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Investigations on the Rust Disease Prevalence on Cowpea in Mandya District and Evaluation of Cowpea Genotypes for its Resistance

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A B S T R A C T

Cowpea is an important grain legume crop. Among various diseases, rust caused by *Uromyces phaseoli* var. *vignae* (Barclay) Arthuris one of the major constraints of cowpea production across all cowpea growing areas of the state, thereby causing severe yield loss. The present study aimed at determining the severity of cowpea rust in six taluks of Mandya district *viz*., Mandya, Maddur, Malavalli, Pandavapura, Srirangapatna and Krishnarajpet during *Kharif* 2017. The maximum mean disease severity was recorded in Mandyataluk (39.14%) followed by Maddur taluk (34.61%) and Pandavapura taluk (31.83%) and minimum mean disease severity of 20.76 per cent was observed in Krishnarajapet taluk followed by Srirangapatna taluk (22.10%) and Malavalli taluk (27.56%). In order to identify the resistant sources against this disease an experiment was conducted to evaluate 57 genotypes under field conditions during *Kharif* 2017 at College of Agriculture, V. C. Farm, Mandya (University of Agricultural Sciences, Bengaluru). The disease severity varied from 0.13 to 81.45%. Out of fifty seven genotypes screened none of them were found to be immune. However, 16 genotypes were resistant, 23 genotypes were moderately resistant, 10 genotypes were moderately susceptible, 7 genotypes were susceptible and variety C-152 showed highly susceptible reaction against rust.

Introduction

Cowpea (*Vigna unguiculata* (L.)Walp.) is an important annual legume among the pulse crops grown in tropical and sub-tropical countries of the world. It is grown through-out India particularly in the Central and Peninsular regions. It is a popular crop due to its rich and cheap sources of high quality protein of about 24.8 per cent, 1.8 per cent fat and 60.3 per cent carbohydrates. It is referred to as 'vegetable meat' because it contains high amounts of protein in grain with good biological value on dry weight basis (Gopalan *et al.*, 2007). Cowpea occupies 3.9 mha of area with 2.2 mt production and 564 kg ha^{-1}

productivity in India (Anon., 2015). In Karnataka, it occupies an area of 0.97 m ha with production of 0.43 m t and productivity of 462 kg ha^{-1} (Anon., 2013). Cowpea is reported to be infected by more than ten diseases. Rust of cowpea caused by *Uromycesphaseolis* var. *vignae* (Barclay) Arthuris widely distributed throughout the country and is responsible for heavy reduction in yield (Chandrashekar*et al.,* 1988).The disease is observed in severe form in July sown crop during southwest monsoon resulting in considerable yield loss (Chandrasekhar *et al.,* 1989).

This disease is widespread in cowpea growing areas of the world and is reported from at least 20 countries causing 10-15 per cent annual losses (Anilkumar*et al.,* 1989). In most of the parts of Karnataka, rust is an economically important and serious disease which affects the production of cowpea. The disease was reported to occur in Dharwad and Mysore (Rangaswamy *etal*., 1989). As the disease progresses, premature defoliation leading to reduced seed size and severe yield loss has been observed (Honnur*et al.,* 2016). Also the significance of disease depends on prevalence of virulent races and their affinity with the genetic constitution of the host in the prevailing environment. The present investigation was undertaken to know the disease incidence and to screen the genotypes against rust disease.

Materials and Methods

A roving survey was conducted during *Kharif* season of 2016-17 in major cowpea growing areas of Mandya district. In each taluk2-7 villages were selected and in each village one to two fields were surveyed for recording the severity of cowpea rust. In each field 50 plants were selected at random for recording the disease severity. Disease scoring is done as per Mayee and Datara (1986) 0-9 scale and Per cent Disease Index (PDI) was calculated using the below mentioned formula.

The cowpea genotypes were screened against rust under field conditions during *Kharif*2017 at College of Agriculture V. C. Farm, Mandya (University of Agricultural Sciences, Bengaluru). Each genotype was sown in two rows of 3m length with 45×10cm spacing and regular agronomic practices were followed. The observations were recorded by using 0-9 scale (Mayee and Datar, 1986) by selecting 5 plants in each row of each genotype. Percent disease index (PDI) will be calculated using the formula mentioned below.

PDI =

$$\frac{\text{Sum of all disease ratings}}{\text{Total number of ratings} \times \text{Maximum disease grade}} \times 100$$

Results and Discussion

A total of six taluks were selected. In Mandyataluk, seven villages were surveyed wherein the highest average disease severity was recorded at Mandya (48.45%) followed by Shivalli village (42.44%), V. C. Farm (40.75%) and Dudda (38.33%). However, least average disease severity was observed in Mallanayakanakatte village (33.48%) followed by Ganadalu (34.44%) and Holalu village (36.11%). Further the average disease severity of 39.14% was recorded in Mandya taluk.

A total of three villages were surveyed in Maddur taluk. The average disease severity of 34.61% was observed in this taluk. The highest average disease severity of 35.50% was recorded in Maddur followed by Honnalagere village (35.00%) and the lowest average disease severity was obtained in Bharatinagar village (33.33%). An average disease severity of 31.83% was recorded from

the six villages of Pandavapura taluk. Among the villages surveyed Cheluvarawinakoppalu recorded highest average disease severity of 34.44% followed by Pandavapura (33.25%), Kanakanamaradi (31.66%) and Jakkanahalli (31.10%) whereas the lowest average severity of disease was observed in Chinakurali (30.00%) followed by Melukote village (30.55%).

Ten villages were surveyed in Malavalli taluk wherein the average disease severity of 27.56% was observed. The highest average disease severity was observed in Malavalli (32.20%) followed by Dubnalli village (32.0%), Devipura (31.85%), Kagepura (31.55%) and Dundanahalli (30.0%) The lowest average disease severity was obtained in Nidagatta village (20.80%) followed by Anjadoddi village (21.4%), Talagawadi (23.33%), Kandegala (25.00%) and Hosalli (27.50%).

In Srirangapatna taluk, the average disease severity of 22.1% was recorded from the two villages surveyed. The survey revealed that the highest average disease severity of 24.20% in Neralekere village. The least average disease severity of 20.0% was observed in Srirangapatna.

In Krishnarajpet taluk, the average disease severity of 20.76% was recorded from two villages surveyed. The highest average disease severity was observed in Krishnarajapet (23.20%) whereas the lowest average disease severity of rust was obtained in Machanahalli village (18.33%)

Among the taluks surveyed in Mandya district, the results revealed the highest average disease severity in Mandya taluk (39.14%) followed by Maddur taluk (34.61%) and Pandavapura taluk (31.83%). The lowest average disease severity was recorded in Krishnarajapet taluk (20.76%) followed by Srirangapatna taluk (22.1%). Among the different villages of six taluks, the highest average disease severity was observed in Mandya village (48.45%) followed by Shivalli village of Mandyataluk (42.44%), whereas the lowest average disease severity was recorded in Srirangapatna village (20.0%) of Srirangapatna taluk followed by Anjadoddi village (21.4%) of Malavalli taluk (Table 1–4).

Table.1 Disease scoring scale description (Mayee and Datar, 1986)

Score	Description	Category
0	No symptoms on leaves	Immune (I)
1	Small, round, powdery brown uredospores covering 1% or less of leaf area	Resistant (R)
3	Typical uredospore covering 1-10% of the leaf area	Moderately Resistant (MR)
5	Typical uredospores covering 11-25% of the leaf area	Moderately Susceptible (MS
7	Typical uredospores covering 26-50% of the leaf area	Susceptible (S)
9	Typical uredospores covering 51% or more of leaf area	Highly Susceptible (HS)

Table.2 The disease severity of cowpea rust in Mandya district

Taluks	Villages	Stage of crop	Variety	Mean disease severity (%)	Mean disease severity of Taluks (%)
Mandya	Holalu	Pod development	C-152	36.11	**39.14**
	Dudda	Flowering	C-152	38.33	
	Mallanayakanakatte	Pod development	C-152	33.48	
	Ganadalu	Pod development	C-152	34.44	
	V. C. Farm	Flowering	C-152	40.75	
	Shivalli	Flowering	C-152	42.44	
	Mandya	Flowering	C-152	48.45	
Maddur	Honnalagere	Flowering	C-152	35.00	**34.61**
	Bharatinagar	Flowering	C-152	33.33	
	Maddur	Flowering	C-152	35.50	
Pandavapura	Chinakurali	Flowering	Pantolab-2	30.00	**31.83**
	Kanakanamaradi	Pod development	Pantolab-2	31.66	
	Cheluvarawinakoppalu	Pod development	Pantolab-2	34.44	
	Melukote	Flowering	Pantolab-2	30.55	
	Jakkanahalli	Flowering	Pantolab-2	31.10	
	Pandavapura	Flowering	Pantolab-2	33.25	
Malavalli	Nidagatta	Flowering	Pantolab-2	20.80	**27.56**
	Anjadoddi	Flowering	Pantolab-2	21.40	
	Kandegala	Flowering	Pantolab-2	25.00	
	Hosalli	Flowering	Pantolab-2	27.50	
	Talagawadi	Flowering	Pantolab-2	23.33	
	Dubnalli	Flowering	Pantolab-2	32.00	
	Devipura	Flowering	Pantolab-2	31.85	
	Dundanahalli	Flowering	Pantolab-2	30.00	
	Kagepura	Flowering	Pantolab-2	31.55	
	Malavalli	Flowering	Pantolab-2	32.20	
Srirangapatna	Neralekere	Flowering	C-152	24.20	**22.10**
	Srirangapatna	Flowering	C-152	20.00	
Krishnarajapet	Machanahalli	Flowering	C-152	18.33	**20.76**
	Krishnarajapet	Flowering	C-152	23.20	

Table.3 Disease severity of cowpea genotypes screened under field conditions

Sl. No.	Genotypes	Per cent disease index (PDI)	Sl. No.	Genotypes	Per cent disease index (PDI)
1.	AV-5	26.77	30.	PV-3	14.54
2.	27	12.00	31.	ArkaSuman	4.57
3.	V-16	0.50	32.	Kashiunnati	0.48
4.	C152XV16	0.23	33.	IC-206240	0.57
5.	K4-1	01.45	34.	PKB-4-2	2.44
6.	120P1-1-1	5.55	35.	IC-402180	0.21
7.	17-1	6.74	36.	PKB-6-2	0.66
8.	61	6.68	37.	APC-668-1	7.78
9.	34	30.00	38.	NBC-25	3.56
10.	22	5.75	39.	C-720	9.88
11.	GC-3	13.44	40.	NBC-38	4.35
12.	IC-2027	15.75	41.	EC-458473	20.98
13.	27749(25)	20.00	42.	Lola	24.65
14.	59	0.13	43.	IC-402104	40.88
15.	NBC-21	23.44	44.	15P2-3	5.64
16.	K4-2	0.34	45.	IC-2591054	6.75
17.	IC-402175	3.68	46.	21-2	0.45
18.	PKB-4-3	0.45	47.	13P1-2	3.33
19.	35-1	4.56	48.	PKB-6-4	0.89
20.	KBC-2	0.52	49.	IC-58905	0.16
21.	IC-25105	3.34	50.	PGCP-11	45.43
22.	AV-7	18.94	51.	Bhagya	4.50
23.	AV-6	2.48	52.	IC-249593	0.13
24.	PKB-3-1	3.22	53.	V-604-7-29-3	34.50
25.	PKB-2	16.76	54.	Genotype-36	32.34
26.	EC-458483	0.32	55.	UPC-5286	2.45
27.	120P1-1-2	6.33	56.	PGCP-6	48.75
28.	PKB-4-4	3.36	57.	C-152	81.45
29.	EC-458480	0.25			

Table.4 Reaction of cowpea genotypes to *U. phaseoli* var. *Vignae* under field conditions

Reaction	Description	No. of genotypes	Genotypes
Immune	No symptoms on leaves	0	-
Resistant	Small, round, powdery brown uredospores covering 1% or less of leaf area	16	C152×V16, 59, K4-2, PKB4-3, Kashiunnati, IC206240, PKB6-2, V-16, EC458483, PKB6-4, EC458480, KBC-2, IC402180, 21-2, IC58905, IC249593
Moderately Resistant	Typical uredospore covering 1-10% of the leaf area	23	K4-1, 120P1-1-1, 17-1, 61, 22, IC402175, 35-1, IC25105, AV-16, PKB3-1, 120P1-1-2, PKB4-4, Arkasuman, PKB4-2, APC668-1, NBC25, C-720, NBC-38, 15P2-3, IC2591054, 13P1-2, Bhagya, UPC-5286.
Moderately Susceptible	Typical uredospores covering 11-25% of the leaf area	10	27, GC-3, IC2027, 27749(25), NBC-21, AV-7, PKB-2, PV-3, EC458473, Lola
Susceptible	Typical uredospores covering 26-50% of the leaf area	7	PGCP-6, AV-5, 34, IC402104, PGCP-11,V-604-7-29-3, Genotype-36
Highly Susceptible	Typical uredospores covering 51% or more of leaf area	1	C-152

In the screening experiment, the results thus obtained revealed that the disease severity ranged between 0.13 to 81.45 per cent. The highest disease severity was recorded in the susceptible check C-152 variety (81.45%) followed by PGCP-6 (48.75%), PGCP-11 (45.43%), IC-402104 (40.88%), V-604-7-29-3 (34.50%) and Genotype-36 (32.34%).

Whereas, least disease severity of 0.13 per cent was recorded in IC-249593 and 59 followed by IC-58905 (0.16%), IC-402180 (0.21%), C152×V16 (0.23%), EC-45480 (0.25%), EC-458483 (0.32%) and K4-2 (0.34%).

Out of fifty seven genotypes screened none of them were found to be immune. However, sixteen genotypes *viz*., C152×V16, 59, K4-2, PKB4-3, Kashiunnati, IC206240, PKB6-2, V-16, EC458483, PKB6-4, EC458480, KBC-2, IC402180, 21-2, IC58905, IC249593were found to be resistant to rust with disease severity ranging between 0.13 to 0.89 per cent.

Twenty three genotypes *viz*., K4-1, 120P1-1-1, 17-1, 61, 22, IC402175, 35-1, IC25105, AV-16, PKB3-1, 120P1-1-2, PKB4-4, ArkaSuman, PKB4-2, APC668-1, NBC25, C-720, NBC-38, 15P2-3, IC2591054, 13P1-2, Bhagya, UPC-5286 were found to be moderately resistant with severity ranging from 1.45 to 9.88 per cent.

Ten genotypes *viz*., 27, GC-3, IC2027, 27749(25), NBC-21, AV-7, PKB-2, PV-3, EC458473, Lola found to be moderately susceptible with disease severity ranging from 12 to 24.65 per cent and seven genotypes *viz*., PGCP-6, AV-5, 34,IC402104, PGCP-11,V-604-7-29-3, Genotype-36 were found to be susceptible with disease severity ranging from 26.77 to 48.75 per cent. The variety C-152 showed highly susceptible reaction for rust with per cent disease severity of 81.45.

The survey results revealed that highest average disease severity in Mandya taluk which may be due to availability of the

inoculums the environmental conditions that must have favored the development of inoculum that subsequently lead to increase in severity of rust. These results are in accordance with those reported by Abdullah *et al.,* (2011) where he observed the disease severity of 26.50 to 50.00 per cent in susceptible C-152 variety grown during *Kharif*-2008, 2009 and 2010 in Bengaluru, Dharwad, Mandya and Pattambi locations. Similar results were recorded by Hiremath *et al.,* (1987) wherein, he recorded a rust severity upto 90-100 per cent in *Kharif* season, caused by same pathogen species (*Uromyces ciceris-arietini*) in chickpea crop Further the data reveals the highest average disease severity during flowering stage of the crop. The results are in accordance with Negussie and Pretorius (2008) who reported that flowering stage of pea is most susceptible to rust disease caused by *Uromyces viciae-fabae* which found to affect the fertile flowers and hence, the number of pods formed.

The host plant resistance is an important choice in the management of crop diseases. As its use in farming is the very effective, simple and economical means in managing the disease. Therefore, identification of resistant sources forms one of the criteria in resistant breeding program. Over 300 races or pathotypes of rust are recognized indicating the broad variability of the rust fungus (Araya *et al.,* 2004). In the present study 57 genotypes of cowpea were screened for rust resistance under natural epiphytotic conditions. None of the genotypes showed immune reaction. However, genotypes C152×V16, 59, K4-2, PKB4-3, Kashiunnati, IC206240, PKB6-2, V-16, EC458483, PKB6-4, EC458480, KBC-2, IC402180, 21-2, IC58905 and IC249593were resistant. In general, over all disease incidence was very high. Similar results were also reported by Anilkumar *et al.,* 1989 and Kale (1992) wherein they observed that among 24 cowpea genotypes screened five genotypes showed immune reaction against rust and C-152 was found to be highly susceptible with 77.24 per cent disease severity. Similarly, Uma and Salimath (2003) also reported that some of varieties of cowpea, such as C-11, C-70 and KM-1 were highly resistant to rust disease.

Realizing the economic importance of the disease and that survey provides an extensive information about the disease severity, a survey on the disease severity was carried out in farmer's fields of Mandya district. Six taluks of Mandya district were surveyed and the disease severity ranged between 20.76 to 39.14 per cent, and that all the villages surveyed revealed the prevalence of the disease. Therefore, understanding the relationship between disease severity and yield loss is useful for the management of the disease.

The present work also demonstrates that the disease severity as high as 81.45 in the susceptible check C-152, thus revealing the important of this disease in cowpea. In this study, genotypes constituting a pool of varieties resistant to rust have been identified and conserved. Among the 57 genotypes, 16 of them were found to be resistant and 23 moderately resistant to the disease. Further research is recommended on the varieties mentioned above at different places for further reliability. Also that, comparison of plant yield with disease can be done.

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