Diversity, community distribution and growth promotion activities of endophytes associated with halophyte *Lycium ruthenicum* Murr

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Abstract

The purpose of this study was to investigate the composition, diversity, distribution, and growth promotion activity of endophytic bacteria isolated from *L. ruthenicum* Murr. Consequently, a total of 109 endophytic bacteria affiliated to 3 phyla, 12 orders and 36 genera were isolated using nine different selective media, from which, *Actinobacteria* was the dominant taxon containing seven orders at the phylum level; *Micrococcales* showed the highest diversity containing 12 genera at the family level. Based on PAST and SPSS analysis, species diversity and abundance were mostly isolated from nutritious soil condition (22 genera) and root tissue (27 genera). Furthermore, growth phase showed significant effect on the endophytic bacteria community (28 genera at dormancy and 17 genera at fluorescence stage). With regard to ex situ plant growth-promoting activities, *Streptomyces* dominated and exhibited broad ability in terms of their potential to grow on nitrogen-free media, synthesize cellulase and lipase enzymes. Characterization of potential plant-beneficial traits indicate that endophytic bacteria exhibited a number of positive activities, including potential diazotrophy ($n=66$), phosphate-solubilizing ($n=6$), production of lipase ($n=21$) and cellulose ($n=35$). Two strains, representing *Bacillus* sp. EGI 63071 and EGI 63106, were found to be effective in promoting the growth of *Triticum aestivum* (wheat: Xindong No.18) seedling under salt stress conditions.

Keywords Environmental microbiology · Endophytes · Diversity · Halophyte · *Lycium ruthenicum* · Growth promotion

The 16S rRNA gene sequences of 109 isolated strains were deposited at NCBI GenBank under accession number (MF416281-MF416316, MK039000-MK039063 and MK045628-MK045636).

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Introduction

Xinjiang is located within an arid and semiarid climatic zone and the major portions of the area are covered by desert or gobi desert (Zhao et al. 2013). Desertification and salinization are the major two serious issues in Xinjiang region due to climate changes, low rainfall, excessive evaporation rate, poor fresh water resource and sparse vegetation (Li et al.

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2018a, b). Consequently, many plants could not survive in such harsh environmental conditions. Halophytes have been able to adapt to the extreme climate and soil conditions. The unique ecological adaptation mechanisms and geographical distribution of halophytes have, therefore, been contributed in comprehending the problems of environment, ecosystem restoration and enhancement of soil nutrient, particularly in the arid region of northwestern China (Jia et al. 2017).

Recently, many types of research have been focused on investigating the halophyte ecological adaptability by physiology method, but few studies investigated the plant-associated microbiome that consists of distinct microbial communities living in the roots, shoots and endosphere (Zhang et al. 2018). Endophytes have been reported to play a vital role in the plant in averting or mitigating abiotic stresses such as drought, salinity and extreme temperature (Egamberdieva et al. 2017). Endophytes associated with medicinal plants have the potential to be beneficial to their host by producing a range of natural products that could be harnessed for potential use in medicine, agriculture or industry (Li et al. 2018a, b). In addition, endophytic bacteria may play a role in soil fertility through phosphate solubilization and nitrogen fixation (Nimaichand et al. 2016). The beneficial microbes associated with the medicinal plant that could positively affect plant growth is highly impressive due to their species diversity and probiotic biosynthesis (Wicaksono et al. 2017). Endophytes colonizing inner plant tissues were reported to produced various biological metabolites, which could improve plant growth and enhance stress tolerance (Bordiec et al. 2011).

In order to understand the function and potential role of endophytic bacteria in developing sustainable systems of the host plant, we have selected the perennial shrub *L. ruthenicum* as the representative plant model for the isolation of endophytes. *L. ruthenicum* belongs to the genus *Lycium* of the family Solanaceae; it mainly grows in central and western Asia, where the dry and saline–alkaline land is an ideal environment for its growth due to its salt and drought resistant characteristics. *L. ruthenicum* is also has a great medical value and had conferred great environmental values due to its alkaline, drought and salt tolerant adaptability (Chen et al. 2008; Cui and Liu 2010). As a perennial halophyte traditional herb and a nutritional food, *L. ruthenicum* was originally recorded in Tibetan medical classic ‘Jing Zhu Ben Cao’. Its ripe fruits had been used for the treatment of heart disease, abnormal menstruation and menopause (Zheng et al. 2011). Moreover, *L. ruthenicum*

was reported to be successfully applied to afforestation in the severe saline–alkaline land area (Zhang et al. 2016; Hao et al. 2016). The objectives of our study were as follows: (1) isolate and identify endophytic bacteria associated with *L. ruthenicum*; (2) investigate the diversity and distribution characteristic of endophytic bacteria from halophyte plant *L. ruthenicum*; (3) evaluate the ability of promising endophytic isolates to stimulate growth of *T. aestivum* (wheat: Xindong No.18) under salt stress conditions.

Materials and methods

Description of study area and plant samples

Six free symptoms plants of *L. ruthenicum* were collected randomly from three sample sites of saline–alkaline soil in Changji, Xinjiang, P.R. China (44°29'N, 86°50'E; Table 1) at dormancy period in January and florescence period in May 2016 respectively. The distance between each site was at least 500 m. The plant samples were transported to the laboratory in sterile plastic bags and processed within 24 h. Three soil samples from each sample collection site were taken for nutrient content analysis at dormancy season in January, 2016. The average temperature during the dormancy period ranges between –18 and –8 °C, but increases to 6–22 °C during the florescence period.

Isolation of endophytes

Each plant sample was separated into leaf, stem and root before being thoroughly washed with tap water to remove the clay and then followed by immersing them in an ultrasonic bath until the water becomes clear. A surface sterilization protocol was adopted for each plant tissue following the method described by Liu et al. (2016). Each plant tissue was separately surface-sterilized by immersing them sequentially, with shaking, in 75% ethanol for 1 min, sodium hypochlorite solution (5%) for 8 min, followed by rinsing with sterile distilled water 4–5 times for each step of surface sterilization protocol. After drying in oven for 1 day at 45 °C, samples were aseptically homogenized using sterile mortar and pestle into semi powder form. The isolation of endophytic bacteria was performed by serial dilution method as described by Jasim et al. (2014) and then 100 µL of each dilution was plated in triplicate onto nine selective isolation media M1–M9 (Liu et al. 2016)

Table 1 Geographical location and study area of the sampling site

Host plant	Growing period	Geo-location	Temperature	Altitude (m)
<i>L. ruthenicum</i>	Dormancy	44°29'N, 86°50'E	–8 °C/–18 °C	396
<i>L. ruthenicum</i>	Florescence	44°29'N, 86°50'E	22 °C/6 °C	396

from reference. All agar plates were incubated at 28 °C and monitored daily for microbial growth. Colonies with distinct colony morphology were picked and re-streaked for purification. The efficiency of surface sterilization was tested by plating 100 µL of the final rinse used for surface sterilization onto tested isolation media at 28 °C for 5 days. No microbial growth was occurring on the isolation media. This result indicated that the two-step surface sterilization protocol was successful in removing or killing epiphytic bacteria; therefore, the isolated strains obtained during the isolation were considered to be true endophytes.

DNA extraction, PCR amplification and 16S rRNA gene sequencing

Genomic DNA of the isolated endophytic strains was extracted by an enzymatic hydrolysis procedure (Liu et al. 2016). PCR amplification of the 16S rRNA gene was performed using the primer pair PA-PB (PA: 5'-CAG AGTTTGATCCTGGCT-3'; PB: 5'-AGGAGGTGATCC AGCCGCA-3') (Li et al. 2007) procured by Sangon Biotech (Shanghai, China). The PCR mixture (50 µL) contained 25 µL 2×PCR master mix, 1 µL DNA template 1 µL of each primer and 22 µL ddH₂O. Amplification of the 16S rRNA genes was performed in a thermal cycler according to the following steps: 94 °C initial denaturation for 10 min, followed by 32 cycles of denaturation at 94 °C for 45 s, annealing at 56 °C for 30 s and extension at 72 °C for 1 min 30 s and a final extension at 72 °C for 10 min. The amplicons were sent to Sangon Biotech Pvt. Ltd (Shanghai) for sequencing. The 16S rRNA sequences were compared with the GenBank database via BLAST using the EzBiocloud server (<http://www.eztaxon.org>) (Yoon et al. 2017) for pairwise sequence comparison with the database containing sequences of type strains with validly described nomenclature. The 16S rRNA sequences have been deposited in GenBank under Accession Numbers MF416281-MF416316, MK039000-MK039063 and MK045628-MK045636.

The phylogenetic dendrogram was generated using the MEGA 7.0 software (Kumar et al. 2016) based on the neighbor-joining method (Saitou and Nei 1987). Bootstrap analysis with 1000 replications was conducted for evaluating the confidence level of the branch nodes (Kumar et al. 2016). The endophytic strains were identified based on the phylogenetic clustering and sequence similarity indices to their closely related homolog (Kim et al. 2014). The diversity of the endophytes was analyzed using the PAST 2.03 software after applying four related statistical parameters Dominance index, Simpson index, Shannon index, and Species evenness (Hammer et al. 2001).

Plant growth promotion assays

All purified endophytic bacterial isolates were screened for nitrogen-free media, phosphate solubilization, cellulase and lipase plant growth-promoting traits. Nitrogen fixation potential was assessed by observing the growth of the bacterial strain both on the nitrogen-free culture (NFC) medium and Ashby medium (Kizilkaya 2009; Liu et al. 2017a). Phosphate solubilization property was screened by culturing the bacteria on Pikovskaya agar medium (Pikovskaya 1948; Li et al. 2018a, b). Cellulase and lipase activities were assayed on media containing carboxymethyl cellulose and victoria blue, respectively (Li 2011; Li et al. 2018a, b). The different levels of endophytes plant growth promoting activities were recorded as high, moderate, low and none, which were distinguished by four different colors red, green, gray and white, and exhibited in a phylogenetic dendrograms by neighbour-joining (Radiation Tree) algorithms.

Strains were positive for at least two plant-beneficial traits were tested individually for investigating the direct effects on plant growth. Representative endophytic bacterial strains EGI 63071 and EGI 63106 were candidates to test their ability to alleviate abiotic stress in vivo conditions. The detail treatments were as follows: (1) the wheat (*T. aestivum*) seeds were surface sterilized by sequential washing in 95% ethanol for 15 min, followed by 25% sodium hypochlorite for 5 min, then all seeds were rinsed thrice with sterilized double distilled water. (2) Sterilized wheat seeds were soaked in an endophytic bacterial suspension of 1×10^8 CFU ml⁻¹ (Egamberdieva et al. 2017) for 10 min, then immediately transplanted 10 seeds into a plastic pot (diameter = 20 cm) containing 500 g mixture soil (sand, peatmoss, stone, perlite) (1:1:1:1) (Li et al. 2018a, b). Each treatment contained ten plants with triplicate and watered once a week with 250 mM saline solution (Wang 2015). The wheat plants were grown in a growth chamber for 15 days with day and night temperatures of 30 and 18 °C, respectively, and with a 16/8-h light/dark cycle (BIC-400, Shanghai Boxun industry Co, Ltd Medical Equipment Factory, Shanghai, China). Plants harvested 15 days after planting for measuring its growth parameters including shoot and root lengths, dry shoot and root weight and germination percentage. Plant material was dried at 40 °C in the oven until constant weight.

Soil nutrient content of the rhizosphere

Three rhizosphere soil samples were collected from three sites at dormancy season in January 2016. All soil samples were air-dried and sieved using a 2 mm sieve to remove any visible plant material. The soil was thoroughly mixed to determine soil available N (SAN), soil available P (SAP) and soil available K (SAK). Representative sub-samples were then passed through another 0.25 mm sieve

Fig. 1 Neighbor-joining tree (Rectangular Tree) showing the phylogenetic relationships of 36 genera based on 16S rRNA gene sequences of the representative strains isolated from *L. ruthenicum*. Bootstrap values (expressed as percentages of 1000 replications) greater than 50% are given at the nodes. Bar 0.02 substitution per nucleotide

for measurements of soil total N (STN), soil total P (STP) and soil total K (STK) (Liu et al. 2017b). Measurement of the nutrients was done by FOSS-fully automatic azotometer, Cary 60-spectrophotometer and flame spectrophotometer at the Research Center for Ecology and Environment of Central Asia.

Statistical analyses

Data obtained from the soil nutrition, the plant morphological and biomass studies subjected to analysis of variance (ANOVA) with SPSS software (version 13). The results presented as average means and standard error (SE). The difference between means compared with a high-range statistical domain (HSD) using Duncan test, and the treatment means separated by the least significant difference (LSD) test at $P < 0.05$. All statistical analyses were conducted using SPSS statistical software (SPSS for Windows, Version 13, Chicago, USA).

Results

Isolation of endophytes and their phylogenetic affiliation

In this study, a total of 109 endophytic strains were isolated from different plant tissues of *L. ruthenicum* samples collected from three sites in Xinjiang province and were further identified by 16S rRNA gene sequencing. The 109 isolates were affiliated to 3 phyla, 12 orders and 36 genera based on 16S rRNA gene identity (Fig. 1). The phylum *Actinobacteria* constituted the highest diversity among all isolates with seven orders *Micrococcales*, *Glycomycetales*, *Streptosporangiales*, *Propionibacteriales*, *Pseudonocardiales*, *Corynebacteriales* and *Streptomycetales* contained; followed by *Proteobacteria* with four orders *Enterobacteriales*, *Pseudomonadales*, *Burkholderiales* and *Rhizobiales*; the infrequent phylum was *Firmicutes*. At the orders level, *Micrococcales* showed the highest diversity with 12 genera *Arthrobacter*, *Brachybacterium*, *Brevibacterium*, *Curtobacterium*, *Kocuria*, *Leucobacter*, *Microbacterium*, *Micrococcus*, *Okibacterium*, *Ornithinimicrobium*, *Promicromonospora* and *Pseudoclavibacter*; followed by *Corynebacteriales* with the isolates affiliated to six genera *Dietzia*, *Gordonia*, *Mycobacterium*, *Nocardia*, *Rhodococcus* and *Williamsia*.

Our results showed that culturable endophytic bacteria strains from *L. ruthenicum* displayed considerable high diversity.

Effects of soil nutrients on the endophytic community

We analyzed nutrition of soil samples from each site to determine the effects of soil nutrients on the endophytic community (Table 2). Among the three sampling sites, the soil from site A represents the highest nutritional values including organic matter, total nitrogen, total phosphorus, available nitrogen, available phosphorus and available potassium compared to site B and C. Whereas, only total soil potassium was the highest in site B.

Among 109 isolates, 41 strains were isolated from site A, 42 and 26 strains were isolated from site B and site C, respectively. In our studies, phylogenetic clustering based on sampling sites indicated that genus *Streptomyces* was the preponderant community at sites A and B (Table 2; Fig. 2), while genus *Kocuria* was the dominant community at site C. Based on the diversity index analysis, Dominance index showed no significant difference between sites B and C; Whereas, Simpson index revealed similarity between sites B and C, The Evenness index was varied in three sites. In addition, the most unique endophytes such as *Aurantimonas*, *Brachybacterium*, *Dietzia*, *Gordonia*, *Glycomyces*, *Lechevalieria* and *Okibacterium* occurred at site A (Fig. 2). Consequently, more endophytes community and unique endophytes were detected at high-nutrition condition site A but less in poor-nutrition condition site B and C.

Effects of the vegetative phase on the endophytic community

Our results revealed that the culturable endophytic bacterial community and diversity in *L. ruthenicum* were strikingly different during the two growth phases. Among 109 isolates, 50 strains affiliated to 17 genera were isolated from samples collected during florescence season, while 59 strains affiliated to 28 genera were isolated from samples collected during the dormancy period (Fig. 3). The diversity indices particularly Shannon, Simpson, and Evenness indicated that plant samples during dormancy period exhibited higher bacterial diversities than florescence. Besides, infrequent taxa (each with 2.0%) *Actinophytocola*, *Aurantimonas*, *Lechevalieria*, *Leucobacter*, *Methylobacterium*, *Micrococcus*, *Nocardia*, and *Williamsia* were isolated only from dormancy period. Among all the endophyte strains isolated from dormancy period, *Streptomyces* constituted 26.0% of the community followed by the *Bacillus* (18.0%) and *Kocuria* (12.0%). Compared with dormancy period, *Streptomyces* dominated 16.9% of florescence period community followed

Table 2 NPK soil analysis of sampling sites

Sites	SOM (g/kg)	STN (g/kg)	STP (g/kg)	STK (g/kg)	SAN (mg/kg)	SAP (mg/kg)	SAK (mg/kg)
A	18.84 ± .770a	1.19 ± .112a	1.53 ± .050a	19.09 ± .518ab	151.75 ± 4.248a	65.86 ± 1.194a	890.4 ± 4.917a
B	10.11 ± 1.181b	0.55 ± .035b	0.87 ± .032b	20.72 ± .806a	83.68 ± 1.290c	17.08 ± .531b	716.2 ± 4.304c
C	6.97 ± .602c	0.48 ± .021b	0.83 ± .020b	17.71 ± .550b	119.18 ± 1.125b	13.2 ± .802c	773.2 ± 3.453b

Three samples per site were analyzed. The data represent the average of those samples. Different letters (a, b, c) in plant growth data indicate significant differences based on Duncan HSD test at $P < 0.05$

SOM soil organic matter, *STN* soil total nitrogen, *STP* soil total phosphorus, *STK* soil total potassium, *SAN* soil available nitrogen, *SAP* soil available phosphorus, *SAK* soil available potassium

Fig. 2 Distribution of endophytic community at the three sampling sites at the generic level

by *Nocardiopsis* (10.2%), *Curtobacterium* (8.5%), and *Rhodococcus* (6.8%).

Composition of endophytic bacterial community on the different plant tissues

In the present work, the diversity of the endophytic bacteria isolated from different plant tissues of *L. ruthenicum* was varied and strongly dependent on the plant tissues. Among 109 isolates, 49 strains were isolated from root tissue, 46 strains were isolated from stem tissue, and 14 strains were isolated from leaf tissue (Supplementary Table S1). The highest number of endophytic bacterial

isolates was from root tissue (27 genera) followed by stem (19) and leaf (6). *Streptomyces* was the dominant genus in bacterial community in both roots and stem, while *Kocuria* was the dominant genus in leaf. The distribution profile of the other major endophytic bacterial genera indicated in Fig. 4. Furthermore, species richness varied based on the plant tissue: the highest number of bacterial species was determined from roots tissue ($n = 27$) followed by stem ($n = 19$), and leaf ($n = 6$). The index values according to Dominance, Shannon, Simpson, and Evenness index indicated that root tissue was found to be a more suitable host for endophytic bacteria as compared with stem and leaf.

Fig. 3 Composition of the endophytic community during the two vegetative phases (A: Dormancy; B: Florescence)

Plant growth promoting activity

With regard to ex situ plant growth-promoting activities, the endophytic bacteria exhibited a number of positive activities, including potential diazotrophy ($n=66$), phosphate-solubilizing ($n=6$), production of lipase ($n=21$), and cellulase ($n=35$). Phylogenetic dendrograms of the endophytic bacteria with the capability of potential diazotrophy, phosphate solubilization, cellulase and lipase activities are presented in Fig. 5. Members affiliated to the genera *Gordonia*, *Mycobacterium*, *Streptomyces*, and *Williamsia* exhibited moderate to high levels of growth on nitrogen-free culture media, but none of these isolates showed phosphate-solubilizing activity. Only a few strains affiliated to genera *Bordetella*, *Brachybacterium*, *Methylopila*, and *Curtobacterium* exhibited low positive activity of growth on nitrogen-free culture media. Our results also demonstrated that only *Rhodococcus* sp. and two *Mycobacterium* sp. showed positive activity for lipase enzyme. In contrast, there are 24 isolates that showed moderate to high level of cellulase activity. In general, strains of the genera *Streptomyces* and *Bacillus* provided the highest level of plant growth

promoting activity, particularly growth on nitrogen-free media and the production of cellulase and lipase enzymes.

Two isolates EGI 63071 and EGI 63106 that belonged to *Bacillus* sp. and were able to grow on nitrogen-free media and produce one hydrolytic enzyme (cellulase) were further selected for salt-tolerance efficiency tests. Strain EGI 63106 was found to be more effective in promoting the growth of wheat seedling under 250 mM salt stress condition: the length of leaf (2.72 cm), dry weight of leaf (5.99 mg), and germination rate (20.57%) were all significantly high ($P < 0.05$), compared to control (0.82 cm, 2.16 mg, and 16.43%, respectively). Strain EGI 63071 slightly promoted the length of root and dry weight of root. Conclusively, significant variation was observed in the root, shoot, and germination percentage when the seedlings were inoculated with the bacterial strains EGI 63071 and EGI 63106 under 250 mM salt stress condition (Table 3).

Fig. 4 Distribution of endophytic genera isolated from three different tissues of *L. ruthenicum*

Discussion

The symbiotic interactions between plants and beneficial microorganisms, such as endophytes, have been studied from various cereal crops and medicinal plants (Lodewyck et al. 2002; Liu et al. 2016, 2017a; Li et al. 2018a, b). However, our current knowledge of the isolation of culturable endophytic bacteria from medicinal plants in the arid regions, and more particularly medicinal halophytes, and their role in desert stratification is still limited. In this study, we explored the effects of soil conditions, phases of desert vegetation, and type of plant tissues in the distribution of endophytic bacteria. The findings from our study indicated that the members of phylum *Actinobacteria*, in particular, genus *Streptomyces*, were prominently present under different conditions of growth of halophytic plants. This observation could most probably be related to the physiological adaptive features of *Streptomyces*, like the formation of spore which helps in dissemination and confer resistance to adverse conditions (Chater 1993; Damodharan et al. 2018). These microorganisms, in turn, play a vital role in maintaining a long-term stability and sustainability of other endophytic community (Egamberdieva et al. 2017).

Numerous researches concluded that soil is the main driving factor for bacterial composition and community distribution associated with host plant (Baath and Anderson 2003; Fierer and Jackson 2006; Lozupone and Knight 2007; Long et al. 2010). In our study, it was observed that endophytes were more abundant in a region with rich nutrient contents. The reason for such findings may be related to the theory that plants can influence the rhizosphere microbiota by regulating the soil conditions in the vicinity of the root system through exudation of sugars, phenolic compounds, and amino acids, which act as signaling molecules for microorganisms in the soil (Liottiet al. 2018). However, in soil with low nutrient contents, the presence of endophytes helped the plant to endure the available nutrients by supplementing growth promoting factors. That may be because endophytic bacteria can convert unusable atmospheric nitrogen and phosphorus into accessible forms by biological nitrogen fixation and phosphate solubilization processes (Meunchang et al. 2006; Nimaichand et al. 2016; Li et al. 2018a, b). In both cases, the presence of endophytes could be associated with the earlier studies which speculated that endophytes are a subset of the rhizoplane community (Germida et al. 1998) and

Fig. 5 Phylogenetic dendrogram Neighbor-joining tree (Radiation Tree) indicating the distribution of the plant-growth-promoting endophytes: **a** use nitrogen-free media, **b** phosphate-solubilizing activity, **c** lipase, and **d** cellulase

Table 3 Effect on growth parameters of wheat plants inoculated with strains EGI 63071 and EGI 63106 under 250 mM salt stress

Treatment	LR/cm	LL/cm	DWR/mg	DWL/mg	GR/%
Control	1.16 ± 0.04b	0.82 ± 0.13c	1.98 ± 0.17b	2.16 ± 0.16c	16.43 ± 0.47c
EGI 63071	1.27 ± 0.05b	1.93 ± 0.07b	2.27 ± 0.71b	4.78 ± 0.04b	18.13 ± 0.25b
EGI 63106	2.18 ± 0.17a	2.72 ± 0.20a	4.02 ± 0.08a	5.99 ± 0.13a	20.57 ± 0.68a

Each treatment contained ten plants with triplicate. Each data from this study represent the average of ten plant experiments after being cultured for 15 days. Different letters (a, b, c) that followed plant growth data in this table indicate significant differences based on Duncan HSD test at $P < 0.05$

LR length of root, LL length of leaf, DWR dry weight of root, DWL dry weight of leaf, GR germination rate

rhizospheric bacteria were laterally transferred towards the internal plant tissues (Santoyo et al. 2016).

Additionally, we try in this investigation to distinguish the difference between the bacterial communities in *L. ruthenicum* during its dormancy period and its blooming season. Interestingly, more endophyte diversity (28 genera) was determined during the dormancy period than in the florescence season. We speculated that the seasonal changes in occurrence and frequency of endophytes are probably related to the unique climate in Xinjiang: it is covered by thick snow and keep humidity in winter but arid in other seasons. Researches have demonstrated that humidity and rainfall are often positively related to infection frequency of horizontally transmitted endophytes in plant (Faeth and Hammon 1997; Schulthess et al. 1998). The previous study also showed that endophytes affected seed dormancy at higher incubation temperatures. But the impact of endophytes on seed dormancy varies depending on the environment under which the seeds had developed (Gundel et al. 2010). Future studies should be focused on the effects of endophyte on the host plants during different growth phases and analyze the relationship between plant dormancy and endophytes.

The distribution of the endophytic bacteria has also been reported to be influenced by different plant tissues (Wang et al. 2016; Li et al. 2018a, b). The plant organ interfered in the characteristics of endophytic bacterial communities, the total number of bacteria strains, richness, and diversity (Liottiet al. 2018). The determination of bacterial community structure in different plant tissue is, therefore, essential for subsequent utilization of endophytic bacteria in the improvement of plant adaptation in extreme environment such as saline soils. This study demonstrated that the composition of the endophytic bacterial community in different tissues was obviously different: Root tissue showed the highest diversity index, followed by stem and leaf tissue. The reason for that is the endophytes can transmit vertically from generation to generation and be a favor mutual-ism between the endosymbionts and hosts (Wang et al. 2016). Jin et al. (2014) analyzed the distribution of endophytic bacteria in various plant tissues by 16S rRNA libraries and recorded that bacterial distribution may be associated with tissue specificity.

Endophytic bacteria are an essential and promising resource for plant growth of valuable bioactive compounds and secondary metabolites (Nimaichand et al. 2016; Mohamad et al. 2018). In addition, there are several endophytic bacteria that showed a potential for improving plant growth and stress tolerance (Abeer et al. 2016; Singh et al. 2017). The genus *Bacillus* is well known for the natural production of secondary metabolites with antibacterial and antifungal activities and has a strong potential to promote plant growth (Li et al. 2018a, b; Mohamad et al. 2018). Strains EGI 63071 and EGI 63106 were effective in terms of stimulated wheat growth under salt stress. We speculate that these results were probably due to the ability of tested strains to convert unusable nitrogen and phosphorus to accessible forms (Meunchang et al. 2006). Cellulase is predicted to participate in the penetration of rhizospheric microorganism into the plant root (Egamberdieva et al. 2013). In view of the importance of endophytes to plant health, many of recent studies have concluded that the genus *Bacillus* was the most promising bioinoculum due to its widespread abundance in different plants (Gao et al. 2017) and its ability to form endospores that are highly resistant to abiotic stresses such as extremes of pH, salinity, and temperature (Horikoshi 2008).

Conclusively, this research reported the endophytic bacteria and their growth promotion ability associated with *L. ruthenicum* in saline soils of Xinjiang province for the first time. In addition, the effects of the external environment on the endophytic bacterial were also expounded. Furthermore, the endophytic bacterial isolates with best plant growth promotion traits were effective in stimulating growth under saline conditions. Our findings demonstrated that a diverse group of bacteria colonizes the interior tissue of medicinal halophyte *L. ruthenicum*. Soil condition, growth phase, and plant tissue exhibited different influence on endophytes' diversity and abundance. These endophytic bacteria are effective plant growth stimulators under saline soil condition. Such plant–microbe interaction provided a promising practical approach to improve soil condition and increase the productivity of crop under salt stress.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no competing interests.

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