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Research article

Genetic diversity and structure analysis of white maize populations

Abhijit Kumar Das[1*], Shubhank Dixit[1], Deepak Bhamare[1], Ramesh Kumar[1], Yathish K. R.[2], Shyambir Singh[1], Bhupender Kumar[3], Suby S. B.[3], Zahoor Ahmed Dar[5], Arushi Arora[6], Santosh Kumar[7] and Sujay Rakshit[4]

[1]ICAR-Indian Institute of Maize Research, Ludhiana-141004, India
[2]ICAR-Indian Institute of Maize Research, Winter Nursery Centre, Hyderabad-500030, India
[3]ICAR-Indian Institute of Maize Research, Delhi Unit, New Delhi-110012, India
[4]ICAR-Indian Institute of Agricultural Biotechnology, Ranchi-834010, India
[5]Dryland Agriculture Research Station, SKUAST-K, Srinagar-191132, India
[6]Punjab Agricultural University, Ludhiana-141004, India
[7]ICAR-Indian Agricultural Research Institute, Gauriakarma-825405, India
[*]Corresponding author email: das.myself@gmail.com

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Abstract

Globally though yellow maize is more popular, white maize has its own niche in specific parts around the world including Central America, southern United States, northern part of South America, Mexico, Africa and some parts of Asia. However, efforts on white maize improvement are very scarce, particularly in India. The aim of the study was to characterize white maize populations for yield traits and to establish heterotic patterns using molecular markers. Twenty seven white maize populations comprising of 16 from CIMMYT, Mexico, 6 from Srinagar and 5 from NBPGR were characterized for yield traits, *viz*., NRPE (number of rows per ear), NKPR (number of kernel per row) and HSWT (hundred seed weight), and also characterized using SSR markers. Six populations were identified for higher NRPE; four populations for higher NKPR and five populations with high HSWT. Structure analysis identified three major populations, *viz*., P1, P2 and P3 consisting five, eleven and ten pure sub-populations, respectively. Principal Coordinate Analysis (PCoA) revealed that all the populations were distributed across the four quadrangles of the scatter plot. Efforts on heterotic grouping identified six populations for NRPE in HG-I (Heterotic Group-I), and three populations in HG-II (Heterotic Group-II). Further, all Indian populations were grouped in cluster A whereas CIMMYT populations are distributed in two different clusters (B and C). The populations were identified for different yield traits belonging to different heterotic groups. The inbred lines derived from these identified populations will have higher yield and will produce superior hybrids upon crossing inbreds from opposite heterotic groups.

Keywords: Genetic diversity, Molecular markers, Structure analysis, White maize, Yield

Introduction

Maize is the third most important cereal after wheat and rice in India and is mainly used as poultry and animal feed. Though yellow maize is globally more popular, white maize is important in many parts including Central America, southern United States, northern part of South America, Africa and some parts of Asia (Sendin *et al*., 2018). México ranks fifth in maize production in the world (FAOSTAT, 2020), and white maize represents about 90% of it (Ramírez-Vega *et al*., 2022). Further, the demand and popularity of white maize is gaining worldwide due to increase in consumer preferences of white maize and Hispanic and Latino populations (Uriarte-Aceves and Sopade, 2021). In India, though yellow maize is more popular, white maize is consumed as food in few parts of the country (Gujarat, Rajasthan, Chhattisgarh, Himachal Pradesh, and Jammu & Kashmir) particularly as *'chapatti'* or flat bread. There are very few reports on improvement and characterization of white maize germplasm.

Understanding the genetic variation in the available germplasm is an important component of crop breeding programmes (Das *et al*., 2021; Venadan *et al*., 2023; Yathish *et al*., 2024; Hundal *et al*., 2024). The diversity and relatedness among the inbred lines derived from various sources is crucial for breeding strategies to maximize the yield potential (Singh *et al*., 2023). The information about the

relationship among the base materials is also critical for developing new superior inbred lines, and to choose the right testers for hybrid development. The development of heterotic hybrids in maize involves deriving homozygous inbred lines and their classification into heterotic groups (HGs) and thereafter crossing them from opposite HGs. Similarly, the source populations can also be classified into different HGs, so that the homozygous inbred lines developed from these populations maintain the heterotic pattern as of their original populations. HGs can be defined as a germplasm collection, upon crossing with the germplasm of an external group, tends to exhibit a higher degree of heterosis compared to crosses of the same group. The genetic diversity among the heterotic groups is maintained and germplasm is improved within the heterotic group through recycling the superior inbred lines and recombining them within a population through reciprocal recurrent selection (Mikel, 2008). Inbred lines developed through this strategy from different populations generally give rise to productive hybrids upon crossing.

The heterotic groups are well established in temperate maize germplasm, such as the three predominant heterotic groups are, *viz*., Stiff Stalk (SS), Non-Stiff Stalk (NS), and Iodent (IO) in the USA (Beckett *et al*., 2017). However, HGs of tropical maize germplasm including Indian maize germplasm, that too of white maize germplasm, is not well defined. The development of productive inbred lines in hybrid breeding is equally important to reduce the cost of hybrid seed production. The best-performing elite inbred lines are frequently used as parents in a hybrid breeding program, however, for complex traits like yield, the line *per se* performance has been reported as a poor predictor of hybrid performance. Hence, simply inherited traits less affected by non-additive effects can be used. In this context, yield-contributing traits like number of rows per ear (NRPE), number of kernels per row (NKPR) and hundred Seed Weight (HSWT) are reported to have high heritability (Xiao *et al*., 2016). These are also positively correlated with grain yield in maize and can be indirectly selected to derive superior inbred lines for hybrid development (Magar *et al*., 2021). The present experiment was designed to establish the heterotic pattern in the exotic maize germplasm received from CIMMYT, Mexico along with the locally available Indian maize populations; and to characterize these populations in terms of yield contributing traits and molecular diversity to identify superior inbred lines for the future hybrid breeding programme.

Materials and Methods

Germplasm collection: Total 27 white maize populations comprising 16 collected from CIMMYT, Mexico, six from Srinagar and five from ICAR-NBPGR, New Delhi were utilized in the study.

Experimentation and phenotypic evaluation: The experiment was conducted during the spring season of 2019 at Ladhowal farm of ICAR-IIMR (30°97 N′, 75°75′ E), Ludhiana. The weather parameters during the crop season were recorded (Fig 1). The populations were evaluated in randomized complete block design (RCBD) with two replications. Each of the populations were grown over 16 rows, the row length was maintained at 3 m with row-to-row distance of 65 cm and plant to plant of 20 cm. Standard agronomic package of practice was used to raise the healthy crop. Individual plants of each of the populations were characterized for yield contributing traits, *viz*., number of rows per ear (NRPE), number of kernels per row (NKPR) and hundred seed weight (HSWT).

Molecular characterization: Genomic DNA was isolated using standard CTAB protocol with minor modification (Murray and Thompson, 1980). The 120 random simple sequence repeat (SSR) markers distributed uniformly throughout the maize genome were selected from maize GDB (www.maizegdb.org) for genetic characterization of populations. Total volume of the PCR reaction mixture was 11 microliter (µl) which consisted of (i) 2.5 µl genomic DNA (20 ng/µl), (ii) 4 µl master mix, (iii) 1.5 µl molecular grade water and (iv) 3 µl primer pairs. PCR products were amplified by following the protocol of Das *et al.* (2019). The amplified products were resolved by using 4% SFR (Super Fine Resolution) agarose at 120 V for 4 hours. Out of 120 SSR markers used, 61 markers were found to be polymorphic among the populations.

Statistical analysis: Analysis of variance (ANOVA) and Duncan's Multiple Range Test (DMRT) test for yield contributing traits was carried out using the SPSS software (SPSS Inc. Released 2007). The data matrix of SSR markers was used for genetic diversity and population structure analysis. Total number of alleles, gene diversity, major allele frequency, heterozygosity and polymorphic information content (PIC) values were calculated using PowerMarker V.3.0 (Liu and Muse, 2005). Principal

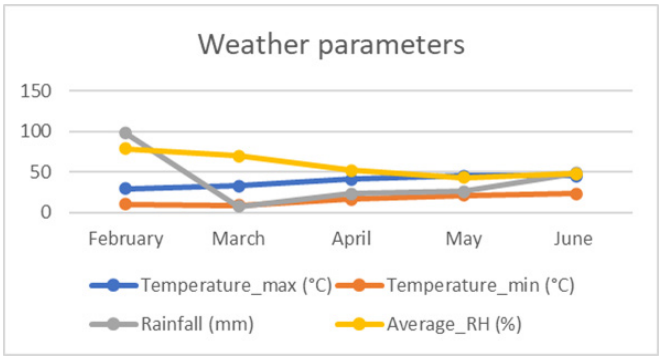

Fig 1. The weather parameters during the crop season at Ludhiana

coordinate analysis (PCoA) and Neighbour-Joining tree with 1000 bootstraps was generated using DARwin-5.0 (Perrier and Flori, 2003). The overall population structure of these populations was determined by Structure v.2.3.4 software (Pritchard *et al*., 2000). The project was run with 5000 burning periods run length followed by 50,000 Markov Chain Monte Carlo (MCMC) replications, admixture ancestry model and correlated allele frequency. The hypothetical number of subgroups (K) was set from 1 to 10 with three runs for each K.

Results and Discussion

Variability for yield contributing traits: Analysis of variance (ANOVA) revealed significant variation for yield contributing traits among the populations (Table 1). Mean NRPE among the 27 populations ranged from 11.39 to 15.33. Similarly, large variation for NKPR (22.99 - 34.64) and HSWT (25.46-35.13 gm) was also observed in these populations. Most promising populations for NRPE were POBLAC 64 (15.33), POBLAC 23 (14.90), POBLAC 29 (14.75), SMP 50 (14.72), POBLAC 22 (14.72), POBLAC 42 (14.68) and POBLAC 92 (14.52l) (Table 2). The populations, *viz*., POBLAC 22 (34.64), POBLAC 29 (33.48), NBPGR 23 (34.44) and POBLAC 44 (34.17) recorded highest NKPR, whereas the most promising populations for HSWT were POBLAC 44 (35.13 gm), POBLAC 102 (33.63 gm), POBLAC 47 (33.41 gm), POBLAC 92 (32.87 gm), KDM3008 (32.70 gm) and KDM 111 (32.70 gm). POBLAC 29 and POBLAC 22 recorded higher NRPE as well as NKPR, similarly, POBLAC 44 recorded higher NKPR and HSWT, whereas POBLAC 92 recorded higher NRPE and HSWT.

The box plot analysis revealed that though seven populations had higher NRPE values, six of them, *viz*., POBLAC 64, POBLAC 23, POBLAC 29, SMP 50, POBLAC 22 and POBLAC 42 recorded higher median values as well (Fig 2). All four populations (POBLAC 22, POBLAC 29, NBPGR 23, POBLAC 44) recorded a high median value for NKPR whereas five (POBLAC 44, POBLAC 102, POBLAC 47, POBLAC 92, KDM3008) of the six populations recorded a high median value for HSWT. Chen *et al*. (2016) reported similar variation for NRPE (12.3-17.0, mean 14.56) whereas much lower variation for HSWT (19.55-29.95 g, mean: 23.46 g) and higher range for NKPR (28.79-51.8, mean 41.7) was reported. Zeng *et al*. (2022) reported much higher variation for HSWT (9.75 to 40.04 g with mean 25.18 g) as well as for NKPR (5.33 to 53.50 with mean 26.46) in the association panel of 291 inbred lines. Similarly, higher range for NRPE were reported by Liu *et al.* (2016a) in the RIL (241) population (4 to 18) and Liu *et al.* (2015) (9.3 to 19.7 with an average of 13.3 ± 1.6) in the diverse inbred panel (368).

The main job of maize breeders is to derive high yielding inbred lines (Liu *et al*., 2016b). The yield components of maize can be summarized by the following equation: Y=PN×E/P×KRN×KPR×KW; where Y is grain yield (g m^{-2}), PN: plant number (m^{-2}), E/P: ears per individual plant, KRN:kernel row number, KPR: kernel per row, KW; mean weight per kernel (g) (Engledow and Wadham, 1923). Further, grain yield in maize is dependent on the relationship between the source produce and the potential of the sink to assimilate this produce. The sink in the maize foundation lines should be of high-effect and high-capacity (Liu *et al*., 2016b). From the equation it is evident that breeders could pay more attention to ear characters of maize as the sink capacity selection index. Hence, the 27 maize populations characterized for yield contributing traits in the current study provide a good opportunity to derive foundation inbred lines.

Correlation among yield contributing traits: As the populations, POBLAC 29, POBLAC 22, POBLAC 44 and POBLAC 92 recorded higher values for more than one yield trait; correlation coefficient values for these traits were estimated particularly for these populations (Fig 3). A significant negative, though small, correlation was present between NRPE and NKPR in POBLC 29 (r=-0.15;

Table 1. Analysis of variance for yield traits

SOV	DF	SS	MS	F	Significance
Population (NRPE)	26	61.87	2.3796	49.2949	<0.001
Replication	1	0.0294	0.0294	0.609	0.4422
Residual	26	1.2551	0.0483	-	-
Population (NKPR)	26	408.4698	15.7104	19.3735	<0.001
Replication	1	13.0439	13.0439	16.0853	<0.001
Residual	26	21.084	0.8109	-	-
Population (HSWT)	26	290.1192	11.1584	3.7009	<0.001
Replication	1	47.9403	47.9403	15.9001	<0.001
Residual	26	78.3925	3.0151	-	-

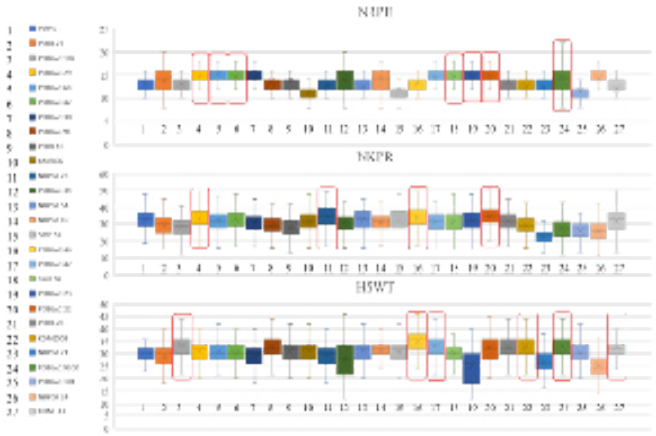

Fig 2. Boxplot analysis of 27 white maize populations

Table 2. Population mean for yield contributing traits of the populations

S. N.	Population	N	Pedigree	Source	NRPE	NKPR	HSWT
1	POP 5	204	Gurez, Tangdar Local	Srinagar	13.27^{fg}	32.45^{ijkl}	29.50^{cde}
2	POOL 27	232	Subtropical temperate early white flint	CIMMYT	13.88^{hij}	29.69^{ef}	28.81 ^{cd}
3	POBLAC 102	242	Precoz Blanco (tropical early white flint/dent)	CIMMYT	13.23^{fg}	28.66^{de}	33.63 ^{m}
4	POBLAC 29	271	Tuxpeño Caribe	CIMMYT	14.75^{mn}	33.48^{lmno}	31.56 ^{hi}
5	POBLAC 64	236	Templado Blanco Dentado QPM	CIMMYT	15.33^{o}	32.22^{hijkl}	30.52^{fg}
6	POBLAC 42	225	ETO Illinois	CIMMYT	14.68^{mn}	32.96^{jklm}	30.43^{efg}
7	POBLAC 30	265	Blanco Cristallino-2	CIMMYT	14.37^{klm}	31.01^{gh}	29.63 ^{def}
8	POBLAC 91	249	Templado Blanco Cristalino	CIMMYT	13.78^{hi}	29.27 ^{def}	32.03^{hijk}
9	POOL 16	287	Tropical early white dent (TEWD)	CIMMYT	13.90^{hij}	28.06 ^{cd}	31.45 ^{h}
10	KDM 3006	187	CML 540 x CML 442-B-B-B-B	Srinagar	11.39^{a}	31.36^{ghi}	31.32^{gh}
11	NBPGR 23	191	IC-0334948	NBPGR	12.97^{ef}	34.44 ^{no}	29.35 ^{cd}
12	POBLAC 34	261	Blanco Subtropical	CIMMYT	14.01^{ijk}	30.46^{fg}	28.56^{c}
13	NBPGR 54	166	IC-0334955	NBPGR	12.55^{d}	32.81^{jkl}	31.54 ^{hi}
14	NBPGR 10	212	IC-0334936	NBPGR	14.26^{jkl}	31.37^{ghi}	31.81^{hij}
15	SMP 54	206	KML225 x NAI 174-B-B-B	Srinagar	11.78^{b}	33.31^{klmn}	30.45^{efg}
16	POBLAC 44	251	(AED) Tuxpeño	CIMMYT	13.56^{gh}	34.17^{mno}	35.13^{n}
17	POBLAC 47	242	Templado Blanco Dentado QPM	CIMMYT	14.34^{klm}	31.62^{ghij}	33.41^{lm}
18	SMP 50	162	CML 440 x CML-349-B-B-B-B	Srinagar	14.72^{mn}	31.27^{ghi}	30.31^{ef}
19	POBLAC 23	207	Blanco Cristallino-1	CIMMYT	14.90^{n}	31.97^{hijk}	25.18^{a}
20	POBLAC 22	215	Mezcla Tropical	CIMMYT	14.72^{mn}	34.64^{o}	32.57^{jkl}
21	POOL 28	139	Subtropical Temperate Early While Dent	CIMMYT	13.53^{gh}	31.70^{ghij}	32.45^{ijkl}
22	KDM3008	187	CML-545 x CMl-540-B-B	Srinagar	12.62^{de}	29.27 ^{def}	32.70^{jklm}
23	NBPGR 21	222	IC-0334973	NBPGR	12.48^{cd}	22.99^{a}	26.98^{b}
24	POBLAC 92C0	271	Blanco Dentado	CIMMYT	14.52^{lmn}	27.13^{bc}	32.87^{klm}
25	POBLAC 101	176	Super Precoz Blanco (tropical extra-early white)	CIMMYT	11.63^{ab}	26.32 ^{b}	30.45^{efg}
26	NBPGR 24	136	IC-0334974	NBPGR	14.15^{ijkl}	26.27^{b}	25.46 ^{a}
27	KDM 111	192	GM-6 x Mahi Dhawal	Srinagar	12.15^{c}	31.90^{hij}	32.70^{jklm}

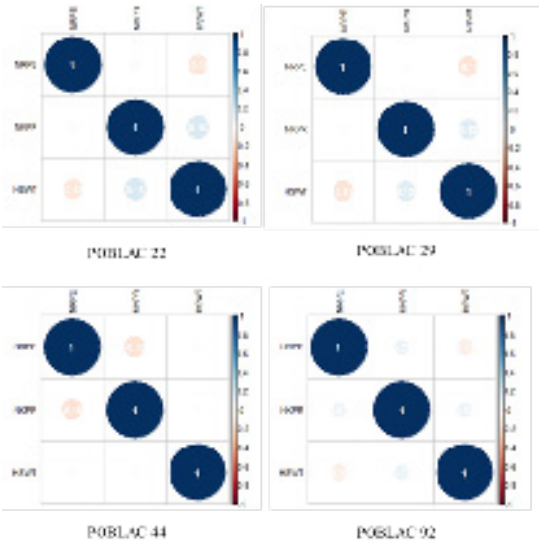

Fig 3. Correlation among yield contributing traits in selected populations

p = 0.01) but the correlation coefficient between NRPE and NKPR was insignificant in the population POBLAC 22 (r=-0.03; *P=0.68*). A significant positive correlation between NKPR and HSWT was present in POBLAC 44 (0.12; *P=0.05*). The correlation coefficient between NRPE and HSWT was negative but insignificant (r=-0.08; *P=0.15*) in the population POBLAC 44. Huo *et al.* (2016) failed to find any significant association between NRPE and NKPR in the two bi-parental populations. Similarly, Magar *et al*. (2021) also did not find any significant association between NRPE, NKPR and HSWT in ten open pollinated varieties (OPVs). Presence of positive correlation helps the simultaneous improvement of both the traits, whereas negative correlation prevents the simultaneous improvement. As the correlation between NRPE and NKPR was insignificant in POBLAC 22 and positive between NKPR and HSWT in POBLAC 44, these populations provide an opportunity for simultaneous improvement for both the traits and derive inbred lines with more than one yield contributing traits.

Genetic diversity and population structure: A total of 165 alleles were amplified by the 61 SSR markers with a mean of 2.73 per marker across the populations. The number of amplified alleles varied from two to five, where 32 molecular markers amplified 2 alleles and five SSRs amplified five alleles. Most of the markers recorded high heterozygosity with a mean of 0.21. Twenty-two markers recorded heterozygosity of > 0.21. The gene diversity varied from 0.08 (*umc1264*) to 0.76 (*umc1772*) with an average of 0.39. The major allele frequency for the markers ranged from 0.35 (*umc1375*) to 0.96 (*umc1264*) with an average of 0.71. The PIC values ranged from 0.07 (*umc1264*) to 0.73 (*umc1772*) with a mean of 0.22. The SSRs, *viz*., *umc1261*, *phi053*, *umc2214*, *umc1459* and *umc1375* recorded PIC >0.5. The larger number of alleles found in these 27 populations may be attributed to the existing heterogeneity of the populations. The mean heterozygosity (0.21) across the populations was also moderately high than the earlier reports such as 0.04 by Das *et al*. (2019) and 0.14 by Devi *et al.* (2023) in inbred lines whereas higher average heterozygosity (0.35) was reported by Mathiang *et al.* (2022) in the 37 landraces. This trend is obvious as populations and landraces are diverse in nature, heterozygous and heterogeneous whereas the inbred lines are expected to be homozygous and homogeneous. Gene diversity is defined as the probability that two randomly chosen alleles from the population are different (Liu and Muse, 2005). Similar range of gene diversity was also reported by earlier workers, *viz*., 0.08 to 0.76 (Das *et al*., 2019), 0.15 to 0.79 (Muthusamy *et al*., 2015), 0.04 to 0.72 (Zunjare *et al*., 2015) and 0.23 to 0.84 (Choudhary *et al*., 2016). Low value of major allele frequency of any marker is indicative of the highly diverse nature of the locus among the selected genotypes and similar results were reported by Kumar *et al*. (2022) and Muthusamy *et al*. (2015). The variation observed in PIC value is corroborated in earlier studies by Muthusamy *et al*. (2015), Das *et al*. (2019) and Kumar *et al*. (2022). These findings indicated that the selected SSR markers were effective in providing valid estimates of genetic diversity parameters for these maize populations.

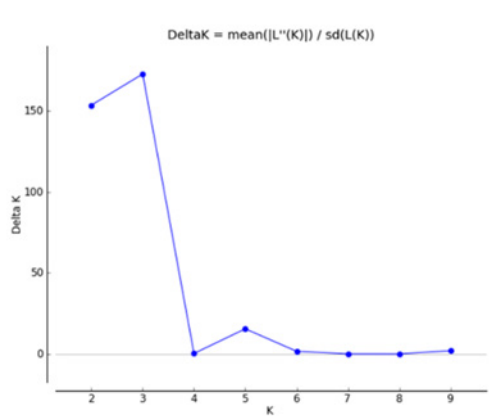

Fig 4. Delta K against estimated K showed a clear peak at the true value of K (3)

The plot generated using delta K against estimated K showed a clear peak at the true value of K = 3 (Fig 4). Structure analysis divided the 27 populations into three major-populations [P1 (Red), P2 (Green) and P3 (Blue)] (Fig 5). As per the membership coefficient (Q) value, populations revealed a Q value ≥0.60 was considered pure, whereas populations with Q<0.60 were regarded as admixture populations (Khan *et al*., 2020). The three major populations, *viz*., P1, P2 and P3 consisted of five, 11 and 10 pure sub-populations, respectively based on Q ≥0.60. However, POBLAC 47 and POBLAC 22 of P1 share a gene flow from P2, similarly POBLAC 42 and POBLAC 30 of P2 share gene flow from P1 and POBLAC 22 from P3. There is also gene flow from P1 to NBPGR 24, NBPGR 10, KDM3008, KDM 3006 and P3 to KDM 3006 of P2. Population KDM 111 showed much complex genetic architecture and shared gene pool of all three populations and was considered as admixture. The mean F_{st} value of P1, P2 and P3 were 0.34, 0.32 and 0.31, respectively which indicated very high differentiation among the populations (Fig 6).

Structure analysis was also done from the marker data which revealed three major populations. The F_{st} value of populations provides an estimate of the degree of differentiation among the populations. F_{st} value can range from 0 (populations can interbreed freely) to 1 (populations do not share any genetic diversity). Generally, F_{st} value<0.05 is considered as small, 0.05 to 0.15 as moderate, 0.15 to 0.25 as great and >0.25 as very great as established by Hartl and Clark (1997). Small α

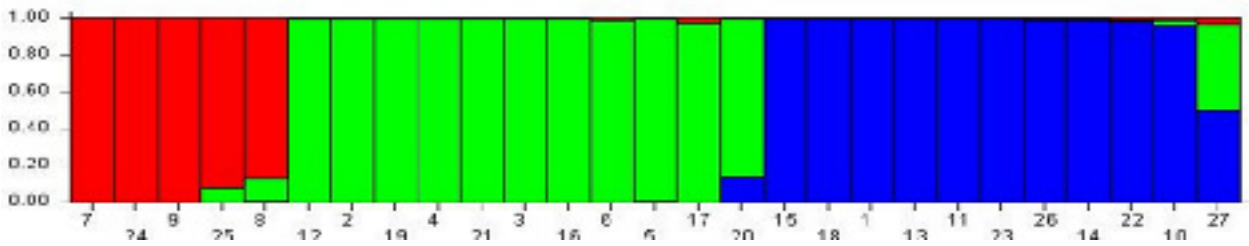

Fig 5. Population structure of white maize populations

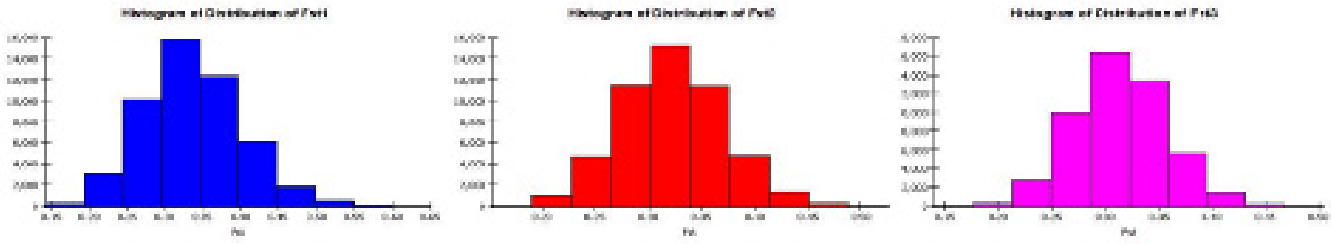

Fig 6. Histogram of distribution of Fst values

suggests that most of the individuals are essentially from one population or another, while $\alpha > 1$ indicates that most of the individuals are admixed in nature. The mean α value of the populations was 0.038, indicating very few individuals with admixture as supported by Q value.

Genetic relationships among the populations: The 27 populations were grouped into three major clusters, viz., A, B and C (Fig 7). Cluster A consisted of 11 genotypes, whereas cluster B and cluster C had seven and nine populations, respectively. The maximum distance was observed between POBLAC 101 of cluster C and SMP 54 of cluster A (0.64) followed by POBLAC 101 cluster C and SMP 50 cluster A (0.63) and the least genetic distance was observed between NBPGR 54 and POP 5 of cluster A (0.10) with overall mean genetic distance of 0.39. The average genetic distance of individual clusters was calculated, and clusters A, B and C had a mean genetic distance of 0.28, 0.24 and 0.36, respectively. The most distant populations were KDM 11 and SMP 54 (0.43), POBLAC 34 and POBLAC 22 (0.31), and POOL 28 and POBLAC 101 (0.51) in cluster A, B and C, respectively. The populations, viz., NBPGR 54 and POP 5 (0.10) inA and POBLAC 23 and POBLAC 102 (0.12) in cluster B shared the least genetic distance, whereas in cluster C, POBLAC 42 and POBLAC 44, as well as POBLAC 32 and POBLAC 90, revealed lowest genetic distance (0.17). Principal Coordinate Analysis (PCoA) was also used to further elucidate the genetic relationships of these 27 populations (Fig 8). Genotypes were distributed across the four quadrangles of the scatter plot. Quadrant 1, 3 and 4 had 11, nine and six genotypes, respectively. However, quadrant 2 had only one genotype.

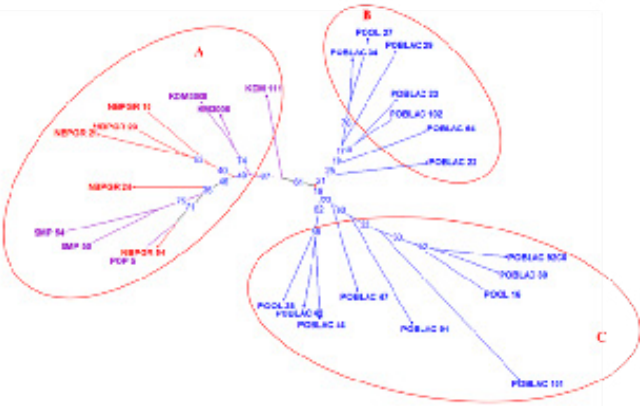

Fig 7. Cluster analysis of white populations

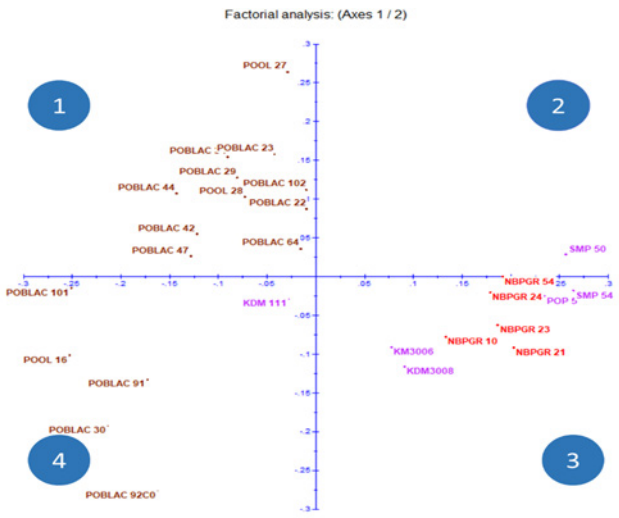

Fig 8. PCA analysis of 27 white maize populations

Out of these 27 populations, 18 populations, *viz.*, POP 5, POOL 27, POBLAC 102, POBLAC 29, POBLAC 64, POBLAC 30, POBLAC 91, KM3006, POBLAC 34, NBPGR 54, NBPGR 10, SMP 54, POBLAC 22, KDM3008, NBPGR 21, POBLAC 92, POBLAC 101 and NBPGR 24 followed same pattern of grouping in structure, cluster and PCoA analysis. POBLAC 30 POBLAC 91, POBLAC 92 and POBLAC 101 can be assigned as overall Heterotic Group I (HG-I: Structure population: 3, PCoA quadrant: 3, Cluster group: C), POOL 27, POBLAC 102, POBLAC 29, POBLAC 64, POBLAC 34 and POBLAC 22 as Heterotic Group II (HG-II: Structure population: 2, PCoA quadrant: 1, Cluster group: B) and POOL 27, POBLAC 102, POBLAC 29, POBLAC 64, POBLAC 34 and POBLAC 22 as Heterotic Group III (HG-III: Structure population: 3, PCoA quadrant: 2, Cluster group: A). However, the rest of the nine populations revealed different patterns of grouping. POBLAC 42, POBLAC 44, POBLAC 47 and POOL 28 revealed similar grouping in structure and PCoA analysis; POOL 16, NBPGR 23 and POBLAC 23 in cluster and PCoA analysis; SMP 50 showed similar pattern in structure and PCoA analysis but remained

isolated in PCoA analysis. KDM 111 revealed admixed nature in structure and also revealed different patterns in cluster and PCoA analysis.

Utilization of the populations identified for yield traits in breeding programme: Out of the six populations identified for NRPE, one population (POBLAC 92) represented HG-I and three population, *viz*., POBLAC 29, POBLAC 64 and POBLAC 22 belonged to HG-II. Similarly, only one (POBLAC 29) of the four populations identified for NKPR represented HG-II, whereas out of the six populations identified for HSWT, one each belonged to HG-I (POBLAC 92), HG-II (POBLAC 102) and HG-III (KDM3008). Hence, the populations identified for different yield traits belonging to different heterotic groups provide a good opportunity to derive superior heterotic inbred lines. The inbred lines from populations with higher NRPE of HG-II are expected to produce heterotic hybrids upon crossing with inbred lines derived from POBLAC 92 of HG-I and KDM3008 of HG-III with higher HSWT. Similarly, inbred lines from populations POBLAC 92 with higher NRPE of HG-I are expected to produce heterotic hybrids upon crossing with inbred lines derived from POBLAC 29 with higher NKPR and POBLAC 102 with higher HSWT of HG-II. Further, the information on the heterotic groups of these populations will help to design the breeding programme with prior knowledge and less resources (Madankar *et al.* 2023).

Conclusion

In the current study, the white maize populations were characterized for yield traits. Out of these 27 populations, those identified with higher NRPE, NKPR and HSWT were six, four and five, respectively. These populations could serve as good sources for deriving inbred lines with higher values of NRPE, NKPR and HSWT. The heterotic pattern of these populations was also determined which classified these identified populations in different HGs. Hence, inbred lines derived from populations with superior yield traits belonging to different HGs are expected to give rise to heterotic maize hybrids.

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