ARTICLE TYPE

Frequency of Red Rot Resistance in the Progeny Population of Various Cross Combinations

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Abstract

Resistance pattern in parents produces resistance progenies predominantly. Inheritance of resistance gene against red rot intensely affected to the degree of frequency in progenies. The present study was commenced to find out the role of parental crosses to develop resistant progenies in the first clonal generation for two consecutive years. Total of 2262 progenies of 143 bi-parental and 27 local cross combinations were evaluated to red rot resistance. CoS 96260, CoS 95255, CoS 8436, Co 0238, CoSe 92423, Co 89003, Co 62198 and CoS 08272 were good parents which involved in bi-parental cross combination, produced predominantly resistant progenies ranging from 40 to 100%. The cross combination Co 8213 × CoS 96260 produced maximum proportion 100% resistant progenies, higher than CoS 95255 × CoA 7602 (83.33 %) and Co 8436 × Co 1148 (80%). These parents identified as a good combiner and also found to inherit resistance gene in bulk of its progenies. These parents could be used as donor parents in red rot resistance breeding programs of sugarcane.

Keywords: *Colletotrichum falcatum*, Parental line, Progenies, Red rot, Resistance, Sugarcane.

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Introduction

Sugarcane progenies derived from various crosses based on their ability to produce high sugar yield and resistance to red rot. The genetic consistency generated not only done by inter-specific hybridization but also backcrossing of major poly, bi-parental, and general crosses for the sustaining of disease resistance and sugar quality (Babu *et al.* 2009). The back cross of hybrids to *S. officinarum* resulted in high sugar yield and red rot resistance in nobilization process (Roach, 1972). Although, the nobilization is highly successful but due to limits of the resistant gene pool in selected parents which exploited during traditional breeding programs, very limited progress has been achieved in increasing red rot resistant progenies with high sugar content and yield (Sreenivasan *et al.* 1987; Lima *et al.* 2002).

The red rot (*Colletotrichum falcatum* Went.) disease susceptibility is a vital limitation of sugarcane improvement in a breeding program. This disease is prevalent almost all the tropical and sub-tropical states in India, and also one of the major constraints in sugarcane advancement. So many good sugarcane cultivars have suffered and left out from general cultivation due to their red rot susceptibility within a short period. Genetic resistance to *C. falcatum* is unstable in certain condition due to the highly variable in nature. The race-specific resistance explored to obtain stable resistance genotypes/varieties to *C. falcatum*. Continuous evaluation processes of the sources of resistance with variable pathotypes are needed in the breeding program (Viswanathan, 2017). Till now, there is no well-known chemical control of this disease. The use of disease-resistant varieties is the easiest and most convenient way of accomplishing disease control. To develop resistant constant and continuous breeding is necessary, as well as testing varieties against pathotypes prevail the area is also needed for resistance sustainability (Satyavir, 2003; Dattamajumder, 2008; Viswanathan, 2010). The resistance clones with good yield and quality alone release for commercial cultivation. Resistant breeding for red rot is complicated by the existence of several races along with good combiners. Susceptible progenies to red rot are eliminated in the first clonal generation of sugarcane, which increases the frequency of resistant progenies and also enhances the selection efficiency for good sugar yield. The exploitation of the resistant gene into progenies depends upon good parental combiners (Ram *et al.* 2005; Babu *et al.* 2010). The present study was undertaken to find out the genetic basis of resistance and identification of suitable parents for the inheritance of red rot resistance gene in sugarcane breeding programs.

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Materials and Methods

An investigation was done to analyze the association of red rot resistance for effective family selection. The present investigation was conducted at the experimental farm of

Sugarcane Research Institute, Shahjahanpur (*Longitude 79^{0}37'E* and *latitude 27^{0}35'N*) over two consecutive years 2015-16 and 2016-17. Evaluation of 2262 progenies of 170 cross combinations comprising to 143 bi-parental and 27 local crosses was done at first clonal generation in breeding division (Table 1). Each progeny was grown in a 4m long plot spaced at 75cm apart. All the agronomical practices and fertilizer dose were adopted as per standard recommendation. Ten stalks of each of 2262 progenies were screened out for red rot resistance by plug method of inoculation using composite inoculum of standard pathotypes Cf 08 and Cf 09 in the second month of August. The temperature ranged from 29–31 degree celsius, and relative humidity varied from 80 to 90% during the inoculation.

Disease Rating

Observations were taken 60 days after inoculation by split open longitudinally of cane. Inoculated canes free from borer infestation and other damages were taken for evaluation. The disease severity was graded on the basis of the standard scale of 0–9. These standard scales of disease were characterized as various patterns followed by 0–2 as resistant (R), 2.1–4 as moderately resistant (MR), 4.1 to 6 as moderately susceptible (MS), 6.1 to 8 as susceptible (S) and above 8 as highly susceptible (HS) (Srinivasan and Bhatt, 1961; Duttamajumder and Singh, 1999).

Results and discussion

Genetic variability for red rot resistance depends on the parental crosses like bi-parental and local crosses. Successful exploitation of this variability in sugarcane crop with a complex ploidy nature and high level of heterozygosity is a complicated process. Total of 2262 progenies were evaluated for red rot resistance. Out of 143 bi-parental crosses, top 30 crosses produced predominantly resistant progenies ranging from 22.22% in CoLk 94184 × BO 130 to 100%. Overall, 11.91% frequency of resistant progenies obtained from bi-parental crosses (Table 1). Cross combination Co 8213 × CoS 96260 produced maximum proportion (100%) of resistant progenies, and it was the best specific combiner. Beside this cross, the other important bi-parental cross combinations CoS 95255 × CoA 7602 (MR × MR), CoS 8436 × Co 1148 (MR × HS), Co 238 × CoS 92423 (MR × S), CoSe 92423 × CoS 8436 (S × MR), Co 8436 × Co 89003 (MR × MR), Co 1158 × Co 62198 (S × S), Co 62198 × CoSe 92423 (S × S), CoS 8436 × CoS 96260 (MR × HS), CoLk 94184 × ISH 150 (MR × MS) and CoS 08272 × Co 1158 (MR × HS) contributed 50 to 83.33 per cent resistant progenies. This indicated that of the all parents only CoS 96260, CoS 95255, CoS 8436, Co 0238, CoSe 92423, Co 89003, Co 62198, CoLk 94184 and CoS 08272 were good general combiner for red rot resistance. These parents were involved in bi-parental cross-combination, produced predominantly resistant progenies ranging from 50 to 100 %. Co 8213 used as a female parent (MR) and CoS 96260 as male parent (S), the proportion of resistant progenies was higher (100%) compared to both susceptible parent CoS 767 and Co 62198 (9.52%). Cross involving female parent as MR and male as HS (CoS 8436 × Co 1148), the proportion of resistant progenies was 80% and both MR parents (CoS 95255 × CoA 7602) was gave 83.33 per cent resistance progenies. The susceptible female (CoSe 92423, Co 1148) and resistant male parents (CoS 8436, Co 89003) produced higher proportion of resistant progenies. This indicates that the resistant parents, either female or male imparted resistance to their progenies (Table 2). Cross-combination such as S.536/99 × S.301/87 and S.4122/03 × S.461/83 produced 66.67 and 60% resistant progenies, respectively in a local cross (Table 3). Resistant progenies found in the cross involving susceptible parents indicate that the role of interaction of genes from both parents. This result indicates the possibilities of exploiting additive gene interaction effect to produce maximum resistant progenies (Alarmelu *et al.* 2010).

These parents identified as a good general combiner and found to inherit resistance gene to the majority of its progenies. These most vital parents produced donor resistant gene in resistance breeding programs of sugarcane. Hence, these crosses may be exploited specifically for red rot resistance. Genetic variability for red rot resistance depends on the various cross combinations (Ram *et al.* 2005). Out of all cross combinations, the top listed bi-parental crosses at least had one moderately resistant parent. This study indicates that the possibility of attaining more resistant progenies is higher by using at least one resistant parent. In general, it was observed that progenies from crosses involving resistant parents tend to be more towards resistant or moderately resistant reaction. This is also an agreement with Alarmelu *et al.* (2010) findings. The occurrence of resistant progenies from resistant parents might be due to the presence of *S. spontaneum* for incorporating resistance against red rot. In the present study, higher proportion was found in all top crosses, it indicates that *S. spontaneum* blood was used as male and female parent were either MR or R**.** The results from the

Table 1: Mean frequency of resistance among all progenies derived from various crosses over two years

			Frequency of disease in percent				
Different crosses	*Total cross*	*Total genotype*	*MR*	*MS*	*S*	*HS*	*Not germinated*
Bi-parental	143	2141	11.91	11.91	20.22	55.07	0.750
Local	27	121	10.74	10.74	28.10	48.76	1.65

MR- Moderately resistant; MS- Moderately susceptible; S- Susceptible; HS- Highly susceptible

Table 2: Detail of top bi-parental crosses and their resistance frequency among progenies

	Parent		*Frequency of disease in percent*			
Sl. No.	*Pistil*	*Male*	*MR*	*MS*	*S*	*HS*
1	Co 8213	CoS 96260	100	-	-	-
2	CoS 95255	CoA 7602	83.33	16.66	-	-
3	CoS 8436	Co 1148	80	20	-	-
4	Co 238	CoS 92423	75	16.67	-	8.33
5	CoSe 92423	CoS 8436	75	-	12.5	12.5
6	Co 8436	Co 89003	75	-	-	25
7	Co 1158	Co 62198	66.67	33.33	-	-
8	Co 62198	CoSe 92423	66.67	0	16.67	16.67
9	CoS 8436	CoS 96260	66.67	33.33	-	-
10	CoLk 94184	ISH 150	60	-	30	10
11	CoH 119	Co 62198	57.14	14.29	28.57	0
12	Co 0239	Co 86011	50	-	-	50
13	CoS 08272	Co 1158	50	-	50	-
14	ISH 100	CoS 96260	50	-	50	-
15	LG 94184	Co 775	50	50	-	-
16	CoSe 92423	CoS 8436	40.54	21.62	10.81	27.02
17	Co 453	Co 86249	40	-	20	40
18	Co 0238	CoSe 92423	34	31.32	22.89	10.84
19	CoLk 94184	BO 96	33.33	33.33	-	33.33
20	LG 95053	BO 91	33.33	-	-	66.67
21	CoS 8436	CoS 96260	33.33	16.67	16.67	33.33
22	CoSe 95422	CoT 8201	33.33	8.33	33.33	25
23	Co 0238	CoSe 92423	33.33	-	16.67	50
24	LG 99122	Co 453	33.33	-	33.33	33.33
25	Co 86011	CoH 70	25	16.67	22.92	35.42
26	Co 98008	Co 775	25	-	-	75
27	BO 91	Co 453	20	40	40	-
28	CoV 89101	CoS 96260	23.81	23.81	19.05	33.33
29	Co 86011	CoH 70	23.08	9.23	27.69	40
30	CoLk 94184	BO 130	22.22	33.33	-	44.44

MR- moderately resistant; MS- moderately susceptible; S- susceptible; HS- highly susceptible

Table 3: Detail of top local crosses and their frequency of resistance among progenies

	Parent		*Frequency of disease in percent*			
Sl. No.	*Pistil*	*Male*	*MR*	*MS*	*S*	*HS*
1	S.536/99	S.301/87	66.67	-	-	33.33
2	S.4122/03	S.461/83	60	20	20	-
3	S.301/87	Sl.200/06	50	-	-	-
4	Sl.265/06	Sl.252/06	50	-	50	-
5	CoSe 08455	S.301/87	33.33	33.33	33.33	-
6	S. 133/87	S.474/83	33.33	33.33	-	33.33
7	S.133/87	S.483/83	33.33	-	33.33	33.33

MR- moderately resistant; MS- moderately susceptible; S- susceptible; HS- highly susceptible

progenies suggest that the utilization of resistant sources in crossing would increase the frequency of red rot resistance in the population (Babu *et al.* 2010; Alarmelu *et al.* (2010).

Other crosses were poor specific combiners for red rot resistance. It is obvious that *S. spontaneum* clones are better donors of resistance in these parents and also provide enough stability against red rot. The segregation pattern of red rot inheritance varied with the crosses and was assumed to be governed by the resistance gene. This may be attributed to the elimination of dominant or recessive *S. spontaneum* genes, which provides resistance or susceptibility in sugarcane. *S. spontaneum* hybrids were identified as potential sources of resistance to red rot (Babu *et al.* 2010; Alarmelu *et al.* 2010; Natarajan *et al.* 2001)

This study has reflected that parental clones can provide a base for imparting resistance in future breeding programs for red rot resistance. The results from the recent study suggest that the utilization of identified resistance sources as donors in crossing would increase the frequency of red rot resistance in the progeny population for making effective selection and production of red rot resistant varieties in sugarcane.

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