mean at 7.43%. Similarly, for "Days to 50 percent silking," the inbred lines displayed variations from 56 to 67 days, with an average of 61 days. Low GCV (4.00%) and PCV (4.78%) were recorded, accompanied by high heritability estimates at 70.00% and a low genetic advance as a percentage of the mean at 6.89%.

"Plant height" demonstrated significant variability, ranging from 102.50 to 180.50 cm, with an average height of 146.31 cm. Moderate GCV (13.53%) and PCV (15.67%) were observed, along with high heritability estimates at 74.50% and a substantial genetic advance as a percentage of the mean at 24.06%. "Ear height" exhibited a wide range from 44.50 to 100.00 cm, with an average ear height of 71.55 cm. The inbred lines showed moderate GCV (17.47%) and high PCV (20.83%), coupled with high heritability estimates at 70.30% and a notable genetic advance as a percentage of the mean at 30.17%. Variability in "Cob length" was observed, ranging from 9.90 to 17.00 cm, with an average length of 13.26 cm. Moderate GCV (11.66%) and PCV (13.18%) were noted, accompanied by high heritability at 78.20% and a substantial genetic advance as a percentage of the mean at 21.24%. For "Cob girth," the inbred lines displayed a range from 2.99 to 4.60 cm, with an average cob girth of 3.64 cm. Moderate GCV (10.62%) and PCV (11.13%) were recorded, along with high heritability at 90.90% and a moderate genetic advance as a percentage of the mean at 20.86%.

"The number of kernel rows per cob" varied from 10 to 16 rows per cob, with an average of 12.81. Moderate GCV (13.87%) and PCV (14.85%) were observed, coupled with high heritability at 87.20% and a notable genetic advance as a percentage of the mean at 26.68%. The "Number of kernels per row" ranged from 15.90 to 38.00, with a mean value of

26.38. Moderate GCV (18.69%) and high PCV (21.75%) were displayed, along with high heritability at 73.80% and a substantial genetic advance as a percentage of the mean at 33.08%.

**Table 2:** Estimation of mean and genetic variability parameters for yield and yield related traits in newly developed inbred lines of maize during *rabi*-2016

| **Sl. No.** | **Characters** | **Range** | | **Mean** | **GCV (%)** | **PCV (%)** | **$h^2$ (bs)** | **GA** | **GAM (%)** |
|---|---|---|---|---|---|---|---|---|---|
| | | **Min** | **Max** | | | | | | |
| 1 | Days to 50 percent tasseling | 55.00 | 65.00 | 60.00 | 4.03 | 4.52 | 79.80 | 4.43 | 7.43 |
| 2 | Days to 50 percent silking | 56.00 | 67.00 | 61.00 | 4.00 | 4.78 | 70.00 | 4.19 | 6.89 |
| 3 | Plant height (cm) | 102.50 | 180.50 | 146.31 | 13.53 | 15.67 | 74.50 | 35.20 | 24.06 |
| 4 | Ear height (cm) | 44.50 | 100.00 | 71.55 | 17.47 | 20.83 | 70.30 | 21.59 | 30.17 |
| 5 | Cob Length (cm) | 9.90 | 17.00 | 13.26 | 11.66 | 13.18 | 78.20 | 2.81 | 21.24 |
| 6 | Cob Girth (cm) | 2.99 | 4.60 | 3.64 | 10.62 | 11.13 | 90.90 | 0.76 | 20.86 |
| 7 | Number of kernel rows per cob | 10.00 | 16.00 | 12.81 | 13.87 | 14.85 | 87.20 | 3.41 | 26.68 |
| 8 | Number of kernels per row | 15.90 | 38.00 | 26.38 | 18.69 | 21.75 | 73.80 | 8.73 | 33.08 |
| 9 | Hundred seed weight | 13.50 | 37.00 | 25.47 | 23.36 | 25.05 | 87.00 | 11.43 | 44.90 |
| 10 | Shelling percentage (%) | 69.08 | 86.95 | 81.92 | 4.81 | 5.07 | 90.10 | 7.71 | 9.42 |
| 11 | Grain yield (t $ha^{-1}$) | 1.81 | 4.94 | 3.18 | 25.65 | 29.42 | 76.00 | 1.46 | 46.08 |

GCV = Genotypic coefficient of variance, PCV = Phenotypic coefficient of variance, $h^2$ (bs) = Broad sense heritability, GA = Genetic advance, GAM = Genetic advance as percent of mean

"Hundred grain weight" ranged from 13.50 to 37.00 g, with an average weight of 25.47 g. High GCV (23.36%) and PCV (25.05%) were observed, along with high heritability at 87.00% and a significant genetic advance as a percentage of the mean at 44.90%. The "Shelling percentage" showed variability from 69.08 to 86.95%, with an average of 81.92%. Low GCV (4.81%) and PCV (5.07%) were noted, coupled with high heritability at 90.10% and a low genetic advance as a percentage of the mean at 9.42%. Finally, "Grain yield per hectare" varied from 1.81 to 4.94 t ha-1, with an average of 3.18 t ha-1, indicating high variability. High GCV (25.65%) and PCV (29.42%) were noticed, along with high heritability at 76.00% and a significant genetic advance as a percentage of the mean at 46.08%.

The estimates of GCV were low as compared to that of PCV for all the traits studied. Lower values of GCV and PCV (< 10%) were noticed for days to 50 percent tasseling, days to 50 percent silking and shelling percentage. Similar results were reported by Grace *et al*. (2018) [2] for days to 50 percent tasseling, days to 50 percent silking and Patil *et al*. (2016) [11] for shelling percentage. For plant height, cob length, cob girth and number of kernel rows per cob moderate (10-20%) GCV and PCV was observed. Similar results were reported by Rajwade *et al*. (2017) [13] for plant height, cob girth, number of kernel rows per cob; Muttappa *et al*. (2018) [9] for cob length. Whereas, hundred seed weight and grain yield recorded high GCV and PCV (> 20%). For hundred seed weight similar results were observed by Grace *et al*. (2018) [2] and Muttappa *et al*. (2018) [9] for grain yield. Moderate GCV (10-20%) and high PCV (> 20%) were observed for ear height and number of kernels per row. Similar observations were recorded by Muttappa *et al*. (2018) [9] but they obtained moderate GCV and moderate PCV. High PCV for these traits are supported by findings of Rajwade *et al*. (2017) [13].

The GCV and PCV for grain yield were high, indicating the existence of wide variation in the material studied. The narrow difference between GCV and PCV indicated the lesser influence of environment on that trait. In addition, high broad sense heritability and GAM for this trait implied that this trait can be improved through selection. However, yield is a complex character and is the function of several component characters and their interaction with the environment. Hence, direct selection based on yield alone will not be very effective in crop improvement programmes. Grafius (1959) [3] pointed out that structure of yield probed through its components rather than directly would be more efficient.

Genetic advance being the function of heritability, selection intensity and phenotypic standard deviation indicates the magnitude of improvement in the desired direction that can be expressed in a particular character by selecting a certain proportion of population. Genetic advance shows the degree of gain obtained in a character under particular selection pressure. Johnson *et al*. (1955) [6] reported that estimates of both heritability and genetic advance are more useful in the choice of selection method rather than heritability or genetic advance alone.

High (> 60%) broad sense heritability was found for all the traits under study. These findings are in agreement with the results of Shazia *et al*. (2017) [14] and Rahul (2017) [12] for days to 50 percent tasseling, days to 50 percent silking, plant height, ear height, number of kernels per row, 100-seed weight and grain yield; Nataraj *et al*. (2014) and Shazia *et al*. (2017) [14] for cob girth. Whereas, Rahul (2017) [12] for cob length; Nataraj *et al*. (2014) and Muttappa *et al*. (2018) [9] for number of kernel rows per cob, Hemavathy *et al*. (2008) [5] and Rahul (2017) [12] for shelling percentage. Genetic advance as percent mean (GAM) was high (> 20%) for plant height, ear height, cob length, cob girth, number of kernel rows per cob, number of kernels per row, 100-seed weight and grain yield per hectare. Similar results of high GAM for plant height, ear height, cob length, number of kernel rows per cob and number of kernels per row were reported by Rahul (2017) [12] and Mohammed *et al*. (2017) [8] for grain yield per hectare; Reddy *et al*. (2012) [20] for cob girth and Shazia *et al*. (2017) [14] for 100-seed weight. Days to 50 percent tasseling, days to 50 percent silking, and shelling percentage revealed lowest (< 10%) genetic advance as percent mean. Similar results were reported by Grace *et al*. (2018) [2] for days to 50 percent tasselling and days to 50 percent silking; Patil *et al*. (2016) [11] for shelling percentage.

The results of the present study indicated the importance of grain yield per hectare and hundred seed weight as they exhibited high heritability, GCV, PCV and GAM. High heritability coupled with high genetic advance indicated that, phenotypic selection would be effective in improvement of such traits. High heritability with moderate GCV and high

PCV coupled high GAM was exhibited by ear height and number of kernels per row suggested selection will also be effective for these traits. High heritability with moderate GCV, PCV and high GAM as revealed by plant height, cob length, cob girth and number of kernel rows per cob indicating the suitability of selection. Days to 50 percent tasseling, days to 50 percent silking and shelling percentage displayed high heritability estimates coupled with low GCV, PCV and GAM suggesting selection will be less effective for these traits.

## Conclusion

The genetic variability study at IARI Regional Research Centre, Dharwad in rabi-2016 on morpho-physiological traits in newly developed maize inbred lines offered insights into variability, heritability, and genetic advance. Analysing 47 elite inbred lines, ANOVA revealed significant variability in all 11 studied traits. Notably, days to 50 percent tasselling, days to 50 percent silking, and shelling percentage had limited genetic variability, while moderate to high GCV and PCV were observed for plant height, ear height, cob length, cob girth, number of kernel rows per cob, number of kernels per row, hundred-seed weight, shelling percentage, and grain yield per hectare. High heritability (>60%) underscored strong genetic control over these traits. Genetic advance as a percentage of the mean (GAM) categorized traits into low, moderate, or high potential for improvement. Promisingly, traits like plant height, ear height, cob length, cob girth, number of kernel rows per cob, number of kernels per row, hundred-seed weight, and grain yield per hectare exhibited high GAM, making them suitable for targeted breeding. In contrast, days to 50 percent tasseling, days to 50 percent silking, and shelling percentage showed low GAM, suggesting less effective direct selection. The study emphasizes considering traits with high heritability and genetic advance in maize breeding for comprehensive improvements. Continuous monitoring of promising inbred lines and exploring underlying genetic mechanisms are crucial for trait stability and integrating molecular insights. In conclusion, the study guides breeders in selecting promising lines for further improvement and adaptation to changing environmental conditions.

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**Supplementary 1:** The list of genetic materials used in the study

| Sl. No. | Line | Sl. No. | Line | Sl. No. | Line | Sl. No. | Line |
|---|---|---|---|---|---|---|---|
| 1 | PDM-116-2 | 14 | DIM-325 | 27 | DIM-311 | 40 | DIM-342 |
| 2 | DIM-329 | 15 | DIM-317 | 28 | PDM-201 | 41 | PDM-136 |
| 3 | DIM-319 | 16 | DDM-2306 | 29 | PDM-4281 | 42 | DIM-346 |
| 4 | DIM-320 | 17 | PDM-79-1 | 30 | PDM-209-1 | 43 | PDM-4641 |
| 5 | DIM330 | 18 | PDM-71-2 | 31 | PDM-106 | 44 | DIM-337 |
| 6 | DIM-307 | 19 | DIM-322 | 32 | DIM-333 | 45 | DDM-2311 |
| 7 | PDM-4121 | 20 | DIM-328 | 33 | PDM-81 | 46 | DIM-304 |
| 8 | DIM-306 | 21 | PDM-10 | 34 | PDM-203 | 47 | DIM-336 |
| 9 | DIM-327 | 22 | DIM-348 | 35 | DDM-2303 |  | Testers |
| 10 | PDM-161-1 | 23 | PDM-95 | 36 | PDM-31-1 | 48 | DC-13 |
| 11 | DIM-318 | 24 | PDM-4031 | 37 | DDM-2301 | 49 | DC-14 |
| 12 | DDM-2304 | 25 | PDM-418 | 38 | PDM-198 | 50 | DC-17 |
| 13 | PDM-137-K | 26 | DIM-324 | 39 | DDM-2310 |  |  |

**Supplementary 2:** Calculation of Grain yield per hectare

Fresh ear weight per plot was recorded at the time of harvest. Grain yield per hectare was calculated by using the formula given below.

At physiological maturity, the cobs were dehusked and harvested in each net plot. The harvested cobs were air dried, shelled, cleaned and weighed. Grain yield per hectare was computed from yield per plot and expressed in t ha$^{-1}$.

$$F = e\frac{100 - d}{100}$$

Where,

e = corrected fresh ear weight on the basis of Av stand at harvest

e = ab/c

a = average stand per plot of the trial

b = fresh ear weight (g)

c = stand at harvest of the respective plot

d = average moisture (%)

f = corrected fresh ear weight at zero per cent moisture

At the time of harvesting, fresh ear weight was recorded in grams per plant. Moisture content in grain at maturity was recorded in shelled samples of five random ears of each plot with the help of electronic moisture meter. The fresh weight of ear data was used to work out the dry weight grain yield per plant at 15 % moisture level. Corrected fresh ear weight at 0 % moisture to be multiplied by correction factor (100/85) for calculation of plot yield at 15 % moisture content.

$$\text{Grain yield (kg ha}^{-1}\text{) at 0\% moisture} = \frac{\text{Fresh ear weight} \times (100 - \text{AVM}) \times \text{S \%} \times 10000}{100 \times \text{plot area}}$$

$$\text{Grain yield (kg ha}^{-1}\text{) at 15 \% moisture} = \frac{\text{Fresh ear weight} \times (100 - \text{AVM}) \times \text{S \%} \times 10000 \times 100/85}{100 \times \text{Plot area}}$$

Where,

AVM = Average moisture content

S % = Shelling Percentage