

Multivariate analysis for morphological traits in newly developed Cytoplasmic lines of wheat

Vinod Kumar Goyal, Suneeta Pandey, R.S. Shukla and Archana Rani

Department of Plant Breeding & Genetics

JNKVV, Jabalpur

Email: shukla.rs90@gmail.com

ABSTRACT

Wheat is the major cereal crop in India on which the food security rests. Determination of the best selection criteria is the most important aim in wheat breeding programs. To achieve high yield potential in wheat, hybrid breeding is a major innovative technique. A total of 17 newly developed CMS lines and seven restorer lines, were used as a experimental material with the objective to identify diverse lines and classify morphological and morpho-physiological traits of wheat genotypes. Principal component analysis indicated that five important components accounted for about 84.53 percent of the total variation among traits. The first component had the contribution from the traits days to 50% heading, days to maturity, plant height and relative water content which accounted 23.44% percent to the total variability. Canopy temperature has contributed 21.35% to the total variability in second principal component. Peduncle length has contributed 15.44% to the total variability in third principal component. The remaining variability of 12.57% and 11.72% was consolidated in fourth and fifth principal component by various traits like chlorophyll content (%) and numbers of tillers/plant. The cumulative variance of 84.53% of total variation among eight traits was explained by the first five axes. Thus the results of principal component analysis revealed, wide genetic variability exists in the CMS lines.

Keywords: Principal component analysis, wheat, CMS lines and morpho-physiological traits

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INTRODUCTION

Wheat (*Triticum aestivum* L.) is the world's second most important staple food crop for more than 35 percent of world's population next to the rice. It produces about 20% food resources of the world with high productivity and occupying a prominent position. India is the second largest wheat producer in the world with a production level of 93.50 million tonnes [4]. Madhya Pradesh is the second largest producer state of wheat with area, production and productivity are 5.94 million hectare, 17.78 million tonnes and 2.9 tonnes respectively [2]. Madhya Pradesh wheat is known for its quality and sale at high premium rate in the market. Looking to the target for wheat production at National Level it is very difficult to meet out the demand of 109 mt by 2020 AD. The innovative approach is one of the alternatives to fulfill the demand. In this direction an effort was made using development of hybrid wheat genotypes using cytoplasmic male sterile lines.

In India, hybrid wheat development programme was initiated under the All India Coordinated Wheat & Barley Improvement Project (AICW&BIP) of the ICAR in 1995 in network mode. Besides three-line breeding approach using CMS system, two-line approach using chemical hybridizing agent (CHA) was also explored. Experimental hybrids through CMS as well as CHA systems were developed, but their commercial exploitation had many bottlenecks. Indeed, first hybrid wheat varieties based on chemical hybridization agent

systems have recently been released in Europe, but high seed production costs are still a crucial limiting factor [7]. A major problem in hybrid seed production of wheat is its low cross-pollination ability. There are several problems in hybrid wheat development and among them, lack of genetic diversity among parents for harnessing heterosis, out-crossing/natural crossing potential, complete fertility restoration and efficient and cost effective hybrid seed production technology are notable. To achieve hybrid vigour, it is necessary to identify, suitable hybrids following cytoplasmic male sterile line approach. Present study was conducted to decipher the extent of genetic variation and relationships among recently developed CMS lines of wheat based on quantitative traits using multivariate analysis and to identify the set of morpho-physiological attributes which could be further utilized in hybrid breeding programs.

MATERIAL AND METHODS

Plant material for the study comprised of newly developed 17 CMS lines and 7 restorer lines, received from IIWBR, Karnal and Division of Genetics, IARI under CRP on hybrid wheat programme. The experiment was planted at Seed Breeding Farm, AICRP on Wheat, Department of Plant Breeding and Genetics, College of Agriculture, J.N.K.V.V., Jabalpur (M.P.) during Rabi season 2017-18. Soil of the experiment is medium black with uniform topography and free from water logged conditions. The region has sub tropical, semi arid climate with about 1200 mm average rainfall. The data recorded were days to 50% heading, days to maturity, plant height (cm), peduncle length (cm), number of tillers/plant, relative water content (%), canopy temperature (%) and chlorophyll content (%). Observations were recorded on randomly selected five competitive plants from each line.

Principal component analysis (PCA) is a standard tool in modern data analysis because it is a simple, non-parametric method for extracting relevant information from confusing data sets. It was calculated using Ingebriston and Lyon (1985) method.

RESULT AND DISCUSSION

Principal component analysis simplifies the complex data by transforming the number of correlated variables into a smaller number of variables called principal components. In present research programme, PCA was performed for quantitative and physiological traits in recently developed CMS lines.

The first principal component accounts for maximum variability in the data with respect to succeeding components [6]. The analysis had grouped the estimated wheat variables into five main components. The first five components with eigen values >0.5 accounted for 84.53% of the total variation of morpho-physiological traits. PC1 accounted for about 23.44% of the variation in morphological traits; PC2 for 21.35%; PC3 for 15.44%; PC4 for 12.56% and PC5 for 11.72% (Table 1).

Out of eight, only six principal components (PCs) exhibited more than 0.5 eigen value, and showed about 91.83% total variability among the traits studied. But, only five PCs were given due importance for further explanation (Table 1). Screen plot explained the percentage of variance associated with each principal component obtained by drawing a graph between eigen values and principal component numbers. PC1 showed 23.44% variability with eigen value 1.87 which then declined gradually. Semi curve line is obtained which after fifth PC tended to straight with little variance observed in each PC. From the graph, it is clear that the maximum variation was observed in PC1 in comparison to other four PCs, which is selected for explain here. So, selection of lines from this PC will be useful (Figure 1 and 2).

Rotated component matrix revealed that each principal component separately loaded with various quantitative and physiological traits under study. The PC1 was more related to the phenological and yield attributing traits viz., days to 50% heading, days to maturity, plant height and relative water content. Thus, PC1 allowed for simultaneous selection of phenological and physiological traits. PC2 exhibited positive effect for canopy temperature. The third principal component was more dominated by Peduncle length whereas, PC4 was more related to chlorophyll content (%). The fifth PC was more related to number of tillers/plant (Table 2 and 3). Similar results were obtained by Leilah and Al-khateeb [6], Sourour *et al.* [9] and Meena *et al.* [8] for plant height; Bhanupriya *et al.* [3] for plant height and days to 50% heading and Ali *et al.* [1] for days to 50% heading.

Principal Component 1 includes RES-10 which had the highest PC score 2.90 value, followed by CMS-96-A (2.02), CMS-92-A (1.38), CMS-83-A (1.29), RES-7 (1.05) and CMS-2046-A (0.82). It indicated that they had high value for phenological traits such as days to 50% heading, days to maturity, plant height and relative water content (Table 4). Principal Component 2 includes the genotypes which had high PC score for CMS-2046-A (2.14), CMS-84-A (2.02), CMS-91-A (1.76), CMS-94-A (1.22), CMS-89-A (1.06) and CMS-2041-A (1.04). It showed that they had high value for canopy temperature.

Table 1: Eigen values, % variance and cumulative eigen values of wheat genotype

Traits	Principal component (PC)	Eigen value	% Variance	Cumulative %
Days to 50% heading	PC1	1.875	23.443	23.443
Days to maturity	PC2	1.708	21.352	44.795
Plant height	PC3	1.235	15.444	60.238
Number of tillers/plant	PC4	1.005	12.568	72.806
Peduncle length	PC5	0.938	11.727	84.533
Chlorophyll content	PC6	0.584	7.306	91.839
Canopy temperature	PC7	0.415	5.190	97.029
Relative water content	PC8	0.238	2.971	100.000

Table 2: Rotation component matrix for eight variables of wheat

Traits	Principal Components				
	PC1	PC2	PC3	PC4	PC5
Days to 50% heading	0.642	-0.621	0.242	0.103	-0.037
Days to maturity	0.570	0.517	-0.079	-0.119	0.220
Plant height	0.685	-0.529	-0.185	-0.144	-0.284
number of tillers/plant	0.101	-0.505	-0.379	-0.246	0.673
Peduncle length	0.151	-0.053	0.734	0.460	0.438
Chlorophyll content	0.093	0.153	-0.661	0.639	0.206
Canopy temperature	0.389	0.558	0.119	-0.462	0.257
Relative water content	0.690	0.426	-0.059	0.256	-0.232

Extraction method: Principal component analysis

Bold value represents more related traits in each principal component

Table 3: Interpretation of rotated component matrix for the traits having values >0.5 in each PCs.

	PC1	PC2	PC3	PC4	PC5
	Days to 50% heading	Canopy temperature	Peduncle length	Chlorophyll content (%)	Number of tillers/plant
	Days to maturity	-	-	-	
	Plant height	-	-	-	
Traits	Relative water content (%)	-	-	-	

Table 4: PC scores of wheat genotype having positive values >0.5 in each PCs.

S. No.	Genotypes	PC1 score	PC2 score	PC3 score	PC4 score	PC5 score
1	CMS-82-A	-0.392	0.856	-1.021	0.103	0.105
2	CMS-83-A	1.298	0.284	-0.217	2.326	1.407
3	CMS-84-A	0.596	2.022	-0.673	1.388	0.608
4	CMS-85-A	-0.413	-0.621	0.393	-1.257	-0.115
5	CMS-86-A	0.739	-0.069	2.520	-2.025	0.128
6	CMS-87-A	0.577	-0.242	1.182	0.581	0.327
7	CMS-88-A	-0.044	0.532	-0.334	1.479	-0.469
8	CMS-89-A	-1.619	1.063	-0.623	-0.952	0.897
9	CMS-90-A	-0.553	0.017	-1.720	-1.039	0.402
10	CMS-91-A	0.128	1.760	-1.256	-1.327	-0.731
11	CMS-92-A	1.382	-0.104	-0.434	0.090	0.202
12	CMS-94-A	-0.167	1.220	-0.631	-0.087	0.116
13	CMS-95-A	0.271	-1.127	0.813	-0.296	1.345
14	CMS-96-A	2.024	-0.334	-0.292	0.454	0.423
15	CMS-97-A	-1.512	1.006	0.493	0.325	0.088

S. No.	Genotypes	PC1 score	PC2 score	PC3 score	PC4 score	PC5 score
16	CMS-2041-A	0.197	1.042	-0.658	-1.658	0.780
17	CMS-2046-A	0.827	2.144	0.688	0.129	-2.553
18	RES-7	1.058	-2.407	-0.943	-0.350	-1.052
19	RES-9	0.724	-2.965	-1.756	0.257	-1.865
20	RES-10	2.903	-0.956	1.389	-0.279	1.029
21	RES-37	-0.721	0.737	2.270	0.783	-1.801
22	RES-38	-1.502	-1.414	-0.457	0.136	0.146
23	RES-936	-2.789	-1.740	1.190	0.553	0.145
24	RES-939	-3.014	-0.703	0.079	0.666	0.438

Table 5: Selection of genotypes on the basis of PC score in decreasing order in each component

PC1	PC2	PC3	PC4	PC5
RES-10	CMS-82-A	CMS-86-A	CMS-83-A	CMS-83-A
CMS-96-A	CMS-2046-A	RES-37	CMS-88-A	CMS-95-A
CMS-92-A	CMS-84-A	RES-10	CMS-84-A	RES-10
CMS-83-A	CMS-91-A	RES-936	RES-37	CMS-89-A
RES-7	CMS-94-A	CMS-87-A	RES-939	CMS-2041-A
CMS-2046-A	CMS-89-A	CMS-95-A	CMS-87-A	CMS-84-A

Figure 1: Screen plot of principal component analysis of wheat genotype between eigen value and principal component

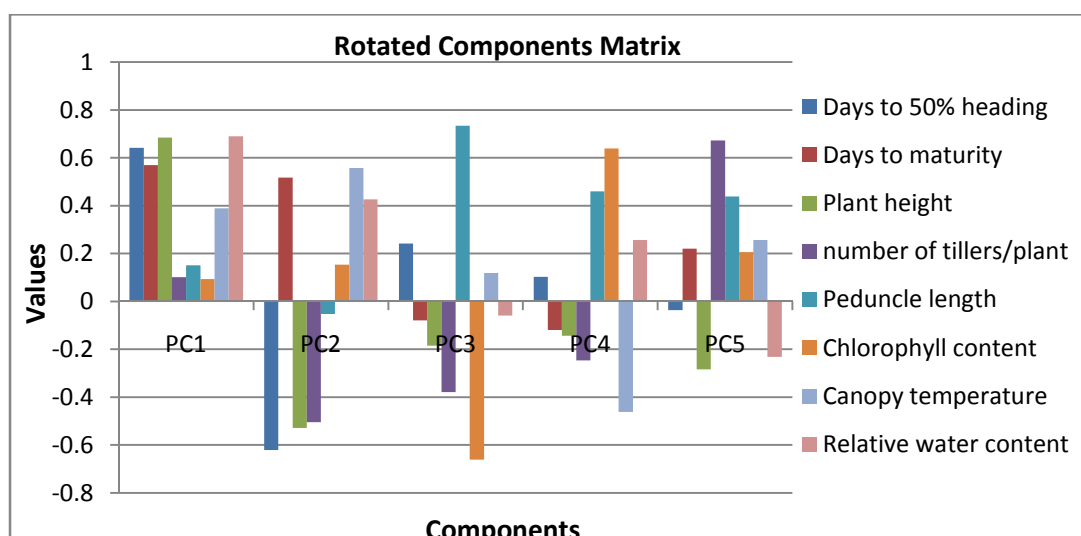
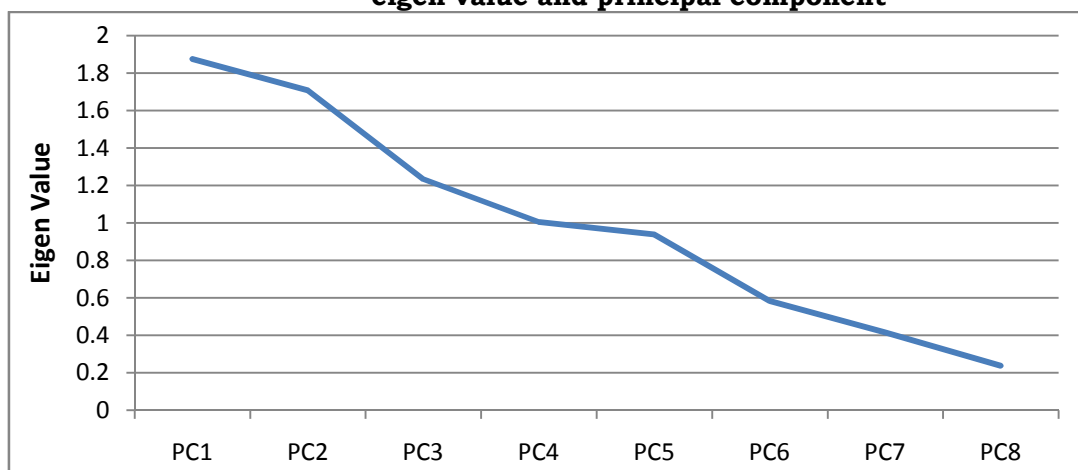


Figure 2: Rotated Component Matrix

Principal Component 3 includes CMS-86-A (2.52), followed by RES-37 (2.27), RES-10 (1.38), RES-936 (1.19), CMS-87-A (1.18) and CMS-95-A (0.81) which exhibited high value

for phenological traits viz., peduncle length. Principal Component 4 includes CMS-83-A, which recorded the highest PC score (2.32), followed by CMS-88-A (1.47), CMS-84-A (1.38), RES-37 (0.78), RES-939 (0.66) and CMS-87-A (0.58) indicated that they had highest value for chlorophyll content. Principal Component 5 includes CMS-83-A (1.40) which exhibited the highest PC score, followed by CMS-95-A (1.34), RES-10 (1.02), CMS-89-A (0.89), CMS-2041-A (0.78) and CMS-84-A (0.60) indicated that they had highest value for number of tillers/plant.

RES-10 was found in PC1, PC3 and PC5 and had maximum PC score, where as CMS-83-A was present in PC1, PC4, PC5 and had the highest traits for phenological and yield. On the basis of top 5 PC scores in each principal component, genotypes are selected and presented as summarized form in table 5.

PC scores were calculated for all the advanced lines in 5 principal components and utilized in finding advanced lines, superior for different combination of phenotypic traits. A high value of PC score of a particular advanced line in a particular PC denotes high value for those variables, in that advanced line which the component is representing. Thus, these score can be utilized to propose precise selection indices, whose intensity can be decided by variability explained by each of the PC.

It can be concluded that PC analysis highlights the characters with maximum variability. So, intensive selection procedures can be designed to bring about rapid improvement of yield attributing traits. PCA also help in ranking of genotypes on the basis of PC scores in corresponding component. From the above discussion, it is clear that in the advanced lines RES-10 hold the first position, followed by CMS-86-A, CMS-83-A and RES-37 on the basis of PC score in all principal components. When we considered the entire PC with PC scores and character basis then RES-10 ranks first because it is present in PC 1, PC 3 and PC 5 also. CMS-83-A, CMS-2046-A, CMS-84-A, CMS-89-A, RES-37, CMS-87-A and CMS-95-A also found in more than one PCs (component having maximum characters). Therefore, these lines should be given due importance in hybrid breeding programme.

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