



Full Length Article

Enhancement of Cellulose Rich Organic Matter Degradation by Inoculation with *Streptomyces* sp. Strains

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Abstract

Microbial degradation of organic matter is a vital part of carbon cycle in nature. Actinobacteria play an important role in the decomposition of cellulose rich organic matter (CROM). *Streptomyces* spp. are abundant in soil, produce various secondary metabolites and secrete extracellular enzymes. The aim of this research was to isolate and select *Streptomyces* strains with the best cellulose degradation abilities. Out of total 32 actinobacteria isolates, four *Streptomyces* strains (CA1, CA10, PA2 and PA7) were subjected to morphological, physiological, biochemical characterization and molecular identification. CROM degradation potential of the strains was investigated on straw and beech briquettes as well as on legume based substrate in *in vitro* condition. *Streptomyces* strains CA1 and CA10 showed the best cellulose production and starch hydrolysis abilities, followed by strains PA2 and PA7. Strain CA1 was also positive to production of pectinase enzymes. *Streptomyces zaomyceticus* CA1 and *S. tanashiensis* CA10 were used as inoculants, which degraded the raw cellulose from 38.38 to 81.69% in the investigated substrates (straw, beech, legume), during a 30-day incubation experiment. CROM inoculation with the selected *Streptomyces* strains improved and accelerated its degradation in controlled conditions. © 2021 Friends Science Publishers

Key words: Cellulose degradation; Actinobacteria; *Streptomyces* sp.; Inoculation; Enzymes

Introduction

Cellulose is a major component of plant biomass and the most common organic compound on earth (Gonzalo *et al.* 2016). By chemical composition, cellulose is a linear polysaccharide composed of glucose molecules connected with β 1–4 glycosid bonding (Hussain *et al.* 2017). Plants produce 4×10^9 tons of cellulose per year (Abedin 2015). The remains of crops rich in cellulose make up 50% of the agricultural organic matter dry mass, whose microbial degradation is a vital part of carbon cycle in the biosphere. The decomposition of that biomass is done by cellulolytic bacteria, fungi and actinobacteria (Haruta *et al.* 2002). Microorganisms produce hydrolytic enzymes called cellulases, a complex of three important enzymes that act synergistically thanks to the crystalline and amorphous complex structure of cellulose. These enzymes hydrolyze cellulose into cellobiosis, glucose and oligo-saccharides.

Actinobacteria play an important role in the degradation of cellulose rich organic matter. About 90% of the total population of actinobacteria is species of the genus *Streptomyces* (Poopal and Laxman 2009). *Streptomyces* are slowly growing filamentous bacteria, abundant in soil, but also in environments with harsh

conditions since they are highly adaptable due to their thermo tolerance and spore forming ability. The genus is mainly known and researched for their production of various secondary metabolites such as antibiotics and volatile compounds (Elardo *et al.* 2009). But they also secrete extracellular enzymes (cellulases and proteases). Cellulose-degrading activity was found in the genus *Streptomyces* in various species and strains (Prasad *et al.* 2013; Devi *et al.* 2018). Research of Berlemont and Martiny (2013), aimed at genomic analyses of 5,123 bacterial genomes from 8 major phyla. It was demonstrated that nearly all *Streptomyces* genomes contained Carbohydrate-Active Enzymes (CAZy). Many authors showed that *Streptomyces* could be a source of CAZy and used in various enzyme based technologies (Saratale *et al.* 2012; Soeka *et al.* 2019). However, the introduction or *Streptomyces* strains to organic matter in order to enhance its decomposition is not enough investigated. Zhao *et al.* (2017) showed that inoculation of compost with *Streptomyces* strains H1, G1, G2, and *Actinobacteria* T9, at different stages improved cellulase activities and accelerated the degradation of cellulose. *Streptomyces albus* BM292 exhibited great potential for bioaugmentation of compost (Jurado *et al.* 2014). Olson *et al.* (2012) also argued that

actinobacteria could be used as inoculants in which cellulose was degraded into desired products.

Therefore, the aim of this research was to isolate and select *Streptomyces* strains with good cellulose degrading abilities. Moreover, another object of the study was to evaluate the CROM degradation potential of the selected strains on different cellulose rich substrates in *in vitro* condition.

Materials and Methods

Isolation of *Streptomyces* strains

Microorganisms were isolated from soil pseudogley (locality village Maovi near Šabac – Pocerina: N 44°41'43,73"; E 19°37'31,04") having the following characteristics: 1.67% CaCO₃; 5.19% humus; 0.26% N; 177.5 mg P₂O₅ in 100 g of soil; 105.34 mg K₂O in 100 g of soil; pH in H₂O 6.78; pH in KCl 5.80.

A 10 g of soil sample was suspended in 90 mL of 0.1 M MgSO₄×7H₂O buffer and shaken for 10 min at 180 rpm on a rotary shaker. The soil suspension was then diluted in four-fold steps in glass tubes to an end point dilution of 10⁻⁵. 100 µL of the dilutions (10⁻¹ to 10⁻⁵) were spread onto Synthetic agar (glucose 10 g L⁻¹, NaNO₃ 10 g L⁻¹, K₂HPO₄ 10 g L⁻¹, KCl 10 g L⁻¹, MgSO₄ × 7H₂O 10 g L⁻¹, agar 15 g L⁻¹), and incubated at 28°C for 7–10 days. Powdery colonies which were established as gram-positive, filamentous bacteria that form a branching network of filaments and produce spores were picked.

Physiological and biochemical characterization of *Streptomyces* isolates

To determine the carbon source utilization, isolates were grown on Hugh-Lifsson medium (pepton 2 g L⁻¹, K₂HPO₄ 0.3 g L⁻¹, NaCl 5 g L⁻¹, carbon source 10 g L⁻¹, brom-thymol blue 0.03 g L⁻¹, agar 3 g L⁻¹) with different carbon source (glucose, fructose, lactose, sucrose, xylose). The change in color, from green to yellow, indicated a positive reaction.

The isolates ability to grow at different temperatures (5, 15, 28, 37 and 45°C), on substrates of different acidity (pH 5, 7 and 9) and on substrates with different NaCl concentrations (3, 5 and 7%) were monitored on potato dextrose agar (PDA). The isolates were incubated for 7 days. The diameter of the isolates colony was measured and compared with the control.

The selected isolates were tested for their resistance to antibiotics (penicillin 10 µg mL⁻¹, novobiocin 5 µg mL⁻¹, tetracycline 30 µg mL⁻¹, chloramphenicol 30 µg mL⁻¹) by disk-diffusion method (Amna *et al.* 2019). After seven days of incubation at 28°C, the results were recorded by measuring the diameter of the inhibition zone around the disks. Completely tolerant isolates were denoted by “-no zone; + zone of inhibition of 0–2 mm; ++ zone of inhibition of 2–5 mm.

In vitro assay of extracellular enzymatic activities

Production of pectinase was tested by the method of agar plates on pectin agar. Incubation lasted 24 h at 37°C, after which colonies were overflowed with lugol. The appearance of uncolored zones around the colony was the evidence of pectinase activity (Soriano *et al.* 2000; Soares *et al.* 2001). Cellulase production was performed by flooding a solution of Congo-red (1 mg cm⁻³ H₂O) on isolates grown on CMC agar (Kasing 1995). The presence of halo zone around the colony was the proof of the cellulose decomposition. Starch hydrolysis was assayed on starch agar, following the protocol as reported by Cappuccino and Sherman (1992).

Urea degradation was tested on Christensen's urea agar (meat peptone 1 g L⁻¹, dextrose 1 g L⁻¹, NaCl 5 g L⁻¹, Na₂HPO₄ 1.2 g L⁻¹, KH₂PO₄ 0.8 g L⁻¹, phenol-red 0.012 g L⁻¹, agar 15 g L⁻¹, urea 20 g L⁻¹). The appearance of the reddish color in the medium indicates the ureolytic activity of the isolate. Lipase production was examined on medium (pepton 10 g L⁻¹, NaCl 5g L⁻¹, CaCl₂ × H₂O 0.1 g L⁻¹, agar 15 g L⁻¹) with Tween 80 addition. Formation the turbid zones around the colony are evidence of lipolytic activity. Hydrolysis of gelatin was tested on deep gelatinous agar (meat extract pepton broth (MPB) + 10–15% gelatin) (Aneja 2003). After incubation, degradation of gelatin in inoculated tubes was proof of the gelatinase activity.

Streptomyces isolates were screened for PGP activities on hydrogen cyanide (HCN) induction medium (Tryptic Soy Broth 30 g L⁻¹, Glycine 4.4 g L⁻¹, agar 15 g L⁻¹), chrom-azuroil S (CAS) medium and tryptone broth (containing 5 mmol L⁻¹ tryptophan) for HCN, IAA and siderophores production, respectively (Schwyn and Neilands 1987; Frey-Klett *et al.* 2005; Etesami *et al.* 2015).

Molecular identification

Actinobacteria DNA extraction was performed using the Gene MATRIX Gram Plus and Yeast Genomic DNA Purification Kit (EURx Ltd.80–297, Gdansk Poland). The amount of DNA from four actinobacteria samples was determined on a QFX Fluorometer apparatus (Denovix Inc, Wilmington, USA). 16s rRNA gene sequences were obtained using two universal actinobacteria primers. The first primer pair was 27F AGAGTTTGATCMTGGCTCAG 1492R GGYTACCTTGTTACGACTT, while the second primer pair was S-C-Act-0235-a-S-20 GGCCTATCAGCTTGTTG S-C-Act-0878-a-ACG CCGG. After sequencing, two 1300 nucleotide length sequences and two 600 nucleotide length sequence were obtained. Further identification was performed using the BLAST algorithm into which the sequences were inserted (<http://www.ncbi.nlm.nih.gov/genbank/>).

Incubation experiment

The incubation experiment was performed on three different

sources of organic matter – straw briquettes, beech briquettes, and legume mix (containing six different beans and peas' varieties mixture). The amount of different fractions in investigated substrates is presented in Table 1.

The substrates were sterilized in autoclave (1 h at 121°C). 10 g of each substrate were measured and placed in sterile Petri dish (9 cm diameter). The treatments were: 1. Control (water); 2. *S. zaomyceticus* CA1; 3. *S. tanashiensis* CA10. Each treatment contained three repetitions. A seven days culture of both strains was used. Spores were counted in the Neubauer chamber, and their number was calculated in 1 mL of liquid nutrient medium. By adding saline, the number was brought to 10⁶ spores in 1 mL of inoculums and 10 mL was used per treatment, respectively.

The incubation experiment lasted 30 days in controlled conditions (constant temperature 25°C, moisture content was maintained at 60% field capacity). The amount of crude cellulose was determined by the filter bags method (Page *et al.* 1982) on the ANCOM 2000 apparatus. The percentage of crude cellulose was calculated using the formula:

$$\% \text{ crude cellulose} = 100 \times (W3 - (W1 \times C1)) / W2$$

Where W1 is the mass of the filter bag; W2 represents the mass of the sample; W3 is the mass of organic matter and C1 is the content-based correction factor.

Statistical analyses

The incubation experiment was conducted in a completely randomized block design with three replications. The data were subjected to analysis of variance (ANOVA) to evaluate the efficiency of *Streptomyces* strains application. The least significant difference test (Fisher LSD) was performed to compare the results between treatments at $P > 0.05$. Software *Statistica*, version 13.3 (TIBCO Software Inc.) was used for statistical analysis.

Results

Selection and identification of *Streptomyces* strains

Total 32 actinobacterial isolates were isolated. Based on colony morphology, color, size and appearance isolates were grouped. The isolates with whitish, compact, large to gigantic colonies with wavy edges were designated as possible *Streptomyces* isolates (11 isolates). Further microscopic observation proved the Gram positive, filamentous spore forming cells in four isolates with numbers CA1, CA10, PA2 and PA7. Those isolates were chosen for further physiological, biochemical characterization and genetic identification.

Physiological characterization of *Streptomyces* strains

To characterize the growth conditions, the selected strains were grown at the specified temperature (5–45°C), pH

(5–9), and NaCl concentrations (3–7%). Several C source (five sugars) and antibiotics were used to test C utilization and resistance, respectively (Table 2). The results showed that the best temperatures for growth were between 28°C to 37°C for all four *Streptomyces* strains. They grew well in neutral pH but also in highly alkaline medium, except strain PA7, indicating its quite wide pH tolerance. It was also found that the strains were not grown even at the lowest tested NaCl concentration (except CA1), suggesting that the strains might be halophobic. CA1 and PA7 used lactose and sucrose as C source, respectively. Only CA10 showed lack of antibiotic resistance towards tetracycline, penicillin and chloramphenicol.

Biochemical characterization of *Streptomyces* strains

Streptomyces strains CA1 and CA10 showed the best cellulose production and starch hydrolysis abilities, followed by strains PA2 and PA7 (Table 3). All four strains were weakly positive to urease test, and also to lipase production. Production of HCN is important for plant pathogen suppression. Only strain PA2 proved negative.

Molecular identification

All four actinobacterial samples were sequenced with two pairs of nucleotides to obtain a sequence of about 1,300 nucleotides in length. After sequencing, two isolates (PA2, CA10) obtained this length, while in PA7 and CA1 isolates, about 600 nucleotides were obtained, which was quite enough to perform the identification up to species level.

CA1 isolate obtained 608 nucleotide sequences. Based on the comparison with the existing sequences from BLAST, the isolate belonged to *S. zaomyceticus*. CA10 isolate obtained 1372 nucleotide sequences. Based on the comparison with the existing sequences from BLAST, the isolate belonged to *S. tanashiensis*. PA2 isolate obtained 1347 nucleotide sequences. Based on the comparison with the existing sequences from BLAST, the isolate belonged to *S. ambofaciens*. PA7 isolate obtained 633 nucleotide sequences. Based on the comparison with the existing sequences from BLAST, the isolate belonged to *S. zaomyceticus*.

Incubation experiment

Thirty-day incubation experiment showed that the amount of raw cellulose in the investigated substrates decreased in all treatments (Table 4).

Percent decrease of the raw cellulose content varied among treatments (Table 5). In straw briquettes treated with *S. zaomyceticus* CA1, the decrease compared to the amount at the beginning of the experiment was 69.65% while this reduction was 65.89% with the addition of *S. tanashiensis* CA10. By adding *S. zaomyceticus* to the beech based substrate, after a month of incubation, there was a 51.57%

decrease in the amount of cellulose compared to the initial stage. *S. tanashiensis* also reduced the cellulose content by 56.49%. In the legume-based substrate, the amount of raw cellulose was reduced by 81.32% after the addition of *S. zaomyceticus* CA1 (Fig. 1). *S. tanashiensis* CA10 decreased the amount of cellulose by 64.2% compared to the initial state.

Discussion

The *Streptomyces* strains were mesophylic, typical for the agroecological conditions of the region they originated from. This is in accordance with the research of Stamenov (2013), who determined that the optimal temperatures for actinobacteria growth were between 28 and 37°C, while no isolate grew at 3 and 45°C. Sreevidya *et al.* (2016) showed that four actinobacterial isolates grew on temperatures between 20 and 40°C and pH ranging between pH 7–11. Our research showed that the tested strains were neither particularly good users of sugars (lactose by CA1 and sucrose by PA7) nor did they grow in medium with added NaCl (only CA1 grew at 3% NaCl). Those results are in contrast to those of Stamenov *et al.* (2016), who concluded that the *Streptomyces* isolates used glucose, galactose, fructose, sucrose, lactose and xylose as C source and grew in media with elevated salinity (added 3–7% NaCl). On the other hand, Dhanasekaran *et al.* (2009) found that *Streptomyces* DPTD-5 and *S. bikiniensis* used sucrose, lactose and fructose as carbon source. Antibiotic resistance test singled out only strain CA10 as susceptible towards antibiotics. In the work of Koushalshahi *et al.* (2012) noted differential sensitivity of *Streptomyces* isolates towards seven antibiotics including nitrofurantoin, nalidixic acid, gentamycin, erythromycin and rifampicin, while they were resistant to penicillin and ampicillin.

Our research showed that actinobacteria strains produced many extracellular enzymes, which participated in the mineralization of investigated organic matter. All four strains produced cellulase, amylase and lipase enzymes while one produced pectinase (CA1) and gelatinase (PA7). Aly *et al.* (2012) found that 20 out of 33 isolates of the genus *Streptomyces* sp. produced lipases. On the other hand, Dhanasekaran *et al.* (2009) found only one isolate, out of 20 to perform hydrolysis of lecithin, lipids, pectin and starch, which is in accordance with our results. Gopalakrishnan *et al.* (2011) also noticed that two of the five investigated actinomycetes produced cellulase and protease enzymes. Research by Alam *et al.* (2004) determined that different *Streptomyces* strains were capable of producing cellulolytic enzymes during growth on various cellulose substrates.

Statistically significant decomposition was achieved by addition of *Streptomyces* strains, though decrease of cellulose content in the watered treatment ranged between 24.23% in straw briquettes and 44.43% in beech briquettes. Those results could be attributed to the process of cellulose natural decomposition which occurs at a very low rate under

Table 1: Basic chemical composition of the substrates - fresh mass (g 100 g⁻¹)

Substrates	Dry matter	Moisture	Raw cellulose	Ash
Straw briquettes	92,06	7,94	39,40	7,06
Beech briquettes	92,26	7,74	55,63	1,04
Legume mix	91,81	8,19	29,65	8,85

Table 2: Physiological characterization and growth conditions

Growth conditions	Strain number			
	CA1	CA10	PA2	PA7
Temperature (°C)*				
5	-	-	-	-
15	+	+	-	-
28	++	++	++	+
37	++	++	++	++
45	-	-	-	-
pH*				
5	-	++	++	-
7	++	++	++	+
9	++	++	+	-
NaCl concentration (%)*				
3	+	-	-	-
5	-	-	-	-
7	-	-	-	-
C source*				
Glucose	-	-	-	-
Fructose	-	-	-	-
Lactose	+	-	-	-
Sucrose	-	-	-	+
Xylose	-	-	-	-
Antibiotics resistance**				
Penicillin 10 µg mL ⁻¹	-	+	-	-
Tetracyclin 30 µg mL ⁻¹	-	++	-	-
Novobiocin 5 µg mL ⁻¹	-	-	-	-
Chloramphenicol 30 µg mL ⁻¹	-	+	-	-

*-negative; + weakly positive; ++ positive

**-no zone; + zone of inhibition of 0–2 mm; ++ zone of inhibition of 2–5 mm

Table 3: Biochemical properties of *Streptomyces* strains

Biochemical properties	Strain number			
	CA1	CA10	PA2	PA7
Pectinase test	+	-	-	-
Cellulase production	+++	+++	+	+
Starch hydrolysis	+++	+++	+	+
Urease test	+	+	+	+
Lipase production	+	+	+	+
Gelatin hydrolyses	-	-	-	-
Production of HCN	+	+	-	+
IAA production	-	+	-	-
Siderophore production	-	-	-	-

-negative; + weakly positive; ++ positive; +++ strongly positive

normal atmospheric conditions (Jeong *et al.* 2012). Thus, little is known about water solubility of cellulose and the reactions needed to break the hydrogen bonds which stabilize the structure of cellulose (Levi *et al.* 2016). It was demonstrated that *S. zaomyceticus* CA1 and *S. tanashiensis* CA10 were particularly good producers of both cellulases and amylases. The results obtained after the one month incubation experiment with CA1 and CA10 strains, showed that the amount of raw pulp decreased between 51.7% (from 554.4 to 268.5 mg g⁻¹) to as much as 81.69% compared to the initial state (295.5 compared to 55.2 mg g⁻¹).

This coincided with the results obtained of Zhao *et al.* (2017), who showed accelerated degradation of cellulose by microorganisms. They added cellulolytic thermophilic actinobacteria to manure and corn straw at different periods (several inoculations during decomposition) and showed that inoculation led to an increase in cellulolytic enzymes activity, accelerated the degradation of cellulose, increased the content of humus substances and changed the structure of the actinobacteria community. In the work of Zhao *et al.* (2016) chicken manure was inoculated with *Streptomyces* sp. and *Micromonospora* sp during composting by different methods of inoculation. The inoculation significantly accelerated the degradation of manure, especially the cellulose fraction, which is consistent with the results of our research. Maximum reduction of raw cellulose content was achieved after inoculation of legume mix substrate with *S. zaomyceticus* CA1. In this perspective, Sanchez *et al.* (2017) concluded that it is necessary to develop technologies that should aim at improvement of the nutritional characteristics of compost. By the addition of nutrients from natural sources as well as microorganisms, the concentration of nutrients in compost that are available to plants could be increased. Varma *et al.* (2017) after a study on the microbial population involved in the degradation of ligno-cellulose during the composting of mixed organic waste (e.g. plant waste, manure fertilizer, dry leaves) concluded that combinations of waste materials had a great influence on microbial degradation of waste material and quality of final compost, due to their physical properties. Heterotrophic bacteria were predominantly active during the initial composting phase due to available organic matter, while actinobacteria were active during the degradation of lingo-cellulose fractions.

Conclusion

S. zaomyceticus CA1 and *S. tanashiensis* CA10, decreased the amount of the raw cellulose between 38.38 and 81.69% in all three investigated substrates (straw, beech, legume), during a 30 day incubation period. The selected strains showed a potential to promote the degradation of cellulose in the substrates. Their application in agriculture, as mineralization enhancer could speed up the biodegradation processes of cellulose rich OM in soil. It could also help to harvest different end products which are formed as a result of fermentation of various materials and wastes rich in carbohydrates.

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Author Contributions

SDj planned the experiments, THJ, DS and BN gathered

Table 4: Cellulose content in investigated substrates (mg g⁻¹)

Substrate	Initial state	øH ₂ O	CA1	CA10
Straw briquettes	392.1b*	297.1k	119.0h	133.7g
Beech briquettes	554.4a	308.1c	268.5d	241.2e
Legume mix	295.5k	165.2f	55.2j	105.8i

*Different letters in subscripts indicate statistically significant difference according to Fisher LSD test (p<0.05)

Table 5: Decrease of raw cellulose content compared to the initial state (%)

Substrate	øH ₂ O	CA1	CA10
Straw briquettes	24.23	69.65	65.9
Beech briquettes	44.43	51.57	56.49
Legume mix	44.1	81.32	64.2



Fig. 1: Substrate of legume mix: control (a) and treatment with *S. zaomyceticus* CA1 (b), 30 days after inoculation

and interpreted the results, VV and DV did the molecular analyses. DS statistically analyzed the data. SDj and THJ wrote the paper.

Conflicts of Interest

All authors declare no conflicts of interest

Data Availability

Not applicable in this paper

Ethics Approval

Not applicable in this paper

References

- Abedin JI (2015). Isolation and identification of cellulose degrading bacteria from soil sample. *Degree Dissertation*. Brac University, Dhaka, Bangladesh
- Alam MZ, MA Manchur, MN Anwar (2004). Isolation, purification, characterization of cellulolytic enzymes produced by the isolate *Streptomyces omiyaensis*. *Pak J Biol Sci* 7:1647-53
- Aly MM, S Tork, S Al-Garni, L Nawar (2012). Production of lipase from genetically improved *Streptomyces exfoliates* LP10 isolated from oil contaminated soil. *Afr J Microbiol Res* 5:1125-1137
- Amna S, B Sarfraz Din, Y Xia, MA Kamran, MT Javed, T Sultan, HJ Chaudhary (2019). Mechanistic elucidation of germination potential and growth of wheat inoculated with exopolysaccharide and ACC-deaminase producing *Bacillus* strains under induced salinity stress. *Ecotoxicol Environ Saf* 183; Article 109466
- Aneja KR (2003). *Experiments in Microbiology Plant Pathology and Biotechnology* (4th edn). New Delhi, India

- Berlemont R, AC Martiny (2013). Phylogenetic distribution of potential cellulases in bacteria. *Appl Environ Microbiol* 79:1545–1554
- Cappuccino JC, N Sherman (1992). *Microbiology: A Laboratory Manual* (3rd edn), pp: 125–179. Benjamin/Cummings Pub. Co., New York, USA
- Devi SS, NG Devi, MC Kalita, NC Talukdar (2018). Isolation and selection of cellulose-degrading microorganisms for utilization along with earthworms in efficient conversion of municipality waste mix to compost. *Curr Sci* 114:1261–1274
- Dhanasekaran D, S Selvamani, A Panneerselvam, N Thajuddin (2009). Isolation and characterization of actinomycetes in Vellar Estuary, Annagkoil, Tamil Nadu. *Afr J Biotechnol* 8:4159–4162
- Elardo PSM, M Scheuermayer, S Kozytska, U Hentschel (2009). *Streptomyces axinellae* sp. isolated from the Mediterranean sponge. *Axinella olypoides* (Porifera). *Intl J Syst Evol Microbiol* 59:1433–1437
- Etesami H, HA Alikhani, HM Hosseini (2015). Indole-3-acetic acid (IAA) production trait, a useful screening to select endophytic and rhizosphere competent bacteria for rice growth promoting agents. *MethodsX* 2:72–78
- Frey-Klett P, M Chavatte, ML Clause, S Courrier, C Le Roux, J Raaijmakers, MG Martinotti, JC Pierrat, J Garbaye (2005). Ectomycorrhizal symbiosis affects functional diversity of rhizosphere fluorescent pseudomonads. *New Phytol* 165:317–328
- Gonzalo DG, DI Colpa, MHM Habib, MW Fraaije (2016). Bacterial enzymes involved in lignin degradation. *J Biotechnol* 236:110–119
- Gopalakrishnan S, S Pande, M Sharma, P Humayun, BK Kiran, D Sandeep, MS Vidya, K Deepthi, O Rupela (2011). Evaluation of actinomycete isolates obtained from herbal vermicompost for biological control of *Fusarium* wilt of chickpea. *Crop Prot* 30:1070–1078
- Haruta S, Z Cui, Z Huang, M Li, M Ishii, Y Igarashi (2002). Construction of a stable microbial community with high cellulose degradation ability. *Appl Microbiol Biotech* 59:529–534
- Hussain AA, MS Abdel-Salam, HH Abo-Ghaila, WK Hegazy, SS Hafez (2017). Optimization and molecular identification of novel cellulose degrading bacteria isolated from Egyptian environment. *J Genet Eng Biotechnol* 15:77–85
- Jeong MJ, AL Dupont, ER de la Rie (2012). Degradation of cellulose at the wet-dry interface: I—study of the depolymerization. *Cellulose* 19:1135–1147
- Jurado M, MJ López, F Suárez-Estrella, MC Vargas-García, JA López-González, J Moreno (2014). Exploiting composting biodiversity: study of the persistent and biotechnologically relevant microorganisms from lignocellulose-based composting. *Bioresour Technol* 162:283–293
- Kasing A (1995). *Cellulase Production, Practical Biotechnology*. Sarawak, Malaysia
- Koushalsahi MB, Kh Issazadeh, A Tehranifard, MRMK Pahlaviani, A Massiha (2012). Isolation of Hg and Cu resistant *Streptomyces* from marine sediments in different regions of the Caspian Sea. *Afr J Microbiol Res* 6:4048–4052
- Levi N, AM Khenkin, B Hailegnaw, R Neumann (2016). Depolymerization of cellulose in water catalyzed by phenylboronic acid derivatives. *ACS Sust Chem Eng* 4:5799–5803
- Olson DG, JE McBride, AJ Shaw, LR Lynd (2012). Recent progress in consolidated bioprocessing. *Curr Opin Biotechnol* 23:396–405
- Page AL, RH Miller, DR Kenney (1982). *Methods of Soil Analysis, Part 2. Chemical and Microbiological Properties*, 2nd edn. American Society of Agronomy, Madison, Wisconsin, USA
- Poopal AC, RS Laxman (2009). Studies on the biological reduction of chromate by *Streptomyces griseous*. *J Haz Mat* 169:539–45
- Prasad P, T Singh, Sh Bedi (2013). Characterization of the cellulolytic enzyme produced by *Streptomyces griseorubens* (Accession No. AB184139) isolated from Indian soil. *J King Saud Univ Sci* 25:245–250
- Sanchez OJ, DA Ospina, S Montoya (2017). Compost supplementation with nutrients and microorganisms in composting process. *Waste Manage* 69:136–153
- Saratale GD, RG Saratale, SE Oh (2012). Production and characterization of multiple cellulolytic enzymes by isolated *Streptomyces* sp. MDS. *Biomass Bioener* 47:302–215
- Schwyn B, JB Neilands (1987). Universal chemical assay for the detection and determination of siderophores. *Anal Biochem* 160:47–56
- Soares MM, R da Silva, EC Carmona, E Gomes (2001). Pectinolytic enzyme production by *Bacillus* species and their potential application on juice extraction. *J Microbiol Biotechnol* 17:79–82
- Soeka YS, S Nandang, T Evi, T Yulinery (2019). Characterization of Cellulase Enzyme Produced by Two Selected Strains of *Streptomyces macrosporeus* Isolated from Soil in Indonesia. *Makara J Sci* 23:65–71
- Soriano M, P Diaz, FIJ Pastor (2000). Pectinolytic systems of two aerobic sporogenous bacterial strains with high activity on pectin. *Curr Microbiol* 50:114–118
- Sreevidya M, S Gopalakrishnan, H Kudapa, RK Varshney (2016). Exploring plant growth-promotion actinomycetes from vermicompost and rhizosphere soil for yield enhancement in chickpea. *Braz J Microbiol* 47:85–95
- Stamenov D, S Đurić, T Hajnal-Jafari, D Jošić, M Manojlović (2016). The use of *Streptomyces* isolate with plant growth promoting traits in the production of English ryegrass. *Rom Agric Res* 33, www.inceda-fundulea.ro DII 2067-5720 RAR 2016-70
- Stamenov D (2013). Karakterizacija mikroorganizama promotora rasta i njihovo preživljavanje u rizosferi engleskog ljujla. *Doctoral Degree Dissertation* Doktorska disertacija. Univerzitet u Novom Sadu, Poljoprivredni fakultet (in Serbian)
- Varma VS, S Das, CV Sastri, AS Kalamdhad (2017). Microbial degradation of lignocellulosic fractions during drum composting of mixed organic waste. *Sustain Environ Res* 27:265–272
- Zhao Y, Q Lu, Y Wei, H Cui, X Zhang, X Wang, S Shan, Z Wei (2016). Effect of actinobacteria agent inoculation methods on cellulose degradation during composting based on redundancy analysis. *Bioresour Technol* 219:196–203
- Zhao Y, Y Zhao, Z Zhang, Y Wei, H Wang, Q Lu, Y Li, Z Wei (2017). Effect of thermo-tolerant actinomycetes inoculation on cellulose degradation and the formation of humic substances during composting. *Waste Manage* 68:64–73