

# In Vitro Antimicrobial Activity of Endophytes, Isolated from *Moringa peregrina* Growing in Eastern Region of Saudi Arabia

Amal Aljuraifani<sup>1</sup>  · Sahar Aldosary<sup>1</sup> · Ibtisam Ababutain<sup>1</sup>

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**Abstract** Seven endophytes bacteria were isolated from *Moringa peregrina* and identified using 16S ribosomal RNA sequences, which revealed two bacterial genera, namely *Proteus mirabilis* and *Bacillus*; three species belong to *Bacillus*: *B. licheniformis*, *B. subtilis* subsp. *Inaquosorum* and *B. pumilus*. The antimicrobial activity of the isolate was screened against 11 human pathogens, and the potency of the selected isolate was qualitatively and quantitatively analyzed by the cross-streak method and minimum inhibitory concentrations (MICs), respectively. Minimum inhibitory concentration (MIC) of the organic extract of selected isolate *B. licheniformis* MpKL1 was found to exhibit appreciable growth inhibition between 125 µg/ml and 500 µg/ml against most tested human pathogens and less influence against *Acinetobacter baumannii*, *Enterobacter aerogenes*, *Streptococcus pyogenes* and *Candida albicans* with MIC > 1000.

**Keywords** Antimicrobial · Endophytes · *Moringa peregrina*

Medicinal plants are the most useful source of lifesaving drugs for humans, animals and plants. Bioactive

compounds that are usually extracted from plants are used as medicines, food, insecticides and other industrially important chemicals. One such medicinal plant is *Moringa peregrina*, belonging to the family Moringaceae, which is mainly found in the tropical and subtropical areas. *M. peregrina* species is commonly known as the miracle tree, ranging in size from a tiny plant to massive tree [1]. Almost all the parts of *M. peregrina* are edible and have been consumed as a vegetable and used to treat many ailments such as tumors, hysteria, scurvy, paralysis, sores and skin infections [2, 3]. *M. peregrina* is an economically important plant of the Arabian and North African region [4, 5]. The occurrence of the associated microbial flora of this important plant is yet to be studied; therefore, looking at the importance and the potential of the plant to withstand extreme environmental conditions, we aimed to assess the endophytes flora of the plant in the present study.

Bacteria and fungi live asymptotically within the plant tissue without manifesting their presence in the host tissue [6].

A wide variety of endophytes can be observed as colonizing the plant parts, these colonies remain symptomless, and the plant tissue remains unaffected and functional. Several endophytes have been isolated from the tissues of aquatic and terrestrial plants [7, 8]. The wide presence of an endophyte in plant tissue creates an effective barrier preventing an attack of the pathogens to the host plant. It has been observed that metabolites produced by endophytes inhibit the growth of pathogens. Furthermore, the endophytic association of plant enables it to withstand the environmental stress and also from various predations. The plant, in turn, provides shelter and nutrients to the endophytes [9]. The present study aims to isolate endophytes from the selected medicinal plant, *M. peregrina*, and to explore their antimicrobial activities against a number of

✉ Amal Aljuraifani  
aaljuraifani@iau.edu.sa  
Sahar Aldosary  
skdosary@iau.edu.sa  
Ibtisam Ababutain  
iababutain@iau.edu.sa

<sup>1</sup> Department of Biology, College of Science, Imam Abdulrahman Bin Faisal University, P.O. Box 1982, Dammam 31441, Saudi Arabia

**Table 1** Endophytic isolates from *M. peregrina* based on the 16S rRNA sequencing

Code number	16rRNA sequence	Name of the organism	Similarity
MpKL1	GKGTMGAGTC TGACGGAGCA CGCCGCGTGA GTGATGAAGG TTTTCGGATC GTAAAACCTCT GTTGTTAGGG AAGAACAAGT ACCGTTTCGAA TAGGGCGGTA CCTTGACGGT ACCTAACCAG AAAGCCACGG CTAACTACGT GCCAGCAGCC GCGTAATAC GTAGGTGGCA AGCGTTGTCC GGAATTATTG GCGTAAAGC GCGCGCAGGC GGTTCYTAA GTCTGATGTG AAAGCCCCCG GCTCAACCGG GGAGGGTCAT TGGAACTGG GGAACCTGAG TGCAGAAGAG GAGAGTGGAA TTCCACGTGT AGCGGTGAAA TGGGTAGAGA TGTGGAGGAA CACCAGTGGC RAAGCGACTC TCTGGTCTGT AACTGACGCT GAGGCGCGAA AGCGTGGGGA GSGAACAGGA TTAGATACYK KGKWRKTCAC	<i>Bacillus licheniformis</i>	98.80
MpDT1	GGTCGCAGCC TGATGCAGCC ATGCCGCGTG TATGAAGAAG GCCTTAGGGT TGAAAAGTAC TTTCAGCSGG GAGGAAGGTG ATAAGGTAA TACCCTTRTC AATTGACGTT ACCCGCAGAA GAAGCACCGG CTAACTCCGT GCCAGCAGCC GCGTAATAC GGAGGGTGCA AGCGTTAATC GGAATTACTG GCGTAAAGC GCACGCAGGC GGTCAATTA GTCAGATGTG AAAGCCCCGA GCTTAACTTG GGAATTGCAT CTGAACTGG TTGGCTAGAG TCTGTAGAG GGGGTAGAA TTCCATGTGT AGCGGTGAAA TGGGTAGAGA TGTGGAGGAA TACCGTGGC GAAGGCGGCC CCCTGGACAA AGACTGACGC TCAGGTGCGA AAGCGTGGGG AGCAAACAGG ATTAGATACC TKGGGGTAGT CCA	<i>Proteus mirabilis</i>	99.53
MpKT2	GMGTAAGTCT GACGGGAGCA CGCCGCGTGA GTGATGAAGG TTTTCGGATC GTAAAAGTCT GTTGTTAGGG AAGAACAAGT ACCGTTTCGAA TAGGGCGGTA CCTTGACGGT ACCTAACCAG AAAGCCACGG CTAACTACGT GCCAGCAGCC GCGTAATAC GTAGGTGGCA AGCGTTGTCC GGAATTATTG GCGTAAAGG GCTCGCAGGC GGTTCTTAA GTCTGATGTG AAAGCCCCCG GCTCAACCGG GGAGGGTCAT TGGAACTGG GGAACCTGAG TGCAGAAGAG GAGAGTGGAA TTCCACGTGT AGCGGTGAAA TGGGTAGAGA TGTGGAGGAA CACCAGTGGC GAAGGCGACT CTCTGGTCTG TAACTGACGC TGAGGAGCGA AAGCGTGGGG AGCGAACAGG ATTAGTTKKG GGGGWWAKTC MAA	<i>Bacillus subtilis subsp. inaquosorum</i>	96.71
MpKT3	AGAGAAAGTCT GACGGAGCAC GCCGCGTGAG TGATGAAGG TTTTCGGATCG TAAAACCTCT GTTGTTAGGGA AGAAYAAGTA CCGTTTCGAAT AGGGCGGTAC CTTGACGGTA CCTAACCAGA AAGCCACGGC TAACTACGTG CCAGCAGCCG CGTAATACG TAGGTGGCAA GCGTTGTCCG GAATTATTGG GCGTAAAGCG CGCGCAGGGC GTTTCTTAA GTCTGATGTG AAGCCCCCGG CTCAACCGGG GAGGGTCATT GGAACCTGGG GAACTTGAGT GCAGAAGAGG AGAGTGGAAAT TCCACGTGTA GCGGTGAAAT GCGTAGAGAT GTGGAGGAAC ACCAGTGGCG AAGGCGACTC TCTGGTCTGT AACTGACGCT GAGGCGCGAA	<i>Bacillus licheniformis</i>	99.23
MpKT4	GMGTAAGTCT GACGGAGCAC GCCGCGTGAG TGATGAAGG TTTTCGGATCG TAAAGCTCTG TTGTTAGGGA AGAACAAGT CGAGAGTAAC TGCTCGCACC TTGACGGTAC CTAACCAGAA AGCCACGGCT AACTACGTG CAGCAGCCGCG GGTAAATACGT AGGTGGCAAG CGTTGTCCGG AATTATTGGG CGTAAAGGGC TCGCAGGCGG TTTCTTAAAG CTGATGTGAA AGCCCCCGG TCAACCGGGG AGGGTCATTG GAACTGGGA AACTTGAGTG CAGAAGAGGA GAGTGAATT CCACGTGTAG CGGTGAAATG CGTAGAGATG TGGAGGAACA CCAGTGGCGA AGGCGACTCT CTGGTCTGTA ACTGACGCTG AGGAGCGAAA GCGTGGGGAG CGAACAGGAT TAGATATKSK GSKWWRKYCA AA	<i>Bacillus pumilus</i>	98.82

**Table 1** continued

Code number	16rRNA sequence	Name of the organism	Similarity
MpDT5	CRKGMGAGT CTGACGGAGC ACGCCGCGTG AGTGATGAAG GTTTTCGGAT CGTAAAGCTC TGTTGTTAGG GAAGAACAAG TACCGTTCGA ATAGGGCGGT ACCTTGACGG TACCTAACCA GAAAGCCACG GCTAACTACG TGCCAGCAGC CGCGGTAATA CGTAGGTGGC AAGCGTTGTC CGGAATTATT GGGCGTAAAG GGCTCGCAGG CGTTTTCTTA AGTCTGATGT GAAAGCCCCC GGCTCAACCG GGGAGGGTCA TTGGAACTG GGGAACTTGA GTGCAGAAGA GGAGAGTGGG ATTCCAGTG TAGCGGTGAA ATGCGTAGAG ATGTGGAGGA ACACCAGTGG CGAAGGCGAC TCTCTGGTCT GTAAGTACG CTGAGGAGCG AAAGCGTGGG GAGCGAACAG GATTAGAACK GKGGGKRWAK YMCA	<i>Bacillus subtilis subsp. inaquosorum</i>	98.34
MpKT6	AKCAGAAGTC TGACGGAGCA CGCCGCGTGA GTGATGAAGG TTTTCGGATC GTAAAGCTCT GTTGTTAGGG AAGAACAAGT CGGAGAGTAA CTGCTCGCAC CTTGACGGTA CCTAACCCAGA AAGCCACGGC TAACTACGTG CCAGCAGCCG CGGTAATACG TAGGTGGCAA GCGTTGTCCG GAATTATTGG GCGTAAAGGG CTCGCAGGCG GTTTCTTAAG TCTGATGTGA AAGCCCCCGG CTCAACCGGG GAGGGTCATT GGAACTGGG AAAGTTGAGT GCAGAAGAGG AGAGTGAAT TCCACGTGTA GCGGTGAAAT GCGTAGAGAT GTGGAGGAAC ACCAGTGGCG AAGGCGACTC TCTGGTCTGT AACTGACGCT GAGGAGCGAA AGCGTGGGGA CGAACAGGA TTAGATACTG GGGKRWKTC AMA	<i>Bacillus pumilus</i>	98.12

human pathogens. This study is driven by the fact that infectious microorganisms are developing resistance to the available antibiotics; hence, there is a need for discovering new antibiotics and therapeutic agents that are highly effective against a wide range of pathogens, less toxic and cost-effective. Endophytes were isolated using the method described by [10]. From the various parts of *M. peregrina* such as the root, twig and leaves, growing in the eastern region (Dammam and Alkobar) of Saudi Arabia, samples were collected from each region in a sterilized poly-bag during transportation and stored at 4 °C until use. Then, they were thoroughly washed in running tap water and surface sterilized with 75% (v/v) ethanol. The outer tissues of the root and twig were removed and cut into smaller pieces, and the leaf tissues were excised and macerated with sterile distilled water by sterile mortar and pestle. Then, they were plated separately into minimal media (agar 1.5% w/v) supplemented with antibiotic cycloheximide 30 µg/ml and incubated at 37 ± 2 °C. The isolates were characterized and identified both morphologically and physiologically. The identification of isolates was based on the 16S ribosomal RNA sequences by the Genetic Unit in the Institute for Research and Medical Consultations. Test organisms included: *E. coli* ATCC25922, *Pseudomonas aeruginosa* ATCC27853, *Klebsiella ocytota* ATCC700324, *K. pneumonia* ATCC100324, *Acinetobacter baumannii* ATCCmra747, *Enterobacter aerogenes* ATCC13048, *Streptococcus dgalacticae* ATCC12336, *Streptococcus pyogenes* ATCC 19615, *Staphylococcus epidermis*

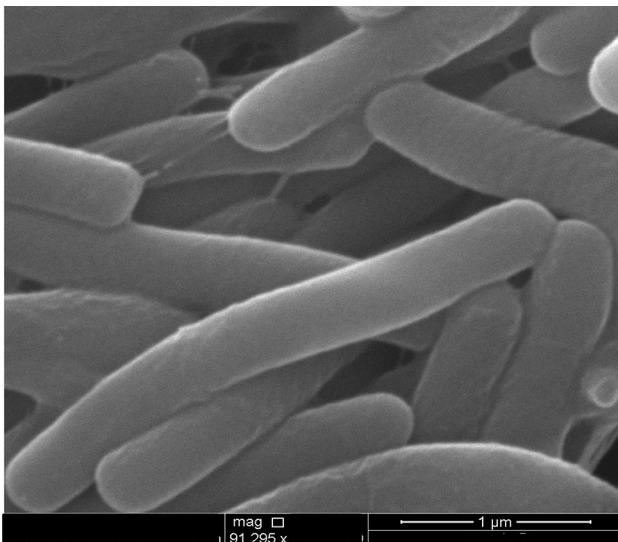
ATCC12228, *Staphylococcus aureus* ATCC24213 and *Candida albicans*. The strains were maintained on agar slants at 4 °C and activated at 37 °C for 24 h on nutrient agar prior to any study. All the endophytes isolates were inoculated on nutrient agar by a single streak of inoculum at the center of the Petri dish, while the unstreaked nutrient agar plate was assigned as a control plate. After 2 days of incubation at 37 °C, all the plates including the control plates were seeded with test bacteria by a single streak at a 90° angle (perpendicular) to the endophytes. Both experimental and the control plates were incubated at 37 °C. The assay was carried out in replicates. Based on the results from the cross-streak method, endophytes isolates from *M. peregrina* leaves (MpKL1) were selected and further inoculated in five numbers of 250-ml Erlenmeyer flasks, each containing 50 ml nutrient broth at 37 °C for 48 h. The seed culture was transferred to five numbers of the 2-L Erlenmeyer flask, each containing 1000 ml nutrient broth at 37 °C for 7 days to obtain a good quantity of pellet. The culture cell pellet was obtained by centrifugation (15000 rpm), and the supernatant was extracted with two types of organic solvents: chloroform/methanol 5:1 (MpKL1 cm) and ethyl acetate (MpKL1ea) in a separating funnel with vigorous shaking. The organic extract was recovered and then the organic solvent was evaporated by rotary evaporation at 30 °C. The dry weight of organic extract was taken and dissolved in dimethyl sulfoxide (DMSO) for further studies [11]. The *Moringa* plant species are a valuable source of useful metabolites that has

**Table 2** Screening of endophytic isolates for their antimicrobial activity using Cross-streak method

Identification results	Isolate code	Test organisms (pathogens)*										
		Gram-negative Bacteria						Gram-positive bacteria				Yeast
		1	2	3	4	5	6	7	8	9	10	11
<i>Bacillus licheniformis</i>	MpKL1=5	+++	+++	+++	+++	++	+	+++	++	+++	+++	+++
<i>Proteus mirabilis</i>	MpDT1	+++	+++	+	-	-	+	++	+	+++	+++	++
<i>Bacillus subtilis subsp. inaquosorum</i>	MpKT2	+	+++	+	+	-	+	-	-	++	-	+
<i>Bacillus licheniformis</i>	MpKT3	+	+++	-	-	-	+	+	++	-	+	
<i>Bacillus pumilus</i>	MpKT4	++	-	-	+	+++	+	-	-	++	-	-
<i>Bacillus subtilis subsp. inaquosorum</i>	MpDT5	+	+	-	-	-	-	-	-	-	+++	++
<i>Bacillus pumilus</i>	MpKT6	-	+	-	-	-	-	-	-	-	-	+

+ = less active, ++ = moderately active, +++ = highly active, - =No activity

\*(1) *E. coli* ATCC25922, (2) *Pseudomonas aeruginosa* ATCC27853, (3) *Klebsiella ocytota* ATCC700324, (4) *Klebsiella pneumonia* ATCC100324, (5) *Acinetobacter baumannii* ATCCmra747, (6) *Enterobacter aerogenes* ATCC13048, (7) *Streptococcus dgalacticae* ATCC12336, (8) *Streptococcus pyogenes* ATCC 19615, (9) *Staphylococcus epidermis* ATCC12228, (10) *Staphylococcus aureus* ATCC24213, (11) *Candida albicans*

**Fig. 1** Scanning electron microscopy of *B. licheniformis* MpKL1

been known for decades. In the present study, seven endophytic isolates were obtained from the samples of *M. peregrina*, and this result emphasizes that all types of plant species harbor endophytic bacteria. This finding is inconsistent with other researchers where they had stated that the aerial plant parts have a higher endophytic content than underground parts [12]. The result based on the 16S rRNA sequencing revealed two bacterial genus *Proteus mirabilis* and *Bacillus*; three species belong to *Bacillus*: *B. licheniformis*, *B. subtilis* subsp. *Inaquosorum* and *B. pumilus*. This finding revealed that the *Bacillus* species is prevalent in this plant (Table 1). Few studies reported endophytic isolate from *M. peregrina*. Khan et al. [13] isolated two fungi genus *Aspergillus caespitosus* LK12 and *Phoma* sp. LK13.

Interestingly, there is one study that reported endophytic bacterial isolate from this plant by Khan *et al.* [14] who isolated five endophytic bacteria: *Methylobacterium radiotolerans*, two species of *Sphingomonas* sp. and two strains of *Bacillus subtilis*. However, isolation of endophytic bacteria from different plants was reported by Amaresan et al. [15] who isolated 37 endophytic bacteria from chili plant. Endophytes are a group of microorganisms that could serve as dependable source of new and highly useful compounds with potential for exploitation in pharmaceutical and agricultural areas [16]. As pathogenic organisms are developing resistance to the majority of antibiotics available, it is important to find new antibiotics to tackle this problem. The result reveals that all endophytic isolates exhibited antagonistic activity against two or more of the pathogenic human microbes (Table 2). Moreover, *M. peregrina* Alkobar leaf 1 (MpKL1) isolate showed promising antimicrobial activity against all the test organisms with moderate to less activity against only a few organisms such as *A. baumannii*, *S. pyogenes* and *E. aerogenes*. The results of this study in agreement with several researches showed endophytic bacteria exhibit antimicrobial activity against human pathogenic microbes [17]. Also, using low concentrations of the active substance negatively affects their efficacy. Thus, it is important to determine the MIC of the active ingredient and, moreover, to reduce the possible cell toxicity risk of the active substance.

MpKL1 was further studied for its MIC values. The MIC of MpKLea (ethyl acetate extract) showed a high inhibitory effect against gram-negative bacteria *E. coli*, *P. aeruginosa* at 125 μg/ml and *K. ocytota*, *K. pneumonia* at 250 μg/ml. Also gram-positive bacteria *S. epidermis* and *S. aureus* highly inhibited at 250 μg/ml (Fig. 1).

**Table 3** MIC ( $\mu\text{g/ml}$ ) determination of the organic extract of MpKL1 against human pathogens (1–11)

Organic extract	Test organisms (pathogens)*										
	Gram-negative bacteria						Gram-positive bacteria				Yeast
	1	2	3	4	5	6	7	8	9	10	
MpKLea	125	125	250	250	>1000	>1000	500	>1000	500	250	500
MpKLcm	250	250	250	250	>1000	>1000	500	>1000	125	500	>1000
Positive control	0.5	2	2	0.5	8	4	8	4	0.25	0.25	4
Ciprofloxacin											

\*(1) *E. coli* ATCC25922, (2) *Pseudomonas aeruginosa* ATCC27853, (3) *Klebsiella ocytota* ATCC700324, (4) *Klebsiella pneumonia* ATCC100324, (5) *Acinetobacter baumannii* ATCCmra747, (6) *Enterobacter aerogenes* ATCC13048, (7) *Streptococcus dgalacticae* ATCC12336, (8) *Streptococcus pyogenes* ATCC 19615, (9) *Staphylococcus epidermis* ATCC12228, (10) *Staphylococcus aureus* ATCC24213, (11) *Candida albicans*

Moreover, MpKLcm (chloroform/methanol extract) also showed high inhibition effect at 250  $\mu\text{g/ml}$  against gram-negative bacteria *E.coli*, *P. aeruginosa*, *K. ocytota* and *K. pneumonia*, whereas MIC of MpKLcm raised up to 500  $\mu\text{g/ml}$  to inhibit the growth of gram-positive bacteria *S. dgalacticae* and *S. aureus*. Also, MIC of MpKLea raised up to 500  $\mu\text{g/ml}$  to inhibit the growth of *S. dgalacticae*, *S. epidermis* and *Candida albicans*. In general, both the extracts were not found very active against *A. baumannii*, *E. aerogenes*, *S. pyogenes* and *Candida albicans* with MIC > 1000. Ciprofloxacin was used as a standard antibiotic (Table 3).

This assay confirms that there is an appreciable degree of antibacterial activity against human pathogenic organisms. The future prospect of the study is the economic feasibility of the antibacterial drug development from these isolated endophytes. This finding is in agreement with several studies which revealed that endophytic bacteria have been proven as reliable sources of novel bioactive compounds and the richest source of secondary metabolites.

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