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Influence of Crop Rotation on Disease Incidence and Population Dynamics of Ginger Wilt inciting Pathogen (*Ralstonia solanacearum)* under Organic Management Practice in Hill Zone of West Bengal

Rakesh Yonzone[1*], Surajit Khalko[2], B.R. Sharma[3], P.M. Bhattacharya[4], S. Bandyopadhyay[2], S. Hembram[5] and Bimal Das[6]
[1]Assistant Professor, Department of Plant Pathology,College of Agriculture (Extended Campus)
Uttar Banga Krishi Viswavidyalaya Majhian, Dakshin Dinajpur, (West Bengal), India.
[2]Associate Professor, Department of Plant Pathology, Uttar Banga Krishi Viswavidyalaya,
Pundibari, Coochbehar, (West Bengal), India.
[3]Professor, Regional Research Station (HZ), Kalimpong, (West Bengal), India.
[4]Professor, Department of Plant Pathology,
Uttar Banga Krishi Viswavidyalaya, Pundibari, Coochbehar, (West Bengal), India.
[5]Assistant Professor, Department of Plant Pathology,
Uttar Banga Krishi Viswavidyalaya, Pundibari, Coochbehar, (West Bengal), India.
[6]Assistant Professor, Department of Genetics and Plant Breeding,
College of Agriculture (Extended Campus), Uttar Banga Krishi Viswavidyalaya, Majhian, Dakshin Dinajpur, (West Bengal), India.

(Corresponding author: Rakesh Yonzone)*

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ABSTRACT: Bacterial wilt disease of ginger also known as "Green wilt disease" caused by *Ralstonia solanacearum* is one of the destructive pathogen causing huge yield losses. Ginger in hill zone of West Bengal are mostly grown organically and infection of *R. solanacearum* if accompanied by favorable environmental condition can result in complete failure of crop growth and production. Due to unavailability of proper organic management practices, farmers are now replacing cultivation of ginger with other crops. A field studies were carried out during 2019 and 2020 under organic management practices with the Rabi crops which are commonly grown in the hill-agro ecological region of West Bengal to determine the effect of ginger based cropping system on the *Ralstonia* population load, disease intensity and yield of the crop. Among the six (06) treatments under study ginger rotation with cabbage showed marked reduction in the population of *R. solanacearum* as compared to the population load in active tillering stage and disease incidence followed by ginger rotation with marigold in both the year. Correlation study of yield with pathogen population at different growth stages of crop indicated the significant negatively correlation. The analysis of pooled data of both the years also revealed the significant effect of ginger rotation with cabbage and marigold in minimizing the disease incidence and increasing the yield. Cabbage and marigold are mostly grown as rabi crops in hill zone, if these crops are incorporated and grown in rotation with ginger it can help in significantly reducing the population load of *R. solanacearum* and disease incidence thereby increasing the fresh rhizome yield.

Keywords: Bacterial wilt, *Ralstonia solanacearum*, Ginger, Crop rotation, Disease incidence.

INTRODUCTION

Ginger (*Zingiber officinale* Rose) is one of the most important commercial spice crop grown in tropical and subtropical area (Jibat and Alo, 2020) and is native to Indo- China region with its main center of diversity in Indo- Malaysia (Jansen, 1981). It is constrained by the diseases of various soil, rhizome, and air-borne pathogens (Rajan *et al.*, 2002) which may be bacteria, fungi, viruses, mycoplasma and nematodes (Paret *et al*., 2010; Sharma *et al*., 2010) that reduces the yield and earning of foreign exchange for the country. Among the various disease, Bacterial wilt caused by *Ralstonia solanacearum* (Smith) is throwing a new challenge among the farmers and scientist. It causes huge devastating losses once the field gets contaminated with the pathogen adding more loss if sufficient moisture and favorable temperature persists. Along with the infection of *R. solanacearum* the increase in losses can be associated with different factors such as varieties, improper cultural and management practices (Raghus 2011). *R. solanacearum* has a broad host range which includes 55 crops and wild species such as potato, tobacco, tomato, eggplant, banana, chili, bell pepper and peanut (Hayward 1991; Bekele *et al*., 2016). It is gram negative, rod shaped and may have one or more polar flagella (motile) or may not have any flagella (non-motile) which produces characteristic fluid smooth white colour colonies with red or pink central whirling pattern (Kadam 2017). The bacteria mostly enter through wounds and multiplies in xylem vesicles causing blockage and finally wilting of the host (Jibat and Alo, 2020). The inherent variability of *R. solanacearum* along with the strong influences of environmental conditions on development of resistance makes it very difficult in managing the disease. The use of chemical practices also for managing the disease is highly challenging in the hill areas since most of the farmers prefer organic management practices to suppress the pathogen. The chemical on the other hand are also very costly and has a hazardous effect not only on soil, but also on environment and quality yield of the ginger. To overcome this challenges of pathogen and disease caused by it crop rotation, prevention and utilization of resistant cultivars are the only solution (Lando, 2002). Therefore, it become very imperative to manage the disease utilizing locally available, ecofriendly management practices with crop-rotation with various commonly growing rabi season crops of the region.

MATERIALS AND METHOD

The entire experimental was conducted at the Farm, Regional Research Station (Hill Zone) of Uttar Banga Krishi Viswavidyalaya, Kalimpong, West Bengal on two consecutive seasons during 2019 and 2020. The experimental plot was ploughed twice with an indigenous plough and level off manually. During final land preparation FYM @ 20t/ha were thoroughly incorporated into the soil. The experiment was planned in taking ginger variety Gorubathaney in Random Block Design (RBD) with four (04) replications and plot size measuring 3 m× 1 m (3 sq. m). No other chemical fertilizer was added and the crop were completely raised organically following recommended package of practices. Altogether six treatment combination (Table 1) were undertaken following crop rotation with commonly grown crop in hills at different season.

Table 1: Treatment combination taken under study.

Treatments	Months		
	April-Oct	Nov-Jan	Feb-March
T1	Ginger	Cabbage	Fallow
T2	Ginger	Garden Pea	Fallow
T3	Ginger	Tomato	Fallow
T4	Ginger	Buck Wheat	Fallow
T5	Ginger	Marigold	Fallow
T6	Ginger	Fallow	Fallow

The rabi plant (mostly cabbage) were incorporated within the soil or left as such after final harvesting of the crop. Soil samples of approximately 250 gms were collected from the rhizosphere following the standard protocol. Plating and enumerated by diluting the bacterial suspension until it reached the dilution of 10^{-4} and grown on Triphenyl Tetrazolium Chloride (TTC) medium as described by at 30±2°C (Kelman, 1954).

The enumeration of the pathogen population was done before sowing, at active tillering and after harvesting of the ginger crop. Colonies were counted using a plate counter. The colonies once counted was multiplied by the appropriate dilution factor to determine the number of CFU/mL in the original sample. It was calculated as-CFU/mL original sample = CFU/plate × (1/mL plated) × dilution factor. The disease incidence was recorded after every fifteen (15) days interval viz., 70, 85, 100, and 115 days after sowing (DAS) and calculated as follow:

Percent Disease Incidence

$$= \frac{\text{No. of plants infected}}{\text{Total no. of plants examined}} \times 100$$

RESULT AND DISCUSSION

A. Estimation of R. solanacearum population by different crop rotation sequences in different growth stages of ginger field

The bacterial population density (*R. solanacearum*) was estimated for both the years (2019 and 2020) in different plant growth stages under different crop rotation sequences. Analysis of variance resulted significant variation among the six different crop rotation sequences (before sowing, active tillering and after harvesting) with different plant growth stages and rhizome yield of ginger. The mean initial population of the *R. solanacearum* in fallow sick soil ranged from 84.25 to 113.00cfu × $10^4$and 77.75 to 117.50 cfu × 10^4in 2019 and 2020, respectively under different growth stages (before sowing, active tillering and after harvesting) of ginger (Table 2).

The maximum population density of *R. solanacearum* was found during active tillering stage (ranging from 55.22 to 113.00 cfu × 10^4 in 2019 and 46.50 to 117.50 cfu × 10^4 in 2020) and minimum was before sowing(ranging from 47.75 to 84.25 cfu × 10^4in 2019 and 39.75 to 94.25 cfu × 10^4 in 2020) among different crop rotation sequences. All the six combinations of crop rotation treatments for management of *R. solanacearum* population density for two-year study in wilt sick soil revealed the reduction in bacterial population in almost all the crop sequences pattern over fallow ginger plot. Further there was a highly significant variation in *R. solanacearum* population due to interaction of different plant growth stages and treatment. After one rotation the population was significantly less in crop rotation Ginger-Cabbage sequences (47.25, 55.25, 48.25 in 2019 and 39.75, 46.50, 45.75 in 2020 in different growth stages viz., before sowing, active tillering and after harvesting of ginger, respectively) followed by Ginger-Marigold and

Ginger-Garden pea sequences. However, the population in other crop rotations was increased or changed slightly in different growth stages of ginger indicating ineffectiveness of these crop rotations in reducing the bacterial population. In the present investigation Ginger-Cabbage sequences, Ginger-Marigold and Ginger-Gardenpea sequences was found significant in reduced the *R. solanacearum* population density in soil indicating either cabbage or marigold should cab be included in the crop rotation sequence in hill cropping sequence with ginger.

Table 2: Influence of bacterial population (cfu ×10^{4}) of *R. solanacearum* by different crop rotation sequences in different growth stages of ginger field.

Treatments	2019			2020		
	Before sowing	Active Tillering	After Harvesting	Before sowing	Active Tillering	After Harvesting
T1-Ginger+Cabbage	47.75	55.25	48.25	39.75	46.50	45.75
T2-Ginger+Gardenpea	59.25	101.25	94.75	78.00	112.50	100.75
T3-Ginger+Tomato	70.00	104.25	104.50	84.25	106.00	99.00
T4-Ginger+Buckwheat	69.50	97.25	92.75	94.25	109.75	89.50
T5-Ginger+Marigold	56.00	71.75	56.25	65.50	74.50	52.50
T6-Ginger(fallow)	84.25	113.00	107.25	77.75	117.50	104.25
C.D. (5%)	13.94	15.90	13.66	18.73	20.70	12.44
SE(m)	4.58	5.23	4.49	6.16	6.81	4.09
SE(d)	6.48	7.39	6.35	8.71	9.62	5.78
C.V.	14.22	11.55	10.70	16.81	14.41	9.98

B. Estimation of disease incidence and rhizome yield under different crop rotation sequences

All the six treatment under study of crop rotation sequences indicated significant effect on disease incidence caused by *R. solanacearum* and rhizome yield of ginger in both the season 2019 and 2020 (Table 3). The bacterial wilt incidences were recorded after every 15 days of interval (70, 85, 100 and 115 days) from the active tillering stages of ginger. A significant variation in bacterial wilt disease incidence percentage was recorded among all the six different treatments at different growth stages of ginger ranging from 16.88% to 72.50% in 2019 and from 14.38% to 68.75 % in 2020 after final recording at 115 DAS. Maximum disease incidence was observed under fallow ginger cultivation (72.50% and 68.75% in 2019 and 2020), whereas minimum disease incidence was recorded under Ginger-Cabbage cropping sequences (16.88% and 14.38% in 2019 and 2020, respectively) followed by Ginger-Marigold (27.50% and 23.75% in 2019 and 2020, respectively) and Ginger-Buckwheat (49.38% and 44.38% in 2019 and 2020, respectively) cropping sequences in both the season. Rotations involving Ginger - Cabbage gave higher rhizome yield (3.08 and 3.22 Kg plot^{-1} in 2019 and 2020, respectively) compared to the other treatments in both the season of ginger cultivation (Table 3). The rhizome yield was minimum in fallow ginger plot (0.76 and 0.93 Kg plot^{-1} in 2019 and 2020, respectively) followed by Ginger-Tomato cropping sequence (1.01 and 1.34 Kg plot^{-1} in 2019 and 2020, respectively) in both the seasons. The pooled analysis (Fig. 1) also signifies the greater effect of Ginger – Cabbage rotation sequence in reducing the population dynamics, disease incidence and increase the rhizome yield.

Table 3: Effect different crop rotation sequences on ginger wilt incidence (PDI) different days after sowing (DAS) and rhizome yield.

Treatments	70(DAS)		85(DAS)		100(DAS)		115(DAS)		Yield (Kg/Plot)	
	2019	2020	2019	2020	2019	2020	2019	2020	2019	2020
T1-Ginger+Cabbage	3.13 (1.94)	0.63 (1.22)	6.25 (2.64)	5.00 (2.42)	10.63 (3.36)	9.38 (3.19)	16.88 (4.22)	14.38 (3.90)	3.08	3.22
T2-Ginger+Gardenpea	10.00 (3.31)	6.88 (2.80)	18.75 (4.43)	11.25 (3.48)	26.88 (5.27)	20.00 (4.54)	51.25 (7.22)	48.75 (7.03)	1.28	1.46
T3-Ginger+Tomato	13.13 (3.76)	11.88 (3.58)	20.63 (4.64)	19.38 (4.51)	40.00 (6.39)	37.50 (6.19)	65.00 (8.11)	60.63 (7.83)	1.01	1.34
T4-Ginger+Buckwheat	8.75 (3.12)	6.25 (2.68)	15.00 (3.99)	9.38 (3.21)	24.38 (5.03)	18.13 (4.36)	49.38 (7.09)	44.38 (6.72)	2.04	2.09
T5-Ginger+Marigold	6.25 (2.68)	5.00 (2.42)	9.38 (3.21)	8.13 (3.00)	15.63 (4.06)	13.13 (3.74)	27.50 (5.31)	23.75 (4.95)	2.56	2.84
T6-Ginger(fallow)	13.13 (3.75)	12.50 (3.64)	28.75 (5.44)	23.13 (4.90)	45.00 (6.77)	41.88 (6.52)	72.50 (8.57)	68.75 (8.34)	0.76	0.93
C.D.	0.50	0.42	0.65	0.43	0.72	0.59	0.66	0.65	0.08	0.05
SE(m)	0.16	0.14	0.22	0.14	0.24	0.20	0.22	0.21	0.03	0.02
SE(d)	0.23	0.19	0.30	0.20	0.33	0.28	0.31	0.30	0.04	0.02
C.V.	10.61	10.02	10.57	7.87	9.13	8.19	6.45	6.59	3.32	1.91

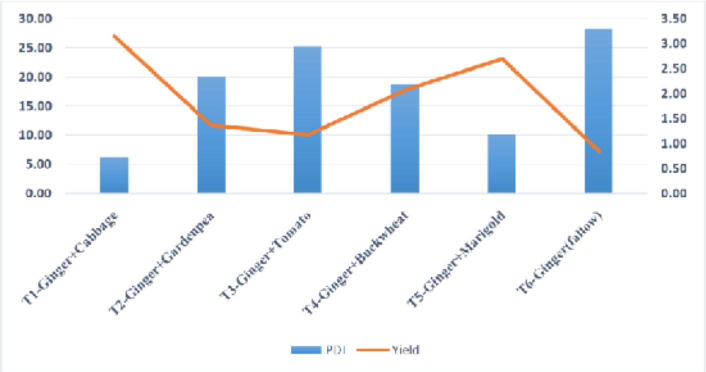

Fig 1: Effect of crop rotation on disease incidence and yield of ginger.

C. Correlation of R. solanacearum population density, disease incidence and rhizome yield of ginger

The correlation coefficient analysis of *R. solanacearum* population density under different growth stages (before sowing, active tillering and after harvesting) resulted significant and positive correlation with *R. solanacearum* disease incidence and significant and negatively correlated with rhizome yield of ginger in both the seasons (Table 4 and 5). On the other hand, rhizome yield was found to be significantly and negatively correlated with percentage of disease incidence (Table 3 and 4). This may due to changes in population density of *R. solanacearum* under different growth stages that causes higher *Ralstonia* infection of ginger field.

Table 4: Estimation of correlation coefficient with population density of *R. solanacearum*, disease incidence and yield of ginger (2019).

	BS	AT	AH	PDI	Yield
BS	1.00				
AT	0.877*	1.00			
AH	0.857*	0.985**	1.00		
PDI	0.919**	0.976**	0.978**	1.00	
YIELD	-0.825*	-0.957**	-0.949**	-0.972**	1.00

*=significant at the 5% level and **= Correlation is significant at the 1% level
[BS=Before sowing; AT= Active Tillering; AH=After harvesting; PDI= Percent disease incidence]

Table 5: Estimation of correlation coefficient with population density of *R. solanacearum*, disease incidence and yield of ginger (2020).

	BS	AT	AH	PDI	Yield
BS	1.00				
AT	0.906*	1.00			
AH	0.835*	0.959**	1.00		
PDI	0.844*	0.912*	0.953**	1.00	
YIELD	-0.805*	-0.917**	-0.968**	-0.985**	1.00

*=significant at the 5% level and **= Correlation is significant at the 1% level
[BS=Before sowing; AT= Active Tillering; AH=After harvesting; PDI= Percent disease incidence]

D. Stepwise regression analysis of disease incidence with population density of R. solanacearum

The multiple regression results presented in Table 6 clearly depicts relationship that exists between the disease incidence and population dynamics with coefficient of determination of 0.981 and 0.911 at different growth stages of ginger crop during both the season of 2019 and 2020 (Fig. 2 and 3). The coefficient of determination generally signifies the fitness of regression equation and indicates proportion of variation in dependent variable Y (disease incidence) explained by independent variables X (population dynamics at different grow stages of crop) for a linear regression model.

Table 6: Multiple regression of population dynamic with the intensity of bacterial wilt.

Year	Model	R²	Adjusted R²	F Value	MSE
2019	**Y=** -37.54+0.484(BS)+0.095(AT)-0.534(AH)	0.981**	0.954	35.90	20.82
2020	**Y=**-16.90-0.177(BS)+0.185(AT)+0.681(AH)	0.911**	0.779	6.90	96.75

**= Correlation is significant at the 1% level

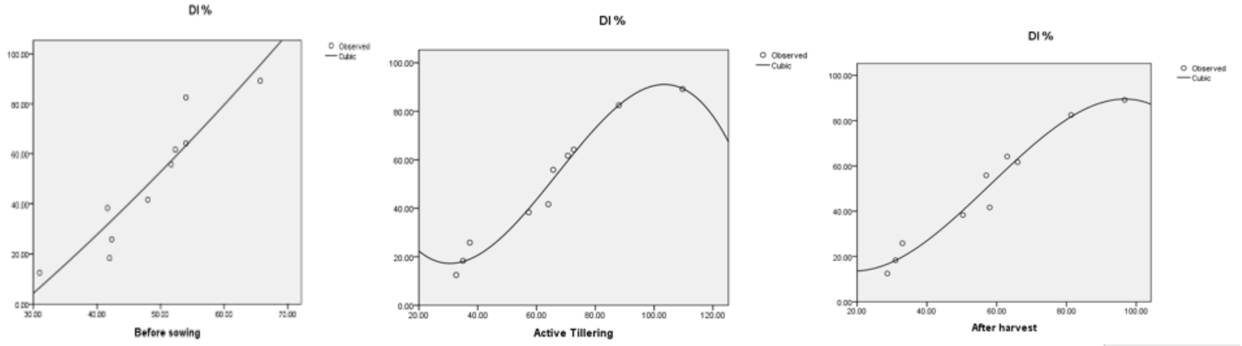

Fig. 2. Disease incidence predicted versus population density at different crop growth stage (2019).

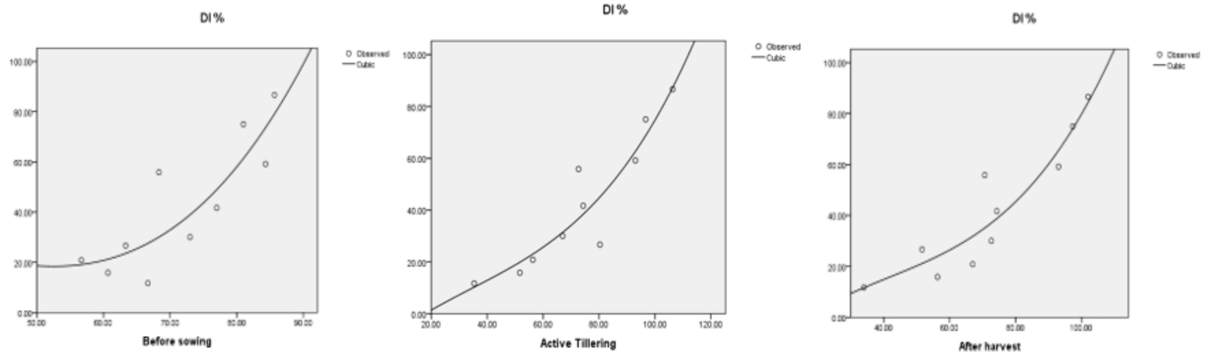

Fig. 3. Disease incidence predicted versus population density at different crop growth stage (2020).

Similar reports of effectiveness in managing soil borne pathogens through crop rotation with Brassica plant such as cabbage have also been reported by many workers. The reduction of *R. solanacearum* population and disease incidence might be through the process of bio fumigation. It is an eco-friendly approach for management of soil borne pathogens where brassica plants are either crop rotated or used as a green manuring crop (Gopi *et al.*, 2016). The pathogen suppression is due to the release of various compounds such as glucosinolates and is othiocyanates by plant which are effective against the pathogen (Kirkegaard *et al.*, 1993). Our finding is in conformity with the work done by Wang *et al.*, (2014) where he reported the effective suppression of soil borne pathogens through bio fumigation using brassica plant. Similar management through bio fumigation also includes the work done by Ojaghian *et al.*, (2012) to overcome *Sclerotinia sclerotiorum*, Neubauer *et al.*, (2014) for managing *Verticillium dahlia* where he found 69.3 to 81.3% efficiency in reduction of the population. The effectiveness of biofumigation with oil against *R. solanacearum* has also been reported by Alves *et al.*, (2014). The effectiveness of biofumigation with cabbage in managing soil borne *R. solanacearum* has also been reported by Bandyopadhyay and Khalko (2016).

CONCLUSION

The results obtained from the above experiment shows that the ginger rotation with cabbage and marigold had a significant influence in reducing the *R. solanacearum* population, minimizing disease incidence and increasing the rhizome yield of ginger. Therefore, these crops can be incorporated in cropping sequence to order reduce the disease incidence of *R. solanacearum* under organic management practices.

FUTURE SCOPE

The actual mechanism involved in controlling the *R. solanacearum* population and the beneficial microorganism that are favored by these cropping sequence under organic management practices need to be determined.

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Conflict of interest. All authors have no conflict of interest.

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