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GENETIC EVALUATION OF CYTOPLASMIC MALE STERILITY BASED WHEAT HYBRIDS

Niharika Shukla[1]*, Stuti Sharma[2], Sanjay Singh[2] and Shweta Kaushal[3]

[1]Scientist (Plant Breeding and Genetics), Krishi Vigyan Kendra, College of Agriculture,
Jawaharlal Nehru Krishi Vishwa Vidhyalaya, Jabalpur - 482 004, M.P., India.
[2]Scientist (Plant Breeding and Genetics), College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidhyalaya,
Jabalpur - 482 004 M.P., India.
[3]Agriculture Extension Officer (Plant Breeding and Genetics), Dewas, M.P., India.
*Corresponding author E-mail : niharikas86@gmail.com

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ABSTRACT

The current research with 54 CMS Based Hybrids (CMS F1) including 4 checks (MP3382, MP 3465, HI 1544, GW 322) were planted in a RCBD with 3 replications obtained from IIWBR, Karnal and the Division of Genetics, IARI New Delhi under the CRP on hybrid wheat program for genetic evaluation of Cytoplasmic Male Sterility based Wheat Hybrids for yield contributing traits. The data on 54 CMS based Hybrids (CMS F_1) including 4 checks (MP3382, MP 3465, HI 1544, GW 322) for 15 yield attributing traits *viz.* Awns length, Spike length, Number of spikelets per spike, sterility Percentage (%), Weight of per spike (g), Number of grain per spike, Harvest index (%), thousand grain weight (g), grain yield/plant (g) and biological yield/plant (g) in wheat was recorded for genetic evaluation in Wheat hybids. The traits like sterility percentage (128.38%), grain yield per plant, and biological yield per plant. these traits have the potential to be utilized for the advancement of hybrid development in wheat. On the basis of mean and range, maximum mean value noted in respective CMS based hybrids *viz.*, grain yield/plant (95A x WH730), thousand grain weights (96A x GW366), harvest index (94A x RAJ3765), number of tillers/plant (91A x RAJ3765). These crosses have the potential to be harnessed for the progress of hybrid development in wheat and it will directly contribute to improving yield and meeting the demand of a growing population, ultimately leading to India achieving self-sufficiency in food security.

Key words : Wheat, CMS based hybrids, Inheritance, Genetic, Grain yield.

Introduction

One of the most significant cereal crops in the world is wheat (Venske *et al.*, 2019). Covering 217 million hectares of the earth's surface, it is the largest food crop, with an annual global production of around 770 million tons (Erenstein *et al.*, 2022). Being the most cultivated food crop globally is commonly referred to as the "King of cereal" crops.

Wheat is counted among the 'three majors' cereal crops, along with corn and rice and it is the most important and strategic food crop for ensuring food security at the global level. The growing population has resulted in a sharp increase in the demand for wheat. Despite its relatively recent origins, bread wheat has enough genetic variability to permit the emergence of over 25,000 varieties that are suitable for a wide range of temperate regions. According to a recent report worldwide wheat production reaches 789.1 million metric tonnes across an area of 225.23 million hectares. The productivity of wheat per hectare is 3.5 metric tonnes (Food and Agriculture Organisation). In terms of both land coverage and quantity of output, wheat is the second most significant cereal crop in India, following rice in the ranking. Wheat production reached a record high of 109.52 mt in 2020–21, with a national productivity average of 3464 kg/ha. Over three billion people worldwide suffer from a diet low in nutrition and about 720 million people experience hunger (Ibba *et al*., 2022). Madhya Pradesh is the third largest state in India in terms of its area, production, and productivity. In Madhya Pradesh, wheat is grown on a total area of 7.15 million hectares, resulting in a production of approximately 24.42 million tonnes according to Madhya Pradesh Economic Survey. India's wheat crop is crucial to the nation's economic expansion, rural area development and food security.

A broad spectrum of inheritable diversity has been documented in wheat germplasm, suggesting the potential for enhancement through the selection process following the hybridization of superior genotypes. However, the efficacy of selection relies on the heritability of a specific trait. Traits that demonstrate heritability offer breeders an advantage by allowing for selection in the early segregating generations with a high level of efficiency and response to selection. Analysing statistical parameters like mean, variance, heritability, genetic advance, etc., is beneficial in assessing the performance of a particular genotype and determining the effectiveness of selection for a specific trait within that genotype. Therefore, the current study was conducted with an objective to evaluate Genetic assessment, variability and inheritance of various yield and related traits, aiming to identify desirable CMS-based wheat hybrids for future breeding endeavours.

Material and Methods

Experimental Material and layout

Present Experiment material consisted of 54 CMS Based Hybrids (CMS F_1) including 4 checks (MP 3382, MP 3465, HI 1544, GW 322) and it is conducted throughout the winter cropping season (*Rabi* season) spanning 2023 to 2024. The trial was conducted within the framework of the CRP on hybrid wheat technology, within the Department of Plant Breeding and Genetics at the Seed Breeding Farm, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, located in Jabalpur (M.P.) The 54 CMS based hybrid (CMS F_1) wheat were planted in a Randomized Complete Block Design with 3 replications. Each plot consists of two rows of 3.0 m long with a 20.0 cm row to row spacing. Under conditions of high fertility, the crop was cultivated with sufficient irrigation and in accordance with recommended agricultural practices, leading to the successful growth of a healthy crop plant. Five competitive plants were randomly taken from each replication and observations were recorded on 15 traits *viz*., days to 50% ear emergence, days to maturity, plant height, number of tillers per plant, peduncle length, awns length, spike length, number of spikelets per spike, sterility percentage, weight of per spike, number of grains per spike, harvest index, thousand grain weight, grain yield/plant and biological yield/plant. A study involving 15 quantitative traits in a randomized complete block design was carried out to ascertain the degree of variability across all the measured traits as well these traits were employed in the evaluation of genetic factors such as mean, range, genotypic and phenotypic coefficient of variability, broad sense heritability, and genetic advance as a percentage of the mean. The Genotypic Coefficients of Variation (GCV) and Phenotypic Coefficients of Variation (PCV) were calculated using the formula proposed by Burton (1952). Broad-sense heritability was determined based on the formula recommended by Hanson *et al*. (1956). Genetic advance was assessed following the approach outlined by Johnson *et al*. (1955).

Results and Discussion

Analysis of variance entails the identification of observable differences in individuals with regard to a particular attribute. The ANOVA indicated that mean sum of square due to CMS Based Hybrids and checks were highly significant for all traits under study *viz*.; tillers per plant, plant height, days to 50% flowering, spike length, spike weight, peduncle length, number of grains per plant, number of grains per spike, days to maturity, thousand grain weight, harvest index, biological yield per plant and grain yield per plant. Hence, the incorporation of these variable CMS-based wheat lines presents a significant opportunity for enhancing yield and its associated traits within breeding programs as well it suggests that a considerable degree of variability has been established and the genetic basis has been expanded for most of the important traits of hybrids produced through the hybridization of multiple parents. For all yield-related

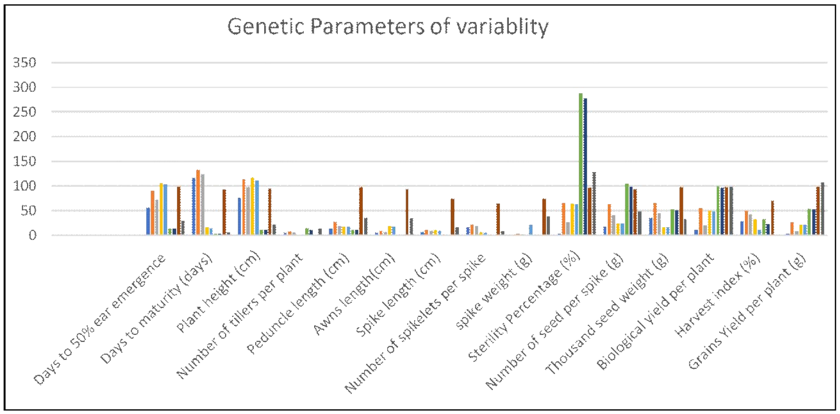

Fig. 1 : Graphical presentation of genetic parameters of variability of CMS based wheat hybrid for quantitative traits.

Table 1 : Analysis of variance for yield and yield attributing traits.

Source of variation	**d.f.**	**Mean sum of Squares**								
		DFF	**DM**	**PH**	**SL**	**NTPP**	**NSPS**	**AL**	**SW**	**PL**
Replication	2	15.26	11.7	92.88	1.24	1.45	0.47	1.28	0.127	8.74
CMS based Hybrids	53	312.98	45.57	338.12	2.41	1.30	3.144	4.20	0.760	34
Error	106	1.48	1.08	6.30	0.25	0.35	0.500	0.09	0.0810	0.28

Source of Variation	**d.f.**	**Mean sum of Squares**					
		SP	**NGPS**	**TSW**	**HI**	**BY**	**GYPP**
Replication	2	42.108	35.38	22.84	71.67	11.62	8.52
CMS based Hybrids	53	843.8	302.49	154.84	77.82	291.54	62.77
Error	106	9.97	6.19	1.24	9.69	2.65	0.40

DFF = Days to 50% ear emergence (days), DAM= days to maturity, PH = Plant height (cm), NTPP = Number of tillers per plant ,PL = Peduncle length (cm) , AL = Awns length (cm), SL = Spike length (cm), NSPS = Number of spirelets per spike, SP= sterility Percentage (%), SW = Weight of per spike (g), NGPS= Number of grain per spike, HI = Harvest index (%) , TGW =Thousand grain weight (g), GYPP = grain yield/plant (g) and BYPP = biological yield/plant (g).

Table 2 : List of Experimental material.

S. no.	**Hybrids**	**S. no.**	**Hybrids**
1.	91A x MP 3288	30.	97A x GW 366
2.	91A x GW 366	31.	97A x GW 190
3.	91A XGW 190	32.	97A x GW 451
4.	91A x GW 451	33.	97A x WH 730
5.	91A x WH 730	34.	97A x VL 3020
6.	91A x RAJ 3765	35.	97A x RAJ 3765
7.	91A x R 2003	36.	97A x R 902
8.	92A x MP 3288	37.	2041A x MP 3288
9.	92A x GW 190	38.	2041A x MP 3211
10.	92A x GW 322	39.	2041A x WH 730
11.	94A x MP 3288	40.	2041A x VL 3020
12.	94A x GW 366	41	2041A x R 10
13.	94A x GW 190	42.	2041A x R 2003
14.	94A x WH 730	43.	2851A x GW 322
15.	94A x VL 3020	44.	2851A x MP 3211
16.	94A x RAJ 3765	45.	2851A x GW 366
17.	95A x GW 366	46.	2851A x GW 190
18.	95A x GW 190	47.	2851A x WH 730
19.	95A x WH 730	48	2851A x VL 3020
20.	95A x VL 3020	49.	2851A x R 10
21.	95A x RAJ 3765	50	2851A x R 2003
22.	95A x R 9		**4 Checks**
23.	96A x MP 3288	1.	**MP 3382**
24.	96A x GW 366	2.	**MP 3465**
25.	96A x GW 190	3.	**HI 1544**
26.	96A x VL 3020	4.	**GW 322**
27.	96A x R 902		
28.	97A x GW 322		

Table 2 continued...

Table 2 continued...

features, similar results have been reported by Kalimullah *et al.* (2012), Choudhary *et al.* (2020), Elahi *et al.* (2020), and Ferede and Worede (2020). Table 3 provides the results for mean and range for all the traits that were examined. There were 72.38 days in the mean performance for days to 50% ear emergence. The minimum and highest ranges were 56 and 90 days, respectively. The mean performance for plant height was 97.37 cm and minimum range was 75.6 cm and maximum 113.9 cm. The trait number of tillers recorded lowest value of range 4.57; highest 7.80 with mean value 5.62 Peduncle length exhibited a mean performance 19.18 cm and ranged from 13.7 to 26.96 cm. The trait awns length recorded mean performance 6.67 cm with lowest value of range 4.63 cm to 9.43 cm there were 124 days in the mean performance for days to maturity, the minimum and highest values were 116 and 133 days. The genetic variability for spike length was as mean 9.19 cm, range minimum 6.82 cm and maximum 11.31 cm. The trait number of spikelets per spike exhibited minimum value 16.2 and maximum value 22.01 with a mean performance 18.62. The genetic variability for trait per spike weight was as mean 2.22 g, range minimum 1.22g to maximum 3.40 g. The trait number of sterility percentage varied from 4.06 to 65.27 with an average value of 26.28. For

Table 3 : Genetic parameters of variability for yield and yield attributing traits.

Characters	Range		Mean	Variance		Coefficient of Variation		h^2B (%)	Genetic advance as 5% of mean
	Min.	Max.		Phenotypic	Genotypic	PCV	GCV		
Days to 50% ear emergence	56	90	72.38	105.31	103.83	14.17	14.07	98.6	28.79
Days to maturity (days)	116	133	124	15.91	14.83	3.21	3.10	93.2	6.17
Plant height (cm)	75.6	113.9	97.37	116.91	110.60	11.10	10.80	94.6	21.64
Number of tillers per plant	4.57	7.80	5.620	0.673	0.314	14.59	9.973	0.467	14.04
Peduncle length (cm)	13.7	26.96	19.18	17.69	17.47	11.52	11.24	97.6	35.56
Awns length(cm)	4.63	9.43	6.67	18.11	17.54	1.46	1.37	93.8	34.99
Spike length (cm)	6.82	11.31	9.19	10.73	9.23	0.974	0.721	74	16.35
Number of spikelets per spike	16.2	22.01	18.62	6.31	5.04	1.382	0.882	63.8	8.29
Spike weight (g)	1.22	3.40	2.22	24..96	21.42	0.308	0.227	73.7	37.88
Sterility Percentage (%)	4.06	65.27	26.28	64.55	63.42	287.94	277.97	96.5	128.38
Number of grains perspike (g)	17.82	63.33	41.19	24.86	24.12	104.96	98.76	94.1	48.20
Thousand seed weight (g)	35.06	64.86	44.94	16.11	15.92	52.44	51.20	97.6	32.40
Biological yield per plant	10.89	55.04	20.24	49.12	48.46	98.95	96.29	97.3	98.43
Harvest index (%)	27.93	48.83	42.54	32.4	11.20	32.4	22.70	70.1	0.981
Grains yield perplant (g)	4.35	26.10	8.68	21.19	20.79	53.03	52.52	98.1	107.15

this trait number of grains per spike the range of variation was 17.82 to 63.33, mean performance was 41.19. The genetic variability for trait thousand grains weight was as mean 44.94 g range minimum 35.06 g and maximum 64.86 g. For the trait biological yield per plant the range of variation was 10.89 g to 55.04 g, mean was 20.24 g. The common mean value for harvest index was recorded 42.54% with lowest range 27.93% and highest range was 48.83%. The trait grain yield per plant showed mean value 8.68 g with range 4.35 g to 26.10 g.

The genotypic and phenotypic coefficient of variation for different traits in the present study is presented in the table. It was observed that the phenotypic coefficient of variation must be greater than the genotypic coefficient of variation overall. This trend was consistent across all characteristics investigated. All of the studied traits are categorized as low, medium, or high GCV and PCV. The examination of the coefficient of variation indicated that the highest estimates of GCV and PCV were observed in the case of sterility percentage (64.55% and 63.42%) followed by grain yield per plant (53.03 and 52.52), Biological yield per plant (49.12% and 48.46%) and weight of per spike (24.96% and 24.12%), Number of grains per spike (24.86% and 24.12%). A moderate estimate of GCV and PCV was found in awns length (18.11% and 17.54%), peduncle length (17.69% and 17.47%), thousand grain weight (16.11% and 15.92%), harvest index (13.38% and 11.20%), spike length (10.73% and 9.23%), plant height (11.10% and 10.80%), Number of spikelets per spike (6.31% and 5.04%), and Number of tillers per plant (14.59% and 9.97%). Conversely, traits such as days to 50% ear emergence (14.17% and 14.07%) and days to maturity (3.21% and 3.10%) displayed low GCV and PCV. The heritability percentage indicates the amount of genetic variability that is transmitted from parents to offspring. In this particular case, a high heritability estimate was recorded for days to 50% ear emergence (98.6%), grain yield per plant (98.1%), thousand grain weight (97.6%), biological yield per plant (97.3%), sterility percentage (96.5%), plant height (94.6%), Number of seed per spike (94.1%), awns length (93.8%), days to maturity (93.2%). Moderate heritability was observed for spike length (74%), weight of per spike (73.7%), harvest index (70.1%). On the other hand, low heritability was noted for the Number of spikelets per spike (63.8%) and Number of tillers per plant (46.7%). Singh *et al.* (2014) obtained similar results for grain yield per plant, thousand grain weight and harvest index; Rajpoot *et al*. (2015), Phougat *et al*. (2017), Pooja *et al*. (2018), Kumar *et al*. (2019), Mishra *et al*. (2019), Elahi *et al*. (2020), Thapa *et al.* (2019), Kumari *et al*. (2020) and Yasin *et al*. (2020).

Genetic advance as percentage of mean estimate high for the sterility percentage (128.38%) followed by grain yield per plant (107.15%) and biological yield per plant (98.48%) exhibited a substantial genetic advance of 5% of the average. Following closely was the number of grains per spike (48.20%), peduncle length (35.56%), spike weight (37.88%), awns length (34.99%), thousand grain weight (32.40%), days of 50% ear emergence (28.79%), and plant height (21.64%). Conversely, harvest index (19.31%), spike length (16.35%), Number of tillers per plant (14.04%) demonstrate a moderate genetic advance, while the Number of spikelets per spike (8.29%) and days to maturity (6.17%) show lower genetic advance. Similar results recorded by Mishra and Shukla (2013).

Conclusion

The CMS Based Hybrids in the present study displayed notable genetic variability for the traits under investigation, suggesting the existence of valuable levels of variability in these hybrids.

- The examination of genotypic and phenotypic coefficient of variation indicated that the PCV values for most traits exceeded the GCV values. There was only a slight disparity between the GCV and PCV values, suggesting minimal impact of environmental factors on the expression of the traits.
- Traits such as sterility percentage, number of grains per spike, grain yield per plant, biological yield per plant, harvest index, and weight per spike exhibited substantial estimates for both GCV and PCV.
- Traits like grain yield per plant, plant height, spike length, thousand grains weight, biological yield per plant and harvest index, plantexhibited high heritability along with significant genetic advance.
- This indicates that these characteristics are predominantly influenced by additive gene action. The desirable and stable hybrids identified in the current study have the potential to be utilized for the advancement of hybrid development in wheat.

A high heritability accompanied by a high genetic advance is the optimal situation for choosing traits in selection. Therefore, measuring genetic progress is also a valuable factor in the process of selection. The degree of heritability, variation in physical characteristics, and genetic progress have been employed to estimate the level of diversity in hybrid wheat types. Thus, the main goal of this research is to evaluate the genetic diversity, inheritability, genetic progress, and relationship of yield-related characteristics in newly created CMS (Cytoplasmic Male Sterility) based wheat hybrids.

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