Analysis of genetic variability in the advanced generation of finger millet [(*Eleusine coracana* (L.) Gaertn.] crosses to isolate improved genotypes for yield and blast resistance

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ABSTRACT

An investigation in finger millet was carried out during summer and kharif 2016 to study variability parameters in F_4 and F_5 progenies of three crosses with contrasting maturity duration with common female parent (PS-1) and different male parents (VL-315, OEB-526 and MR-6). The F_5 progenies were also screened for reaction to neck and finger blast under natural infection conditions at two locations. The PCV and GCV values were moderate to high for number of tillers, ear weight, grain yield and straw yield. Significant positive association of grain yield was evident with earhead weight, total tillers, productive tillers and fingers ear ¹Maximum progenies recorded a resistant score (<5) for neck blast infection. For finger blast, most progenies belonging to PS-1 × VL-315 and PS-1 × OEB-526 were resistant or moderately resistant. However, most progenies from the cross PS-1 × MR-6 were moderately susceptible to finger blast. The progenies with high grain yield and appreciable resistance to blast infection were identified in each of the crosses. Among these, the progenies PSVL-16 (PS-1 × VL-315), PSOB-12 (PS-1 × OEB-526) and PSMR-30 (PS-1 × MR-6) showed comparatively better performance.

Keywords: Finger millet, genetic advance, heritability, neck blast, finger blast

Finger millet (2n=4x=48) is a small seeded coarse cereal and has the largest genome size (1.5 Gb) among all the small millets (Vetriventhan *et al.*, 2020). It originated about 5000 years ago in the highlands of Eastern Africa (from Western Uganda to Ethiopia) by domestication of wild weedy forms. Evidences show that its cultivation was being practised in India about 3000 years ago (Jansen and Ong, 1996). This crop is traditionally consumed as a staple in many parts of Africa and South Asia. Finger millet is adaptable to a wide range of climatic conditions. It performs equally well in the tropical climate of South India and the low temperature situations in the North Indian hills. Though Karnataka alone accounts for 65% of the production and 60% of the area under finger millet in India, it is widely cultivated in many other states like Andhra Pradesh, Tamil Nadu, Uttarakhand, Orissa, *etc*. Finger millet grains contain 7.7 % protein, 1.5% fat and 2.7 % minerals and are widely consumed by diabetic patients worldwide in various forms. It is the richest source of Calcium (350mg/100g) among all the cereals (Kumar *et al.*, 2016). Due to the low productivity of this crop (1390 kg ha⁻¹) compared with other cereals like wheat (3507 kg ha⁻¹) and rice (2553 kg ha⁻¹), the area under this crop has been decreased by 49 % from 2000-01 to 2018-19. In order to encourage farmers to cultivate this crop, yield and quality improvement is a foremost requirement.

Many workers have characterised genetic variability parameters in germplasm collections (Reddy *et al.*, 2013; Chaudhari *et al.*, 2014; Jadhav *et al.*(2015); Patro and Madhuri, 2014; Ulaganathan and Nirmalakumari, 2013) as well as segregating generations obtained after crossing parents with complementary and/or diverse characters (Patnaik *et al.*, 2004; Shet *et al.*, 2009; Krishnappa *et al.*, 2009). A thorough insight into the genetic variability parameters is important for every new genetic material produced because it lays a foundation of decision making for future cycles of selection and evaluation. Besides, the biotic and abiotic factors responsible for reducing the yield of the crop should be systematically controlled. Finger millet can tolerate prolonged drought and infertile soils and is in fact a model to develop climate resilient genotypes in other important crop species. However, the blast disease caused by *Pyricularia oryzae* is a major challenge in its production and can result in almost 88 % yield loss (Rao, 1990; Nagaraja *et al.*, 2007). The pathogen is active at a temperature ranging from 26⁰C-32C⁰ and relative humidity of 89.9 % with high rainfall (Patro and Madhuri, 2014). All growth stages of the crop are vulnerable to the infection. In leaf blast, infectious

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lesions appear on the leaves in initial stage which expand and coalesce in susceptible genotypes. Neck blast breaks the connection between vascular tissues at the point of infection leading to death of the parts above the neck portion. The panicle or finger blast is the most infectious stage. Poorly filled grains or shrivelled grains or complete absence of grain formation occurs in this stage (Takan *et al.* 2004; Takan *et al.*, 2012; Manyasa *et al.*, 2019). A number of genotypes resistant or moderately resistant to blast have been released (VL-146, VL-149, Gautami and Sharda). However, we still don't have a spectrum of genotypes for the farmer to choose which are not only highly resistant to blast but also fit to the desired maturity duration. The present study was designed with the objective of evaluating three finger millet crosses segregating for maturity durations (early, medium and late), yield parameters and reaction to finger millet blast. The superior genotypes thus identified hold great hope to add to the list of varieties desired by farmers throughout the country.

MATERIALS AND METHODS

Plant material

The starting material for the experiment comprised of F_4 generation seeds belonging to three crosses with variable maturity durations. The female parent (PS-1 *i.e.* male sterile version of GPU-28) was common for the three crosses while the male parents were VL-315, OEB-526 and MR-6. For each of the three populations, thirty F_4 progenies selected from superior F_3 plants were sown in summer 2016. Each progeny was sown following plant-to-row method in 3 rows of 1.5 m length with a spacing of 30 x 10 cm.

Experimental design and statistical analysis

Augmented design was used with the four parents as checks repeated at regular intervals. The progenies as well as checks were evaluated for ten quantitative traits (Table 2) which were found to be directly or indirectly related to grain yield in previous studies. Among the F_4 progenies evaluated, thirty best performing progenies were selected in each cross based on the maturity date and yield contributing traits to raise the F_5 generation. The same ninety F_5 progeny families (thirty for each population) were raised in *kharif* 2016 following similar layout and design as for the F_4 generation. The recommended package of practices for nutrients, weed and pest management were followed to achieve a healthy crop in both the seasons.

Biometric observations were recorded on a sample of ten plants in each progeny row during both the seasons and the average was used for data analysis. Descriptive statistics for each trait were obtained using IBM SPSS statistics (version 19). Analysis of variance was performed to partition the total variation following an augmented design (Federer, 1956). The phenotypic and genotypic coefficients of variability were estimated as per the method of Burton and De Vane (1953). Broad sense heritability (H^2) and genetic advance for each trait was estimated by following the method of Johnson *et al.*(1955). Analysis was done using "Windostat" computer program for each cross separately.

Disease screening

For pathological investigation, the F_5 progenies were evaluated at GKVK, Bengaluru and Agricultural Research Station (ARS), Vizianagram, Andhra Pradesh. Vizianagram is an important hotspot for blast disease in India. After every five family progeny rows, two infector rows were sown to ensure adequate availability and spread of the inoculum. Udurumallige, a medium duration finger millet genotype highly susceptible to blast disease was used as the infector row. The scoring for neck and finger blast incidence was carried out using per cent disease infection (PDI) as outlined by Patro and Madhuri (2014). The progenies were classified into highly resistant (PDI= 0, score 1), moderately resistant (PDI= 5.01-10.00, score 2), resistant (PDI<5, score 3), moderately susceptible (PDI=10.01-25, score 4), susceptible (PDI=25.01-50, score 5) and highly susceptible (PDI > 50, score 6). The observations for per cent neck blast and finger blast incidence were normalized using arc sine transformation and then subjected to statistical analysis.

RESULTS AND DISCUSSION

Yield and yield components

Estimation of genetic variability in a population is preliminary to design a breeding programme, irrespective of the traits concerned. The variability parameters are not just a virtual tool for selection, but they also indicate the possible number of genes which might govern a character. This information gives an idea about the number of generations required to achieve improvement in the desired direction.

The estimates of mean, range, phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as per cent of mean for the three crosses are presented in Table 2, 3 and 4, respectively. In the F_4 and F_5 generations of the three crosses, the PCV and GCV were moderate to high for total number of tillers, ear weight, straw yield and grain yield, moderate productive tillers and finger length and low for plant height, days to 50 per cent flowering thousand grain weight and number of fingers per ear. Shet *et al.* (2009), Patil and Mane (2013), Srilakshmi (2013), Chaudhari *et al.* (2014) and Das *et al.* (2016) observed similar trend in finger millet. Haradari *et al.*
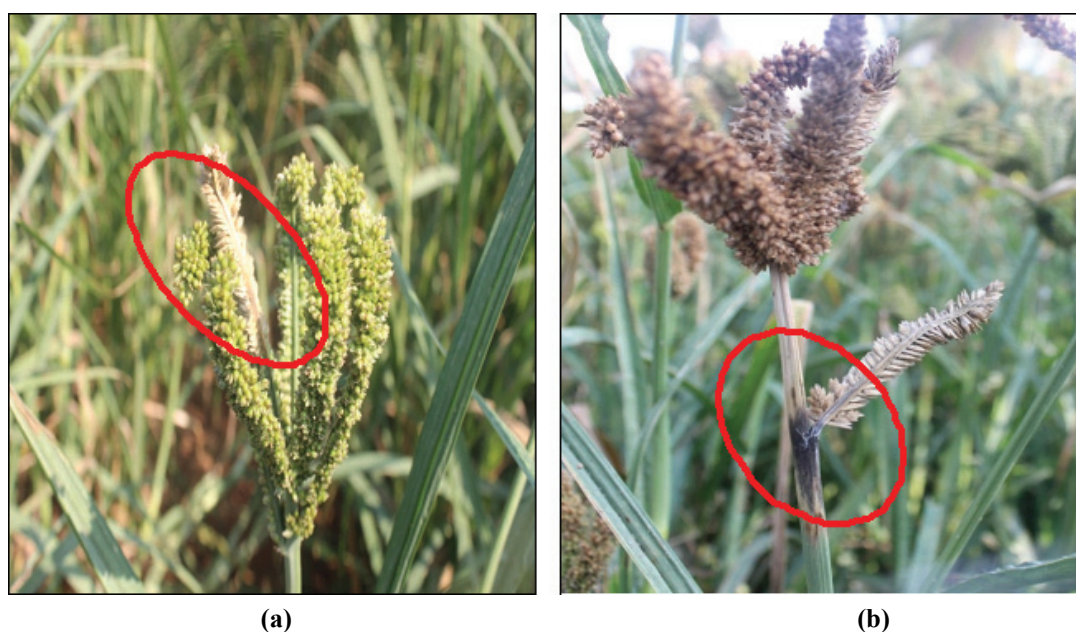
(a)   **(b)**

Fig. 1: Close view of (a) finger blast and (b) neck blast disease on finger millet

(2012) also obtained lower variability for days to 50 per cent flowering as compared to ear weight and grain yield in 1000 accessions of finger millet. Low genetic variability was observed for thousand grain weight. On account of high magnitude of PCV and GCV, more emphasis should be given to characters such as total tillers, ear weight, grain yield and straw yield.

The ratio of genotypic and phenotypic variance *i.e.* heritability is an indicator of genotypic variation. Heritability was high or moderate for all the traits examined except number of fingers per ear and plant height (in the cross PS-1× OEB-526), where low values of heritability were observed in at least one of the generations. This is in consonance with the findings of Srilakshmi (2013) and Mahanthesha *et al.*(2017). On the other hand, John (2006), Reddy *et al.* (2013), Kausar *et al.* (2013) observed high heritability for all the yield contributing traits. Narrow sense heritability and intergeneration correlation between the F_4 and F_5 generations was also estimated and has been detailed separately (Dubey and Rangaiah, 2019).

Heritability gives an idea about the breeding value of a trait that will be transferred to the next generation upon selection. Consideration of genetic advance along with heritability can lead to more efficient selection. Genetic advance is more realistically calculated as *per cent* of mean. In this study, genetic advance as per cent of mean was found to be high for total number of tillers, finger length, productive tillers, ear weight, grain yield and straw yield. It was low to moderate for rest of the characters. This is in consonance with the results of Hardari *et al.* (2013), Das *et al.*(2016), Mahanthesha *et*

al. (2017) in finger millet and Nirmalakumari *et al.*(2010) in little millet. Grain yield per plant had the highest genetic advance. Ulaganathan and Nirmalakumari (2013) also obtained highest genetic advance for single plant grain yield.

High values for heritability and genetic advance generally indicate that additive gene action predominates in the expression of a trait (Panse and Khargonkar,1957). In such a situation, a response to selection can be expected by using simple selection procedures. However, high heritability and low genetic advance and low heritability and high genetic advance values indicate the presence of both additive and non-additive types of gene action with predominance of non-additive gene action. This hold true in case of days to 50 per cent flowering and thousand grain weight. The selection methods should also take into consideration multi environment testing and multi-location testing to have an actual idea of the trait inheritance and selection should be based on the inferences so drawn. For instance, in this experiment, total tillers per plant and finger length exhibited moderate values for PCV and GCV but high heritability. Ear head weight and grain yield plant[-1] showed high values for PCV and GCV as well as high heritability and genetic advance. Though these traits are highly influenced by the environment and also by a large number of genes, efficient selection for these traits can only be carried out if the environmental component of variance is controlled and a large population is raised in the early generations. On the contrary, days to 50 per cent flowering, plant height and thousand grain weight showed low values for PCV, GCV, high heritability and

Table 1: Mean, range and genetic variability parameters for yield and its contributing traits in F₄ and F₅ generation of the cross PS-1 × VL-315

Characters	Mean ± S.E.		Range Minimum		Range Maximum		Standardised Range		PCV (%)		GCV (%)		H² (BS)		Expected GAM (%)	
	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5
Days to 50 % flowering	61.36 ± 0.85	58.06 ± 0.66	54	49	73	65	0.31	0.28	7.17	5.9	7.14	5.72	99.14	94.31	14.65	11.46
Plant height (cm)	98.12 ± 1.61	90.16 ± 1.64	76.6	70.7	121.9	106.7	0.46	0.4	8.49	9.7	8.09	6.41	90.82	43.89	15.89	8.75
Total tillers per plant	8.37 ± 0.32	6.31 ± 0.28	5.4	3.4	12.25	10.4	0.82	1.11	19.55	23	18.01	17.49	84.89	60.41	34.19	28
Fingers per ear	6.80 ± 0.16	6.17 ± 0.14	5	4	10	7.2	0.73	0.52	11.99	12	9.54	6.21	63.23	26.3	15.63	6.56
Finger length (cm)	6.22 ± 0.17	5.52 ± 0.14	4.23	3.99	8.25	6.99	0.65	0.54	13.94	13	12.79	12.75	84.23	92.14	24.19	25.21
Productive tillers	3.56 ± 0.13	3.84 ± 0.08	2.2	3.1	5.6	4.7	0.95	0.42	19.75	11	13.99	9.47	50.19	76.1	20.43	17.03
Ear weight per plant (g)	36.47 ± 1.75	22.10 ± 1.19	23.35	9.5	58.94	35.65	0.92	1.18	25.17	28	21.68	23.67	74.16	73.12	38.46	41.7
Grain yield	25.88 ± 1.45	14.32 ± 0.82	13.18	5.89	42.85	22.08	1.12	1.13	28.49	29	25.29	28.03	78.82	93.19	46.26	55.74
Thousand grain weight	2.67 ± 0.02	2.77 ± 0.04	2.46	2.23	2.95	3.05	0.18	0.3	4.42	6.8	4.42	6.77	99.65	99.86	9.08	13.94
Straw yield (g)	52.37 ± 2.35	29.89 ± 1.22	32.25	16.15	81.44	47.65	0.94	1.05	23.62	21	18.84	14.11	63.4	44.19	30.9	19.19

Table 2: Mean, range and genetic variability parameters for yield and its contributing traits in F₄ and F₅ generation of the cross PS-1 × OEB-526

Characters	Mean ± S.E.		Range Minimum		Range Maximum		Standardized range		PCV (%)		GCV (%)		H² (BS)		Expected GAM (%)	
	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5	F_4	F_5
Days to 50 % flowering	66.16 ± 0.72	61.46 ± 0.48	59	53	74	66	0.23	0.21	5.6	4.13	5.6	3.73	98.81	81.83	11.47	6.95
Plant height (cm)	110.25 ± 1.49	96.51 ± 1.26	96.18	78.8	127.8	107.8	0.29	0.3	7.4	6.94	3.17	4.38	18.56	39.84	2.81	5.69
Total tillers per plant	6.96 ± 0.32	4.74 ± 0.22	4.63	2.78	11.4	7.11	0.97	0.91	24	25.13	21.08	20.62	78.92	67.31	38.59	34.84
Fingers per ear	7.92 ± 0.14	7.05 ± 0.17	6.1	5.44	10.8	9.9	0.59	0.63	9.8	12.39	5.76	9.67	34.34	60.95	6.95	15.55
Finger length (cm)	6.87 ± 0.11	6.26 ± 0.14	5.45	4.76	7.87	7.85	0.35	0.49	8.8	11.74	5.95	11.52	45.38	96.31	8.26	23.29
Productive tillers	3.25 ± 0.06	3.71 ± 0.13	2.5	2.22	4.2	4.8	0.52	0.69	10	17.93	8.51	17.21	73.01	92.11	14.98	34.01
Ear weight per plant (g)	37.38 ± 1.52	24.67 ± 1.51	19.56	7.9	52.33	46.5	0.88	1.56	22	32.34	13.21	25.05	36.63	60	16.47	39.99
Grain yield	24.05 ± 0.90	16.58 ± 1.52	14.36	6.71	36.87	34.84	0.94	1.7	20	35.23	13.07	29.46	42.68	69.9	17.6	50.75
Thousand grain weight	2.67 ± 0.05	2.82 ± 0.04	2.1	2.31	3.01	3.09	0.34	0.28	9.9	6.43	9.93	6.42	99.84	99.8	20.43	13.22
Straw yield (g)	68.76 ± 3.82	32.25 ± 2.63	27.48	16.2	119.7	60.7	1.34	1.38	27	41.1	17.51	34.22	34.75	69.3	10.63	58.68

Table 3: Mean, range and genetic variability parameters for yield and its contributing traits in F$_4$ and F$_5$ generation of the cross PS-1 × MR-6

Characters	Mean ± S.E.		Range Minimum		Range Maximum		Standardized range		PCV (%)		GCV (%)		H²(BS)		Expected GAM (%)	
	F$_4$	F$_5$	F$_4$	F$_5$	F$_4$	F$_5$	F$_4$	F$_5$	F$_4$	F$_5$	F$_4$	F$_5$	F$_4$	F$_5$	F$_4$	F$_5$
Days to 50 % flowering	71.33 ± 0.54	65.10 ± 0.38	64	62	75	70	0.15	0.12	3.98	3.08	3.39	2.44	73.05	62.66	5.98	3.98
Plant height (cm)	120.29 ± 1.34	104.17 ± 1.14	101	86.9	131	120.5	0.26	0.32	5.74	5.64	5.73	5.38	99.49	90.9	11.76	10.56
Total tillers per plant	6.87 ± 0.19	3.71 ± 0.21	4.7	1.7	8.8	6.5	0.6	1.29	14.88	30.4	12.91	22.91	75.2	56.7	23.06	35.56
Fingers per ear	7.90 ± 0.13	7.19 ± 0.12	7	5.7	10.2	8.6	0.4	0.4	8.37	9.44	7.73	0.7	85.25	0.55	14.69	0.11
Finger length (cm)	7.79 ± 0.103	7.71 ± 0.29	6.87	6.19	9.32	9.02	0.31	1.19	6.99	19.81	4.88	19	48.87	91.9	7.04	37.54
Productive tillers	3.35 ± 0.08	3.05 ± 0.11	2.56	1.9	4.3	4.2	0.52	0.75	12.57	18.54	9.24	16.98	54	83.8	13.98	32.02
Ear weight per plant (g)	47.99 ± 1.74	23.21 ± 1.47	35.44	10.67	86.4	43.5	1.06	1.41	18.87	33.66	16.16	23.12	73.38	47.15	28.52	32.69
Grain yield	24.27 ± 1.12	15.06 ± 0.89	13.59	6.76	37.89	25.02	1	1.21	23.91	30.71	21.16	27.51	78.35	80.2	38.58	50.76
Thousand grain weight	2.73 ± 0.02	3.01 ± 0.02	2.42	2.59	3	3.25	0.21	0.22	4.42	3.42	4.42	3.32	99.88	93.9	9.09	6.62
Straw yield (g)	83.00 ± 2.51	38.43 ± 2.07	50.05	22.3	112.39	71.25	0.75	1.27	15.59	26.88	15.27	21.95	95.96	66.67	30.82	36.91

Table 4 : Number of progenies (%) corresponding to different disease response groups for neck blast finger blast in F$_5$ generation of three finger millet crosses across Vizianagaram (VZM) and Bengaluru

Score	Crosses — Disease response groups (Per cent infection)	Neck Blast PS-1 × VL-315 Bengaluru	VZM	PS-1 × OEB-526 Bengaluru	VZM	PS-1 × MR-6 Bengaluru	VZM	Finger Blast PS-1 × VL-315 Bengaluru	VZM	PS-1 × OEB-526 Bengaluru	VZM	PS-1 × MR-6 Bengaluru	VZM
1	Highly resistant (0.00)	4 (13.3%)	6 (20%)	2 (6.7)	9 (30%)	11 (36.7%)	1 (3.3%)	0	0	0	0	0	0
2	Resistant (less than 5)	26 (86.7%)	24 (80%)	28 (93.3%)	21 (70%)	19 (63.3%)	27 (90%)	8 (26.6%)	12 (36.6%)	21 (66.7%)	12 (40%)	16 (53.3%)	2 (6.6%)
3	Moderately resistant (5.01-10)	0	0	0	0	2 (6.7%)	0	10 (33.3%)	15 (50%)	6 (20%)	7 (23.3%)	8 (26.6%)	3 (10%)
4	Moderately susceptible (10.01-25)	0	0	0	0	0	0	12 (40%)	3 (10%)	2 (6.66%)	8 (26.6%)	6 (20%)	13 (43.3%)
5	Susceptible (25.01-50)	0	0	0	0	0	0	0	0	1 (3.33%)	2 (6.66%)	0	10 (33.3%)
6	Highly susceptible (More than 50.00)	0	0	0	0	0	0	0	0	0	1 (3.33%)	0	2 (6.66%)
	Total	30	30	30	30	30	30	30	30	30	30	30	30

Table 5: Superior progenies selected in the three crosses for neck and finger blast resistance, high grain yield and maturity duration (early, medium or late)

Progeny no.	Neck blast Score	Finger blast Score	Grain yield (g)	Days to 50 % flowering
PS-1 × VL-315				
PSVL-16	2	3	21.44	56
PSVL-18	1	3	21.11	61
PSVL-23	2	3	18.47	52
PSVL-30	2	3	23.09	58
PS-1 × OEB-526				
PSOB-12	1	2	24.11	61
PSOB-23	1	2	23.42	64
PSOB-9	2	3	20.64	59
PSOB-19	1	3	22.29	63
PS-1 × MR-6				
PSMR-29	1	2	22.89	64
PSMR-30	0	3	24.86	67

low to moderate genetic advance. The number of genes governing these traits were smaller which allow little interference of the environment if controlled systematically. Therefore, molecular breeding for these traits might prove to be quite useful.

Reaction to neck and finger blast

The progenies in the cross PS-1 X VL-315 showed more variation for neck and finger blast infection as compared to the other two crosses at Vizianagram whereas at Bengaluru, the progenies exhibited significant variation only for the crosses PS-1 x OEB-526 and PS-1 x MR-6 (data not included). The typical symptoms of finger blast and neck blast as observed in the experiment are shown in Fig. 1.

At Vizianagram, the F_5 progenies in the crosses PS-1 x OEB-526 and PS-1 x MR-6 showed resistant reaction to neck blast. More than half of the progenies from the cross PS-1 × OEB-526 showed resistant or moderately resistant reaction to finger blast, whereas maximum progenies from the cross PS-1 × MR-6 showed susceptible or moderately susceptible reaction to finger blast. For the progenies evaluated at Bengaluru, significant difference was observed only in the crosses PS-1 × VL-315 and PS-1 × OEB-526 (data not included). Hence, the progenies showing resistant reaction at both the locations can be used as a source of resistance genes.

Table 4 shows that most progenies in all the crosses were resistant to neck blast. However, in crosses PS-1 ×OEB-526 and PS-1 × MR-6, few progenies that showed highly resistant reaction at Bengaluru showed susceptible reaction at Viziangaram.

Finger blast

The progenies of the cross PS-1 × VL-315 showed nearly comparable finger blast incidence at both the locations. However, the progenies falling in moderately susceptible category were higher in Bengaluru (40%). In cross PS-1 × OEB-526, maximum progenies were found to show resistant reaction to finger blast. In addition to this, the progenies showing susceptible reaction to finger blast were found to be higher in Vizianagaram than Bengaluru. On comparing finger blast incidence at the two locations for the cross PS-1 × MR-6, it was observed that at Bengaluru, most progenies were found to be resistant (53.3 %) or moderately resistant (26.6%), while at Vizianagaram, most progenies were found to be moderately susceptible (43.3%) or susceptible (33.3 %). The temperature and relative humidity conditions prevalent at Bengaluru did not provide sufficient chances for the inoculum spread and lower disease incidence was observed in the healthy crop also.

Finally, top performing progenies were selected in each of the crosses on the basis of yield performance, maturity duration and blast reaction (Table 8).

Four progenies were identified in the cross PS-1 × VL-315, namely PSVL-16, PSVL-18, PSVL-23 and PSVL-30. The progeny PSVL-16 showed grain yield comparable to the checks, high number of tillers per plant, short stature coupled with resistant reaction to neck and finger blast. Four progenies were identified in the cross PS-1 × OEB-526, namely PSOB-9, PSOB-12, PSOB-19 and PSOB-23.The progeny PSOB-12 was found to flower in 61 days, gave higher mean grain yield (24.11 g) as well as straw yield than the checks and was

highly resistant to neck and finger blast. Two progenies were identified in the cross PS-1× MR-6, namely PSMR-29 and PSMR 30. The progeny PSMR 30 was found to flower in more than 65 days, had higher grain yield as well as straw yield compared to the checks and showed moderate resistance to neck and finger blast.

Among all the three populations, best progenies superior to their respective parents were selected based on grain yield, reaction to neck and finger blast and maturity duration. Progenies of the cross PS-1 × VL-315 were found to be comparatively superior over other population for grain yield and resistance to neck and finger blast. The superior progenies identified in each of the crosses could be subjected to few more cycles of pedigree selection to recover stable high yielding and blast resistant genotypes. The genotypes so obtained would be evaluated in different locations and/or years to assess their stability for important economic traits to recommend them for particular agroclimatic zones.

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