

## A BRIEF STUDY ON THE COMBINING ABILITIES OF QUANTITATIVE TRAITS IN FIELD PEA (PISUM SATIVUM L.)

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### ABSTRACT

The objective of this research was to investigate and estimates of the general combining ability (GCA) and specific combining ability (SCA) for the yield-related traits (plant height; height to first pod; number of pods per plant; seeds per plant; seeds per pod; number nodes per plant; inter-node distance; seed weight per plant and 1000 seed weight) in forage pea varieties for identifying suitable parents for pea - breeding programs. The 12 F1's and 12 F2's progenies of four divergent parents (Pleven 10, Mir and EFB33) mated in full diallel scheme. The results of the analysis of combinative ability of the investigated traits showed high significant variance of SCA for all traits both generations with the exception of 1000 seed weight in F1 and seeds per pod in F2. High significant variance of GCA is showed from 1000 seed weight in F1. The additive gene effects play a more important role in the inheritance of seeds per pod, seed weight per plant and 1000 seed weight, in F1 and seeds per pod and inter-node distance in F2. Whereas for the traits plant height; height to first pod; pods per plant; seeds per plant; nodes per plant; fertile nodes per plant in both generations have an influence on non-additive genetic interactions, where SCA was observed to be of higher magnitude than GCA. The parent Mir was found to be good general combiner for traits - plant height, pods, and nodes per plant, Kerpo for seeds weight per plant, Pleven 10 for 1000 seed weight and E.F.B.33 for inter-node distance. The best hybrid combinations due to their desired SCA effects were identified crosses P2 × P4 for number pods, seeds, nodes and fertile nodes per plant, P3 × P1 for plant height, height to first pod and 1000 seed weight and P1 × P3 for number seed per pod. These findings can be utilized further in selection program to enhance the yield potential of pea genotypes.

**Keywords:** forage pea, diallel analysis, combining ability, productivity

### 1. INTRODUCTION

The structure of the gene effects, i.e. the combinative ability is indicator for assessment of selection value on the parental forms, that is being carried broadly in breeding and genetical researches. It has special important meaning of the choice of the parents who will be used in the creation of new constant and heterotic varieties. It is known that hybrids with higher yield are received by genotypes (sorts and lines) with high combinative ability [Turbin et al. (1974)]. Combining ability studies are more reliable as they provide useful information for the selection of parents in terms of performance of the hybrids and elucidate the nature and magnitude of various types of gene actions involved in the expression of quantitative trait. Combining ability such as general combining ability (GCA) and specific combining ability (SCA) studies are useful in classifying parental lines in terms of their hybrid performance. As well it gives opportunity to be forecast who combinations will bring in consequential generations to formation of desired transgressive forms. The diallel scheme of crossing based on data of the hybrids F1, are much accurate method for its determination [Csizmadia, (1994), Sharma et al. (1999), Srivastava et al. (2000), Bourion et al. (2002)]. They allow to be determined as the additive effects so and specific combinative ability and the quantity of the effective factors at inheritance of the concrete character. In self-pollinated crops like pea, these studies are useful in assessing the combining

ability of the parents which, when crossed, would give more desirable segregates [(Hasan et al. (2004), Nikolov et al. (2004), Kalapchieva, (2010)].

The purpose of this study was to estimate general and specific combining ability values for yield - related traits among four pea varieties and to identify appropriate parents and crosses for the traits evaluated to assess their potential use in pea breeding programs.

### Materials and methods

The experimental study was conducted during the period 2009-2011 in second experimental field of the Institute of Forage Crops, Pleven. As parental component are using the following varieties forage pea: spring form Kerpo (*Pisum sativum ssp.sativum*) and winter types pea - Pleven 10, Mir and EFB33 (*Pisum sativum ssp.arvense*). These forms were crossed by hand in 2009. The experiment was laid out in a complete block design with two replications during winter season of 2010-2011. The parental forms (P1 and P2) first and second generations (12 F1 and 12 F2) are sown at scheme P1 , F1 , F2 , P2 with unit plot size (2 m × 1 m) on a row spacing 20 cm, distance in row 5 cm and plot to plot distance was 0.70 m. Hand planting was applied with depth of sowing 5 cm. The forage pea is grown by approved technology of the Institute of Forage Crops - Pleven. In the hybridization were included

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all direct and reciprocal crosses (full diallel scheme). From each genotype were used for analyzed follow quantitative traits such as - plant height (cm); height to first pod (cm); number of pods per plant; seeds per plant; seeds per pod; number nodes per plant; inter-node distance (cm); seed weight per plant (g); 1000 seed weight (g); fertile nodes per plant of parental components (P1 and P2) and crosses of first and second hybrid generations (F1 and F2). The individual number measurement of the each traits on one plant are 40 plants from F1, F2, P1 and P2. The combining ability analysis and estimates of gca and sca effects were computed according to Method 2 Model I of Griffing (1956), using the computer programs DIALL [Ukai, (1989)] and Genes 2009 v.7.0 [(Cruz, 2006)].

## Results and discussion

### Diallel ANOVA analysis by Griffing

Usually SCA effects do not contribute to tangible bettering the self-pollinated cultures with exception of these that the trade uses of heterosis is acceptable. SCA consists dominance-epistatic genetic interactions that can be related with heterosis. In the self-pollinated crops as like pea type of interaction additive  $\times$  additive could be fixed in the later generations and obtaining of more strong as well transgressive segregates. From viewpoint of these the selectionists could apply a good general combiner in specific specific breeding programs for bettering the traits [(Griffing, 1956, Jinks and Jones, (1958), and Joshi et al. (2004)].

Aghav et al. (1998) reported significant GCA and SCA variances for yield and yield contributing traits (pods per plant, seeds per pod, 1000 seed weight and seed weight per plant in pigeon pea (*Cajanus cajan*). SCA was observed to be of higher magnitude for the traits like plant height, height to first pod, pods/plant, seeds, nodes and fertile nodes per plant and inter-node distance in F1 and F2 selfsame trait also seed weight per plant and 1000 seed weight indicating the importance of additive gene action.

The mean sum of squares due to specific combining ability (SCA) for F1 was highly significant for all the characters with the exception of 1000 seed weight. For this trait was significant general combining ability (GCA). Similar is the mean sum of squares (SCA) in F2. It was highly significant with the exception of number pods per plant in F2. GCA was not significant. This indicating that both the additive and non-additive gene actions were predominant for the expression of these traits (Table 1 and Table 2). For all the traits (with the exception 1000 seed weight) are established significant difference between crosses and its reciprocal in F1 and F2 generation, that show there is presence of varied selection material.

The GCA and SCA ratio were more than one for the characters pods and fertile nodes per plant and seed weight per plant for F1 and number pods and inter-node distance, indicating that these characters were predominantly under additive genetic control [Hasan et al. (2006)]. Similarly, Dhameliya et al. (1994) reported higher GCA values for ten yield related traits in pigeon pea. The non-additive components of variance

were also involved in the inheritance of 50% germination, plant height and days to maturity.

The detailed results of combining ability analysis are presented traits wise as follows: Variance due to SCA was highly significant for plant height (for F1 and F2), indicating the presence of both additive and non-additive gene action. Srinivas et al. (1998b) also reported higher significant SCA variance for this traits in pigeon pea. Highest positive assessment GCA effect was produced by parent Mir (F1 - 13.20 and F2 - 12.20), Kerpo exhibited highest negative GCA (-28.83; -28.31). Positive SCA effect is preferable for plant height. The highest SCA effect (Table 3 and Table 4) was showed by P3  $\times$  P1 (5.54) followed by P2  $\times$  P1 (5.18) in F1 and by P2  $\times$  P4 (19.88) and P3  $\times$  P4 (15.53) in F2. On the other hand, the highest negative SCA effect demonstrated by P4  $\times$  P1 (-11.45). Form including of Kerpo in hybridization could be expected hybrids with a lower height of the plant for selection of genotypes for higher grain yield. The height first pod correlate positive with plant height and the results are analogous. The variance due to SCA was highly significant. The highest positive GCA effect was observed for Pleven 10 (7.18; 6.71) and Mir (7.02; 6.93). Whereas the highest negative GCA effect was found in Kerpo for both generations (-15.89; 15.50). The crosses P3  $\times$  P4 (6.86) showed highest positive SCA effect for F1 and P3  $\times$  P1 (5.58) for F2. The hybrid P2  $\times$  P3 (-31.04) exhibited highest negative SCA effect in F1, P1  $\times$  P2 (-36.65) in F2. It was observed that Mir showed negative effect for most cross combination indicating that it is the worst general combiner.

Combining ability analysis for pods per plant showed significant SCA variance. The highest positive GCA was exhibited by Mir (2.22- F1; 1.75- F2) whereas the parent Kerpo (-4.38; -3.99) showed highest negative GCA. So, Mir was the best general combiner for pods per plant. The highest positive SCA effect (5.43; 9.99) was exhibited by the hybrid P2  $\times$  P4.

Variance due to SCA revealed that both additive and non-additive gene actions were involved for seeds per plant. It was observed that the GCA effect was positive for the parents E.F.B.33 (11.80; 11.36) and Mir (11.70; 15.68) for both generations. Kerpo exhibited highest negative GCA effect (-21.68; -28.79) following from Pleven 10 (-1.83 for F1), which indicates that they not were good general combiner for this trait. The highest positive SCA effect was observed for P2  $\times$  P4 for both F1 and F2 (28.18; 37.50) followed by P2  $\times$  P1 (20.74; 28.08).

Analysis of variance due to SCA was highly significant for seeds per pod only for F1. The GCA variance is higher than SCA variance indicating that additive gene action is important for the expression of the trait. The highest positive GCA showed that parent E.F.B.33 (0.08) in F1 and Mir (0.20) in F2 were the best and Pleven 10 (-0.20; -0.06) was the poor general combiner. The SCA effect showed that P1  $\times$  P3 (0.57; 0.58) was the best specific cross combination for seeds per pod in both generations. On the other hand, the hybrids P4  $\times$  P2 (-0.63 for F1) and P2  $\times$  P4 (-0.31 for F2) exhibited negative SCA effect which indicating the crosses are poor specific

combiners. This result also have the close agreement with the findings of Sharma et al. (2000).

The overall length of the plant was determined as quantifiable sum by the number nodes per plant and the inter-node distance. The obtained results for these traits were showed high GCA for Mir (0.70 for F1 and 1.10 for F2), E.F.B.33 (1.01 for F1 and 0.71 for F2) for secong triat. Variety Kerpo showed negative values of GCA for both generations. The highest positive SCA effect for these traits were observed for P3 × P4 (6.11) and P2 × P1 (2.48) for F1 and P2 × P4 (6.30 and 4.31) for F2 (28.18; 37.50). This indicated that is possible to be selected hybrids with low number nodes and long inter-node distance.

Mean square due to SCA was highly significant for seed weight per plant. This result was supported by Singh et al. (1996) in pigeon pea. Positive GCA and SCA would reflect combining ability for high grain yield. Highest positive GCA was demonstrated by Kerpo (37.35 for F1; 40.48 for F2) whereas other parents exhibited high negative GCA. So, for seed weight per plant, Kerpo was the best general combiner. The SCA effect was highest negative for the P2 × P4 (-30.42) and the P1 × P4 (-25.17) for F1 and for the P3 × P4 (-20.56) for F2. The highest positive SCA effect was exhibited by the hybrid P4 × P2 (32.19) in F1 and P2 × P3 (22.93) in F2.

Highly significant GCA variance showed expression of 1000 seed weight only for F1. GCA is higher than SCA meaning that additive gene action was predominant. Similar result was also reported by Singh et al. (1996) in pigeon pea. Pleven 10 showed the highest positive GCA effect (0.23; 0.36) for both F1 and F2 followed by Mir (0.13 for F1) and E.F.B.33 (0.13 for F2). These three parents were the good general combiners for 1000 seed weight. Pleven 10 was the best general combiner. The highest positive SCA effect was exhibited by the hybrid P3 × P1 (0.83 in F1) followed by P2 × P1 (0.46 in F2).

The mean square due to SCA were highly significant for fertile nodes per plant. The parent Pleven 10 (2.40) for F1 and Mir (1.58) for F2 showed highly positive estimate of GCA which reflects combining ability for high number fertile node per plant. On the contrary Kerpo exhibited highly negative (-3.10; -2.56), it means combining ability for small number fertile nodes. For SCA effect, crosses P3 × P1(5.54) in F1 and P2 × P4(7.70) in F2 showed highest positive effect. Pleven 10 exhibited negative effect for most crosses that determine Pleven 10 like was the worst combiner for fertile nodes per plant.

The values of GCA for traits seeds/pod, seed weight/plant and 1000 seed weight, in F1, and seeds/pod and inter-node distance in F2 is found higher than these of SCA. This indicated that in the inheritance of these traits predominated additive gene effects. The similar result was reported by Sharma et al. (2000), Singh and Mishra (1996). Other outors are established epistatic and non-additive genetic effect in the inheritance of the main traits as number nodes per plant, days to first picking, pods per plant, and shelling [Kalia and Singh (1996), Sharma (1999), Bourion et al. (2002)].

## Conclusion

The results of the analysis of combinative ability of the investigated traits showed high significant variance of SCA for all traits both generations with the exception of 1000 seed weight in F1 and seeds per pod in F2. High significant variance of GCA is showed from 1000 seed weight in F1. The additive gene effects play a more importance a role in the inheritance of seeds per pod, seed weight per plant and 1000 seed weight, in F1 and seeds per pod and inter-node distance in F2. Whereas for the traits plant height; height to first pod; pods per plant; seeds per plant; nodes per plant; fertile nodes per plant in both generations have an influence on non-additive genetic interactions, where SCA was observed to be of higher magnitude than GCA. The parent Mir was found to be good general combiner for traits - plant height, pods, and nodes per plant, Kerpo for seeds weight per plant, Pleven 10 for 1000 seed weight and E.F.B.33 for inter-node distance. The best hybrid combinations due to their desired SCA effects were identified crosses P2 × P4 for number pods, seeds, nodes and fertile nodes per plant, P3 × P1 for plant height, height to first pod and 1000 seed weight and P1 × P3 for number seed per pod.

## References

1. Aghav SB, Kharpe PR. and Narladkar VW (1998). Combining ability analysis in pigeon pea.
2. Annal. Agril. Res. 19 (3): 241 - 244.
3. Bourion V, Fouilloux G, Le Signor C, and Lejeune-Henaut I (2002). Genetic studies of selection for productive and stable peas. *Euphytica*, 127: 261-273.
4. Cruz CD (2006). Programa Genes: Biometria. Editora UFV. Vicosia (MG): 382.
5. Csizmadia I (1994). Inheritance of earliness in a diallel cross of garden pea varieties, *Zoldsegetermeszteszi -Kutato Intezet Bulletinje*, 26: 19-32.
6. Dhameliya HR, Pathak AR and Zaveri PP (1994). Genetic analysis of heterogeneous population in pigeon pea (*Cajanus cajan* L). *Gujarat Agril. University Res. J.* 20 (1): 46 - 51.
7. Griffing B (1956). A generalized treatment of the use of diallel cross in quantitative inheritance. *Heredity*, 10:31-50.
8. Hasan M. K. M., A. K. M. A. Islam, J. U. Ahmed and M. A. K. Mian (2004) Combining ability for yield related characters in pea (*Pisum sativum* L.). *Asiat. Soc. Bangladesh. Sci.*, 30 (2):55-62.
9. Mitu HMK, Islam AK, Rasul MG and Mian MAK (2006). Genetic Analysis of Yield Related Characters in Pea (*Pisum sativum* L). *J. Asiat. Soc. Bangladesh. Sci.*, 32 (1): 111 - 120
10. Jinks JL and Jones RM (1958). Estimation of components of heterosis. *Genet.* 43:223-234.
11. Joshi SK, Sharma SN, Singhanian DL, and Sain RS (2004). Combining ability in the F1, and F2; generations of diallel cross in hexaploid wheat (*Triticum aestivum* L.). *Hereditas*, 141:115-121.
12. Kalapchieva S (2010). Studies of combining ability in garden pea through morphological characters. *Genetika, oplemenjivanje bilja i sjemenarstvo* 45. hrvatski i 5. me?unarodni simpozij agronoma: 437-441.
13. Kalia P, and Singh Y (1996). Heterosis and combining ability studies for the some quantitative traits in pea. *Haryana J. Hotr. Sci.* 25 (2): 54-57.
14. Nikolov E (2004). Assessment breeding value of varieties and lines origin eastern Balkan and tekne. 2. Genetic analysis for nicotine content in raw tobacco. Scientific conference with international participation "Stara Zagora, 204": 250-253.
15. Sharma TR (1999). Combining ability and heterosis in garden (*Pisum sativum* var. *arvense*) in the cold desert Himalayan region. *Indian J. Agric. Sci.* 69:386-388.

16. Sharma DS, Adarsh B, Chaudhary D and Bala A (1999). Studies on combining ability and gene action in pea (*Pisum sativum* L.). *Indian Journal of Hill Farming*, 12 (1-2): 32-36.
17. Sharma MK, Ratsogi KB, and Korla BN (2000). Combining ability analysis for yield and yield components in pea (*Pisum sativum* L.). *Crop Res. Hisar.*, 19 (3): 500-504.
18. Singh RN and Mishra GM (1996). Heterosis and combining ability in pea (*Pisum sativum* L.). *Hort. J.*, 9 (2):129-133.
19. Srinivas T, Jain KC and Reddy MS (1998). Combining ability studies of medium and long duration pigeon pea (*Cajanus cajan* L.). *Annal. Agril. Res.*, 19 (3): 299-303.
20. Srivastava C, Tyagi M, Agrawal R and Rai B (2000). Combining ability analysis for seed yield and related traits in peas of Indian and exotic origin. *Madras Agricultural Journal*, 86 (7-9): 366-370.
21. Turbin N, Khotyleva L and Tarutina L (1974). Diallel analysis in plant breeding. "Science and Technology, Minsk: 184.
22. Ukai Y (1989). A microcomputer program DIALL for diallel analysis of quantitative characters. *Jpn. J. Breed.*, 39:107-109.

## APPENDIX

### TABLES

**Table 1.** Analysis of variance for combining ability in F1 generation of pea

Source of variation	df	Mean square									
		Plant height (cm)	Height to first pod (cm)	Pods/plant (No.)	Seeds/plant (No.)	Seeds/pod (No.)	Nodes/plant (No.)	Inter-node distance (cm)	Seed weight/plant (g)	1000 Seed weight (g)	fertile nodes/plant
Replication	3	22.22	5.44	2.74	135.63	0.06	0.75	0.92	1.81	1.52	1.11
GCA	3	2791.29	224.38	16.06	1676.04	1.75	0.3	2.7	5.32	26.56*	0.2
SCA	2	3604.40**	1537.15**	67.75**	2390.65**	1.30**	18.82**	7.22**	4.76**	0.52	17.89**
Reciprocal	6	2125.75**	743.21**	225.56**	2867.88**	1.88**	68.60**	9.40**	26.59**	4.61	71.78**
Error	33	28.55	17.72	3.56	112.37	0.16	31.27	64.44	34.17	11.92	65.54
GCA/ SCA		0.77	0.15	0.24	0.7	1.35	0.02	0.37	1.12	51.08	0.01

\* significant at 5% level, \*\* significant at 1% level

**Table 2.** Analysis of variance for combining ability in F2 generation of pea

Source of variation	df	Mean square									
		Plant height (cm)	Height to first pod (cm)	Pods/plant (No.)	Seeds/plant (No.)	Seeds/pod (No.)	Nodes/plant (No.)	Inter-node distance (cm)	Seed weight/plant (g)	1000 Seed weight (g)	fertile nodes/plant
Replication	3	64.78	37.48	87.46**	4141.78**	0.31	52.08**	0.31	94.41	185.69	11.67**
GCA	3	1137.58	176.77	38.27	3614.54	4.08	65.52	1.38	7.06	448.56	14.17
SCA	2	3612.00**	1632.02**	258.94**	8909.40**	0.33	150.66*	0.65*	177.75*	1192.**	31.08**
Reciprocal	6	2242.83**	171.56**	153.48**	6654.25**	2.17**	112.23*	1.08**	68.23**	763.98	26.50**
Error	33	30.95	48.12	6.06	794.56	0.28	9.09	0.15	14.11	93.76	2.24
GCA/ SCA		0.31	0.11	0.15	0.41	12.36	0.43	2.12	0.04	0.38	0.46

\* significant at 5% level, \*\* significant at 1% level

**Table 3.** Estimates of general combining ability (GCA) effects for different traits of pea parent forms

Parents	Plant height (cm)		Height to first pod (cm)		Pods/plant (No.)		Seeds/plant (No.)		Seeds/pod (No.)		Nodes/plant (No.)		Inter-node distance (cm)		Seed weight/plant (g)		1000 Seed weight (g)		fertile nodes/plant	
	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2
P1 (Mir)	13.2	12.2	7.02	6.93	2.22	1.75	11.7	15.68	0.05	0.2	0.7	1.1	0.71	0.56	15.9	-15.8	0.13	0.07	1.4	1.58
P2 (Pleven 10)	2.69	5.21	7.18	6.71	0.82	0.96	-1.83	1.75	-0.2	-0.06	-0.4	0.49	0.62	0.58	-10.08	-7.84	0.23	0.36	2.4	0.35
P3 (E.F.B.33)	12.93	10.9	1.69	1.86	1.79	1.29	11.8	11.36	0.08	0.12	0.49	-0.28	1.01	0.71	-11.36	-16.84	0.07	0.13	-0.71	0.62
P4 (Kerpo)	-28.83	-28.31	-15.89	-15.5	-4.83	-3.99	-21.68	-28.79	0.08	-0.25	-0.79	-1.31	-2.35	-1.85	37.35	40.48	-0.42	-0.56	-3.1	-2.56

SE	25.03	17.03	14.17	16.98	1.24	1.73	24.38	18.08	0.03	0.03	0.98	0.08	0.3	0.2	0.28	0.28	153.1	42.85	0.3	0.2
Variations of GCA	174	71.09	14.02	11.04	1.04	2.39	104.7	225.9	0.11	0.25	1.29	4.09	0.22	0.86	4.86	0.44	251.3	215.5	0.18	0.88

**Table 4.** Specific combining ability effects for different traits in 12 F1 and F2 diallel pea hybrids

Hybrids	Plant height (cm)		Height to first pod (cm)		Pods/plant (No.)		Seeds/plant (No.)		Seeds/pod (No.)		Nodes/plant (No.)		Inter-node distance (cm)		Seed weight/plant (g)		1000 Seed weight (g)		fertile nodes/plant	
	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2
P1× P2	0.76	-47.66	-30.91	-36.65	-0.06	-3.79	-8.06	-6.35	-0.25	0.4	-1.89	-3.21	0.31	-1.41	1.17	-7.18	-1.58	-1.33	0.76	-3.36
P1× P3	-6.49	-13.25	-5.43	-3.21	-1.22	1.39	13.86	30.24	0.57	0.58	2.38	5.32	-0.32	0.46	9	12.41	-0.29	-0.51	-6.49	0.55
P1× P4	3.43	-1.6	-10.6	-9.78	2.9	3.74	12.06	6.74	0.07	-0.29	1.5	1.41	1.93	2.95	-25.17	-19.33	-0.23	-0.58	3.43	3.58
P2× P1	5.18	5.83	3.19	0.64	4.9	-1.99	20.74	28.08	-0.03	1.19	2.64	2.04	2.48	-0.93	1.25	-7.6	-0.14	0.46	5.18	-3.36
P2× P3	-3.67	-48.7	-31.04	-30.81	-5.55	-5.43	-18.65	-17.71	0.28	0.28	0.36	0.51	-3.1	-2.77	23.56	22.93	-1.13	-1.08	-3.67	-4.93
P2× P4	3.68	19.88	3.32	5.4	5.43	9.99	28.18	37.5	0.05	-0.31	2.61	6.3	2.62	4.31	-30.42	-16.26	-0.58	-0.82	3.68	7.7
P3× P1	5.54	12.73	1.1	5.58	-3.81	3.71	-7.14	34.88	0.4	0.36	1.79	3.04	-2.06	1.3	16.38	-6.69	0.83	0.06	5.54	2.72
P3× P2	2.25	7.67	1.31	2.84	1.7	4.04	5.43	24.95	-0.1	0.15	2.15	4.63	1.07	2.09	10.33	7.46	-0.2	-0.45	2.25	4.37
P3× P4	0.73	15.53	6.86	2.24	4.85	1.8	20.85	7.46	-0.12	-0.06	6.11	2.21	2.14	0.8	-7.52	-20.56	0.28	0.37	0.73	0.36
P4× P1	-11.45	-35.76	-16.15	-9.45	-11	-6.92	-38.49	-21.68	0.5	0.28	-5.91	-2.14	-5.48	-2.68	-0.64	8.12	0.77	-0.23	-11.45	-5.6
P4× P2	1.62	-1.49	16.23	4.9	1.72	-5.25	-12.58	-30.91	-0.63	-0.22	2.87	-3.04	1.07	-2.08	32.19	12.66	-0.07	0.45	1.62	-4.36
P4× P3	-8.68	6.3	-4.43	0.28	-2.23	1.27	-3.13	12.29	0.25	0.22	-0.76	0.5	-1.34	0.63	-1.95	-11.92	0.05	-0.01	-8.68	1.31
SE	7.14	7.74	4.43	12.03	0.89	1.51	28.09	198.64	0.04	0.07	0.77	3.53	0.2	0.56	72.29	23.44	0.05	0.04	0.92	2.27
Variations of SCA	450.54	45.15	192.14	204	8.46	32.36	298.13	1113.6	0.16	0.04	1.83	22.21	1.83	3.88	18.92	149.04	0.16	0.08	8.12	18.75