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Magnitude of heterosis in hybrids derived from diverse cytoplasmic male sterility sources of pearl millet [*Pennisetum glaucum* (L.) R. Br.]

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Abstract
To assess the magnitude heterosis in hybrids carrying different cytoplasms for different traits. The 300 hybrids were developed by crossing of five different cytoplasmic male sterile lines and 60 diverse restorers in Line × tester design. The hybrids were grouped by their cytoplasmic sources (A_1, PT732A and A_4). The mean and range of heterosis and number of desirable crosses were calculated in each of the group for ten traits. The results revealed that, considerable and differential expression of heterosis was observed for different quantitative characters in hybrids based on different cytoplasm. The lesser magnitude of heterosis was observed for days to 50% flowering and days to maturity in A_1 sources as compared to PT732A and A_4 cytoplasmic source and vice versa for plant height and productive tillers per plant. But for other traits the cytoplasmic effect was conspicuous. These results suggest that there exists ample opportunity to exploit these diverse sources in pearl millet hybrid breeding to raise the productivity in Pearl millet.

Keywords: Pearl millet, heterosis, cytoplasmic male sterile line and restorers

Introduction
Pearl millet is a *kharif* season cereal crop in India, predominantly cultivated as a staple food and fodder crop. It is getting importance as climate resilient cereal crop for present harsh climatic condition. It provides staple food and nutritionally support for many people living in India, while it's dry fodder makes important feed for livestock.

In India first Pearl millet hybrid HB-1 was released after that several promising hybrids have been developed and released for general cultivation which lead to increased pearl millet productivity. However, in a short period of time most of hybrids failed due to their susceptibility to downy mildew disease and which was common in all the hybrids (Safeeulla, 1977) [8]. It was later realized that downy mildew susceptibility is associated with Tift 23A cytoplasm.

After that continuous research work the several alternative sources like, A_2, A_3, A_4, A_5 and PT732A (Bellary) cytoplasm are identification in pearl millet, since after, in India many number of hybrids were developed in Pear millet, have largely based on the A_1 CMS system except two (GHB 316 on A_3, HHB 216 on A_4 CMS system) hybrids.

The dependence on single cytoplasm makes the pearl millet hybrid seed industry vulnerable to pest and disease epidemics. The diversification of cytoplasmic background of hybrids insures the crop against any risk associated with cytoplasm and also adds flexibility and nuclear diversity in Pearl millet. Hence extensive research was needed for genetic diversification of cytoplasmic and nuclear genome of parental lines and development of divers cytoplasmic based stable potential hybrids for present climatic condition.

However systematic studies on identification of restorers on identified diverse cytoplasms are meager and good restorer availability on these sources is a limiting factor in the development of potential hybrids. Though highly stable A_4 and A_5 sources were found but utility is restricted due to non-availability of good fertility restorers (Rai *et al.*, 2006) [7].

Hence in present study heterosis was accessed for grain yield and yield related traits in hybrids derived from diverse sources of cytoplasmic male sterile line and restorers parents in Pearl millet.

Materials and Methods

The research material for the present investigation comprises of five female lines from diverse cytoplasmic male sterility sources (A_1, PT732A and A_4) and 60 divers restorers. The three female parents 841A, 863A and ICMA9422A (A_1 cytoplasm), ICMA01555 (A_4 cytoplasm) and PT732A (Bellary cytoplasm) and the 60 restorers were crossed in LxT mating design following Kempthorne (1957) [4] developed 300 hybrids. The total 375 genotypes (300 crosses + 60 male lines + 5 female and five corresponding B lines + five checks) were laid out in a randomized block design with two replications during *kharif* 2019. The seed of each entry was sown in a single row of 4-meter length. Intra row spacing was 15 cm and inter row spacing was 45 cm. The parents were grown in a separate adjoining block. Hybrids (F_1's) and parents were randomized among themselves only. Recommended package of practices were followed to raise the crop. Weeding, inter cultural operation and plant protection measures were taken up as and when needed. The 300 hybrids involving five lines and 60 testers and checks mean value for each trait was used for the estimation of heterosis. The heterosis of all F_1 crosses over their mid parent (MP), better parent (BP) and standard check (SC) were computed by the method suggested by Turner (1953) [9] and Hayes *et al.* (1955) [3].

Results and Discussion

The analysis of variance for line x tester (Including parents) is presented in table 1. The mean sums of squares due to genotypes for all characters were highly significant. The genotypes were further partitioned in to the mean sum of the squares due to parents (P), crosses and P vs C. The parents, crosses, parent's vs crosses and Line x Tester interactions were highly significant for all the characters. The lines were also highly significant for all the characters except for the days to 50% flowering, plant height and grain yield per plant. While, sum of squares due to testers and contrast parents were highly significant for all the characters. These results revealed presence of high amount of variability for all the characters. This is in the lines of expectation as the parental material comprised different cytoplasms like A1, A4 and PT732A and hence in the hybrids as well. Similar results were reported by Alidad Amiribezadi *et al.* (2012) [1] and Rafiq *et al.* (2016) [6].

Table 1: Analysis of variance for Line X Tester (Including parents) for 10 different characters in pearl millet hybrids and parents

Sources	DF	Days to 50% flowering	Days to maturity	Plant height (cm)	Productive tillers/ plant	Panicle Length (cm)	Panicle girth (cm)	Peduncle length (cm)	Earhead weight (g)	Grain yield/ earhead (g)	Grain yield/plant (g)
Replication	1	156.50**	0.02	35.51	2.56**	6.13*	0.003	1.28	126.31**	7.81	487.89**
Genotypes	364	15.83***	41.67**	1033.80**	0.61**	41.53**	1.31**	35.51**	377.28**	225.22**	818.97**
Crosses	299	12.19**	44.85**	1095.07**	0.61**	35.70**	1.41**	27.28**	340.79**	215.07**	654.76**
Line(c)	4	127.08**	1904.75**	43514.14**	19.61**	1033.52**	44.30**	147.12**	1736.22**	3467.86**	2578.90**
Tester (c)	59	15.63	22.17	525.40	0.40	22.91	1.04	29.50	311.07	160.12	835.29**
LXT (c)	236	9.38**	19.00**	518.52**	0.34**	21.99**	0.78**	24.70**	324.57**	173.68**	577.01**
Parents	64	17.36**	25.23**	446.40**	0.47**	27.42**	0.35**	37.34**	63.14**	53.89**	97.23**
Line (p)	4	9.85	43.90**	287.90	0.29*	5.21*	1.72**	3.39*	30.69**	6.26*	10.27
Tester (p)	59	17.19**	22.27**	448.52**	0.48**	28.72**	0.22*	38.65**	66.26**	56.19**	98.05**
L(P)vT(P)	1	57.31**	125.23**	955.67**	0.59*	39.74**	2.56**	95.77**	8.76	108.89**	396.75**
Cross vs parent	1	1007.04**	142.54**	20307.19**	10.95**	2686.20**	32.32**	2378.68**	31392.76**	14224.40**	96110.48**
Error	364	2.14	2.87	44.54	0.12	1.41	0.15	1.14	7.69	8.29	21.22

*, ** Significant at 5% and 1% level of significance, respectively

Magnitude of heterosis in hybrids carrying different cytoplasms for ten different characters.

To assess the magnitude heterosis in hybrids carrying different cytoplasms for different traits the hybrids were grouped by their cytoplasmic sources (A_1, PT732A and A_4). The mean and range of heterosis and number of desirable crosses were calculated in each of the group for all the ten traits (table 2) the results were discussed in the below.

For days to 50 percent flowering, the minimum mid parent heterosis mean (1.53) was registered from 863A based hybrids (A_1) and maximum (7.42) by ICMA94222 (A_1) based hybrids. The minimum mean heterosis over better parent was registered from 863A based hybrids (A_1). However, A_4 based hybrids registered highest heterosis mean over checks. Degree of heterosis exhibited by F_1's over their mid parent values were within the range of-11.44 (A_1) 863A based hybrids to 21.11 PT732A based hybrids. Total sixteen hybrids showed significant negative heterosis of them maximum crosses (8) registered from 863A based hybrids (A_1). The range of heterosis over better parent was from-13.89(A_1) 863A based hybrids to 13.27 percent (PT732A).A total of 40 crosses showed significant negative heterosis over their better parent of them maximum crosses (20) registered from 863A based hybrids (A_1). However, none of the crosses revealed significant negative heterosis over early flowered national check GHB-558.While maximum crosses (170) exhibited significant negative heterosis over zonal private check kaveri super boss.

The mean heterosis for days to maturity over mid parent, better parent and over checks were low in ICMA94222 based hybrids (A_1). While maximum heterosis mean was registered from PT732A based hybrids over better parents and checks.Degree of heterosis exhibited by F_1's over their mid parent values was the ranged from-11.82 (PT732A) to 15.24 (A_4) and total 71 hybrids showed significant negative heterosis among them ICMA94222 based hybrids (A_1) recorded higher (35) significant negative heterosis. The range of heterosis over better parent was from-16.30 (A_1) to 13.17 percent (A_4). The total 117 crosses showed significant negative heterosis among them 56 crosses from ICMA94222 based hybrids (A_1). However, heterosis exhibited by F_1's over national check was ranged from-11.38 (A_1) to 13.17 (PT732A and A_4) and 66 crosses revealed significant negative heterosis among them 58 crosses from ICMA94222 based hybrids (A_1). While 76 and 282 crosses registered significant negative heterosis over private commercial and zonal checks respectively.

The Plant height (cm) trait highest heterosis mean over mid parent was noticed in ICMA94222 based hybrids (A_1) and over checks was observed in 863A based hybrids. The range of percent heterosis of the hybrids over their respective mid parent values varied from-29.62 (PT732A) to 61.11 percent in 841A(A_1) based hybrids. Out of 229 crosses that showed significant mid parent heterosis, maximum crosses were registered by 841A based hybrids (A_1). Significant better parent heterosis was observed in 141 crosses, of which 863A based hybrids (A_1) showed highest positive heterosis crosses (47). The total of, nearly 56 hybrids were found to be significantly taller than the best check. Out of which 841A based hybrids (A_1) registered highest (26) positive heterosis crosses.

Number of productive tillers per plant exhibited lowest MP, BP and standard heterosis mean were observed in A_4 based hybrids and highest MP and BP heterosis was in 841A based hybrids (A_1). While highest heterosis over checks, was observed in ICMA94222 based A_1 hybrid. The magnitude of heterosis over mid parent and better parent was ranged from-44.13 and-53.83 (A_4) to 96.29 and 80.79 percent in 841A based hybrids (A_1) respectively. With respect to heterosis over better national check, 47 crosses registered significant heterosis and the maximum crosses (24) were registered from ICMA94222 based hybrids (A1).

The panicle length (cm), exhibited highest heterosis mean value over mid parent (42.29 cm), better parent (28.75 cm) and checks (28.56) were highest in 863A (A_1) based hybrids. The heterosis percent over mid parent value varied from-49.44 (A_4) to 106.25 percent 863A (A_1) based hybrids and highest positive (58) significant crosses recorded in 863A based hybrids (A_1). The lowest (-56.74) and highest (82.46) percent heterosis over better parent was observed in (A_4) based hybrids. The 863A based crosses exhibited more number of (51) significant positive from the better parent. With respect to heterosis over best private zonal check (Kaveri super boss), total of 25 hybrids showed significant positive heterosis and the maximum number (19) was recorded by 863A based hybrids.

With respect to Panicle girth (cm) trait, among the hybrids of different cytoplasmic source, ICMA94222 based hybrids exhibited highest mid parent (35.84) and better parent (27.93) heterosis mean value. The highest heterosis mean over checks was recorded by A_1 based hybrids (863A).Among the hybrids of different cytoplasmic source, the maximum number of mid parent heterosis desirable crosses (41) was registered by ICMA94222 based (A1) crosses and maximum significant positive crosses (22) over better parent heterosis was was observed on ICMA94222 A_1 source. As many as 60 hybrids exhibited significant heterosis over best commercial check (86M86) among them maximum crosses (38) registered from 863A based hybrids (A_1).

The highest Peduncle length (cm) mid parent (27.48) and better parent (11.15) heterosis mean value was registered from of A_1 based hybrids (841A).While all cytoplasmic based hybrids registered negative heterosis mean value over checks except over commercial private check 86M86. The highest significant mid parent heterosis was observed in 44 crosses of ICMA94222 based hybrids (A_1). As regards better parent heterosis, 841A based hybrids (A_1) showed more number (27) significant positive heterosis. With respect to heterosis over best check (Kaveri super boss), total 17 crosses exhibited significant positive heterosis out of which 841A based hybrids (A_1) recorded more number of crosses (9).

With respect to expression of heterosis for Ear head weight (g) traits. The highest mid and better parent heterosis mean was observed in A_1 based hybrids (841A). With respect to heterosis over standard checks, PT732A based hybrids recorded the maximum heterosis mean. The highest significant mid (56) and better (50) parent heterosis crosses were observed ICMA94222 based hybrids (A_1). With respect to heterosis over best check, total 47 crosses exhibited significant positive heterosis out of which PT732A based hybrids (Bellary) recorded more number of crosses (16).

With respect to grain yield per ear head (g) mid parent, better parent heterosis ICMA94222 based hybrids recorded highest heterosis mean. On other hand PT732A based hybrids recorded highest heterosis mean over checks. The ICMA94222 A_1 based hybrids fallowed by ICMA01555 A_4 based hybrids recorded higher mid and better parent heterosis among the different cytoplsam based hybrids. While A_4 and fallowed by PT732A based hybrids recorded highest heterosis over checks for grain yield per ear head. As regards to the number of desirable heterosis in mid parent, better parent and heterosis over best check among five different crosses showed that, PT732A based hybrids registered maximum crosses.

Expression of heterosis for grain yield per plant (g) among the different cytopasmic hybrids showed that, highest heterosis mean of mid parent, better parent and heterosis over checks were registered from 841A based A_1 hybrids fallowed by PT732A based hybrids except for mid parent heterosis mean. The extent of mid parent heterosis was ranged from-61.14 863A based A_1 hybrids to 375.69 841A based A_1 hybrids and maximum significant crosses (56) registered on ICMA94222 based hybrids (A1). The lowest (-67.33) and highest (332.63) percent heterosis over better parent was observed in 841A based A_1 hybrids. With respect to heterosis over better check (Kaveri super boss), 61 crosses showed significant positive heterosis out of which PT732A based hybrids recorded more number of crosses (17). The maximum expression of heterosis over checks was observed in A_4 based hybrids fallowed by PT732A and A_1 cytoplasm based hybrids for grain yield per plant.

In general, the expression of heterosis mean among the three sources of cytoplasm revealed that, days to flowering, days to maturity and plant height traits was low and high for remaining studied traits. The mean heterosis in hybrids grouped by cytoplasmic type appeared to be of lesser magnitude for days to 50% flowering and days to maturity in A_1 sources as compared to PT732A and A_4 cytoplasmic source and vice versa for plant height and productive tillers /plant. But for other traits the cytoplasmic effect was conspicuous. The A_1 and PT732A cytoplasmic source exhibited pronounced heterotic effect on panicle length, ear head weight, grain yield /ear, grain yield /plant compared to A_4 source. Similarly, A_1 and A_4 cytoplasmic source had greater heterotic effect on panicle girth trait. The highest heterotic values, for grain yield per se traits in pearl millet were in confirmation with Vetriventhan *et al.* (2008) [10], Dangaria *et al.* (2009) [2] and Alidad Amiribezadi *et al.* (2012) [1], Rafiq *et al.* (2016) [6] Kumara *et al.* (2023) [5].

Table 2: Magnitudes of heterosis expressed for ten traits in pearl millet hybrids carrying different cytoplasms

Cytoplasm source	Days to 50% flowering					Days to Maturity				
	Mid parent	Better parent	GHB-558	86 M 86	Kaveri Super Boss	Mid Parent	Better parent	GHB-558	86 M 86	Kaveri Super Boss
841A (A_1)										
Mean	1.68	-1.95	2.77	-4.85	-8.75	3.07	-1.02	1.80	0.00	-10.53
Min.	-10.14	-13.89	-3.16	-10.68	-14.02	-5.36	-10.67	-5.99	-7.65	-17.37
Max.	16.40	11.11	15.79	10.68	2.80	10.78	10.06	10.78	8.82	-2.63
No. of Significant crosses	4	9	0	24	51	2	16	2	6	59
ICMA94222 (A_1)										
Mean	7.42	4.73	4.05	-4.03	-7.62	-4.08	-9.56	-7.00	-8.64	-18.25
Min.	-4.17	-10.38	-4.21	-11.65	-14.95	-9.15	-16.30	-11.38	-12.94	-22.11
Max.	16.76	13.19	12.63	3.88	0	11.46	8.022	4.79	2.94	-7.89
No. of Significant crosses	0	2	0	14	32	35	56	57	58	60
863A (A_1)										
Mean	1.53	-3.49	4.77	-3.37	-6.98	0.77	-0.79	4.35	2.51	-8.28
Min.	-11.44	-13.59	-6.32	-13.59	-16.82	-6.52	-8.15	-1.80	-3.53	-13.68
Max.	17.84	7.77	16.84	7.77	3.74	10.06	6.90	11.38	9.41	-2.11
No. of Significant crosses	8	20	0	20	37	9	16	0	0	54
PT732A										
Mean	4.18	0.76	4.77	-3.37	-6.98	1.67	0.04	4.68	2.83	-7.99
Min.	-9.18	-11.32	-6.32	-13.59	-16.82	-11.82	-12.57	-8.38	-10.00	-19.47
Max.	21.11	13.27	16.84	7.77	3.74	12.84	9.88	13.17	11.18	-0.53
No. of Significant crosses	3	8	0	20	35	11	12	3	4	52
ICMA01555 (A_4)										
Mean	6.87	2.72	8.58	0.15	-3.60	0.97	-1.08	2.43	0.62	-9.97
Min.	-7.39	8.74	-1.05	-8.74	-12.15	-10.14	-13.26	-7.19	-8.82	-18.42
Max.	19.58	13.00	18.95	9.71	5.61	15.24	13.17	13.17	11.18	0.53
No. of Significant crosses	1	1	0	5	15	14	17	4	8	57
Total significant crosses	16	40	0	83	170	71	117	66	76	282
Check mean			48	52	54			84	85	95
SE	1.26	1.46	1.11			1.46	1.69	1.11		
CV%	2.97		3.15			2.00		1.87		
CD(0.05)	2.86		3.08			3.32		3.10		
CD(0.01)	3.77		4.06			4.37		4.08		

Cytoplasm source	Plant Height (cm)					Number of Productive Tillers per Plant				
	Mid parent	Better parent	GHB-558	86 M 86	Kaveri Super Boss	Mid Parent	Better parent	GHB-558	86 M 86	Kaveri Super Boss
841A (A_1)										
Mean	25.48	19.54	22.14	4.96	5.62	33.61	20.93	15.70	26.90	31.03
Min.	-19.50	-25.82	-20.00	-31.25	-30.82	-18.29	-30.02	-26.49	-19.37	-16.75
Max.	61.11	57.36	48.00	27.19	27.99	96.29	80.79	51.66	66.34	71.75
No. of Significant crosses	56	45	52	26	24	30	18	17	24	27
ICMA94222 (A_1)										
Mean	26.46	14.03	14.75	-1.39	-0.77	28.30	15.53	24.71	36.79	41.23
Min.	-7.14	-17.31	-14.91	-26.88	-26.42	-39.09	-42.40	-32.23	-25.67	-23.25
Max.	56.99	51.13	38.18	18.75	19.5	95.69	78.32	86.98	105.08	111.75
No. of Significant crosses	51	31	38	14	16	30	17	24	34	34
863A (A_1)										
Mean	20.66	15.97	23.10	5.79	6.46	6.65	-6.55	10.32	21.01	24.94
Min.	-3.73	-13.89	8.36	-6.88	-6.29	-33.46	-34.37	-20.75	-13.08	-10.25
Max.	50.09	40.85	45.45	25.00	25.79	34.57	12.78	32.45	45.28	50.00
No. of Significant crosses	53	47	58	15	15	7	0	1	6	9
PT732A										
Mean	-10.22	-13.65	-9.97	-22.63	-22.14	0.95	-12.43	6.75	17.09	20.90
Min.	-29.62	-34.62	-27.27	-37.50	-37.11	-27.13	-42.36	-30.02	-23.24	-20.75
Max.	15.45	4.01	4.36	-10.31	-9.75	68.45	29.09	56.73	71.91	77.50
No. of Significant crosses	35	0	0	0	0	7	1	5	13	16
ICMA01555 (A_4)										
Mean	7.78	2.51	4.45	-10.24	-9.68	-12.72	-20.95	-22.56	-15.06	-12.30
Min.	-16.25	-24.45	-1382	-25.94	-25.47	-44.13	-53.83	-48.79	-43.83	-42.00
Max.	45.9	42.38	39.27	16.69	20.44	44.18	37.50	30.68	43.34	48.00
No. of Significant crosses	34	18	17	1	1	3	1	0	2	1
Total significant crosses	229	141	165	56	56	77	37	47	79	87
Check Mean			138	160	159			2.26	2.07	2.00
SE	5.77	6.67	4.95			0.29	0.34	0.24		
CV%	4.45		4.59			14.38		14.05		
CD(0.05)	13.08		13.74			0.66		0.66		
CD(0.01)	17.21		18.09			0.87		0.87		

Cytoplasm source	Panicle length (cm)					Panicle girth (cm)				
	Mid parent	Better parent	GHB-558	86 M 86	Kaveri Super Boss	Mid Parent	Better parent	GHB-558	86 M 86	Kaveri Super Boss
841A (A_1)										
Mean	18.12	19.57	10.33	-8.91	-16.06	28.19	17.49	13.63	-0.06	12.65
Min.	-8.02	-25.82	-27.23	-32.94	-36.67	67.32	53.77	31.30	15.49	30.17
Max.	55.18	40.35	8.72	0.20	-5.37	-8.35	-21.62	-13.26	-23.71	-14.01
No. of Significant crosses	38	29	0	0	0	20	9	0	0	0
ICMA94222 (A_1)										
Mean	16.00	6.75	-10.51	-17.53	-22.11	35.84	27.93	33.13	17.10	31.99
Min.	-13.22	-27.85	-30.79	-36.22	-39.76	7.72	5.27	10.65	-2.68	9.7
Max.	48.97	31.63	17.06	7.88	1.89	73.15	64.01	65.43	45.51	64.01
No. of Significant crosses	34	25	0	0	0	41	22	27	4	27
863A (A_1)										
Mean	42.29	28.75	16.23	7.12	1.17	17.86	-6.58	51.91	33.61	50.60
Min.	-5.70	-10.01	-12.77	-19.61	-24.07	-29.82	-44.79	-10.22	-21.03	-10.99
Max.	106.25	65.70	45.96	34.51	27.04	55.94	19.39	94.13	70.75	92.46
No. of Significant crosses	58	51	35	26	19	28	0	49	38	48
PT732A										
Mean	28.73	15.06	7.86	-0.60	-6.13	-10.38	-16.31	-18.67	-28.47	-19.37
Min.	-13.18	-19.80	-23.40	-29.41	-33.33	35.4	34.07	18.91	4.59	17.89
Max.	82.63	59.91	47.66	36.08	28.52	-49.3	-55.26	-49.13	-55.26	-49.57
No. of Significant crosses	50	39	29	12	5	2	0	0	0	0
ICMA01555 (A_4)										
Mean	7.37	-3.50	-10.78	-17.78	-22.35	0.03	-20.66	29.01	13.47	27.89
Min.	-49.44	-56.74	-47.87	-51.96	-54.63	-84.29	-86.63	-78.26	-80.88	-78.45
Max.	82.65	82.46	65.96	52.94	44.44	127.93	63.77	166.30	134.23	164.01
No. of Significant crosses	23	18	8	3	1	15	0	27	18	26
Total significant crosses	203	162	72	41	25	106	31	103	60	101
Check Mean			23.50	25.50	27.00			2.30	2.62	2.32
SE	1.02	1.18	0.89			0.33	0.38	0.28		
CV%	5.32		5.46			14.26		14.33		
CD(0.05)	2.32		2.49			0.75		0.78		
CD(0.01)	3.06		3.27			0.99		1.03		

Cytoplasm source	Peduncle length (cm)					Ear head weight (g)				
	Mid parent	Better parent	GHB-558	86 M 86	Kaveri Super Boss	Mid Parent	Better parent	GHB-558	86 M 86	Kaveri Super Boss
841A (A_1)										
Mean	27.49	11.18	-2.75	22.68	-11.25	99.30	79.89	13.61	2.14	-9.94
Min.	-40.48	-47.74	-56.28	-44.85	-60.11	-50.63	-58.27	-72.87	-75.61	-78.49
Max.	162.94	126.81	89.74	139.35	73.15	256.19	225.35	89.91	70.73	50.54
No. of Significant crosses	38	27	17	39	9	51	47	31	24	14
ICMA94222 (A_1)										
Mean	22.48	5.62	-2.55	22.93	-11.07	83.90	67.61	0.89	-9.30	-20.03
Min.	-16.45	-23.91	-25.18	-5.62	-31.72	-29.56	-42.36	-54.16	-58.79	-63.67
Max.	69.95	43.13	28.82	62.50	17.55	168.89	138.08	34.67	21.07	6.75
No. of Significant crosses	44	22	1	47	0	56	50	13	3	0
863A (A_1)										
Mean	13.79	-0.41	-14.31	8.10	-21.80	77.05	61.07	-6.33	-15.78	-25.75
Min.	-29.22	-37.23	-40.24	-24.62	-45.47	-65.78	-67.24	-83.60	-85.26	-87.00
Max.	74.34	45.55	19.21	50.38	8.79	288.43	260.22	80.30	62.10	42.92
No. of Significant crosses	36	19	2	24	0	42	39	17	13	7
PT732A										
Mean	26.87	10.79	-4.54	20.42	-12.88	93.97	72.93	17.92	6.01	-6.52
Min.	-33.21	-41.16	-51.81	-39.21	-56.02	-43.30	-50.00	-59.03	-63.17	-67.53
Max.	97.40	68.89	39.89	76.47	27.66	196.72	149.29	62.66	46.23	28.94
No. of Significant crosses	38	27	12	32	7	52	49	42	29	16
ICMA01555 (A_4)										
Mean	18.43	0.84	-2.00	23.62	-10.57	47.01	25.80	-1.30	-11.26	-21.76
Min.	-18.03	21.52	-24.32	-4.53	-30.94	-65.79	-69.60	-69.80	-72.85	-76.06
Max.	54.41	46.80	40.50	77.24	28.21	162.19	107.45	66.83	49.99	32.25
No. of Significant crosses	41	12	3	46	1	40	27	21	14	10
Total significant crosses	197	107	35	188	17	241	212	124	83	47
Check Mean			21.44	17.00	23.50			36.86	41.00	46.50
SE	0.09	1.06	0.80			2.40	2.77	2.06		
CV%	5.47		5.6			7.78		7.55		
CD(0.05)	2.08		2.23			5.43		5.72		
CD(0.01)	2.75		2.94			7.15		7.54		

Cytoplasm source	Grain yield per head (g)					Grain yield per plant (g)				
	Mid parent	Better parent	GHB-558	86 M 86	Kaveri Super Boss	Mid Parent	Better parent	GHB-558	86 M 86	Kaveri Super Boss
841A (A_1)										
Mean	95.15	73.40	11.70	-12.51	-30.92	159.84	130.70	32.62	9.70	2.43
Min.	-56.74	-68.73	-74.47	-80.00	-84.21	-26.22	-40.26	-65.06	-71.10	-73.02
Max.	253.82	236.05	96.94	54.24	21.79	375.69	322.03	91.57	58.47	47.97
No. of Significant crosses	52	43	15	6	1	55	55	48	25	16
ICMA94222 (A_1)										
Mean	120.68	98.20	25.53	-1.69	-22.37	111.11	90.41	9.71	-9.25	-15.26
Min.	-23.39	-47.26	-53.19	-63.34	-71.05	-42.71	-44.90	-72.26	-77.05	-78.57
Max.	282.46	260.65	81.62	42.24	12.32	241.96	214.63	71.51	41.87	32.47
No. of Significant crosses	51	43	33	14	0	56	49	19	8	3
863A (A_1)										
Mean	41.89	27.81	-17.11	-35.08	-48.74	133.01	97.72	12.27	-7.13	-13.28
Min.	-69.93	-70.32	-84.55	-87.90	-90.45	-61.14	-67.33	-81.47	-84.67	-85.69
Max.	211.01	197.47	72.17	34.84	6.47	361.50	332.63	91.15	58.12	47.64
No. of Significant crosses	26	23	7	2	0	54	48	28	13	10
PT732A										
Mean	118.03	93.84	45.70	14.11	-9.90	129.93	109.61	26.02	4.24	-2.66
Min.	-46.47	-56.61	-63.83	-71.67	-77.63	-47.27	-47.60	-73.28	-77.90	-79.37
Max.	249.57	200.41	102.62	58.69	25.30	256.97	239.51	95.11	61.39	50.7
No. of Significant crosses	55	50	46	32	7	53	51	35	20	17
ICMA01555 (A_4)										
Mean	95.78	76.33	19.28	-6.58	-26.24	122.96	102.07	18.53	-1.95	-8.45
Min.	-65.68	-75.57	-68.09	-75.00	-80.26	-27.08	-29.51	-64.04	-70.25	-72.22
Max.	269.62	254.19	104.15	59.89	26.25	290.30	276.92	97.56	63.43	52.60
No. of Significant crosses	49	40	23	16	3	55	48	27	14	15
Total significant crosses	233	199	124	70	11	273	251	157	80	61
Check Mean			23.50	30.01	38.00			48.66	58.82	63.00
SE	2.49	2.87	2.17			3.98	4.60	3.49		
CV%	11.32		11.18			8.7		8.48		
CD(0.05)	5.64		6.03			9.02		9.69		
CD(0.01)	7.43		7.94			11.88		12.75		

Conclusion

These results indicate the differential effect of diverse cytoplasm on the expression of different quantitative characters. The considerable expression of heterosis was observed in hybrids based on different cytoplasm particularly for productivity traits suggest that there exists ample opportunity to exploit these diverse sources in pearl millet hybrid breeding to raise the productivity to a greater level.

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