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Effect of silicon on soil micro flora in rice

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Abstract
The field experiment conducted during kharif 2017 at the Department of Entomology, College of Agriculture, OUAT, Bhubaneswar on the efficacy of silicon applied on rice through inorganic and organic sources either alone or in combination with bio fertilizers on dehydrogenase and microbial population revealed that out of twelve treatments the treatment RHA+PF+KSB and CaSiO 3 +PF+KSB supported higher population of bacteria, CaSiO 3 +KSB and RHA+KSB supported higher population of fungus and CaSiO 3 +PF+KSB and CaSiO 3 +PF supported higher population of actinomycetes, RHA+PF+KSB and RHA+KSB treatments contained higher amount of dehydrogenase activities at vegetative and reproductive stage, respectively. The total bacteria, fungal and actinomycetes population was positively and significantly correlated to dehydrogenase activity at both the stages of rice crop.

Keywords: Soil, silicon, micro flora and dehydrogenase

Introduction
Rice is the staple food of people of India for which rice cultivation will go on for many more years to come. The rice grain yield largely depends upon the availability of nutrient and nutritional availability greatly depends upon the congenial Physio-chemical properties of soil. Moreover, such conducive properties of soil are reflected due to microbial activity following application of fertilizer and other amendments in soil. Silicon is one source essential element which on application in rice improves the soil characteristics and augments the availability of other nutrient to the crop. With this background, attempt was made to study the effect of silicon on various micro floral activity in soil and subsequent dehydrogenase activity.

Methods and Materials
The field experiment was taken up during *kharif*, 2017 at the Research Farm of Department of Entomology, College of Agriculture, OUAT, and Bhubaneswar. A total of twelve treatments including a control involving both organic and inorganic sources of silicon were applied in rice either alone or in combination with various bio fertilizers and the details of the treatments has been presented in Table 1. The experiment was laid out in RBD with rice variety TN1 and each replication was replicated thrice. Seedlings of TN1 were raised as per the agronomic recommendation and twenty one days old seedlings were transplanted in main field after adequate puddling and levelling. All the treatment components were added in soil as basal application with recommended dose of fertilizers. Soil samples were collected at vegetative state (60 DAT) and before harvesting stage (80 DAT) for enumeration of total bacterial, fungal and actinomycetes population.

Bacterial population
Enumeration of bacteria was carried out in soil extract agar medium using standard dilution plating technique. One gram g of soil sample was serially diluted by 10 fold series using sterile water blank up to 10^{-6} and one ml of aliquot from 10^{-6} dilution was taken and dispensed in sterile petri-plates with soil extract agar medium. The bacterial colonies were enumerated after 48 hrs of incubation at 37 °C and expressed as number of cfu/g dry weight of soil (James, 1958) [3].

Fungal population
Enumeration of fungi was carried out in Rose Bengal Agar medium. One gram of soil sample was serially diluted by 10 fold series using sterile water blank up to10^{-4} and one ml of aliquot from 10^{-4} dilution was taken and dispensed in sterile petriplates with Rose Bengal Agar medium. The fungal colonies were enumerated after 3 days of incubation at 37°C and expressed as number of cfu/g dry weight of soil (Parkinson, *et al.*, 1971) [4].

Actinomycetes population

Enumeration of actinomycetes was carried out in Kenknight's Agar medium. One g of soil sample was serially diluted by 10 fold series using sterile water blank up to 10^{-5} and one ml of aliquot from 10^{-5} dilution was taken and dispensed in sterile petriplates with Kenknight's Agar medium. The actinomycetes colonies were enumerated after 4 days of incubation at 37 °C and expressed as number of cfu/g dry weight of soil (Wellingtonn and Toth, 1963) [6].

Dehydrogenase activity

The dehydrogenase activity was also assessed in laboratory from same soil samples. DHA assessment was done by following the laboratory procedure developed by Casida *et al*. (1964) [1]. The specific dyes such as the triphenyltetrazolium chloride (TTC) specifying the flow of electrons were utilized as indicators of electron transport system (ETS) activity. By the reduction of colorless, water soluble substrate (TTC) by dehydrogenases present in the soil sample, an insoluble product with red color (Triphenylformazan-TPF) was formed. TPF was then quantified calorimetrically at the range of visible light (485 nm). It was presumed that if the red colors of soil samples prepared for spectrophotometer analyses are more intensive, then the measured level of DHA is higher. Consequently, soil samples without red colors or those with light red color were characterized by lower DHA values.

Results and Discussion

Effect of silicon and bio-fertilizers on microbial activity of soil

The data on total bacteria, fungal and actinomycetes population from soil samples collected and analysed both at vegetative and reproductive stage under the influence of various treatments imposed during period of study has been presented in Table 1. A perusal of data from Table 1 indicated that the treatment T_8, T_7 and T_5 supported higher bacterial population (41×10^6, 40×10^6 and 35×10^6 cfu/ g soil) at vegetative stage having no difference between themselves whereas, at reproductive stage, T_5 supported a population of 31×10^6 cfu/ g soil followed by T_8 (30×10^6 cfu/ g soil) and T_3 (28×10^6 cfu/ g soil). It was observed that bacteria population marginally decreased in some treatments whereas, in some other, it was drastically reduced. However, the control treatment which supported 24×10^6 cfu/ g soil and 20×10^6cfu/ g soil at vegetative and reproductive stage, respectively was at par with a number of treatments. It can be stated that organic source of silicon with bio-fertilizers supported higher bacteria population as compared to inorganic source of silicon and bio-fertilizers. It was evidenced from the same Table that total fungal population was more in T_4 (21×10^4cfu/ g soil) followed by T_8 (20×10^4cfu/ g soil) and T_3 (19×10^4cfu/ g soil), respectively. The control treatment supported 11×10^4 cfu/ g soil at vegetative stage which was significantly different from above treatments. At reproductive stage, T_7, T_8 and T_3 were better treatments in order of efficacy and remained superior over control and the treatments consisting of only bio-fertilizers. As regards to total actinomycetes population at vegetative stage it can be seen from Table 1 that T_5, T_4 and T_3 were favourable treatments for actinomycetes (40×10^4cfu/ g soil, 39×10^4cfu/ g soil and 37×10^4cfu/ g soil). Other treatments like T_8, T_1 and T_2 were also at par with former three treatments. However, the control treatment supporting 22×10^4 cfu/ g soil actinomycetes population was only at par with T_{11} (24×10^4cfu/ g soil). At pre harvesting stage there was a change in order of efficacy among the treatments. The treatment T_3 supported (33×10^4 cfu/ g soil) population followed by T_6 (31×10^4 cfu/ g soil) and T_8 (30×10^4 cfu/ g soil).

Dehydrogenase activity

The dehydrogenase activity being influenced by Si and bio-fertilizers recorded from soil samples (*kharif*, 2017) has been presented in Table 2. The dehydrogenase activity was found to be maximum in T_8 (51.07 µg TPF/g/hr) followed by T_7 (49.44 µgTPF/g/hr) and T_5 (46.99 µg TPF/g/hr) having no significant difference among themselves. Similarly at reproductive stage, T_7 had the highest dehydrogenase activity (40.04 µg TPF/g/hr) followed by T_5 (36.77 µg TPF/g/hr) and T_6 (33.09 µg TPF/g/hr) in which T_7 was at par with T_5 but the treatment T_5 was at par with T_6,T_4, T_8 and T_3 treatments. It can be stated that dehydrogenase activity was the resultant effect of higher microbial activity in soil and silicon amendments from organic source (RHA) favoured more microbial activity than inorganic source ($CaSiO_3$).

Correlation between soil dehydrogenase activity and microbial activity

It can be observed from the Table 3 that the total bacteria population was positively and significantly correlated to dehydrogenase activity at vegetative stage of the crop (r=0.865) and only positively correlated at reproductive stage (r=0.547). Similarly, the total fungal population was positively and significantly correlated with dehydrogenase activity both at vegetative and reproductive stage (r=0.637 and r=0.707, respectively). The actinomycetes population was also observed to be positively correlated with dehydrogenase activity at vegetative stage (r=0.427) and significantly and positively correlated at pre harvest stage (r=0.655).

From the entire investigation it can be witnessed that the treatment T_8 was a common treatment which favoured higher population of all the three types of microbes observed under study. Dehydrogenase activity in soil due to microflora under the influence of silicon has been referred in Table 2. It was observed that organic source of silicon supplemented with bio fertilizers caused enhanced dehydrogenase activity. At both the crop stages, T8 (RHA+PF+KSB) caused higher concentration of dehydrogenase in soil samples. Higher dehydrogenase activity is the outcome of higher micro floral activity. Quilchno and Maranon, 2002 [5] ; Gu *et al.*, 2009 [2] have opined in the same line that among all the enzymes in soil dehydrogenases are most important and used as an important indicator of soil microbes activity. The correlation study between various microflora and dehydrogenase activity (Table 3) also indicated significant positive relationship and the strengthened our finding.

Table 1: Effect of silicon and bio fertilizers application on the microbial activity of soil during *kharif*, 2017

	Treatments	Total bacterial population (data $\times 10^6$ cfu per g of soil)		Total fungal population (data $\times 10^4$cfu per g of soil)		Total actinomycetes population (data $\times 10^5$ cfu per g of soil)	
		Vegetative stage (60 DAT)	Before harvest (80 DAT)	Vegetative stage (60 DAT)	Before harvest (80 DAT)	Vegetative stage (60 DAT)	Before harvest (80 DAT)
T_1	$CaSiO_3$	27	19	13	10	35	24
T_2	RHA	25	22	12	11	32	20
T_3	$CaSiO_3$ + Pf	30	28	19	13	37	33
T_4	$CaSiO_3$+KSB	26	23	21	11	39	26
T_5	$CaSiO_3$ + Pf + KSB	35	31	16	10	40	28
T_6	RHA + Pf	33	26	15	12	29	31
T_7	RHA + KSB	40	21	17	15	33	29
T_8	RHA + Pf + KSB	41	30	20	14	36	30
T_9	Pf	31	20	13	9	30	23
T_{10}	KSB	30	23	14	12	31	27
T_{11}	Pf + KSB	29	21	12	9	24	25
T_{12}	Control	24	20	11	8	22	14
	SE(m) ±	2.351	1.806	1.151	0.848	2.345	1.808
	CD (P = 0.05)	6.89	5.29	3.37	2.48	6.87	5.30

Table 2: Effect of silicon and bio fertilizers application on the dehydrogenase activity of soil during *kharif*, 2017

Sl. No	Treatments	Vegetative stage (60 DAT)	Before harvest (80 DAT)
		(µg TPF/g/hr)	
T_1	$CaSiO_3$	37.60	24.51
T_2	RHA	31.46	27.37
T_3	$CaSiO_3$ + Pf	36.36	30.64
T_4	$CaSiO_3$+KSB	42.90	32.69
T_5	$CaSiO_3$ + Pf + KSB	46.99	36.77
T_6	RHA + Pf	43.72	33.09
T_7	RHA + KSB	49.44	40.04
T_8	RHA + Pf + KSB	51.07	32.08
T_9	Pf	35.95	21.65
T_{10}	KSB	40.45	30.23
T_{11}	Pf + KSB	38.81	28.19
T_{12}	Control	34.73	23.70
SE(m) ±		2.844	2.150
CD (P = 0.05)		8.34	6.30

Table 3: Correlation between soil dehydrogenase activities with soil microbial activity during *kharif*, 2017

Microbial activity	Vegetative state (60 DAT)	Before harvest (80 DAT)
Total bacteria population vs Dehydrogenase activity	0.865**	0.547
Total fungus population vs Dehydrogenase activity	0.637*	0.707*
Total actinomycetes population vs Dehydrogenase activity	0.427	0.655*

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