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## Selection of good combiner for further crop improvement by diallel analysis for central plan zone in winter wheat (*Triticum aestivum* L.)

**Nageshwar, Som Veer Singh, Mahak Singh, Lokendra Singh, Sarvendra Kumar, Nand Kumar and Anjani Kumar Singh**

### Abstract

The F<sub>1</sub> 45 genotypes and F<sub>2</sub> 45 genotypes including ten - parents' produced through diallel cross (excluding reciprocal) of wheat (*Triticum aestivum* L.) were analyzed for combining ability for yield and yield associated traits. Highly significant variances due to gca and sca in both the generations of present study for all the traits revealed that additive as well as non-additive genetic effects were involved in determining the traits. The analysis of variance indicated significant differences among the treatment for all the characters. Among the parents based on *per se* performance and gca effects, good general combiners, namely, HD3086, K8962 and K1314 for days to 75 per cent heading, HD3086, DBW88 and K8962 for days to maturity, HD2733 and K0307 for plant height (cm), K0307 and K1601 for number of productive tillers, DBW88 for spike length (cm), DBW88 for number of spikelets per spike, DBW88, HD2733, K0307, HD2967 and K0402 for number of grains per spike, HD3086, HD2733 and K0402 for 1000-grain weight (g), HD3086, K0307, HD2967 and K0402 for grain yield per plant (g), DBW88 and K0402 for biological yield (g), HD3086, DBW39, K0307, HD2967 and K0402 for Harvest index (%), DBW88, K0307 and K0402 for protein content (%) were common in both F<sub>1</sub> and F<sub>2</sub> generations. On the basis of *per se* performance and positive significant gca effect the cross combinations, viz., HD 3086 X K 1601 and HD 2967 X K 1314 proved to be the best specific combiner in both the generation. The crosses involving good general combiners and showing high sca effects may be utilized for further breeding purposes.

**Keywords:** Combining ability, diallel crosses, genotypes, additive gene

### Introduction

Wheat (*Triticum aestivum* L.) is one of the leading food crops of the world farming and occupies significant position among the cultivated cereals. Wheat is a member of the Poaceae family and a self-pollinated crop. The wheat plant has long slender leaves and stems that are hollow in most varieties. The inflorescences are composed of varying numbers of minute flowers, ranging from 20 to 100. The flowers are borne in groups of two to six in structures known as spikelets, which later serve to house the subsequent two or three grains produced by the flowers. Wheat (*Triticum*) and rye (*Secale*) together with *Aegilops*, *Agropyron*, *Eremopyron* and *Haynalidia* form the subtribe *Triticineae*. Linnaeus in 1753 first classified wheat. In 1918, Sakamura reported the chromosome number sets (genomes) for each commonly recognized type. This was a turning point in *Triticum* classification. Depending on ploidy levels, wheat is of three types viz., Diploid 14 (n=7), allotetraploid 28 (n=14) and allohexaploid 42 (n=21). The haploid DNA content of hexaploid wheat (*Triticum aestivum* L. em Thell, 2n=42, AABBDD) is approximately 1.7 x 10<sup>10</sup> bp, about 100 times larger than the *Arabidopsis* genome, 40 times that of rice and about 6 times that of maize (Bennett and Smith, 1976; Amuruganathan and Earle, 1991).

Wheat is most successfully grown between the latitude of 30°-60°N and 27°-40°S (Nuttonson, 1955), but it can be grown under wide range of climatic conditions from Arctic Circle to equator. The optimum temperature for wheat growth is 25 °C with minimum and maximum growth temperatures of 30 °C to 40 °C and 30 °C to 32 °C, respectively (Briggle, 1980). Wheat grown under a wide range of climates and soils, wheat is best adapted to temperate regions with rainfall between 30 and 90 cm (12 and 36 inches). Mostly wheat is grown for human food and about 10 percent is retained for seed and industry (for production of starch, paste, malt, dextrose, gluten). Wheat grain contains essential nutrients; about 12% water, carbohydrates (60-80% mainly as starch), proteins (8-15%) containing essential amino acids (except lysine, tryptophan and methionine), fats (1.5-2%), minerals (1.5-2%), vitamins (such as B complex, vitamin E) and 2.2% crude fibers.

Flour made from the whole kernel is called graham flour and becomes rancid with prolonged storage because of the germ-oil content retained. White flour, which does not contain the germ, preserves longer. Wheat is of two types winter and spring based on winter intensity. Therefore, today wheat is grown all over the world, with different varieties according to the various climates. World's main wheat producing countries are China, India, United States, Russian Federation, France, Australia, Germany, Ukraine, Canada, Turkey, Pakistan, Argentina, Kazakhstan and United Kingdom. Most of the currently cultivated wheat varieties belong to hexaploid wheat (*Triticum aestivum* L.), which is known as common bread wheat for bread making. Wheat ranks first among the world food crops, in terms of cultivated area 221.18 mha and production 774.74 mmt with productivity of 35 qha-1 (USDA 2021).

In India, wheat is the second most important cereal crop next only to rice, India stands second among wheat producing countries after China. During the crop year 2020-2021, wheat was grown over an area of 31.47 million hectares with the production of 109.52 million metric tonnes and during 2019-2020 was 32.72 million hectares with the production of 101.20 million tonnes and average productivity was 34.24 q/ha. (Project Director's Report, IIW&BR 2018-19). The demand of wheat in India by 2022 has been projected to be between 1010-115 million tonnes as against 109.50 million tonnes production of present day. Uttar Pradesh state ranks first in both area and production. Among states, Uttar Pradesh produces a significant level of wheat record production of 35.47 mt (34%) with 36.04 mt productivity in the area of 9.84 mh, followed by Punjab (19.78 mt: 18%), Madhya Pradesh (18.35 mt: 17%), Haryana (12.65 mt: 12%), Rajasthan (9.60 mt: 9%) and Bihar (6.02 mt: 6%).

## Materials and methods

Ten genotypes of wheat (*Triticum aestivum* L. Em. Thell) namely HD3086, DBW88, HD2733, DBW39, K0307, HD2967, K0402, K1601, K8962 and K1314as basic material which had been taken on the basis of their differences in origin, adaptability and morphological characters from the germplasm maintained at Section of Economic Botanist (Rabi Cereals), C.S. Azad University of Agriculture and Technology, Kanpur. All these parents have genetic variability for yield level as well as for various good yield components. In the present investigation all possible crosses among the selected parents were made in one direction only, i.e. direct crosses. Here each parent was used either as male or as female in the mating. The number of single crosses attempted was equal to  $[n(n-1)/2]$ , where n is the number of parents used. Half diallel design was used in the present study because reciprocal differences are not significant in wheat crops.

All possible single crosses were made during the year 2018-19 to complete a 10x10 half diallel set without reciprocal due to absence of extra nuclear inheritance in wheat (Whitehouse, at al.1958) The experiment was conducted in randomized block design (RBD) with 45 F<sub>1</sub>, 45 F<sub>2</sub> with ten diversified parents during the year 2019-2020) at Crop Research Farm, Nawabganj, Kanpur. The experimental material was sown in each replication, parents and F<sub>1</sub>s were sown in single row while F<sub>2</sub>s were sown in two rows. The length of each row was 3.0m with inter and intra-row distance of 25 and 10cm respectively. Recommended doses of fertilizers @ 120 kg N + 60 kg P<sub>2</sub>O<sub>5</sub> + 40 kg K<sub>2</sub>O per hectare were applied in the

experimental area along with four irrigations at all critical stages.

Quantitative data were collected on five plants in each row. Days to 75% heading, days to maturity, plant height, number of productive tillers, spike length, number of spikelets per spike, number of grains per spike, 1000-grain weight, and grain yield per plant, biological yield per plant, Harvest index, and protein content. Regarding statistical analysis data recorded on parents with forty five F<sub>1</sub> and forty five F<sub>2</sub> were analyzed together.

The combining ability analysis was worked out in diallel analysis mating design by following Griffings (1956 b).

## Results and Discussion

### Combining ability variances

Diallelanalysis of variance for combining ability was carried out for all the 12 characters, namely, Days to 75% heading, days to maturity, plant height (cm), number of productive tillers, spike length (cm), number of spikelets per spike, number of grains per spike, 1000-grain weight (g), grain yield per plant (g), biological yield (g), Harvest index (%), and protein content (%), in both F<sub>1</sub> and F<sub>2</sub> generations.

The combining ability analysis provides useful information in the screening of desirable strains and their cross combinations for their utilization. Such knowledge is a pre-requisite in order to frame a systematic breeding programme leading to rapid and sustained improvement.

The aforesaid analysis involves per se performance, gca and sca effects to determine the potentiality of parents/crosses for mobilizing them in efficient hybridization programme. The different standard methods for combining ability estimates (Griffing, 1956b; Kempthorne, 1957; Kempthorne and Curnow, 1961; Fyfe and Gilbert, 1963; Gardner and Eberhart, 1966)<sup>[10, 4, 6]</sup> may or may not be compatible with one another with equal weightage and in the same order of ranking. On the other hand, a plant breeder is mainly concerned with relative ranking coupled with desirable and significant combining abilities rather than absolute values.

Highly significant variances due to gca and sca in both the generations of present study for all the traits revealed that additive as well as non-additive genetic effects were involved in determining the traits. Estimated variances indicated higher contribution on non-additive gene effects for all the characters in both the generations. Genetic components analysis also indicated predominance of non-additive genetic estimate for all the characters. Such results have also been reported by Zalewski (2001, Arshad and Chowdhry (2002)<sup>[18, 1]</sup>, Manmohan *et al.* (2003)<sup>[13]</sup>, Siddique *et al.* (2004)<sup>[15]</sup>, Joshi *et al.* (2004)<sup>[8]</sup>, Awan *et al.* (2005)<sup>[2]</sup>, Vanpariya *et al.* (2006)<sup>[17]</sup>, Soyly and Akgün (2007)<sup>[16]</sup>, Murphy *et al.* (2008)<sup>[14]</sup>, Kapoor *et al.* (2011)<sup>[9]</sup>, Jatav *et al.* (2014)<sup>[7]</sup>, Verma *et al.* (2016), Yadav (2017), Khaled *et al.* (2020)<sup>[11]</sup> and Emam *et al.* (2021)<sup>[3]</sup>.

### General combining ability (GCA) effects

The GCA effects include both additive and additive x additive interaction components of genetic variability (Griffing, 1956b; Sprague, 1966) which represents fixable genetic variance as also reported by Gilbert (1967). The additive parental effects as measured by GCA effects are of practical use, whereas non-allelic interactions are unpredictable and cannot be easily manipulated.

The per se performance of the parents was compared with their GCA effects in both the generations for all the characters

under study. It was concluded that the parents having high per se performance were proved to be the best general combiners for all the traits. It may be noted that if the character is unidirectionally controlled by a set of alleles and additive effects are important, choice of the parents on the basis of per se performance in most of the cases may be correct. But the choice of parents should be made on the basis of their combining ability estimates where non-allelic interactions are important.

Considering simultaneously the per se performance and gca effects, good general combiners common in the F1 and F2 generations were HD3086, K8962 and K1314 for days to 75 per cent heading, HD3086, DBW88 and K8962 for days to maturity, HD2733 and K0307 for plant height (cm), K0307 and K1601 for number of productive tillers, DBW88 for spike length (cm), DBW88 for number of spikelets per spike, DBW88, HD2733, K0307, HD2967 and K0402 for number of grains per spike, HD3086, HD2733 and K0402 for 1000-grain weight (g), HD3086, K0307, HD2967 and K0402 for grain yield per plant (g), DBW88 and K0402 for biological yield (g), HD3086, DBW39, K0307, HD2967 and K0402 for Harvest index (%), DBW88, K0307 and K0402 for protein content (%). The consistency of aforesaid combiners for yield and quality contributing traits in both the generations indicated that good general combiners were stable in their performance over generation.

On the basis of overall performance, parents HD3086, K0307, HD2967 and K0402 were best general combiners for grain yield and other important yield contributing characters as well as quality characters. These parents may be used for simultaneous improvement in grain yield and quality attributes through an inter-mating population involving all possible combinations among themselves.

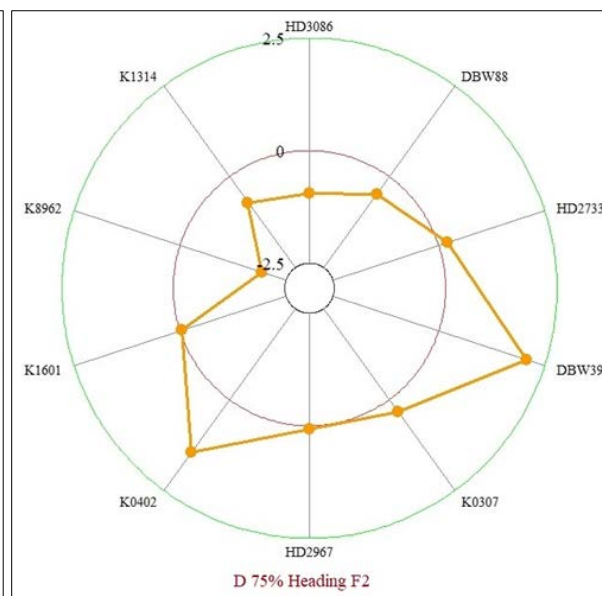
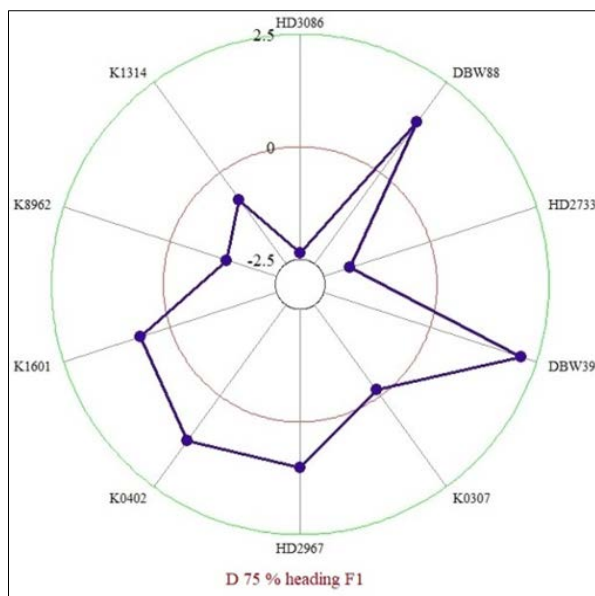
### Specific combining ability (sca) effects

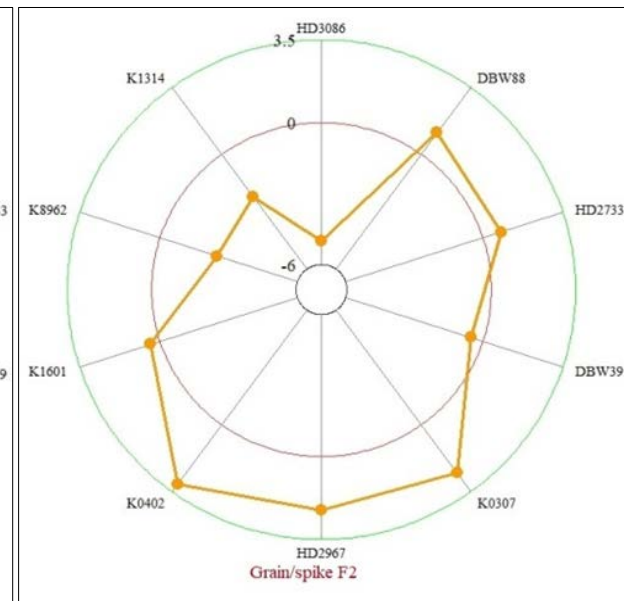
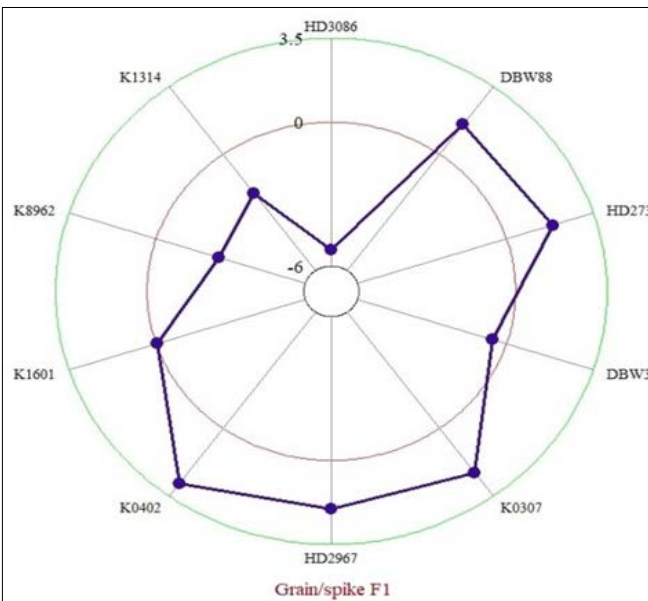
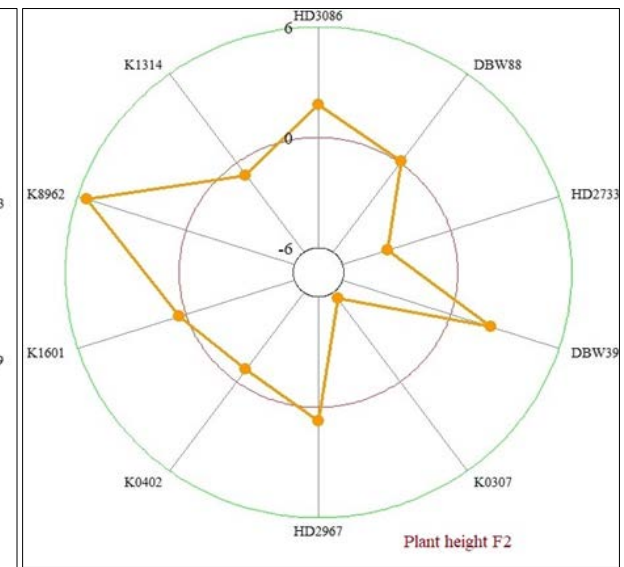
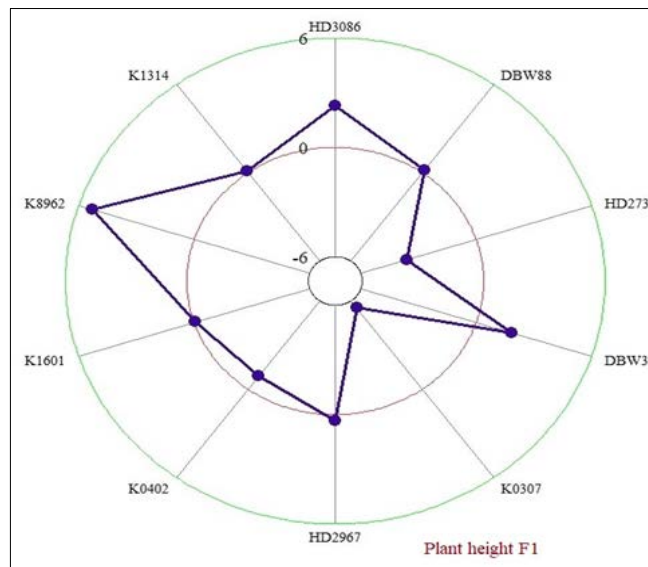
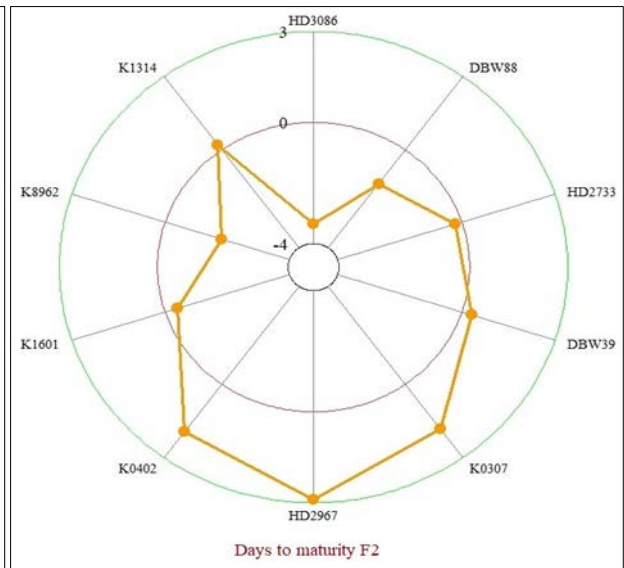
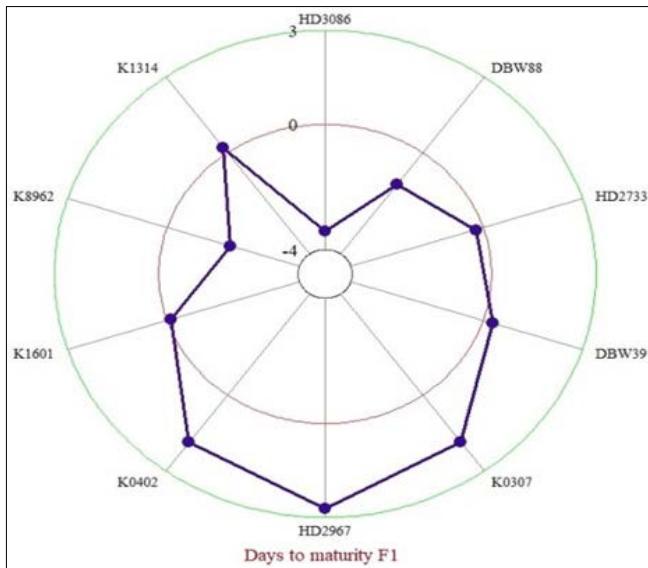
The sca effects representing dominance and epistatic component of genetic variability would not contribute much for improvement of self-pollinated crops except where commercial exploitation of heterosis is feasible. The crosses involving good general combiners and showing high sea effects may be utilized for further breeding purposes. Desirable transgressive segregant are expected to be produced by making a large number of crosses (Khrostovska, 1975) Jinks and Jones (1958) also suggested that the superiority of

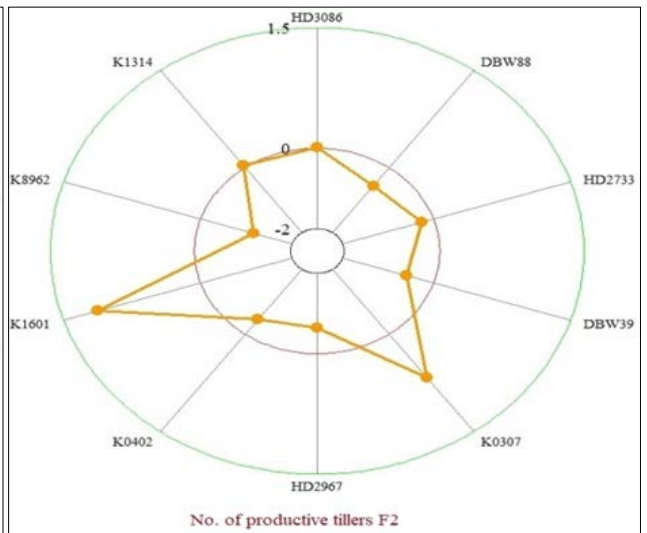
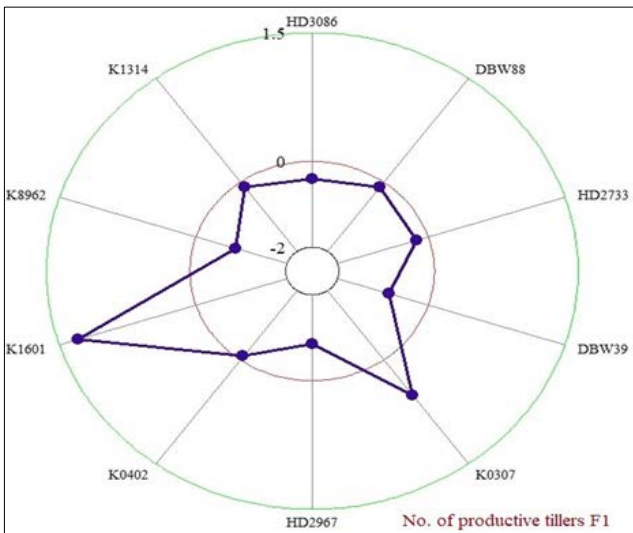
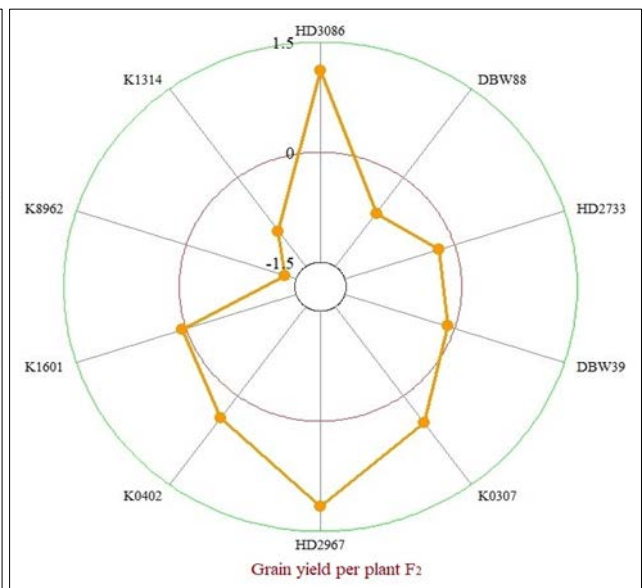
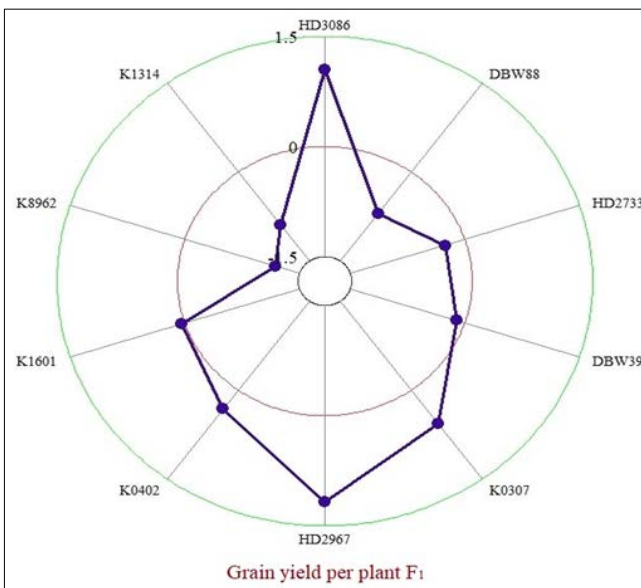
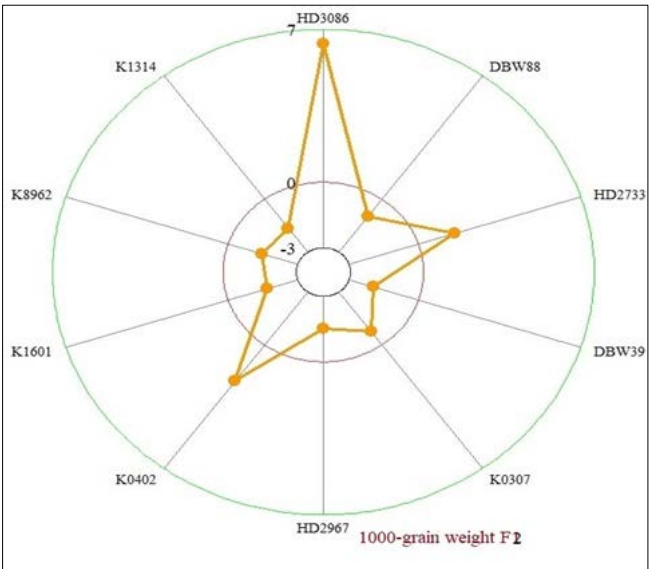
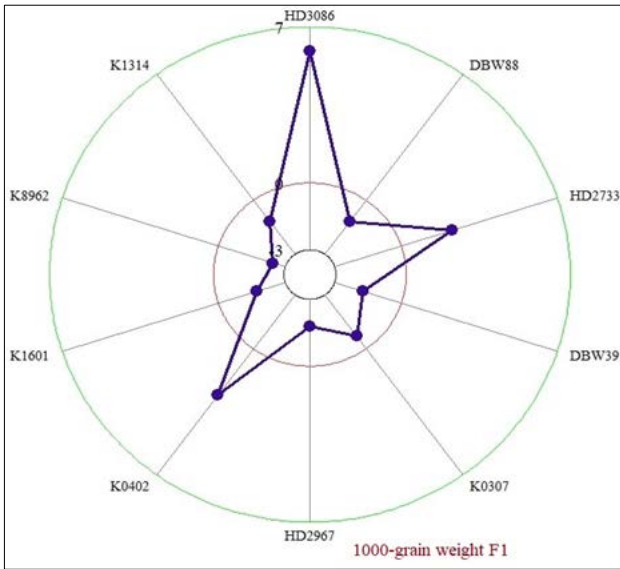
many hybrids may not be indicated by their ability to produce transgressive segregants due to non-fixable gene action would be important for grain yield. In respect of grain yield per plant; the positive and significant values of sca were associated with four combinations with high mean per se performance like HD-3086 X HD-2733, HD-3086 X K0307, HD-3086 X HD-2967, HD-3086 X K1601 and HD-2967 X K1314 were observed good specific combiner in F1 and four crosses, namely HD-3086 X K1601, HD-2967 X K0402, HD-2967 X K1601 and HD-2967 X K1314 were observed good specific combiner in F2 Only two crosses combination, HD-3086 X K1601 and HD-2967 X K1314 proved to be the best specific combiner on the basis of per se performance and positive significant gca effect in both the generation. Table 11(d). All the three possible combinations namely, high x high, high x low and low x low were observed between the parents of high and low gca effects. Relatively higher estimates of sca effects were recorded in those crosses which involved diverse parents.

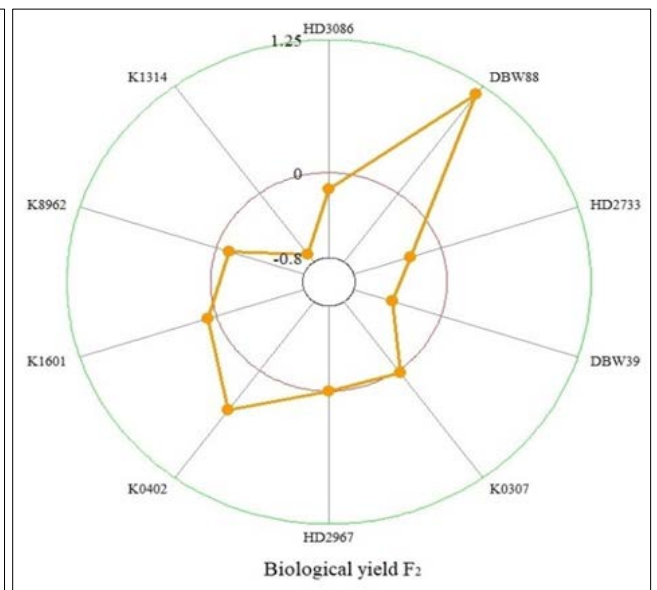
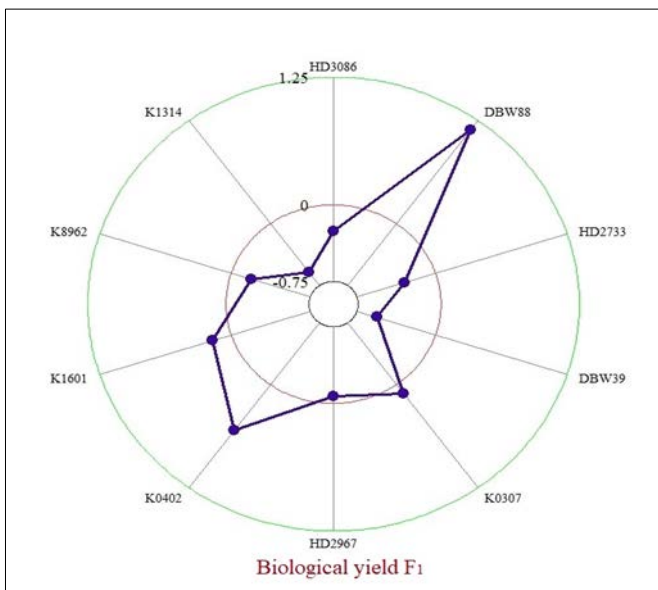
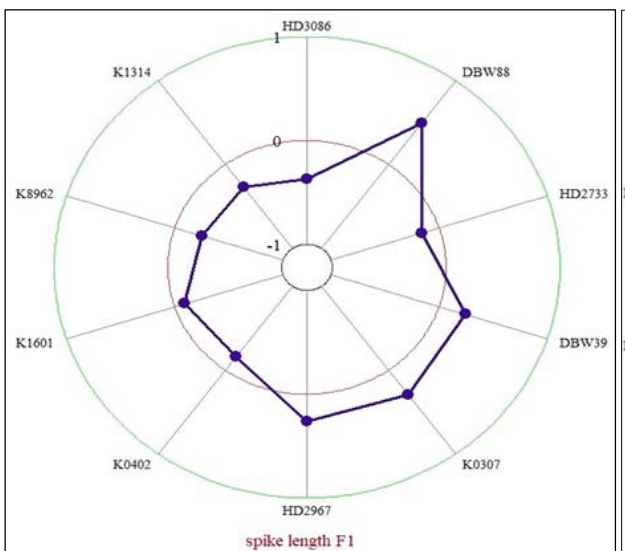
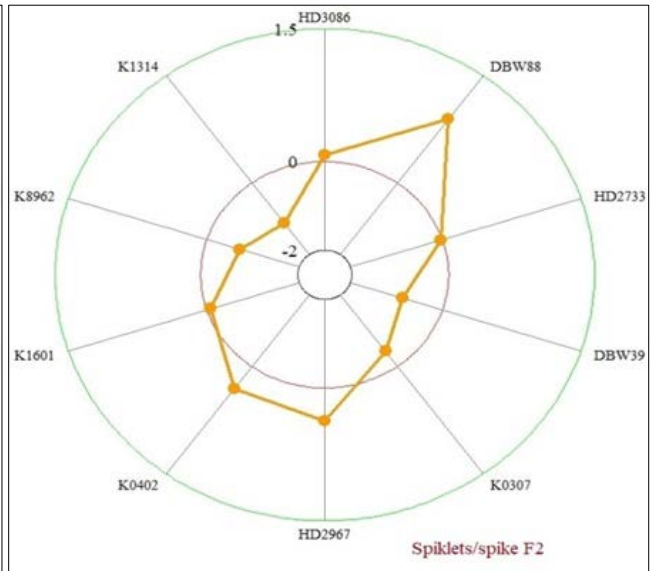
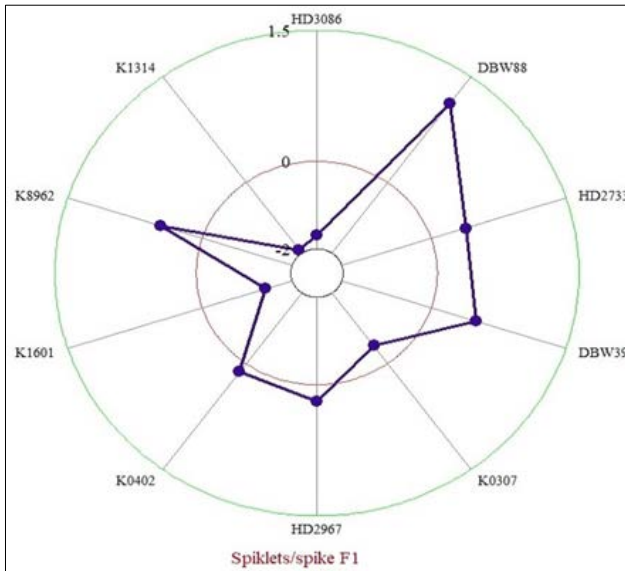
The category of contribution for high x low gca effects played an important role in the expression of positive and significant sca effects. These crosses showing high sea effects with at least one good general combiner could produce desirable transgressive segregants in subsequent generations: Vanpariya *et al.* (2006) [17], Soylu and Akgün (2007) [16], Murphy *et al.* (2008) [14], Kapoor *et al.* (2011) [9], Jatav *et al.* (2014) [7], Verma *et al.* (2016), Yadav (2017), Khaled *et al.* (2020) [11] and Emam *et al.* (2021) [3], Shahidet *et al.* (2005) and Zahidet *et al.* (2007) also came to the same results. For better utilization of these crosses, the inter se crossing of F1 hybrids in all possible combinations for multiple parents is put into a common gene pool, which will lead to realization of better recombinants and also help in breaking up of the genetic barriers, if present (Jensen 1970). Later, Redder and Jensen (1974), demonstrated significant gain in seed weight through mass selection with concurrent random mating and suggested that this technique could be a useful breeding procedure for wheat.

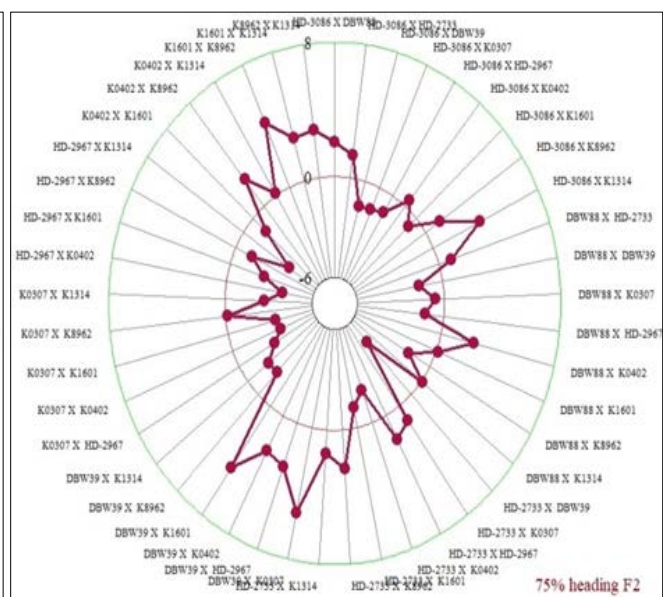
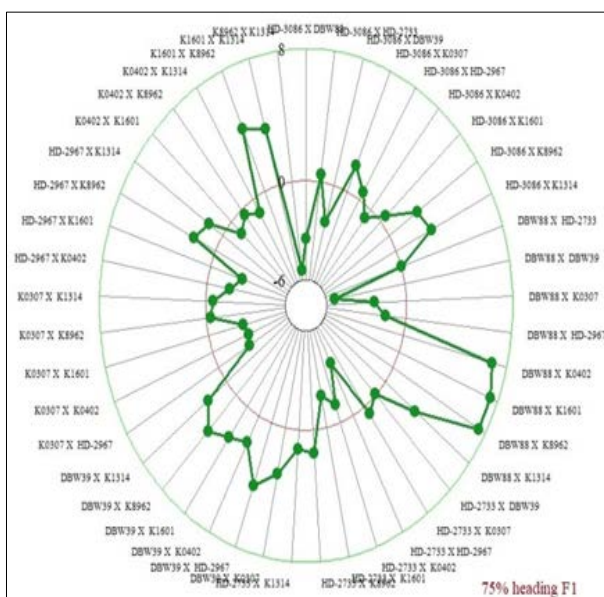
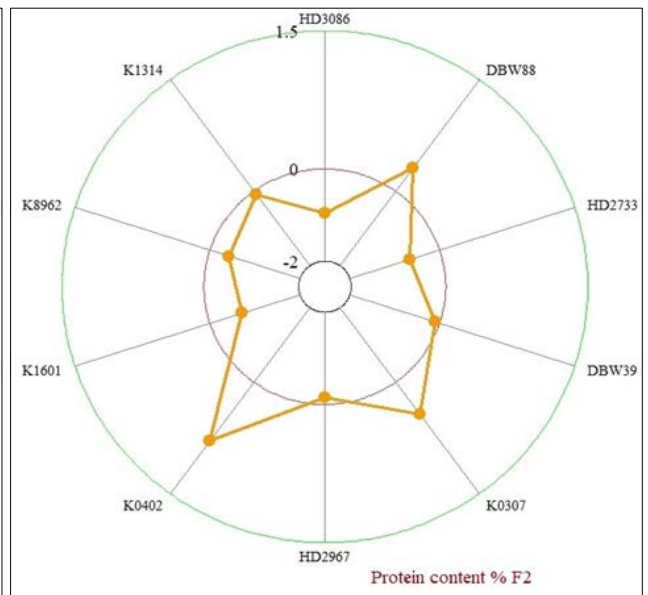
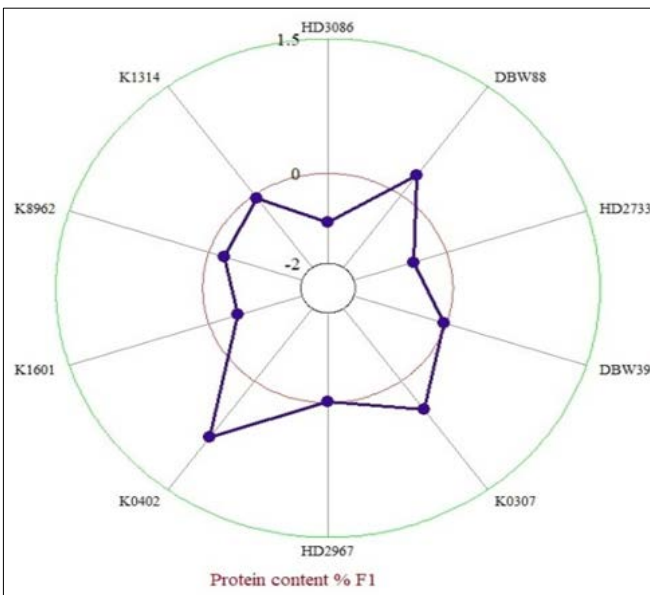
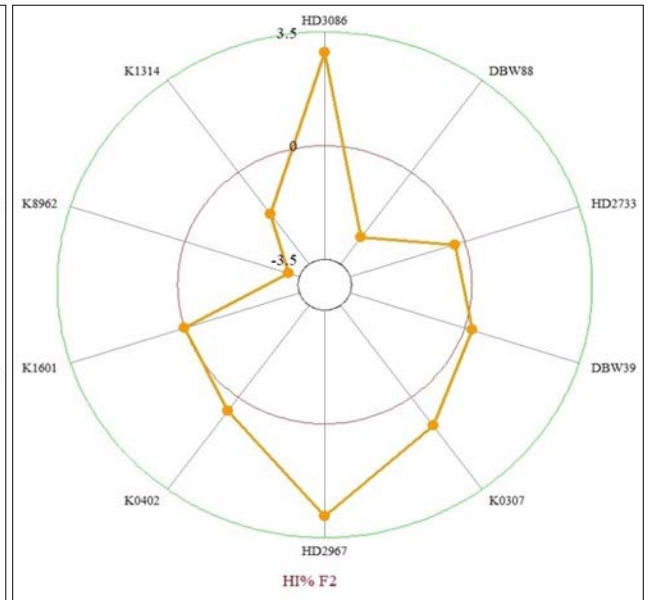
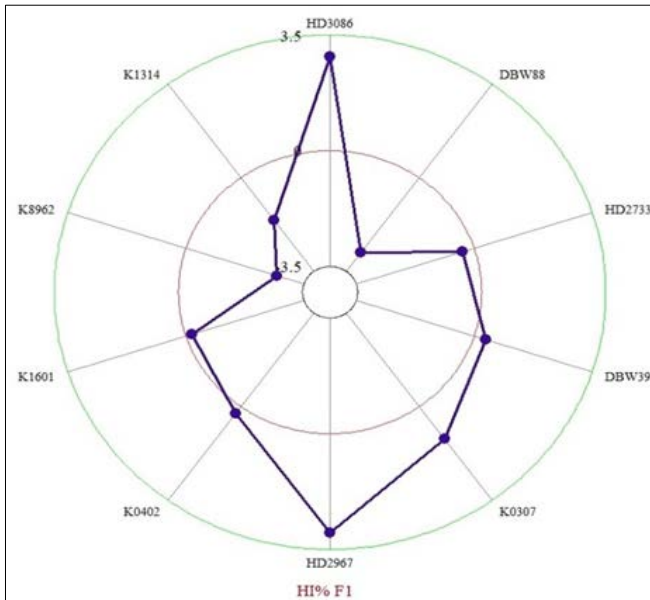
The cross combinations possessing low x low effects in both the-generations such types of hybrids might be due to non-additive gene effects and could not be easily exploited in further segregating generations. Hence these crosses could be used in production of multiline variety combining other desirable attributes of economic value.

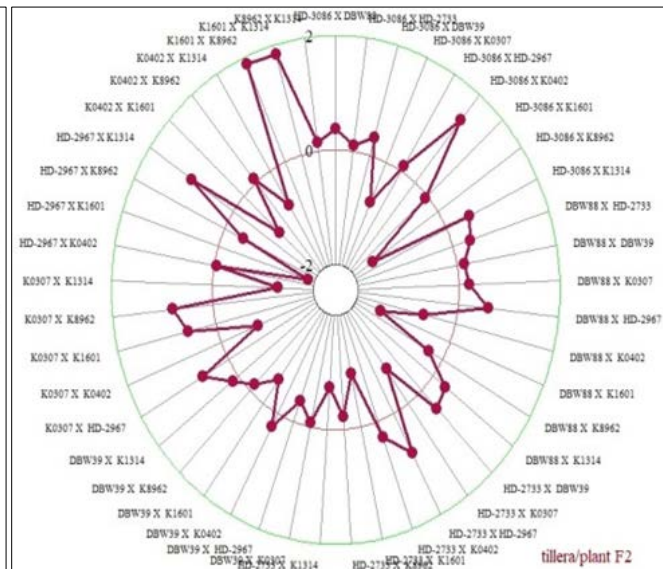
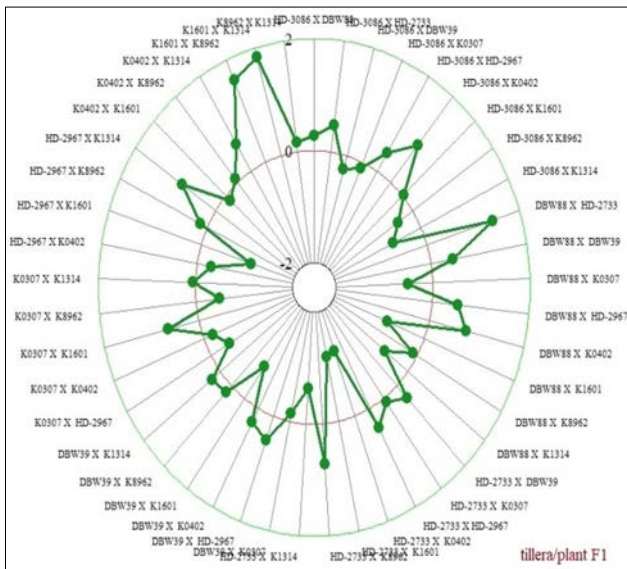
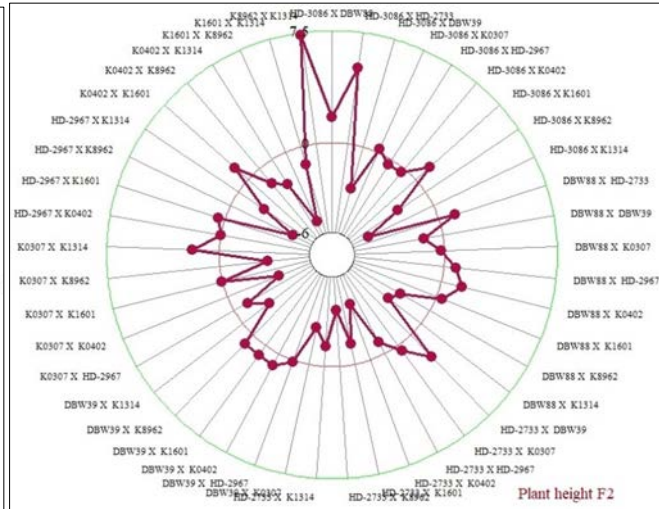
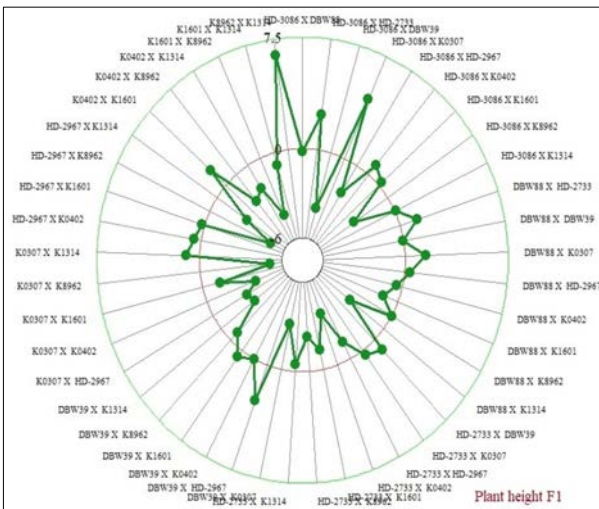
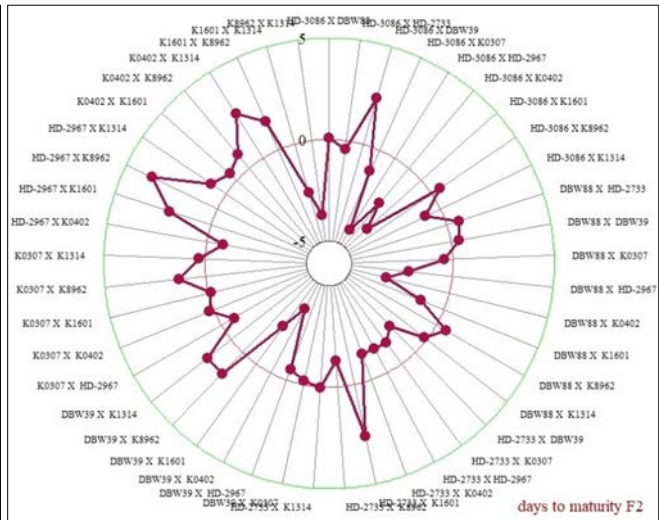
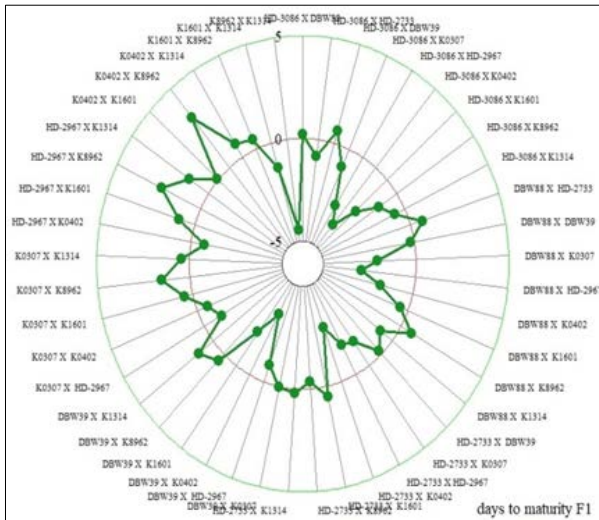




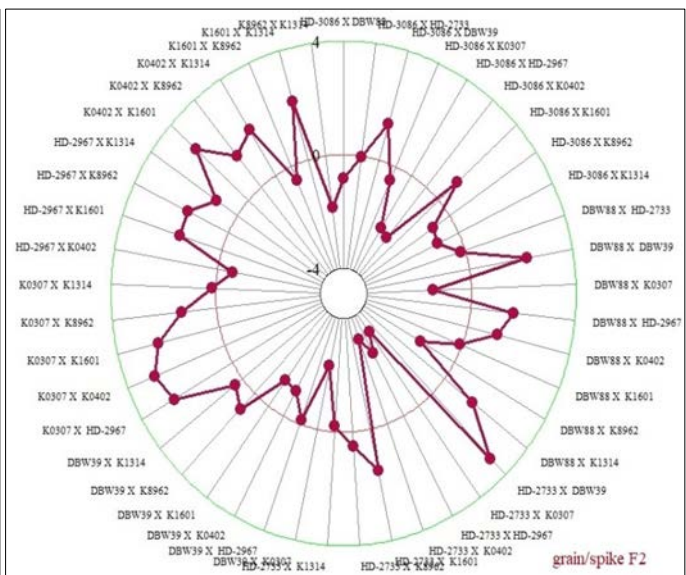
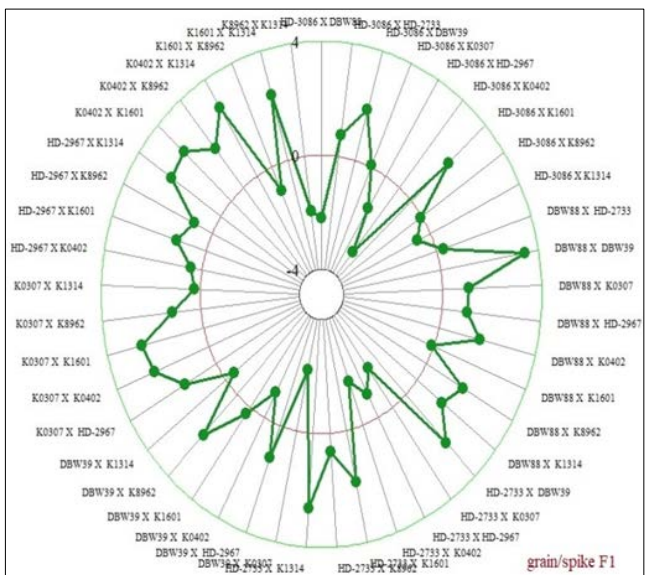
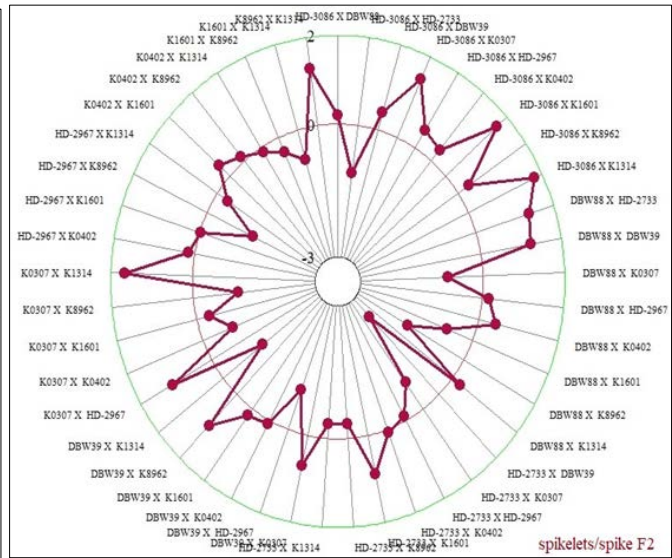
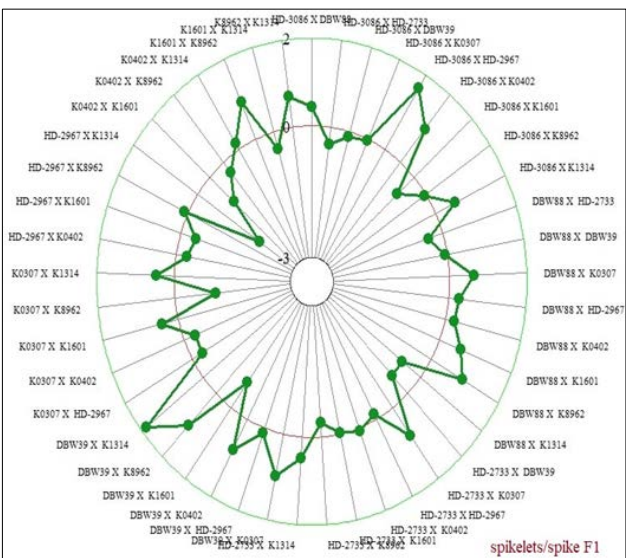
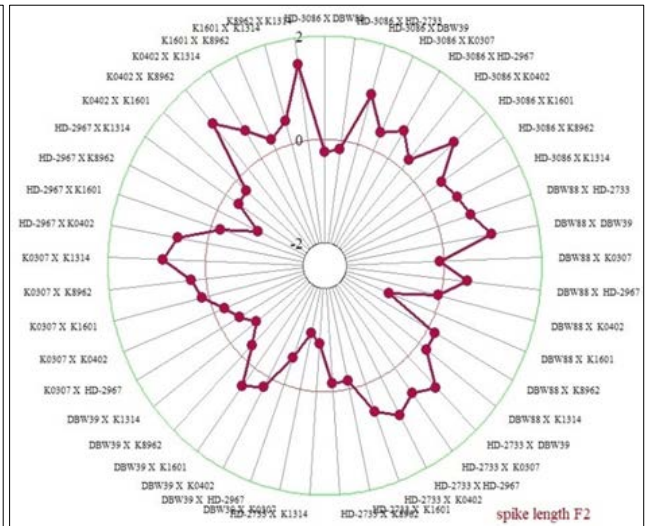
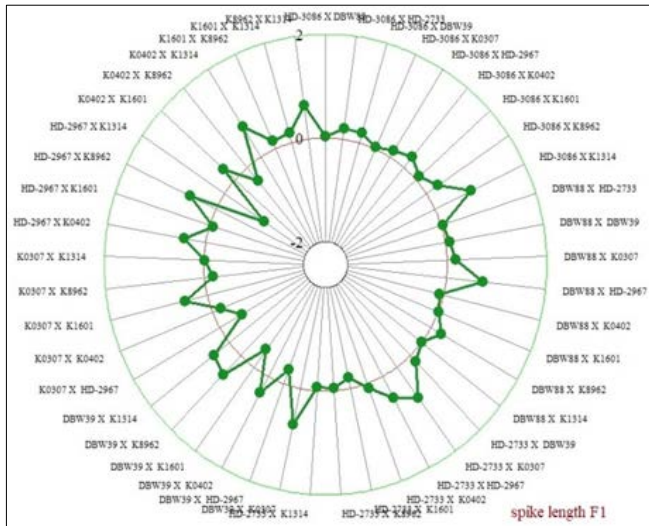


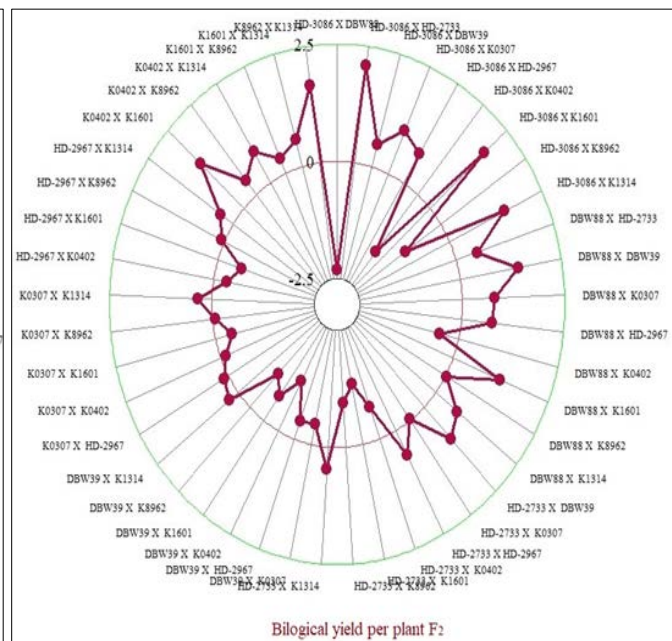
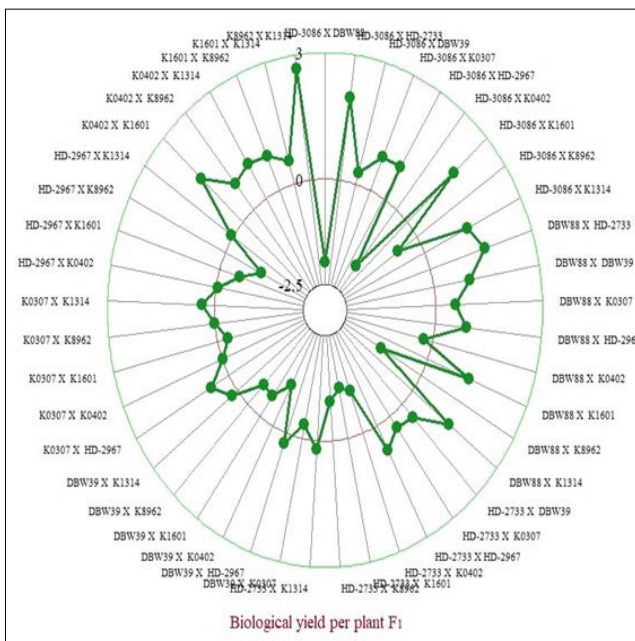
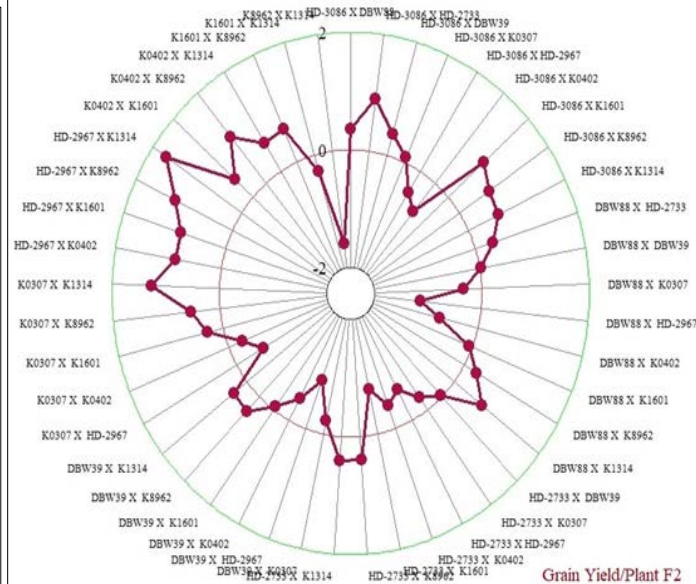
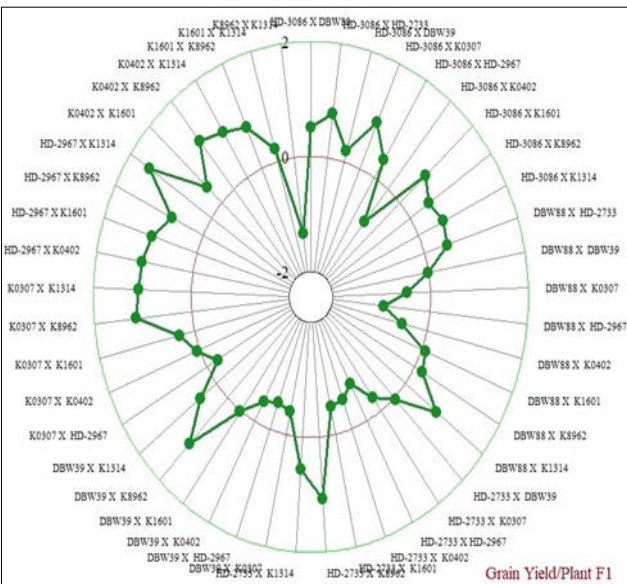
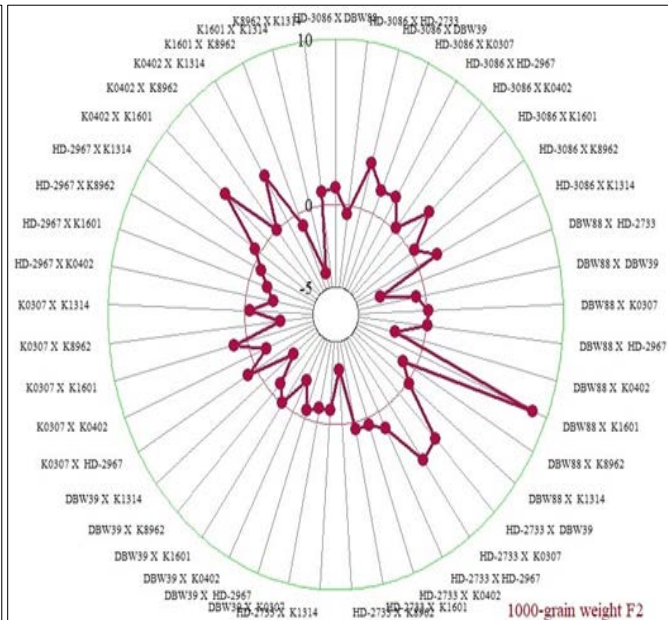
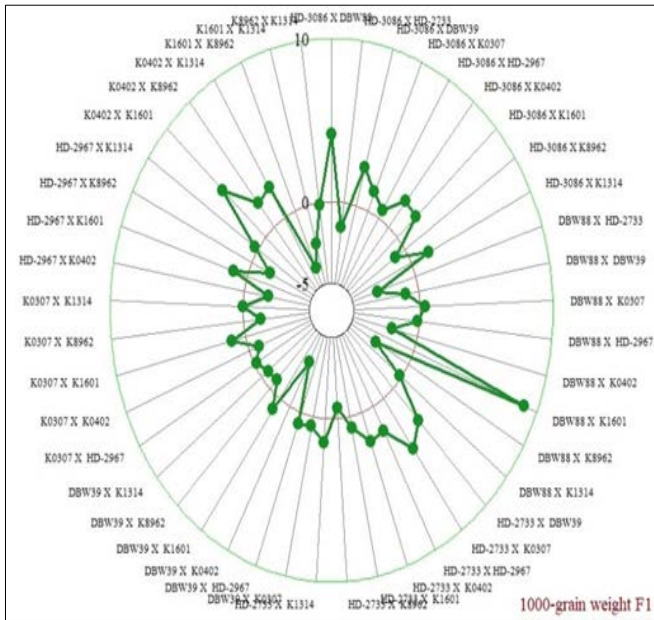


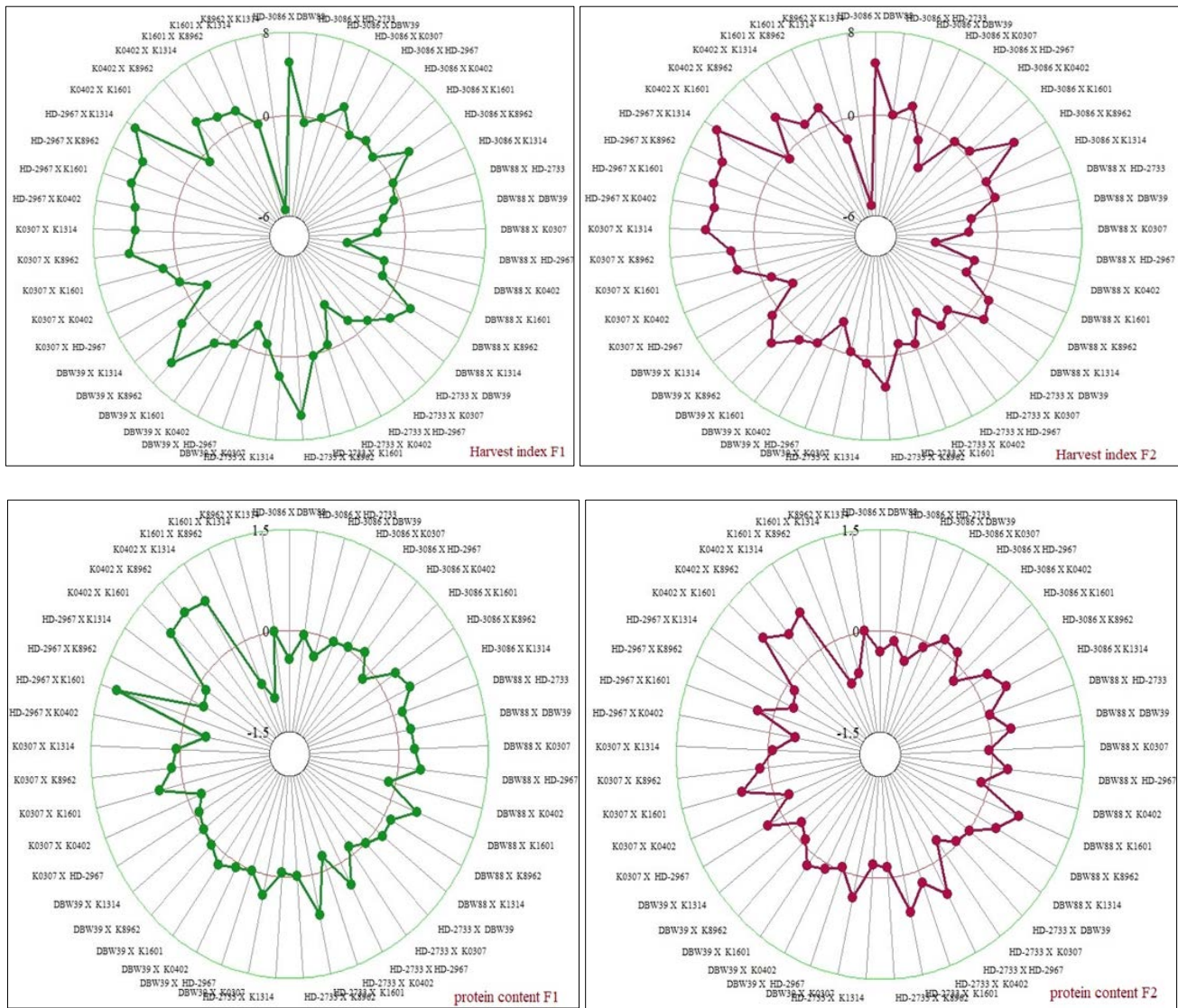












**Graphs 1:** Specific Combining Ability with ten diverse parents and their different characteristics in F<sub>1</sub> and F<sub>2</sub> generations

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