Sugar Tech (Sept-Oct 2022) 24(5):1479–1496
https://doi.org/10.1007/s12355-021-01070-7

RESEARCH ARTICLE

Varietal Break Down to Red Rot in the Sugarcane Variety Co 0238 Mimics Vertifolia Effect: Characterizing New *Colletotrichum falcatum* Pathotype CF13

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Received: 22 May 2021 / Accepted: 13 October 2021 / Published online: 29 January 2022

Abstract Red rot, a fungal disease caused by *Colletotrichum falcatum* Went is the major constraint for sugarcane production in India and many other Asian countries. Recurrent epidemics of the disease cause varietal breakdown in popular varieties, thereby elite varieties with red rot resistance succumb to new variants of the pathogen and cause huge economic losses. We investigated on the recent devastating red rot epidemic that struck the popular cv Co 0238, cultivated in ~ 2.2 M ha in Uttar Pradesh (UP) (82.21% cane area) and 0.16 M ha in Bihar (64.12% cane area) states by pathotyping of 67 *C. falcatum* isolates including 45 from the cv Co 0238 and 22 from other varieties along with seven designated pathotypes on a set of 20 host differentials. The differential interaction studies conducted at five locations in the states of UP, Haryana and Punjab revealed that all the Cf0238 isolates maintained a discrete pathogenicity pattern of infecting the host cv Co 0238. Further, all the designated pathotypes and other host isolates did not show their virulence on the cv Co 0238. Similarly, all the Cf0238 isolates (45) maintained an avirulence behaviour on CoJ 64, the susceptible differential at all the locations. These pathogenicity data of new *C. falcatum* isolates from Co 0238 and other varieties on the host differentials clearly showed emergence of a specific pathotype capable of infecting the predominant variety under cultivation Co 0238 in the subtropical region. Reason for the sudden outbreak and extensive crop losses in thousands of hectares is attributed to monoculture of the variety in more than 80% area in the region due to 'Vertifolia effect'. The monoculture also created a selection pressure from the pathogen to adapt to the host and caused breakdown of resistance favoured by waterlogging and flooding in the region. We have designated the new virulent isolate from Co 0238 as a new *C. falcatum* pathotype CF13 based on detailed characterization for pathogenicity and is recommended for screening sugarcane varieties for red rot resistance. This study also indicated repeat of boom and bust cycle in sugarcane–red rot interaction due to monoculture, leading to emergence of a virulent pathotype and large-scale destruction of the crop under cultivation.

Keywords Sugarcane · Red rot · Vertifolia effect · Monoculture · Epidemics · Pathotype · Virulence

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Introduction

The sugarcane productivity in India has been static for several decades from 1970 and an increase in cane and sugar production was achieved by expansion in the cane area. The cane production of ~ 140 MT in the 1970s has nearly doubled during 2000 with major increase in area from 2.7 M Ha to 4.4 MHa with a certain improvement in cane productivity during the period (https://sugarcane.icar.gov.in/). However, cane productivity in the country remained low as compared to the potential achievable yield. Partly it was also due to growing of only a few varieties across the country in the past decades. From 1970 onwards only a handful of varieties such as Co 6304, Co 62175, Co 7805, CoC 671, CoJ 64, CoS 767, CoS 8436, Co 86032, CoSe 92423, CoSe 95422, etc. occupied major area in both the tropical and subtropical states. Among these varieties, almost all the varieties except Co 86032 were withdrawn from cultivation mostly due to their breakdown to red rot or varietal degeneration caused by non-fungal diseases (Viswanathan, 2016, 2021a; b). Hence quantum leap in cane productivity could not be achieved. Although more than 200 varieties were released for commercial cultivation many of them have not succeeded in the field or occupied a limited area (Hemaprabha et al. 2020). But with identification and release of the variety Co 0238 during 2009 for the subtropical states, landscape of sugarcane cultivation has changed; cane productivity in the country has increased to ~ 80 t/ha during 2017–2018 from 70 t/ha (Ram and Hemaprabha 2020). The country reached a record sugar production of 33.1 MT from 5.5 M Ha during 2018–2019 (ISMA 2021).

The Indian sugarcane breeding programme mainly focus on development of high yielding sugarcane varieties with higher sucrose and red rot resistance. In India, red rot of sugarcane caused by *Colletotrichum falcatum* Went is the most damaging disease and this determines field life of the released varieties. Since the pathogenic fungus infects stalk tissues, affected cane tissue rots and finally entire stalk dies. Apart from this, the pathogenic fungus causes inversion of stored sucrose in the stalks to reducing sugars in the partially damaged canes; thereby sugar extraction is significantly affected in the mills (Viswanathan 2010). In India, several epidemics have been recorded for more than a century; each of the epidemics led to severe devastation in sugarcane growing areas especially in the subtropical region comprising Uttar Pradesh (UP), Bihar, Haryana and Punjab and east coastal region in the tropical states (Chona 1980; Viswanathan et al. 2003; Viswanathan 2017, 2021a,b). History of these epidemics reflected a clear 'boom' and 'bust' cycle after adoption of a single variety over a large areas.

Red rot epidemics in sugarcane not only caused severe economic losses to the sugar industry but also led to emergence of new variants of the pathogen capable of knocking down host resistance referred as 'varietal breakdown' (Viswanathan and Selvakumar 2020). Detailed studies in the past characterized new variants in different occasions and designated many *C. falcatum* pathotypes after phenotyping their pathogenicity on a set of host differentials. So far, 12 pathotypes were designated and used for screening new varieties in the respective region (Viswanathan, 2017, 2018). Of the total cane area in the country, UP state alone grows nearly 50% of sugarcane. Recently, due to the better cane and sugar yield, the cane area of the variety Co 0238 has reached 82.21% of its total cane area in the state during 2019–2020 from mere 3.1% during 2013–2014 (Ram and Hemaprabha 2020). Coinciding with the huge expansion of the variety in the state, incidences of red rot were noticed in the endemic locations from 2016 onwards. However, the spread of the disease was rapid and increased in larger area over the last few seasons and the disease engulfed a large cane area in UP and adjoining Bihar. This has become a major catastrophe in the region and an estimated loss of 1.0 to 1.414 billion US$ occurred in the sugar season 2020–2021 (Viswanathan 2021a). The cv Co 0238 was resistant to the prevailing *C. falcatum* pathotypes CF07, CF08 and CF09 at the time of its release for cultivation. From the first incidence onwards the pathogenic isolates were collected from different districts of UP, Bihar, Haryana and Punjab states and we investigated on the pathogenicity of the 67 new isolates along with the existing seven pathotypes on 20 differential host varieties at different centres. The objective of the study was to critically analyse evolution of new *C. falcatum* pathotype with higher virulence to knockdown disease resistance and disease outbreak in the widely cultivated cv Co 0238 in India. The outcome of the study revealed that all the 45 new isolates recovered from the red rot affected cv Co 0238 had a similar pathogenicity pattern among themselves with a clear deviation from the prevailing pathotypes in the region. The study surmises that large scale cultivation of the variety triggered a clear 'Vertifolia effect' and gain of virulence by the pathogen to cause devastations in the major sugarcane growing belt in the country. The study clearly revealed that monoculture of a single variety creates a selection pressure in favour of the pathogen to develop a specific pathotype capable of overcoming host resistance.

Materials and Methods

Collection of *C. falcatum* Isolates and Their Maintenance

Under All India Coordinated Research Project (AICRP) on Sugarcane operated by Indian Council of Agricultural Research (ICAR), surveys for natural occurrence of diseases on important sugarcane varieties were conducted by the different centres and collected red rot affected canes of Co 0238 and other varieties (Table 1; Fig. 1). All the newly collected *C. falcatum* isolates (67) were assessed for their pathogenicity at Shahjahanpur, Seorahi and Lucknow in Uttar Pradesh state, Kapurthala in Punjab state and Karnal in Haryana state along with the seven designated pathotypes viz., CF01, CF02, CF03, CF07, CF08, CF09 and CF11 of the subtropical region. The new isolates (67) were mostly originated from Co 0238 (45) followed by CoS 8436 (5), Co 89003 (5), CoJ 85 (3), CoPk 05191 (2), CoJ 64 (1), CoJ 88 (1), CoS 07250 (1), CoS 97264 (1), CoLk 8102 (1), CoLk 94184 (1) and CoS 08279 (1). The new isolates were maintained on oat meal agar in pure form after single spore isolation and sub-cultured periodically. The isolate names were prefixed 'Cf' followed by variety name and isolate numbers assigned by the research centres.

Plug Method of Inoculation and Pathogenicity Assay

The individual isolates were grown on oatmeal agar and the fresh conidial suspensions were prepared (1×10^6 conidia/ml) from 7-day-old cultures with distilled water for inoculation. Pathogenicity assays were conducted on 20 host differentials comprising 17 hybrid varieties and one each from *Saccharum officinarum, S. sinense* and *S. spontaneum,* routinely used to assess variation in pathogenicity of *C. falcatum* isolates under AICRP on sugarcane (https://iisr.icar.gov.in/iisr/aicrp/index.htm). The host varieties were grown in six metre rows by following standard agronomical practices for the respective locations. A minimum of 10 healthy canes free from wilt and termite or other insects attack were selected for inoculating each pathotype/isolate. The designated seven pathotypes maintained at all the centres along with the newly collected isolates were inoculated in the middle of the 3rd internode above the soil level of the standing canes following the standard plug method (Mohanraj et al. 2012). About 0.5 ml of the conidial suspension was placed with a Pasteur pipette onto the bore-hole in each cane and bore holes were sealed with plastic clay after placing the tissue core. The inoculation was performed during second fortnight of July in the centres and 60 days after inoculation, the canes were split open longitudinally along the point of inoculation. Inoculated canes free from borer infestation were considered for evaluation. The disease reactions were scored based on a 0–9 rating scale of Srinivasan and Bhat (1961) and categorised into resistant (R), moderately resistant (MR), moderately susceptible (MS), susceptible (S), and highly susceptible (HS). To assess pathogenic variation among the isolates, these reaction categories were further grouped as resistant (R + MR) (0.0–4.0) intermediate (MS) (4.1–6.0) and susceptible (S + HS) (6.1–9.0) and analysed. To denote the pathogenicity, these reactions were referred as less virulent, moderately virulent and virulent, respectively (Viswanathan et al. 2017a).

The disease reactions were graded following 0–9 scale considering (1) Condition of tops (weightage-1) Green—0, yellow/dry-1; (2) Lesion width (weightage-3) in the internodes above the inoculated internode is assigned the scores of 1, 2 or 3 in relation to cane width; (3) White spot (weightage-2) restricted -1; progressive -2; (4) Nodal transgression of red rot lesion above the inoculated internode (weightage-3); 1-if one node crossed; 2-if two nodes crossed, 3-if three or more nodes crossed. Then average score was calculated following the formula: Average score = Total score/Number of canes evaluated. Recently characteristic symptoms with each of the disease reactions were described by Viswanathan et al. (2021).

To establish the relationship or proximity for pathogenicity among the isolates tested, the phylogenetic analyses were conducted using MEGA version 5 (Kumar et al. 2018). The red rot reactions of R, S and I expressed by each of the isolates on the differentials were converted into FASTA format. Then the isolates were aligned and the phylogeny was constructed keeping the cut off value for condensed tree at 65% using Unweighted Pair Group method (UPGMA).

Results

Pathogenicity of *C. falcatum* Isolates/Pathotypes

At Lucknow, out of 11 new isolates evaluated, all the eight Cf0238 isolates showed virulent behaviour on Co 0238, whereas the variety exhibited R reaction to two isolates from CoS 8436 and the pathotypes CF07, CF08 and CF09 and intermediate reaction to an isolate from CoLk 8102 and the pathotype CF11. Similarly, the Cf0238 isolates exhibited virulent to moderate virulent behaviour on the differentials Co 419, Co 975, Co 62399, BO 91, Co 7805, Co 86002, Co 86032, Baragua and Khakai. The two new isolates from the cv CoS 8436 caused virulent reactions on their host variety and behaved differently with Co 0238 by less virulent behaviour. The susceptible differential CoJ 64 exhibited S reactions to other isolates/pathotypes whereas

Table 1 Details of *Colletotrichum falcatum* isolates collected in sugarcane fields of subtropical India (2016–2020)

No	Pathotype/isolate	Host source	Year	Location of collection
Designated pathotypes				
1	CF01	Co 1148	1997	Karnal, Haryana
2	CF02	Co 7717	1997	Karnal, Haryana
3	CF03	CoJ 64	1997	Karnal, Haryana
4	CF07	CoJ 64	2006	Karnal, Haryana
5	CF08	CoJ 64	2006	Karnal, Haryana
6	CF09	CoS 767	2006	Karnal, Haryana
7	CF11	CoJ 64	2006	Lucknow, UP
Lucknow, U.P				
8	Cf0238IR-184	Co 0238	2020	Rosa, UP
9	Cf0238IR-185	Co 0238	2020	Rosa, UP
10	Cf0238IR-186	Co 0238	2020	Harinagar, Bihar
11	Cf0238IR-187	Co 0238	2020	Kaptanganj, UP
12	Cf0238IR-188	Co 0238	2020	Rankola, UP
13	Cf0238IR-189	Co 0238	2020	Seorahi, UP
14	Cf0238IR-190	Co 0238	2019	Majhaulia, Bihar
15	CfS8436IR-191	CoS 8436	2019	Hariyawan, UP
16	CfS8436IR-192	CoS 8436	2020	Hariyawan, UP
17	Cf0238IR-193	Co 0238	2020	Ajbapur, UP
18	CfLk8102IR-194	CoLk 8102	2020	Haidergargh, UP
Shahjahanpur, U.P				
19	Cf0238-1	Co 0238	2016	Nigohi, UP
20	Cf0238-2	Co 0238	2017	Hargaon, UP
21	Cf0238-3	Co 0238	2018	Pilibhit, UP
22	Cf0238-4	Co 0238	2018	Gularia, UP
23	Cf0238-5	Co 0238	2018	Hariyawan, UP
24	Cf0238-6	Co 0238	2018	Rupapur, UP
25	Cf0238-7	Co 0238	2019	Khabharkheda, UP
26	Cf0238-LKO	Co 0238	2020	IISR, Lucknow, UP
27	Cf0238-R 1602	Co 0238	2016	Nigohi, UP
28	Cf0238-R 1702	Co 0238	2017	Hargaon, UP
29	Cf0238-R 1705	Co 0238	2017	Gola, UP
30	Cf0238-R 1707	Co 0238	2017	Hargaon, UP
31	Cf0238-R 1711	Co 0238	2017	Ajbapur, UP
32	Cf0238-R 1802	Co 0238	2018	Ajbapur, UP
33	Cf0238-R 1807	Co 0238	2018	Palia, UP
34	Cf0238-R 1808	Co 0238	2018	Kumbhi, UP
35	Cf0238-R 1810	Co 0238	2018	Pilibhit, UP
36	Cf0238-R 1811	Co 0238	2018	Gularia, UP
37	Cf0238-R 1814	Co 0238	2018	Hargaon, UP
38	Cf0238-R 1817	Co 0238	2018	Hariyawan, UP
39	Cf0238-R 1820	Co 0238	2018	Loni, UP
40	Cf0238-R 1821	Co 0238	2018	Rupapur, UP
41	Cf0238-R 1903	Co 0238	2019	Khabharkheda, UP
42	Cf0238-R 1924	Co 0238	2019	Seorahi, UP
43	Cf0238-R 1938	Co 0238	2019	Rupapur, UP
44	Cf0238-R 2001	Co 0238	2020	Nababganj, UP

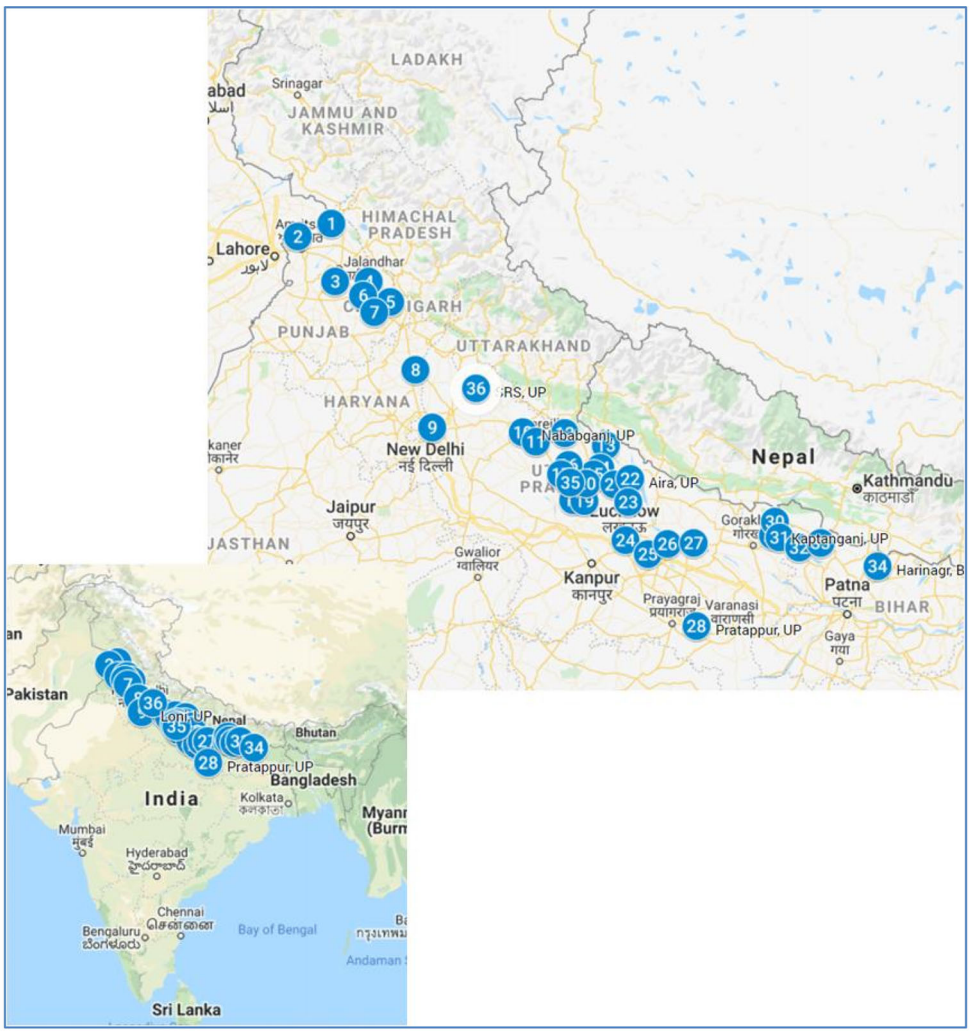
Table 1 continued

No	Pathotype/isolate	Host source	Year	Location of collection
45	Cf0238-R 2003	Co 0238	2020	Gola, UP
46	CfPk05191-R1941	CoPk 05191	2019	Palia, UP
47	CfPk05191-R2005	CoPk 05191	2020	Biswan, UP
48	CfS07250	CoS 07250	2013	Gularia, UP
49	CfS08279-R1945	CoS 08279	2019	SRS, UP
50	CfS8436	CoS 8436	2011	Gola, UP
51	CfS97264	CoS 97264	2017	Tilhar, UP
Seorahi, U.P				
52	Cf8436-R1702Seo	CoS 8436	2017	Khadha, UP
53	Cf0238-R1801Seo	Co 0238	2018	SiswaBajar, UP
54	Cf0238-R1802Seo	Co 0238	2018	Rauzagaon, UP
55	Cf0238-R1803Seo	Co 0238	2018	Kaptanganj, UP
56	Cf0238-R1904Seo	Co 0238	2019	Pratappur, UP
57	Cf0238-R1905Seo	Co 0238	2019	Seorahi, UP
Karnal, Haryana				
58	Cf0238-LKO	Co 0238	2020	IISR, Lucknow, UP
59	Cf0238-1	Co 0238	2020	Afjalgarh, Haryana
60	Cf0238-2	Co 0238	2020	Ajbapur, Haryana
61	Cf0238-3	Co 0238	2020	Faridpur, Haryana
62	Cf89003	Co 89003	2020	Karnal, Haryana
63	CfS8436	CoS 8436	2020	Karnal, Haryana
64	CfLk94184	CoLk 94,84	2020	Karnal, Haryana
Kapurthala, Punjab				
65	Cf0238-LKO	Co 0238	2020	IISR, Lucknow, UP
66	CfJ64	CoJ 64	2020	Nakodar, Punjab
67	CfJ85-1	CoJ 85	2020	Nakodar, Punjab
68	CfJ85-2	CoJ 85	2020	Gurdaspur, Punjab
69	CfJ85-3	CoJ 85	2020	Morinda, Punjab
70	CfJ88	CoJ 88	2020	Bhudewal, Punjab
71	Cf89003-1	Co 89003	2020	Morinda, Punjab
72	Cf89003-2	Co 89003	2020	Ajnala, Punjab
73	Cf89003-3	Co 89003	2020	Nawanshahr, Punjab
74	Cf89003-4	Co 89003	2020	Amloh, Punjab

UP Uttar Pradesh

it showed intermediate reactions to Cf0238 isolates. The variety Co 0238 remained resistant to all the new isolates from other hosts and the designated pathotypes, except CF11. Although there were an apparent similarity in the behaviour of Cf0238 isolates on the 20 differentials, there were few deviations occurred on BO 91, Baragua, Co 7805 and Co 86032 (Table 2).

At Shahjahanpur, a total of 33 *C. falcatum* isolates comprising of 27 from Co 0238 and six isolates from CoPk 05191 (2), CoS 07250 (1), CoS 09279 (1), CoS 8436 (1) and CoS 97264 (1), were evaluated. It was interesting to note that as in Lucknow centre, all the Cf0238 isolates were able to cause virulent reactions on their host Co 0238, whereas three isolates from the cvs CoS 8436, CoS 97264 and CoS 07250 and the designated pathotypes did not infect Co 0238 except CfS08279-R1945. All the designated pathotypes behaved as less virulent on Co 0238 except one intermediate reaction by the pathotype CF11. These results indicated that the new isolates originated from Co 0238 have a different pathogenic behaviour as compared to the designated *C. falcatum* pathotypes/isolates (Table 2). The Cf0238 isolates also exhibited a deviation in their behaviour on the differentials Co 62399, CoJ 64, Baragua, Khakai and Co 7805 than the other isolates/pathotypes (Table 2).



1	Gurdaspur, Punjab	13	Palia, UP	25	Haidergargh, UP
2	Ajnala, Punjab	14	Gola, UP	26	Rauzagaon, UP
3	Nakodar, Punjab	15	Kumbhi, UP	27	Khadha, UP
4	Nawanshahr, Punjab	16	Nigohi, UP	28	Pratappur, UP
5	Morinda, Punjab	17	Tilhar, UP	29	Kaptanganj, UP
6	Bhudewal, Punjab	18	Rupapur, UP	30	SiswaBajar, UP
7	Amloh, Punjab	19	Hariyawan, UP	31	Rankola, UP
8	Karnal, Haryana	20	Ajbapur, UP	32	Seorahi, UP
9	Loni, UP	21	Hargaon, UP	33	Majhaulia, Bihar
10	Nababganj, UP	22	Aira, UP	34	Harinagr, Bihar
11	Gularia, UP	23	Biswan, UP	35	Rosa, UP
12	Pilibhit, UP	24	Lucknow, UP	36	SRS, UP

Fig. 1 Location of *C. falcatum* isolates collected during the survey in the subtropical region of India; In the above figure the map is enlarged

In Seorahi centre, six isolates comprising of five from Co 0238 and one isolate from CoS 8436 were tested (Table 2). As in Lucknow and Shahjahanpur centres, the Cf0238 isolates behaved differently from other isolates and pathotypes. The variety Co 0238 behaved as S to its isolates and remained R to other isolates/ pathotypes. Similarly, the Cf0238 isolates exhibited virulent behaviour of the differentials Co 975, Co 62399, CoC 671, Co 86002 and CoV 92102 whereas on the other differentials the behaviour was less virulent or moderate virulent. Further,

Table 2 Pathogenic reactions of *Colletotrichum falcatum* isolates and pathotypes on host differentials in three centres in Uttar Pradesh

No	Pathotype/ isolate	Co 419	Co 975	Co 997	Co 1148	Co 7717	Co 62399	CoC 671	CoJ 64	CoS 767	CoS 8436	BO 91	Baragua	Khakai	SES 594	Co 7805	Co 86002	Co 86032	CoSe 95422	CoV 92102	Co 0238
Pathotype																					
1	CF01	S	R	S	S	R	I	I	S	R	R	R	R	S	R	R	R	I	R	I	R
2	CF02	R	R	S	R	S	R	S	I	I	R	R	R	S	R	R	I	R	R	I	R
3	CF03	I	R	S	R	I	R	S	S	R	R	R	R	S	R	I	R	R	R	R	R
4	CF07	R	R	S	I	R	R	I	S	S	R	R	R	S	R	R	I	R	R	I	R
6	CF08	R	R	S	I	R	R	I	S	S	R	R	R	S	R	I	S	R	R	I	R
7	CF09	S	R	S	R	R	R	I	S	S	R	R	R	S	R	I	S	R	R	I	R
8	CF11	S	S	S	S	S	S	S	S	S	R	R	R	S	R	I	S	S	R	S	I
Lucknow (11 Nos.)																					
9	Cf0238IR-184	I	S	R	R	I	S	S	I	R	R	I	I	I	R	I	S	I	I	S	S
10	Cf0238IR-185	I	S	R	R	I	S	S	I	R	R	I	R	I	R	I	S	R	I	S	S
11	Cf0238IR-186	I	S	R	R	I	S	S	I	R	R	R	I	I	R	I	S	I	I	S	S
12	Cf0238IR-187	I	S	R	R	I	S	S	I	R	R	I	I	I	R	S	S	I	I	S	S
13	Cf0238IR-188	I	S	R	R	I	S	S	I	R	R	I	R	I	R	I	S	R	I	S	S
14	Cf0238IR-189	I	S	R	R	I	S	S	I	R	R	I	I	I	R	I	S	I	I	S	S
15	Cf0238IR-190	I	S	R	R	I	S	S	I	R	R	I	I	I	R	I	S	R	I	S	S
16	CfS8436IR-191	S	R	R	R	I	I	S	S	R	S	R	R	S	R	R	I	R	I	S	R
17	CfS8436IR-192	S	R	R	R	I	I	S	S	R	S	R	R	S	R	R	I	R	I	S	R
18	Cf0238IR-193	I	S	R	R	I	S	S	I	R	R	I	I	I	R	I	S	R	I	S	S
19	CfLk8102IR-194	R	S	R	R	S	I	S	S	I	R	R	R	S	R	I	I	I	S	I	I
Shajahanpur (33 Nos.)																					
20	Cf0238-1	I	I	S	R	I	S	S	R	R	R	R	R	S	R	I	I	S	R	R	S
21	Cf0238-2	I	I	S	I	I	S	S	I	R	R	R	R	S	R	I	I	S	R	R	S
22	Cf0238-3	R	R	R	R	I	S	S	R	R	R	R	I	S	R	I	S	S	R	S	S
23	Cf0238-4	S	I	I	I	R	S	S	I	R	R	R	I	S	R	S	I	S	R	R	S

Table 2 continued

No	Pathotype/ isolate	Co 419	Co 975	Co 997	Co 1148	Co 7717	Co 62399	CoC 671	CoJ 64	CoS 767	CoS 8436	BO 91	Baragua	Khakai	SES 594	Co 7805	Co 86002	Co 86032	CoSe 95422	CoV 92102	Co 0238
24	Cf0238-5	I	I	S	I	I	S	S	R	R	R	R	I	S	R	I	S	S	R	R	S
25	Cf0238-6	S	R	I	I	R	S	S	S	R	R	R	R	S	R	S	S	S	R	S	S
26	Cf0238-7	R	R	S	I	R	S	S	S	R	R	R	I	S	R	S	S	S	R	I	S
27	Cf0238-LKO	R	I	R	R	R	S	S	R	R	R	R	R	I	R	S	R	S	R	S	S
28	Cf0238-R 1602	I	I	S	R	I	S	S	R	R	R	R	R	S	R	I	I	S	R	R	S
29	Cf0238-R 1702	R	I	R	R	R	S	S	R	R	R	R	R	I	R	I	S	S	R	R	S
30	Cf0238-R 1705	R	R	S	R	R	S	S	R	R	R	R	R	I	R	I	R	S	R	S	S
31	Cf0238-R 1707	R	S	R	R	R	S	S	R	R	R	R	R	I	R	R	R	S	R	R	S
32	Cf0238-R 1711	R	I	S	R	R	S	S	R	R	R	R	R	I	R	R	S	S	R	I	S
33	Cf0238-R 1802	R	I	R	R	R	S	S	R	R	R	R	R	I	R	I	S	S	R	R	S
34	Cf0238-R 1807	R	R	R	R	R	S	S	S	R	R	R	R	I	R	S	S	R	R	S	S
35	Cf0238-R 1808	R	I	R	R	I	S	S	R	R	R	R	S	R	R	I	S	S	R	R	S
36	Cf0238-R 1810	R	R	R	R	I	S	S	R	R	R	R	I	S	R	I	S	S	R	S	S
37	Cf0238-R 1811	S	I	I	I	R	S	S	I	R	R	R	I	S	R	S	I	S	R	R	S
38	Cf0238-R 1814	R	I	S	R	R	S	S	R	R	R	R	R	S	R	I	I	S	R	I	S
39	Cf0238-R 1817	I	I	S	I	I	S	S	R	R	R	R	I	S	R	I	S	S	R	R	S
40	Cf0238-R 1820	R	R	S	I	R	S	S	R	R	R	R	I	R	R	R	S	R	R	R	S
41	Cf0238-R 1821	S	R	I	I	R	S	S	S	R	R	R	R	S	R	S	S	S	R	S	S
42	Cf0238-R 1903	R	R	S	I	R	S	S	S	R	R	R	I	S	R	S	S	S	R	I	S
43	Cf0238-R 1924	R	R	R	R	R	S	S	R	R	R	R	R	R	R	R	R	S	R	R	S
44	Cf0238-R 1938	R	S	R	R	R	S	S	R	R	R	R	R	I	R	R	R	S	R	I	S

Table 2 continued

No	Pathotype/ isolate	Co 419	Co 975	Co 997	Co 1148	Co 7717	Co 62399	CoC 671	CoJ 64	CoS 767	CoS 8436	BO 91	Baragua	Khakai	SES 594	Co 7805	Co 86002	Co 86032	CoSe 95422	CoV 92102	Co 0238
45	Cf0238-R 2001	R	S	R	R	R	S	S	R	R	R	R	R	R	R	I	R	S	R	R	S
46	Cf0238-R 2003	R	S	I	R	R	S	S	R	R	R	R	R	I	R	R	R	S	R	S	S
47	CfPk05191-R1941	R	I	S	R	R	S	S	R	R	R	R	R	I	R	S	I	S	R	S	S
48	CfPk05191-R2005	R	I	S	R	I	S	S	R	R	R	R	R	I	R	S	I	S	R	I	S
49	CfS07250	S	R	S	S	I	S	S	S	I	R	S	R	S	R	S	I	S	I	I	R
50	CfS08279-R1945	R	I	I	R	I	S	S	R	R	R	R	R	S	R	R	R	S	R	S	S
51	CfS8436	S	I	S	S	I	I	S	S	R	S	R	R	S	R	I	R	S	R	S	R
52	CfS97264	R	R	S	I	R	R	I	I	I	R	I	R	S	R	R	S	R	I	R	R
Seorahi (5 Nos.)																					
53	Cf8436-R1702Seo	R	I	I	S	I	I	R	I	I	S	R	R	I	R	I	S	S	R	S	R
54	Cf0238-R1801Seo	I	S	R	R	I	S	S	I	R	R	R	I	R	R	I	S	R	R	S	S
55	Cf0238-R1802Seo	I	S	R	R	I	S	S	I	R	R	R	R	I	R	I	S	R	R	S	S
56	Cf0238-R1803Seo	I	S	R	R	I	S	S	I	R	R	R	I	R	R	I	S	R	R	S	S
57	Cf0238-R1904Seo	I	S	R	R	I	S	S	I	R	R	R	R	R	R	I	S	R	R	S	S
58	Cf0238-R1905Seo	I	S	R	R	I	S	S	I	R	R	R	I	R	R	I	S	R	R	S	S

R Resistant, *I* Intermediate, *S* Susceptible

Table 3 Pathogenic reactions of *Colletotrichum falcatum* isolates and pathotypes on host differentials in Haryana

No	Pathotype / isolate	Co 419	Co 975	Co 997	Co 1148	Co 7717	Co 62399	CoC 671	CoJ 64	CoS 767	CoS 8436	BO 91	Baragua	Khakai	SES 594	Co 7805	Co 86002	Co 86032	CoSe 95422	CoV 92102	Co 0238
Pathotype																					
1	CF01	S	R	S	S	S	S	S	S	I	R	I	R	R	R	I	S	R	I	S	S
2	CF02	S	R	S	S	S	S	S	S	R	R	I	R	I	R	R	S	I	R	R	I
3	CF03	R	R	S	S	R	R	S	S	R	R	R	R	R	R	R	S	R	R	R	R
4	CF07	R	R	S	R	R	I	S	S	R	R	R	R	R	R	S	S	R	R	S	R
5	CF08	R	R	S	S	R	S	I	S	R	R	R	R	R	R	S	S	R	R	I	R
6	CF09	R	R	I	I	I	R	S	S	R	R	R	R	I	R	S	R	R	R	R	R
7	CF11	S	S	S	R	S	S	S	S	R	R	I	R	I	R	I	S	S	I	I	R
Isolate																					
8	Cf0238-LKO	R	S	S	R	R	S	S	R	R	R	R	R	R	R	S	I	S	R	R	S
9	Cf0238-1	R	I	S	R	I	S	S	R	R	R	I	R	R	R	R	R	S	R	R	S
10	Cf0238-2	R	S	S	R	I	S	S	I	R	R	I	R	R	R	S	S	S	R	R	S
11	Cf0238-3	R	R	S	R	R	S	S	R	R	R	R	R	R	R	R	R	S	R	I	S
12	Cf89003	S	S	S	R	R	S	S	S	R	S	R	R	S	R	S	R	S	R	R	S
13	CfS8436	S	I	R	R	R	I	S	S	R	S	R	R	I	R	S	S	R	R	R	S
14	CfLk94184	I	R	R	I	R	S	S	R	R	R	R	R	R	R	S	S	R	R	R	I

R Resistant, *I* Intermediate, *S* Susceptible

Table 4 Pathogenic reactions of *Colletotrichum falcatum* isolates and pathotypes on host differentials in Punjab

No	Pathotype/ Isolate	Co 419	Co 975	Co 997	Co 1148	Co 7717	Co 62399	CoC 671	CoJ 64	CoS 767	CoS 8436	BO 91	Baragua	Khakai	SES 594	Co 7805	Co 86002	Co 86032	CoSe 95422	CoV 92102	Co 0238
1	CF01	S	I	S	S	I	I	S	I	R	R	R	R	S	R	R	R	R	R	I	R
2	CF02	I	R	S	S	S	S	I	S	R	R	R	R	S	R	R	R	R	R	I	R
3	CF03	I	R	S	I	I	R	S	S	R	R	R	R	S	R	I	R	I	R	R	R
4	CF07	I	R	S	I	R	R	S	S	I	R	R	R	S	R	R	I	I	R	R	R
5	CF08	S	S	S	S	I	S	S	S	I	R	R	R	S	R	S	I	R	R	R	R
6	CF09	I	I	I	S	R	R	S	S	S	R	R	R	S	R	I	I	R	R	R	R
Isolates																					
7	Cf0238-LKO	I	I	R	I	I	S	S	I	R	R	R	R	S	R	S	I	S	R	I	S
8	CfJ64	S	S	S	S	I	S	S	S	S	R	R	R	S	R	I	I	R	R	R	R
9	CfJ85-1	S	I	S	S	R	S	S	S	S	R	R	R	S	R	S	R	R	R	R	R
10	CfJ85-2	S	S	S	S	I	S	S	S	S	R	R	R	S	R	I	I	R	R	R	R
11	CfJ85-S	S	S	I	S	I	S	S	S	I	R	R	R	S	R	I	I	R	R	R	R
12	CfJ88	S	I	S	I	I	S	S	S	I	R	R	R	S	R	I	R	R	R	R	R
13	Cf89003-1	I	I	I	S	I	S	I	S	I	R	R	R	S	R	I	R	R	R	R	R
14	Cf89003-2	I	I	S	S	I	S	I	S	R	R	R	R	S	R	I	R	R	R	R	R
15	Cf89003-3	S	S	S	S	I	S	S	S	I	R	R	I	S	R	S	I	R	R	R	R
16	Cf89003-4	S	S	S	I	I	S	S	S	I	R	R	R	S	R	I	R	I	R	R	R

R Resistant, *I* Intermediate, *S* Susceptible

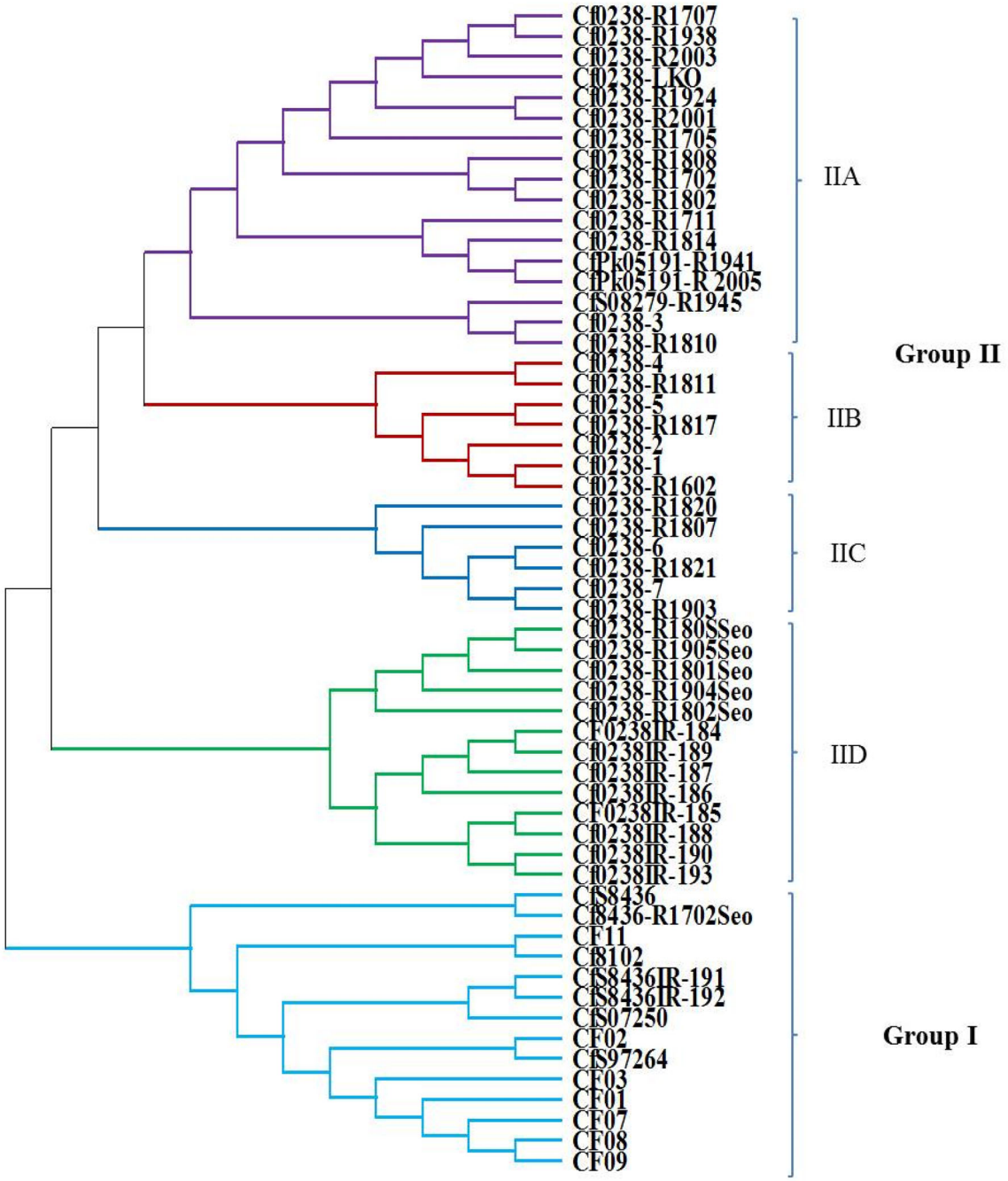


Fig. 2 Grouping of disease reactions of 7 pathotypes and 50 new isolates of *Colletotrichum falcatum* from Uttar Pradesh on 20 sugarcane host differentials after phylogenetic analyses using MEGA version 5

all the Cf0238 isolates behaved uniformly on the 20 differential hosts and the isolates did not exhibit virulent reactions on the susceptible differential for the sub-tropical zone CoJ 64 (Table 2).

At Karnal, Haryana, seven *C. falcatum* isolates and seven pathotypes were evaluated for red rot reactions and of these, four Cf0238 isolates exhibited virulent behaviour on their matching host variety and similar behaviour was observed on the differentials Co 997, Co 62399, Co 86032 and CoC 671. However, these isolates behaved as less virulent on the susceptible differential CoJ 64. In contrast, all the designated pathotypes CF01, CF02, CF03, CF07, CF08, CF09 and CF11 and the isolates from the cvs Co 89003 and CoS 8436 behaved as virulent on this

differential (Table 3). However, the differential Co 0238 behaved as S to CF01, Cf89003 and Cf8436 and intermediate to CF02 and CfLk94184 and such behaviour was found only at Karnal. The new Cf0238 isolates also exhibited a differential behaviour with other isolates/pathotypes on the differentials Co 419, Co 975, Co 1148, Co 7805 and Co 86032.

At Kapurthala in Punjab 10 *C. falcatum* isolates and six pathotypes were evaluated and the differential Co 0238 behaved as R to all the other isolates/pathotypes except its own isolate Cf0238-LKO. When all the other isolates/pathotypes exhibited virulent behaviour on the differential CoJ 64 the isolate Cf0238-LKO behaved as moderately virulent. In addition, this isolate had exhibited a differential behaviour with other isolates/pathotypes on the host differentials Co 997, Co 62399, Co 7805, Co 86032 and CoV 92102 (Table 4). Incidentally, four of the isolates from Co 89003 behaved comparatively more virulent in this location.

Pathogenicity of New Isolates Originated from Co 0238

In Shahjahanpur, it is interesting to note that all the 27 isolates originated from Co 0238 variety were less virulent on the resistant differentials like CoS 767, CoS 8436, BO 91, SES 594 and CoSe 95422. On the differential Co 62399, all the Cf0238 isolates exhibited virulent behaviour whereas it was less virulent against the designated pathotypes CF02, CF03, CF07, CF08, CF09 except CF11 with virulent and CF01 with moderate virulent behaviours. The differential CoC 671 showed S reactions against all the 27 isolates derived from Co 0238. At the same time, the known resistant differential Baragua behaved moderately virulent to nine new Cf0238 isolates (33.3%) whereas all the designated pathotypes exhibited less virulence and expressed R reactions. Similarly all the designated pathotypes behaved as virulent on the differential Khakai, whereas 14 (51.8%) Cf0238 isolates behaved as virulent, 8 (29.6%) moderately virulent and 4 (14.8%) less virulent, indicating a clear variation in the pathogenicity of the new isolates from the designated pathotypes. The differentials Co 7805, Co 86002, Co 86032 and CoV 92102 showed differential reactions against all the new isolates where R, I and S reactions were recorded. Of the 27 Cf0238 isolates 8 (29.62%) expressed virulence on Co 7805 whereas 14 (51.8%) expressed less virulence on CoV 92102. On Co 86002, 14 (51.8%) isolates expressed virulence, seven less virulence and six moderate virulence. On the differential Co 86032, 25 (92.6%) of 27 new Cf0238 isolates showed virulence and two were less virulent.

The pathogenicity pattern of all the 50 pathotypes/ isolates collected and tested at Lucknow (11), Sahjahanpur (33) and Seorahi (6) centres from UP state and seven designated pathotypes were analysed and a dendrogram was constructed. In that, the pathotypes/ isolates were separated into two major groups (Fig. 2). The major group-I grouped all the designated pathotypes CF01, CF02, CF03, CF07, CF08, CF09, CF11 and newly collected isolates CfS8436, Cf8436-R1702Seo, CfLk8102IR-194, CfS8436IR-191, CfS8436IR-192, CfS07250 and CfS97264 which were less virulent on Co 0238 together. All these pathotypes were less virulent on Co 0238 except CF11 and Cf8436-R1702Seo which behaved as less virulent expressing intermediate reaction on Co 0238.

The second major group II clustered all the other 43 isolates which exhibited virulence on the cv Co 0238. This major group was further divided into four subclusters IIA, IIB, IIC and IID based on red rot reactions on the differential hosts. The subcluster IIA separated 14 isolates obtained from Co 0238 and the two isolates Cf05191R1941 and Cf05191R2005 originated from CoPk 05191 and another isolate Cf08279R1945 from CoS 08279 virulent on Co 0238. All these isolates were found to be less virulent on the differential CoJ 64. The isolates which showed intermediate reaction on the differential Co 975 but virulent on Co 0238 formed the subcluster IIB. This group consisted of seven Cf0238 isolates originated from the variety Co 0238. The subgroup IIC separated six isolates from Co 0238 which were virulent on Co 86032 and Co 0238 but were less virulent on the differentials Co 975 and Co 7717. The last subcluster IID comprised of the 13 Cf0238isolates which were moderately virulent on the differentials CoJ 64 and Co 419 and less virulent on CoSe 95422 and Co 997 but virulent on Co 0238 (Fig. 2).

Discussion

Variability in *C. falcatum* was first known in 1930s in India after the historical red rot epidemics on the then ruling variety Co 213 which caused severe damages as we are witnessing in the states of UP and Bihar (Chona and Padwick 1942). During the same time, Abbott (1938) characterized virulent and avirulent strains in Louisiana. The virulent light types were differentiated from less virulent dark types based on high sporulating behaviour of white coloured mycelium. Later, many workers reported the pathogenic variation in *C. falcatum* regularly in the past (Beniwal et al. 1989; Chona and Srivastava 1960; Padmanaban et al. 1996; Srinivasan 1962). The emergence of highly sporulating light coloured strains was correlated with the large scale red rot epidemics in subtropical sugar belt in India (Chona and Padwick 1942; Rafay and Singh 1957). Although there were lesser disease outbreaks in 1950s and 1960s, severe red rot outbreak occurred after the

Fig. 3 Large-scale destruction of sugarcane after varietal breakdown to red rot in the variety Co 0238 in Uttar Pradesh state, India

breakdown of the popular variety Co 1148 and caused huge damages, followed by epidemics on Co 7717 in Haryana and CoJ 64 in the subtropical region. Hence earnest efforts were made to characterize the pathotypes using a set of host differentials and identified different pathotypes (Beniwal et al. 1989; Padmanaban et al. 1996; Satyavir 2003). Two designated pathotypes of *C. falcatum* CF01 and CF02 were well differentiated by pathogenicity, serological and molecular studies (Mohanraj et al. 2002; Viswanathan et al. 2003).

Breakdown of the popular variety CoJ 64 led to emergence of new isolates with high virulence and from that new pathotypes were characterized and designated viz CF03, CF07, CF08 and CF11 during different occasions. Additionally, CF09 pathotype was designated from CoS 767, a popular variety in the state of UP (Viswanathan 2021b). Characterization of *C. falcatum* pathotypes under AICRP on Sugarcane is a national programme of ICAR in the country to designate the pathotype(s) and use them for screening sugarcane varieties in different agro-climatic zones (Viswanathan, 2018). This system ensures uniformity in the pathogenic flora used to screen the same set of varieties across the centres in a zone. Designating a new pathotype and using it for screening of the new varieties for red rot resistance mimics testing with current pathogenic flora that occur in the region. In the subtropical region, we have discontinued old pathotypes CF01, CF02 and CF03 and currently use CF07, CF08 and CF09 for red rot screening. Similarly use of CF04, CF05 and CF10 were discontinued and CF06 and CF12 are used for screening sugarcane varieties for red rot resistance in the tropical region (Viswanathan, 2018).

During 2009, Co 0238 the high yielding and high sugar variety was released for commercial cultivation as an early maturing variety in North-West Zone (NWZ) comprising the states of Haryana, Punjab, Western and Central UP, Uttarakhand and Rajasthan. The variety was preferred by both the farmers and sugar industry as it combined both high cane yield (81 t/ha) and 20% sucrose in juice (Ram and Hemaprabha 2020). Since 2013–2014, the area under Co 0238 has been increasing at a faster rate in all the five major sugarcane growing states, viz. Punjab, Haryana, Uttarakhand, UP and Bihar in the subtropical India. Though, this variety was released and notified for NWZ, it has crossed the boundaries of the zone to reach Eastern UP, Bihar and Madhya Pradesh. During 2013–2014, the cv Co 0238 had a coverage of 0.11 M ha of the total cane area of 2.76 M ha in the sub-tropical India accounting for only $\sim$ 4.3%. Punjab had the maximum coverage (27.8%) followed by Haryana (12.6%), UP (3.1%), and Uttarakhand (1.4%). There was a huge jump in the area covered by the variety as it occupied 66.10% (78,306 ha) in Punjab, 60.20% (83,937 ha) in Haryana, 82.21% (22,02,385 ha) in Uttar Pradesh, 64.12% in Bihar (1,59,198 ha) and 75.71% (64,303 ha) in Uttarakhand (Ram and Hemaprabha 2020). To be precise, this single variety Co 0238 occupied the area of 25,88,129 ha (79.15%) in the sub-tropical India covering all the five states (Ram and Hemaprabha 2020). The

variety replaced many of the popular varieties CoJ 64, CoJ 85, CoH 119, CoS 767, CoS 8436, CoSe 92423, CoSe 95422 etc. under cultivation in the region.

During the time of release of Co 0238 for the subtropical region, red rot was a menace up to 10% in CoS 767 and Co 1148 and severe upto 75% in CoPant 84211 and CoJ 84 and upto 100% in CoPant 84212 and CoJ 83 in UP. There was a severe red rot outbreak on the predominant variety CoS 8436 in Haryana and UP. In Punjab, CoJ 64, CoJ 82 and CoJ 84 had infections upto 80%. In Bihar, many varieties were showing red rot-wilt complex in the field on varieties CoSe 92423, BO 70, BO 74, BO 102, BO 120, Co 1148, CoLk 8001, CoS 687 and CoS 767 (Viswanathan 2010). Until 2010, there was no record of any new virulent pathotype in Lucknow areas. Whereas in Shahjahanpur, the isolate R0401 originated from the cv CoS 8436 displayed variable pathogenic reactions on CoS 8436 and the pathogenic behaviour speculated emergence of a new pathotype along with the existing pathotypes CF08 and CF09 in UP (Viswanathan et al. 2011). During 2016, red rot was observed on the cv Co 0238 with incidences of 5–15%, 1–2%, 2–10%, 40% from Nigohi, Rosa, Hargaon and Gola, respectively in the UP state. Overall, the variety had low to moderate incidences of red rot (3–8%) in different cane growing areas of UP. Whereas other cvs CoS 8436, CoS 92423, CoLk 8102, CoS 91269 and CoSe 95422 recorded severe disease incidences in the state (Viswanathan et al. 2017b). In the successive years, the incidences of red rot have rapidly increased in different districts of the UP state. During 2017–2018, the cv Co 0238 recorded 3 to 20% red rot at several locations in the command areas of different sugar mills in UP. Additionally in some fields up to 30% red rot incidences were recorded in the cvs CoSe 95422, CoS 8436, and CoSe 92423. In Bihar also red rot was recorded in the varieties namely CoSe 95422, Co 0238 and BO 130 to the tune of 3–7% (Viswanathan et al. 2018). Subsequently both the states UP and Bihar witnessed huge devastations of red rot and brought downfall of the cv Co 0238 (Viswanathan 2021a,b).

The cv Co 0238 exhibited MR reactions to *C. falcatum* pathotypes CF08 and CF09 used for screening at the time of release and in our present studies also it maintained its resistance against the seven designated pathotypes from the subtropical region and new isolates from other varieties (Tables 2, 3, 4). However, all the Cf0238 isolates originated from Co 0238 had a killing effect on its host variety. This finding clearly depicts a clear emergence of new *C. falcatum* pathotypes in tune with the varieties under cultivation. Historically we have witnessed failure of popular varieties like Co 213, Co 312, Co 419, Co 658, Co 997, Co 1148, Co 7717, CoC 671, CoJ 64, etc. after their adoption in large areas in the past due to emergence of new pathotypes with acquired virulence to cause varietal breakdown (Chona 1980; Viswanathan, 2017, 2018, 2021). Earlier, adaptation of *C. falcatum* to the new varieties was speculated thereby the new pathogenic variants make the incompatible host cytoplasm to compatible (Srinivasan 1962, 1965). Adaptation of *C. falcatum* pathotypes CF01 and CF02 on their respective incompatible host varieties Co 7717 and Co 1148 was demonstrated. In that, by repeated inoculations on the incompatible hosts, the pathotypes acquired virulence to make the interactions compatible (Malathi et al. 2006). Subsequently, pathogenicity determinants of *C. falcatum* that aid in pathogenicity were identified (Malathi et al. 2012a, b). Recently adaptation *C. falcatum* to sugarcane varieties was clearly demonstrated under field conditions with different sources of inoculum and varieties varying in red rot resistance (Viswanathan et al, 2020a; b). We have clearly established the role of soil borne inoculum sources in inciting attempted infections and gradually causing death of the infected stools under field conditions (Viswanathan and Selvakumar 2020). Since *C. falcatum* survives in the soil especially in crop debris for varying periods (Viswanathan 2010), the inoculum already available from the infected varieties like CoS 8436, CoSe 92423, CoSe 95422, BO 130 etc. in the endemic regions would have served as the source for new infections in Co 0238.

Given the nature of agro-climatic zones of central and eastern UP and Bihar, where, flooding and waterlogging are common during southwest monsoon months of July to September; the inoculum is easily spread through the flood water to vast areas of Indo-Gangetic plains of these states. Further, flooding or water stagnation favours emergence of new variants in *C. falcatum* through hyphal fusion or fusion of germ tube hyphae (Duttamajumder et al. 1990; Viswanathan et al. 2003). Probably under high soil moisture stress, the host resistance will be compromised and favoured the pathogen entry into the host tissues (Pappelis and Katasanos 1965). Earlier, evolution of new pathogenic variants with higher virulence capable of knocking down R genes was demonstrated in many host–pathogen interactions; Van der Plank (1963) first documented such phenomenon in potato variety Vertifolia where the pathogen *Phytophthora infestans* overcame R genes and made the variety susceptible. Later such events in plant breeding and plant pathology were referred as 'Vertifolia effect' and are portrayed by erosion of horizontal resistance to a disease in a crop due to strong presence of vertical resistance characterized by the presence of R genes. Recently, Viswanathan (2021b) documented boom and bust cycle with respect to red rot epidemics in the past and the present scenario also reflects the same. Earlier, Natarajan et al. (1998) also opined monoculture of a variety favouring boom and bust cycle of red rot in UP and Bihar.

Presently, monoculture of the variety Co 0238 to more than 80% of total cane area in the UP state created a selection pressure on the pathogen and the host variety acts as strong selection agent and specific variant capable of infecting the popular sugarcane variety emerged. Due to monoculture of the variety, the new pathotype would have spread very fast probably through flood water in large areas of sugarcane especially during monsoon months. This may be a reason we observed uniform behaviour of the Cf0238 isolates on the differentials and this may also be due to rapid increase in frequency in the new variants of the pathogen population. The new variants could have either evolved from the already existing pathogenic flora, perhaps, in a very low frequency or new variants as discussed earlier. Grouping of pathogenic reactions on the host differentials clearly separated all the Cf0238 isolates in a major group II whereas all the previously designated pathotypes were grouped in group I (Fig. 2). This finding indicates that the newly emerged isolates on the variety Co 0238 might have a different source(s) of origin. The varieties Co 1148, CoJ 83, CoJ 84, CoLk 8102, CoPant 84211, CoPant 84212, CoPk 05191, CoS 767, CoS 8436, CoS 91269, CoS 08279, CoSe 92423 and CoSe 95422 exhibited red rot to varying intensities before and after breakdown of Co 0238 in UP (Viswanathan et al. 2011, 2017b, 2018). Among the isolates of other varieties, the isolates from CoPk 05191 and CoS 08279 alone grouped with Cf0238 isolates in the subcluster IIA (Fig. 2). The distinct pattern of Cf0238 isolates in pathogenicity suggests that new virulent isolates could have been emerged from infections on other varieties occurred in the field that have not been characterized so far. Further, at Shahjahanpur, of the 27 Cf0238 isolates, 18 (66.7%) were less virulent on the susceptible differential CoJ 64 whereas all the designated pathotypes were virulent and expressed S reactions, indicating the origin of these Cf0238 isolates is from other host varieties. After the emergence of a new virulent pathotype, its frequency reaches a threshold at which it incites an epidemic in the variety, hitherto resistant to red rot. Generally, the disease epidemic builds up after a few seasons or more, since the first detection of the virulent pathotype and rapidity of an epidemic depends on the area under the variety is grown. In such situation, selection pressure will be in favour of the virulent pathotype on the variety (Van der Plank 1963). In the present situation, all the phases involved in boom and bust cycle viz. unscientific spread of Co 0238 to more than 80% sugarcane area in the UP state, breakdown of resistance to red rot, emergence of new virulent pathotype capable of overcoming resistance in Co 0238, build-up and spread of red rot epidemic and large-scale destruction of the crop, happened without any limitation (Fig. 3). Although proper warning has been given by the sugarcane pathology group during 2017, the advisory was ignored and undermined the probable catastrophe of huge crop losses of several millions of US$.

The earlier reports from Punjab clearly indicated that the new isolates CF271 and CF273 from CoJ 88, CF268 from CoJ 83 and CF270 from CoJ 82 were more virulent than the old pathotypes CF01, CF03 and CF09 (Viswanathan et al. 2011). At the same time in Haryana, the pathotypes CF02, CF03 and CF09 showed more virulence than the pathotypes CF08, CF01 and CF11. The new isolates from CoS 8436 were found to be less virulent and caused susceptible reaction on three known susceptible hosts and not in the differential CoS 8436 (Viswanathan et al. 2011). Probably before the domination of Co 0238 in the region during 2014–2015, there was a mix up of different varieties although none of them were resistant or recently succumbed to the disease. Since the spread of the affected varieties formed a mosaic pattern in the districts, probably the newly emerged pathotypes could not make an epidemic of large scale destruction. The disease incidences were continued to be low to moderate, however, greedy expansion of a single variety to cover entire command area in the UP and Bihar states caused boom and bust cycle facilitated by 'Vertifolia effect'. Although most of the Cf0238 isolates were comparatively less virulent than the designated pathotypes (Tables 1, 2, 3), they only caused disease in the variety Co 0238 and severe crop losses.

Conclusion

Sugarcane cultivation in the subtropical region witnessed a kind of sugar revolution after the release of red rot resistant variety Co 0238 with high yield and sugar during the last decade and became popular among the farmers and covered larger area in a short span of time (Ram and Hemaprabha 2020). That resulted in repeat of 'boom and bust' cycle experienced in the previous decades due to 'Vertifolia effect' and evolution of a new pathotype probably matching with the R genes present in the variety. The increase in frequency of the new pathotype(s) resulted in red rot epidemics in the fields covering larger areas. The record of many new isolates which are specifically virulent on Co 0238 indicated the emergence of a new pathotype in the region and it is designated as *C. falcatum* "CF13". Immediately, the affected variety Co 0238 has to be replaced with new varieties with red rot resistance in large proportion, to save the sugar industry. Since entire command area is saturated with this pathotype CF13, it has to be used to screen new sugarcane varieties before their cultivation in place of CF07 and CF09 in the subtropical region along with CF08. The results of our study clearly established that emergence of new virulent pathotype on the popular cv Co 0238 mimics 'Vertifolia effect' as a

result of monoculture of single sugarcane variety in the subtropical region. Red rot epidemic curtailed the boom and initial years of success could not be sustained for an extended period. Sugarcane researchers should also realize the potential of the dynamic pathogen like red rot which can devastate the crop if we ignore initial infections on a popular variety. Policy makers should not misadventure unscientific varietal deployment and a proper varietal planning will prevent such huge catastrophe due to boom and bust cycle and 'Vertifolia effect' in the future.

Funding The centres Shahjahanpur, Seorahi, Kapurthala and Pusa acknowledge the financial support received from the Project Coordinator, All India Coordinated Research Project on Sugarcane, ICAR-IISR, Lucknow, UP, India. All the authors acknowledge support from AICRP on Sugarcane of ICAR, New Delhi.

Declarations

Conflict of interest The author declare that they have no conflict of interest.

Human and rights statement The present research did not involve human participants and/or animals.

Informed consent Informed consent was obtained from all individual participants included in the study.

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