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# Combining Ability and Heterosis Analysis for Seed Yield and Yield Related Traits in Table Pea [*Pisum sativum* (L.) var. *hortense*]

Archi Gupta[1,2], Bijendra Singh[1], Mukesh Kumar[1], V.R. Sharma[3],
Charupriya Chauhan[2], Sanghamitra Rout[4], Satish K. Yadav[5]

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## ABSTRACT

**Background:** A study was carried out to estimate the general and specific combining abilities, as well as heterosis for seed yield and yield associated traits in pea lines.

**Methods:** Twenty-eight cross combinations were generated using half-diallel mating design with eight parental lines. The mean values of seed yield and its contributing traits of parental lines and their offspring for each replication were used for statistical analysis *viz.,* GCA, SCA and Heterosis.

**Result:** The GCA and SCA were significant and indicating the presence of both additive and non-additive types of gene actions. AP-3, VL-7, Kashi_Nandini and PC-531 were identified as promising parents due to significant GCA effects on seed yield and other traits. Among the crosses Kashi_Nandini × PC-531, VL-7 × PMR-53, Arkel × Vl-7 and VL-7 × Kashi_uday hybrids were the most promising, with significantly higher SCA effects for seed yield and yield related traits. Seed yield showed significantly high heterosis ranged from -2.00% to 8.77 % (AP-3 × PC-531 and Arkel × PMR-53, respectively) and relative heterosis ranged from -0.75% to 14.10% (Kashi_uday × PC-531 and Arkel × PMR-53 respectively) significantly exhibited positive heterosis for seed yield over better parent and mid-parent.

**Key words:** Combining ability, Half di-allele, Heterosis, Table pea.

## INTRODUCTION

The garden pea (*Pisum sativum* L. var. *hortense*; 2n=14) is the cool season legume belongs to family Leguminosae and widely used as seed vegetable. It is highly self-pollinated crop and native to South-West Asia (Kumari *et al.,* 2015). India contributes around 21% of world pea production with an area and production, 0.54 million hectares and 5.45 million metric tons, respectively. (Anonymous, 2017).

Pea is cherished for its nutrition's as its seeds contains 20-30% protein. Aside from that, it is a good source of essential amino acids such as lysine and tryptophan. Furthermore, it contributes to better human health by lowering the risk of heart disease, diabetes and other ailments (Kumari *et al*., 2015). Due to these characteristics pea promises an excellent research potential as compared to other pulses but yet to be exploited at desired levels. To meet the demands of an ever-increasing population, pea genotypes must be genetically improved in order to produce high-yielding, disease-resistant varieties. (Halil and Uzan, 2019). Hybridization is one among the most effective method employed in plant breeding to enhance the quality and yield of vegetable crop produce. The selection of desirable parents with desired characteristics is important pre-requisite to for developing high yielding and disease resistant genotypes in hybridization program (Inamullah *et al.*, 2006).

Combining ability is important in plant breeding because it aids in determining the nature and magnitude of genetic effects governing quantitative traits to identify the best performing lines (Basbag *et al.,* 2007). The general combining ability (GCA) indicates the presence of additive gene effect (main effect), which aids in the selection of parental lines based on average performance in a series of hybrid combinations, whereas the specific combining ability (SCA) reveals the presence of non-additive (interaction effect), which aids in the identification of better hybrid combinations based on hybrid vigour or heterosis. Heterosis is an important tool for genetic improvement of quantitative traits which is the superiority of $F_1$ hybrid over its mid-parental value in terms of yield and its related traits. Therefore, exploitation of hybrid vigor in improvement of yield and its

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[1]Department of Horticulture, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut-250 110, Uttar Pradesh, India.
[2]School of Agriculture, Lovely Professional University, Phagwara-144 411, Punjab, India.
[3]CSIR-National Botanical Research Institute, Lucknow-226 001, Uttar Pradesh, India.
[4]Department of Genetics and Plant Breeding, Centurion University of Technology and Management, Gajapati-761 211, Odisha, India.
[5]ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi-110 012, India.

**Corresponding Author:** Archi Gupta, Department of Horticulture, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut-250 110, Uttar Pradesh, India. Email: archigupta22@gmail.com

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related traits could be a key technique for breaking existing yield barriers. In addition, study of heterosis in self-pollinated crops offers an opportunity to breeders to identify promising crosses in early generation that can give transgressive segregants in later segregating generations. The purpose of this study was to assess the general and specific combining ability, heterosis and heterobeltiosis for nine quantitative traits for future breeding programmes.

## MATERIALS AND METHODS

The current study was conducted at the Horticulture Research Centre (HRC) of the S.V.P University of Agriculture and Technology, Meerut during *rabi,* of 2018-19 and 2019-20. Twenty-eight cross combinations were generated using half-diallel mating design with eight parental lines. During *Rabi* 2018-19, the parental lines were grown in a randomised block design (RBD) with three replications. When the flowers are at a mature bud stage, the female parents were emasculated in the evening. The emasculated flower is then bagged before tagging in order to restrict unwanted pollination. Pollination was done consecutive next day morning by using pollen collected from the selective male parent. The pods obtained from the cross were separately harvested and seeds were stored.

The seeds of F1 hybrids and parental lines were grown in RBD with three replications. The observations were recorded for seed yield and its contributing characters *viz*., DF 50%- Days to 50% flowering, PH- Plant height (cm), NFFN- No. of first fruiting node, LFFN- Length of first fruiting node, NPP- No. of pods/plant, LP- Length of pod, WP- Width of pod, NSP-No. of seeds/pod, SYP- Seed yield/plant (g). The experimental data was analyzed using mean values of each observation for parental lines and their offspring for each replication on five randomly selected plants. Analysis of variance was carried out as explained previously by Panse and Sukhatme (1967). The combining ability analysis was performed by preceding the procedures earlier detailed by Kempthorne (1957). Estimation of heterosis over mid-parent and better parent (heterobeltiosis) was done following procedures earlier outlined by Fonseca and Petterson (1968).

## RESULTS AND DISCUSSION

Analysis of variance revealed significant difference among all the among parents and their hybrid combinations for the nine quantitative traits studied. The interaction between parent and hybrids was found to be significant for the all the nine traits (Table 1). The combining ability is of two types, general and specific for the quantitative genetics. General combining ability (GCA) reveals the average performance of a parental lines in a series of crosses which indicates the additive gene effect (main effect). Whereas the specific combining ability (SCA) is the deviation in the performance of hybrids from the parents which indicates the presence of

**Table 1:** Analysis of variance for parent, hybrids and combing ability for nine quantitative traits.

| SV | df | DF50% | PH | NFFN | LFFN | NPP | LP | WP | NSP | SYP |
|---|---|---|---|---|---|---|---|---|---|---|
| REP | 2 | 0.45 | 0.22 | 0.11 | 0.10 | 0.02 | 0.16 | 0.0013 | 0.01 | 0.11 |
| Treatment | 35 | 104.87** | 515.62** | 10.91** | 28.57** | 20.33** | 3.60** | 0.0069** | 0.911** | 167.92** |
| PAR | 7 | 199.37** | 868.94** | 6.65** | 43.48** | 33.92** | 0.73 | 0.0128** | 1.06** | 341.88** |
| F1 | 27 | 78.72** | 437.87** | 10.58** | 23.94** | 16.17** | 2.73** | 0.0055** | 0.81** | 127.21** |
| P x F1 | 1 | 149.22** | 141.90** | 49.73** | 49.16** | 37.55** | 47.28** | 0.0056** | 2.71** | 49.44** |
| Error | 70 | 0.55 | 0.21 | 0.08 | 0.07 | 0.05 | 0.09 | 0.0014 | 0.03 | 0.12 |
| GCA | 7 | 141.91** | 793.70** | 11.52** | 39.92** | 26.99** | 1.37** | 0.0106** | 0.955** | 273.41** |
| SCA | 28 | 8.22** | 16.42** | 1.67** | 1.92** | 1.73** | 1.16** | 0.0002 | 0.141** | 1.62** |
| Error | 70 | 0.18 | 0.07 | 0.03 | 0.02 | 0.02 | 0.03 | 0.0005 | 0.011 | 0.04 |
| GCA/SCA ratio |  | 17.27 | 48.35 | 6.91 | 20.76 | 15.64 | 1.19 | 45.71 | 6.78 | 169.24 |

SV-Source of variation; df- Degrees of freedom; *, ** Significant at 5% and 1% level, respectively.

**Table 2:** Estimation of general combining ability (GCA) effects of parents for nine quantitative traits in pea.

| Parents | DF-50% | PH | NFFN | LFFN | NPP | LP | WP | NSP | SYP |
|---|---|---|---|---|---|---|---|---|---|
| AP-3 | -2.08** | 8.68** | 1.18** | 1.59** | 2.17** | 0.44** | 0.02** | 0.59** | 7.73** |
| Kashi_Nandini | -3.65** | -8.35** | -0.06 | -0.36** | -1.57** | -0.05 | 0.00 | -0.08 | -4.13** |
| Arkel | -1.12** | -7.44** | -0.75** | 0.04 | -1.15** | -0.19** | -0.06** | -0.34** | -3.89** |
| VL-7 | -1.78** | 14.44** | 0.71** | 2.90** | 1.73** | 0.53** | 0.02** | -0.31** | -0.03 |
| PMR-53 | 0.38 | 4.29** | 0.64** | -1.25** | -1.18** | -0.26** | 0.02** | 0.14** | -4.54** |
| Kashi_uday | -2.92** | -10.17** | -1.55** | -3.86** | -1.96** | -0.57** | 0.00 | -0.12** | -5.15** |
| PC-531 | 7.35** | -4.18** | -1.27** | 0.36** | 0.68** | -0.12** | 0.04** | 0.24** | 6.03** |
| AP-1 | 3.82** | 2.73** | 1.09** | 0.57** | 1.30** | 0.21** | -0.03** | -0.13** | 3.99** |
| *SE* (gi) | 0.400 | 0.079 | 0.050 | 0.046 | 0.037 | 0.051 | 0.007 | 0.031 | 0.059 |
| *SE* (gi-gj) | 0.191 | 0.119 | 0.075 | 0.070 | 0.055 | 0.077 | 0.031 | 0.046 | 0.089 |

SE-Standard error; *, **Significant at 5% and 1% level, respectively.

non-additive (interaction effect) effect may be due to dominance or epistasis interaction (Kumari *et al.,* 2015).

The analysis of variance for combining ability revealed that the GCA and SCA effects were highly significant for all traits. except with trait WP indicating for SCA (Table 1). The estimates of GCA effects for parental lines were presented in Table 2. The parents AP-1 and AP3 were showed positive significant GCA effects for more than six traits hence they can be considered as good general combiners. The parents AP-3, PC-531 and AP-1 showed significantly high positive GCA effect for SYP and they can be used as good general combiners for seed yield. VL-7 proved to be a good general combiner for plant height and length of the pod. PC-531 and AP-1 are good combiners for DF 50% as they report highly significant GCA effect in positive direction in contrast to Kashi Nandini and Kashi uday showed for DF 50% in negative direction. AP-3, VL-7, AP-1 and PC-531 were good combiners for NPP because they had a significant GCA effect in the positive direction. AP-3, PC-531 and PMR-53 were good combiners for NSP and had a significant positive GCA effect. These good general combiners can be used in specific breeding programs by the breeder for the genetic improvement of pea varieties.

The lines with high GCA mostly due to additive gene effect have good breeding value with significant genetic gains with larger adaptability. Moreover, high GCA have less environmental effect and less gene interaction and therefore can be used for the selection of desired parents (Griffing, 1956). Earlier, in a similar investigation Dagla *et al.* (2013) stated that variance due to *gca* was highly significant for DF-50%, PH, NPP and SYP in Pea, indicating the importance of both the additive and non-additive genetic components variation. Similar studies were reported earlier in pea by Nageshwar *et al.* (2020), Katoch *et al.* (2019), Shivaputra *et al.* (2018),), Suman *et al.* (2017), Dar *et al.* (2017), Joshi *et al.* (2015), Kumari *et al.* (2015), Mishra *et al.* (2014), Patel (2012) and Sharma *et al.* (2007).

The estimates of SCA effects for twenty-eight crosses were presented in the Table 3. The SCA effects represents dominance or epistasis interaction used for the particular cross combination can be used for the exploitation of heterosis. For SYP, eleven cross (AP-3 × Kashi-Nandini,

**Table 3:** Estimation of specific combined ability (SCA) effects of hybrids for nine quantitative traits in pea.

| Hybrids | DF-50% | PH | NFFN | LFFN | NPP | LP | WP | NSP | SYP |
|---|---|---|---|---|---|---|---|---|---|
| AP3 × Kashi-Nandini | -0.69 | -1.12** | 0.67** | 0.38* | 0.24* | 0.83** | 0.03 | -0.04 | 0.57* |
| AP3 × Arkel | 0.44 | 1.85** | 1.77** | 2.15** | 0.79** | 0.14 | 0.00 | 0.43** | 1.77** |
| AP3 × VL-7 | -0.56 | -0.02 | 0.92** | -0.10 | -0.01 | -0.60** | 0.03 | 0.45** | 0.27 |
| AP3 × PMR-53 | -1.39** | 0.17 | -0.31** | 0.34* | -0.02 | 0.43* | -0.01 | -0.09 | 0.14 |
| AP3 × Kashi-Uday | -0.43 | 1.94** | 1.62** | 1.53** | 1.53** | 1.49** | -0.01 | 0.24* | 0.88** |
| AP3 × PC-531 | 0.31 | 0.63 | -0.75** | -0.72** | -1.11** | -0.35* | 0.00 | 0.49** | -0.52* |
| AP3 × AP 1 | -1.83** | -0.52 | -0.12 | -0.36** | 0.33** | 0.85** | 0.01 | -0.27* | -0.44* |
| Kashi-Nandini × Arkel | 2.34** | -2.06** | -0.96** | -0.42** | -0.39** | -0.11 | -0.01 | 0.33** | 0.24 |
| Kashi-Nandini × VL-7 | 2.34** | -0.98** | -0.09 | 0.88** | -0.06 | 0.71** | 0.00 | 0.26* | 0.10 |
| Kashi-Nandini × PMR-53 | 0.17 | -0.59** | 0.88** | 0.75** | 1.11** | 0.42* | 0.01 | 0.35** | 0.23 |
| Kashi-Nandini × Kashi-Uday | -0.86* | -2.09** | -0.31 | -0.81** | -0.76** | -0.50** | -0.01 | -0.24* | -0.12 |
| Kashi-Nandini × PC-531 | -1.13 | 0.05 | 0.75** | 1.74** | 2.01** | 0.78** | 0.01 | 0.05 | 2.07** |
| Kashi-Nandini × AP 1 | -2.59** | 16.48** | 1.50** | 0.51** | -0.03 | 0.15 | 0.00 | 0.22* | 0.23 |
| Arkel × VL-7 | -6.53** | 0.84** | 0.15 | 1.56** | 0.45** | 1.15** | 0.01 | -0.14 | 1.11** |
| Arkel × PMR-53 | 2.64** | 1.35** | 1.16** | -0.34* | 0.94** | -0.84** | 0.01 | -0.10 | 1.40** |
| Arkel × Kashi-Uday | 1.61** | -0.03 | -0.62** | -0.33* | -0.73** | -0.33 | 0.02 | -0.08 | -0.54* |
| Arkel × PC-531 | 0.34 | -1.36** | -1.28** | -1.81** | -1.35** | 0.79** | -0.01 | -0.29* | -2.92** |
| Arkel × AP1 | 0.87* | 0.21 | 1.61** | 1.01** | 0.75** | 1.65** | 0.01 | 0.04 | 1.31** |
| VL- 7 × PMR 53 | -3.69** | 8.73** | 1.62** | 3.22** | 3.45** | 1.43** | 0.01 | 1.02** | 0.61* |
| VL-7 × Kashi-Uday | -2.73** | 0.79** | 0.57** | 0.18 | 0.70** | 0.56** | 0.00 | -0.26* | 0.22 |
| VL-7 × PC-531 | -2.66** | -0.07 | 1.00** | 0.18 | 0.28* | 0.12 | 0.00 | -0.15 | 1.39** |
| VL-7 × AP 1 | -2.46** | -2.16** | -0.48** | -1.16** | -0.02 | 0.90** | 0.00 | -0.07 | 0.10 |
| PMR-53 × Kashi-Uday | -1.56** | -1.03** | -0.80** | -0.45** | -0.56** | -0.13 | -0.01 | 0.38** | 0.29 |
| PMR-53 × PC-531 | -0.16 | 0.02 | 1.90** | 0.62** | 0.22 | 1.32** | 0.02 | -0.18 | -0.24 |
| PMR-53 × AP1 | -2.29** | -1.52** | 0.41** | 0.96** | 0.13 | 0.47** | 0.01 | -0.07 | 1.48** |
| Kashi-Uday × PC-531 | -1.53** | 0.68* | -0.63** | -0.15 | -0.55** | -0.32* | 0.00 | 0.01 | -0.39* |
| Kashi-Uday × AP 1 | 4.01** | -1.37** | 0.94** | 1.07** | 1.88** | 0.02 | 0.02 | 0.07 | 0.71** |
| PC-531 × AP 1 | 0.41 | -1.66** | -0.96** | -0.36* | -0.38** | -1.16** | -0.02 | 0.03 | 0.18 |
| *SE* (sij) | 0.388 | 0.242 | 0.152 | 0.141 | 0.112 | 0.157 | 0.020 | 0.094 | 0.181 |
| *SE* (sij-sik) | 0.574 | 0.357 | 0.225 | 0.209 | 0.166 | 0.232 | 0.029 | 0.139 | 0.268 |

AP-3 × Arkel, AP3 × Kashi-uday, Kashi-Nandini × PC-531, Arkel × VL-7, Arkel × PMR-53, Arkel × AP1, VL- 7 × PMR-53, VL-7 × PC-531, PMR-53 × AP-1, Kashi-uday × AP-1) exhibited significant SCA effect in positive direction and they can be used as good specific combiners for SYP. Among them Kashi-Nandini × PC-531 showed with the highest SCA effects, can be used as best specific combination for SYP. The crosses AP-3× Kashi-uday and VL-7 and PMR-53 exhibited significant positive SCA effect for all traits except for DF 50%. Twelve crosses showed significant negative SCA effect for DF 50% and among them the cross Arkel x VL-7 showed highest SCA effect in negative direction and can be used as good specific combiner with desirable traits. VL-7 × PMR 53 was good specific combiner for NPP and NSP with high SCA effect in positive direction. Recently, Moses *et al.* (2020) also noticed a high positive significant SCA effects for SYP in pea. The SCA effect on yield and its related characteristics has previously been reported by Nageshwar *et al.* (2020), Katoch *et al.* (2019), Halil *et al.* (2019), Suman *et al.* (2017), Kumari *et al.* (2015), Cehyan *et al.* (2008), Ceyhan (2003). For SYP, the cross AP-3 × Arkel showed high significant positive SCA effect (high × low GCA) that showed the additive and epistatic interaction. The cross Kashi-Nandini × PC-531 and PMR-53 × AP-1 also showed significant positive GCA effect (low × high GCA) that implies the epistatic × additive interaction. Moreover, Arkel × PMR-53 (low × low GCA interaction) showed the dominance × dominance type of interaction with high positive significant SCA affect. These cross combinations can be used as good specific combiners for the seed yield.

The estimate of heterosis over superior parent and mid-parent for 9 characters in parents and $F_1$ hybrids for yield and its contributing traits (Tables 4 and 5.). For SYP wider range of heterobeltiosis ranged from -2.00% to 8.77%, respectively and mid-parent heterosis ranged from -0.75% to 14.10%, respectively was recorded. Arkel × VL-7 and Arkel × PMR-53 exhibited positive significant maximum heterosis for SYP over better parent and mid-parent, respectively. Significant and negative heterosis was regarded as desirable for DF 50%, whereas positive and significant heterosis was regarded as desirable for other characters. DF 50% showed broad range of heterobeltiosis (-0.88% to 27.10%) and mid heterosis (-0.41% to 7.08%). VL-7 × PMR-53 and Arkel × VL-7 were significantly negative for DF-50%, over better parent and mid-parent respectively. VL-7 × PMR-53 exhibited positive significant maximum heterosis for LP and NPP over better parent and mid-parent respectively in positive direction. In addition, VL-7 × PMR-53 also showed high

**Table 4:** Estimation of heterosis for seed yield/plant and yield contributing traits (% increase/decrease over better parent).

| Hybrids | DF 50% | PH | NFFN | LFFN | NPP | LP | WP | NSP | SYP |
|---|---|---|---|---|---|---|---|---|---|
| 1 | 1.87 | -18.35** | 11.74** | 0.16** | -16.67** | 19.12** | 2.44 | -1.21 | -22.04** |
| 2 | 0.84 | -14.08** | 15.38** | 6.87**** | -10.55** | 9.91* | -3.33 | 1.41 | -18.87** |
| 3 | -5.74** | -2.22** | 20.76** | 2.84** | 2.68 | 9.76* | 2.85 | 1.98 | -13.64** |
| 4 | -2.46 | -3.03** | 9.35** | -2.71** | -15.86** | 12.43** | 0.22 | 0.93 | -23.91** |
| 5 | -0.88 | -16.98** | 7.03** | -7.09** | -10.97** | 20.71** | 0 | 1.65 | -23.62** |
| 6 | 18.85** | -11.84** | -11.38** | -1.02 | -10.93** | 5.36 | -1.48 | 8.99* | -2.00** |
| 7 | 4.92** | -5.51** | 12.24** | 0.75 | 2.11 | 22.34** | -1.33 | -4.56 | -6.33** |
| 8 | 13.08** | -4.30** | -4.51 | 0.3 | -5.92 | 10.72** | -3.39 | 7.69 | 5.43** |
| 9 | 11.21** | -20.14** | 9.36** | 0.02 | -7.21 | 27.06** | -0.22 | 7.08 | -7.17** |
| 10 | 11.21** | -12.07** | 26.82** | 4.82** | 31.43** | 16.44** | 0.66 | 10.55** | 6.97** |
| 11 | -0.93 | -1.5 | -6.01 | -9.73** | -1.15 | 1.49 | -0.45 | -2.03 | 2.44 |
| 12 | 27.10** | -7.36** | 8.01 | 2.45** | -4.83 | 16.62** | -2.12 | -3.66 | -19.13** |
| 13 | 13.08** | 13.37** | 15.60** | 1.33 | -11.54** | 15.65** | -1.13 | 3.21 | -16.36** |
| 14 | -15.97** | -17.42** | 5 | 3.17** | -0.25 | 30.58** | -3.51 | -0.34 | -2.91** |
| 15 | 12.61** | -8.51** | 22.57** | -2.42* | 11.56** | 4.13 | -3.53 | 0.95 | 8.77** |
| 16 | 7.08** | -3.95** | -6.02 | -11.06** | -13.40** | 5.6 | -2.47 | -3.29 | -2.77 |
| 17 | 24.37** | -8.11** | -10.51** | -7.47** | -25.64** | 15.16** | -6.99 | -10.85** | -30.10** |
| 18 | 16.81** | -6.90** | 10.60** | 4.23** | -2.72 | 31.65** | 0 | -2.59 | -12.84** |
| 19 | -19.29** | 2.13** | 32.39** | 4.23** | 21.89** | 33.19** | 1.32 | 16.64** | -6.87** |
| 20 | -6.19** | -20.19** | 1.43 | -12.25** | -4.45 | 19.15** | -0.66 | -5.23 | -10.31** |
| 21 | -3.52** | -15.08** | 8.18** | 0.08 | 6.32** | 15.73** | -0.85 | -8.82* | -11.26** |
| 22 | -10.56** | -10.28** | 5.14** | -3.24** | 12.84** | 31.22** | -2.41 | -3.71 | -5.72** |
| 23 | 2.65 | -14.90** | -5.79 | -1.95 | 12.61** | 7.35* | -0.88 | 9.46* | 7.03** |
| 24 | 7.86** | -6.09** | 24.90** | -3.88** | -14.74** | 20.53** | -0.21 | -3.66 | -25.42** |
| 25 | -4.29** | 0.6 | 12.27** | -0.06 | -7.48** | 16.94** | -1.32 | 2.32 | -14.11** |
| 26 | 21.24** | -9.13** | -10.80** | -14.52** | -25.71** | -1.96 | -2.97 | -4.63 | -27.19** |
| 27 | 26.55** | -12.60** | -2.07 | -8.10** | -0.37 | 7.96* | -0.45 | 0.76 | -17.82** |
| 28 | 3.82** | -5.07** | -16.01** | -1.24 | -1.39 | -2.72 | -5.93 | -4.43 | -4.77** |
|  | 0.71 | 0.32 | 0.23 | 0.18 | 0.17 | 0.23 | 0.04 | 0.15 | 0.24 |

significant positive heterosis for NSP over both better parent and mid-parental heterosis. Previously, Rebika (2017) also observed heterobeltiosis and standard heterosis for seed yield along with most of its yield components in pea which have the immense potential to exploit hybrid vigour or to isolate desirable segregants. Similar findings in pea have been reported by Nageshwar *et al*. (2020), Katoch *et al* (2019), Halil *et al.* (2019) and Kumari *et al.* (2015).

**Table 5:** Estimation of heterosis for seed yield/plant and yield related traits (% increase/decrease over mid-parent).

| Hybrids | DF 50% | PH | NFFN | LFFN | NPP | LP | WP | NSP | SYP |
|---|---|---|---|---|---|---|---|---|---|
| 1 | -4.80** | 2.81** | 21.37** | 6.41** | 10.03** | 24.22** | 3.36 | 6.52 | 6.21** |
| 2 | -0.41 | 3.70** | 32.09** | 10.95** | 10.42** | 17.10** | 1.16 | 10.31** | 8.97** |
| 3 | -12.88** | 2.60** | 25.57** | 5.71** | 11.12** | 13.46** | 3.53 | 13.92** | 5.07** |
| 4 | -9.16** | 3.14** | 17.66** | 8.36** | 14.93** | 23.13** | 0.55 | 6.97 | 5.45** |
| 5 | -4.68** | 3.28** | 29.50** | 9.48** | 19.89** | 28.05** | 0.56 | 7.28 | 5.50** |
| 6 | -3.65** | 1.18* | 2.14 | -0.1 | -5.97** | 7.31 | 0.87 | 9.43* | 0.07 |
| 7 | -8.24** | 3.08** | 13.55** | 2.75** | 9.75** | 25.92** | 1.83 | 0.3 | 2.70** |
| 8 | 7.08** | 0.99 | 1.15 | 2.73** | 2.83 | 13.23** | 0.23 | 8.71* | 7.72** |
| 9 | -4.42** | 4.19** | 14.47** | 9.03** | 15.48** | 28.22** | 1.34 | 11.27* | 7.50** |
| 10 | -3.64** | 5.42** | 28.13** | 10.25** | 38.23** | 22.56** | 1.9 | 12.59** | 9.90** |
| 11 | -3.64** | 0.09 | 5.83 | 0.85 | 1.77 | 3.32 | -0.11 | 0.23 | 4.70** |
| 12 | -4.90** | 3.39** | 15.26** | 7.90** | 20.81** | 19.46** | 1.09 | 3.49 | 8.67** |
| 13 | -8.33** | 32.91** | 26.91** | 5.65** | 10.71** | 17.21** | 1.16 | 6.06 | 6.68** |
| 14 | -23.37** | 3.52** | 16.09** | 9.97** | 15.23** | 34.73** | 1.62 | 2.62 | 10.37** |
| 15 | 3.47** | 4.77** | 31.10** | 4.99** | 27.63** | 7.25 | 1.27 | 3.79 | 14.10** |
| 16 | 4.31** | -0.19 | 0.29 | 1.49 | -2.82 | 6.08 | 1.52 | -0.14 | 1.48 |
| 17 | -0.67 | -2.49** | -9.80** | -4.79** | -12.17** | 20.57** | -0.45 | -3.39 | -7.42** |
| 18 | 0.72 | 4.09** | 27.87** | 6.15** | 13.08** | 36.41** | 1.44 | 1.02 | 9.41** |
| 19 | -19.86** | 13.64** | 37.19** | 18.95** | 57.56** | 41.41** | 1.65 | 23.37** | 10.32** |
| 20 | -16.86** | 2.95** | 18.84** | 5.75** | 21.55** | 22.39** | 0.55 | 0.67 | 5.78** |
| 21 | -14.64** | 1.53** | 20.46** | 3.79** | 9.15** | 17.49** | 0.86 | 1.49 | 6.16** |
| 22 | -15.05** | 2.26** | 10.54** | 1.37 | 13.68** | 31.78** | 1.37 | 2.71 | 5.85** |
| 23 | -8.30** | 0.7 | 7.04 | 4.50** | 15.11** | 11.06** | 0 | 9.95* | 7.59** |
| 24 | -5.33** | 1.88** | 34.58** | 6.18** | 12.27** | 29.79** | 1.84 | 1.72 | 2 |
| 25 | -9.76** | 3.37** | 22.09** | 9.35** | 20.22** | 24.67** | 2.17 | 3.24 | 11.70** |
| 26 | -6.16** | -0.04 | -5.51 | -0.04 | -3.67* | 2.2 | -0.11 | 0.26 | -0.75 |
| 27 | 5.93** | 1.09 | 19.58** | 6.52** | 27.43** | 11.37** | 2.19 | 1.21 | 6.48** |
| 28 | -2.98** | 0.39 | -2.24 | -0.2 | 0.5 | -1.67 | -0.67 | 0.04 | 2.41** |
|  | 0.56 | 0.3 | 0.2 | 0.18 | 0.15 | 0.21 | 0.03 | 0.13 | 0.23 |

**Table 6:** Estimation of genetic parameters for nine quantitative characters in pea.

| Parameters | DF 50% | PH | NFFN | LFFN | NPP | LP | WP | NSP | SYP |
|---|---|---|---|---|---|---|---|---|---|
| D | 66.28±3.33** | 289.58±15.82** | 2.19±0.32** | 14.47±0.68** | 11.69±0.62** | 0.21±0.20 | 0 | 0.34±0.08** | 113.92±0.84** |
| $H_1$ | 36.19±7.66** | 67.57±36.37 | 6.17±0.74** | 7.43±1.56** | 7.07±1.42** | 3.84±0.45** | 0 | 0.56±0.19** | 5.87±1.92** |
| $H_2$ | 24.78±6.66** | 59.19±31.64 | 5.16±0.64** | 6.06±1.35** | 5.43±1.24** | 3.39±0.40** | 0 | 0.43±0.16** | 4.99±1.67** |
| $H_3$ | 24.40±4.47** | 23.25±21.22 | 8.15±0.43** | 8.06±0.91** | 6.15±0.83** | 7.74±0.26** | 0 | 0.44±0.11** | 8.09±1.12** |
| Sqrt ($h_1$/d) | 0.74 | 0.48 | 1.68 | 0.74 | 0.79 | 4.25 | 0 | 1.28 | 0.23 |
| $H_2/4h_1$ | 0.17 | 0.22 | 0.21 | 0.2 | 0.19 | 0.22 | 0.11 | 0.19 | 0.21 |
| $^bK_D/K_R$ | 1.55 | 0.82 | 0.54 | 0.93 | 1.24 | 0.95 | 0 | 1.15 | 1.28 |
| $H^2/H_2$ | 0.98 | 0.39 | 1.58 | 1.33 | 1.13 | 2.28 | 0 | 1.02 | 1.62 |
| Heritability (narrow) | 80.7 | 75.09 | 20.48 | 63.54 | 68.51 | 5.03 | 64.24 | 38.74 | 100.33 |

D = Component of variation due to additive effect. $H_1$= Component of variation due to dominance effect. $H_2$= $H_1$ (1-(u-v)2), where u = Proportion of positive genes in parents, v = Proportion of negative genes in parents and (u-v) = 1. $h_2$= Dominance effect (as the algebraic sum over all loci in heterozygous phase in all crosses). sqrt $H_1$/D = Mean degree of dominance in F1. $H_2/4h_1$= Proportion of genes with positive and negative effects in the parents. $h_2/H_2$ = No. of groups of factors controlling the characters and exhibiting dominance. bKD/ KR= [($4DH_1$)0.5 + F / ($4DH_1$)0.5 - F] = Proportion of dominance and recessive gene.

SYP is controlled by additive gene effect and the dominance component (H1) and dominance component (H2) were found to be significant for all the characters except plant height. The value of Additive variance (D) was observed higher than the H1 and H2 for all traits except for NFFN, LP and NSP (Table 6). The proportion of genes with positive and negative effects of parents ($h_2/4h_1$) showed that all traits showed the positive direction. The no. of groups of controlling factors and exhibiting dominance were shown more in LP. The proportion of dominant genes to receive genes was more than a unity in DF-50%, NSP and SYP. All the traits high heritability ($h^2$) except NFFN and LP. The estimates of additive genetic component (D) were found to be significant for all the characters except NFFN, LP and NSP. Previously, Singh *et al*. (2019) found significant estimates of both additive (D) and dominance (H) components for all pea characters except pod length. Similar findings in pea have been reported by Katoch *et al.* (2019), Halil and Uzun (2019), Kumari *et al.* (2015) and Cehyan *et al.* (2008).

## CONCLUSION

The AP-3, VL-7, Kashi-Nandini and PC- PC-531 were identified as promising parents due to significant GCA effects on seed yield and other traits. Among the crosses Kashi-Nandini × PC-531 VL-7 × PMR-53, Arkel × Vl-7 and VL-7 × Kashi-uday hybrids were the most promising because they had high SCA effects for seed yield/plant as well as other yield contributing characters. Lines with significant desirable GCA and SCA effects could be used to develop high yielding pea varieties. For seed yield, Arkel × VL-7 and Arkel × PMR-53 showed the maximum positive heterosis over the better parent and mid-parent, respectively. These genotypes can be used in future pea breeding programmes.

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