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2 **Isolation, Identification and Evaluation of the**  
3 **Plant Growth Promoting Activities of**  
4 **Endophytic *Stenotrophomonas maltophilia* to**  
5 **Stimulate Growth of Clover Plants under Salt**  
6 **Stress**

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12 **ABSTRACT**  
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Two endophytic bacterial isolates were obtained from root nodules of clover plants grown in the salt-affected clay soil of Egypt. Based on the sequencing and phylogenetic analysis of *16S rRNA* genes, the isolates were closely linked to *Stenotrophomonas maltophilia* strains IPR-Pv696 and 262XG2 and deposited in GenBank with accession numbers OM980221.1 (Am1) and OM980223.1 (Am2), respectively. We evaluated the potential of both isolates to promote plant growth and found that the two isolates, IPR-Pv696 and 262XG2, respectively, produced indole-3- acetic acid (30.26 & 31.15 µg/ml) and exopolysaccharides (13.57 & 13.68 g/l). In addition, there was a difference in their nitrogen fixation activity and their ability to solubilize phosphate, 278 & 208 mg/l, and potassium, 33.5 & 32.9 µg/ml), respectively. Under salty soil field conditions, both isolates increased clover plant growth, chlorophyll, carbohydrate content, and nutrient uptake while lowering proline levels. Our results highlight the advantages of applying *Stenotrophomonas maltophilia* as a biofertilizer for clover and possibly for other crops in sustainable agriculture.

14 *Keywords: Endophytic bacteria; Stenotrophomonas; PGPR; 16S rRNA; Phylogenetic tree*

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16 **1. INTRODUCTION**  
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18 Using biofertilizer as an alternative to chemical fertilizers is safer, cost-effective, and  
19 ecologically beneficial [1]. These biopreparations are known to have a variety of plant  
20 growth-promoting (PGP) traits, which improve plant health, growth, and production [2].  
21 Endophytic bacteria from root nodules have recently drawn increased interest as unique  
22 resources for enhancing plant development. The endophytic bacteria reside inside plant  
23 tissues without any observed alteration of the morphology of their hosts. They significantly  
24 impact the plants' capacity to absorb nutrients because they are more efficient in nutrient  
25 transformation, mobilization, and solubilization [3,4]. Additionally, they benefit host-plants by  
26 fixing nitrogen, solubilizing phosphate, and producing indole-3- acetic acid (IAA) [5]. It was  
27 thought that the only rhizobial bacteria found in the root nodules of leguminous plants were  
28 endophytic bacteria; however, a variety of non-rhizobial bacteria are also housed in root  
29 nodules and have a noticeable impact on the crop's survival, nodulation, and grain yield  
30 [6,7,8]. *Stenotrophomonas* bacteria received increased attention because they could serve  
31 as efficient bioinoculants for promoting plant development and controlling various diseases  
32 [9]. *S. maltophilia*, a species of *Stenotrophomonas*, is recognized as a crucial species for  
33 boosting plant development in agriculture [10]. Gram-negative bacteria of the  
34 *Stenotrophomonas* genus are members of the *Xanthomonadaceae* family. Endophytes and  
35 free-living bacteria, *Stenotrophomonas* species, have been identified as the major species in

36 the bacterial community linked with plants [11, 12]. In prior research, the *Stenotrophomonas*  
37 genera were shown to be effective phosphate solubilizers and biofertilizers [13]. According to  
38 [9], *S. maltophilia* can fix nitrogen in plants, including peanuts, wheat, maize, and rice [14].  
39 The *Stenotrophomonas* genus has been used as a rhizospheric microbiota of different crops,  
40 including corn [15, 16]. [17] confirmed the plant growth-promoting potential of *S. maltophilia*  
41 in wheat plants, along with resistance against biotic and abiotic stress.

42 The 16S rRNA genes are present in all prokaryotes and code for the RNA component of the  
43 ribosomal 30S subunit that has an essential role in translation [18]. Sequencing the 16S  
44 rRNA gene is the most effective method for identifying unknown bacteria. A root represents  
45 a phylogenetic tree's bacterial taxonomic origin pattern [19, 20].

46 Egyptian clover (*Trifolium alexandrinum* L.) is Egypt's primary annual winter forage  
47 leguminous crop. Berseem clover is highly nutritious for the animal field and improves soil  
48 fertility and its physical characteristics [21]. Berseem forage is superior to grasses in protein  
49 and mineral contents [22].

50 The present work intends to isolate and identify two bacterial isolates using 16S rRNA  
51 technology and study plant growth-promoting activities of *Stenotrophomonas maltophilia*  
52 isolated from the nodules of clover plants to determine the effect of their inoculation to plants  
53 under salinity stress conditions.

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## 55 **2. MATERIAL AND METHODS**

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### 57 **2.1 Isolation of nodule endophytes**

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59 Nodules were collected randomly from each clover plant, washed with sterile distilled water  
60 to remove soil particles and surface sterilized with 95 % alcohol for 30 seconds and 0.1 %  
61 HgCl<sub>2</sub> (w/v) for 2 min before being rinsed 6-8 times with sterile distilled water to remove  
62 HgCl<sub>2</sub> completely. For the isolation of endophytic bacteria, the surface-sterilized nodules  
63 were crushed and streaked on yeast-extract-mannitol agar (YEMA) plates as indicated by  
64 [23, 24] and Luria Bertani agar medium based on the modified method of [25]. Single  
65 colonies were purified further by repeatedly streaking on the same medium for three days at  
66 30 °C. The isolates were kept at -20 °C in glycerol (20% v/v).

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### 68 **2.2 Molecular characterization**

#### 69 **2.2.1 DNA isolation**

70 Total genomic DNA was isolated and purified following the technique described in [26]. The  
71 quality of the extracted DNA from several bacterial species was assessed On a 1% Agarose  
72 gel.

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#### 74 **2.2.2 Identification of isolates by 16S rRNA sequencing**

75 Isolated DNA was amplified with 16S rRNA in a PCR tube and 20 µl of the reaction solution. The  
76 PCR amplification was performed using 27F/1492R universal primers [27], as shown in Table 1. The  
77 amplification took place over 35 cycles for 45 sec at 94° for denaturation, 55°C for 60 sec for  
78 annealing, and extension at 72°C for 60 sec. The PCR include a positive control (*E. coli* genomic  
79 DNA) and a negative control. The PCR amplicon purification was completed using a column-based  
80 technique and the Montage PCR Clean-up kit (Macro gen). The purified PCR products were  
81 sequenced using two primers, as described in table 1. Big Dye Terminator Cycle Sequencing Kit was

82 used for the sequencing, and an Applied Biosystems model 3730XL automated DNA sequencing  
83 device was used to resolve the results (Applied BioSystems, USA).

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### 85 **2.2.3 Nucleotide sequence accession numbers**

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87 The *16S rRNA* gene sequences of chosen isolates were compared to the *16S rRNA* gene  
88 sequences using BLASTN in the GenBank database. A phylogenetic tree was constructed  
89 using the Neighbor joining method.

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91 **Table 1. The sequences of the forward and reverse primers used for 16S rRNA**  
92 **amplification and sequencing**

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Primers	Sequences
Amplification primers	27F 3' AGA GTT TGA TCM TGG CTC AG 5'
	1492R 3' TAC GGY TAC CTT GTT ACG ACT T 5'
Sequencing Primers	518F 3' CCA GCA GCC GCG GTA ATA CG 5'
	800R 3' TAC CAG GGT ATC TAA TCC 5'

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## 97 **2.3 Plant growth promoting attributes**

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### 98 **2.3.1 Indole acetic acid (IAA) production**

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Using the colorimetric technique outlined by [30], IAA production was quantified. In LB broth with L-tryptophan added, the isolated bacteria's pure colony grew for three days at  $30 \pm 2^\circ\text{C}$ . After incubation, bacteria were extracted using a centrifuge set at  $3824 \text{ xg}$  for 15 minutes, and 2 ml of the supernatant was mixed with two drops of orthophosphoric acid and 4 mL Salkowski's reagent, then measured at 530 nm by spectrophotometry.

### 105 **2.3.2 Exopolysaccharides (EPS) production**

To estimate EPS production, bacterial strain was inoculated into conical flasks containing 100 ml of YEM broth. The inoculated flasks were incubated at  $30 \pm 1^\circ\text{C}$  on a rotary shaker at 200 rpm for 72 h. After incubation, the culture broth was centrifuged at  $3500 \text{ xg}$ , and the supernatant was mixed with two volumes of acetone. The crude polysaccharides developed were collected by centrifugation at ( $3500 \text{ xg}$ ) for 30 min. The EPS was washed with distilled water and acetone alternately, transferred onto a filter paper and the amount of exopolysaccharides was calculated by dry-weight measurements as g/l according to [31].

### 114 **2.3.3 Nitrogen Fixing Activity**

Nitrogen-fixing activity was examined using Jensen's medium and Bromothymol Blue (BTB) as a colour indicator, according to [32].

### 118 **2.3.4 Estimation of phosphate solubilization**

119 Qualitative determination of phosphate solubilization was performed on Pikovskaya's agar  
120 plate (PVK) medium [33]. Isolate was spot inoculated and incubated at  $28 \pm 2^\circ\text{C}$ . The size of  
121 the halo corresponding to phosphate solubilization was measured after 3-7 days of  
122 incubation. Phosphate solubilization was expressed as solubilizing efficiency (SE %) [34,  
123 35]. Quantitative estimation of tri-calcium phosphate solubilization was performed by growing  
124 the bacterial strain in Pikovskaya's broth. The concentration of the soluble phosphate was  
125 determined from the culture supernatant.

126 Phosphate solubilization efficiency = (Solubilization diameter (S) x 100)/(growth diameter)

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### 128 **2.3.5 Estimation of potassium solubilization**

129 The spotting method was used to investigate potassium solubilization by bacterial isolates  
130 on Aleksandrov medium plates containing insoluble mica powder as a potassium source  
131 [36]. Plates were incubated for seven days at  $28^\circ\text{C} \pm 2$ . The ability of bacterial isolates to form  
132 solubilization zones was used to detect potassium solubilization. Quantitative estimation of  
133 potassium release was performed by growing bacterial isolates in Aleksandrov broth  
134 medium and incubating for seven days at  $28^\circ\text{C} \pm 2$ . Following the incubation, the broth  
135 cultures were filtered through Whatman No. 1 filter paper and centrifuged for 20 minutes at  
136 12,000 rpm. The soluble K content in the supernatant was measured using a flame  
137 photometer [37].

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## 139 **2.4 Field Experiment**

140 To elucidate the role of the isolated bacteria in alleviating salt stress in Clover plants grown  
141 in saline soil compared to *R. leguminosarum* bv. *trifolii* strain 102, specific to Clover plants, a  
142 field experiment was carried out at El-Rowad village farm, Sahl El-Hussinia, El-Sharkia  
143 Governorate, Egypt, with a randomized complete block design and three replicates. Seeds  
144 of clover plants were inoculated with gamma-irradiated vermiculite-based inoculants. All  
145 treatments received the half-recommended dose of phosphorus, potassium and nitrogen.  
146 The treatments were as follows:

- 147 1. Control (Recommended dose of NPK)
- 148 2. *R. Leguminosarum* bv. *trifolii* strain 102 + half dose of NPK
- 149 3. *S. maltophilia* strain IPR-Pv696 + a half dose of NPK
- 150 4. *S. maltophilia* strain 262XG2 + a half dose of NPK

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## 152 **2.5 Plant growth parameters**

153 Each plot's fresh yield was measured immediately after harvesting to prevent humidity loss.  
154 A 500 g sample from each plot was dried at room temperature without exposure to sunlight  
155 to determine the forage's dry weight. After a few days, when samples showed a stable  
156 weight over three additional days, the weight obtained was scored as an approximation of  
157 the dry weight percentage of the dry matter produced by each treatment. Shoots'  
158 carbohydrate and chlorophyll contents were measured. Dry samples were ground and

159 digested utilizing the H<sub>2</sub>SO<sub>4</sub> and HClO<sub>4</sub> acid mixture [38]. The method described by [39]  
 160 was used to determine the plants' N, P, and K content in the plant digests.

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## 162 2.6 Proline determination

163 Proline was extracted from the shoot, and its concentration was determined using the [40].  
 164 Using a standard curve, the proline content was determined by spectrophotometer at 520  
 165 nm as  $\mu$  mole proline / g of fresh weight material.

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## 167 2.7 Soil analysis

168 A surface soil sample (0–30 cm) was air dried, sieved using a 2 mm sieve, and thoroughly  
 169 mixed. According to [41], calcium carbonate, soil organic matter (SOM), total soluble ions,  
 170 and electrical conductivity (EC) were all measured in the saturated soil paste extract. The pH  
 171 of soil suspension (1: 2.5) was measured using a pH meter (Table 2). [38] measured the  
 172 available nitrogen using the modified Kjeldahl method. Following the methodology outlined  
 173 by [42], the available phosphorus, potassium, and micronutrients (Mn, Fe, and Zn) were  
 174 extracted using ammonium bicarbonate, and their concentrations were assessed using an  
 175 ICP Spectrometer (model 400).

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177 **Table 2. Physical and chemical properties of the soil sample before planting**

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Coarse sand (%)	Fin sand (%)	Silt (%)	Clay (%)	Texture	O.M (%)	CaCO <sub>3</sub> (%)		
4.2	15.2	35.5	45.3	Clay	0.47	11.5		
pH (1:2:5)	EC (dS/m)	Cations (meq <sup>-1</sup> )			Anions (meq <sup>-1</sup> )			
		Ca <sup>++</sup>	Mg <sup>++</sup>	Na <sup>+</sup>	K <sup>+</sup>	HCO <sub>3</sub> <sup>-</sup>	Cl <sup>-</sup>	SO <sub>4</sub> <sup>-</sup>
8.12	12.82	22.61	35.61	68.5	1.48	4.61	95.61	27.98
N	P	K	Zn	Mn	Fe	Cu		
PPM								
107.1	2.95	171.16	0.868	2.16	1.85	0.61		

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## 180 2.8 Statistical analysis

181 Data were statistically analyzed using the general linear model's procedure of SAS [43]. The  
 182 significant differences between treatments were statistically tested using Duncan's multiple-  
 183 range tests.

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