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Early generation selection for yield and heat tolerance in bread wheat (*Triticum aestivum* L.)

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Abstract

Thirteen families (F_2 crosses) each with 5 progenies were grown in compact family block design with three replications in two environments normal sowing (E_1) and very late sowing (E_2) environments at Udaipur. Data recorded for grain yield, its twelve component traits and seven heat tolerant parameters were analysed to identify superior crosses and their progenies for yield and heat tolerance so as to exploit these for getting desirable sergeants in advanced generations. The analysis of variance revealed significant differences among the families for grain yield and all other traits in both the environments. However, the variations among the progenies within a family varied from character to character and environment to environment. In normal sowing environment, C_{12} family was the best among the eight families depicting significantly higher grain yield than the standard check. While in E_2 late sown environment, C_1 could be considered as one of the best family for yield and other attributes. Of heat tolerance traits, the family C_6 proved its worthiness. Based on the *per se* performance and estimation of variability parameters, $C_{12}P_2$, $C_{11}P_5$ and $C_{13}P_5$ were most promising progenies for normal conditions, while C_1P_3, C_1P_1, C_6P_4, C_8P_1 and C_4P_5 were promising for very late sown conditions. Selection from these families in advanced generations could provide desirable segregants for high yield and heat tolerance.

Key words: Grain yield, heat tolerance, families, progenies, segregants

Introduction

Heat stress is a major limitation to wheat (*Triticum aestivum* L.) productivity in arid, semi-arid, tropical and sub-tropical regions of world [1]. During grain filling stage this abiotic stress reduces the yield considerably at the rate of 270 kg/ha/degree rise in temperature above 11°C [2]. In India, NW plain zone area under delayed planting has been increasing very fast due to rice-wheat rotation, leads to expose the wheat plants to high temperature at the post anthesis phase. The other areas experiencing similar stress is, wheat growing regions of central and peninsular India. Hence, now breeding for heat tolerance has become an integral component of wheat improvement at both National and International level. However the progress to breed for high temperature tolerance has been handicapped due to inadequate knowledge about the morpho-physiological parameters and their sophisticated measurement techniques. But in recent past a few desirable heat tolerance parameters with high heritability have been identified for their use in breeding programme notably membrane stability or relative heat injury, canopy temperature depression (CTD), seedling vigor index, heat susceptibility index and melandialdehyde content (Stress accelerate lipid peroxidation).

The present investigation was therefore, an attempt to make use of these parameters in identifying superior crosses and their progenies for heat tolerance with high yield and their selection in F_3 generation based on their *per se* performance and estimation of variability parameters that may give an idea about the efficiency of selection in advanced generations.

Materials and methods

Out of 48 line × tester crosses [3], which depicted high heterosis along with non-significant SCA effects involving good general combiners, were advanced in F_2 generation and evaluated in normal and very late sowing environments. From each of these crosses, 5 plants with good *per se* performance in very late sowing were selected to raise F_3 generation, where each cross was designated as a family and plant to row as progeny. All these families and progenies, along with five checks, namely Raj 3077, Lok 1, Raj 3777, HD 2189 and Ajantha, were grown in compact family block design with three replications in each of two environments *viz.*, normal sowing or E_1 (25th November, 2003) and very late sowing or E_2 (6th January 2004) environments at Experimental Farm of Department of Plant Breeding and Genetics, Rajasthan College of Agriculture, Udaipur. Each progeny was grown in 4 m long single row spaced at 22.5 cm apart and plant to plant within row spaced at 10 cm apart. All the recommended cultural and management practices were followed to raise a healthy crop. Data were recorded on 5 randomly competitive plants for each progeny per replication for

13 agronomical traits including yield in both the environments and seven heat tolerance parameters in either single or both the environments, where measurements (twice) for canopy temperature depression (CTD) at grain filling stage was followed by Reynolds *et al.* [4], and for malondialdehyde (MDA) content by Health and Packer [5], for stomatal frequency (SF) by Punia [3], seedling vigor index (SVI) by Nayeem and Mahajan [6], germination stress index (GSI) by Behl [7], relative heat injury (RI) in E_1 as stress is uniformity subjected in laboratory for comparing different genotypes by Sullivan [8] and for heat susceptibility index (HSI) by Fischer and Maurer [9].

The above data so obtained were subjected to analysis of variance as given by Panse and Sukhatme [10] while estimates of variability parameters *viz.*, PCV and GCV were followed by Burton [11], heritability by Burton and Devane [12] and genetic gain by Johnson *et al.* [13]. The superior crosses were identified as depicting high *per se* performance for yield and other traits as compared to the check means along with high variability for intra family progenies having significant difference while for superior progenies were identified based on their mean *per se* performance having higher or *at par* as compared to the best checks for respective traits.

Results and discussion

Agronomical traits: The analysis of variance revealed significant differences among the families for grain yield and all other traits in both the environments indicated that plants in selected F_2 crosses depicted larger variation for these traits. On the other hand, differences among the progenies within a family (cross) varied from family to family for various traits in E_1 and E_2 environment. High family and progeny mean *per se* performance for grain yield and its contributing traits like harvest index, biological yield, grain number, effective tiller etc. indicated better expression of genotypes in normal sown condition (E_1 environment) than late sown condition i.e. E_2 environment, showing considerable effect of heat stress (Tables 1 and 2). Variability parameters were calculated for all those families which exhibited significant progeny differences. The highest magnitude of heritability, and genetic gain was recorded by family C_8 followed by C_{11} and C_{13} for plant height in both the environments and C_{10} in E_1 environment only. For grain yield and biological yield, family C_{11} again showed high genetic gain with moderate heritability in E_1 environment. These families also had high heritability estimates for days to 50% flowering and maturity. Heritability estimates in general were comparatively higher under heat stress environment E_2 than under normal E_1, indicating better chance of selection under stress environment. This may be due to the expression of resistance under stress conditions.

In normal sowing E_1, family C_{12} was found to be the best performer with highest *per se* mean grain yield followed by C_9, C_7, C_1, C_{13}, C_5, C_{11} and C_{12}, all had significantly higher grain yield than check mean (Table 1). Of these families, C_1, C_7, C_9 and C_2 depicted non-significant difference within their progenies for grain yield in this environment. This might be due to fixation of genes and hence lesser chance of segregation in advance generations. Similarly for grain yield contributing traits *viz.*, biological yield, 100 grain weight, number of effective tillers, flag leaf area days to flowering, maturity, number of grains except C_2, within progenies differences were also non-significant. Thus selection of progenies would be effective by considering high *per se* grain yield only. With regards to *per se* performance of these four families for yield contributing traits, significantly higher mean than the check mean was observed for biological yield, number of grains, spike length, flag leaf blade area and number of tillers in C_2, C_9 (except tiller number), C_1 (except flag leaf and tiller no.) family, while in C_7 significant superior performance was for biological yield and number of tillers and *at par* to other traits. As far as performance of progenies of these families were concerned, only one progeny C_7F_5 had significantly higher grain yield than the best check variety. This might be considered for selection in this generation but unfortunately with its tallness and soft straw, it could pose a problem of lodging and hence was not desirable.

On the other hand in another group of superior families *viz.*, C_5, C_{11}, C_{12} and C_{13} in E_1, within progenies variation for grain yield was found significant. This indicates chances of further segregation in advance generations and hence selection of high yielding segregants can be possible. Superiority of these families were also noticed for yield contributing traits too *viz.*, C_{12} for duration from flowering to maturity, spike length, grain number and biological yield, C_5 for plant height, flag leaf blade area, grain number and harvest index, C_{13} for flag leaf blade area, grain number and biological yield, C_{11} for duration from flowering to maturity, and harvest index. These findings showed that yield potential of different families may be governed by buffering action of different characters, and high grain yield *per se* in F_2 was not only due to genetic potential of the genotypes, but the environment had masking effect on grain yield of F_2 plants selected. Estimation of variability parameters in this group of families revealed that maximum GCV, PCV and CV for grain yield were recorded for C_{11} followed by C_{12}, C_5 and C_{13}. Variability for component traits too confirmed the significant variation among the progenies within these high yielding superior families. Moderate to high magnitude of variability parameters were recorded for days to

Table 1. Family means for various agronomical traits in F_3 generation of bread wheat in E_1 and E_2 environments

Families	Days to 50% flowering		Days to 50% maturity		Duration from flowering to maturity		Plant height (cm)		Number of tillers per plant		Flag leaf blade area (cm^2)		Spike length (cm)		Number of grains/ spike		100-grains weight (g)		Biological yield (g/plant)		Grain yield (g/plant)		Harvest index (%)	
	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
C_1	77.7	70.2	113.4	95.7	35.7	25.5	100.9	88.9	8.4	7.2	32.6	29.0	12.0	11.3	55.5	50.6	4.0	3.8	39.0	28.7	16.3	12.3	41.3	43.8
C_2	79.7	69.8	113.7	94.2	34.0	24.5	107.8	75.1	9.4	6.2	38.1	24.5	11.5	51.8	51.0	3.4	4.0	3.9	39.1	22.3	15.3	7.4	38.7	34.6
C_3	88.2	71.3	117.9	97.0	29.7	25.6	90.8	66.9	8.7	6.5	38.7	24.5	11.4	10.8	54.2	46.1	3.6	3.8	35.6	23.2	13.9	9.1	39.5	38.8
C_4	78.1	70.0	114.9	94.1	36.8	24.1	91.8	74.4	9.4	7.3	35.17	25.62	9.63	9.85	48.00	47.41	4.34	4.30	35.25	25.08	14.57	10.03	43.40	40.45
C_5	81.0	69.3	115.7	96.1	34.6	26.8	82.2	65.5	8.8	6.7	34.66	24.95	10.33	9.62	51.30	49.40	4.16	4.21	34.31	21.87	15.63	10.29	45.27	48.52
C_6	78.8	68.8	113.9	93.5	35.0	24.6	90.5	74.6	8.0	6.91	30.97	25.54	10.54	10.12	50.64	50.27	4.02	3.92	32.40	22.70	13.57	10.26	42.59	45.30
C_7	91.0	74.2	117.9	100.0	26.9	25.7	117.6	89.5	10.1	7.49	32.23	20.90	9.64	9.79	49.12	46.48	4.27	3.86	43.49	26.35	16.85	8.87	38.74	33.54
C_8	87.4	71.6	115.67	96.1	27.6	24.5	101.9	80.6	9.2	7.0	34.18	25.45	12.15	11.04	56.76	52.96	3.46	3.83	37.87	23.81	12.52	9.07	35.20	39.73
C_9	79.3	68.5	113.9	92.8	34.6	24.2	98.1	78.6	8.4	5.84	36.52	23.15	11.03	10.52	55.28	52.24	3.99	3.97	40.05	22.69	17.29	9.61	42.94	42.28
C_{10}	82.9	69.7	114.9	94.2	31.9	24.5	99.8	74.2	8.0	6.1	33.81	22.03	11.92	11.33	54.72	51.52	3.62	3.95	34.2	19.85	12.96	5.72	38.29	28.75
C_{11}	83.7	70.1	115.7	94.5	32.1	24.3	88.3	65.3	8.4	5.8	35.91	26.09	10.00	9.30	49.78	45.40	4.01	3.86	35.05	19.14	15.61	7.53	45.07	37.80
C_{12}	87.7	69.5	116.2	96.7	28.5	27.2	102.1	73.7	9.8	6.9	32.57	23.78	10.82	10.18	55.24	49.28	3.87	4.07	43.55	24.14	18.21	9.92	41.41	41.23
C_{13}	85.6	71.9	115.8	96.7	30.4	24.8	106.6	86.7	9.3	7.5	33.43	26.57	10.69	10.38	53.84	48.88	4.41	4.24	40.88	27.55	16.04	10.48	39.46	38.74
Checks	79.2	71.0	113.5	96.8	34.3	25.8	88.4	80.3	8.4	8.15	30.76	26.85	10.30	10.01	48.40	43.73	4.31	4.04	32.45	26.15	13.23	11.19	41.38	43.41
CD 5%	2.2	0.7	0.7	1.3	2.2	1.2	3.7	2.8	1.0	0.7	2.59	1.75	0.40	0.34	2.03	2.30	0.22	0.17	5.07	2.86	2.19	1.24	1.81	2.77

Notes: C_1-Raj 3777 × HD 2189; C_2Ajantha × WH 542; C_3-WH 542 × PBN 51; C_4-HD 2389 × HD 2189; C_5-HD 2389 × PBN 51; C_6-Raj 3077 × Kailash; C_7-C 306 × PBN 51; C_8-Raj 1482 × Ajantha; C_9-Kalyansona × HD 2189; C_{10}-Kalyansona × Ajantha; C_{11}-Kalyansona × PBN 51; C_{12}-GW 190 × HD 2189 and C_{13}-HI 977 × HD 2189

Table 2. Promising progeny means for various agronomical traits in F_3 generation of bread wheat in E_1 and E_2 environments

No.	Progenies	Days to 50% flowering		Days to 50% maturity		Duration from flowering to maturity		Plant height (cm)		Number of tillers/ plant		Flag leaf blade area (cm^2)		Spike length (cm)		Number of grains/ spike		100-grains weight (g)		Biological yield (g/plant)		Grain yield (g/plant)		Harvest index (%)	
		E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2	E_1	E_2
1	C_1P_1	75.3	69.7	113.0	95.0	37.7	25.3	98.5	86.8	9.3	7.5	29.5	27.3	11.8	11.2	57.6	48.4	3.8	3.6	41.7	30.3	18.0	13.2	43.1	43.7
2	C_1P_2	75.0	69.3	113.3	95.7	38.3	26.3	99.7	88.4	7.4	6.5	35.2	28.8	12.2	11.8	54.8	51.2	4.2	4.0	38.3	27.9	15.5	12.2	40.6	44.4
3	C_1P_3	79.3	70.7	114.0	96.7	34.7	26.0	97.1	87.7	8.3	7.1	36.2	32.6	12.4	11.6	58.4	52.4	3.9	3.7	37.3	30.7	15.3	13.3	38.6	43.0
4	C_1P_4	81.3	71.3	114.0	95.7	32.7	24.3	104.3	90.0	8.9	7.4	29.0	28.2	11.7	11.2	54.0	52.0	4.1	3.9	39.9	25.7	16.7	10.1	42.9	44.5
5	C_4P_5	82.0	72.0	116.7	98.3	34.0	26.3	83.8	67.1	10.7	8.9	37.3	26.4	9.1	10.1	52.0	46.8	4.5	4.6	40.1	28.3	15.1	11.5	45.9	41.1
6	C_5P_3	82.0	70.7	117.0	97.7	35.0	27.0	80.4	65.6	8.6	6.4	36.9	26.7	11.6	10.3	55.6	51.6	4.6	4.6	38.5	24.0	17.9	12.0	46.4	51.7
7	C_5P_4	77.7	69.0	115.3	95.0	37.7	26.0	89.1	68.9	10.9	7.5	33.6	23.6	10.7	9.8	52.0	48.7	4.1	4.2	41.5	25.3	19.3	11.9	46.9	47.2
8	C_6P_4	81.7	69.7	114.0	94.7	32.3	25.0	92.8	76.6	7.6	7.4	29.9	24.8	11.3	10.7	52.8	53.2	4.0	4.0	37.6	22.7	16.1	10.5	42.2	44.8
9	C_7P_5	89.3	72.7	117.0	98.0	27.7	25.3	117.8	88.9	9.5	6.3	31.8	23.9	10.3	10.7	51.2	47.9	4.4	3.9	50.8	28.2	20.9	10.0	41.4	35.7
10	C_8P_1	91.7	73.7	116.3	97.3	24.7	23.7	127.1	97.3	10.8	8.0	30.4	24.8	11.4	10.9	56.4	54.4	3.6	3.6	44.8	30.5	14.4	10.8	34.2	35.8
11	C_9P_2	81.3	68.3	114.3	93.7	33.0	25.3	98.4	78.7	10.0	5.9	35.1	21.8	11.0	10.9	55.2	52.0	3.9	3.9	44.9	25.9	19.0	11.4	42.4	42.7
12	$C_{11}P_5$	85.7	71.3	115.3	97.3	29.7	26.0	101.6	72.1	10.2	5.7	36.0	23.2	9.6	8.7	52.1	47.3	4.1	3.9	53.5	19.6	22.9	7.1	42.7	34.6
13	$C_{12}P_2$	87.3	67.7	116.0	96.0	28.7	28.3	98.6	75.9	10.6	7.0	7.3	3.0	21.6	10.9	10.3	55.0	48.4	4.0	4.2	54.0	28.1	23.3	11.4	44.0
14	$C_{13}P_5$	90.7	73.0	117.0	99.0	27.3	26.0	98.5	76.3	11.0	8.5	35.1	24.9	10.7	10.0	55.6	48.8	5.0	4.6	51.0	29.5	20.3	10.4	40.4	35.9
Best checks		74.3	69.3	112.7	94.3	29.3	24.7	82.4	76.1	9.0	10.1	33.3	29.0	11.4	11.0	53.6	45.2	4.6	4.5	34.9	30.4	14.7	12.7	42.5	46.7
CD 5%		5.0	1.7	1.7	2.9	4.9	2.8	8.2	6.2	2.2	1.5	5.8	3.9	0.9	0.7	4.5	5.1	0.5	0.4	11.3	6.4	4.9	2.8	4.0	6.2

flowering, duration from flowering to maturity, plant height (C_{11}, C_{13}), spike length (C_{11}, C_{12}), 100 grain weight (C_{13}), biological yield (C_{11}) and harvest index (C_{12}). Among the progenies of these families, $C_{12}P_2$, $C_{11}P_5$ and $C_{13}P_5$ were depicting significantly higher means than the best check for grain yield, biological yield as well as *at par* mean for number of tillers, flag leaf blade area, spike length, number of grains, and 100 grain weight (Table 2). But efficiency of selection of genotypes requires the great magnitude of variability, high heritability and genetic gain along with its greater contribution [14]. Based on this, $C_{11}P_5$ and $C_{12}P_2$ (belongs to families with high variability) were the most promising progeny that could be exploited for desirable segregants in advance generations. The other desirable progenies $C_{13}P_5$ belongs to superior family with low heritability for biological yield and grain yield could also be exploited for single plant selection in advance generations.

In E_2 environment (late sown condition), C_1 could be considered as one of the best family with maximum grain yield *per se* though *at par* to check mean. This family also depicted significantly higher mean than the check mean for component traits too *viz.*, early flowering, high flag leaf blade area, spike length and number of grains per spike. However progeny differences within this family was non-significant for grain yield and all other traits, indicating fixation of genes and attainment of homozygosity for these traits. Among the progenies of this family, the most promising ones with higher grain yield were C_1P_1, C_1P_3 and C_1P_2. Their superiority were also evident by significantly higher mean performance than the best check for component traits too like grain number (C_1P_3 and C_1P_2) and *at par* mean values for biological yield, flag leaf blade area, harvest index, spike length and days to 50% maturity (Table 2). The other promising family in stress environment (E_2) was C_5. Contrary to C_1, significant variation within its progenies for grain yield, 100 grain weight and spike length was recorded. The family mean for grain yield was *at par* to the best check with high variability (CV, PCV, GCV). But with low heritability, selection for yield itself in advance generation may not be effective. However contribution of component traits can be used as yield potential selection criteria rather than yield only. Because this family depicted significant superiority over best check for days to flowering, plant height, number of grains and harvest index (Table 1). The best progeny belonging to this family was C_5P_3 depicting high grain yield, biological yield, harvest index, 100 grain weight *at par* to best check and significantly higher number of grains with short plant height than the check in this environment. All these above said progenies C_1P_1, C_1P_2, C_1P_3 and C_5P_3 could be exploited for desirable segregants in advance generations for late sown conditions.

Heat tolerant parameters: Significant differences between families for all the heat tolerance traits indicated considerable variability among crosses for these traits. However with regards to differences among the progenies within family, seedling vigour index (SVI) at 30°C was the trait for which maximum number of seven families showed variation followed by SVI at 35°C (five families). Stomatal frequency (upper), stomatal frequency (lower) and SVI at 25°C with 3 families each. This differential response indicating heterozygosity is still there in F_3 for these traits, hence further selection is required in advance generations. On the other hand progenies within each family were depicting uniform behaviour for canopy depression temperature and relative heat injury indicating fixation of genes for these traits. Most of the progenies had relative injury *at par* to the best check Raj 3777.

Table 3. The high yielding families and their heat tolerant parameters mean in F_3 generation of bread wheat in E_1 and E_2 environments

No.	Families	CTD (°C)		SF		SVI			RI (%)	GSI (%)	HSI (%)	MDA content (m. moles/100mg)	
				Lower	Upper								
		E_1	E_2	E_1	E_1	25°C	30°C	35°C	E_1	E_1	E_1/E_2	E_1	E_2
1	C_1	27.85*	30.29	27.58	41.13	445.55	357.67	313.12	51.47	75.37	0.60	5.92	6.95
2	C_2	28.27	30.89¯*	26.51	41.02	505.70	389.05*	290.75	52.66	73.52	1.34¯*	5.61	7.27
3	C_3	27.89	30.60¯*	28.60	43.82	429.03¯*	341.93	254.42¯*	55.66	68.91¯*	0.89'*	4.72	6.11
4	C_4	27.64*	30.63¯*	29.69	45.80	473.13	389.22	299.97	50.36	76.18	0.81¯*	5.15	6.27
5	C_5	29.00	30.36	31.31¯*	46.91	427.72¯*	319.82'*	239.57¯*	40.74*	76.31	0.78'*	5.82	7.32
6	C_6	27.80*	30.25	26.84	44.87	458.07	376.80*	293.49	43.34*	71.78	0.58	3.38*	4.50*
7	C_7	28.27	30.21	33.40¯*	50.45*	537.29*	392.80*	280.23	41.84*	80.79*	1.14¯*	4.73	6.15
8	C_8	28.49	29.84	27.89	42.11	477.33	389.83*	284.90	36.16*	77.00	0.75	4.91	5.71
9	C_9	28.74	30.67¯*	28.98	44.22	472.22	358.53	285.95	54.42	74.59	1.18¯*	4.94	6.73
10	C_{10}	28.53	31.34¯*	28.07	44.44	464.58	376.40	291.02	49.18	73.60	1.52¯*	5.53	7.21
11	C_{11}	28.45	31.60¯*	30.25	44.78	412.21¯*	349.41	259.59*	41.33*	73.26	1.19¯*	5.11	6.58
12	C_{12}	27.60*	30.21	34.04¯*	48.91*	444.58	353.79	290.69	52.21	76.70	1.16¯*	5.96	7.27
13	C_{13}	27.49*	30.45¯*	26.82	43.38	516.80*	423.33*	323.43*	47.63	72.51	0.90	5.40	6.61
Checks		28.60	29.92	27.20	43.44	471.65	364.45	295.81	51.37	75.06	0.38	5.10	6.21

Notes: *Significantly inferior to best checks at 5% level; *Significantly superior to best checks at 5% level and others: *at par* to best checks

Looking to the response of individual family, C_6 was found to be depicting desirable mean performance for most of these traits (Table 3). It was followed by C_7, C_8, C_{13} and C_1 with non-significant differences within their progenies with high heritability (C_8 and C_{13} only) for most of the traits. A number of progenies from these families have done fairly well for most of the heat tolerant traits. The promising ones were C_1P_3, $C_{13}P_1$, $C_{13}P_2$, C_7P_3 and C_4P_5. Besides these, some high yielding progenies *viz.*, C_1P_3, C_1P_1, $C_{13}P_5$, C_6C_4 and C_8P_1 were also exhibiting desirable performance for these traits. With regards to the reliability of the heat tolerant parameters in screening heat tolerant genotypes, estimation of heat susceptibility index (HSI) indicates a perfect relationship with grain yield under stress environment, this was closely followed by relative heat injury with some exception.

Table 4. The high yielding progenies and their heat tolerant parameters mean in F_3 generation of bread wheat in E_1 and E_2 environments

No.	Progenies	Mean grain yield (g/plant)	CTD		SF		SVI			RI (%)	GSI (%)	HSI (%)	MDA content (m. moles/100mg)	
					Lower	Upper								
		E_1 and E_2	E_1	E_2	E_1	E_1	25°C	30°C	35°C	E_1	E_1	E_1/E_2	E_1	E_2
1	$C_{12}P_2$	17.29	27.30	30.00	33.22–*	49.89	438.67	352.00	283.20	46.83	82.32	1.34–*	5.69	6.72
2	C_1P_1	15.61	28.27	30.38	29.00	45.67	435.07	347.40	306.53	49.37–*	75.76	0.65	5.38	6.56
3	C_5P_4	15.60	28.25	30.28	27.44	42.89	449.33	328.67–*	241.93–*	40.16	75.78	0.98–*	7.03–*	7.86–*
4	C_7P_5	15.44	28.57	30.52	36.89–*	49.22	500.33	417.33	301.83	43.12	75.71	1.30–*	3.98	5.27
5	$C_{13}P_5$	15.34	27.30	30.12	29.78	47.22	446.75	399.33	328.67	46.65	73.79	1.29–*	5.63	6.46
6	$C_{11}P_5$	15.00	27.67	32.15–*	30.67	47.89	419.17	409.33	259.67	39.34	75.16	1.59–*	4.55	5.94
7	C_5P_3	14.96	28.37	29.98	31.22	47.22	425.33	313.37–*	226.00–*	40.03	77.74	0.54	6.72–*	7.34
8	C_1P_3	14.29	27.03	30.33	21.33	27.89*	408.00	340.53–*	324.00	46.41	77.24	0.33	6.20–*	7.39
9	C_1P_2	13.86	27.75	30.37	29.56	46.56	428.33	348.43	313.47	55.25–*	69.25–*	0.56	5.94–*	6.87
10	C_1P_4	13.40	27.78	30.23	24.78	39.11	473.67	364.67	308.93	50.68–*	79.77	1.01*	6.77–*	7.44
11	C_4P_5	13.33	27.23	30.00	30.45	46.67	464.00	380.20	305.33	50.18–*	72.05	0.76	5.43	6.41
12	C_9P_2	13.33	27.75	29.98	30.67	47.33	531.33	350.00	283.60	41.84	83.56	0.71	4.86	7.13
13	C_6P_4	13.29	27.32	29.77	29.00	42.11	464.67	380.00	292.00	43.53	78.64	0.73	2.79	3.41
14	C_8P_1	12.80	27.50	30.10	28.78	43.56	576.33	470.43*	319.33	32.93	75.96	0.63	5.48	6.46
Best checks		12.77	27.87	29.65	24.44	41.67	499.33	391.33	300.50	37.10	81.54	0.09	3.41	4.65

Notes: –*Significantly inferior to best checks at 5% level; *Significantly superior to best checks at 5% level and others: *at par* to best checks.

Based on the present findings, none of families and their progenies could be considered as the best one for all agronomical and heat tolerant traits, showing variable response. Hence utmost care is to be taken while rejecting progenies. However, some progenies $C_{12}P_2$, $C_{11}P_5$ and $C_{13}P_5$ could be considered the most promising to obtain desirable segregants for normal sown conditions, while another group of progenies *viz.*, C_1P_3, C_1P_1, C_6P_4, C_8P_1 and C_4P_5 could be exploited for very late sown condition. All these were high yielding and in some cases *at par* to the best check for grain yield and some of the component traits like biological yield, harvest index, number of grains and spike length as well as many of the heat tolerant traits with less than 1.0 heat susceptibility index.

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