

Accelerated generation of inbred lines through DH Technology VS conventional bred QPM germplasm: Inbred and hybrid performance for higher genetic gains

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Abstract

Doubled haploid (DH) lines can be developed in shorter time frame than conventionally bred inbred lines, hence their use in developing new high yielding hybrids is gaining popularity rapidly. The present study was carried out to assess the per se performance of inbred lines developed through DH technology vs conventionally bred lines and to compare the test cross performance of 100 doubled haploid and back crossed maize inbred lines along with four checks across two locations. The first two principal components explained 51.4% of the total variance, with Dim1 and Dim2 accounting for 29.2% and 22.2%, respectively. The genotypes G5, G18, G6 showed maximum mean grain yield of 31.29, 30.03, 29.23 q/ha, respectively in per se performance observed in 100 inbred lines. A total of 87 testcross progenies along with four checks were evaluated for grain yield at two locations. At both locations, hybrids H73 (QIL 4-3401 x LM 13 Q3), H64 (QIL 4-3370 x LM 19 Q3-1) and H61 (QIL 4-3366 x LM 13 Q3) had recorded highest grain yield with 111.6 q/ha, 111.4 q/ha and 111.2 q/ha, respectively. All these three hybrids were derived from back cross derived populations.

Introduction

Maize (*Zea mays* L.) is grown throughout the world in a range of agro-ecological environments. Maize breeding revolves around the development of improved inbred lines (either using conventional breeding methods or DH technology) and identifying the best parental combinations for creating hybrids that are high yielding than their parents (Duvick, 2001). Maize inbred lines are primarily developed by crossing elite lines within heterotic groups, while hybrids are produced by crossing inbred lines that belong to different heterotic groups. The genetic uniformity of hybrids depends on the genetic purity of the parents used in making the cross. Grain yield is a complex trait and difficult to improve without targeting the improvement of grain yield attributing traits, which are relatively less complex in nature. Breeders must develop improved maize hybrids that are able to give maximum yield as well as stability across differential environments.

In maize breeding, doubled haploid (DH) lines generated by in vivo induction of maternal haploids, are frequently utilized. In contemporary plant breeding, doubled haploid (DH) technology has established itself as a reliable method for quickly creating homozygous lines. To achieve this, haploid plants with a single set of chromosomes are created, and then their haploid genomes are doubled. DH technique has many advantages, including a more effective selection method than selection among segregating families and a reduction in the time and expenses associated with the creation of inbred lines by recurrent self-pollination. Because DH lines are homozygous, plant populations are homogeneous, which makes it possible for breeders to precisely assess the performance of various genetic materials in breeding operations.

Compared to inbred lines created using traditional breeding techniques, the utilization of doubled haploids provides two benefits. First of all, it saves time since homozygous plants with 100% homozygosity are created in a single generation. After five generations of selfing, the traditional inbreeding approach yields an average level of homozygosity of 96.9% (Briggs and Knowles, 1967). Second, compared to traditional breeding techniques like pedigree selection or single seed descent, the genetic variety of a segregating population can be utilized more quickly (Bordes et al., 2007). DH can also increase the effectiveness of recurrent selection, especially for low heritability traits (Bouchez and Gallais, 2000).

The ability to generate haploids is essential for the successful application of DH technology in maize breeding projects. This is accomplished by pollinating the source germplasm from which DH lines will be created using pollen from haploid inducers (Chaikam et al., 2019). The haploid induction rate (HIR) is the percentage of seeds with haploid embryos found among all the seeds harvested on the source germplasm (Prigge et al., 2012). Based on the initial Stock 6 genotype, more sophisticated inducers with a high HIR (8%–10%) have been produced during the last 15–20 years, making it possible to produce maize DH lines on a large scale (Geiger and Gordillo, 2009).

Improved modern inducers include RWS, RWK- 76, UH400, and UH600 (University of Hohenheim, Germany), the PHI series (Procera, Romania), CAU5 (China Agricultural University, China), the BHI series (Iowa State University, USA), and the TAIL series (Tropical Adapted Inducer Lines, CIMMYT) (Trentin et al., 2020; 2023). Because of the genetic, methodological, and logistic advantages, further progress in maize breeding is expected to increase considerably with the development of DH lines (Gordillo and Geiger, 2008).

Back cross populations in maize are used to transfer specific traits (high yield, disease resistance etc.) from a donor line to a recipient line. They are widely used in crop breeding programmes in order to have trait introgression, QTL identification as well as for superior hybrid development. In a study done by Eagles et al. (1989), backcross populations of maize (*Zea mays* L.) were produced by crossing the early maturing inbred line W153R with the highland Mexican race Conico then backcrossing to W153R (Q1 population) and by crossing W153R with the highland Peruvian race San Gerónimo then backcrossing to W153R (Q3 population). Testcrosses were produced from S₀ plants. Many testcrosses were higher yielding than check hybrids of W153R, but most were later maturing.

Kumar et al., (2024), aimed to identify quantitative trait loci (QTLs) linked with grain yield and yield attributing traits in teosinte derived back cross populations. Two BC₂F₂ populations developed from the cross of LM13 with *Zea parviglumis* (population 1) and LM14 with *Zea*

parviglumis (population 2) were genotyped and phenotyped. BC₂F_{2.3} lines in both populations were phenotyped again for grain yield and attributing traits in the spring season. In total, three QTLs each for ear height (EH), two QTLs for flag leaf length (FLL) and one QTL each for ear diameter (ED), plant height, flag leaf length (FLL), flag leaf width and 100 kernel-weight were identified in population 1. In population 2, two QTLs for kernel row per ear (KRPE) and one QTL for FLL were detected in. QTLs for EH, FLL and KRPE showed consistency across seasons. Among the identified QTLs, six QTLs were found to be co-localized near identified genomic regions in previous studies, validating their potential in contributing to trait expression.

Among various multivariate techniques, PCA and cluster analysis have proven to be highly effective in selecting genotypes for breeding programs aligned with a breeder's objectives. PCA simplifies the selection process by reducing the dimension of the data and gives the foremost components that majorly contribute to yield, particularly when addressing the morphological and physiological variations commonly observed in crop species. Principal component analysis is a sort of multivariate analysis where canonical vectors or roots representing different axes of differentiation and amount of variation accounted for each of such axes, respectively, are derived (Rao, 1952). It is called principal component analysis as it reflects the importance of the largest contributor to the total variation at each axis of differentiation.

In descriptive statistics, boxplot is a convenient way of graphically depicting groups of numerical data through their quartiles. Box plots are non-parametric and they display variation in samples of a statistical population without making any assumptions of the underlying statistical distribution. The spacings between the different parts of the box indicate the degree of dispersion (spread) in the data, and show outliers (Rousseeuw et al., 1999). The objective of the present study was to evaluate the performance of doubled haploid and back crosses derived maize testcrosses as well as per se performance of parental lines across two locations in India.

Materials and methods

Genetic materials

A total of 100 inbred lines were used for assessing *per se* performance and making test crosses with two testers. Out of 100 inbred lines, 50 lines were DH lines whereas other 50 lines were developed by back cross breeding procedure. The 50 DH lines were derived from three populations namely QIL-4-2192 x QIL-4-2916, QIL-4-2192 x QIL-4-3149, MB-67 x E2-20-2. QIL-4-2192 is an elite QPM rich inbred line, also used as parental line of QPM hybrid IQMH 202, whereas QIL-4-2916, QIL-4-3149, E2-20-2 are methionine rich inbred lines. MB 67 (pedigree LM13-Q6) is a normal maize background line converted to QPM version. A total of 50 lines developed from these three populations. The F₂ populations and inducer lines were sown in ratio of 3:1 to generate DH lines. F₂ was detasseled and D₀ generation was obtained and further maintained in seasons (*kharif 2021*) and multiplied during *kharif, 2022*. The DH lines were developed by means of in vivo haploid induction and later chromosome doubling was done at VPKAS, Almora.

The QPM based inbred lines (QIL-4-2034, QIL-4-2047, QIL-4-2192, QIL-4-2209-10, QIL-4-2234, QIL-4-2243, QIL-4-2261-1, QIL-4-2295, QIL-4-2306, QIL-4-2311, QIL-4-2317, QIL-4-2038, QIL-4-2099, QIL-4-2124, QIL-4-2184, QIL-4-2215-2, QIL-4-2300, QIL-4-2192, QIL-4-2234, QIL-4-2124) were crossed with CP 858 (a private sector hybrid by Charoen Popkhand Seeds Pvt Ltd), Bio 9544 (a private sector hybrid by Bioseeds Pvt Ltd), UMI 1200 and UMI 1201 (female parents of hybrid (CMH 08-282 & CMH 08-292, respectively) in *Kharif 2021* at ICAR-IIMR, Ludhiana. The F₁s were further backcrossed with CP 858, Bio 9544, UMI 1200 and UMI 1201 in *Rabi 2021* at RMR & SPC, Begusarai. The BC₁F₁ generation was obtained after making these backcrosses, which were further progressed to BC₂F₁ in *Kharif 2022* and selfing was done at ICAR-IIMR in order to develop the BC₂F₂ and BC₂F₃ progenies in next seasons. Total 50 back cross progenies were used as study material in current research.

In 12 backcrosses, the QPM lines QIL-4-2034, QIL-4-2047, QIL-4-2192, QIL-4-2209-10, QIL-4-2234, QIL-4-2243, QIL-4-2261-1, QIL-4-2295, QIL-4-2306, QIL-4-2311, QIL-4-2317 were used as male parent and CP 858 was used as female parent, then F₁s were back crossed with CP 858. In five back crosses, QIL-4-2038, QIL-4-2099, QIL-4-2124, QIL-4-2184, QIL-4-2215-2 and QIL-4-2300 were used as female parent and CP 858 was used as male parent. The QPM lines QIL-4-2192, QIL-4-2234, QIL-4-2124 and QIL-4-2192 were used as male parent and UMI 1200, UMI 1201 were used as female parent, subsequently F₁s were used for back crossing with UMI 1200 and UMI 1201. Both the hybrids CP 858 and Bio 9544 and UMI lines were used in order to overcome the yield penalty in the QPM background.

Per se performance of inbred lines was assessed in *kharif 2024* seasons at Ludhiana and Karnal locations. The checks (inbred lines) namely QIL-4-2209, QIL-4-2192, DMRQPM 106 and HKI 193-1 were also used in *per se* performance experiment. QIL-4-2209, QIL-4-2192 and DMRQPM 106 are the parental inbred lines of QPM hybrids IQMH 202 and IQMH 203 released by ICAR-IIMR whereas, HKI 193-1 is female parent of QPM hybrid HQPM 1. HQPM 1 (High Quality Protein Maize 1) is a single-cross hybrid developed by the CCS Haryana Agricultural University (HAU), Regional Station, Uchani, Karnal. The 104 inbred lines were sown in alpha lattice design in 3.0 m long single row with 2

replications. The seeds were sown with a spacing of 60 × 25 cm and standard cultivation practices were carried out as recommended. The detailed pedigree of the study material is given in Table 1.

Table 1
Details of the study material used

S. No.	Genotype	Inbred line	Pedigree
		DH lines	
1	G1	QIL-4-3279	QIL-4-2192 x QIL-4-2916 : P-1
2	G2	QIL-4-3282	QIL-4-2192 x QIL-4-2916 : P 7
3	G3	QIL-4-3286	QIL-4-2192 x QIL-4-2916 : P 16
4	G4	QIL-4-3287	QIL-4-4 2192 x QIL-4-3149: P 135
5	G5	QIL-4-3288	QIL-4-4 2192 x QIL-4-3149: P 136
6	G6	QIL-4-3290	QIL-4-4 2192 x QIL-4-3149: P 138
7	G7	QIL-4-3294	QIL-4-4 2192 x QIL-4-3149: P 141
8	G8	QIL-4-3295	QIL-4-4 2192 x QIL-4-3149: P 142
9	G9	QIL-4-3296	QIL-4-4 2192 x QIL-4-3149: P 143
10	G10	QIL-4-3297	QIL-4-4 2192 x QIL-4-3149: P 144
11	G11	QIL-4-3298	QIL-4-4 2192 x QIL-4-3149: P 145
12	G12	QIL-4-3300	QIL-4-4 2192 x QIL-4-3149: P 147
13	G13	QIL-4-3301	QIL-4-4 2192 x QIL-4-3149: P 148
14	G14	QIL-4-3302	QIL-4-4 2192 x QIL-4-3149: P 149
15	G15	QIL-4-3303	QIL-4-4 2192 x QIL-4-3149: P 150
16	G16	QIL-4-3304	QIL-4-4 2192 x QIL-4-3149: P 152
17	G17	QIL-4-3306	QIL-4-4 2192 x QIL-4-3149: P 154
18	G18	QIL-4-3307	QIL-4-4 2192 x QIL-4-3149: P 155
19	G19	QIL-4-3310	QIL-4-4 2192 x QIL-4-3149: P 158
20	G20	QIL-4-3315	QIL-4-4 2192 x QIL-4-3149: P 163
21	G21	QIL-4-3317	QIL-4-4 2192 x QIL-4-3149: P 165
22	G22	QIL-4-3319	QIL-4-4 2192 x QIL-4-3149: P 167
23	G23	QIL-4-3320	QIL-4-4 2192 x QIL-4-3149: P 168
24	G24	QIL-4-3321	QIL-4-4 2192 x QIL-4-3149: P 169
25	G25	QIL-4-3322	QIL-4-4 2192 x QIL-4-3149: P 170
26	G26	QIL-4-3323	QIL-4-4 2192 x QIL-4-3149: P 171
27	G27	QIL-4-3324	QIL-4-4 2192 x QIL-4-3149: P 172
28	G28	QIL-4-3325	QIL-4-4 2192 x QIL-4-3149: P 173
29	G29	QIL-4-3326	QIL-4-4 2192 x QIL-4-3149: P 174
30	G30	QIL-4-3327	QIL-4-4 2192 x QIL-4-3149: P 175
31	G31	QIL-4-3328	QIL-4-4 2192 x QIL-4-3149: P 176
32	G32	QIL-4-3330	QIL-4-4 2192 x QIL-4-3149: P 178
33	G33	QIL-4-3333	QIL-4-4 2192 x QIL-4-3149: P 182
34	G34	QIL-4-3335	QIL-4-4 2192 x QIL-4-3149: P 184
35	G35	QIL-4-3336	QIL-4-4 2192 x QIL-4-3149: P 185
36	G36	QIL-4-3337	QIL-4-4 2192 x QIL-4-3149: P 186

S. No.	Genotype	Inbred line	Pedigree
DH lines			
37	G37	QIL-4-3339	QIL-4-4 2192 x QIL-4-3149: P 188
38	G38	QIL-4-3340	QIL-4-4 2192 x QIL-4-3149: P 189
39	G39	QIL-4-3342	MB 67 x E2-20-2 : P 192
40	G40	QIL-4-3343	MB 67 x E2-20-2 : P 193
41	G41	QIL-4-3344	MB 67 x E2-20-2 : P 194
42	G42	QIL-4-3347	MB 67 x E2-20-2 : P 198
43	G43	QIL-4-3348	MB 67 x E2-20-2 : P 201
44	G44	QIL-4-3349	MB 67 x E2-20-2 : P 202
45	G45	QIL-4-3352	MB 6 x E2-20-2 : P 205
46	G46	QIL-4-3353	MB 67 x E2-20-2 : P 206
47	G47	QIL-4-3357	MB 67 x E2-20-2 : P 212
48	G48	QIL-4-3358	MB 67 x E2-20-2 : P 213
49	G49	QIL-4-3359	MB 67 x E2-20-2 : P 214
50	G50	QIL-4-3360	MB 67 x E2-20-2 : P-215
Back cross population			
51	G51	QIL-4-3361	(CP 858 x QIL-4-2034) x CP 858 : 1-1
52	G52	QIL-4-3362	(CP 858 x QIL-4-2034) x CP 858 : 1.2
53	G53	QIL-4-3363	(CP 858 X QIL-4-2047) x CP 858 : 2.1
54	G54	QIL-4-3364	(CP 858 X QIL-4-2047) x CP 858 : 2.2
55	G55	QIL-4-3365	(CP 858 X QIL-4-2192) x CP 858 : 3.1
56	G56	QIL-4-3366	(CP 858 X QIL-4-2192) x CP 858 : 3.2
57	G57	QIL-4-3367	(CP 858 X QIL-4-2192) x CP 858 : 3.3
58	G58	QIL-4-3368	(CP 858 X QIL-4-2192) x CP 858 : 3.5
59	G59	QIL-4-3369	(CP 858 x QIL-4- 2209-10) x CP 858 : 4 - 1
60	G60	QIL-4-3370	(CP 858 x QIL-4- 2209-10) x CP 858 :4 - 3
61	G61	QIL-4-3371	(CP 858 x QIL-4- 2209-10) x CP 858 : 4-6
62	G62	QIL-4-3372	(CP 858 x QIL-4- 2209-10) x CP 858 : 4-8
63	G63	QIL-4-3373	(CP 858 x QIL-4-2234) x CP 858 : 5 - 1
64	G64	QIL-4-3374	(CP 858 x QIL-4-2234) x CP 858 : 5 - 2
65	G65	QIL-4-3375	(CP 858 x QIL-4-2234) x CP 858 : 5 - 3
66	G66	QIL-4-3376	(CP 858 x QIL-4-2234) x CP 858 : 5-5
67	G67	QIL-4-3377	(CP 858 x QIL-4-2243) x CP 858 : 6 - 1
68	G68	QIL-4-3379	(CP 858 x QIL-4-2261-1) x CP 858 : 7 - 6
69	G69	QIL-4-3381	(CP 858 x QIL-4-2261-1) x CP 858 : 7-8
70	G70	QIL-4-3382	(CP 858 x QIL-4-2261-1) x CP 858 : 7-9
71	G71	QIL-4-3384	(CP 858 x QIL-4-2295) x CP 858 : 9 - 1
72	G72	QIL-4-3385	(CP 858 x QIL-4-2295) x CP 858 : 9 - 3

S. No.	Genotype	Inbred line	Pedigree
		DH lines	
73	G73	QIL-4-3386	(CP 858 x QIL-4-2295) x CP 858 : 9 – 4
74	G74	QIL-4-3387	(CP 858 x QIL-4-2295) x CP 858 : 9 – 5
75	G75	QIL-4-3388	(CP 858 x QIL-4-2299) x CP 858 : 10 – 2
76	G76	QIL-4-3389	(CP 858 x QIL-4-2306) x CP 858 : 11 – 1
77	G77	QIL-4-3390	(CP 858 x QIL-4-2306) x CP 858 : 11 – 2
78	G78	QIL-4-3397	(CP 858 x QIL-4-2306) x CP 858 : 11 – 9
79	G79	QIL-4-3401	(CP 858 x QIL-4-2306) x CP 858 : 11 – 13
80	G80	QIL-4-3402	(CP 858 x QIL-4-2311) x CP 858 : 12 – 1
81	G81	QIL-4-3405	(CP 858 x QIL-4-2317) x CP 858 : 13 – 1
82	G82	QIL-4-3407	(CP 858 x QIL-4-2317) x CP 858 : 13 – 3
83	G83	QIL-4-3413	(QIL-4- 2038 x CP 858) x CP 858 : 2–4
84	G84	QIL-4-3414	(QIL-4- 2038 x CP 858) x CP 858 : 2–5
85	G85	QIL-4-3417	(QIL-4- 2099 x CP 858) x CP 858 : 5 – 1
86	G86	QIL-4-3418	(QIL-4-2099 x CP 858) x CP 858 : 5 – 2
87	G87	QIL-4-3419	(QIL-4-2124 x CP 858) x CP 858 : 6 – 1
88	G88	QIL-4-3420	(QIL-4-2124 x CP 858) x CP 858 : 6 – 3
89	G89	QIL-4-3421	(QIL-4-2124 x CP 858) x CP 858 : 6 – 5
90	G90	QIL-4-3422	(QIL-4-2184 x CP 858) x CP 858 : 7 – 2
91	G91	QIL-4-3423	(QIL-4-2184 x CP 858) x CP 858 : 7–7
92	G92	QIL-4-3424	(QIL-4-2184 x CP 858) x CP 858 : 7.9
93	G93	QIL-4-3426	(QIL-4-2215-2 x CP 858) x CP 858 : 8.2
94	G94	QIL-4-3434	(QIL-4-2300 x CP 858) x CP 858 : 10.4
95	G95	QIL-4-3445	QIL-4-2293 x (Bio 9544 x QIL-4-2293) : 5.1
96	G96	QIL-4-3451	(UMI 1200 x QIL-4-2192) x UMI 1200 : 2.6
97	G97	QIL-4-3452	(UMI 1201 x QIL-4-2234) x UMI 1201: 3.2
98	G98	QIL-4-3453	(UMI 1201 x QIL-4-2124) x UMI 1201: 4.2
99	G99	QIL-4-3455	(UMI 1201 x QIL-4-2192) x UMI 1201: 5.2
100	G100	QIL-4-3456	(UMI 1201 x 2234) x UMI 1201 : 6.1
101	G101	Check QIL-4-2192	Su2Su20202 Comp(R)-BBB-1-1-1
102	G102	Check QIL-4-2209	WNCQPM 10033-2-1
103	G103	Check CLQRCY 40	DMRQPM 106
104	G104	Check HKI 193-1	HKI 193-1
105	G105	Tester MB 109	LM 19-Q3-1
106	G106	Tester MB 122	LM 13-Q3

Generation of Testcrosses

Inbred lines derived from the backcross and DH induction were crossed with two testers namely LM 19 Q3-1 (MB 109) and LM 13 Q3 (MB 122) which are the converted version (QPM) of a released hybrid PMH 6's parental lines. PMH 6 (Punjab Maize Hybrid 6) is a maize hybrid developed by the Punjab Agricultural University (PAU), Ludhiana. The DH and BCs lines were used as the females while the testers were used as the male parent. The test crosses were made during *rabi* 2024 season at RMR & SPC, Begusarai (Bihar). However, at end of harvesting season, only 87 test crosses with both testers produced enough seeds. Among these total crosses, 55 were derived from DH lines whereas 32 crosses belonged to BC-based parental lines

Field evaluations of the DH and back cross population-based testcrosses

Eighty-seven hybrids and 4 checks (QPM hybrids: IQMH 202 & IQMH 203; Field corn Hybrids: BIO 9544 and ADV 765) were evaluated in an alpha lattice field experimental design with two replications per location during the *kharif* 2025 season. Checks IQMH 202, IQMH 203 are the QPM based maize hybrids released by ICAR-Indian Institute of Maize Research (IIMR). Bio 9544 and ADV 765 are the field corn hybrids released by private sector (Bioseeds Pvt Ltd and Advanta seeds, respectively). The field evaluations were done at Ludhiana and Karnal locations. The agro climatic description for the tested sites is given in Table 2.

Table 2 Agro-climatic description of the site where the testcross hybrids were evaluated					
S. No.	Location	Latitude	Longitude	Elevation	Soil type
1.	Ludhiana	30°54'N	75°51'E	244 m	Sandy loam to loamy sand
2.	Karnal	29.686°N	76.989°E	252 m	sandy loam to clay loam

Data collection

Evaluation of yield related components

Grain yield (GY) and yield related components viz., days to 50% anthesis (DA)-duration from planting to 50% of the pollen shedding; days to 50% silking (DS)-duration from planting to 50% silk emergence were recorded; plant height (PH)-five plants were randomly selected, and their height from the base to the tassel-bearing node at maturity was measured in centimetres using a measuring rod, and the average plant height was calculated; ear height (EH)-measured at the dry silk stage in centimetres from the base of the plant to the base of the highest cob on the same randomly selected 5 plants whose plant height was recorded, and the average was calculated; cob length (CL)-measured in centimetres from the base to the filled grain point of three cobs collected from the all plants; cob girth (CG)-measured in centimetres at the centre of each cob from three cobs collected from the all plants, and the mean was calculated; number of kernels/row (NOK)-number of seeds per row in 3 randomly selected ears of all plants were counted and averaged; number of rows (NOR)-the number of kernel rows in three ear of all plants were counted and averaged and grain yield (GY)-calculated in q/ha by considering the plot size and yield per plot. Furthermore, using the above parental lines, the developed hybrids were further evaluated for grain yield.

Statistical analysis

Data analysis

Analysis of variance (ANOVA) for each of the trait was performed in the Agricolae package in R software (Mendiburu and Simon, 2009). The R software “variability” package (version 4.2.1) was used for the principal component analysis. Box plots and scree plot were also generated following the procedure.

Results

Analysis of variance for grain yield and associated traits in inbred lines

It revealed significant differences among the inbred lines for all the observed traits. The significant variation in the inbred lines suggested that the variability present in the inbreds and will be helpful to develop the hybrids with a higher yield potential. However, non-significant differences among replications were observed for DA, DS, PH, EH, CL, CG and NOR. There were significant differences among replications for the NOK as well as for GW. Environments also possessed significant differences for studied traits. The interaction between genotype and environment ($G \times E$) also exhibited a significant difference ($p < 0.001$) for DA, DS, PH, EH, CL and CG (Table 3).

Table 3. ANOVA for grain yield and associated traits in maize inbred lines

Source of variation	Df	DA	DS	PH	EH	CL	CG	NOR	NOK	GW
Genotype	103	16.06***	14.38***	940.7***	301.5***	6.54***	84.1***	4.37***	68.44***	14.01***
Replication	1	0.00	2.24	17.72	0.566	0.61	1.80	0.51	76.16***	455.25***
Environment	1	1811.12***	549.24***	30795.9***	13188.5***	44.55***	63.59***	23.71***	1.62	391.94***
G × E	103	14.24***	11.57***	654.7***	243.5***	4.24***	44.81***	2.00	7.17	7.39
Residuals	207	3.06	2.89	74.8	29.2	0.56	4.45	1.88	6.91	7.57

***significant at 0.001 % level of significance

Abbreviations: DA-Days to 50% Anthesis, DS-Days to 50% Silking, PH-Plant height, EH-Ear height, CL-Cob length, CG-Cob girth, NOR-Number of rows/ear, NOK-Number of kernels/ear and GW-Grain yield/plot

Analysis of variance for grain yield in test cross population

The ANOVA (Analysis of Variance) of grain yield revealed significant variation among the genotypes at a 0.001% level of significance. Both the environments as well as the interaction between genotype and environment (G × E) were also found to be differed significantly. It signifies that the both the locations pose a significant effect on the grain yield of the genotypes. Replications were observed non-significant in analysis of variance (Table 4).

Table 4. ANOVA for grain yield in maize hybrids

S. No.	Source of variation	Df	SS	MSS	F	***significant at 0.001 % level of significance
1	Genotype	90	73128.425	812.538	8.426***	Analysis of grain yield between DHs and BCs derived lines using t test
2	Replication	1	46.072	46.072	0.477	
3	Environment	1	113637.891	113637.891	1178.443***	The t test revealed statistically non-significant variation (p=0.411) between grain yield of test crosses of DH and BC at Ludhiana location whereas a statistically significant difference (p=0.000132) was observed between sets of hybrids derived from DH and BC lines
4	G × E	90	46213.427	513.483	5.325***	
5	Residuals	181	17550.365	96.431	-	

at Karnal location at p=0.05 level of significance. This signifies that the both the sets performed comparably well under Ludhiana location however, their performance was differential in terms of grain yield under Karnal location. These findings also indicate that environment and G × E interaction also plays a major role in deciphering the performance of hybrids.

Variation for yield and its related traits in individual location

At Ludhiana (E1) location, the days to 50 % anthesis and days to 50 % silking ranged from 51 to 65 days and 53 to 66 days, respectively. The values for plant height and ear height ranged between 63.50 to 178.33 cm and 31.50 to 94.17 cm, respectively. Whereas CL, CG, NOR, and NOK ranged from 6.9 to 15.4 cm, 20.5 to 52.8 cm, 7 to 14 and 4 to 29. The grain yield (q/ha) ranged between 21.21 q/ha to 33.33. This indicates a high level of variability among the genotypes for grain yield.

At Karnal (E2) location, the range for days to anthesis is from 48 to 60 days. This relatively narrow range indicates low variability among the genotypes for maturity. Days to silking ranged from 50.5 to 62.5 days and plant height varies from 63 cm to 177.5 cm. The range for ear height is from 10 cm to 91.5 cm, giving a difference of 81.5 cm. Cob length ranged from 7.97 cm to 15.35 cm. Cob girth shows a wide range from 12.25 cm to 54.75 cm, this high variability suggests significant differences among genotypes. The number of rows ranges from 8 to 13 whereas the number of kernels ranges from 7 to 23.5. Grain yield ranges from 18.62 q/ha to 31.91 q/ha.

The highest grain yield at E1 was recorded in inbred line QIL-4-3294 and QIL-4-3288 (33.30 q/ha) followed by 32.63 q/ha (QIL-4-3287) and 29.78 q/ha (QIL-4-3282). The DA were lowest for genotypes QIL-4-3352, QIL-4-3357 and QIL-4-3359 (51 days) whereas genotypes QIL-4-3382 and QIL-4-3418 had DA of 65 and 64 days, respectively. The genotypes QIL-4-3352 and QIL-4-3364 both recorded lowest DS (53 days) whereas genotypes QIL-4-3360 and QIL-4-3418 had highest DS (66 and 65 days). The highest plant height as well as ear height was observed in genotypes QIL-4-3455 and QIL-4-3279 (178.33 and 170.95 cm; 94.17 and 88.58), respectively.

Among the 104 inbred lines, the maximum cob length (15.4 and 15.3 cm) was observed in genotypes QIL-4-3279 and QIL-4-3455. The cob girth is a yield-related trait and it also offer scope for further selection, was observed maximum at 52.8 cm in genotype QIL-4-3348 followed

by 41.4 cm in genotype QIL-4-3455. The maximum number of rows (14) and maximum number of kernels (29) were observed in genotypes QIL-4-3455, QIL-4-3453, QIL-4-3413 and QIL-4-3420, QIL-4-3279, QIL-4-3417, respectively (Table 5).

Table 5. Per se performance of 100 inbred lines at Ludhiana location

S. No.	Inbred line	DA	DS	PH	EH	CL	CG	NOR	NOK	GW (q/ha)
1	QIL-4-3279	54	54	170.95	88.58	15.4	40.0	12	29	29.56
2	QIL-4-3282	57	58	104.83	46.67	7.8	26.7	14	6	29.78
3	QIL-4-3286	60	62	108.00	45.83	9.0	24.9	11	13	29.23
4	QIL-4-3287	60	61	107.33	40.00	9.9	20.5	12	15	32.63
5	QIL-4-3288	58	59	108.00	53.33	10.5	35.2	12	15	33.30
6	QIL-4-3290	59	57	112.50	44.42	11.1	30.6	13	12	28.74
7	QIL-4-3294	57	58	99.17	52.08	9.5	27.7	12	7	33.33
8	QIL-4-3295	55	55	108.50	57.00	11.4	30.3	12	13	28.71
9	QIL-4-3296	54	56	126.17	62.50	12.9	33.1	12	12	28.47
10	QIL-4-3297	55	57	118.00	62.50	13.1	31.9	14	14	26.96
11	QIL-4-3298	56	57	114.33	46.17	11.2	28.2	12	7	28.80
12	QIL-4-3300	57	58	121.50	57.50	10.3	27.8	12	11	28.71
13	QIL-4-3301	53	55	114.67	44.17	10.0	30.0	13	13	27.77
14	QIL-4-3302	55	56	117.13	53.33	10.7	33.6	13	10	27.18
15	QIL-4-3303	57	58	114.00	51.33	10.1	32.8	14	16	27.88
16	QIL-4-3304	55	57	131.33	59.83	9.7	32.1	13	11	28.96
17	QIL-4-3306	56	57	118.00	49.17	12.9	30.8	12	18	26.74
18	QIL-4-3307	57	58	124.67	50.00	12.3	26.3	12	14	28.15
19	QIL-4-3310	56	56	101.75	45.42	10.2	27.6	11	9	27.51
20	QIL-4-3315	59	60	101.72	47.33	9.4	26.6	12	9	28.96
21	QIL-4-3317	55	56	115.17	62.50	9.6	32.7	12	11	26.75
22	QIL-4-3319	55	57	113.33	57.42	9.7	31.6	12	8	28.00
23	QIL-4-3320	57	58	118.00	54.17	8.6	29.6	12	6	26.92
24	QIL-4-3321	58	59	97.50	35.00	10.1	25.7	11	8	27.44
25	QIL-4-3322	59	61	100.67	45.83	8.8	30.8	11	8	25.81
26	QIL-4-3323	57	58	103.00	38.75	9.4	28.9	11	10	26.34
27	QIL-4-3324	63	64	82.00	38.00	9.6	31.6	12	8	26.85
28	QIL-4-3325	58	59	122.00	63.50	10.1	28.5	11	9	28.68
29	QIL-4-3326	61	62	79.75	41.25	10.6	22.1	10	10	27.21
30	QIL-4-3327	54	58	117.50	65.00	11.1	25.9	12	12	27.70
31	QIL-4-3328	59	57	123.00	54.17	10.8	30.8	9	8	26.64
32	QIL-4-3330	57	58	107.83	51.00	11.8	28.2	13	9	26.82
33	QIL-4-3333	57	58	83.00	42.50	9.9	23.6	12	8	26.63
34	QIL-4-3335	58	58	96.50	39.17	8.4	26.7	11	8	28.45
35	QIL-4-3336	60	61	96.67	42.50	9.6	24.7	9	5	25.99
36	QIL-4-3337	58	60	96.67	36.67	10.9	30.5	12	18	27.45
37	QIL-4-3339	55	57	121.67	46.67	11.6	30.9	12	10	25.93
38	QIL-4-3340	53	55	102.74	49.17	10.8	28.3	10	10	26.54

39	QIL-4-3342	64	65	142.50	52.50	11.5	30.1	10	15	28.60
40	QIL-4-3343	54	56	95.50	44.17	11.8	33.2	13	16	25.02
41	QIL-4-3344	60	61	117.00	50.00	11.9	29.4	13	15	28.44
42	QIL-4-3347	61	62	84.00	42.50	8.0	28.2	8	8	25.86
43	QIL-4-3348	54	57	121.00	53.50	9.7	52.8	9	8	25.60
44	QIL-4-3349	58	59	91.00	39.17	9.7	30.9	13	12	25.97
45	QIL-4-3352	51	53	120.00	45.50	11.2	34.0	10	10	27.71
46	QIL-4-3353	61	62	128.00	63.33	10.9	30.8	12	16	28.53
47	QIL-4-3357	51	55	128.00	66.00	11.0	31.5	9	8	27.42
48	QIL-4-3358	58	58	90.67	42.50	8.8	27.9	10	9	28.08
49	QIL-4-3359	51	55	127.00	66.00	9.6	22.0	11	10	27.24
50	QIL-4-3360	62	66	101.00	51.25	10.2	28.3	11	9	26.94
51	QIL-4-3361	60	62	103.83	46.67	10.7	30.2	14	12	28.20
52	QIL-4-3362	57	59	167.50	47.00	14.7	34.2	13	16	27.14
53	QIL-4-3363	57	59	107.50	49.17	12.3	31.8	13	14	27.19
54	QIL-4-3364	54	53	118.83	59.17	10.4	30.0	12	15	27.27
55	QIL-4-3365	61	62	112.00	61.25	11.3	34.6	13	11	26.73
56	QIL-4-3366	57	57	128.50	85.92	10.8	30.4	9	10	28.10
57	QIL-4-3367	56	57	136.50	63.75	10.0	30.6	11	15	24.79
58	QIL-4-3368	59	60	105.83	58.33	11.1	26.3	9	11	25.49
59	QIL-4-3369	61	59	113.25	66.25	9.5	29.8	11	14	27.79
60	QIL-4-3370	56	56	112.08	60.00	10.5	30.8	11	13	24.04
61	QIL-4-3371	59	60	115.33	59.17	8.3	31.4	12	9	23.50
62	QIL-4-3372	57	59	99.17	57.92	11.2	27.4	10	11	27.00
63	QIL-4-3373	55	56	106.17	43.33	9.9	31.5	11	11	26.09
64	QIL-4-3374	56	57	108.08	43.33	11.5	28.0	12	12	23.93
65	QIL-4-3375	57	58	111.67	45.83	13.3	27.2	11	17	28.95
66	QIL-4-3376	59	60	94.17	50.00	10.8	32.0	12	27	26.31
67	QIL-4-3377	58	59	128.33	55.00	12.3	29.7	11	8	27.97
68	QIL-4-3379	56	58	63.50	38.75	10.0	23.7	10	6	28.40
69	QIL-4-3381	61	62	112.83	50.00	11.5	31.7	12	8	24.42
70	QIL-4-3382	65	65	76.50	46.50	9.5	29.3	11	11	26.20
71	QIL-4-3384	57	58	114.17	55.50	12.3	35.8	11	15	27.99
72	QIL-4-3385	54	55	124.17	54.17	14.8	33.4	13	25	27.42
73	QIL-4-3386	58	60	81.00	42.00	9.3	21.0	8	9	24.38
74	QIL-4-3387	60	60	107.50	42.50	7.8	26.1	9	6	23.67
75	QIL-4-3388	57	58	129.17	56.25	7.8	31.8	12	8	29.69
76	QIL-4-3389	57	58	98.67	46.67	11.6	31.7	11	17	26.80
77	QIL-4-3390	56	58	95.92	42.92	8.3	34.9	14	9	24.39

78	QIL-4-3397	56	57	130.17	52.50	8.3	28.0	12	10	24.61
79	QIL-4-3401	57	58	92.67	47.33	10.3	27.8	11	11	24.99
80	QIL-4-3402	59	60	140.17	67.33	10.9	32.8	11	11	26.31
81	QIL-4-3405	59	61	107.25	61.25	8.8	22.6	10	4	26.61
82	QIL-4-3407	58	56	64.83	31.50	8.1	28.5	13	12	25.85
83	QIL-4-3413	59	60	134.67	80.50	9.5	32.8	14	11	25.25
84	QIL-4-3414	61	62	116.83	71.58	11.8	33.1	11	11	28.47
85	QIL-4-3417	61	62	88.75	42.50	14.1	31.9	11	29	25.63
86	QIL-4-3418	64	65	114.50	60.00	8.8	30.2	11	11	24.80
87	QIL-4-3419	53	55	147.50	68.00	10.0	30.5	10	17	24.79
88	QIL-4-3420	59	60	132.08	67.50	13.8	33.2	14	29	26.46
89	QIL-4-3421	56	58	136.50	69.00	11.0	34.9	12	16	25.80
90	QIL-4-3422	57	58	107.75	56.58	11.7	32.5	13	17	26.30
91	QIL-4-3423	62	65	110.67	59.17	7.9	29.5	11	9	25.02
92	QIL-4-3424	59	60	100.50	50.25	11.0	26.7	12	10	24.87
93	QIL-4-3426	59	60	107.33	59.17	6.9	26.8	7	5	25.91
94	QIL-4-3434	57	58	121.67	50.83	13.9	31.1	13	13	27.11
95	QIL-4-3445	58	59	121.17	71.00	11.9	31.5	13	9	24.46
96	QIL-4-3451	55	56	109.67	54.17	12.9	31.6	13	16	26.35
97	QIL-4-3452	56	57	138.67	67.50	11.1	33.0	13	11	25.00
98	QIL-4-3453	58	60	141.67	67.50	12.8	40.5	14	21	24.52
99	QIL-4-3455	57	58	178.33	94.17	15.3	41.4	14	26	23.98
100	QIL-4-3456	57	58	142.67	70.83	11.2	32.6	13	13	27.20
101	Check QIL-4-2192	60	60	112.17	54.17	10.3	31.5	10	15	23.71
102	Check QIL-4-2209	58	59	70.00	32.50	9.5	27.6	9	6	24.04
103	Check QIL-4-CLQ 40	57	58	100.83	51.83	10.0	33.7	11	17	28.00
104	Check HKI 193-1	55	58	98.50	61.50	11.8	23.7	11	11	21.21

Table 6. Per se performance (mean) of inbred lines at Karnal location

S. No.	Inbred line	DA	DS	PH	EH	CL	CG	NOR	NOK	GW (q/ha)
1	QIL-4-3279	52	54.5	121.5	57.5	14.9	38.5	11	21	26.05
2	QIL-4-3282	57.5	59.5	140.5	73.5	11.2	22.5	13	8	24.38
3	QIL-4-3286	51.5	54.5	121	71.5	9.3	28.5	11	10	26.78
4	QIL-4-3287	52	54.5	149	74.5	10.4	25.5	12	13	24.77
5	QIL-4-3288	57.5	59.5	126.5	73.5	12.1	32.8	11	13	29.28
6	QIL-4-3290	52	54.5	120.5	73.5	11.4	34.5	13	11	29.73
7	QIL-4-3294	50.5	53	119	59	11.5	31.5	10	8	23.62
8	QIL-4-3295	52.5	55.5	123	63.5	10.5	29.5	11	14	26.39
9	QIL-4-3296	59	61.5	133.5	71	10.4	14.5	10	14	24.39
10	QIL-4-3297	53	55.5	131	64	11.8	22.6	11	12	26.60
11	QIL-4-3298	52	54.5	141	74	12.4	27.7	12	7	25.44
12	QIL-4-3300	50.5	54.5	121.5	53.5	10.1	21.5	11	11	26.30
13	QIL-4-3301	49	51.5	111	59	9.8	19.5	11	12	28.28
14	QIL-4-3302	52	54.5	143	79.5	10.4	21.4	10	14	26.32
15	QIL-4-3303	50.5	54.5	151	83.5	11.4	18.4	11	12	20.69
16	QIL-4-3304	52	54.5	163.5	80.5	11.5	14.3	12	11	23.92
17	QIL-4-3306	50	53.5	141	64.5	12.2	24.8	12	16	28.44
18	QIL-4-3307	49	52	139	61.5	11.1	18.6	11	13	31.92
19	QIL-4-3310	50.5	54.5	151	71	12.6	27.3	9	10	24.61
20	QIL-4-3315	55.5	58.5	96.5	44	9.8	23.3	10	10	28.17
21	QIL-4-3317	51.5	55	106	53	11.9	37.3	11	11	28.53
22	QIL-4-3319	50.5	54.5	119	63.5	8.1	30.5	12	8	25.25
23	QIL-4-3320	52.5	55.5	96.5	52.5	9.0	29.5	10	9	26.10
24	QIL-4-3321	51.5	54.5	141	83.5	11.6	28.6	11	10	23.60
25	QIL-4-3322	51.5	53.5	141	74	11.1	31.5	12	11	28.84
26	QIL-4-3323	48	50.5	121	63.5	8.9	24.5	10	11	28.00
27	QIL-4-3324	48.5	51.5	120.5	67.5	10.8	33.6	12	10	28.34
28	QIL-4-3325	60	62.5	121.5	64	11.0	28.5	11	10	27.41
29	QIL-4-3326	50.5	54	121	69	9.7	23.3	11	11	23.12
30	QIL-4-3327	53.5	57.5	116.5	63.5	11.1	26.3	10	14	26.05
31	QIL-4-3328	50.5	52.5	142.5	63	10.6	32.3	10	7	23.43
32	QIL-4-3330	49.5	51.5	140	62	8.9	27.5	11	11	28.94
33	QIL-4-3333	51.5	54.5	112.5	59	10.7	28.8	12	11	21.40
34	QIL-4-3335	50.5	55	132.5	73	9.6	30.0	10	12	27.05
35	QIL-4-3336	51.5	55.5	141	77.5	8.9	26.3	11	9	23.56
36	QIL-4-3337	52.5	55.5	142.5	57.5	8.5	24.8	11	14	22.61
37	QIL-4-3339	52.5	56.5	146.5	72	12.7	24.5	11	12	18.63
38	QIL-4-3340	50.5	53.5	171	86.5	11.4	16.8	10	10	26.01

39	QIL-4-3342	53.5	57.5	169	66.5	14.3	18.0	11	15	24.23
40	QIL-4-3343	52.5	56.5	141	71	12.7	30.5	12	15	24.34
41	QIL-4-3344	50.5	53.5	140.5	66.5	13.3	35.3	11	13	28.78
42	QIL-4-3347	53.5	57.5	138.5	66	11.6	28.8	11	9	23.19
43	QIL-4-3348	53	56.5	124.5	54.5	10.6	54.8	10	11	29.26
44	QIL-4-3349	54	56.5	126.5	53.5	9.7	31.3	12	12	25.49
45	QIL-4-3352	50.5	52.5	117.5	46.5	11.9	34.3	11	13	26.91
46	QIL-4-3353	55.5	57	147	77	14.3	35.5	11	16	24.42
47	QIL-4-3357	51.5	54.5	127	67	11.8	32.8	10	13	22.98
48	QIL-4-3358	50.5	54.5	142.5	73.5	15.4	43.5	12	11	25.98
49	QIL-4-3359	52	54.5	127	68.5	9.6	23.4	10	7	28.13
50	QIL-4-3360	52.5	55.5	142	84	10.5	34.6	11	11	27.68
51	QIL-4-3361	55.5	58.5	152.5	73.5	11.0	37.5	12	11	23.48
52	QIL-4-3362	59.5	61.5	123.5	68	8.2	26.3	10	14	22.67
53	QIL-4-3363	57.5	60.5	124	66	11.0	26.7	12	15	30.60
54	QIL-4-3364	51.5	55	112.5	63	11.7	26.3	11	16	28.13
55	QIL-4-3365	48.5	52	121.5	69	13.5	31.0	11	15	22.25
56	QIL-4-3366	56.5	58	127	57.5	12.8	29.5	8	13	28.36
57	QIL-4-3367	50.5	53.5	162	82.5	10.0	32.5	11	12	24.17
58	QIL-4-3368	58.5	60.5	115	57	11.1	42.5	10	15	22.51
59	QIL-4-3369	57.5	59.5	130.5	48.5	11.3	35.5	12	14	23.16
60	QIL-4-3370	51.5	54.5	128.5	72.5	10.6	31.5	12	15	21.90
61	QIL-4-3371	52.5	54.5	112.5	61	11.3	31.5	12	11	22.61
62	QIL-4-3372	52.5	56.5	127	69	11.5	34.0	10	16	22.03
63	QIL-4-3373	51.5	54.5	112	52.5	10.0	31.5	10	10	22.69
64	QIL-4-3374	51.5	54.5	128	68	12.2	29.5	12	12	21.12
65	QIL-4-3375	51.5	54.5	117.5	67.5	13.6	33.5	10	15	22.49
66	QIL-4-3376	51.5	54	122	62.5	12.6	36.3	12	19	21.60
67	QIL-4-3377	57.5	60.5	122.5	68.5	12.8	32.3	12	10	27.81
68	QIL-4-3379	55.5	58.5	104.5	58.5	9.6	28.3	10	7	20.57
69	QIL-4-3381	53.5	56.5	114.5	73.5	10.0	33.1	12	8	23.66
70	QIL-4-3382	52.5	56	177.5	81	8.0	30.5	12	11	24.06
71	QIL-4-3384	51.5	55	153	78	11.5	28.3	11	13	24.42
72	QIL-4-3385	56.5	58	107.5	63	13.8	29.0	12	21	22.04
73	QIL-4-3386	58.5	60	91.5	49.5	9.2	20.5	10	13	20.54
74	QIL-4-3387	54.5	57.5	141.5	53	12.8	25.3	8	9	27.57
75	QIL-4-3388	51.5	53.5	126.5	62.5	9.3	33.4	12	11	28.63
76	QIL-4-3389	52.5	56	116.5	68	10.7	34.6	12	16	22.69
77	QIL-4-3390	51.5	55	115.5	56	12.8	33.6	11	10	24.94

78	QIL-4-3397	52.5	56	139	66	11.5	22.4	12	8	24.03
79	QIL-4-3401	50.5	55.5	145.5	50	10.7	42.3	12	11	25.23
80	QIL-4-3402	52.5	56.5	116.5	56.5	11.3	16.6	11	11	23.97
81	QIL-4-3405	57.5	60.5	116.5	59.5	11.4	31.5	11	7	27.32
82	QIL-4-3407	52.5	56.5	140	61.5	9.6	12.3	11	11	24.64
83	QIL-4-3413	52.5	56	154.5	91.5	13.7	39.5	12	11	21.90
84	QIL-4-3414	51.5	55.5	164.5	88	14.3	37.2	13	11	23.24
85	QIL-4-3417	50.5	54	129.5	57.5	8.8	34.8	12	24	21.87
86	QIL-4-3418	50.5	54.5	141	77.5	9.8	27.8	12	11	22.58
87	QIL-4-3419	51.5	55	147	68	10.8	28.5	11	13	22.50
88	QIL-4-3420	51.5	55.5	176	73	11.5	28.8	11	23	23.98
89	QIL-4-3421	52.5	56.5	139	68	12.8	32.3	11	17	25.98
90	QIL-4-3422	56.5	60	124.5	63	11.6	31.3	11	21	22.33
91	QIL-4-3423	55.5	57.5	141	69	11.2	31.4	12	11	23.82
92	QIL-4-3424	54.5	57.5	131.5	63.5	10.6	39.0	13	8	23.64
93	QIL-4-3426	54.5	57.5	150	63.5	13.8	41.3	10	7	26.66
94	QIL-4-3434	54.5	57	137.5	62.5	13.8	17.7	10	11	23.59
95	QIL-4-3445	58.5	60.5	129.5	63	9.6	32.3	10	8	22.66
96	QIL-4-3451	57.5	59.5	131	53	8.3	25.5	10	16	26.50
97	QIL-4-3452	56.5	59.5	122.5	62.5	11.3	32.8	13	11	22.88
98	QIL-4-3453	54.5	57.5	144	67.5	11.2	32.3	12	16	25.10
99	QIL-4-3455	53.5	56.5	122.5	67.5	13.0	33.5	12	18	21.58
100	QIL-4-3456	59.5	61.5	132.5	68	11.4	32.6	11	15	24.87
101	Check QIL-4-2192	58.5	60	63	10	9.2	26.9	10	15	24.12
102	Check QIL-4-2209	50.5	54.5	64	31	9.2	29.5	10	7	22.61
103	Check QIL-4-CLQ 40	51.5	55.5	69	32	10.6	28.6	12	15	30.33
104	Check HKI 193-1	53.5	57	96.5	61.5	10.3	24.3	11	11	23.49

At Karnal location, the genotypes QIL-4-3307 and QIL-4-3363 were highest performing with grain yield of 31.92 and 30.60 q/ha, respectively. Both the genotypes surpassed the check (CLQRCY 40) which showed grain yield of 30.33 q/ha. The minimum DA as well as DS were observed in genotype QIL-4-3323 with 48 and 51 days respectively. Regarding Plant height and ear height, the taller plants were in genotype QIL-4-3382 and QIL-4-3420 (177.5 cm and 176 cm) and considerable ear height was in genotypes QIL-4-3413 and QIL-4-3414 (91.5 cm and 88 cm). The observed maximum values for post-harvest traits (cob length and cob girth) were 15.4 cm (QIL-4-3358); 14.9 (QIL-4-3279) and 54.8 (QIL-4-3348); 43.5 (QIL-4-3358). The number of rows (14) were highest in genotypes QIL-4-3452, QIL-4-3424, QIL-4-3414, QIL-4-3290 and QIL-4-3282. The number of kernels were reported highest in genotype QIL-4-3417 (24) followed by QIL-4-3420 (23 kernels) and 21 kernels in genotypes QIL-4-3279, QIL-4-3422, QIL-4-3385 (Table 6).

Mean grain yield averaged across locations

Analysing the mean grain yield data across both the locations, the genotypes QIL-4-3288, QIL-4-3307, QIL-4-3290 recorded maximum mean grain yield of 31.29, 30.03, 29.23 q/ha, respectively followed by DMRQPM 106 (check) (29.17 q/ha). The genotypes G37 had lowest mean grain yield of 22.28 q/ha.

Variation for grain yield among DH inbred lines and backcross populations across locations

The DH lines QIL-4-3294, QIL-4-3288, QIL-4-3287, QIL-4-3282 and QIL-4-3279 recorded highest grain yield (33.33 q/ha, 33.30 q/ha, 32.63 q/ha, 29.78 q/ha and 29.56 q/ha) at E1 whereas maximum grain yield at location E2 was observed in genotypes QIL-4-3307, QIL-4-3290, QIL-4-3288, QIL-4-3348 and QIL-4-3330 with 31.92 q/ha, 29.73 q/ha, 29.28 q/ha, 29.26 q/ha and 28.94 q/ha respectively. The highest mean grain yield (31.29 q/ha and 30.03 q/ha) across both locations E1 and E2 was observed in DH line QIL-4-3288 and QIL-4-3307.

Among the lines derived from back cross populations, the maximum grain yield at E1 was observed in genotypes QIL-4-3388 and QIL-4-3375 (29.69 and 28.95 q/ha) followed by genotypes QIL-4-3314, QIL-4-3379, QIL-4-3361 (28.47, 28.40, 28.20 q/ha). At second location E2, only one genotype QIL-4-3363 recorded maximum average grain yield of 30.60 q/ha as compared to check DMRQPM 106 (check) (30.33 q/ha). The genotypes QIL-4-3388 and QIL-4-3366 also had considerable good yield of 28.63 and 28.36 q/ha, respectively.

Across both locations, the maximum mean grain yield was recorded by check (DMRQPM 106) (29.17 q/ha) closely followed by genotypes QIL-4-3388 (29.16 q/ha) and QIL-4-3363 (28.90 q/ha).

PCA and Box plot analysis

The first two principal components explained 51.4% of the total variance, with Dim1 and Dim2 accounting for 29.2% and 22.2%, respectively. The PCA biplot revealed a clear separation of studied traits along this axis. The blue points represent inbred lines, which are scattered around the origin. Along Dim1, observations extend more widely, suggesting greater variability captured by this component. Along Dim2, the spread is somewhat narrower but still meaningful. Some observations also appear as outliers at the extremes of the plot. The red arrows represent the observed traits and their loadings on the principal components: Variables such as PH, EH, NOK, CL, and NOR are oriented toward the positive side of Dim1, indicating strong positive contributions to this component and a tendency to be positively correlated with each other. In contrast, DS and DA showed strong positive association on Dim2. The angles between vectors indicated that PH, CL, EH, CG, NOK and GW were positively correlated with each other, while DS and DA were negatively correlated (Fig.1).

PCA differentiation between DHs and BC derived inbred lines

The PCA biplot distributed the 100 genotypes (named as 1-50 for DHs and 51-100 for BCs) and 4 checks into four quadrants based on the first two principal components (PC1 and PC2). Genotypes located in first quadrant (+PC1 and +PC2) differentiated into 6 DHs and 20 BC lines. There were 11 DHs and 15 BCs located in second quadrant (-PC1 and +PC2). Genotypes located in third quadrant (-PC1 and -PC2) were 17 DHs and 6 BC lines. Genotypes located in first quadrant (+PC1 and -PC2) were distributed as 16 DHs and 9 BC lines. This distribution clearly shows that quadrant 1 and 2 occupied majority of BCs derived inbred lines whereas quadrant 3 and 4 had mostly DHs in them. Quadrants 3 and 4 showed association towards traits like grain weight, number of rows and cob length. Quadrants 1 and 2 showed association with cob girth, number of kernels, ear height, plant height, days to 50% anthesis and days to 50% silking.

Principal components (Eigen value greater than one), Eigen values (Latent Root), per cent variability, cumulative per cent variability and component loading of different characters are presented in table 7. In the present study, the 5 principal components with Eigen values greater than one contributed 100 per cent towards the total variability. Therefore, it was inferred that the essential features of data set had been represented in the five principal components. The first principal component contributed maximum towards variability (29.22). The significant factors loaded in PC1 towards maximum genetic divergence were PH (plant height), CL (cob length), EH (ear height) and NOK (number of kernels). The second principal component (PC2) described 22.16 per cent of total variance and the characters viz. days to 50% silking and days to 50% tasseling contributed significant factor loadings. The third principal component (PC3) explained 12.70 per cent of total variance and the characters viz., NOK (number of kernels), PH (plant height) were the contributors for the maximum variance in this principal component (Table 8).

Table 7. Eigen values, proportion of the total variance represented by principal components, cumulative percent variance

	Eigenvalue	Percentage of variance	Cumulative percentage of variance
comp 1	2.630059806	29.22288673	29.22288673
comp 2	1.995150309	22.16833676	51.39122349
comp 3	1.143561691	12.70624102	64.09746451
comp 4	0.949057041	10.54507824	74.64254275
comp 5	0.89795915	9.977323885	84.61986663
comp 6	0.750815666	8.342396285	92.96226292
comp 7	0.366069476	4.067438617	97.02970153
comp 8	0.220852507	2.453916748	99.48361828
comp 9	0.046474355	0.51638172	100

Table 8. Component loading of different characters in maize inbred lines

	Dim.1	Dim.2	Dim.3	Dim.4	Dim.5
DA	0.310337	46.84905	0.07607	2.868294	0.007688
DS	0.299956	47.93439	0.165527	0.857573	0.003739
PH	23.07912	0.077593	20.36044	2.807965	0.007573
EH	21.4395	0.833085	21.10735	6.296644	0.130339
CL	22.80093	0.003006	5.026744	0.078711	0.509523
CG	6.582387	0.430126	9.697634	1.015346	56.26945
NOR	9.441713	0.006026	0.883539	15.40136	35.32785
NOK	16.03472	0.001841	26.3617	2.257525	2.436291
GW	0.011334	3.864878	16.321	68.41658	5.307548

Box plot

In a box plot, a wider box indicates greater variability in the middle 50% of the data. Longer whiskers indicate higher variability outside the middle 50%. The bold line represents the median. Box plot analysis revealed substantial overlap between the DHs and BC derived inbred lines for most observed traits, indicating their comparable overall performance. BC derived lines showed greater phenotypic variability for flowering time (DA and DS), plant height, ear height, cob girth, and kernel number in general, whereas DH lines showed a higher median grain yield. The larger dispersions showed that several cultivars showed themselves as outliers, as they are scattered as extreme values (Fig. 2A-2I).

Scree plot

The first principal component (PC1) accounts for approximately 29.2% of the total variance, followed by PC2 with 22.2%. Together, these two components explain over half of the dataset's variability (51.4%), indicating that a substantial amount of the underlying structure can be captured in a reduced two-dimensional space. The third principal component contributes an additional 12.7%, increasing the cumulative explained variance to approximately 64.1%. Beyond the third component, the contribution of each subsequent component declines steadily. The components before this point are generally considered significant, as they capture most of the data's variance (Fig. 3). PC4 and PC5 explain about 10.5% and 10.0% of the variance, respectively, while later components (PC6–PC9) each contribute less than 10%, with the final components accounting for only negligible proportions. The scree plot exhibits a noticeable inflation point around the third to fourth principal component. This pattern suggests that the first three to four components capture the most meaningful variance in the data, while additional components contribute relatively little information.

Mean performance in test cross hybrids

Among the 87 test crosses evaluated at location E1, hybrids QIL-4-3288 x LM 19 Q3-1 and QIL 4-3361 x LM 19 Q3-1 out yielded the check ADV-765 (Check) (91.3 q/ha), however genotypes QIL 4-3367 x LM 13 Q3, QIL 4-3370 x LM 13 Q3 and QIL-4-3347 x LM 13 Q3 showed

considerable good grain yield of 86.9, 83.8 and 83.2 q/ha respectively. At E2, hybrids QIL 4-3401 x LM 13 Q3 and QIL 4-3421 x LM 19 Q3-1 were among the best performing ones with grain yield of 153.4 and 148.3 q/ha respectively followed by QIL 4-3366 x LM 13 Q3 (145.7 q/ha), QIL-4-3322 x LM 13 Q3 (144.3 q/ha), QIL 4-3370 x LM 19 Q3-1 (142.6 q/ha) and QIL 4-3375 x LM 13 Q3 (142.6 q/ha). The greater values of grain yield at Karnal region owes to the climatic conditions as well as the clay loam soil texture.

Among DH, hybrids QIL-4-3288 x LM 19 Q3-1 and QIL-4-3347 x LM 13 Q3 among the top performing ones with grain yield of 92.7 and 83.2 q/ha at E1, whereas at E2, hybrids QIL-4-3322 x LM 13 Q3 and QIL-4-3300 x LM 13 Q3 outperformed with grain yield of 144.3 q/ha and 135.6 q/ha. Superior test-cross performance of some DH lines may be correlated with the proportion of donor parent genome and the parental combination used in the original crosses.

Among BC lines-based test crosses, at E1, hybrids QIL 4-3361 x LM 19 Q3-1 and QIL 4-3367 x LM 13 Q3 were best ones with 91.9 q/ha and 86.9 q/ha. At E2, the BC populations-based hybrids QIL 4-3401 x LM 13 Q3 and QIL 4-3421 x LM 19 Q3-1 were top performing with yield potential of 153.4 q/ha and 148.3 q/ha, respectively (Table 9).

Table 9. Mean grain yield (q/ha) of test cross populations under locations E1 and E2

S. No.	Nomination	Hybrid	Ludhiana (E1)	Karnal (E2)
1	H1	QIL-4-3279 x MB-109	56.7	73.6
2	H2	QIL-4-3279 x MB-122	56.7	82.5
3	H3	QIL-4-3282 x MB-109	57.9	59.6
4	H4	QIL-4-3282 x MB-122	58.7	74.4
5	H5	QIL-4-3286 x MB-109	50.8	64.3
6	H6	QIL-4-3286 x MB-122	70.2	76.6
7	H7	QIL-4-3287 x MB-109	74.3	119.8
8	H8	QIL-4-3287 x MB-122	72.7	110.6
9	H9	QIL-4-3288 x MB-109	92.7	109.4
10	H10	QIL-4-3288 x MB-122	61.5	109.8
11	H11	QIL-4-3290 x MB-109	68.0	107.7
12	H12	QIL-4-3290 x MB-122	60.4	108.6
13	H13	QIL-4-3294 x MB-109	78.7	91.4
14	H14	QIL-4-3294 x MB-122	75.4	107.4
15	H15	QIL-4-3295 x MB-109	52.2	116.3
16	H16	QIL-4-3295 x MB-122	74.4	102.5
17	H17	QIL-4-3296 x MB-109	66.0	119.8
18	H18	QIL-4-3296 x MB-122	65.4	121.5
19	H19	QIL-4-3297 x MB-109	67.9	131.4
20	H20	QIL-4-3297 x MB-122	62.9	107.3
21	H21	QIL-4-3298 x MB-109	60.8	94.3
22	H22	QIL-4-3298 x MB-122	81.8	116.9
23	H23	QIL-4-3300 x MB-109	69.7	65.3
24	H24	QIL-4-3300 x MB-122	73.1	135.6
25	H25	QIL-4-3301 x MB-109	61.8	133.9
26	H26	QIL-4-3301 x MB-122	78.0	103.2
27	H27	QIL-4-3302 x MB-109	63.7	112.6
28	H28	QIL-4-3302 x MB-122	55.0	116.8
29	H29	QIL-4-3303 x MB-122	76.5	118.5
30	H30	QIL-4-3304 x MB-109	68.4	114.9
31	H31	QIL-4-3304 x MB-122	70.3	126.5
32	H32	QIL-4-3306 x MB-122	71.1	109.3
33	H33	QIL-4-3310 x MB-122	63.1	133.0
34	H34	QIL-4-3319 x MB-109	69.5	99.0
35	H35	QIL-4-3319 x MB-122	70.1	99.4
36	H36	QIL-4-3320 x MB-109	46.9	98.5
37	H37	QIL-4-3321 x MB-122	83.1	112.9
38	H38	QIL-4-3322 x MB-122	64.4	144.3

39	H39	QIL-4-3323 x MB-109	80.5	127.1
40	H40	QIL-4-3324 x MB-122	57.7	104.0
41	H41	QIL-4-3325 x MB-109	39.7	100.2
42	H42	QIL-4-3325 x MB-122	57.4	88.9
43	H43	QIL-4-3326 x MB-109	49.2	88.9
44	H44	QIL-4-3326 x MB-122	60.8	91.4
45	H45	QIL-4-3328 x MB-109	60.5	106.1
46	H46	QIL-4-3333 x MB-109	63.8	102.8
47	H47	QIL-4-3335 x MB-109	55.4	105.7
48	H48	QIL-4-3342 x MB-109	61.0	102.6
49	H49	QIL-4-3342 x MB-122	51.8	118.8
50	H50	QIL-4-3343 x MB-122	59.3	76.2
51	H51	QIL-4-3344 x MB-109	49.7	76.5
52	H52	QIL-4-3344 x MB-122	48.2	102.5
53	H53	QIL-4-3347 x MB-109	63.7	103.7
54	H54	QIL-4-3347 x MB-122	83.2	117.5
55	H55	QIL-4-3348 x MB-109	47.3	47.0
56	H56	QIL 4-3361 x MB-109	91.9	73.1
57	H57	QIL 4-3361 x MB-122	79.5	75.8
58	H58	QIL 4-3363 x MB-109	66.7	87.8
59	H59	QIL 4-3363 x MB-122	59.3	102.4
60	H60	QIL 4-3366 x MB-109	80.0	87.9
61	H61	QIL 4-3366 x MB-122	76.7	145.7
62	H62	QIL 4-3367 x MB-109	64.6	73.6
63	H63	QIL 4-3367 x MB-122	86.9	103.8
64	H64	QIL 4-3370 x MB-109	80.1	142.6
65	H65	QIL 4-3370 x MB-122	83.8	94.7
66	H66	QIL 4-3375 x MB-109	69.0	94.0
67	H67	QIL 4-3375 x MB-122	77.0	142.6
68	H68	QIL 4-3376 x MB-109	73.2	120.1
69	H69	QIL 4-3376 x MB-122	45.9	107.4
70	H70	QIL 4-3390 x MB-109	72.8	122.4
71	H71	QIL 4-3390 x MB-122	71.3	102.1
72	H72	QIL 4-3401 x MB-109	61.8	70.0
73	H73	QIL 4-3401 x MB-122	69.7	153.4
74	H74	QIL 4-3402 x MB-109	76.5	100.6
75	H75	QIL 4-3402 x MB-122	56.9	79.9
76	H76	QIL 4-3407 x MB-109	82.1	97.5
77	H77	QIL 4-3407 x MB-122	53.3	94.2

78	H78	QIL 4-3419 x MB-109	81.6	62.3
79	H79	QIL 4-3419 x MB-122	73.3	103.0
80	H80	QIL 4-3421 x MB-109	66.9	148.3
81	H81	QIL 4-3421 x MB-122	64.3	103.4
82	H82	QIL 4-3422 x MB-109	53.8	55.9
83	H83	QIL 4-3422 x MB-122	45.9	78.0
84	H84	QIL 4-3423 x MB-109	52.1	56.5
85	H85	QIL 4-3423 x MB-122	65.6	108.4
86	H86	QIL 4-3424 x MB-109	45.8	102.0
87	H87	QIL 4-3424 x MB-122	61.3	53.8
88	H88	IQMH-202 (Check)	61.5	75.8
89	H89	IQMH-203 (Check)	47.9	107.0
90	H90	BIO-9544 (Check)	81.3	101.8
91	H91	ADV-765 (Check)	91.3	109.8

Considering the mean grain yield among both locations E1 and E2, hybrids QIL 4-3401 x LM 13 Q3, QIL 4-3370 x LM 19 Q3-1 and QIL 4-3366 x LM 13 Q3 were the highest yielders with 111.6 q/ha, 111.4 q/ha and 111.2 q/ha, respectively. All these three hybrids were derived from back cross derived populations. The parental inbred lines QIL-4-3401, QIL-4-3370 and QIL-4-3366 of these identified best test crosses showed grain yield of 25.11 q/ha, 22.97 q/ha and 28.23 q/ha in per se performance as compared to check DMRQPM 106 (29.17 q/ha). A wide variation in grain yield showed that superior as well as diverse inbred lines were used for making test crosses.

Discussion

The present study is exclusively based on a set of 100 doubled haploid and back cross derived inbred lines as the parental lines in maize. The novelty of the work lies in the assessment of comparative performance (grain yield and associated traits) of doubled haploid inbred lines to back cross derived inbred lines. Our research stands out differently at many points when it is compared to earlier literature cited. First and foremost, in majority of the past studies on evaluation of maize germplasm, researchers used either back crosses generated inbred lines or DHs or DHs derived from back cross populations. This is the first kind of study in which comparative evaluation of DH and BCs together were done.

The analysis of variance revealed highly significant differences which indicates the presence of substantial genetic variability within the germplasm used. Genetic diversity is the main prerequisite for any crop improvement programme as it generates chances for obtaining best performing cultivars. The significant environmental effects were also significant which indicate that the both testing locations differed considerably in their environmental conditions.

The significant variation for grain yield was observed between test crosses which shows the considerable genetic variation for hybrid performance. The genotype × environment interaction was also found to be significant which shows that performance of genotypes does vary according to prevailing environmental conditions. This also emphasizes the need of multilocation testing for any set of genotypes.

In line with the present study, Beyene et al., (2011) observed significant location, genotype and genotype x location effects for grain yield and anthesis-silking interval (ASI) in 75 doubled haploid maize testcrosses and six checks tested across four locations. They detected that, 15 DH testcross hybrids yielded equivalent to or more than the commercial check, WH505, averaged across four locations. Three hybrids yielded significantly higher than the best commercial check. Bordes et al., (2007) found that maize lines generated by the doubled haploid method from a broad-base population were as good as those produced by SSD methods for grain yield, kernel moisture, plant height, and ear height and leaf length. Mwangangi et al., (2026) stated that the top-performing hybrids yielded 7.4–8.2 t ha⁻¹, representing a 29%–79% advantage over commercial checks. The hybrids were derived from crossing 244 DH lines with six testers. Significant genetic variation was observed among genotypes, environments and their interactions.

The proportion of variance explained by PC1 (29.2%) and PC2 (22.2%) indicates that both these components effectively captured the major sources of variation. Similar levels of variation explained by the first two principal components have been reported in literature in maize germplasm studies. In a study conducted by Sneha et al. (2026), Dim 1 and Dim 2 contributed for 36.1 and 15.7 % variation in PCA biplot

created for 100 inbreds in maize. Principal Component Analysis (PCA) revealed the first three components accounted for 64% of the total variation with tassel length, plant height and leaf width were contributing highly to the variation. Suryanarayana et al., (2017) observed that the six principal components with Eigen values greater than one contributed 85.31 per cent towards the total variability in a research study using 30 genotypes in maize. The first principal component contributed maximum towards variability (39.65).

There was considerable overlapping between DH and BC derived inbred lines for most yield related traits in the box plot analysis. It strongly reflects that both breeding methods have comparable performance for the observed traits. Both sets can be used as the elite source for maize improvement. The BC derived lines showed greater variability for flowering traits (days to anthesis and days to silking), plant height, ear height, cob girth, and number of kernels. It implies that sufficient recombination and segregation took place as result of back cross methods. On the other hand, DH lines possessed a higher median grain yield which shows that double haploid method was proved to be useful in fixation of favourable alleles. The resultant homozygous lines produced as result of DH induction proved to be a useful breeding approach. Li et al., (2025) estimated dry matter (DM) accumulation and harvest index (HI) on 468 plots containing 263 maize hybrids. The DM and HI both are key factors that determine the final grain yield. The box plots were created using observed data. Each side of the box plot has a kernel density estimate to show the distribution shape of the data. Grain leaf ratios were also estimated using box plots.

Among the DH-derived test crosses, hybrid QIL-4-3288 × LM 19 Q3-1 and QIL-4-3347 × LM 13 Q3 were the highest yielding at E1, with grain yields of 92.7 and 83.2 q/ha, respectively. At E2, hybrid QIL-4-3322 × LM 13 Q3 exhibited the highest grain yield (144.3 q/ha), followed by QIL-4-3300 × LM 13 Q3 with 135.6 q/ha. This superior performance showed that the interaction between DH lines and testers contributed considerably in determining hybrid performance. Among the BC-derived test crosses, hybrid QIL 4-3361 × LM 19 Q3-1 and QIL 4-3367 × LM 13 Q3 were the top performers at E1 with grain yields of 91.9 and 86.9 q/ha. At E2, QIL 4-3401 × LM 13 Q3 and QIL 4-3421 × LM 19 Q3-1 recorded the highest grain yield of 153.4 and 148.3 q/ha. At E2, the BC-derived hybrids outperformed the highest-yielding DH-derived hybrids which implies that backcross-derived lines had more favourable donor alleles while recovering the recurrent parent genome.

Beyene et al., (2011) indicated that maize testcrosses developed from DH lines produced high grain yield and as acceptable agronomic traits as the commercial hybrids developed through conventional pedigree methods. Ogugo et al., (2015) derived the six DH populations from BC₁. these DH lines were 97 % genetically pure, with ~2 % heterogeneity. Donor parent introgression up to 32 % showed significant positive correlation with grain yield under drought and optimum environments. The plants in the BC₁ generation are heterozygous than expected for randomly drawn BC plants. They also possess a higher proportion of the donor genome, which shifts their distribution in the direction of F₂-derived progeny. For this reason, DH populations were generated from BC₁ lines. Seitz (2005) compared testcross performance of DH lines with conventionally derived lines, and found substantial variation. Wilde et al., (2010) found that mean testcross performance of the three DH-line groups developed from three European landraces did not differ significantly from the average testcross performance of their parental landraces, but yielded 22-26% lower than that of present elite flint lines. In present study, based on the mean grain yield across both environments (E1 and E2), hybrids QIL 4-3401 × LM 13 Q3, QIL 4-3370 × LM 19 Q3-1, and QIL 4-3366 × LM 13 Q3 emerged as the top-performing test crosses, with mean grain yields of 111.6, 111.4, and 111.2 q/ha, respectively. Notably, all three superior hybrids were derived from backcross (BC)-derived populations, which shows the effectiveness of the BC breeding approach in generating elite parental lines with high hybrid performance.

Efficient production of maize DH lines through the in vivo method provided breeders with a tool to produce pure lines within one to two generations and an increase in genetic advance per unit of time at the level of hybrid development. DH technology provides the opportunity to shorten the time required for the development of homozygous lines and to increase the genetic gain per unit of time. Combined analysis of variance showed that all sources of variations were significant in per se performance among inbred lines. This study first underlines the magnitude of the first two principal components which explained 51.4% (almost half) of the total variance. From the analysis of range, it can be concluded that traits such as plant height, ear height, and cob girth exhibit high variability, indicating strong potential for selection and genetic improvement. Traits like days to anthesis, days to silking, and number of rows show low variability, suggesting stability among genotypes. Meanwhile, cob length, number of kernels, and grain weight display moderate variability and offer some scope for improvement. Cob girth also provides good potential for selection in breeding programs. Our results indicated that performance of hybrids as well as different environments and G × E were also statistically significantly different. Maize testcrosses developed from Back cross based lines produced higher grain yield. For Back crossed based lines, expected PGC with Mendelian inheritance is 75 % for the recurrent parent and 25 % for the donor parent. However, newly developed cultivars need to be tested over more locations for several years to determine the performance and adaptability of the cultivar before commercial release. In general, DH based test crosses also performed well and we may diversify the parental material used for developing DH lines so that more and more diverse lines can be developed in fast manner and high yielding heterotic hybrids may be released for commercial cultivation for increasing maize production and productivity.

Declarations

Funding and Competing interests

No funding was received for conducting this study. The authors declare that there are no conflicts of interest in this submission.

Author Contribution

RK, CGK, AKD, SR and HS Jat contributed to the study conception and design. Material preparation, data collection and analysis were performed by YK, SK, RK Khulbe, PS. The first draft of the manuscript was written by RK and all authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

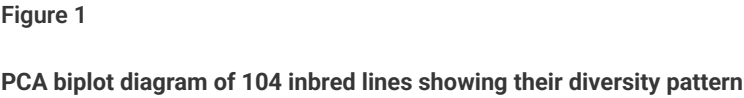
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References

1. Beyene, Y., Mugo, S., Mutinda, C., Tefera, T., Karaya, H., Ajanga, S., Shuma, J., Tende, R. & Kega, V. (2011). Genotype by environment interactions and yield stability of stem borer resistant maize hybrids in Kenya. *African Journal of Biotechnology*, 10, 4752–4758.
2. Bordes, J., Charmet, G., Dumas de Vaulx, R., Pollacsek, M., Beckert, M., Gallais, A. & Lapierre, A. (2007). Doubled-haploid versus single-seed descent and S1-family variation for testcross performance in a maize population. *Euphytica*, 154, 41–51.
3. Bouchez, A. & Gallais, A. (2000). Efficiency of the use of doubled-haploids in recurrent selection for combining ability. *Crop Science*, 40, 23–29.
4. Briggs, F. N. & Knowles, P. F. (1967). *Introduction to Plant Breeding*. Reinhold Publishing Corporation, USA, New York, pp. 236–272.
5. Chaikam, V., Molenaar, W., Melchinger, A. E. & Boddupalli, P. M. (2019). Doubled haploid technology for line development in maize: technical advances and prospects. *Theoretical and Applied Genetics*, 132(12), 3227–3243.
6. Duvick, D. N. (2001). Biotechnology in the 1930s: the development of hybrid maize. *Nature Reviews Genetics*, 2, 69–74.
7. Eagles, H. A., Hardacre, A. K. & Bansal, R. K. (1989). Testcross performance of maize lines from backcross populations containing highland Mexican or highland Peruvian germplasm. *Euphytica*, 41, 263–272.
8. Geiger, H. H. & Gordillo, G. A. (2009). Doubled haploids in hybrid maize breeding. *Maydica*, 54, 485–499.
9. Gordillo, G. A. & Geiger, H. H. (2008). Optimization of DH-line based recurrent selection procedures in maize under a restricted annual loss of genetic variance. *Euphytica*, 161, 141–154.
10. Kumar, P., Choudhary, M., Sheoran, S., Longmei, N., Kumar, B., Jat, B. S., Dagla, M. C., Bhushan, B., Aggarwal, S. K., Bagaria, P. K. & Sharma, A. (2024). Teosinte-derived advanced backcross population harbors genomic regions for grain yield attributing traits in maize. *International Journal of Molecular Sciences*, 25(19), 10300.
11. Li, R., Zhang, G., Xie, R., Hou, P., Ming, B., Xue, J., Wang, K. & Li, S. (2025). Dynamics of high-yielding maize genotypes under intensive management across multiple environments. *European Journal of Agronomy*, 162, 127368.
12. Mendiburu, F. & Simon, R. (2009). Agricolae - a free statistical toolbox for agricultural experiments. *15th Triennial Symposium of the International Society for Tropical Root Crops*, Lima, Peru, Nov. 2–6, 2009.
13. Mwangangi, W., Gowda, M. & Amadu, M. K. (2026). Yield Performance, Combining Ability and Stability of Early- to Medium-Maturing Doubled-Haploid Maize Lines in Eastern Africa. *Plant Breeding*, 1–16.
14. Ogugo, V., Semagn, K. & Beyene, Y. (2015). Parental genome contribution in maize DH lines derived from six backcross populations using genotyping by sequencing. *Euphytica*, 202, 129–139.
15. Prigge, V. & Melchinger, A. E. (2012). Production of haploids and doubled haploids in maize. In: Loyola-Vargas, V. M. & Ochoa-Alejo, N. (eds), *Plant Cell Culture Protocols*. Springer, New Jersey, pp. 161–172.
16. Rao, C. R. (1952). *Advanced Statistical Methods in Biometrical Research*. John Wiley and Sons Inc.
17. Rousseeuw, P. J., Ruts, I. & Tukey, J. W. (1999). The bagplot: a bivariate boxplot. *The American Statistician*, 53(4), 382–387.
18. Seitz, G. (2005). The use of doubled haploids in corn breeding. *41st Annual Illinois Corn Breeders' School*, Univ Illinois Urbana-Champaign.
19. Sneha, S., Sathya Sheela, K. R. V., Ravi Kesavan, R., Selvakumar, T., Babu Rajendra Prasad, V., Siva Kumar, S., Kumari Vinothana, N. & Deepika, V. (2026). Identification of maize inbreds for hybridization using agro-morphological traits and SSR markers through clustering and population structure analysis. *Molecular Biology Reports*, 53, 632.

- ## Figures



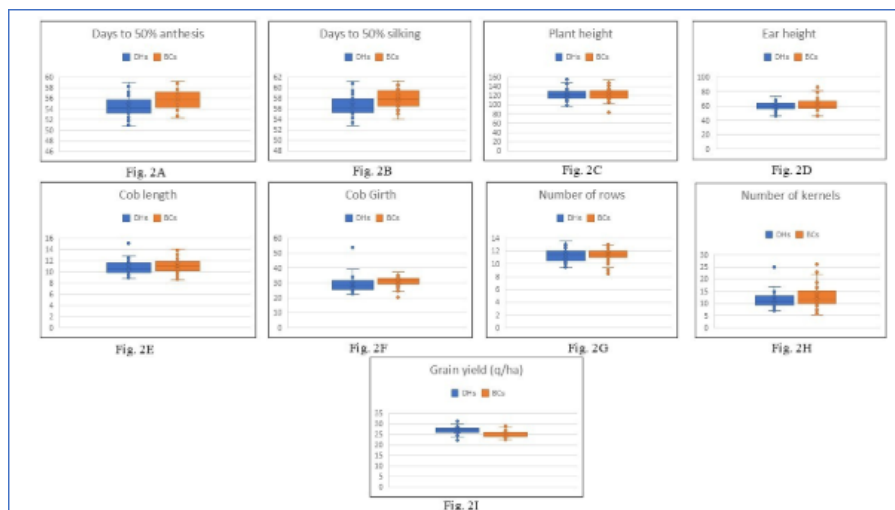


Figure 2

2A-2I. Box plots of all recorded traits for 100 inbred lines

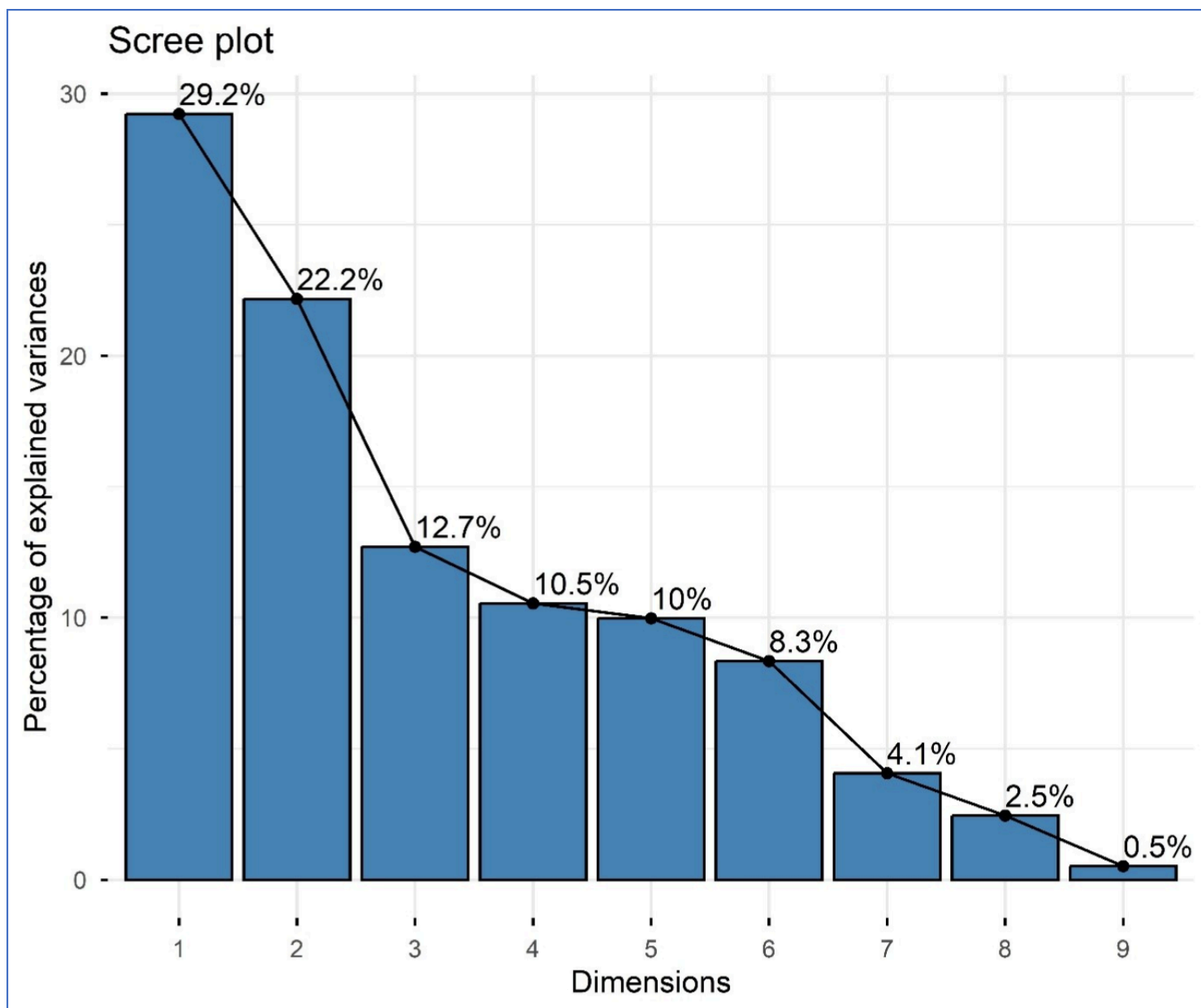


Figure 3

Scree plot diagram of principal components plotted against eigen value

