

## Study of Wheat Genotypes for Yield and Associated Traits

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### Abstract

Genetic variety is the main selection criteria to improve crops yield. The study was carried out at Agriculture Research Station Swabi, Khyber Pakhtunkhwa. Tested nine advanced wheat lines, along with one check, was used for the assessment of their yield and variety of traits in a Randomized Complete Block Design in 2022–2023. Genotypes for each of the chosen traits had non-significant variances for other metrics but substantial ( $P \leq 0.01$ ) differences for grain weight spike<sup>-1</sup>, thousand grain weight, grain yield, biological yield, and harvest index. The check variety took minimum days to maturity (121 days each) while CIM-8 took minimum days. For CIM-4, the minimum plant height was 90.66 cm. The highest spike length obtained by the CIM-3 genotype was 14.3 cm. The maximum grains spike<sup>-1</sup> was expressed by CIM-7 (81.33 grains). The maximum grain weight spike<sup>-1</sup> for genotype CIM-5 was 3.66 g, while the maximum weight for thousand grains was 51.3 g for genotype CIM-3. Genotype CIM-7 (12148 kg ha<sup>-1</sup>) yielded the highest biological yield, while genotype CIM-5 (6666 kg ha<sup>-1</sup>) produced the maximum grain yield. The CIM-5 genotype reported the highest harvest index value (60.16). The study shows that sufficient variation exists in the breeding material and these genotypes must be studied further for obtaining any best line. Furthermore, these genotypes' genetic material might be used in a future breeding system.

**Keywords:** Genetic variation, Wheat, Genotype, Morphological traits, yields

### Introduction

The hexaploid species known as wheat (*Triticum aestivum* L.), which belongs to the Poaceous (Gramineae) family, has chromosomal number  $2n=6x=42$ . Originating in South Eastern Turkey, wheat is a self-pollinating annual crop. Pakistani people mostly depend on it as a staple food, and its production exceeds that of other crops in the country (Chandio *et al.*, 2016; Gadde & Kalli, 2020a). Three quarters of the country's total land is used for wheat cultivation, which makes up to 70% of all grains. Pakistan produced 25.60 million tons of wheat

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in 2018–19, compared to 766.9 million tons worldwide (Gadde & Kalli, 2021a; Ploschuk *et al.*, 2020).

Pakistan is among the nations with the highest wheat production, but even so, our output is insufficient to support the world's growing population. The primary causes of decreased crop productivity include crop area reduction, population growth, climate change, decreased availability of inputs (fertilizers, pesticides, etc.), and decreased availability of irrigation water (Gadde & Kalli, 2021a). These circumstances forced plant breeders to create crop genotypes that can withstand harsh environments without experiencing a reduction in yield. Wheat has frequently been the subject of extensive study for yield improvement. The most intricate of its constituent sub-characters, grain yield is influenced by genes, interactions, and the environment (Pauzi *et al.*, 2019; Novoselovic *et al.*, 2004). During a breeding programme, direct selection based only on visual observation is not very effective. Genetic variants, heritability estimates, and the correlation between grain yield and agro-morphological traits are the foundations of effective selection (Gadde & Kalli, 2020b). Correlation studies and heritability estimates offer a more simpler method of establishing a relationship between critical features and grain yield (Gul *et al.*, 2019; Rahim *et al.*, 2019). Selection is made more beneficial by knowledge of genetic variations, heritability coefficients, the connection between associated morphological features and grain yield. Correlation analyses and heritability estimations offer the simplest way to connect key traits with grain yield (Gul *et al.*, 2020; Kumar *et al.* 2019).

Crop improvement was greatly aided by the genetic concepts used in numerous breeding programmes. Plants that are selected with considerable environmental variation are less likely to have genotypes that are selected with hereditary differences (). In contrast, selection is more likely to occur when environmental variability is smaller than genetic variability. When working with the crop improvement programme, it is highly advised to have a sufficient understanding of heredity and response to selection. Choosing traits with high heritability early in the breeding programme can facilitate progress (Jan *et al.*, 2023; Khan *et al.*, 2008). Grain yield is a polygenic characteristic that depends on selection, environment, and related traits. Thus, the characters who contribute to yield ought to be highlighted. Understanding the interaction between the various features that contribute to yield is just as important as knowing about heredity (Zareef *et al.*, 2023; Zeeshan *et al.*, 2014). In order to select the most promising wheat lines for next wheat breeding programmes, the current study focuses on the genetic diversity of wheat lines.

### Materials and Methods

The current study, titled "Study of wheat genotypes for yield and associated traits," was carried out in Rabi, 2022–2023 at the Agriculture Research Station (ARS) Swabi. Ten sophisticated exotic wheat lines and one local check cultivar (PS-19) made up the testing materials. Three replications of a Randomised Complete Block Design were used in the experiment. Four rows made up each plot in which a genotype was planted. Every row of every plot measured three metres in length, with a 30-centimeter gap between each row. During the crop season, recommended cultural procedures were implemented to minimise experimental error and preserve the crop's health.

**Table 1**  
*List of genotypes used during study*

S. No	Genotype	Parentage
1	CIM-101	NELOKI//SOKOLL/EXCALIBUR
2	CIM-102	KRL 19/QUAIU #1//BECARD/QUAIU #1
3	CIM-103	SUP152*2//TECUE #1//FRNCLN*2//TECUE #1
4	CIM-104	MUU/KBIRD//KACHU/KIRITATI
5	CIM-105	BECARD/QUAIU #1//BORL14
6	CIM-106	MUCUY
7	CIM-107	KACHU #1/YUNMAI 47//KACHU/4/MUU #1//PBW343*2//KUKUNA/3/MUU/5/KUTZ
8	CIM-108	TRCH/SRTU//KACHU/3//BORL14
9	CIM-109	PRL/2*PASTOR//PBW343*2//KUKUNA/3//ROLF07/4//KFA/2* KACHU
10	CHK	PS19

### Traits Measured

A random selection of ten plants was made, and information was provided for below traits.

#### Days to 50% Heading

Approximately from the time of planting to the end of heading, half of the plants in each plot displayed days to 50% head production.

#### Days to Maturity

The period from planting until the physiological maturity of the crop was observed by tracking the number of days it took for 50% of plants in each plot to experience the loss of green pigment from spikes containing peduncles.

#### Plant Height

Plant height was measured by excluding awns and recorded at the point at which plants of each genotype attained maturity. The measurement was taken from the soil surface to the tip of the terminal spikelet.

#### Spike Length

For each genotype in each plot, the length of the five plants selected at random, the length of each spikelet, from the base at the start of the spikelet to the tip at the terminal site, was measured in centimeters. We measured ten randomly chosen spikes but did not measure the awns.

#### Grains Spike<sup>-1</sup>

The grain count per spike was determined by manually threshing ten randomly selected spikes. The average of the total grains from the ten spikes was calculated by counting them.

#### Grain weight spike<sup>-1</sup>

The weight of grains per spike was collected for ten randomly chosen spikes after manually threshing each individual spike. After that, the spikes were weighed on an electronic scale, and the grain weight spike<sup>-1</sup> data was analyzed using the average data.

#### 1000-Grains Weight

To determine the weight of the grains, three arbitrary samples of thousand grains were collected from each plot's yield. A digital balance was used to measure the weight of three randomly selected thousand grain samples. The weight of the 1000 grains was then calculated from the average of the three samples.

#### Biological Yield

After sun-drying for two to three days, each genotype was picked independently at maturity and weighed in order to collect biological yield data.

Biological yield (kg ha<sup>-1</sup>) = (Biological yield plot<sup>-1</sup>/ Plot area m<sup>2</sup>) × 10000 m<sup>2</sup>

### Grain Yield

To determine grain yield, each plot's crop was completely thrashed, and the following formula was used to weigh the total amount of grain produced in each plot individually.

$$\text{Grain yield (kg ha}^{-1}\text{)} = (\text{Grain yield plot}^{-1}/\text{plot area m}^2) \times 10,000 \text{ m}^2$$

### Harvest Index (%)

Information regarding the harvest index was calculated using the formula provided, which involves the ratio of grain yield to biological yield. Harvest index (%) = (Grain yield plot<sup>-1</sup> / Biological yield plot<sup>-1</sup>) × 100

### Statistical Analysis

Statistic 8.1 Software was used to do an analysis of variance on statistical data that was collected for the several attributes that were the focus of the study (Rehman *et al.*, 2015).

## Results and Discussion

### Days to Heading

Days to heading showed non-significant differences (Table 2). Genotype no. 8 (124) had a maximum day to heading mentioned, but genotype no. 10 (121) had a minimum day to heading noted. The total mean of all genotypes was found to be 122.67 (Table 1). Because it facilitates the insect's escape mechanism, early heading is crucial. The findings of Kumar *et al.* (2020), who observed significant variations for these attributes among various genotypes, are not consistent with our results. Given that their backgrounds are comparable; the lack of significant differences may be due to genetic similarities.

### Days to Maturity

Days to maturity showed non-significant differences (Table 2). The genotypes no. 1 and no. 3 had maximum days to maturity (169) and genotype no. 5 had minimum days to maturity (165). With an aggregate mean of 167.83, all genotypes were present (Table 1). According to a study by Simmons (1987), a plant is considered mature when its senescence, which began just before anthesis, and reduction of leaf area occur. The crop may be exposed to un-favourable climatic conditions including lodging, sprouting, and other issues that lower yield, so information on maturity time is crucial.

### Plant Height

Regarding plant height, there were no discernible variations (Table 2). Genotype number 9 had the highest plant height measured

at 99.66 cm, while genotype number 4 had the lowest plant height measured at 90 cm. Table 1 displays all genotypes with an overall mean of 93.26. Given its correlation with grain yield, plant height is an important factor in breeding programmes. Short-stemmed plants will respond more strongly to fertilisers and have less lodging (Khan *et al.* 2007).

#### *Spike Length*

Regarding spike length, there were non-significant variations found (Table 2). The genotype number 3 showed the maximum spike length of 14.33 cm, while the genotype number 6 showed the minimum spike length of 11.66 cm. Table 1 displays the genotypes with an overall mean of 12.8cm. Spike length is strongly connected with grain yield spike-1, which is why plant breeders are constantly drawn to long spikes (Okuyama *et al.* 2005). Long spike increases photosynthetic rate since it remains green for a longer period of time (Sharma *et al.* 2003).

#### *Grains Per Spike*

For grains per spike, non-significant differences were found (Table 2). For genotype no. 7, the maximum number of grains per spike (81.33) was recorded, whereas genotype no. 4 had the lowest number of grains per spike (59). Table 1 displays all genotypes with an overall mean of 68.63. The yield is dependent on the maximum number of grains spike-1, with grains spike-1 being a significant factor in wheat crop productivity. For the purpose of creating better varieties, grains spike-1 can be used as a selection feature (Shpiler and Blum, 1991).

#### *Grain weight Per Spike*

For this feature, highly significant differences were found. (Refer to Table 2) The genotype no. 5 showed the highest grain weight per spike (3.6g), while the genotype no. 4 showed the lowest grain weight per spike (1.8g). Table 1 displays all genotypes with an overall mean of 2.84g. Grains weight spike-1 is a significant characteristic that depends on the amount of grains and their physiological growth. Since grain weight spike-1 directly affects the harvest index, it plays a significant role in the yield generation process. Grain weight plant-1 is a direct indicator of the effective usage of nutrients and their transfer into generative regions of the plant (Borojevich, 1983).

#### *Thousand Grain Weight*

For this feature, there were very substantial differences found. Table 2 Genotype number 3 had the highest recorded weight of 1,000 grains (51.33g), whereas genotype number 8 had the lowest weight (37g). With an overall mean of 43.2g, all genotypes were present. Table 1 Grain yield is directly correlated with thousand grain weight. Grain yield will increase with a higher 1000-grain weight value. Significant differences in 1000-grain weight were also noted by Ashfaq *et al.* (2003) between 15 genotypes of bread wheat. By computing the significant difference between genotypes using 30 wheat genotypes, Bhushan *et al.* (2013) supports our findings.

#### *Biological Yield*

For this feature, highly significant differences were found. (Refer to Table 2) Genotype No. 7 showed the highest biological yield (12148 kg/ha), while genotype No. 6 showed the lowest biological yield (6056 kg/ha). The average genotype mean across all samples was 9471 kg/ha. (Table 1). The outcomes of our study closely align with those of Mohsin *et al.* (2009), who published the findings of their investigation involving the testing of 95 artificial wheat lines.

#### *Grain Yield*

For this feature, there were extremely substantial variances (Table 2). The genotype no. 5 showed the highest grain yield (6666 kg/ha), whereas the genotype no. 6 showed the lowest grain yield weight (2588 kg/ha). The average genotype mean across all samples was 4288 kg/ha. (Table 1). Grain yield is the most important factor in wheat crops. Breeders are very interested in this attribute. Additionally, Zare *et al.* (2015) found that three wheat cultivars differed significantly in terms of grain yield and other characteristics.

#### *Harvest Index*

For this feature, highly significant differences were found (Table 2). Genotype number 5 (60.14) had the highest Harvest index, whilst genotype number 3 (26.17) had the lowest. With an average mean of 45.32, all genotypes were present. Table 1 For cereal crops, a direct correlation exists between the grain yield and the harvest index. The ratio of total biological yield to economic production will rise in tandem with the harvest index's increase. The findings of the current study were in line with those of Zeashan *et al.* (2014).

#### **Conclusion**

Genotypic and phenotypic correlations are significant statistical techniques that help assess the degree of relationship

between various yield-contributing features and can help wheat breeders choose greater yields. For the purpose of indirect selection for grain yield, highly heritable traits that have a beneficial correlation with grain yield are crucial. The highest grain yield was given by entry no 5 followed by entry no seven. So, these lines have the potential to add towards the yield increase. And these lines are selected for future wheat breeding program.

**Table 2**  
Mean data of genotypes used during study

	DT H	DT M	PH	SL	GP S	G WP S	TG W	BY	GY	HI
1	122. 6A	169. 6A	92. 6A	13.3 AB	64.0 AB	2.6 B	43.0 BC	9500A BCD	4055.6 CD	42.4 BC
2	123. 6A	167. 6AB	87. 2A	13.3 AB	66.3 AB	2.6 B	48.3 AB	10556 ABC	3500.0 CD	33.9 CD
3	123. 6A	169. 6A	93. 4A	14.3 A	70.6 AB	3.0 B	51.3 A	11537 AB	2992.6 CD	26.1 D
4	122. 0A	168. 6AB	90. 6A	13.0 AB	59.0 B	1.8 C	43.6 ABC	7389C D	3322.2 CD	45.2 BC
5	122. 0A	168. 3AB	95. 8A	12.0 B	68.0 AB	3.6 A	42.6 BC	11241 AB	6666.7 A	60.1 A
6	122. 0A	167. 0AB	90. 7A	11.6 B	72.0 AB	3.0 B	39.0 C	6056D D	2588.9 D	41.8 BC
7	122. 0A	168. 6AB	90. 8A	12.0 B	81.3 A	3.1 AB	43.6 ABC	12148 A	6490.0 AB	53.3 AB
8	124. 3A	165. 6B	99. 4A	12.3 B	75.3 AB	2.8 B	37.0 C	8241B CD	4559.3 BCD	54.4 AB
9	123. 0A	166. 0AB	99. 6A	13.3 AB	69.0 AB	2.9 B	40.6 BC	9148A BCD	4811.1 ABC	52.2 AB
10	121. 3A	167. 0AB	92. 0A	12.6 AB	60.6 B	2.7 B	42.6 BC	8904A BCD	3896.3 CD	43.3 BC
Mean of 6 Genot ypes	122. 6	167. 83	93. 2	12.8 0	68.6	2.8	43.2	9471.9	4288.3	45.3
CV (Co- Efficie nt of Variat ion)	1.55	1.36	9.0 7	8.33	16.3	13. 6	10.6	21.99	28.31	17.4
LSD (Least Signifi cant Differ ences)	3.2	3.9	14. 5	1.82	19.2	0.6	7.8	3572	2082	13.5

DTH (Days of heading), DTM (Days to maturity), PH (Plant height), SL (Spike length), GPS (Grains per spike), GWPS (Grain weight per spike), TGW (Thousand per weight), BY (Biological weight), GY (Grain yield), HI (Harvest Index)



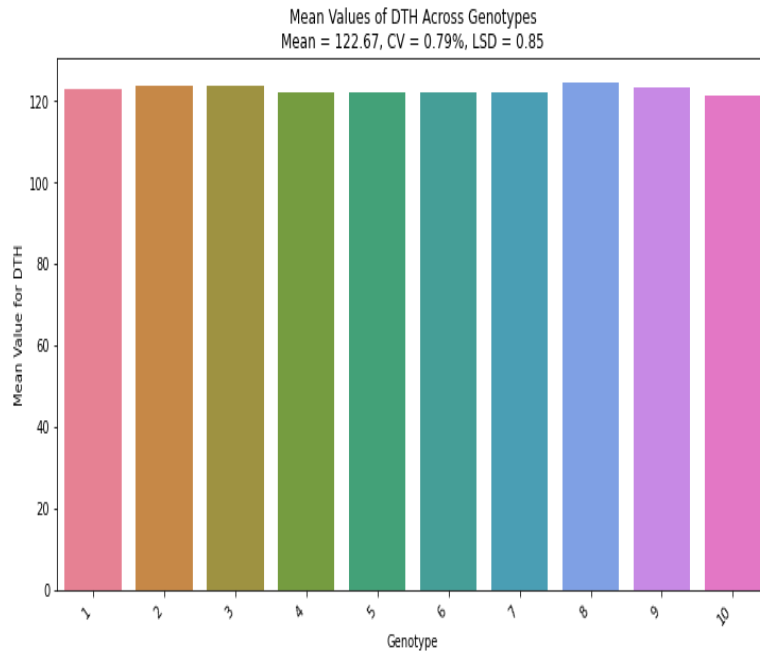


Figure 4.1: Mean value of DTH across Genotypes CIM-01 to CIM-09 and CHK-10

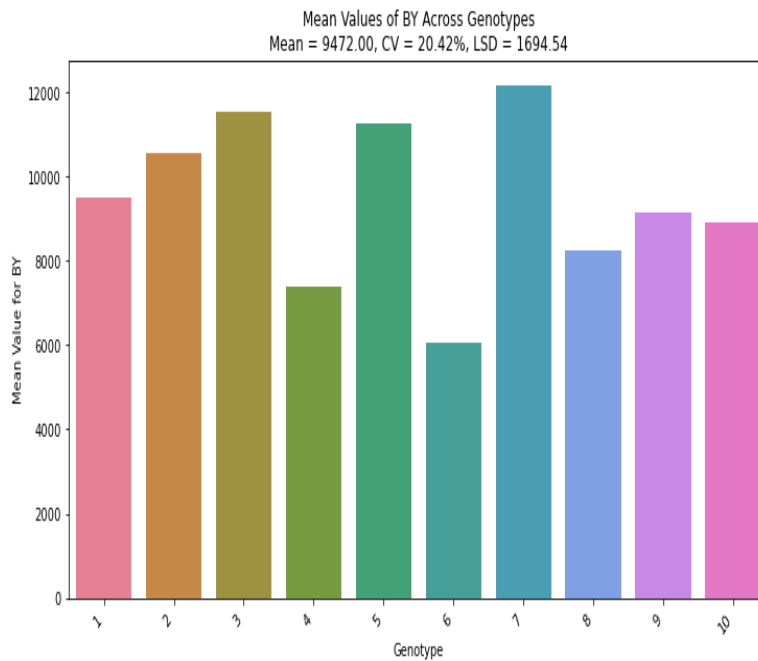


Figure 4.2: Mean value of DTM across genotypes CIM-01 to CIM-09 and CHK

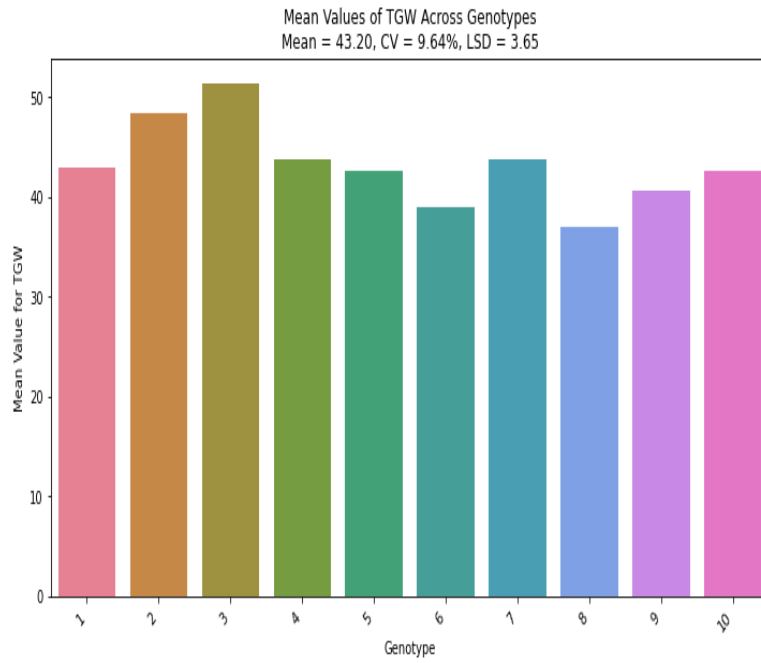


Figure 4.3: Mean value of PH across genotypes CIM-01 to CIM-09 and CHK

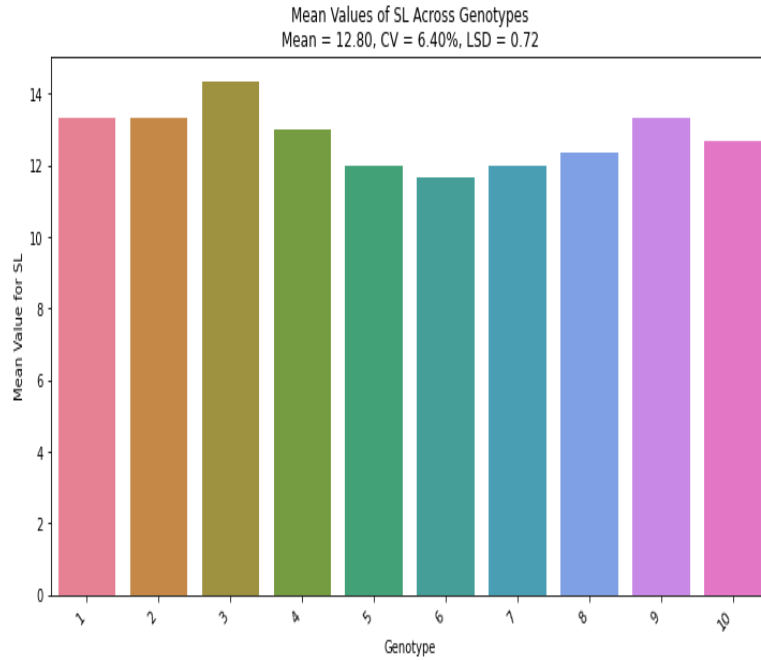


Figure 4.4: Mean value of SL across genotypes CIM 01 to CIM -09 and CHK

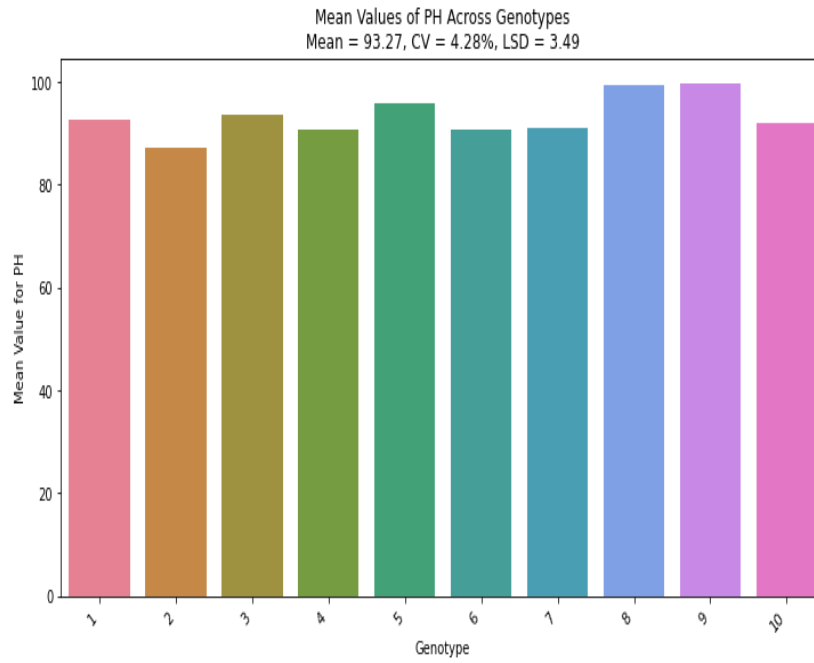


Figure 4.5: Mean value of GPS across genotypes CIM-01 to CIM-09 and CHK-10

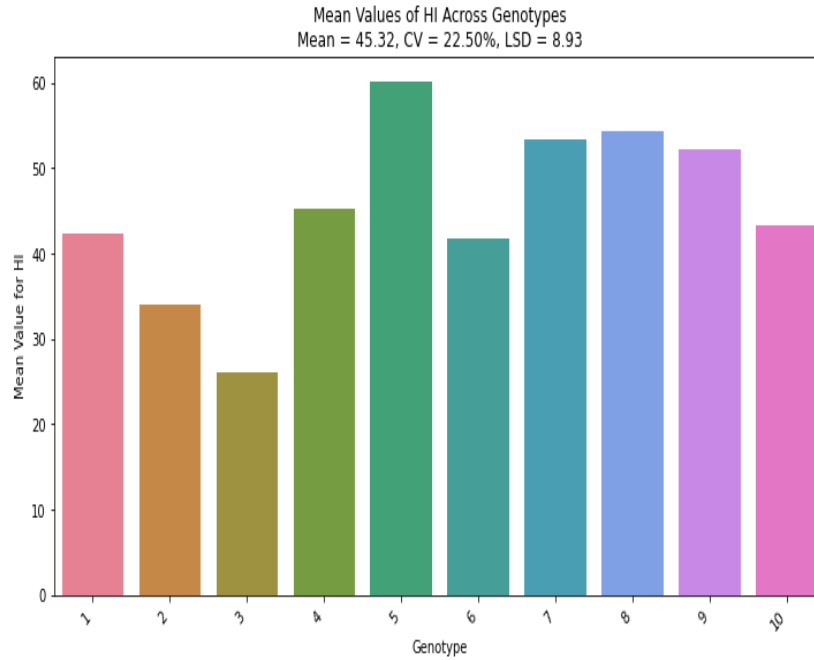


Figure 4.6: Mean value of GWPS across genotypes CIM-01 to CIM-09 and CHK-10

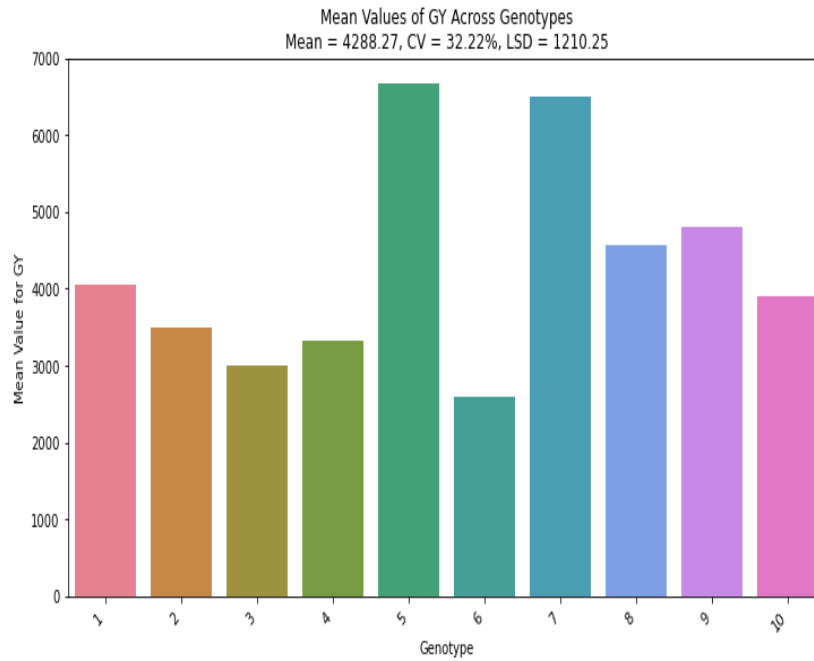


Figure 4.7: Mean value of TGW across genotypes CIM-01 to CIM-09 and CHK-10

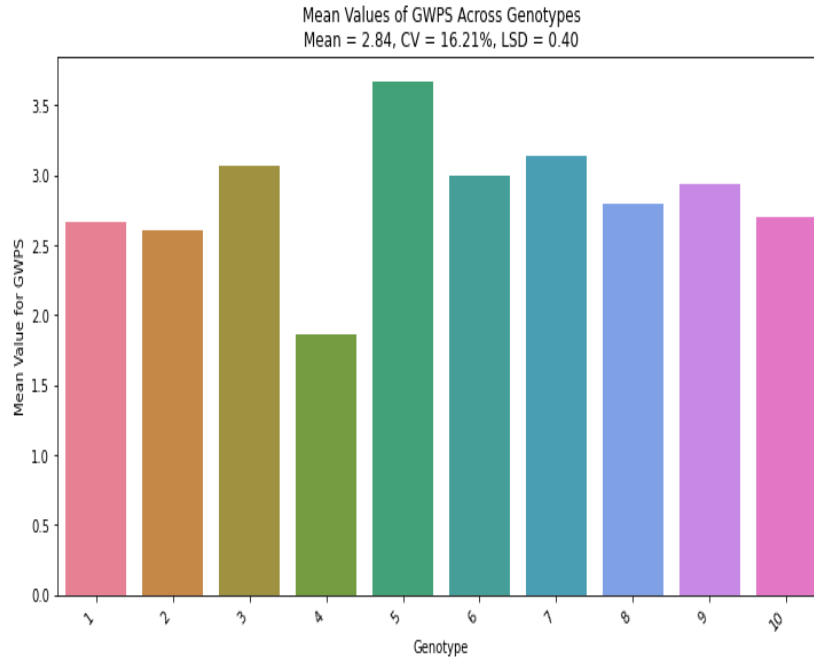


Figure 4. 8: Mean value of BY across genotypes CIM-01 to CIM-09 and CHK-10

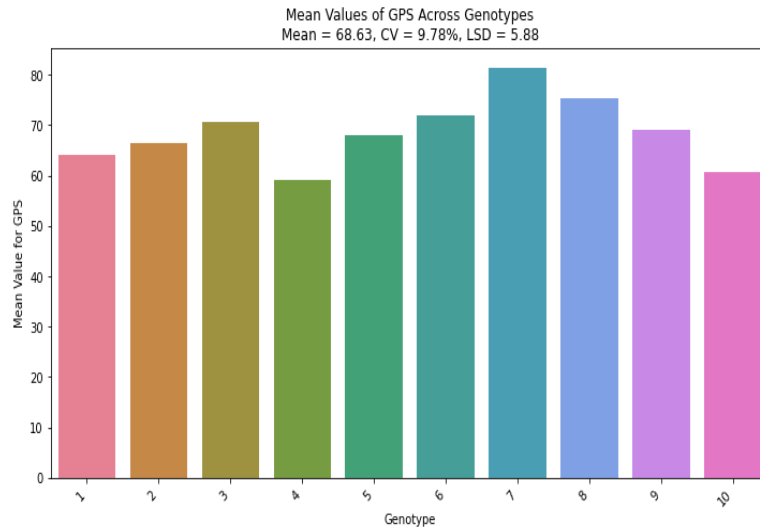


Figure 4.9: Mean value of GY across genotypes CIM-01 to CIM-09 and CHK-10

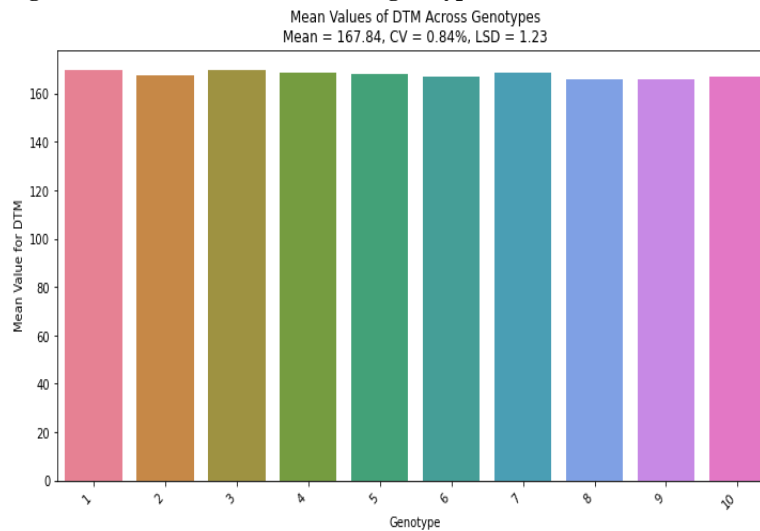


Figure 4.10: Mean value of HI across genotypes CIM -01 CIM-09 and CHK-10

Table 3

Mean squares of Genotypes

Source	DT H	DT M	PH	SL	GPS	GW PS	TG W	BY	GY	HI
Replication	0.03	7.63	24.1	2.10	71.63	0.05	1.60	2074	27847	38.21
Genotypes	2.81	5.94	47.7	2.01	135.0	0.63	52.0	1.12	57267	311.9
Error	3.62	5.18	71.5	1.13	126.1	0.15	20.9	4338	14741	62.44
	5	8	74	7	1	0	70	232	87	8

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