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Research Article

Heterosis and combining ability analysis for yield and yield related traits in greengram (*Vigna radiata* L.)

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Abstract

The present study was conducted in Line x Tester mating design using 40 hybrids 14 parents to estimate the combining ability effects and heterosis for yield and yield attributing traits in greengram. Combining ability analysis indicated the preponderance of non-additive gene action for all the traits studied. Considering the *per se* performance and *gca* effects VBN 2 and ADT 3 (Lines) and IPM-02-03, Pusa 0871 and EC 398897 (Testers) were adjudged as best parents and crosses involving these are expected to throw desirable segregants. Considering the *per se* performance, significant *sca* effects and desirable heterosis, the hybrids ADT 3 x IPM-02-03, ADT 3 x IPM-02-14, ADT 3 x PDM 139, ADT 3 x TM-11-34, IPM-409-04 x EC 398897, SML 1074 x PUSA 0871, VBN 2 x EC 398897 and VBN 2 x PUSA 0871 were found to be superior for number of pod clusters per plant, number of pods per plant and single plant. These hybrids can be utilized to develop high yielding varieties with desirable traits. Gene action analysis revealed preponderance of both additive and non-additive genes for yield and its contributing characters. Hence, these combinations are the best for the current study and they can be directly utilized for realizing improved greengram yield without much compromise on other desirable traits.

Key words
Greengram, line × tester analysis, *per se* performance, heterosis, combining ability

Introduction

Mungbean or greengram (*Vigna radiata* (L.) Wilczek) is one of the important grain legume crops in Asian countries. It is one of the important pulse crops after chickpea and pigeonpea, because of its adaptation to short growth duration, low water requirement, soil fertility, easy digestibility and low production of flatulence (Shil and Bandopadhya, 2007). India is the largest producer of greengram with more than 50 % of the world's production, but the productivity of the crop is 481 kg/ha and remain at low yield level (Annual Report, DPD 2016-17). The first step in a successful breeding program is to select appropriate parents. However, a major issue is selection of parents based on *per se* performance which lacks fidelity and obvious failures to identify better parents. Therefore, it is essential to identify parents based on nicking ability in cross combinations rather than *per se* performance only. In order to choose appropriate parents and crosses, and to determine the combining abilities of parents in early generation, the line x tester analysis method has been widely used by plant breeders. This method was applied to improve self and cross-pollinated plants (Kempthorne, 1957). Line x Tester analysis provides a systemic approach for identification of appropriate parents and crosses superior in terms of investigated traits.

In the available literature, both additive and non-additive gene actions are reported to control seed yield and yield-relating traits in greengram (Barad *et al*. (2008); Marappa (2008); Sathya and Jayamani (2011); Sujatha and Kajjidoni (2013) and Suresh (2014)). However, the major part of genetic variation for yield and its components has been reported to be under control of non-additive genetic effects. Genetic information, especially about the nature of gene action, combining ability and heterosis are required for selecting suitable parents and designing appropriate breeding programmes. The present study was undertaken to estimate the heterosis, combining ability effects and variances for yield and its components traits in greengram.

Materials and Methods

The study was conducted at Rice Research Station, Tamil Nadu Agricultural University, Tirur, Thiruvallur, Tamil Nadu. The material used for the present study was developed by crossing four Mungbean Yellow Mosaic Virus (MYMV) susceptible genotypes *viz.,* ADT 3, IPM-409-04, SML 1074 and VBN 2 taken as lines and ten resistant/tolerant genotypes *viz.,* CO (Gg) 7, EC 398897, IPM 02-03, IPM 02-14, MH 521, PDM 139, Pusa 0672, Pusa 0871, TM 11-07 and TM 11-34 taken as testers. Crossing was taken up as per the method suggested by Sen and Ghosh (1959) in a line x tester fashion as proposed by Kempthrone, 1957. The 40 crosses along with their parents were raised in randomized block design with two replications at Rice Research Station, Tirur. The experimental materials were raised in two rows of 6 m length with the spacing of 30 × 10 cm. Recommended agronomic practices and need based plant protection measures were followed under irrigated conditions.

Five randomly selected plants were tagged for each entry in each replication for recording the data. Observations were recorded for nine biometrical traits *viz.*, days to 50 % flowering (DFF), plant height (PH), number of branches per plant (NBP), number of pod clusters per plant (NPC), pod length (PL), number of pods per plant (NPP), number of seeds per pod (NSP), 100 seed weight (HSW), and seed yield per plant (SYP).

Average data recorded on each character from the tagged plants represented the mean of that replication. The data on the hybrids and parents were subjected to L × T analysis. The general combining ability effects of the parents and specific combining ability effects of the crosses were worked out as suggested by Kempthorne 1957. The ratio of GCA/SCA was worked out for each trait to find out the predominance of additive or non-additive gene action assuming the adequacy of additive dominance model. The magnitude of heterosis in hybrids was expressed as percentage of increase or decrease of a character over standard hybrid (d_{iii}) was estimated using the formula of Fonseca and Patterson (1968). The significance of magnitude of the relative heterosis, heterobeltiosis and standard heterosis was tested at error degrees of freedom by the formula suggested by Turner (1953).

Result and Discussion

The analysis of variance showed significant differences among parents and hybrids for all the characters under study. The analysis of variance for combining ability (Table 1) revealed highly significant differences among the parents and line x tester component for all the traits studied. Similarly, the testers component exhibited significant variability for all the characters except plant height.

The GCA variances were lower than SCA variances for all the characters studied as indicated by their lower ratios revealing the predominance of non-additive gene action in the inheritance of these traits (Table 1). This result suggests that pedigree selection will be ineffective and better segregating progenies has to be selected in later generations of selection cycle. The findings of Anbumalarmathi *et al.* (2005), Marappa (2008), Barad *et al.* (2008), Sathya and Jayamani (2011), Sujatha and Kajjidoni (2013), Narasimhulu *et al* (2014) and Suresh (2014) support the above results.

For rapid success in any hybridization programme, the choice of parents which can produce superior off-springs is very much essential. The parents with high *per se* would be of greater importance in breeding programme (Singh *et al*., 1983). In choice of parents, high mean performances are generally preferred for all the traits except days to 50 per cent flowering as earliness is the preferred attribute. Based on the *per se* performance IPM-409-04 among the lines and IPM-02-03 and Pusa 0871 among the testers were found significantly early in flowering. The lines, SML 1074 registered significant *per se* value for the traits *viz.*, number of branches per plant, pod length and hundred seed weight followed by ADT 3 for number of seeds per pod and single plant yield. Among the testers, Pusa 0871 recorded significant mean values for all the traits studied except plant height followed by IPM-02-14 for four important yield contributing traits *viz.*, Number of branches per plant, number of pod clusters per plant, number of pods per plant and hundred seed weight. ADT 3 among lines and Pusa 0871 among testers recorded maximum mean values for single plant yield. Considering the *per se* performance of the parents, the lines ADT 3 and SML 1074 and the testers Pusa 0871 and IPM 02-14 were found to be better parents and crosses involving these will be expected to throw desirable segregants for yield attributing characters.

The good breeding methodology rests on a correct understanding of the gene effects involved. The *gca* effects represent the additive nature of gene action. A best general combiner is characterized by its better breeding value when crossed with number of other parents ((Fischer *et al.,* 2008). Besides, mean performance of a parent is also considered with *gca* effects, since the former offers reliability / authenticity to *gca* effects as a guide in selection of parents.Among the lines, VBN 2 registered significant positive *gca* value for five traits *viz.*, plant height, number of pods per plant, pod length, hundred seed weight and single plant yield. ADT 3 recorded positively significant *gca* effects for number of branches per plant, number of pod clusters per plant, number of pods per plant and single plant yield (Table 2).

Among the testers, IPM-02-03 showed positively significant *gca* effecs for seven traits *viz.*, days to 50 per cent flowering, plant height, number of pods clusters per plant, number of pods per plant, number of seeds per pod, hundred seed weight and single plant yield and Pusa 0871 for seven yield traits *viz.*, days to 50 per cent flowering, number of branches per plant, number of pods clusters per plant, number of pods per plant, number of seeds per pod, hundred seed weight and single plant yield followed by EC 398897 for six traits *viz.*, plant height, number of pods clusters per plant, number of pods per plant, pod length, hundred seed weight and single plant yield. Among the parents, the lines ADT 3 and VBN 2 and the testers EC 398897, IPM 02-03, IPM 02-14 and Pusa 0871 registered significant *gca* effects for single plant yield.

Based on the *per se* performance and *gca* effects, the parents VBN 2 and ADT 3 among the lines and IPM 02-03, Pusa 0871 and EC 398897 among the testers were identified as best general combiners to produce superior segregants with favourable combination of alleles for most of the yield attributing traits. The mean performance of hybrids for the yield and other related traits is given in Table 3. Among the hybrids, ADT 3 x IPM 02-03 showed superior mean performance for eight traits *viz.*, days to 50 per cent flowering, plant height, number of pods clusters per plant, pod length, number of pods per plant, number of seeds per pod, hundred seed weight and single plant yield followed by the hybrids ADT 3 x IPM 02-14, IPM 409-04 x EC 398897, SML 1074 x Pusa 0871, VBN 2 x IPM 02-03 and VBN 2 x Pusa 0871 which excelled in mean performance for five traits each. Similarly the hybrids, SML 1074 x IPM 02-03, ADT 3 x PDM 139, ADT 3 x TM 11-34, VBN 2 x EC 398897 and VBN 2 x PDM 139 had a significant mean performance for three traits each.

Specific combining ability estimates revealed a very wide range of variation for all the characters. High *sca* effects mostly from the dominance and interaction effects existed between the hybridizing parents (Narasimulu *et al.* 2014). In greengram owing to its autogamous genetic nature, sca effects are not readily useful. However, if *sca* is due to additive × additive gene action, it is fixable at later generations and superior transgressive segregants can be isolated from such crosses (Shinde and Deshmukh 1989). In the present investigation, the hybrids ADT 3 x IPM 02-03, ADT 3 x TM 11-07, IPM 409-04 x PDM 139, IPM 409-04 x Pusa 0672, SML 1074 x Co 7, SML 1074 x TM 11-34, VBN 2 x IPM 02-14 and VBN 2 x MH 521 registered negative *sca* effects for days to 50 per cent flowering (Table 4).

The hybrid IPM 409-04 x EC 398897 found to have positive *sca* effects for six traits *viz.*, plant height, number pod clusters per plant, pod length, number of pods per plant, number of seeds per pod and single plant yield followed by IPM 409-04 x Pusa 0672 for days to 50 per cent flowering, plant height, number pod clusters per plant, hundred seed weight and single plant yield. The cross VBN 2 x Co 7 showed significant *sca* effects for four traits *viz.*, number of pod clusters per plant, number of pods per plant, hundred seed weight and single plant yield. The next superior hybrids were ADT 3 x IPM 02-03, ADT 3 x IPM 02-14, ADT 3 x PDM 139, ADT 3 x TM 11-34, IPM 409-04 x TM 11-07, SML 1074 x IPM 02-14, SML 1074 x Pusa 0871, VBN 2 x EC 398897, VBN 2 x MH 521 and VBN 2 x Pusa 0871 for three traits each. These crosses could be exploited effectively through heterosis breeding programme for getting desirable recombinants from the segregating population.

Based on *per se* performance, significant *sca* effects and desirable heterosis, the hybrid IPM 409-04 x EC 398897 was highly suitable for heterosis breeding since it expressed high *per se* performance, *sca* effects and standard heterosis for four traits including number of pod clusters per plant, number of pods per plant, pod length and single plant yield. The cross combinations ADT 3 x IPM 02-14, SML 1074 x Pusa 0871 and VBN 2 x EC 398897 could be finalized as next best as it showed desirable mean, *sca* effects and standard heterosis for a maximum of three traits such as number of pod clusters per plant, number of pods per plant and single plant yield in ADT 3 x IPM 02-14 and VBN 2 x EC 398897 and number of pods per plant, hundred seed weight and single plant yield in SML 1074 x Pusa 0871.

Thus in the present study, the parents Pusa 0871 and EC 398897 were adjudged as best parents based on *per se* performance and *gca* effects. The hybrids ADT 3 x IPM 02-03, ADT 3 x IPM 02-14, ADT 3 x PDM 139, ADT 3 x TM 11-34, IPM 409-04 x EC 398897, SML 1074 x Pusa 0871, VBN 2 x EC 398897 and VBN 2 x Pusa 0871 were found to be superior based on high *per se* performance, significant *sca* effects and standard heterosis. These hybrids can be utilized for to develop high yieilding varieties with desirable traits. In the present study it is noted that additive and non-additive gene actions are found important in the evolution of high yielding genotypes and improvement can be expected by delaying the selection to later generations, when the dominance and epistatic gene interactions disappear, restoring to intermating of segregants followed by recurrent selection.

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Table 1. Analysis of variance of combining ability for yield and yield components of greengram

Source	df	Mean squares								
		DFF	**PH (cm)**	**NBP**	**PCP**	**PL (cm)**	**NPP**	**NSP**	**100SW (g)**	**SYP (g)**
Replication	1	0.23	1.12	0.05	0.10	0.17*	6.13	0.05	0.01	0.15
Hybrids	39	26.59*	108.83*	0.26*	12.17*	0.84*	123.96*	2.11*	0.78*	18.68*
Lines	3	218.18*	237.10*	0.38*	13.14*	4.40*	490.59*	2.00*	1.57*	54.42*
Testers	9	12.77*	58.07	0.53*	14.06*	0.72*	151.27*	2.77*	1.26*	21.02*
Line x Tester	27	9.91*	111.50*	0.16*	9.20	0.48*	74.13*	1.90*	0.53*	13.93*
Error	39	1.92	10.98	0.11	1.15	0.09	10.18	0.87	0.03	0.90
gca Variance		0.41	0.07	0.003	0.08	0.01	1.23	0.005	0.01	0.12
sca Variance		3.99	50.26	0.03	4.03	0.2	31.97	0.52	0.25	6.51
σ^2A		0.82	0.14	0.004	0.16	0.02	2.46	0.01	0.02	0.24
σ^2D		3.99	50.26	0.03	4.03	0.2	31.97	0.52	0.25	6.51
Ratio σ^2A/ σ^2D		0.206	0.003	0.133	0.04	0.1	0.077	0.019	0.08	0.037

*** Significant at 5 % level**

Table 2. Estimates of general combining ability (*gca*) effects of the parents for yield and its component traits.

Parents	**DFF**	**PH (cm)**	**NBP**	**PCP**	**PL (cm)**	**NPP**	**NSP**	**100SW (g)**	**SYP (g)**
Lines									
ADT 3	0.17	0.98	0.16*	1.63*	-0.09	6.33*	0.16	-0.02	1.93*
IPM-409-04	-4.72*	-3.48*	-0.17*	-1.42*	-0.49*	-3.75*	-0.01	0.39*	-2.03*
SML 1074	2.17*	-1.86*	0.01	-0.48	-0.06	-4.13*	0.29	0.27*	-0.33
VBN 2	2.38*	4.36*	0.00	0.26	0.64*	1.56*	-0.44*	0.11*	0.43*
SE	0.49	1.17	0.08	0.24	0.15	0.71	0.21	0.06	0.21
CD $_{0.05}$	1.39	3.33	0.21	0.68	0.30	2.03	0.59	0.17	0.60
Testers									
CO (Gg) 7	-0.15	-1.84	0.14	-0.28	-0.35*	-2.57*	-0.41	0.10	-0.87*
EC 398897	2.35*	3.21*	0.13	1.53*	0.26*	4.43*	-0.47	0.53*	1.88*
IPM-02-03	-2.15*	4.58*	0.02	1.91*	0.21	3.87*	0.71*	0.59*	1.96*
IPM-02-14	0.47	0.96	0.08	-0.15	0.23*	2.09	0.52	-0.31*	1.34*
MH-521	-0.28	-1.29	0.33*	0.22	0.51*	-4.38*	0.34	-0.50*	-0.55
PDM-139	0.22	-2.74*	-0.14	-1.00*	-0.14	-1.05	-0.04	-0.17*	-0.62
Pusa 0672	-0.15	-3.29*	-0.45*	-1.28*	0.04	-3.69*	-0.54	-0.12	-1.08*
Pusa 0871	-1.02*	0.39	0.38*	1.78*	-0.15	8.18*	0.84*	0.45*	1.95*
TM-11-07	-0.77	-2.17	-0.06	-1.59*	-0.43*	-3.50*	-0.91*	-0.35*	-1.90*
TM-11-34	1.48*	2.21	-0.27*	-1.15*	-0.18	-3.38*	-0.04	-0.23*	-2.12*
SE	0.31	0.74	0.12	0.38	0.09	1.13	0.33	0.04	0.34
CD $_{0.05}$	0.88	2.11	0.34	1.08	0.19	3.21	0.94	0.11	0.95

* Significant at 5 % level

Table 3. Standard Heterosis (%) for yield and component traits in greengram

Hybrids	**DFF**	**PH (cm)**	**NBP**	**NPC**	**PL (cm)**	**NPP**	**NSP**	**100SW (g)**	**SYP (g)**
ADT 3/CO (Gg) 7	11.94*	-21.55*	46.30*	9.09	-1.42	-8.93	-10.53	10.78*	11.43
ADT 3/EC 398897	13.43*	-22.41*	48.15*	30.30*	2.13	30.36*	-2.63	17.96*	40.00*
ADT 3/IPM 02-03	-7.46	-5.17	66.67*	60.61*	7.09	74.11*	21.05*	21.56*	88.57*
ADT 3/IPM 02-14	5.97	-5.17	57.41*	72.73*	-4.75	64.29*	15.79	-13.77*	97.14*
ADT 3/MH 521	10.45*	-6.90	44.44	39.39*	5.67	21.43	0.00	-17.96*	42.86*
ADT 3/PDM 139	8.96*	-22.41*	55.56*	42.42*	-3.90	50.18*	10.53	5.99	65.71*
ADT 3/ Pusa 0672	11.94*	-37.93*	33.33	15.15	-7.80	24.11*	-10.53	-16.17*	11.43
ADT 3 Pusa 0871	8.96*	-15.52*	70.37*	48.48*	-1.42	66.07*	-5.26	3.59	45.71*
ADT 3/TM 11-07	-7.46	-29.31*	29.63	6.06	-9.93*	1.79	-10.53	-11.98*	0.00
ADT 3/TM 11-34	-10.45*	-14.22*	29.63	36.36*	-13.83*	36.61*	13.16	16.17*	60.00*
IPM 409-4/CO (Gg) 7	16.42*	-27.59*	55.56*	-15.15	5.32	3.57	-15.79	-16.17*	-6.00
IPM 409-4/EC 398891	0.00	0.00	11.11	42.42*	9.57*	38.39*	10.53	2.40	58.57*
IPM 409-4/IPM 02-03	-14.93*	-12.07*	51.85*	12.12	-8.16	8.93	-5.26	-13.17*	1.43
IPM 409-4/IPM 02-14	-8.96*	-46.55*	-3.70	-6.06	-2.13	5.36	10.53	-4.19	13.43
IPM 409-4/MH 521	-1.49	-41.38*	48.15*	3.03	3.55	-19.64	15.79	-12.57*	-2.86
IPM 409-4/PDM 139	-7.46	-48.97*	11.11	-9.09	-21.28*	-9.82	-10.53	-16.17*	-14.29
IPM 409-4/Pusa 0672	-14.93*	-8.62	-18.52	24.24	-10.64*	-7.14	0.00	12.57*	26.57*
IPM 409-4/Pusa 0871	-11.94*	-37.07*	74.07*	-30.30*	-7.09	-1.79	15.79	4.19	-42.86*
IPM 409-4/TM 11-07	-4.48	-15.52*	-7.41	-9.09	-5.67	0.00	-10.53	-17.37*	2.86
IPM 409-4/TM 11-34	1.49*	-19.83*	11.11	-21.21	-9.01*	-17.86	-7.89	-20.96*	-27.14*
SML 1074/CO (Gg) 7	5.97	-29.31*	62.96*	12.12	-8.51*	-4.46	15.79	5.15	7.14
SML 1074/EC 398891	23.88*	-10.34	66.67*	-3.03	0.00	-7.14	-5.26	36.29*	14.86*
SML 1074/IPM 02-03	17.91*	-24.14*	-7.41	42.42*	-6.38	33.93*	10.53	26.95*	51.43*
SML 1074/IPM 02-14	26.87*	-8.62	44.44	12.12	9.57*	23.21*	-2.63	-0.60	40.00*
SML 1074/MH 521	10.45*	-39.66*	81.48*	24.24	10.64*	-10.71	7.89	-13.53*	25.71*
SML 1074/PDM 139	11.94*	-23.06*	18.52	-34.85*	6.03	-28.57*	0.00	-14.97*	-14.29
SML 1074/Pusa 0672	11.94*	-36.21*	-14.81	-27.27*	5.32	-19.64	-13.16	8.14*	-2.86
SML 1074/Pusa 0871	5.97	-15.52*	55.56*	63.64*	-5.32	52.68*	21.05*	25.87*	94.29*
SML 1074/TM 11-07	10.45*	-24.14*	57.41*	9.09	-4.26	-21.43	-5.26	6.71	-1.43
SML 1074/TM 11-34	7.46	-18.53*	1.85	6.06	-10.99*	-31.25*	5.26	-4.19	-11.43
VBN 2/CO (Gg) 7	17.91*	-13.28*	20.37	45.45*	5.46	26.79*	-5.26	15.09*	44.29*
VBN 2/EC 398891	17.91*	-24.14*	57.41*	69.70*	4.96	55.36*	-21.05*	-1.20	69.43*
VBN 2/IPM 02-03	5.97	-6.03	38.89	42.42*	21.13*	-8.04	5.26	26.35*	44.86*
VBN 2/IPM 02-14	8.96*	-12.07*	22.22	-21.21	12.06*	-9.38	0.00	-6.59	7.14
VBN 2/MH 521	4.48	0.00	66.67*	9.09	10.64*	0.00	-7.89	0.60	5.71
VBN2/PDM 139	16.42*	-3.45	18.52	18.18	13.12*	26.79*	0.00	13.77*	31.43*
VBN 2/Pusa 0672	16.42*	-18.97*	11.11	-9.09	17.02*	3.57	2.63	-10.78*	12.29
VBN 2/Pusa 0871	11.94*	-8.19	57.41*	69.70*	7.30	53.57*	5.26	14.61*	88.57*
VBN 2/TM 11-07	19.40*	-25.00*	48.15*	-18.18	-2.84	23.21*	-10.53	-5.99	8.57
VBN 2/TM 11-34	19.40*	-11.21	20.37	-12.12	6.38	17.86	-10.53	-8.38*	-21.43

* Significant at 5 % level0a0a0a

Table 4. Estimates of specific combining ability (*sca*) effects of the hybrids for yield and its component traits.

Cross Combinations	**DFF**	**PH (cm)**	**NBP**	**NPC**	**PL (cm)**	**NPP**	**NSP**	**100SW (g)**	**SYP (g)**
ADT 3/CO (Gg) 7	1.70	1.50	-0.16	-1.95*	0.32	-10.01*	-0.79	0.28*	-2.18*
ADT 3/EC 398897	-0.30	-1.00	-0.13	-2.01*	-0.05	-6.01*	0.03	0.15	-2.43*
ADT 3/IPM 02-03	-2.80*	-0.50	0.23	0.12	0.35	6.80*	1.09	0.24	1.74*
ADT 3/IPM 02-14	-0.93	-2.13*	0.21	3.18*	-0.50*	5.83*	0.78	-0.33*	3.12*
ADT 3/MH 521	1.33	-2.88*	-0.38	0.05	-0.04	0.30	-0.54	-0.31*	0.25
ADT 3/PDM 139	0.33	0.63	0.24	1.52	-0.07	5.02*	0.84	0.35*	2.32*
ADT 3/ Pusa 0672	1.70	1.00	0.25	-0.45	-0.52*	0.36	-0.66	-0.63*	-1.97*
ADT 3 Pusa 0871	1.57	0.37	-0.08	-0.76	0.11	0.24	-1.54*	-0.37*	-2.00*
ADT 3/TM 11-07	-4.18*	2.63*	-0.19	-0.88	-0.21	-6.08*	-0.29	-0.22	-2.15*
ADT 3/TM 11-34	1.57	0.37	0.02	1.18	0.62*	3.55	1.09	0.84*	3.32*
IPM 409-4/CO (Gg) 7	-0.90	0.78	0.30	-0.90	-0.17	3.57	-1.11	-0.44*	0.26
IPM 409-4/EC 398891	0.10	11.73*	-0.30	2.04*	0.87*	6.32*	1.45*	-0.09	3.15*
IPM 409-4/IPM 02-03	-0.40	3.36	0.37	-0.83	-0.33	-1.37	-1.24	-0.80*	-1.92*
IPM 409-4/IPM 02-14	-1.03	-13.02*	-0.28	-0.27	0.08	-0.59	0.45	0.48*	-0.24
IPM 409-4/MH 521	2.22*	-7.77*	0.01	0.10	0.20	-1.12	1.14	0.32*	0.22
IPM 409-4/PDM 139	-0.28	-10.72*	-0.03	0.32	-0.91*	-1.70	-0.99	-0.17	-0.72
IPM 409-4/Pusa 0672	-2.40*	13.23*	-0.12	3.35*	-0.33	1.69	0.51	0.98*	3.32*
IPM 409-4/Pusa 0871	-0.53	-6.95*	-0.30	-4.21*	0.10	-8.68*	0.64	0.06	-5.78*
IPM 409-4/TM 11-07	1.72	8.11**	-0.36	0.92	0.49*	3.50	-0.11	-0.04	2.06*
IPM 409-4/TM 11-34	1.47	1.23	0.11	-0.52	0.00	-1.62	-0.74	-0.30*	-0.35
SML 1074/CO (Gg) 7	-2.30*	-1.84	0.22	0.42	-0.22	1.69	1.59*	-0.21	-0.28
SML 1074/EC 398891	1.20	4.11	0.27	-2.65*	-0.24	-6.06*	-0.35	0.67*	-2.36*
SML 1074/IPM 02-03	3.70*	-5.27*	-0.61*	0.73	-0.63*	6.00*	-0.04	0.21	0.76
SML 1074/IPM 02-14	4.08*	7.36*	0.19	0.29	0.47*	4.79*	-1.10	-0.03	0.38
SML 1074/MH 521	-0.67	-8.39*	0.28	0.92	0.27	1.75	0.09	-0.38*	1.02
SML 1074/PDM 139	-0.67	2.68	-0.11	-2.74*	0.59*	-6.57*	-0.29	-0.77*	-2.41*
SML 1074/Pusa 0672	-0.30	-4.39	-0.25	-1.83*	0.36	-1.43	-1.04	0.14	-0.95
SML 1074/Pusa 0871	-1.42	3.92	-0.13	2.60*	-0.20	6.94*	0.84	0.31*	4.52*
SML 1074/TM 11-07	-0.17	1.48	0.34	1.48	0.16	-2.12	0.09	0.31*	-0.01
SML 1074/TM 11-34	-3.42*	0.36	-0.20	0.79	-0.57*	-5.00*	0.21	-0.26*	-0.67
VBN 2/CO (Gg) 7	1.50	1.24	-0.35	2.43*	0.07	4.75*	0.31	0.37*	2.20*
VBN 2/EC 398891	-1.00	-10.11*	0.16	2.62*	-0.58*	5.75*	-1.13	-0.74*	1.64*
VBN 2/IPM 02-03	-0.50	-0.99	0.02	-0.01	0.61*	-11.43*	0.19	0.35*	-0.58
VBN 2/IPM 02-14	-2.13*	-0.86	-0.11	-3.20*	-0.05	-10.03*	-0.12	-0.12	-3.26*
VBN 2/MH 521	-2.88*	8.39*	0.09	-1.07	-0.43*	-0.93	-0.69	0.37*	-1.49*
VBN2/PDM 139	0.63	7.83*	-0.10	0.90	0.39	3.24	0.44	0.59*	0.82
VBN 2/Pusa 0672	1.00	-0.61	0.11	-1.07	0.49*	-0.62	1.19	-0.49*	-0.39
VBN 2/Pusa 0871	0.37	1.95	-0.09	2.37*	-0.01	1.50	0.06	0.00	3.26*
VBN 2/TM 11-07	2.63*	-5.24	0.22	-1.51	-0.44*	4.69*	0.31	-0.06	0.10
VBN 2/TM 11-34	0.37	-1.61	0.06	-1.45	-0.04	3.07	-0.56	-0.28*	-2.31*
SE	0.98	2.34	0.24	0.76	0.30	2.26	0.66	0.12	0.67
CD $_{0.05}$	2.79	6.66	0.67	2.16	0.60	6.41	1.88	0.34	1.91

* Significant at 5 % level


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