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Analysis of *Streptomyces* spp. Native to Mahikeng Soils in South Africa

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Streptomyces **species were isolated from rhizospheric soils collected from different localities in Mahikeng, North West Province of South Africa. A total of 84 isolates were obtained from 5 rhizospheric soil samples, highest number of isolated were recovered from maize (*Zea mays*) rhizosphere. The genus *Streptomyces* was identified by cultural, morphological, physiological and molecular analyses. 26 culturally distinct isolates were identified to the species level by 16S rDNA gene sequence analysis. The sequences of 16S rDNA gene of the isolates matched with Streptomyces but different species in BLAST analysis, similarities ranging between 100%-91%. Rhizosphere can be considered as inexhaustible resource of microorganisms that can be harness for possible exploration.**

Key Words: *Streptomyces*; rhizosphere; characterization; 16S rDNA gene.

Rhizosphere is the soil immediately surrounding the plant root system where the biotic and abiotic factors of the soil are influence by the root. This zone is greatly influenced by the root exudates and microorganisms [1]. Microbiological activity in the rhizosphere is greater than the bulk soil [2]. The rhizosphere depicts the centre of intense biological activity due to the food supply provided by the root exudates [2]. The physical properties of the soil like pH, moisture content, mineral composition, organic matter and environmental factors can influence the microbial diversity and forms in the rhizosphere [3]. The forms of life found in the rhizosphere include bacteria, protozoa, fungi, nematode, virus and insect but bacteria are the most abundant. The plant bacteria interactions in the rhizosphere can be harmful, beneficial or of no effect. Interaction that are beneficial to plants include mycorrhizae, legume nodulation, production of plant hormones, production of antimicrobial agents that inhibit the growth of plant pathogens and production of communication molecules that encourage plant growth [4].

Streptomyces are one of the major groups of soil inhabitants and are extensively distributed in nature. *Streptomyces species* are the largest and the most important genus in the order actinomycetales. They are prolific producer of medical and agricultural useful compounds. *Streptomyces* are aerobic, filamentous, Gram positive bacteria with high Guanine and cytosine content in their genome [5]. They exhibit characteristic morphology and form extensive branching substrate and aerial mycelia. They are responsible for the soil prudent smell due to the production of geosmin [6]. They are flexible nutritionally and can aerobically degrade resistant

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substances such as pectin, lignin, chitin, keratin, latex and aromatic compounds [7].

Streptomyces is one of the well known secondary metabolites producers, has attracted considerable research interest due to ability to produce substances that are of agricultural and pharmaceutical interest [8,9]. *Streptomyces* are responsible for quite a considerable number of important compounds in use in agriculture and medicine including cycloheximide, erythromycin, streptomycin, azalomycin F, munumbicin, salinomycin and rapamycin [10,11]. *Streptomyces* can degrade an enormous number and variety of organic compounds and are extremely important in the mineralization of organic matter. They are found to be of used in biological control of plant pathogens and also perform significant biogeochemical roles in soils. As soil bacteria, they help in crop production, promote plant nutrition, and improve soil fertility. *Streptomyces* as plant growth promoting rhizobacteria play substantial role in transformation, mobilization and solubilization of nutrients from the soil and consequential uptake of elemental nutrients by plants help to actualize realise their full genetic potential. Some *Streptomyces species* produce antimicrobial agents that may be involve in the mutualistic relationship with the host plant in the rhizosphere.

A need for better and more environmental friendly ways to cultivate the world food indicates new methods of controlling pathogens and pests are needed. Since chemical compounds are either harmful to the environment or recalcitrant [12]. Recently, there has been increased interest in using more friendly methods in agricultural production. It now appears that there is a relatively untapped source of microbial diversity for use in agriculture. The use of molecular approaches to describe microbial diversity has greatly enhanced the knowledge of population structure in microbial communities. Cloning and sequencing of the 16S rRNA gene give data that can describe complete microbial community composition and can indicate genes that can be explore from these microbes based on information already available for known phylogenetic relatives [13]. The application of knowledge on microbial diversity will enhance the ability to explore and manage the rhizosphere that will lead to advancement in food production. In this study, we report on the isolation and characterization of *Streptomyces* species from rhizospheric soils. This can be further explored for plant growth promoting activities that will help enhance food production.

MATERIALS AND METHODS

A total of seventeen soil samples were collected from the rhizosphere of maize, onion, cabbage, spinach and sunflower around Mahikeng, North West Province, South Africa. From each location about 100 g of sample was collected at 5 to 10 cm depth from each of the surfaces. Soil samples were placed in sterile plastic bags to avoid contamination and taken to the laboratory. The soil samples were air-dried at room temperature for 5 to 7 days and stored at 4°C in plastic containers until further use

One gram of soil sample were suspended in 100 ml of sterile distilled water and homogenized by vortexing for 30 min at 150 rpm. The suspension was serially diluted up to 10^{-6} dilution. For each dilution 0.1 ml was spread plated on starch casein agar (SCA) (Soluble starch, 10.0 g; Casein hydrolysate, 0.3 g; KNO_3, 2.0 g NaCl, 2.0 g; K_2HPO_4, 2.0 g; $MgSO_4.7H_2O$, 0.05 g; $CaCO_3$, 0.02 g; $FeSO_4.7H_2O$, 0.01 g; Agar, 15.0 g; pH, 7.3) in triplicates. The agar was supplemented with 10 µg ml^{-1} cycloheximide and 25 µg ml^{-1} streptomycin to inhibit fungal and bacterial contamination respectively. All the inoculated plates were incubated at 25°C for 1-2 weeks. After incubation period, the plates were examined for the presence of actinomycetes colony. The suspected colonies were picked and purified on yeast malt extract agar (Merck), and incubated at room temperature for 4-7 days. The suspected pure actinomycetes isolates were inoculated on actinomycetes agar slants and also stored in 20% glycerol kept at -20°C.

Cultural, morphological and physiological characteristics of the strain were studied according to the standard procedures [14]. Biochemical tests: catalase, oxidase, nitrate reduction, citrate utilization, gelatin liquefaction, starch hydrolysis, indole production, hydrogen sulphide production, esculin degradation, casein hydrolysis, tween 20, Methyl red and Voges-Proskauer tests were carried out on the bacterial cultures. Utilization of carbon source was using

ISP-9 as a basal medium containing different carbon sources at 1% concentration [15].

The isolates were grown for 7 days on actinomycetes agar slant at 25°C. 2 ml of spore suspension were inoculated into LB broth and incubated for 4 days on a shaker incubator at 200 rpm and 30°C to form a pellet of vegetative cells (pre-sporulation). Extraction of genomic DNA was conducted using ZR Soil Microbe DNA MiniPrep™ (Zymo Research, USA) extraction kit according to the manufacturer's instructions.

PCR amplification of the 16S rDNA gene of the isolates was conducted using two primers, StrepF: 5'-ACG TGT GCA GCC CAA GAC A-3' and StrepR: 5'-ACA AGC CCT GGA AAC GGG GT-3'. PCR was performed in a total volume of 50 µl containing 30-50 ng DNA, 100 mM each primer, 0.05 U/µl *Taq* DNA polymerase, 4 mM $MgCl_2$, and 0.4 mM of each dNTP. The thermal cycling conditions were: 5 min at 94°C for initial denaturation; 30 cycles of 30 s at 95°C, 1 min at 54°C, 2 min at 72°C; and fin al extension for 5 min at 72°C. The amplification reaction was performed with a DNA Engine DYAD Peltier thermal cycler (BioRad, USA). For each reaction, a negative control lacking DNA template was included. The PCR amplicons were analysed by electrophoresis in 1% (w/v) agarose gel. The gel containing ethidium bromide (10 µg ml^{-1}) was view under Syngene Ingenius Bioimager (UK) to confirm the expected size of the product. The remaining mixture was purified using NucleoSpin Gel and PCR Clean-up kit (Macherey-Nagel, Germany).

Sequencing of the purified PCR products were conducted at facilities of Inqaba Biotechnical Industrial (Pty) Ltd, Pretoria, South Africa using ABI PRISM® 3500XL DNA Sequencer (Applied Biosystems). The obtained 16S rDNA sequences were compared to sequences in the NCBI genebank database with the Basic Alignment Search Tool (BLAST) [16].

RESULTS AND DISCUSSION

From the rhizospheric soil samples collected from Mahikeng, it was observed that *Streptomyces* are predominate genus in the soil; this suggests their wide distribution in association with plants in the natural environment [17]. A total of 84 isolates were isolated from 5 different rhizospheric soil samples collected from different crops in Mahikeng. The distribution of total *Streptomyces species* in the rhizospheric soils collected from different location in Mahikeng is shown in Table 1. From this study, it was noted that the number and diversity of *Streptomyces* isolated from maize (*Zea mays*) were higher compare to other rhizosphere soils. This might be due to differences in the composition and amount of root exudates and rhizodepositions among the five rhizospheric soils. The ability of certain rhizobacteria to colonize or occupy a niche in the rhizosphere (rhizosphere competence) might also be responsible for host-plant specificity [18]. Reports indicated that rhizosphere represent a unique biological niche that supports abundant and diverse microorganisms because of the presence of root exudates [19].

The *Streptomyces* present in this soil community is identified through cultural, morphological, biochemical, physiological and molecular analyses. The isolates were small to medium sized; purple, brown, cream, gray and pure white in colour; and round, powdery with irregular margin. All the selected isolated are tough, leathery and filamentous colonies that were hard to pick from the culture plates, showing morphology typical of *Streptomyces.* The 84 isolates were classified into 26 groups according to their cultural characteristics. Morphological studies of the isolates revealed that all the isolates were filamentous and Gram positive rods. The cultural characteristics of the isolates on starch casein agar were given in Table 2. The 26 isolates designated as MRSS1-MRSS26 were tentatively assigned to the genus *Streptomyces* bases on their macro- and micro-morphological and cultural characteristics [14]. The isolates showed growth from abundant to moderate**.** The colour of the substrate mycelium varied from white to reddish brown and aerial mycelium varied from white to grey. This result is similar to previous results reported by grey [20]. Only isolates MRSS16 and MRSS20 produced diffusible pigment.

Taxonomic characteristics of the isolates were summarized in Tables 3-5. The biochemical studies on Table 3 showed that all the isolates were catalase positive, able to hydrolysed starch and utilized tween 20. Twenty-two isolates were able to utilize tween 60 and 20 utilize tween 80.

Eleven isolates were able to produce enzyme catalase. Seven isolates were able to hydrolyze casein. Six different isolates were able to utilize citrate, degrade casein and reduce nitrate. Only 3 isolates, MRSS3, 4 and 11 were able to produce H_2S. Only 1 isolate MRSS4 tested positive for methyl red, all the other isolates were positive for Voges-Proskauer tests indicating. None of the isolates liquefied gelatin or produced indole. All the isolates grew on minimal media and utilize a good number of the carbon sources. Table 4 shows the carbon source utilization of the isolates; all the isolates were able to utilize glucose. From the table it is evident that the *Streptomyces* isolates were able to utilize quite a number of carbon sources. *Streptomyces sp* are saprophytes; this might be

Table 1. The distribution of total *Streptomyces species* isolated from rhizospheric soils in Mahikeng

Crop	Sample code	GPS Co-ordinates	Presumptive isolates	Confirmed isolates
Onion	MO1	S25° 53.318'	25	18
Maize	MM2	S25° 53.296'	29	32
Cabbage	MC3	S25° 53.276'	15	11
Spinach	MS4	S25° 56.946'	26	6
Sunflower	MS5	S25° 56.657'	23	17
Total			118	84

Table 2. Cultural characteristics of the isolates on starch casein agar

Isolate	Growth	Elevation	Colour	Mycelium type	Pigmentation	Margin	Reverse colony colour
MRSS1	Good	Raised	White	Substrate	No	Smooth	Creamish
MRSS2	Good	Convex	White	Substrate	No	Ciliate	Creamish
MRSS3	Good	Convex	Cream	Substrate	No	Woolly	Brownish
MRSS4	Good	Convex	White	Aerial	No	Smooth	Creamish
MRSS5	Good	Convex	Dull white	Aerial	No	Smooth	Yellowish
MRSS6	Good	Convex	Creamish white	Aerial	No	Smooth	Yellowish
MRSS7	Abundant	Convex	Dull white	Aerial	No	Wavy	Yellowish
MRSS8	Good	Convex	White	Substrate	No	Wavy	Yellowish
MRSS9	Good	Convex	Grey	Aerial	No	Ciliate	Brownish
MRSS10	Moderate	Convex	Cream	Substrate	No	Smooth	Yellowish
MRSS11	Good	Convex	White	Substrate	No	Smooth	Brownish
MRSS12	Good	Convex	Dull white	Substrate	No	Woolly	Creamish
MRSS13	Good	Dome	Dull white	Substrate	No	Ciliate	Creamish
MRSS14	Good	Convex	White	Substrate	No	Ciliate	Creamish
MRSS15	Good	Convex	Grey	Substrate	No	Wavy	Creamish
MRSS16	Good	Dome	Brown	Substrate	Brownish	Woolly	Whitish
MRSS17	Good	Convex	Dull powdery white	Substrate	No	Ciliate	Brownish
MRSS18	Good	Raised	Dull white	Substrate	No	Ciliate	Creamish
MRSS19	Good	Convex	White	Substrate	No	Woolly	Creamish
MRSS20	Good	Flat	White	Substrate	Purplish	Woolly	Brownish
MRSS21	Good	Convex	White	Substrate	No	Smooth	Creamish
MRSS22	Good	Convex	White	Substrate	No	Smooth	Brownish
MRSS23	Good	Dome	White	Substrate	No	Wavy	Blackish
MRSS24	Good	Convex	White	Substrate	No	Ciliate	Creamish
MRSS25	Moderate	Hilly	White	Substrate	No	Woolly	Brownish
MRSS26	Good	Convex	White	Aerial	No	Smooth	Yellowish

Table 3. Biochemical characteristics of *Streptomyces* isolates

Isolates code	Gram Staining	Catalase	Oxidase	Citrate Utilization	Gelatin Liquefaction	Starch Hydrolysis	Casein hydrolysis	Esculin Degradation	Nitrate production	H_2S production	Indole production	Methyl red	Voges-Proskauer	Tween 20	Tween 60	Tween 80
MRSS1	+	+	+	-	-	+	+	+	-	-	-	-	+	+	+	+
MRSS2	+	+	+	-	-	+	-	-	-	-	-	-	+	+	+	+
MRSS3	+	+	+	-	-	+	-	-	-	+	-	-	+	+	+	+
MRSS4	+	+	-	-	-	+	-	-	-	+	-	+	-	+	+	+
MRSS5	+	+	-	-	-	+	-	-	-	-	-	-	+	+	+	+
MRSS6	+	+	-	-	-	+	-	-	-	-	-	-	+	+	+	+
MRSS7	+	+	-	-	-	+	-	-	+	-	-	-	+	+	+	±
MRSS8	+	+	-	-	-	+	-	-	-	-	-	-	+	+	+	+
MRSS9	+	+	-	-	-	+	-	-	-	-	-	-	+	+	+	+
MRSS10	+	+	-	-	-	+	+	-	-	-	-	-	+	+	+	+
MRSS11	+	+	-	-	-	+	-	-	-	+	-	-	+	+	±	-
MRSS12	+	+	-	-	-	+	+	-	-	-	-	-	+	+	-	-
MRSS13	+	+	-	-	-	+	+	+	-	-	-	-	+	+	+	+
MRSS14	+	+	-	+	-	+	-	+	+	-	-	-	+	+	+	+
MRSS15	+	+	+	-	-	+	-	-	-	-	-	-	+	+	+	+
MRSS16	+	+	-	+	-	+	+	+	+	-	-	-	+	+	+	+
MRSS17	+	+	-	-	-	+	-	-	-	-	-	-	-	+	+	+
MRSS18	+	+	+	-	-	+	-	-	-	-	-	-	+	+	+	+
MRSS19	+	+	+	+	-	+	-	+	-	-	-	-	+	+	+	+
MRSS20	+	+	+	+	-	+	-	-	+	-	-	-	+	+	-	-
MRSS21	+	+	-	+	-	+	-	-	±	-	-	-	+	+	+	-
MRSS22	+	+	+	-	-	+	+	+	-	-	-	-	+	+	+	+
MRSS23	+	+	+	-	-	+	-	-	-	-	-	-	+	+	-	-
MRSS24	+	+	-	-	-	+	-	-	-	-	-	-	-	+	-	-
MRSS25	+	+	+	+	-	+	-	+	+	-	-	-	+	+	+	+
MRSS26	+	+	+	-	-	+	-	-	-	-	-	-	+	+	+	+

-= negative result; += positive result

Isolates code	Glucose	Sucrose	Sorbitol	Mannitol	Fructose	Lactose	Galactose	Rhamnose	Cellulose	Mannose	Inositol	Raffinose	Maltose	Xylose

Table 4. Carbon source utilization by *Streptomyces* isolates

Isolates code	Glucose	Sucrose	Sorbitol	Mannitol	Fructose	Lactose	Galactose	Rhamnose	Cellulose	Mannose	Inositol	Raffinose	Maltose	Xylose
MRSS1	++	+	-	+	+	-	+	+	±	++	-	+	+	-
MRSS2	++	++	-	++	++	-	++	++	±	++	++	++	++	++
MRSS3	++	±	-	++	+	+	+	+	-	+	++	+	++	-
MRSS4	++	+	-	+	+	-	+	+	-	±	+	+	+	-
MRSS5	++	+	-	+	+	-	+	-	-	+	++	-	+	-
MRSS6	++	+	-	-	+	-	+	+	++	+	±	+	+	+
MRSS7	++	+	-	++	+	+	-	-	-	+	++	-	+	-
MRSS8	++	-	±	±	+	±	-	-	-	±	-	-	±	-
MRSS9	++	-	-	-	+	-	-	+	-	±	+	+	-	-
MRSS10	++	+	-	++	-	-	++	-	±	-	-	-	±	-
MRSS11	++	-	-	±	+	+	±	+	-	±	+	+	-	-
MRSS12	++	+	-	+	+	++	++	+	±	++	++	++	+	+
MRSS13	++	-	-	++	±	++	+	+	-	++	-	+	++	+
MRSS14	++	+	-	+	++	++	++	++	±	++	++	++	+	+
MRSS15	++	++	±	-	±	-	+	±	-	+	++	-	±	-
MRSS16	++	±	-	++	+	-	++	++	-	++	±	++	++	+
MRSS17	++	++	-	+	-	-	±	-	-	±	+	-	-	-
MRSS18	++	+	±	+	++	-	++	-	+	+	++	-	+	+
MRSS19	++	+	-	±	+	+	-	+	-	+	+	+	+	-
MRSS20	++	++	-	++	+	++	++	++	±	++	++	++	++	+
MRSS21	++	-	-	-	-	++	-	+	-	-	-	-	+	-
MRSS22	++	+	±	++	++	++	++	+	±	++	++	++	++	++
MRSS23	++	-	-	-	++	-	-	++	-	++	+	++	+	+
MRSS24	++	++	-	++	++	++	++	++	-	++	++	++	++	+
MRSS25	++	+	-	±	±	-	+	+	-	+	+	+	+	-
MRSS26	++	+	-	++	++	-	+	+	-	+	+	+	+	-

Table 5. Physiological characteristics of Streptomyces isolates

Isolates code	Growth under anaerobic conditions	Growth on MacConkey agar	Optimum pH for growth	Optimum temperature for growth (°C)	NaCl tolerance (%)
MRSS1	+	-	7	28	6
MRSS2	-	-	6.5	25	7
MRSS3	+	-	8	30	7
MRSS4	+	-	7	30	7
MRSS5	-	-	7	27	5
MRSS6	+	-	7	28	7
MRSS7	+	-	7	28	7
MRSS8	-	-	7	27	6
MRSS9	+	-	8	29	7
MRSS10	+	-	7	27	8
MRSS11	+	-	7	28	7
MRSS12	+	-	7	28	7
MRSS13	+	-	8	28	7
MRSS14	+	-	7	28	7
MRSS15	+	-	9	25	8
MRSS16	+	-	7	30	7
MRSS17	-	-	7	27	7
MRSS18	+	-	8	28	7
MRSS19	-	-	7	29	7
MRSS20	+	-	8	28	7
MRSS21	-	-	8	25	6
MRSS22	-	-	7	27	7
MRSS23	+	-	7	28	7
MRSS24	+	-	7	28	7
MRSS25	+	-	6	28	7
MRSS26	+	-	6	25	7

-=no growth, += growth

Table 5. Results of similarity searches between 16S rDNA genes isolated in the present investigation

Isolate Code	Highest Identical species	Matched sequence accession No	Sequence identity (%)	E-value
NWU1	*Streptomyces cyaneus*	AY232254	99	0
NWU2	*Streptomyces werraensis*	AB184381	100	0
NWU7	*Streptomyces espinosus*	X808261	99	0
NWU8	Uncultured *Streptomyces sp*	JQ358574	97	0
NWU9	Uncultured *Streptomyces sp*	JQ358602	91	0
NWU10	*Streptomyces coelicolor*	HQ848084	99	0
NWU11	*Streptomyces sp*	JN936842	99	0
NWU12	*Streptomyces sp*	GU263865	99	0
NWU13	*Streptomyces heliomycin*	EU593729	97	0
NWU14	*Streptomyces sp*	FJ626659	99	0
NWU15	*Streptomyces griseus*	AB184821	99	0
NWU16	*Streptomyces platenis*	FJ486292	99	0
NWU17	*Streptomyces tricolor*	FJ532433	100	0
NWU18	*Streptomyces lividans*	JQ309923	100	0
NWU19	*Streptomyces griseorubens*	JN180193	99	0
NWU20	*Streptomyces griseoloalbus*	DQ442503	100	0
NWU21	*Streptomyces californicus*	JQ218934	99	0
NWU22	*Streptomyces albogriseolus*	JQ619482	99	0
NWU23	*Streptomyces thermoluteus*	AB184581	99	0
NWU24	*Streptomyces sporovirgulis*	JQ654447	99	0
NWU25	*Streptomyces humidus*	HQ607425	99	0
NWU26	*Streptomyces hygroscopicus*	FJ406123	99	0

due to the capability to produce large and diverse range of hydrolytic enzymes that help in degradation of different types of organic molecules [21,22]. *Streptomyces species* have been identified as industrial source of enzymes such as amylase, cellulase, lipase and xylanase. Previous research works have shown that the predominant of *Streptomyces* in the rhizosphere soils is due to their enzymatic activities and ability to produce a vast array of secondary metabolites [22-24]. These attributes help them to out-compete other microorganisms and even to strive in the soil [25].

Figure 1, shows PCR amplification of the genomic DNA with *Streptomyces* specific forward and reverse primers resulted in approximately 1100 bp amplicons. The 16S rDNA sequence thus obtained was subjected to BLAST search using the NCBI data base. The BLAST analysis of partial 16S rDNA gene sequences showed that all the isolates were closely related to member of the genus *Streptomyces* with similarities ranging between 100% and 91% (Table 6). Identification of microorganisms to the species level is important; this helps to ascertain if the organism is novel and to know secondary metabolites produced by closely related species [26].

Streptomyces species had been reported to act as biocontrol agents in the rhizosphere. According to different researches, *Streptomyces* acts as biocontrol against blast and sheath blight disease in rice [27], tomato disease [28] and damping off disease in wheat [29]. *Streptomyces* spores are major constituent of some commercial biocontrol products use in agricultural production such as Mycostop, Actinovate, and ActinoIron [30]. This shows the acceptance of this genus as biocontrol agents. *Streptomyces* acts against various soil-borne plant pathogens; this attribute is due to the production of different secondary metabolites in the rhizosphere. Their mechanisms of action as biocontrol agent can be due to induction of systemic resistance in host plant, production of siderophores or antibiotics [31]. This prevalent inhabitant of soil is widely recognized as a powerful biocontrol agent, this is ascribe to its broad host range, its ability to form spores and produce different bioactive compounds with a broad spectrum of activity in the rhizosphere.

The potential uses of biofertilizers in agriculture play an important role of providing an economically viable level for achieving the ultimate goal to enhance food productivity. Microorganisms that are potential biofertilizers are either nitrogen fixing (symbiotic and non-symbiotic), or phosphorous solubilizing microorganisms. *Streptomyces sp* have been reported as potential biofertilizer, due to its ability to solubilize phosphorus [32]. The bacterial phosphate solubilization ability is due to the production of extracellular enzymes that aids in the degradation of mineral phosphate. It had been reported that phosphate solubilization can be influenced by specific root exudates of different rhizosphere of plant. Through the utilization of the root exudates

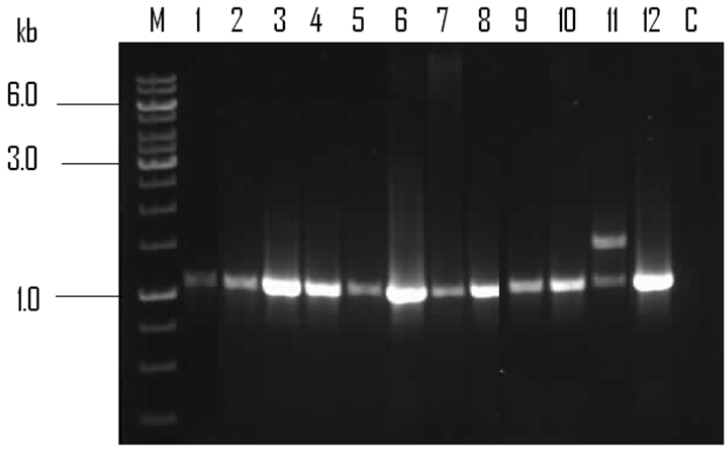

Fig. 1. Agarose gel photograph indicating the positive band of approximately 1.1 kb for *Streptomyces* signatures nucleotide amplification

and other carbon sources by these microbes, phosphorus is supply to plant in the rhizosphere. Hamdali et al[29] reported that the amount of phosphorus released from mineral phosphate was higher in the presence of the actinomycete strains than in the presence of the plant alone, indicating the important contribution of mineral phosphate-solubilizing actinomycetes in the improvement of plant growth.

Streptomyces lydicus was isolated from the rhizosphere o f linseed plant [33]. This strain is the active constituent present in commercial biopesticides, Actinovate and ActinoGrow used in the control of powdery mildew caused by *Podosphaera xanthii* and black scurf and stem cancer caused by *Rhizoctonia solani* respectively.

CONCLUSION

From this study it is clear that rhizospheric soil provide a rich source of *Streptomyces* species, which can be explore in agricultural production. *Streptomyces* species have been inadequately researched despite the evidence of their ability to serve as plant growth promoters. This is unexpected as *Streptomyces* accounts for an abundant percentage of the soil microflora and also active inhabitant of the soil. Rhizosphere bacteria that promote plant growth are considered an alternative to the use of chemicals in agriculture. *Streptomyces* have desirable characteristics including effective colonization of the rhizosphere, formation of spores, production of enormous array of potent secondary metabolites, and high-quality enzymatic activities. Furthermore, these isolates will be screened for plant growth promoting activities *in vitro* and *in vivo*. The isolates that showed activities are likely to be potential candidates for biocontrol, biofertilizer, biopesticide, bioherbicide and biotechnological application of commercial value. Thus, in food production *Streptomyces* sp have potential as replacement for agricultural inorganic compounds. The rhizosphere can be considered as inexhaustible resource for possible exploration.

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