

Identification of Resistant F₆ Recombinant Inbred Lines (RILs) of Finger Millet for Neck and Finger Blast Disease Infection under Natural Hotspot

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ABSTRACT

Finger millet (*Eleusine coracana* L. Gaertn.) is one of the most important staple food crops in India. Blast disease caused by the fungus *Pyricularia grisea* (Cooke) is the most important biotic production constraint which affects different aerial parts of the plant at all plant growth stages. Three hundred and sixty F₆ finger millet RILs derived from the cross PR 202 × GPU 48 were evaluated during 2015 rainy season at Vizianagaram (natural hotspot for finger millet blast disease) for blast disease reaction. ANOVA revealed highly significant mean squares attributable to 'RILs' and 'check varieties' for both neck and finger blast disease. The estimates of PCV, GCV and heritability were high for both neck and finger blast disease. Most of the RILs were moderately resistant whereas, a few RILs were resistant. The best five resistant RILs for neck and finger blast disease were identified.

FINGER millet (*Eleusine coracana* L. Gaertn.) belonging to the family poaceae, an allotetraploid with 2n=4x=36 chromosomes, is the most important staple food crop among small millets. Wider adaptability, higher nutritional quality, higher multiplication rate and longer shelf life under ambient conditions, makes finger millet an ideal crop for use as a staple food and famine reserve (Upadhyaya *et al.*, 2007). Though finger millet is considered as one of the hardiest crops, its production is constrained by several biotic and abiotic stresses. Among the several production constraints, blast (neck and finger blast) caused by the fungus *Pyricularia grisea* (Cooke) affects different aerial parts of the plant at all plant growth stages beginning from seedling to grain formation. The average yield loss due to blast is estimated as 28 per cent (Vishwanath *et al.*, 1997). Under pathogen favourable conditions, losses may reach up to 50 per cent (Seetharam, 1982). Appearance of brown and subsequently blackening of the area immediately below the ear is an indication of neck blast. Finger blast usually begins from the apical portion and runs toward the base of the finger (Patro and Madhuri, 2014). Host plant resistance (HPR) is considered as the most eco-friendly and economical method of mitigating losses due to neck and finger blast. The objective of the present study was to identify blast disease resistant finger millet F₆ recombinant inbred lines (RILs) derived from the cross involving

blast susceptible and blast resistant parents for use as varieties if found high yielding or in breeding blast resistant varieties.

The material for the present study consisted of 360 RILs derived from the cross PR 202 × GPU 48 following ear-to-row method. While, the female parent PR 202 is a blast disease susceptible variety, the male parent GPU 48 is a blast disease resistant variety. The 360 F₆ RILs along with their two parents and blast disease susceptible check, *Uduru mallige* were evaluated during 2015 rainy season at Vizianagaram (recognised as natural hotspot for finger millet blast disease in India) for response to neck and finger blast disease infection following augmented design (Federer, 1956). The seeds of RILs were sown in eighteen blocks. Each block consisted of 20 RILs, three checks (PR 202, GPU 48 and *Uduru mallige*) replicated twice and two boarder rows. The RILs, parents and checks were planted at a spacing of 10 cm × 22.5 cm. Recommended crop production practices were followed during the crop growth period.

Infector-row method was followed to screen the RILs for responses to blast disease infection. After every five rows of RILs, single infector row consisting of blast susceptible genotype (*Uduru mallige*) was sown to ensure sufficient inoculum load and disease

spread. The neck blast incidence (NBI) and finger blast incidence (FBI) on RILs, parents and checks were scored and expressed in per cent using the following formulae.

$$\text{NBI (\%)} = \frac{\text{Number of ears showing infection on peduncle per unit area}}{\text{Total number of ears in a unit area}} \times 100$$

$$\text{FBI (\%)} = \frac{\text{Number of infected fingers / unit area}}{\text{Average number of fingers / ear} \times \text{Total number of ears / unit area}} \times 100$$

Analysis of variance (ANOVA) was performed to partition the total variance of entries (RILs + parents + check) into those attributable to 'RILs', 'checks' and 'RILs vs checks' as per augmented design. The mean NBI and FBI of each of the 360 RILs were adjusted for block effect. The effect of each block (B_j) was estimated as,

$$B_j = X_j - X_{..}$$

Where,

X_j = The mean NBI and FBI of check entries in j^{th} block

$X_{..}$ = The mean NBI and FBI of all the checks in all the blocks.

The estimate of B_j was used to adjust the NBI and FBI mean of the RILs relevant to the block. Thus, the mean NBI and FBI of each RIL evaluated in j^{th} block was adjusted by subtracting the block effect ' B_j ' of the j^{th} block from actual NBI and FBI of the RILs. Adjusted mean NBI and FBI values were used for estimating descriptive statistics such as mean NBI and FBI, standardised range, phenotypic (PCV) and genotypic co-efficient of variation (GCV) (Burton and De Vane, 1953). Heritability in broad-sense (h^2) was estimated as $h^2 = (Vg/Vp) \times 100$ where, Vg = Genotypic variance, Vp = Phenotypic variance.

Based on NBI and FBI, as measured on a 0-5 scale; RILs were classified as immune (0), highly resistant (0.1-2.0%), resistant (2.01-10.0%), moderately resistant/susceptible (10.01-25.0%), susceptible (25.01-50.0%) and highly susceptible (>50%). The significance of differences in NBI and FBI of RILs classified into different groups was tested

using one way ANOVA. Based on the mean NBI and FBI the best RILs with higher level of resistance to neck and finger blast were identified.

Analysis of variance revealed highly significant mean squares attributable to 'RILs' and 'check varieties' for both NBI and FBI (Table I). Mean squares attributable to 'RILs vs check varieties' were

TABLE I

Analysis of variance for response to disease infection in F₆ generation of finger millet

Source of variation	Degrees of freedom	Neck Blast (%)	Finger Blast (%)
Blocks	17	5.7	9.659
RILs + Checks	362	198.95 **	177.71 **
RILs	359	88.13 **	94.49 **
Checks	02	15456.89 **	12711.27 **
Checks vs. RILs	01	9468.07 **	4986.37 **
Error	34	5.46	6.17

* and ** indicates significance at 0.05 and 0.01, respectively.

significant for NBI and FBI. These results suggested significant differences among the RILs and they differed from the checks for NBI and FBI, Lule *et al.* (2013) also reported significant variations among finger millet genotypes for blast disease infection. The distribution of RILs for NBI and FBI were normal (Fig. 1 and Fig. 2). The estimates of range of NBI and FBI provide clues about the occurrence of genotypes with resistant and susceptible expression

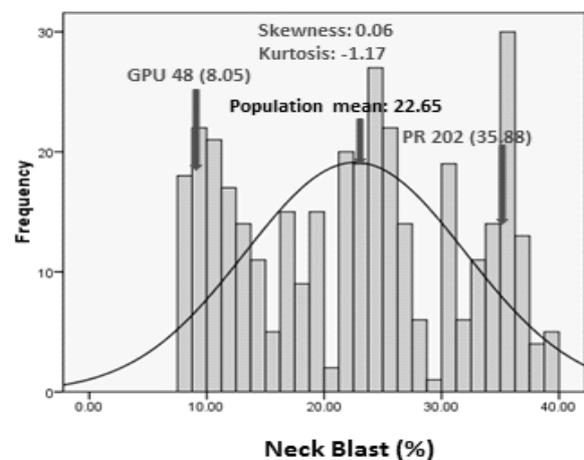


Fig. 1: Graph depicting frequency distribution of response of RILs to neck blast disease infection in natural disease hotspot (Vizianagaram, AP)

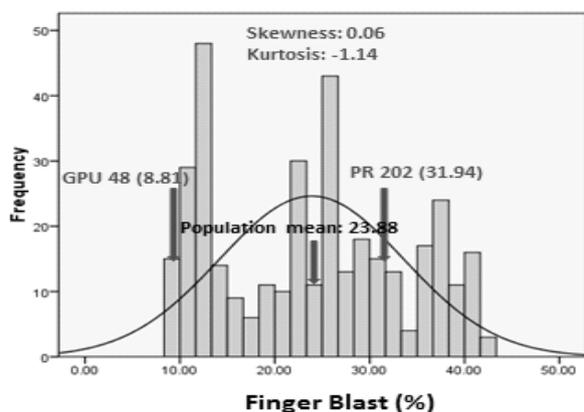


Fig. 1 : Graph depicting frequency distribution of response of RILs to finger blast disease infection in natural disease hotspot (Vizianagaram, AP)

(Table II). The estimates of PCV and GCV were high for both NBI and FBI. Narrow difference between the estimates of PCV and GCV indicated limited influence of environment for the incidence of neck and finger blast disease.

The coefficient of variation indicates only the extent of total variability and does not demarcate the variability into heritable and non-heritable components. Hence the estimate of heritability, which indicates

precisely the heritable expected gain, assumes importance. The information on heritability alone may not help in formulating suitable breeding procedures. Nevertheless, the heritability estimates in conjunction with predicted genetic advance will be more reliable. The heritability was high for both NBI and FBI. A fairly high predicted genetic advance as per cent mean (GAM) (Table II) suggested possibility of selection of finger millet genotypes for resistance to neck and finger blast disease.

Significant differences of RILs belonging to different response groups for mean disease response suggested efficiency of classifying RILs into different response groups (Table III). Most of the RILs were either classified under moderately resistant/susceptible category (179 and 181 RILs for neck and finger blast, respectively) or susceptible category (146 and 162 RILs for neck and finger blast, respectively). On the other hand, only a few RILs were classified under resistant group (35 and 17 RILs for neck and finger blast, respectively). None of the RILs were immune or highly resistant to blast disease infection. Several earlier researchers have also reported wide differences

TABLE II

Descriptive statistics for F6 finger millet RILs for response to neck and finger blast disease infection under natural hotspot (Vizianagaram, AP)

Parameters	Mean±SE	Minimum	Maximum	Standardised Range	GCV (%)	PCV (%)	$h^2_{(BS)}$	GAM (%)
Neck Blast(%)	22.65±0.5	7.15	41.85	1.53	38.21	39.58	0.93	76.00
Finger Blast(%)	23.88±0.52	7.69	43.99	1.52	37.47	38.89	0.93	74.38

TABLE III

Frequency of F6 finger millet RILs and their mean disease scores corresponding to disease response groups

Parameters	Immune (0)	Highly Resistant (0.1-2.0)	Resistant (2.01-10.0)	Moderately resistant/	Susceptible (10.01-25.0)	Highly Susceptible (>50)	F ratio probability indicating significance of mean disease score
Neck Blast (%)	0	0	35(8.55)	179(17.67)	146(32.26)	0	<0001
Finger Blast (%)	0	0	17(9.03)	181(17.10)	162(33.11)	0	<0001

Figures in parenthesis indicates mean disease score

TABLE IV

The best five F₆ finger millet RILs showing resistance response to neck and finger blast infection

RILs	Neck Blast (%)	Finger Blast (%)	RILs	Finger Blast (%)	Neck Blast (%)
176	7.15	13.42	349	7.69	10.72
216	7.19	13.45	347	7.89	10.22
150	7.29	11.42	47	8.02	9.62
175	7.35	11.22	65	8.09	10.69
215	7.39	11.25	49	8.22	9.02
PR 202 (Susceptible parent)	35.88	31.94	PR 202 (Susceptible parent)	31.94	35.88
GPU48 (Resistant parent)	8.05	8.81	GPU48 (Resistant parent)	8.81	8.05
Uduru mallege (Susceptible check)	66.63	61.81	Uduru mallege (Susceptible check)	61.81	66.63
SEm±	0.50	0.52	SEm±	0.52	0.50
CD @ 5%	5.81	6.18	CD @ 5%	6.18	5.81

in responses of finger millet genotypes ranging from resistant to highly susceptible reactions (Kumar and Kumar, 2009). Best five neck and finger blast resistant RILs that transgressed GPU 48 (resistant parent/check) were identified (Table IV). These RILs could be used in breeding finger millet varieties with neck and finger blast disease resistance.

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