

Evaluation of Impact of Infection with *Pseudomonas syringae* pv. *syringae* on Biochemical Constituents and Enzymatic Activity in Pearl Millet [*Pennisetum glaucum* (L.) R. Br.] Seeds

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Abstract

It is crucial to provide access to affordable indigenous food sources as alternative to traditional food in order to combat under nutrition and improve food security. Pearl millet crop suffers from many serious diseases of which bacterial brown spot disease caused by *Pseudomonas syringae* pv. *syringae* (*Pss*) is an important disease in pearl millet crop. The current study, the biochemical as well as physiological alterations brought about by naturally occurring *Pss* infection in seed samples of pearl millet collected through various areas of Marwar region in Rajasthan were evaluated. Diseased seed samples had considerably higher protein value compared with healthy check samples but lower values of moisture, crude fiber, crude fat, total carbohydrate and total soluble sugar content. The seed samples infected with *Pss* showed a significantly rise in total phenols and in defense enzymes viz catalase, polyphenoloxidase and peroxidase. The findings show that *Pss*-host interaction disrupts host metabolism and several protective enzymes as well as secondary metabolites produce symptoms on pearl millet seeds. The results show the change in biochemical constituents of seeds due to *Pss* infection in pearl millet.

Key words: Food security, *Pseudomonas syringae* pv. *syringae* (*Pss*), Pearl millet, Marwar region, Defense enzymes

Asia and Africa continents are where pearl millet is most commonly farmed. It is one of the ancient edible crops in the world and is native to the Sahalian region of African continent [1]. Rajasthan, Maharashtra, Gujarat, Haryana and Uttar Pradesh are major producing states in India [2]. In Rajasthan, Barmer district is a largest sowing area but Alwar district is major producing area of pearl millet. Depending on the location and people's dietary preferences, it is consumed in numerous cuisine forms in India. In the recent years, interest of people are being increased for using pearl millet due to absence of gluten [3] presence of minerals (Ca, Fe, Zn, Mg), vitamins C & B-complex and low glycemic index [4] useful phenolic acid (trans-cinnamic, gentisic, caffeic, p-coumaric) [5] and high level of fiber [6]. The seeds are remarkable source of natural antioxidants for preventing contagious as well as non-contagious diseases and supporting good health due to the abundance of bioactive chemicals and phenols [7-9].

There are many pathogens that affects pearl millet but *Pseudomonas syringae* pv. *syringae* (*Pss*) causing bacterial brown spot or brown spot disease is one of the most significant one. The oozing, yellow to brown rotting on margins of leaf

and necrotic symptoms on the plant are the major symptoms which lead to a significant yield loss [10-11]. Changes in the host plant's metabolism are common occurrence following pathogen invasion and these changes are linked to certain important biochemical abnormalities in tissues of host. Additionally, plants produce enzyme like pathogen related (PR) protein and derivatives of phenolic substances in an effort to defend their cells against the pathogens by initiating a series of defense response mechanism [12]. It is clear from the biophysiological changes in the host that the changed host metabolism caused by pathogenic infection can be detected including defense-enhancing enzyme production viz. catalase, peroxidase, polyphenol oxidase and other secondary metabolites [13-14].

It becomes necessary to quantify the ash, moisture, fiber, fat, protein, carbohydrate and enzyme levels in order to have proper insight of the interaction between host and the pathogen. Therefore, an effort has been undertaken to research the modifications in biochemical constituents of healthy and diseased pearl millet seeds having *Pss* infection.

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MATERIALS AND METHODS

Isolation and categorization

Seed samples of pearl millet collected from Jodhpur, Barmer, Jaisalmer, Jalore, Nagaur and Pali districts of Rajasthan, India were categorized into healthy (accession numbers PM-13, PM-44 and PM-92) and infected (accession numbers PM-17, PM-32 and PM-67) on the basis of exomorphic symptoms such as shriveling, rotting and browning on seed coat on investigation of dry seeds. After being sterilized with solution of 2% of sodium hypo chlorite, the samples were placed directly on nutrient agar (NA) medium and King's B agar medium, kept in an incubator at 28 ± 2 °C for 2 days. Group of bacterial cells exhibiting *Pss*-specific characteristics were purified on NA by using the technique of re-streaking. The pure colonies were subjected to biochemical assays and confirmed by host-pathogen test on pearl millet and other plants.

Biochemical changes

Three seed samples each of healthy (check) and diseased pearl millet was used for estimation of biochemical changes.

The standard methods were used [15-18] for estimation of the content. 10 g powder of seeds of pearl millet was taken and dried in hot air oven at 110 °C. Crude fat estimation action was done in moisture free 2 g powder of seeds by Soxhlet apparatus through solvent extraction method. Crude fiber was estimated by using 2 g moisture and fat free powder of seeds using alkali wash method. Kjeldahl method was used for estimation of nitrogen content present in dry seed powder.

Ash was estimated by dry ashing method using muffle furnace. The total content of carbohydrates was calculated by difference = $100 - (\text{ash}\% + \text{crude fat}\% + \text{moisture}\% + \text{total protein}\% + \text{crude fiber}\%)$ [2] [16] [19].

Total phenol content estimation by Folin's Ciocalteu phenol reagent method was done. The procedure based on the production of a blue color as a result of the interaction between phenol and oxidizing agent phosphomolybdate. In a

spectrophotometer, the reaction's absorbance of blue color at 670 nm was measured. Similarly, a blank was prepared by using of distilled water. A standard graph and solution of standard phenol (50µg/ml) were used to calculate the quantity of total phenol content [16] [20-21].

Enzymatic activity

Each sample of 300 mg of incubated seeds using standard blotter method were milled in 3 ml of 0.1 M sodium phosphate buffer at pH 6.5. The supernatant from the centrifugation of homogenate for 15 min at 10000 rpm for 4 °C was utilized for an enzyme assay. The solution of 0.2 ml hydrogen peroxide (0.2M) was added into cuvette, measurement of the sample taken at 470 nm in spectrophotometer. The initial absorbance A_0 was measured and then again at intervals of 30 sec. to record activity of peroxidase [22-23].

Similarly, the change caused by the oxidized catechol was recorded at 420 nm every 30 sec. for five minutes to estimate polyphenol oxidase activity [22] [24-25].

A method described by [26] was used to assess the enzyme catalase. The solution of 0.1 M of 2.7 ml phosphate buffer at pH 6.5 and stored at 4 °C. The enzyme was measured by using of spectrophotometer at 250 nm for 2 min on every 15 second interval.

RESULTS AND DISCUSSION

The samples taken from diverse fields of the Marwar region Rajasthan showed that the pearl millet seeds had varying degrees of infection and showed substantial alteration in their biochemical constituents. In the current investigation, the three selected infected seed samples had lower moisture contents (4.90) than the healthy (check) samples (6.41) (Table 1). The three pearl millet seed samples that were affected with the disease had a greater protein content in comparison to check healthy samples (Table 1).

Table 1 Changes in biochemical constituents of pearl millet seeds due to *Pseudomonas syringae* pv. *syringae* infection

Biochemical constituents										
S. No.	Sample accession No.	Replicates of samples	Moisture (%)	Crude fiber (%)	Crude fat (%)	Crude protein (%)	Ash (%)	Total carbohydrate (%)	Total soluble sugar (%)	Phenol (%)
Check samples										
(i)	PM-13	R ₁	6.54	2.97	1.73	7.71	1.08	61.42	48.25	1.86
		R ₂	6.29	2.66	2.19	7.54	1.21	62.23	49.49	2.71
		R ₃	5.83	3.22	1.48	7.87	1.34	63.75	51.57	2.68
(ii)	PM-44	R ₁	4.69	3.96	2.29	6.31	1.17	59.32	43.26	1.82
		R ₂	4.91	4.17	2.47	6.12	1.34	57.21	45.97	1.64
		R ₃	5.11	3.28	1.63	5.94	0.91	58.93	45.89	1.95
(iii)	PM-92	R ₁	7.75	4.57	2.70	6.67	1.91	67.12	53.41	1.79
		R ₂	8.49	4.92	1.95	6.54	2.13	65.44	52.37	2.14
		R ₃	8.12	5.13	2.61	7.29	1.61	65.31	54.19	1.63
	Mean		6.41	3.88	2.12	6.89	1.41	62.30	49.38	2.02
	SD		1.428	0.889	0.442	0.726	0.399	3.376	3.802	0.410
	SEM		0.476	0.296	0.147	0.242	0.133	1.125	1.267	0.137
Infected seed samples										
(i)	PM-17	R ₁	4.41	1.62	1.15	10.25	1.72	47.11	38.83	2.92
		R ₂	4.74	1.85	1.21	9.87	2.29	49.93	37.95	3.52
		R ₃	5.06	2.32	1.49	10.32	1.93	48.84	38.59	3.24
(ii)	PM-32	R ₁	6.29	1.96	1.29	6.91	1.19	52.62	40.86	2.42
		R ₂	5.31	2.32	0.84	7.25	1.66	53.41	42.11	1.91
		R ₃	5.64	1.83	0.97	7.47	1.49	52.96	41.34	2.72
(iii)	PM-67	R ₁	4.25	3.17	1.50	8.67	2.31	46.12	34.71	2.79
		R ₂	3.89	2.64	1.76	8.32	1.27	44.33	35.39	3.34
		R ₃	4.51	2.79	2.03	9.71	2.36	44.41	34.85	2.83

Mean	4.90	2.28	1.36	8.75	1.80	48.86	38.29	2.85
SD	0.753	0.514	0.377	1.340	0.448	3.600	2.830	0.492
SEM	0.251	0.171	0.126	0.447	0.149	1.200	0.943	0.164
Difference (2-1)	-1.51	-1.60	-0.76	1.86	0.39	-13.44	-11.09	0.83
SEd	0.538	0.342	0.194	0.508	0.200	1.645	1.580	0.213
t- Value	2.815	4.669	3.905	-3.671	-1.955	8.172	7.017	-3.888
DF	16	16	16	16	16	16	16	16
P	0.012	0.000	0.001	0.002	0.048	0.000	0.000	0.001

SD- Standard deviation; **SEM-** Standard error of mean; **SEd-** Standard error of difference; **DF-** degree of freedom

Table 2 Changes in enzymatic activity in seeds of pearl millet naturally infected with *Pseudomonas syringae* pv. *syringae*

Enzymatic activity					
S. No.	Sample accession No.	Replication of samples	Peroxidase	Polyphenoloxidase	Catalase
Check (Healthy seed samples)					
1	PM-13	R ₁	0.776	0.043	0.328
		R ₂	0.947	0.021	0.295
		R ₃	0.832	0.034	0.341
2	PM-44	R ₁	0.610	0.031	0.457
		R ₂	0.665	0.059	0.463
		R ₃	0.583	0.026	0.449
3	PM-92	R ₁	1.198	0.033	0.211
		R ₂	1.251	0.051	0.194
		R ₃	1.173	0.064	0.236
	Mean		0.893	0.040	0.330
	SD		0.262	0.015	0.107
	SEM		0.087	0.005	0.036
Sample naturally infected					
1	PM-17	R ₁	1.315	0.469	1.248
		R ₂	1.617	0.527	1.574
		R ₃	1.421	0.374	1.423
2	PM-32	R ₁	2.983	0.722	1.057
		R ₂	2.861	0.569	1.113
		R ₃	3.103	0.647	1.147
3	PM-67	R ₁	2.121	0.313	2.031
		R ₂	1.703	0.426	1.989
		R ₃	1.896	0.388	1.763
	Mean		2.113	0.493	1.483
	SD		0.696	0.135	0.376
	SEM		0.232	0.045	0.125
	Difference (2-1)		1.221	0.453	1.152
	SED		0.248	0.045	0.130
	t- Value		-4.925	-9.998	-8.838
	Df		16	16	16
	P		0.000	0.000	0.000

SD- Standard deviation; **SEM-** Standard error of mean; **SEd-** Standard error of difference; **DF-** degree of freedom

The crude fat content of seed samples analyzed has decreased. This decrease may be due to the lipid molecule being break down by lypolytic activity. Similar research has been published on *Pss* infected sunflower plant [27] and in barley [28]. In the current investigation, the infected seed samples had lower crude fiber contents than the healthy (check) samples (Table 1). Similar kind of results observed in various microbe infected pearl millet [29] and in Ajwain seeds compromised with pathogenic attack [30]. The lower value of crude fiber may be due to decomposition of cellulose during cellulolytic activity [31]. The infected seed samples had lower in total carbohydrate and total soluble sugar contents than the healthy (check) samples (Table 1). The ability of the pathogen to regulate itself own unique method to consume host carbohydrates consequently, the ratio of sucrose to hexose may gradually decline [32]. Similar carbohydrate reduction outcomes were observed in peanut [33] and cowpea [34]. The decline in total soluble sugar in *S. orientale* L. have been also reported [35].

The infected seed samples had increase in total phenols than the healthy (check) samples (Table 1). In earlier investigation, a protein that help in defense mechanism also known as pathogen related (PR) protein synthesized the host by pearl millet [36]. PR proteins commonly known as first line defense immune response and increases in production during biotic stress condition [12]. It was also observed in bacterial infected *Capsicum annum* [37]. Phenolics are naturally existing plant molecules that are widely known for their antibacterial activities and ubiquitination [38]. Increase in phenolic substances was found to be significantly greater in infected pearl millet seed samples than in check samples (Table 1). Numerous studied have examined the rise in phenolic components in crop caused by microbes' infection. Phenolic compounds secreted against *Pss* and pathovars of *Pseudomonas syringae* in infected plants such as in sweet cherry [39] and in *Arabidopsis thaliana* [40] have been reported.

An efficient plant defense system against pathogen attack is demonstrated in the current investigation by study on enzymatic activity. The infected seed samples of seeds showed noticeably higher catalase (1.483), peroxidases (2.113) and polyphenyl oxidases (0.493) as compared to healthy check samples (0.330), (0.893) and (0.040) respectively (Table 2). Catalase (CAT), polyphenol oxidase (PPO), peroxidase (POD), and chitinase are most significant defense enzymes found to defend plants from biotic stress [41]. Stressed plants go through a number of inherent equilibrium for initial stress step sensing, including signal cascade, expression of genes and metabolic alterations of defense chemicals to avoid unfavorable situations [42]. Additionally, increased phenylalanine lyase (PAL) and superoxide dismutase (SOD) activity in infected cells as well as the accumulation of phenolic contents in highly diseased tissue [43]. Similar findings have been also found in tobacco [44], soyabean [25] and rice [45] due to the involvement of oxidative enzymes in the defense system that caused these plants to react against pathogenic infection. The high CAT, PPO and POD activities can be attributed to their probable function in the first line of defense, which alters secondary metabolism and eventually lead in order to resist the pathogens [46]. These enzymes have been found located in the seed coat, endosperm and cotyledon of seeds [47-49].

CONCLUSION

The pathogen's capacity to successfully enter host cells to occupy the space of apoplastic region as well as cytosol is used evaluated the effects of infection on the host crop and emergence a chain reaction of bio-physiological changes in the crop's overall system that also activates its defenses. Each form of host-pathogen interaction type affects the start and appearance of every defensive molecule in response to each pathogen invasion. These protective and defensive biochemical investigations together with research on other biochemical constituents (crude fiber, fat, carbohydrate, total soluble sugars) can be used as indicator to track infections. The present research work has shown that the chemicals that actively participate in the defensive mechanism of pearl millet seeds against *Pss* are total protein, phenolic compounds, PPO, POD and CAT. Therefore, it can be concluded that when *Pss* comes into contact with seeds of pearl millet, there is correlation between variance in these biochemical constituents, enzymes and the development of disease.

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