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Impact of brewery wastewater sludge on microbiological quality of agricultural soil

C. Ike Christian¹, C. Odika Prince²*, E. Okorie Peace³

¹Department of Biological Sciences (Microbiology Unit), Rhema University, Aba, Nigeria, ²Department of Chemical Sciences (Biochemistry Unit), Rhema University, Aba, Nigeria, ³Department of Biochemistry, Michael Okpara University of Agriculture, Umudike, Nigeria.

ABSTRACT

Impact of brewery wastewater sludge on microbiological quality of agricultural soil was studied using standard methods. Different concentrations of brewery wastewater sludge were added to soil sample collected from abandoned farm land to produce test soil samples A to C; and a control (without sludge). The samples were allowed to stay for 80 days with exposure to same environmental condition. Standard methods were deployed to isolate and group organisms from the soil samples. Important microbes such as Streptococcus sp., Klebsilla sp., Proteus sp., Vibrio sp., Shigella sp., Micrococcus sp., Pseudomonas sp., Enterobacter sp., Escherichia sp., and Bacillus sp amongst others were isolated. The isolated organisms and their loads were more on the test soil samples against the control. These could be indication of the impact of the brewery sludge on the soil. Organisms isolated and grouped have one or more beneficial role to play with relevance to agricultural soil. This study has revealed the impact of brewery wastewater sludge on microbiological quality of agricultural soil.

KEYWORDS: Brewery sludge, microbiological quality, agricultural soil

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*Corresponding Author: C. Odika Prince Email: prince.odika@yahoo. co.uk

INTRODUCTION

Apart from turning raw materials into furnished goods, the industries are also known to turn out chunk of wastes as industrial wastes [1]. These wastes when improperly disposed pollute the environment adversely [2]. Brewery wastewater sludge is amongst the wastes turned out as industrial wastes in brewery industry [3]. Brewery wastewater sludge is generated from brewing industry [2,3] by discharging 70% of the intake water as effluent [4,5] Analysis of brewery wastewater sludge has reviewed important elements such as nitrogen, phosphorus, potassium as well as volatile fatty acids and others nutrients [6].

Fertilizers and organic manures are materials used to improve the fertility of the soil for better crop yield. However, the quest to fashion out a more eco-friendly method of improving agricultural soil fertility for better yield has led to the possible utilisation of brewery sludge [7]. Brewery sludge can be applied directly to agricultural soil or it can be composted as organic manure before utilizing for plant growth [8]. Existing studies on brewery sludge [8-18] have addressed certain areas. However, the studies on impact of brewery sludge in agricultural soil with special emphasis to microbes and environment are scanty. This study investigated the impact of brewery wastewater sludge

on microbiological quality of agricultural soil using a case of abandoned farmland.

MATERIALS AND METHODS

Sludge and Soil Sample Collection

The sludge was collected from the Wastewater Treatment Plant (WWTP) of Nigerian Breweries Plc. Aba, Abia State, Nigeria. Soil sample used for this study were collected from an abandoned, refuge dump farmland in Eboh Lane in Isiala Ngwa North Local Government of Abia State, Nigeria. The samples were transported to Rhema University laboratory for further treatment before usage.

Sludge and Soil Mixture

At the laboratory, the soil sample was separated into four samples (three test specimen as test soil samples A to C; and a control) and each test soil sample was homogenously mixed with different concentration of the brewery sludge. For property mixing, each test sample had two subsets (T and J), contained 20 kg of soil to 5 kg of sludge; Group B, which also has two

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subsets (T and J), contained 20 kg of soil to 10 kg of sludge; Group C, with two subsets (T and J), contained 20 kg of soil to 15 kg of sludge; the control soil sample, was mixed with no sludge at all. All the samples were allowed to stay for 80 days while exposing them equally to same environmental condition. The two subsets for each test soil sample were pulled together as one sample before analysis.

Microbiological Isolation, Identification and Grouping

Bacterial isolates were identified by carrying out series biochemical test as stipulated by Holt [19]. Total heterotrophic bacterial counts (THBC), total viable bacterial count (TVBC), total coliform bacterial count (TCBC), total nitrifying bacterial count (TNBC) and total fungal count (TFC) were determined using the methods of Prescott et al. [20] and Barnett and Hunter [21].

RESULTS AND DISCUSSION

The roles of soil microorganism have been noted [22-23], and their function in soil has been explained earlier [24] like changing of nutrients from inaccessible to usable forms by bacteria. Microbes isolated and identified from the soil samples after 80 days are presented in Tables 1-4. Microbes such as Streptococcus sp., Klebsilla sp., Proteus sp., Vibrio sp., Shigella sp., Micrococcus sp., Resudomonas sp., Enterobacter sp., Escherichia sp., and Bacillus sp., were isolated from control sample. Pseudomonas sp., Bacillus sp., Staphylococcus sp., Micrococcus sp., Lactobacillus sp., Streptococcus sp., Klebsilla sp., Vibrio sp., Salmonella sp., Escherichia sp., Citrobacter sp., Proteus sp., Enterobacter sp., and Shigella sp., were isolated from test soil sample A.

Pseudomonas sp., Bacillus sp., Staphylococcussp., Micrococcus sp., Lactobacillus sp., Lactobacillus sp., Klebsilla sp., Salmonella sp., Escherichia sp., Citrobacter sp., Acinetobactor sp., Serratia sp., Proteus sp., Enterobacter sp., and Vibrio sp., were isolated from test soil sample B. Bacillus sp., Staphylococcus sp., Lactobacillus sp., Streptococcus sp., Achromobacter sp., Klebsilla sp., Salmonella sp., Escherichia sp., Acinetobactor sp., Serratia sp., Proteus sp., Enterobacter sp., Vibrio sp., Shigella sp., Flavobacterium sp., Citrobacter sp., Micrococcus sp., and Pseudomonas sp., were isolated from test soil sample C. The brewery sludge may have influence the increased isolates from the test soil samples against the control. These microorganisms become important when their individual functions and relevance to agricultural soil are considered [25-27]. Flavobacterium sp. has been known to increase the length of rots significantly [28]. Bacillus sp. has been known to increase the uptake of cadmium and significantly increases root and shoot dry weight [29]. It also stimulates plant growth and decreases Cr6+ content [30,31]. Generally, all the individual organisms isolated has one or more beneficial roles to play in agricultural soil.

Results of microbiological load of studied soil samples after 80 days are represented in Table 5. From the Table, THBC ranged from $2.10 \times 10^5 - 4.50 \times 10^5$ CFU/g, TVBC ranged

Probable organism Gas H_2S Butt Slant Oxidation and Citrate Maltose Suce Fermentation	Gas H	S ₂	ıtt Slar	nt Oxidation and Citr Fermentation	rate M	laltose Suc	rose Lac	Tose di	מומכחסב בנמכוחסב	Maillion	Urease	Starcii Hydrolysis	Voges Proskeaur	Red	Indole	Catalase	0xidase	Spore staining	Motility	r ology F	Gram teaction
Streptococcus sp.	,	۷ .	⋖	ш		'	'	'	Ŋ	ı	,	+		,		+			იე -	Cocci	+ve
Klebsilla sp.	+	۷ .	\leq	- 0/F	+	,	AG	A A G	∢	,	+	,	+	+	,	+		,	- Rod	þ	-ve
Proteus sp.	+	4	⋖	Ш	····	5	⋖	⋖	,	∢	ı	,	+	+	+	+	,	ı	+ Rod	po	-ve
Vibrio sp.	+	۷ .	\leq	- 0/F	+	•	⋖	⋖	Ŋ	AG	ı	,	+	+	ı	+	+	ı	+ Rod	þ	-ve
Shigella sp.	+	۲	\leq	0/F	۷ -	1	⋖	1	⋖	⋖	ı	,	,	+	1	+	,	ı	- Rod	þ	-ve
Micrococcus sp.		۷ .	\leq	0	5	1	1	1		∢	1	,	+	+	1	+	,	1	° Co	Cocci	+
Pseudomonas sp.	,	\leq	\leq	0		+	ŋ	1	Ŋ	∢	,		+	+	,	+	+	1	+ Rod	po	-ve
Enterobacter sp.	+	۷ ,	\leq	· L	+	1	G	1		∢	,	ı	+	,	,	+	,	1	+ Rod	p	-ve
Escherichia sp.	+	۷ ,	⋖	L		1	⋖	⋖	⋖	ı	,			1	+	+	,	1	+ Rod	po	-ve
Bacillus sp.	,	۷ ,	⋖	ш	<u>ں</u>	٠	1	•	ഗ	⋖	ı	+	+	,	ı	+	,	+	+ Rod	р	+ve

Table 2: Bacterial isolates from test soil sample A

Probable organism	Gas	H ₂ S B	utt SIa	Gas H ₂ S Butt Slant Oxidation and Citrate Maltose Fermentation	and Citration	te Ma	Itose Sucro	Sucrose Lactose Glucose	se Glucos	e Fructo	Fructose Manitol	Urease	Starch Hydrolysis	Voges Proskeaur	Methyl Red	Methyl Indole Red	Catalase	0xidase	Spore staining	Motiliț	y Cellular Morphology	Gram Reaction
Pseudomonas sp.		×	\leq	0	'	G	+	ŋ	,	G	⋖	,		+	+		+	+		+	Rod	-ve
Bacillus sp.	,	۷ .	⋖	ட	•		ı	ı	,	Ŋ	⋖	,	+	+	1	,	+	,	+	+	Rod	+ve
Staphylococcus sp.		_	\leq	ட	+	ഗ		,	,	,	⋖	,			1	•	+	,	ì	•	Cocci	+ve
Micrococcus sp.	,	۷ -	\leq	0	+		1	,	,	,	⋖	1	,	+	+	1	+	,	,	•	Cocci	+ve
Lactobacillus sp.	+	4	⋖	0/F	•	•	ı	AG	ŋ	,	,	,	,		1	,	+	,	,	•	Rod	+ve
Streptococcus sp.		۷ '	⋖	ட	•	ഗ		,	,	Ŋ		,	+		1	•	+	,	ì	•	Cocci	+ve
Klebsilla sp.	+	۷ -	\leq	0/F	+	1	ı	AG	AG	⋖	,	+	,	+	+	ı	+	,	,	1	Rod	-ve
Vibrio sp.	+	۷ .	\leq	0/F	+	1	ı	⋖	⋖	Ŋ	AG	,	,	+	+	,	+	+	,	+	Rod	-ve
Salmonella sp.	+	4	\leq	0/F	+	ഗ	⋖	⋖	⋖	⋖		,			+	•	+	,	ì	+	Rod	-ve
Escherichia sp.	+	۷ '	⋖	ட	•	1	•	⋖	⋖	⋖		,			1	+	+	,	·	+	Rod	-ve
Citrobacter sp.	+	4	⋖	ட	+	⋖	⋖	⋖	⋖	⋖	,	,		1	+	,	+		,	+	Rod	-ve
Proteus sp.	+	4	⋖	ட	+	ഗ	Ŋ	⋖	⋖	ì	⋖	,		+	+	+	+	,	ì	+	Rod	-ve
Enterobacter sp.	+	۷ '	\leq	ட	+	1	•	Ŋ	,	,	⋖	,		+	1		+	,	·	+	Rod	-ve
Shigella sp.	+	۷ -	\leq	0/F	1	⋖	1	⋖		⋖	⋖			1	+	1	+	1	1	•	Rod	-ve

-ve = Gram negative; +ve = Gram positive; + = positive; - = negative; A = Acid; G = Gas; O = oxidation; F = Fermentation; K = Alkaline, TSI = Triple sugar iron aga.

Table 3: Bacterial isolates from test soil sample B

Probable organism	Gas	H ₂ S	Butt	Slant	Gas H ₂ S Butt Slant Oxidation and Citrate Maltose Fermentation	ıd Citra 1	te Malt	ose Sucrose		se Glucc	Lactose Glucose Fructose Manitol	e Manitol	Urease Starch Hydrolys	- :8	Voges Proskeaur	Methyl Red	Indole (Indole Catalase Oxidase		Spore l staining	¶otility	Motility Cellular Morphology	Gram Reaction
Pseudomonas sp.	٠	١.	$ $ \leq		0	'	G	+	IJ	,	IJ	۷			+	+		+	+		+	Rod	-ve
Bacillus sp.	1	1	⋖	⋖	ш	1	ŋ	•			Ŋ	⋖	i	+	+	,	i	+	ì	+	+	Rod	+ve
Staphylococcus sp.	1	1	\leq	\leq	ш	+	ŋ	•	,			⋖	,	,		,	,	+	ı	,		Cocci	+ve
Micrococcus sp.	1	1	⋖	\leq	0	+	ŋ	٠	ı	,		⋖		,	+	+	,	+	,	,		Cocci	+ ve
Lactobacillus sp.	+	+	⋖	⋖	0/F	1	,	•	AG	Ŋ			i	,		,	i	+	ì	,		Rod	+ *
Lactobacillus sp.	1	1	⋖	⋖	ш	1	ŋ	•			Ŋ		,	+		,	,	+	ı	,		Cocci	+ve
Klebsilla sp.	+	1	⋖	\leq	0/F	+	ı	٠	AG	AG	⋖		+	,	+	+	,	+	,	,		Rod	-ve
Salmonella sp.	+	+	⋖	\leq	0/F	+	ŋ	⋖	⋖	⋖	⋖		i	,		+	i	+	ì	,	+	Rod	-ve
Escherichia sp.	+	1	⋖	⋖	ш	1	ı	•	⋖	⋖	⋖		,	,		,	+	+	ı	,	+	Rod	-ve
Citrobacter sp.	+	+	⋖	⋖	L	+	⋖	⋖	⋖	⋖	⋖	,	,	,		+	,	+	ı	,	+	Rod	-ve
Acinetobactor sp.	•	1	\leq	\leq	0	•	,	•	⋖	⋖	⋖	⋖				+	i	+	ì			Rod	-ve
Serratia sp.	1	1	⋖	\leq	ш	+	ŋ	Ŋ	,		⋖	+	,	,	+	,	,	+	ı	,	+	Rod	-ve
Proteus sp.	+	+	⋖	⋖	ш	+	G	IJ	⋖	⋖	,	⋖	,	,	+	+	+	+	,	,	+	Rod	-ve
Enterobacter sp.	+	•	⋖	\leq	L	+	,	•		,	,	⋖		,	+	,	,	+	,	,	+	Rod	-ve
Vibrio sp.	+	1	⋖	\leq	0/F	+	,	٠	⋖	⋖	Ŋ	ВB	,	,	+	+	,	+	+	,	+	Rod	-ve
Flavobacterium sp.	•	1	⋖	\leq	0	•	ЯĠ	AG	ı	٨	1	G				,				1	1	Rod	-ve

-ve = Gram negative; +ve = Gram positive; + = positive; - = negative; A = Acid; G = Gas; O = oxidation; F = Fermentation; K = Alkaline, TSI = Triple sugar iron agar.

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Table 4: Bacterial isolates from test soil sample C

Probable organism	Gas 1	2S Bu	tt Slar	Gas $H_2 S$ Butt Slant Oxidation and citrate Maltose Sucrose Fermentation	citrate	Maltose	Sucrose	Lactose	الاردة الاردة	Lactose Glucose Fructose Manitol		U rease H	starcn Hydrolysis	voges Proskeaur	Red	Metnyi indole Catalase Red		Uxidase	Spore	Motility	Cellular Morphology	Gram Reaction
Bacillus sp.		۷ .	⋖	L		G				9	4		+	+			+		+	+	Rod	+ ve
Staphylococcus sp.	,	∠	\leq	ட	+	ŋ				-	⋖	1	,		ı	,	+	,	,	1	Cocci	+ ^
Lactobacillus sp.	+	⋖ +	⋖	0/F	•			AG	5			1		,	1	,	+			1	Rod	+
Streptococcus sp.	,	۷ .	⋖	ட	,	ŋ		1		5		1	+	,	1	,	+	,	,	ı	Cocci	+ve
Achromobacter sp.	,	∠	\leq	,	+	AG	,		AG	AG		+	+	,	ı	,	,	+	,	+	Rod	-ve
Klebsilla sp.	+	۷ -	\leq	0/F	+	,		AG	AG	⋖		+		+	+	,	+			1	Rod	-ve
Salmonella sp.	+	∢ +	\leq	0/F	+	ŋ	⋖	⋖	⋖	⋖		,	,	,	+	,	+	,		+	Rod	-ve
Escherichia sp.	+	۷ .	⋖	ட	1	,		⋖	⋖	⋖	,	ı	,	,	ı	+	+	,	ı	+	Rod	-ve
Acinetobactor sp.	,	∠	\leq	0	•	,	1	⋖	⋖	A	~	1		,	+	,	+			1	Rod	-ve
Serratia sp.	,	۷	\leq	ш	+	ഗ	ŋ			, 4	+	,	,	+	,	,	+	,	,	+	Rod	-ve
Proteus sp.	+	∢ +	⋖	ட	+	Ŋ	Ŋ	⋖	⋖	-	~	,	,	+	+	+	+	,	,	+	Rod	-ve
Enterobacter sp.	+	۷ -	\leq	ட	+	,		ű		-	۷	1		+	1	,	+			+	Rod	-ve
Vibrio sp.	+	۷ .	\leq	0/F	+	,		⋖	⋖	9	AG	1	,	+	+	,	+	+	,	+	Rod	-ve
Shigellasp	+	۷	\leq	0/F	1	⋖	,	⋖		4	~	,	,	,	+	,	+	,	,	ı	Rod	-ve
Flavobacterium sp.	,	۷	\leq	0	1	AG	AG		⋖	-	(5	,			,	i			,	,	Rod	-ve
Citrobacter sp.	+	ح +	⋖	ட	+	⋖	⋖	⋖	⋖	⋖		,	,	,	+	,	+			+	Rod	-ve
Micrococcus sp.		۷	\leq	0	+	ŋ		,		-	⋖	,	,	+	+	,	+		,	,	Cocci	+ ve
Pseudomonas sp.		∠	\leq	0	٠	ŋ	+	ŋ		9	⋖	,		+	+	,	+	+		+	Rod	-ve

Table 5: Results of microbial load of soil samples

Load (CFU/g)	Control	Test soil sample A	Test soil sample B	Test soil sample C
THBC (×10 ⁵)	2.10	3.90	4.50	4.20
TVBC (×104)	1.30	2.50	3.20	2.30
TCBC (\times 10 ³)	4.20	1.30	1.90	1.10
TNBC (\times 10 2)	0.40	0.80	1.00	1.20
TFC (×10 ⁵)	4.10	5.90	6.50	6.90

Total Heterotrophic Bacterial Count (THBC), Total Viable Bacterial Count (TVBC), Total Coliform Bacterial Count (TCBC); Total Nitrifying Bacterial Count (TNBC); and Total Fungal Count (TFC).

from 1.30 x 10^4 – 3.20 x 10^4 CFU/g, TCBC ranged from 1.10 x 10^3 – 4.20 x 10^3 CFU/g, TNBC ranged from 0.40 x 10^2 – 1.20 x 10^2 CFU/g and TFC ranged from 4.10 – 6.90 x 10^5 CFU/g. Heterotrophic bacteria breakdown carbohydrates and sugars and make them available to the soil [32,33].

CONCLUSION

The increased number of isolates from test soil samples (soil mixed with brewery wastewater sludge) and increased microbial loads as observed in the present study could be indication that brewery sludge can impact positively on agricultural soil. Bacteria and fungi are emerging indicators of soil condition, and all the isolated and grouped organisms of the present study has one or more beneficial role to play with relevance to agricultural soil. This study has revealed the impact of brewery wastewater sludge on microbiological quality of agricultural soil.

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