



Article Estimation of Heterosis and the Combining Ability Effect for Yield and Its Attributes in Field Pea (*Pisum sativum* L.) Using PCA and GGE Biplots

Amit Sharma¹, Rajesh Yadav¹, Ravika Sheoran¹, Deepak Kaushik¹¹⁰, Tapan Kumar Mohanta², Kartik Sharma³, Alpa Yadav⁴, Parmdeep Singh Dhanda⁵ and Prashant Kaushik^{6,*0}

- ¹ Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar 125004, Haryana, India
- ² Natural and Medical Sciences Research Center, University of Nizwa, Nizwa 611, Oman
- ³ Department of Agronomy, Punjab Agricultural University, Ludhiana 141004, Punjab, India
- ⁴ Department of Botany, Indra Gandhi University, Rewari 122502, Meerpur, India
- ⁵ Department of Biochemistry, Punjab Agricultural University, Ludhiana 141004, Punjab, India
- ⁶ Instituto de Conservación y Mejora de la Agrodiversidad Valenciana, Universitat Politècnica de València, 46022 Valencia, Spain
- * Correspondence: prakau@doctor.upv.es

Abstract: Field pea (Pisum sativum L.) is a highly nutritious winter-season pulse crop. It is used as food, feed, and fodder and offers nutritional security to low-income people in developing countries. Different graphical approaches like Principal Component Analysis (PCA) and Genotype + Genotype \times Environment (GGE) biplots were used along with the conventional line \times tester to identify efficient parents, combining ability effects and distinct heterotic groups in field pea (Pisum sativum L.). The study used a line tester design (9 \times 3) for seed yield and its associated traits. In the conventional analysis, lines Aman and HFP 715 and the tester GP02/1108, as well as crosses HFP 715 \times GP02/1108, Aman \times GP02/1108, and Pant P-243 \times HFP 1426 showed the best GCA (General Combining Ability) and SCA (Specific Combining Ability) effects, respectively, for seed yield and its attributes. The σ^2 SCA > σ^2 GCA, and σ^2 D > σ^2 A in almost all the traits indicated control of non-additive gene effects. High manifestations of heterobeltiosis for seed yield were evidenced by the superiority of 24 out of 27 crosses over the better parent. The highest significant heterobeltiosis was observed in the cross HFP 715 × GP02/1108, followed by IPF 14-16 × GP02/1108, IPF 14-16 × HFP 1426, DDR-23 × HFP 1426, DDR-23 \times GP02/1108, and Aman \times GP02/1108 for yield and its attributes. The biplot techniques were used to analyze data and compare their results with conventional line \times tester analysis. Overall, graphical analysis results were very similar to those of traditional analysis. Consequently, it can surely be assumed that these methods could be helpful in presenting data from field pea breeding experiments carried out with line \times tester design.

Keywords: biplots; heterobeltiosis; GCA; non-additive; Pisum sativum L.; SCA; seed yield

1. Introduction

Field pea (*Pisum sativum* L., Family Leguminosae, subfamily Papilionoideae, and tribe Fabaceae) is the world's second-most crucial food legume and a major pulse crop in the winter season. It is diploid (2n = 14), predominantly self-pollinated, and is considered to be native to the Near East and Mediterranean [1]. It is one of the oldest cultivated pulse crops, first appearing in the Mediterranean between 7000 and 6000 BC and continuing to be grown today [2]. It is an important economic and nutritional crop that is commonly referred to as "poor man's meat" due to its high protein (25.10%), fiber (13.40%), vitamin and mineral content, and prebiotic carbohydrate (61.80%) content while being affordable to lower-income consumers [3]. Additionally, it significantly impacts the control of Type



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Copyright: © 2023 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). 2 diabetes, body weight, blood cholesterol, cardiovascular health, and gastrointestinal function. So, high yield is one of the main breeding goals in field pea (*Pisum sativum* L.). Besides, these play a vital role in sustainable agriculture and soil health improvement via fixing atmospheric nitrogen through symbiosis, making them valuable in terms of both economics and nutrition [4]. Field pea, in particular, is naturally high in iron and zinc and hence has the potential to address two of the world's most common micronutrient deficiencies [5]. Despite the potential for increased consumption of field peas to help alleviate hidden hunger, more progress has yet to be achieved in increasing production, and yields have lagged behind those of cereals [5]. In India, the situation is grimmer, and its productivity lags far behind that of other countries like Canada, Russia, Australia, China, France, etc. Hence, there is enough scope for the enhancement of the production and productivity of field peas in India.

Seed yield in field peas is a multiplex quantitative trait influenced by many other morphological and physiological traits. Although many high-yielding field pea varieties have been developed over the past 2-3 decades, they needed help to overcome the hurdles in production improvement due to their vulnerability to biotic and abiotic stresses [6,7]. The environment plays a vital role in crop production by interacting with genetic architecture. In pure lines, hybrids, synthetics, or any other material used for breeding, genotypic and environmental interactions are typically present under all circumstances, complicating the breeding work and forbidding the progress of crop improvement programs. For example, selecting a good general combiner in a single or multilocation environment helps in the production of hybrids that perform better under different $G \times E$ interaction. Despite rigorous research efforts, stagnancy in productivity has been observed in the last few decades. This happened mainly because of the continued use of existing varieties and a few selected genotypes as parents in the hybridization program. Further, due to continuous selection pressure for specific traits like yield, the varieties have become more vulnerable to biotic and abiotic stresses, which has jeopardized their potential for long-term sustained genetic improvement.

Since Gregor Mendel's pioneering work in the nineteenth century, pea genomics has received much research [8]. Recombinant breeding is the most successful approach to increasing the productivity of self-pollinated crops like field pea. From a genetic standpoint, the most crucial step in the hybridization program is the selection of superior genotypes to produce new genotypes with desirable characteristics [9]. A high-performance genotype may not inevitably create better hybrids and transgressive segregants when employed in hybridization. Different types of breeding designs, like diallel, test crosses, bi-parental, line \times tester, and multiple crosses, are used to evaluate breeding material [10]. The primary goal of these designs is to assess the GCA and SCA impacts on parental lines, the SCA and heterosis of crossings, and the heredity of the traits [11]. Line tester analysis ($l \times t$), a modified version of the top cross design, is usually used for determining combining ability (GCA and SCA), identifying parental lines based on hybrid performance, and estimating various sorts of gene activities [12]. The $l \times t$ design has been used earlier to study field pea yield and agronomic traits [13–15]. However, breeders look for alternatives to conventional methods to make results more comprehensive and easily interpretable with enhanced visual quality. Nowadays, graphical methods are gaining importance in expressing the outcome of crop breeding experiments. Among the various graphical methods, mainly principal component analysis (PCA), and genotype + genotype \times environment (GGE) biplot analysis are being used to exhibit the combining abilities of parents and crosses in other crops. However, no such depiction was observed in the field pea. Keeping the above aspects in mind, the present study was planned to estimate combining ability effects, gene action, and heterobeltiosis using $l \times t$ for yield and its attributes and to compare GGE and PCA biplots to visualize them. The information gathered will be helpful for developing hybrid field peas with high seed yields. With this analysis, breeders can choose which inbreds are to be combined to achieve better hybrid performance if they have a better grasp of the pattern of combining ability in this germplasm.

2. Materials and Methods

2.1. Experimental Material, Design, Layout, and Experimental Site (Geography and Climate)

Nine female lines (Pant P-243, DDR-23, HFP 715, IPF 14-13, IPF 14-16, RFP 2009-2 Pant P-200, RFPG 79, Aman) and three male testers (HFP 1545, HFP 1426, GP02/1108) were crossed in line \times tester (l \times t) fashion to generate 27 crosses of field pea during rabi 2019-20 at Pulses Research Area, Department of Genetics and Plant Breeding, CCS, Haryana Agricultural University, Hisar. All these were sown in a randomized block design with three replications. Each genotype was planted in a single row of 4m length with 45 \times 10 cm spacing. All the recommended agronomic practices were adopted to raise a good crop. The brief characteristics of the lines and testers used in the study are described in Table 1.

Table 1. Salient features of the lines and testers used.

Genotype	Salient Features
Lines	
Pant P-243	Tall, early, rust tolerant
HFP 715	Dwarf, early maturity Dwarf, early maturity, high yielding, leaflet less and powdery mildew Resistant
IPF 14-13	Medium tall, rust resistant, late flowering and maturity
IPF 14-16	Tall, rust resistant and high yielding
RFP 2009-2	Dwarf, rust and PM resistance, early flowering and maturity
Pant P-200	Dwarf, rust and powdery mildew resistant
RFPG 79	More number of primary, and secondary branches and, Ascochyta blight and powdery mildew resistant
Aman	Tall tendril type, late maturing, and high yielding
Testers	
HFP 1545	Dwarf, early flowering, high yielding
HFP 1426	Late maturity, more number of pods and, high yielding
GP02/1108	Dwarf with short inter-nodal length, more nodes, and pods, small pods, blue green foliage with pinkish flowers, poor seed yield, and quality

The experimental site was situated at 29.10° N latitude and 75.46° E longitude, at an elevation of 215.2 m above mean sea level. Extreme high and low temperatures, dryness, and scanty rainfalls characterized the sea level. It lies on the outer margin of the southwest (SW) monsoon region and has a tropical dry climate. The mean weekly weather parameters during Rabi 2019–2020 are depicted in Figure 1. The meteorological conditions (temperature and rainfall) that prevailed during the growing season were recorded as per the procedure given by Khichar and Niwas, 2013.

2.2. Data Collection and Statistical Analysis

Data on days to flowering and maturity, a number of primary and secondary branches per plant, nodes per plant, the height of the first pod, plant height, pods per plant, seeds per pod, test weight (100-seed weight), biological and seed yield per plant, and harvest index were recorded from five randomly selected plants except for days to maturity and flowering, where observations were taken on a plot basis. Data were analyzed using the computer program Windowstat 8.0 (INDOSTAT Services Limited, Hyderabad). The combining ability effects (GCA and SCA) were done as per Kempthorene [12], Arunachalam [16], $(\sigma^2 \text{gca}/\sigma^2 \text{sca})$ and $(\sigma^2 D/\sigma^2 A)^{-1/2}$ ratios, which were used to rate the relative weight of additive versus the non-additive type of gene actions [17]. Heterosis was estimated from mean values, and its significance was be tested using a t-test. PCA biplots were created using the R studio BiplotGUI program [18] using numerical findings from the traditional $1 \times t$ analysis. Data was transformed using the center and scale transformations, and biplots for parents and crosses were constructed independently. Similarly, GGE biplots were created using the GGEBiplotGUI program in R statistical software [19].



Figure 1. Comparison of weather parameters across two years. Max = maximum temperature; Min = minimum temperature; $^{\circ}C = degree$ Celsius; mm = millimeter.

3. Results

3.1. Line \times Tester Analysis

3.1.1. ANOVA for Line \times Tester Analysis

The perusal of ANOVA (Table 2) revealed that the mean squares due to lines were highly significant for all the traits, with the number of primary branches per plant as an exception. At the same time, the tester showed a significant mean square for all characters except secondary branches per plant, nodes per plant, pods per plant, and harvest index. The parents contributions to these characteristics' GCA variance components were strongly shown by the mean squares owing to lines and testers, and the absence of a substantial variance for a few traits suggested minimal variability among the testers for these characters.

As it was observed that proportional contributions of total variance due to the line were significant and higher in magnitude than the tester for most of the yield-contributing traits, it could be inferred that more significant variability is present among the lines for these characters. Considerable variation owing to line tester interaction was seen for all features except days to maturity, number of primary branches per plant, and number of seeds per pod, indicating a significant contribution of F1 to SCA components. A comparison of mean squares owing to parent vs. hybrid plants revealed the presence of overall heterosis for all characteristics except the number of nodes per plant. Subdividing the treatment variance into parents' crosses and parents versus crosses revealed significant mean squares for all characters attributable to parents and crosses, while highly substantial mean squares due to parent vs. cross were revealed for all the characters except the number of nodes

per plant, exhibiting thereby the existence of a sufficient magnitude of heterosis for the character under study.

3.1.2. General Combining Ability (GCA) Effects of Parents

It was revealed that (Table 3) the lines DDR-23, RFP 2009-2, and Pant P-200 were superior in early flowering, as indicated by their highly significant and negative general combining ability (GCA) effects. In addition, for days to maturity, similar effects of GCA were shown by parents, viz., DDR-23, HFP 715, and RFP 2009-2. Based on their highly significant and positive GCA effects, the lines HFP 715, RFPG 79, and DDR-23 were found to be the best combiners for several primary branches per plant; RFPG 79 and Aman for several secondary branches per plant; DDR-23, HFP 715 and RFPG for several nodes per plant; Pant P-243, IPF 14-13, IPF 14-16, RFPG 79 and Aman for the height of first pod; DDR-23, HFP 715, RFP 2009-2 and Pant P-200 for plant height; HFP 715, IPF 14-13, IPF 14-16 and Pant P-200 for 100-seed weight; HFP 715, IPF 14-16 and RFPG 79 for several pods per plant; HFP 715 and RFP 2009-2 for seeds per pod; IPF 14-16, RFPG 79 and Aman for biological yield; HFP 715, IPF 14-16 and Aman for seed yield per plant; DDR-23 and HFP 715 for harvest index. Among the testers, HFP 1545 was identified as a good general combiner for days to 50% flowering, plant height, and the number of seeds per plant; HFP 1426 for the height of the first pod; and GP02/1108 for almost all traits except the height of the first pod, plant height, harvest index, and a number of seeds per pod.

3.1.3. Specific Combining Ability (SCA) Effects of Crosses

Table 4 accounts for the specific combining ability (SCA) effects of 27 different crosscombinations. Based on it, the cross combinations viz., Aman \times GP02/1108, P-243 \times HFP 1426, HFP 715 \times GP02/1108, and RFP 2009-02 \times HFP 1545 had the best SCA effects for seed yield per plant.

Likewise, cross HFP 715 × HFP 1426 for both early flowering and early maturity; IPF 14-16 × GP02/1108, RFPG 79 × HFP 1426 and HFP 715 × GP02/1108 for a number of primary branches per plant; Aman × GP02/1108 for of secondary branches per plant; HFP 715 × GP02/1108 and RFPG 79 × GP02/1108 for a number of nodes per plant; IPF14-16 × HFP1426 for the height of the first pod; Pant P-200 × GP02/1108, Aman × HFP 1426, HFP 715 × HFP 1545, RFPG 79 × GP02/1108, IPF 14-13 × HFP 1426 and Pant P-243 × HFP 1426 for 100-seed weight; RFPG 79 × HFP 1545, HFP 715 × GP02/1108 and Aman × GP02/1108 for a number of pods per plant, HFP 715 × HFP 1426, RFPG 79 × HFP 1545, Aman × GP02/1108 and Pant P-243 × GP02/1108 for a number of pods per plant, HFP 715 × HFP 1426, RFPG 79 × HFP 1545, Aman × GP02/1108, RFP 2009-02 × HFP 1545 and DDR 23 × HFP 1426 for biological yield per plant, RFP 2009-02 × GP02/1108, Pant P 243 × HFP 1426 and Pant P 200 × HFP 1426 for harvest index had best SCA effects. Where none of the crosses are for dwarf plant height. Based on overall performance, the cross combinations viz., Aman × GP02/1108 and HFP 715 × HFP 1545 were found to be good specific combiners for most yield-attributing traits.

A perusal of Table 5 revealed that the ratio of $(\sigma^2 SCA / \sigma^2 GCA)$ was greater than unity for almost all the traits except the number of nodes per plant. Similarly, the degree of dominance $(\sigma^2 D / \sigma^2 A)^{-1/2}$ was greater than unity for most of the traits with the exception of secondary branches per plant and days to maturity, indicating control of non-additive gene effects and the predominant role of dominance gene action. Table 6 shows lines, testers, and crosses possessing good GCA and SCA effects for different traits.

Characters	d.f.	DF	DM	NPB	NSB	NN	Ht. of the First Pod	PH	100-SW	NPP	NSP	BY	SYP	HI
Rep.	2	0.18	11.61 **	0.60 **	0.34	13.20 **	138.64 **	96.44	0.91 *	1.56	0.22	1.482	3.309	20.07
Treat.	38	30.29 **	20.95 **	0.25 **	1.34 **	4.52 **	373.81 **	1978.30 **	4.17 **	99.70 **	0.77 **	183.41 **	46.43 **	105.03 **
i. Parents	11	39.04 **	27.35 **	0.20 *	1.36 **	6.48 **	367.91 **	1688.45 **	5.91 **	82.86 **	0.94 **	206.40 **	20.46 **	88.16 **
ii.Crosses	26	25.47 **	18.87 **	0.20 **	1.22 **	3.80 **	368.94 **	1993.49 **	2.84 **	89.14 **	0.65 **	114.72 **	23.83 **	61.34 **
ii.a. due to lines	8	38.37 **	29.85 **	0.11	1.58 **	7.59 **	318.62 **	1528.08 **	5.53 **	82.83 **	0.80 **	214.11 **	19.32 **	104.76 **
ii.b. due to tester	2	53.44 **	31.44 **	0.64 **	0.28	0.44	91.00 **	114.11 *	9.28 **	18.32	1.90 **	100.24 **	23.72 **	10.98
iii.c. line \times tester	1	15.56 **	1.33	0.44	1.81 *	9.60 *	1316.00 **	6120.08 **	2.16 *	212.24 **	0.11	356.98 **	23.07 *	109.67 **
Parents vs. crosses	1	59.59 **	4.65 *	2.02 **	4.06 **	1.73	565.25 **	4771.44 **	19.50 **	559.41 **	2.16 **	1716.71 **	919.7 **	1426.39 **
Error	76	0.26	0.69	0.73	0.17	1.14	11.72	36.33	0.2	10.46	0.1	7.6	1.98	8.47

Table 2. Analysis of variance for combining ability in field pea.

*, ** significant at 5% and 1%, respectively, of DF: Days to 50% flowering; DM: Days to maturity; NPB: Number of primary branches per plant; NSB: Number of secondary branches per plant; NN: Number of nodes per plant; Ht. of the first pod: height; Height of the first pod; PH: Plant height; 100-SW: 100-seed weight; NPP: Number of pods per plant; NSP: Number of seeds per pod; BY: Biological yield per plant; SYP: Seed yield per plant; HI: Harvest index.

Table 3. GCA effects of lines and testers for different char	acters in field pea.
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Characters	DF	DM	NPB	NSB	NN	Ht. of the First Pod	РН	100-SW	NPP	NSP	BY	SYP	HI
Lines													
Pant P-243	0.185	-0.568	-0.146	-0.081	0.198	6.654 **	13.914 **	-0.381 *	-1.965	-0.244 *	0.738	-0.862	-4.069 **
DDR-23	-2.148 **	-2.457 **	0.188 *	0.096	1.420 **	-12.457 **	-29.086 **	-1.627 **	-6.832 **	0.044	-2.637 **	0.564	6.472 **
HFP 715	1.185 **	-1.123 **	0.268 **	-0.593 **	1.425 **	-12.235 **	-30.642 **	0.707 **	3.299 *	0.422 **	-4.057 **	2.540 **	2.772 **
IPF 14-13	0.852 **	1.543 **	-0.127	-0.348 *	-0.247	7.654 **	23.691 **	0.502 **	-0.432	-0.200	1.076	-0.795	-4.287
IPF 14-16	-0.259	0.099	-0.262 **	0.141	-1.420 **	8.654 **	17.914 **	0.529 **	3.546 **	0.067	7.368 **	2.509 **	-3.054
RFP 2009-2	-1.926 **	-1.457 **	-0.252 **	-0.348 *	-0.869*	-10.012 **	-25.198 **	0.086	-3.632 **	0.267 *	-7.684 **	-4.907 **	1.868
Pant P-200	-1.481 **	-0.123	-0.101	-0.123	-0.958 *	-10.457 **	-24.309 **	0.325 *	-4.810 **	0.111	-4.804 **	-3.925 **	1.468
RFPG 79	0.407 *	1.210 *	0.254 **	0.785 **	0.953 *	10.654 **	27.136 **	0.034	9.879 **	-0.467 **	2.391 *	0.590	-1.964 *
Aman	3.185 **	2.877 **	0.165	0.474 **	-0.491	11.543 **	26.580 **	-0.175	1.146	0.000	7.609 **	4.166 **	0.793
Testers													
HFP 1545	-0.222 *	-0.309	-0.560	-0.111	-0.351	-2.309 **	-5.605 **	-0.025	-0.973	0.207 *	-0.357	0.010	0.461
HFP 1426	2.444 **	2.358 **	-0.057	-0.311 **	-0.188	2.951 **	2.691 *	-0.395 **	-1.884 *	0.148 *	-2.407 **	-1.053 **	0.145
GP02/1108	-2.222 **	-2.049 **	0.615 **	0.422 **	0.538 *	-0.642	2.914 *	0.420 **	2.857 **	-0.356 **	2.763 **	1.043 **	-0.605

*, ** significant at 5% and 1%, respectively, DF: Days to 50% flowering; DM: Days to maturity; NPB: Number of primary branches per plant; NSB: Number of secondary branches per plant; NN: Number of nodes per plant; Ht. of the first pod: height; Height of the first pod; PH: Plant height; 100-SW: 100-seed weight; NPP: Number of pods per plant; NSP: Number of seeds per pod; BY: Biological yield per plant; SYP: Seed yield per plant; HI: Harvest index.

	Table 4. 5	CA effects of	different cro	sses for diffe	erent charact	ers in neid pea	1.						
Characters Crosses	DF	DM	NPB	NSB	NN	Ht. of the First Pod	РН	100-SW	NPP	NSP	ВҮ	SYP	HI
Pant P-243 × HFP 1545	-0.667 *	0.420	-0.062	-0.133	-0.649	-1.580	-5.506	0.170	-2.96	-0.541 **	-0.250	-0.268	-0.459
Pant P-243 \times HFP 1426	0.667 *	-0.580	0.123	0.467	0.588	3.494	6.531 *	0.550*	2.551	0.019	2.004	2.838 **	5.64 **
Pant P-243 × GP02/1108	0.789	0.160	-0.162	-0.333	0.062	-1.914	-1.025	-0.719 **	-1.590	0.422 *	-1.753	-2.571	-5.18 **
DDR-23 \times HFP 1545	1.667 **	0.309	0.138	0.289	-0.538	0.531	1.494	0.420	-1.894	-0.130	0.198	0.202	0.030
DDR-23 × HFP 1426	-1.333 **	-0.691	0.057	0.156	0.032	-4.395 *	-3.136	-0.773	1.751	-0.104	3.695 *	1.342	-2.097
$DDR-23 \times GP02/1108$	-0.333	0.383	-0.195	-0.444	0.506	3.864	1.642	0.354	-2.143	0.133	-3.892 *	-1.544	2.067
HFP 715 \times HFP 1545	-0.667 *	-0.358	0.160	0.311	-0.827	-1.025	3.383	0.755 **	1.106	-0.207	-0.929	-1.090	1.714
HFP 715 \times HFP 1426	-1.667 **	-1.025 *	-0.421 **	-0.156	-0.723	0.716	-2.914	-0.025	-2.783	0.452 *	-2.602	-1.417	-0.707
HFP 715 × GP02/1108	2.333 **	1.383 **	0.360 *	-0.156	1.551 *	0.309	-0.469	-0.730 **	6.323 **	-0.244	3.531 *	2.807 *	-1.007
IPF 14-13 \times HFP 1545	-0.333	-0.691	0.116	-0.333	0.795	2.086	-1.284	0.037	-1.894	0.171	-0.922	-0.459	0.846
IPF 14-13 × HFP1426	2.333 **	0.975	-0.099	0.067	-0.901	3.160	0.753	0.568 *	-1.316	0.141	-0.125	0.191	0.555
IPF 14-13 \times GP02/1108	-2.000 **	-0.284	-0.017	0.267	-0.494	-5.247*	0.531	-0.605	2.810	-0.222	1.048	-0.332	-1.401
IPF 14-16 \times HFP 1545	0.111	-0.580	-0.328 *	0.311	0.528	-3.247	-3.173	0.353	-1.138	0.215	-2.000	-0.549	0.907
IPF 14-16 \times HFP 1426	-0.222	0.420	-0.143	0.111	0.699	5.160 *	3.531	-0.460	-2.360	-0.459 *	2.684	1.907	-0.343
IPF 14-16 \times GP02/1108	0.111	0.160	0.472 **	-0.422	-1.227	-1.914	-0.358	0.107	2.499	0.244	-0.683	-0.549	-0.563
RFP 2009-02 × HFP 1545	-0.556	0.309	0.116	0.133	-0.516	0.753	3.938	0.386	0.773	0.148	5.398 **	2.290 *	-1.042
RFP 2009-02 × HFP 1426	0.778 *	-0.025	-0.232	-0.267	0.254	-0.506	-3.958	-0.533 *	1.217	0.141	-3.499 *	-3.147 **	-5.392 **
RFP 2009-02 × GP02/1108	-0.222	-0.284	0.116	0.133	0.262	-0.247	-1.580	0.147	-1.990	-0.289	-1.899	0.857	6.974 **
Pant P-200 \times HFP 1545	-0.333	-0.025	0.027	-0.289	0.640	2.531	5.649	-1.069 **	0.617	0.237	0.244	-0.262	-1.482
Pant P-200 \times HFP 1426	1.333 **	-0.025	0.079	0.178	-0.990	-5.728 **	-4.914	-0.242	-0.938	0.163	0.428	1.411	4.91 **
Pant P-200 × GP02/1108	-1.000 **	0.049	-0.106	0.111	-0.049	3.198	0.864	1.312 **	0.321	-0.400 *	-0.672	-1.149	-3.432 *
RFPG 79 \times HFP 1545	-1.222 **	-0.025	-0.128	0.333	0.862	-2.247	-3.395	-0.498	6.728 **	0.548 **	2.907	0.617	-2.020
RFPG 79 \times HFP 1426	1.778 **	0.309	0.457 **	-0.067	0.499	3.494	5.642 *	-0.161	-3.560	-0.393 *	-0.823	-0.377	0.077
RFPG 79 × GP02/1108	0.556	-0.284	-0.328 *	-0.267	1.360 *	-1.247	-2.247	0.660 *	-5.168 *	-0.156	-2.083	-0.240	1.943
Aman \times HFP 1545	2.000 **	0.642	-0.040	-0.622 *	-0.994	2.198	0.494	-0.553 *	-3.338	-0.452 *	-4.645 **	-1.783 *	1.506
Aman \times HFP 1426	-3.667 **	0.642	0.079	-0.489	-1.457 *	-5.395 **	-3.136	1.078 **	0.040	0.141	-2.161	-1.937 *	-2.111
Aman \times GP02/1108	1.667 **	-1.284 **	-0.04	1.111 **	0.751	3.198	2.642	-0.525 *	6.299 **	0.421 *	6.085 **	3.270 **	0.605

Table 4. SCA effects of different crosses for different characters in field pea.

*, ** significant at 5% and 1%, respectively, DF: Days to 50% flowering; DM: Days to maturity; NPB: Number of primary branches per plant; NSB: Number of secondary branches per plant; NN: Number of nodes per plant; Ht. of the first pod: height; Height of the first pod; PH: Plant height; 100-SW: 100-seed weight; NPP: Number of pods per plant; NSP: Number of seeds per pod; BY: Biological yield per plant; SYP: Seed yield per plant; HI: Harvest index.

Characters Variances	DF	DM	NPB	NSB	NN	Ht. of the First Pod	РН	100-SW	NPP	NSP	ВҮ	SYP	HI	
σ ² GCA	0.78	1.911	0.002	0.114	0.225	0.030	25.532	0.043	4.078	0.018	-1.467	0.291	1.739	
σ ² SCA	5.1	2.224	0.38	0.107	0.129	143.030	754.335	0.859	14.941	0.104	38.618	5.928	14.124	
σ^2 GCA/ σ^2 SCA	0.153	0.859	0.005	1.065	1.744	0.0002	0.034	0.050	0.273	0.173	-0.038	0.049	0.123	
$\sigma^2 D$	5.1	2.224	0.038	0.107	0.129	143.030	754.335	0.859	14.941	0.104	38.618	5.928	14.124	
$\sigma^2 A$	1.567	3.822	0.004	0.227	0.451	0.060	51.065	0.085	8.156	0.036	-29.33	0.582	3.477	
$(\sigma^2 D/\sigma^2 A)^{-1/2}$	3.254	0.582	9.50	0.471	0.286	2383.833	14.772	10.106	1.832	2.889	-1.317	10.185	4.062	

 Table 5. Fixed types of variances for various characters in field pea.

DF: Days to 50% flowering; DM: Days to maturity; NPB: Number of primary branches per plant; NSB: Number of secondary branches per plant; NN: Number of nodes per plant; Ht. of the first pod: height; Height of the first pod; PH: Plant height; 100-SW: 100-seed weight; NPP; Number of pods per plant; NSP: Number of seeds per pod; BY: Biological yield per plant; SYP: Seed yield per plant; HI: Harvest index.

Table 6. Lines, testers, and crosses possess good GCA and SCA effects for different traits in field pea.

Sr. No.	Characters	Lines	Testers	Crosses
1	Days to 50% flowering	DDR-23, RFP 2009-2, Pant P-200	HFP 1545, GP02/1108	Pant P-243 × HFP 1545, DDR-23 × HFP 1426, HFP 715 × HFP 1545, HFP 715 × HFP 1426, IPF 14-13 × GP02/1108, Pant P-200 × GP02/1108, RFPG 79 × HFP1545, Aman × HFP 1426
2	Days to maturity	DDR-23, HFP 715, RFP 2009-2	GP0 2/1108	HFP 715 \times HFP 1426, Aman \times GP02/1108
3	Number of primary branches per plant	DDR-23, HFP 715 RFPG 79	GP02/1108	HFP 715 \times GP02/1108, IPF 14-16 \times GP02/1108, RFPG 79 \times HFP 1426
4	Number of secondary branches per plant	RFPG 79, Aman	GP02/1108	Aman \times GP02/1108
5	Number of nodes per plant	DDR-23, HFP 715, RFPG 79	GP02/1108	HFP 715 × GP02/1108, RFPG 79 × GP02/1108
6	Height of first pod (cm)	Pant P-243, IPF 14-13, IPF 14-16, RFPG 79, Aman	HFP 1426	IPF 14-16 × HFP 1426
7	Plant height (cm)	DDR-23, HFP 715 RFP 2009-2, Pant P-200	HFP 1545	-
8	100-seed weight (g)	HFP 715, IPF 14-13, IPF 14-16, Pant P-200	GP02/1108	Pant P-243 × HFP 1426, HFP 715 × HFP 1545, IPF-14-13 × HFP1426, PantP-200 × GP02/1108, RFPG 79 × GP02/1108, Aman × HFP 1426
9	Number of pods per plant	HFP 715, IPF 14-16, RFPG 79	GP02/1108	HFP 715 \times GP02/1108, RFPG 79 \times HFP 1545, Aman \times GP02/1108
10	Number of seeds per plant	HFP 715, RFP 2009-2	HFP 1545, HFP 1426	Pant P-243 \times GP02/1108, HFP 715 \times HFP 1426, RFPG 79 \times HFP 1545 and Aman \times GP02/1108
11	Biological yield per plant (g)	IPF 14-16, RFPG 79, Aman	GP02/1108	DDR-23 × HFP 1426, HFP 715 × GP02/1108, RFP 2009-02 × HFP 1545, Amanx GP02/1108
12 13	Seed yield per plant (g) Harvest index (%)	HFP 715, IPF 14-16, Aman DDR-23 HFP 715	GP02/1108	Pant P-243 × HFP 1426, HFP 715 × GP02/1108, RFP 2009-02 × HFP 1545, Aman × GP02/1108 Pant P-243 × HFP 1426, RFP 2009-02 × GP02/1108, Pant P-200 × HFP 1426
15	marvest mdex (%)	DDK-25, HFP 715	-	rain r-245 × mrr 1420, Krr 2007-02 × Gr02/1108, rain r-200 × mrr 1420

3.1.4. Heterosis (heterobeltiosis) Analysis

More results from conventional line × tester analysis were those of heterobeltiosis in crosses for the observed traits (Table 7). For early flowering, 23 out of 27 crosses exhibited significantly negative heterobeltiosis; superior among them were IPF-14-13 × GP02/1108, RFPG 79 × GP02/1108, DDR-23 × HFP 1426, Pant P-200 × GP02/1108, RFP 2009-02 × GP02/1108, and Aman × HFP 1426. These results indicated that early flowering in these crosses was due to the involvement of one early line (DDR-23) and two early testers, viz., GP02/1108 and HFP 1426. Likewise, desirable crosses exhibiting negative and significant heterobeltiosis for early maturity were RFPG 79 × GP02/1108, Aman × GP02/1108, RFPG 79 × HFP 1545, RFP 2009-02 × GP02/1108, and Aman × HFP 1545.

Four crosses, viz., IPF 14-16 × GP02/1108, RFPG 79 × HFP 1426, RFP 2009-02 × GP02/1108, and DDR-23 × HFP 1545, depicted significant positive heterobeltiosis for a number of primary branches per plant. Similarly, plants containing more secondary branches provide greater opportunity for higher yield. Five crosses showed significant positive heterobeltiosis for this trait, viz., DDR-23 × HFP 1545, Aman × GP02/1108, DDR-23 × HFP 1426, IPF 14-16 × HFP 1545, and Pant P -200 × GP02/1108. Positively significant heterotic effects for a number of nodes per plant were found only in one cross, HFP 715 × GP02/1108.

For plant height, positive heterobeltiosis is desirable in the tall genotype and also for the height at the first pod, whereas negative heterosis is desirable in dwarf types. Desirable positive significant heterobeltiosis for number of nodes per plant were found in crosses viz., IPF 14-16 × GP02/1108, DDR-23 × GP02/1108, DDR-23 × HFP 1426, IPF 14-16 × HFP 1545, IPF 14-16 × HFP 1426, Pant P-243 × GP02/1108, Aman × GP02/1108, and RFPG 79 × HFP1545. The cross Pant P-243 × HFP 1426 exhibited the highest positive value of heterobeltiosis, followed by RFPG 79 × HFP 1426 and IPF 14-13 × HFP1426, all of which involved tall parents. Likewise, only one cross (IPF 14-16 × HFP 1545) exhibits a negative value of heterobeltiosis for the height of the first pod, the tall ones.

Out of 27 crosses, a high manifestation of significant positive heterobeltiosis for 100seed weight was exhibited by IPF 13-14 × HFP 1426, Pant P-243 × HFP 1426, Pant P-200 × HFP 1426, Aman × HFP 1426, IPF 14-13 × HFP 1545, RFP 2009-02 × HFP 1545, and HFP 715 × HFP 1545. The heterosis results for this trait depicted that only two crosses (DDR-23 × GP 02/118 and IPF 14-16 × GP 02/1108) showed significant positive heterobeltiosis. A higher number of seeds per plant is generally associated with a higher seed yield.

Out of 27 crosses, 15 exhibited a significant positive heterobeltiosis for biological yield per plant, ranging from 19.09 (DDR-23 × HFP 1545) to 90.79 (HFP 715 × GP02/1108). The high manifestation of heterosis for seed yield was evidenced by the superiority of 24 out of 27. Very high heterosis was observed in crosses HFP 715 × GP02/1108, IPF 14-16 × GP02/1108, IPF 14-16 × HFP 1426, DDR-23 × HFP 1426, and DDR-23 × GP02/1108 for yield and its attributes. Desirable positive heterobeltiosis for harvest index was observed in 12 crosses out of 27, and it was observed as its maximum in cross RFP 2009-02 × GP02/1108.

	Characters	DE	ЪΜ	NIDD	NCD	NINI	Ht. of the	DLI	100 SW	NIDD	NCD	DV	CVD.	ш
Crosses		Dr	DIVI	INFD	INSD	ININ	First Pod	rп	100-577	INFF	INSP	DI	511	пі
Pant P-243	× HFP 1545	-1.76 **	-1.07	-2.56	-19.05	-6.97	3.31	-4.58	3.33	10.78	-14.29 **	30.89 **	30.15 **	-0.61
Pant P-243	imes HFP 1426	-2.08 **	-1.32 *	0.00	9.52	3.48	28.93 **	20.83 **	11.34 **	29.90	-6.25	50.44 **	82.01 **	10.46 *
Pant P-243 $ imes$	GP02/1108	-3.52 **	-0.27	15.62	4.76	4.98	6.61	11.67	-12.03 **	32.99 *	2.86	56.95 **	4.04 **	-7.37
DDR-23 \times	HFP 1545	-0.45	-2.67 **	17.95 *	160.00 **	-9.61	-5.13	-6.20	-3.18	11.76	1.30	19.09 *	46.92 **	20.26 **
DDR-23 \times	HFP 1426	-7.50 **	-2.89 **	10.26	110.00 *	-4.80	-14.77	2.33	-5.26 *	49.61 **	-5.00	76.54 **	105.50 **	15.04 **
DDR-23 \times	GP02/1108	-1.86 **	-0.55	8.11	53.33	3.06	14.10	13.95	-13.02 **	67.97 **	20.00 **	69.19 **	101.82 **	22.33 **
HFP 715 $ imes$	HFP 1545	-3.0 **	-2.14 **	5.13	77.78	-5.41	-12.50	-0.81	6.21 **	-2.78	5.19	8.82	29.27 *	19.17 **
HFP 715 $ imes$	HFP 1426	-3.75 **	-2.11 **	-17.95 *	0.00	-3.24	3.41	5.79	-0.77	-14.44	8.75	32.13 *	50.55 **	11.52 *
HFP 715 $ imes$	GP02/1108	-1.72 **	-1.61 **	11.11	13.33	23.76 **	-1.25	12.40	-5.87 **	7.22	2.74	90.79 **	134.48 **	18.47 **
IPF 14-13 ×	< HFP 1545	-5.83 **	-0.27	7.69	-60.00 **	2.54	3.73	7.97	8.23 **	-17.92	-1.30	-3.53	21.24 *	1.78
IPF 14-13 >	× HFP1426	0.83	1.58 **	-5.13	-48.00 *	-4.57	17.91 **	20.32 **	19.52 **	-17.69	-5.00	-7.30	15.44	-1.01
IPF 14-13 $ imes$	GP02/1108	-10.42 **	-1.07	0.00	8.00	-0.51	-8.96	20.32 **	-6.33 **	12.26	-8.70	11.75	30.68 **	0.99
IPF 14-16 ×	< HFP 1545	0.00	-1.34 *	-7.69	92.86 *	-13.33 *	-15.44 **	-2.75	1.50	36.93 *	6.49	39.28 **	57.47 **	4.61
IPF 14-16 ×	< HFP 1426	-3.75 **	0.00	-5.13	50.00	-11.25	12.08	14.90 *	-5.60 *	34.90 *	-11.25 *	49.10 **	119.84 **	-0.29
IPF 14-16 $ imes$	GP02/1108	-2.68 **	-1.35 *	30.56 **	60.00	-18.75 **	-9.40	10.59	-2.10	78.19 **	13.85 *	55.83 **	125.22 **	5.85
RFP 2009-02	imes HFP 1545	-4.82 **	-1.87 **	5.13	70.00	-6.49	-2.38	2.19	6.79 **	5.92	2.44	19.71 *	32.92 **	8.74
RFP 2009-02	\times HFP 1426	-4.58 **	-1.58 **	-12.82	-20.00	1.08	6.82	6.57	-1.55	3.74	1.22	2.82	0.35	-2.43
RFP 2009-02	× GP02/1108	-7.02 **	-2.96 **	21.21 *	66.67	13.14	0.00	8.76	-4.40 *	10.90	-15.85 **	39.97 **	72.09 **	23.66 **
Pant P-200	imes HFP 1545	-3.95 **	-1.07	2.56	7.69	2.16	2.38	0.70	-0.15	4.58	3.75	10.54	20.81 *	1.99
Pant P-200	imes HFP 1426	-3.33 **	-0.53	0.00	38.46	-6.49	-12.50	-0.70	9.88 **	-1.74	1.25	13.46	29.68 *	14.44 **
Pant P-200 \times	GP02/1108	-7.46 **	-1.08	8.82	86.67 *	6.08	10.71	11.97	3.62	29.51	-18.75 **	31.54 **	25.47 *	-4.18
RFPG 79 \times	K HFP 1545	-7.11 **	-3.36 **	7.50	-11.90	8.33	-2.17	11.34	-4.96 *	27.09 **	2.60	-5.66	18.07*	0.59
RFPG 79 \times	K HFP 1426	-0.42	-1.03	25.00 **	-33.33 *	6.86	21.74 **	32.39 **	-5.17 *	-0.40	20.00 **	20.29 **	3.83	2.98
RFPG 79 \times	GP02/1108	-8.79 **	-4.91 **	-2.50	-14.29	-1.47	3.62	23.08 **	-1.77	2.99	0.00	-10.40	19.29 *	14.28 *
Aman \times	HFP 1545	-3.23 **	-2.06 **	10.26	-5.26	-9.00	2.03	-2.73	-0.04	-9.56	-7.79	-2.30	40.33 **	14.37 **
Aman \times 1	HFP 1426	-6.85 **	0.00	10.26	-10.53	-9.00	-2.70	2.05	9.23 **	0.00	-1.25	-1.09	30.96 **	4.21
Aman \times C	GP02/1108	-6.05 **	-4.88 **	7.69	173.68 **	5.50	7.43	8.19	-9.74 **	31.01 *	7.25	38.45 **	90.64 **	17.61 **

 Table 7. Estimates of heterobeltiosis for different characters in field pea.

*, ** significant at 5% and 1%, respectively, DF: Days to 50% flowering; DM: Days to maturity; NPB: Number of primary branches per plant; NSB: Number of secondary branches per plant; NN: Number of nodes per plant; Ht. of the first pod: height; Height of the first pod; PH: Plant height; 100-SW:100-seed weight; NPP: Number of pods per plant; NSP: Number of seeds per pod; BY: Biological yield per plant; SYP: Seed yield per plant; HI: Harvest index.

3.2. Graphical Analysis and Presentation

3.2.1. PCA-Biplot Analysis for Line \times Tester Analysis

Figure 2 summarizes the means and GCA values of parents (Figure 2a–c) and SCA values of crosses (Figure 2d–f) by PCA biplot. As portrayed in PCA biplots, the best parents based on good general combining ability were DDR-23 and GP02/1108 for days to flowering and days to maturity; RFPG 79 for a number of secondary branches per plant; DDR-23 and GP 02/1108 for a number of nods per plant; and HFP 715, IPF 14-16, and GP02/1108 for number of pods per plant (Figure 2a). The parents HFP 715 and HFP 1545 had significant and positive GCA effects for both plant height and number of seeds per plant, whereas the parents GP02/1108, IPF 14-16, and HFP 715 for 100-seed weight and the parents IPF 14-16, RFPG 79, and GP02/1108 for biological yield per plant had high GCA values. These genotypes also had high means for these components (Figure 2b). Parents having high GCA effects for the height of the first pod were Aman, IPF 14-16, IPF-14-13 and RFPG 79, whereas DDR-23, GP 02/1108 and HFP 715, IPF14-16, GP02/1108 has high GCA effects for the number of primary branches per plant and seed yield per plant, respectively (Figure 2c).



Figure 2. Principal component analysis (PCA) biplot diagrams for parents (**a**–**c**) and crosses (**d**–**f**) represent means and combining abilities.

Figure 2d demonstrates crosses that showed high SCA values for days to flowering: Pant P-243 \times HFP 1545 and DDR-23 \times HFP 1426, and for days to maturity: HFP 715 \times HFP 1426. Further, cross combinations HFP 715 \times GP02/1108 and RFPG 79 \times GP02/1108 had significant and positive SCA effects for the number of nodes per plant, whereas the cross Aman \times GP02/1108 was for a number of secondary branches per plant. Crosses Aman \times GP02/1108, HFP 715 \times GP02/1108, and RFPG 79 \times HFP 1545 had significantly positive SCA effects on the number of pods per plant. As per Figure 2e, significantly positive crosses depicted SCA effects for plant height Pant P-243 \times HFP 1426, RFPG 79 \times HFP 1426, and IPF-14-13 \times GP02/1108, while crosses DDR-23 \times HFP 1426 and HFP 715 \times GP02/1108 were better specific combiners for biology yield per plant; Pant P-243 \times GP02/1108 and HFP 715 imes HFP 1426 for 100-seed weight, and Pant P-243 imes GP02/1108 and HFP 715 imesHFP 1426 for number of seeds per plant. From Figure 2f, it can be deduced that the cross IPF 14-13 \times HFP 1426 showed a high SCA for height at the first pod, whereas crosses Pant $P-243 \times HFP$ 1426 and HFP 715 \times GP02/1108 showed high seed yield per plant, Pant $P-243 \times HFP$ 1426 and IPF 14-16 $\times GP2/1108$ showed a high number of primary branches per plant, and crosses DDR-23 imes HFP 1545, RFP 2009-02 imes HFP 1545, and HFP 715 imesGP02/1108 for harvest index. Mean performance and heterotic values both are presented in Figure 3a–c by PCA biplots. The PCA biplots depicted that the crosses IPF-14-13 \times GP02/1108 and RFPG 79 \times GP02/1108 exhibited desirable negative heterobeltiosis for days to flowering, while RFPG 79 \times GP02/1108 and Aman \times GP02/1108 exhibited desirable negative heterobeltiosis for days to maturity. Crosses DDR-23 \times HFP 1545 and IPF 14-16 \times HFP 1545 had significantly positive heterobeltiosis for a number of secondary branches per plant, while crosses, IPF 14-16 \times GP02/1108 and DDR-23 \times GP02/1108 had desirable significant positive heterosis for a number of pods per plant. The cross generated from HFP 715 and GP02/1108 had a greater number of nods per plant, whereas other crosses showed superiority in 100-seed weight: IPF 13-14 \times HFP 1426 and Pant P-243 \times HFP 1426. Only one cross, i.e., IPF 14-16 \times HFP 1545, exhibited negative heterobeltiosis for the height of the first pod. Crosses showed the heterotic effect for a number of seeds per pod, DDR-23 \times GP 02/1108 and IPF 14-16 \times GP 02/1108, whereas cross generated from HFP 715 and GP02/1108 had high positive heterosis for biological yield per plant. The cross RFPG 2009-02 \times GP02/1108 showed the maximum heterosis for harvest index. The results obtained from graphical analysis were very similar to those obtained from traditional methods (Table 4). Thus, we can say that the PCA biplot is a good choice to graphically represent the heterosis analysis results.

3.2.2. GGE Biplot Analysis for Line \times Analysis

GGE biplot outputs were generated using the mean vs. stability option, and the first component of the GGE biplot justified most of the variation, as shown for different traits in Figure 4. It explained 88.78% variation for all the traits. Three components explain the combining abilities of GGE biplot. The first one is a thick red line that passes through the plot origin called the tester coordinate (TC), while the other one is a thick red line that passes through the plot origin and is perpendicular to the tester coordinate, referred to as the perpendicular coordinate (PC), and the last one is a group of lines parallel to the perpendicular line (Yan, 2001), as shown in Figure 4 [20]. A graphic analysis, as seen in Figure 4a,b, revealed that negative and highly significant GCA were found in the parents, DDR-23, HFP 715, and RFP-2009 for days to 50% flowering and days to maturity, respectively. Therefore, these parents produced desirable cross-combinations upon crossing.



Figure 3. Principal component analysis (PCA) biplot diagrams for heterosis and mean values for crosses are shown in separate diagrams (**a**–**c**).



Figure 4. Cont.



Figure 4. Cont.



Figure 4. Bioplot diagrams of genotype + genotype x environment (GGE) for all traits studied. Plotting parameters were Transform = 0, Scaling = 0, Centered = 2, SVP = 2.

On the basis of their highly significant and positive GCA and SCA effects, the lines RFPG 79 and DDR-23 and their crosses, IPF 14-16 \times GP02/1108 and RFPG 79 \times HFP 1426, found the best general and specific combiners for a number of primary branches per plant (Figure 4c). In contrast, high GCA effects for a number of secondary branches per plant were observed in parents viz., RFPG 79 and Aman and SCA effects in crosses Aman \times GP02/1108 as shown in Figure 4d. As shown in Figure 4e, the best general and specific combiners for the number of nodes per plant were HFP 715 and RFPG 79, and HFP 715 \times GP02/1108 and RFPG 79 \times GP02/1108, respectively. Negative and highly significant GCA and SCA as the best combiners of parental lines for height at the first pod were observed in parents Pant P-243, IPF 14-13, IPF 14-16, and crosses IPF14-16 \times HFP1426, respectively (Figure 4f). Perusal analysis of Figure 4g revealed negative and highly significant GCA in the parental lines for dwarfness: DDR-23, HFP 715, and Pant P-200. As shown in Figure 4h, the best general combiners for pods per plant were HFP 715 and IPF 14-16, whereas the best specific combiners were RFPG 79 imes HFP 1545 and HFP 715 \times GP02/1108; likely the best general and specific combiners for a number of seeds per pod were HFP 715 and RFP 2009-2, HFP 715 imes HFP 1426, RFPG 79 imes HFP 1545 and Aman imesGP02/1108, respectively (Figure 4i). For 100-seed weight parents, HFP 715, IPF 14-13, IPF 14-16, and Pant P-200 showed positive and significant SCA effects, whereas crosses showed positive and significant GCA effects for this character: Aman \times HFP 1426, HFP 715 \times HFP 1545 and RFPG 79 \times GP02/1108 (Figure 4j). Positive and significant GCA and SCA effects for biological yield per plant were shown by IPF 14-16, RFPG 79 and Aman and crosses, Aman \times GP02/1108, RFP 2009-02 \times HFP 1545, and DDR 23 \times HFP 1426, respectively (Figure 4k). A graphic analysis, as seen in Figure 4l, revealed that the best general combiner for seed yield per plant was HFP 715 and RFP 2009-2, and the best specific combiners were HFP 715 \times HFP 1426 and RFPG 79 \times HFP 1545. A perusal of Figure 4m revealed positive and highly significant GCA for harvest index parental lines DDR-23 and HFP 715 and similarly positive and highly significant SCA for crosses Pant P-243 imes HFP 1426 and Pant P 200 \times HFP 1426. Overall, parent testers HFP 1545 and HFP 1426, lines Pant P-243, DDR-23, and RFPG 79 best and crosses IPF 14-16 \times GP02/1108, Pant P-243 \times GP02/1108, DDR-23 \times HFP 1426, and IPF 14-16 \times HFP 1545 were observed to be the best for yield and its attributes.

4. Discussion

For any plant breeding effort to be successful, there must be sufficient genetic diversity among the selected lines. When attempting to hybridize in a particular mating design, determining the best parental genotype combinations allows breeders to take advantage of their heterotic effects and demonstrates that superior transgressive segregants are accessible in the F₂ and the following generations. In the analysis of variance, the mean squares due to replication and genotype were highly significant ($p \leq 0.01$) for almost all the traits examined, indicating that there were large genotypic variations for these characters among the investigated genotypes. ANOVA revealed the importance of their orthogonal components, i.e., parents, crosses, and against parents, crosses, for most of the examined traits. This implied that a high amount of genetic diversity is present in parents and their hybrids, allowing them to explore their genetic variation by combining ability analysis and heterosis for these traits. These results were in agreement with previous findings by Singh and Saini [21], Halil and Uzun [22], and Kumar et al. [23], who also found highly significant differences for the means squared of the studied traits. These outcomes specify that there is ample scope for improvement through the selection of germplasm and its utilization in heterosis breeding.

Line \times Tester analysis is the best method for evaluating the combining ability of contrasting lines and testers for various traits. The general combining ability (GCA) value is directly connected with the reproductive value of a parent and is associated with additive gene effects, while the specific combining ability (SCA) is related to non-additive gene activity, which is mostly contributed by dominance, epistasis, or genotype-environment interaction effects, and both GCA and SCA impacts are significant in the development of the breeding population. In this study, all the lines and testers showed significant favorable (positive/negative) GCA effects for at least one of the parameters. The presence of significant GCA effects indicated that continued progress could be possible through breeding for yield and yield components in field pea. These results were in accordance with the findings of Askander and Osman [24] and Borah et al. [25]. Kumar et al. [26]. Genotypes HFP 715 and Aman among lines and GP02/1108 among testers appeared to be the best general combiners for yield and its attributing traits. HFP 715, the best line observed in this study, was a good general combiner for days to maturity, number of primary branches per plant, number of nodes per plant, plant height, 100-seed weight, number of pods per plant, and harvest index, and the tester, GP02/1108, proved to be a consistently good general combiner for seed yield, biological yield, number of pods per plant, 100-seed weight, number of nodes per plant, number of secondary branches per plant, days to flowering, and days to maturity. The study of SCA effects of crosses and GCA effects of parents revealed that no generalization regarding SCA effects of crosses based on the GCA value of parents could be made for the various characters under study. These results concurred with the findings of previous combining ability studies by Kumar et al. [23], which found four parental lines, viz., PB-01, Jyoti, PB-89, and DS-10, had a significant GCA effect on seed yield. In the same study, five lines, namely pear polo, DS-10, G-10, AP-3, and VRPE-24, were good combiners for the trait plant height. Similarly, Mishra et al. [27] found that an inbred P-1457-7-1 was a good combiner for the trait seed yield per plant in field peas. Likewise, the study by Kumar et al. [26] revealed that Makyatmubi exhibits sound GCA effects for traits nodes to first flowering, number of seeds pod^{-1} , seed yield plant⁻¹, and harvest index.

Whereas SCA effects represent non-fixable (non-heritable) components of variation, which are dominance, additive x dominance, and dominance x dominance. To confirm whether the crosses selected on the basis of specific combining ability effects were the best-performing ones, the superior crosses on the basis of specific combining ability effects were selected. Out of the 27 cross combinations, only four crosses, namely Aman × GP02/1108, Pant P-243 × HFP 1426, HFP 715 × GP02/1108, and RFP 2009-02 × HFP 1545, were found to be positive and significant specific combiners for seed yield per plant. The performance of different crosses based on SCA was used to construct the gene action. High SCA effects resulting from crosses involving both parents with good general combiners (e.g., HFP 715 × GP02/1108 for a number of pods per plant and seed yield per plant; for seed and biological yield per plant) may be attributed to additive × additive gene action whereas, high SCA effects derived from crosses including good × poor general combiners (e.g., Aman × GP02/1108 and RFPG 79 × HFP 1545 for a number of pods per plant; P-243 × HFP 1426 for harvest index for a number of seeds per pod; Pant P-243 × HFP 1426 for harvest index for a number of seeds per pod; Pant P-243 × HFP 1426 for harvest index for a number of seeds per pod; Pant P-243 × HFP 1426 for harvest index for a number of seeds per polat; P-243 × HFP 1426 for harvest index for a number of seeds per polat; P-243 × HFP 1426 for harvest index for a number of seeds per polat; P-243 × HFP 1426 for harvest index for a number of seeds per polat; P-243 × HFP 1426 for harvest index for a number of seeds per polat; P-243 × HFP 1426 for harvest index for a number of seeds per polat; P-243 × HFP 1426 for harvest index for a number of seeds per polat; P-243 × HFP 1426 for harvest index for a number of seeds per polat; P-243 × HFP 1426 for harvest index for a number of seeds per polat; P-243 × HFP 1426 for harvest index for a number of seeds per polat; P-243 × HFP 1426 for harvest

combiner parent and epistatic effects of the poor general combiner, and high SCA effects manifested by low × low crosses (e.g., RFPG 79 × HFP 1545 for a number of seeds per pod and Pant P-243 × HFP 1426 and RFPG 2009-02 × HFP 1545 for seed yield per plant) may be caused by dominance × dominance type of non-allelic interaction. Similarly, Zaman and Hazarika [28] reported that the cross combinations Rachna × Azad, Rachna × HUDP 6, Rachna × HUP 2, and Azad × HUP 2 had significant SCA values for pods per plant, plant height, and days to flowering. Furthermore, Askander and Osman [24] found that the hybrid (Thomas laxton × Petit provencal) exhibited a significant SCA effect in a desirable direction for plant height, no. of branches plant⁻¹, pod weight plant⁻¹, no. of pods plant⁻¹, no. of seeds plant⁻¹, and seed yield plant⁻¹. Likewise, Kumar et al. [26] observed that the crosses Makyatmubi x VL-58 and Makyatmubi x Prakash showed significant SCA effects for 100 seed-weight and seed yield plant⁻¹.

The σ^2 SCA has been observed to be higher than σ^2 GCA in almost all the traits except the number of secondary branches and the number of nodes per plant, indicating control of non-additive gene effects. These results confirm the findings of the SCA analysis. The role of non-additive gene action in the expression of these characters in field pea was also reported earlier by Askander and Osman [24], which differ from the one (5.0) only in one trait seed pod⁻¹ and plant height (1.66), respectively. Likewise, Yadav et al. [29] and Kumar et al. [23] revealed less than one ratio (σ^2 GCA/ σ^2 SCA) for all the traits studied. The general assessment of the results from these studies indicated that yield and its contributing traits are under the control of additive and non-additive genes. To utilize both types of gene actions, a breeding program involving some inter-mating in segregating generations to infuse genes in a population, like the diallel selective mating system suggested by Jensen [30], or multiple crossings or mass selections followed by inter-mating as suggested by Redden and Jensen [31], might be helpful in breaking yield barriers in this crop.

Heterosis, or hybrid vigour, is a phenomenon where hybrid progeny has superior performance compared to their parental inbred lines. It is a function of the number of loci at which the parent carries different alleles and the magnitude and direction of the non-additive effects within or between those loci in hybrid combinations. Negative heterobeltiosis is useful regarding days of flowering and days to maturity because it transfers the vegetative phase energy to the reproductive phase early, and this probably aids in the enhancement of seed yield. These genotypes, besides fitting well in different crop rotations of intensive agriculture systems, suffer fewer losses due to biotic and abiotic stresses and vacate the field for the succeeding crop by providing sufficient time for seeding. Positive heterosis is desirable for a number of primary branches because, for plants with robust stature, having more primary branches provides an excellent opportunity for higher yields. Similar consonance of result is obtained from the study of Kumar et al. [23] in field peas, which recorded that the cross DS-10 \times Shilpa-10 had the highest significant heterobeltiosis for days to flowering in, while, the cross Pear polo \times Rachana had the highest significant heterobeltiosis for days to maturity. Furthermore, Askander and Osman [24] found that cross Avola \times Local exhibited desirable significant heterosis over better parent (-2.33) for days to 50% flowering.

Negative heterosis is desirable for the character plant height because dwarf genotypes are advocated to attain the potential yield due to their ability to withstand winds and other weather vagaries (lodging resistant). In the current investigation, no desirable heterotic crosses were found for this character. At the same time, more nodes per plant are desired, as they will bear more pods. More pods per plant are associated with a higher yield, so significant positive heterobeltiosis is desirable for both these traits. Similar results were in accordance with the previous results of Kumar et al. [26], which observed no desirable significant heterosis for plant height. Still, they found that crosses Makuchabi × VL-58 (69.57) and Makyatmubi × KPMR-851 (69.57) exhibited significant heterobeltiosis for several pods' plant⁻¹, and crosses Makyatmubix Makuchabi (25.64) and Makyatmubi × Prakash (25.64) showed the highest desirable heterosis for a number of pods plant⁻¹ in the

cross Sel 3-25 \times USA1 and for a number of seeds plant⁻¹ in the cross Sel 3-25 \times Ardahan. Furthermore, Askander and Osman [24] investigated the highest heterobeltiosis for a number of pods plant⁻¹ and the number of seeds plant⁻¹.

Overall, in the present study, high manifestations of heterobeltiosis for seed yield were evidenced by the superiority of 24 out of 27 crosses over the better parent. High heterobeltiosis was observed in the cross HFP 715 × GP02/1108, followed by IPF 14-16 × GP02/1108, IPF 14-16 × HFP 1426, Aman × GP02/1108, and DDR-23 × GP02/1108 for yield and its attributes. These may be utilized in crop improvement programs to obtain transgressive segregants in later generations. Similarly, Singh et al. [13] found that the hybrid PRAKASH × IPFD 10–13 expressed the highest heterobeltiosis (82.54%) for seed yield plant⁻¹. Likewise, in the study of Halil and Uzun [22], Sel 3-25 × Kirazli was the best hybrid for seed yield and most of its associated traits. Similarly, Kumar et al. [23] and Askander and Osman [24] obtained similar results of seed yield and its attributing traits.

Our interpretation and analysis based on the Fisher infinitesimal model describe one or more quantitative traits as the sum of a genetic and a non-genetic component, with the first component distributed within families as a normal random variable with a variance unrelated to the parental traits and centered at the average of the parental genetic components. In comparison to Mendel's qualitative traits-based analysis, this model explained the quantitative traits like yield and its component more efficiently.

Regarding $G \times E$ interaction, in the present investigation, among parents, lines DDR-23 and HFP 715 were found to be stable as they flowered earlier and had a stable yield under $G \times E$ interaction. Whereas traits, viz., the height of the first pod and plant height, exhibit strong G \times E interaction. So, parents DDR-23 and HFP 715 are good general combiners for producing hybrids for higher yield that perform better in a single or multi-location environment. Here, the graphical approach of the GGE biplot explains 88.78% variation for all the traits. As a result, because the GGE biplot provided the highest explanation of variance, its proficiency for all tested qualities was more accurately shown in the graphical analysis. The best parents cross, combining ability and heterotic patterns shown by GGE biplot were analogous to conventional line \times tester results, indicating that it can be used as a reliable statistical tool to estimate the combining ability of parents by means of line \times tester data. In the case of the common bean, using just one multiplicative component from the AMMI model was adequate to explain a substantial proportion of the pertinent data [32]. Likewise, PCA biplot and GGE biplot analysis are best for the characterization of stable and good general combiners in crops like field pea. In maize, Badu-Apraku and Akinwale [33] and Momeni et al. [34] also reported close correspondence between conventional and graphical methods of $l \times t$ analysis.

Based on the genetic data, it is recommended that untested breeding material be selected using genomic selection (GS), which can assist breeding organizations in reducing the costs and time associated with phenotyping [35]. So, in conventional breeding approaches like line × tester, the genomic prediction of the inbred lines, or how well inbred lines perform in hybrid combinations, is always evaluated and may be measured in single or multiple-location trials. So, ensuring knowledge about genomic prediction breeding values may strengthen field trial accuracy and contribute to revamping genetic improvement programs [36]. Similar to this, genomic estimated breeding value (GEBV) may assist in an early recurrent selection in field pea breeding by choosing the most promising inbreds and crosses for subsequent intermating, especially for traits that are challenging to assess. The estimated combining ability is gathered from genetic tests such as progeny trials, and parental re-selection gives a more boost in achieving the goal of isolating superior inbred lines or transgressive segregants.

5. Conclusions

Although considerable progress is being made in field pea improvement, it should continue. Combining ability studies may contribute to achieving this objective. The results reported here clearly demonstrated heterosis, combining ability, precocity, and yield in field pea. In the present study, combining ability analysis has successfully identified good parents and crosses that can be used as stepping stones for evolving a well-defined approach for field pea improvement. Simultaneously exploiting the additive and nonadditive components of genetic effects would help improve such character easily. The analysis of variances offered the conclusion that lines, testers, and their crosses exhibited highly significant differences ($p \le 0.01$) for all the traits studied. Here, in the present study, the lines Aman and HFP 715 and the tester GP02/1108 and the crosses HFP 715 \times GP02/1108, Aman \times GP02/1108, and Pant P-243 \times HFP 1426 were observed to be the best general and specific combiners, respectively, for seed yield and its attributes. HFP 715 \times GP02/1108 and IPF 14-16 \times GP02/1108 were identified as superior hybrids in terms of heterobeltiosis for seed yield. The inheritance of yield and its components demonstrated a predominance of non-additive gene action (dominance), which suggested that heterosis breeding would be preferable to achieve rapid gains in field pea. Later generations can benefit from isolating desirable transgressive segregants by utilizing the superior lines and crosses. In addition, a comprehensive analysis of the capabilities and limitations of several graphical methods for presenting experimental data was conducted. Results from the GGE biplot were highly congruent with those from traditional line imestester techniques, establishing the GGE biplot as a credible statistical tool for estimating the parents' combining ability in line-tester data.

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Abbreviations

PCA: Principal Component Analysis, GGE: Genotype + Genotype × Environment, GCA: General Combining Ability, SCA: Specific Combining Ability.

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