Stress-Tolerance and Taxonomy of Culturable Bacterial Communities Isolated from a Central Mojave Desert Soil Sample

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Abstract: The arid Mojave Desert is one of the most significant terrestrial analogue objects for astrobiological research due to its genesis, mineralogy, and climate. However, the knowledge of culturable bacterial communities found in this extreme ecotope’s soil is yet insufficient. Therefore, our research has been aimed to fulfil this lack of knowledge and improve the understanding of functioning of edaphic bacterial communities of the Central Mojave Desert soil. We characterized aerobic heterotrophic soil bacterial communities of the central region of the Mojave Desert. A high total number of prokaryotic cells and a high proportion of culturable forms in the soil studied were observed. Prevalence of Actinobacteria, Proteobacteria, and Firmicutes was discovered. The dominance of pigmented strains in culturable communities and high proportion of thermotolerant and pH-tolerant bacteria were detected. Resistance to a number of salts, including the ones found in Martian regolith, as well as antibiotic resistance, were also estimated.

Keywords: physiology of bacteria; extremotolerance; antibiotic resistance; soil; microbial communities; Mars analogue site

1. Introduction

One of the main tasks of modern astrobiology is studying environmental factors of different space bodies and outer space and to determine surviving and functioning limits of terrestrial life forms under extraterrestrial conditions [1,2].

It is known that potentially habitable space objects are exposed to a number of extreme abiotic factors, including high-intensity ionizing radiation, reduced pressure, contrast temperature conditions, low water availability, etc. [3–5]. Up to date, a large amount of data on physicochemical properties of regolith and climatic and cosmic regimes of various extraterrestrial bodies, in particular Mars, have been accumulated [6]. Based on these data, it can be stated that in today’s biosphere of the Earth there are ecosystems that possess some environmental parameters similar to those found on extraterrestrial bodies. Hot-arid and cold-arid deserts, permafrost sedimentary rocks and some arid soils are considered as terrestrial analogues of extraterrestrial regolith [7–9] and are used as model objects in astrobiological research.

Microorganisms of arid ecosystems are exposed to a wide spectrum of stress factors such as water and organic matter deficiency, exposure to winds and high-intensity ultraviolet (UV) radiation, and significant temperature fluctuations. However, these areas are not lifeless and are characterized by
significant richness and diversity of prokaryotes [10,11]. Many astrobiological studies consider the Atacama Desert [12–14], the Sonora Desert [15], and the Dry Valleys of Antarctica [16] to be the main objects of research. However, it is important to investigate different ecosystems that are exposed to extreme environmental factors [17]. The Mojave Desert is one of such analogue ecosystems. It is characterized by relief and mineralogy that are close to those found on Mars [18–20]. There are several reasons as to why edaphic (i.e., associated with soil) bacterial communities of hot deserts should be studied, such as the lack of culturable communities’ research and the possible biotechnological potential of bacterial strains that inhabit the ecosystems and its highly valuable and significant properties for further research [21].

The Mojave Desert is located in the southwest of the United States and covers an area of approximately 150,000 km². It is characterized by altitudes of 600–1500 m above sea level and arid-semiarid climate with an average annual precipitation of less than 300 mm (the average annual precipitation is 137 mm/year). Temperatures range from −10 to 50 °C; frequent winds are also observed in this area [22,23]. The average annual temperature is 20 ± 0.5 °C, annual heat-moisture index (AHM) is 230 ± 19 [24].

Ten thousand years ago this territory was characterized by a humid climate and well-formed soil coverage, but the aridization of weather conditions and desertification of the region have led this area to its present state [23]. The region is characterized by volcanogenic geology and topography, a high degree of weathering of surface sedimentary rocks [25] and extremely poor vegetation [19]. The total organic matter content in the soils of this desert is very low (it ranges from 145 to 260 µg of C per gram of soil). Carbon to nitrogen ratio is about 9.5 [26].

All the aforementioned properties of the Mojave Desert make it a suitable terrestrial analogue to Mars, particularly because of the climate changes that had happened here and of the ongoing geological and climatic processes [24]. The soil of this desert has a mineralogical composition close to that of the Martian regolith [27]. As well as that, it also has a similar composition of mineral salts [8,18,28]. Worth noticing is the fact that in the past the territory of modern Mojave Desert had been coated by mature soil coverage, which could contain diverse soil microbial communities. However, as time has been progressing, this region was subjected to long-lasting drought periods and microbial communities have been forced to adapt and alter their metabolism under conditions of moisture and nutrients deficiency and high-stress load. Supposedly the same happened to the Martian regolith [19,28]. The soils of this desert have already been used in model astrobiological studies and in The Mojave Mars simulant (MMS) in particular as a regolith model of Mars [29]. Bacterial isolates from the soils of this desert served as model organisms for studying lithopanspermia processes [15].

Earlier studies revealed a large number and variety of phototrophic organisms in the soil of Mojave confined to hypolith communities and able to carry out photosynthesis under aggressive environmental conditions in situ (i.e., in natural soil conditions) and in vitro (i.e., in laboratory conditions) [8,30].

Presence and metabolic activity of phototrophic and chemotrophic prokaryotes have also been confirmed, as well as presence of nitrogen-fixing bacteria and ability of those organisms to produce primary organic matter (references herein and [10,21]). Thus, it becomes obvious that along with the autotrophic community, there must be a heterotrophic community in the soil of this desert.

In general, previous studies have discovered a similar structure of edaphic bacterial communities at the phylum level in the soils of cold and hot deserts: among aerobic heterotrophic bacteria, representatives of the phyla Actinobacteria, Proteobacteria, Acidobacteria, and Bacteroidetes are the most common [10].

In the surface soil of The Mojave Desert, 48 different taxonomic units of bacteria were found by molecular cloning [31]. Biological soil crusts (BSC) confined to the surface layers of soil are common in the Mojave Desert. The next generation sequencing of 16S rRNA genes from the soil under BSC revealed the following phylogenetic structure of the bacterial community: Proteobacteria (23 ± 5%), Actinobacteria (20 ± 5%), and Chloroflexi (18 ± 3%), representatives of the genus Rubrobacter were the most dominant
among actinobacteria. **Acidobacteria** (10 ± 2%), **Bacteroidetes** (6.5 ± 2.0%), and **Cyanobacteria** (11 ± 10%); **Gemmatimonadetes**, **Armatimonadetes**, **Planctomycetes**, **Nitrospirae**, **Chlorobi**, and **Verrucomicrobia** (<5% altogether) representatives have also been identified [32].

**Proteobacteria** (~45% operational taxonomic units (OTU)), **Actinobacteria** (~12% OTU), and **Firmicutes** (~10% OTU) phyla have been found as the most abundant ones by metagenomic analysis of the soils of the desert. The authors have concluded that there was a high number and high taxonomic diversity of bacteria inhabiting the arid soils of the Mojave Desert. They have also concluded that the desert soils were rich with unidentified bacteria species, supporting this with molecular-genetical data obtained [21].

Based on the high-throughput DNA sequencing and shotgun-metagenomic study of the Mojave Desert soils performed by the several research groups, a high relative abundance **Proteobacteria** and **Cyanobacteria** phyla and presence of representatives of the phyla **Actinobacteria**, **Bacteroidetes**, **Verrucomicrobia**, **Acidobacteria**, **Firmicutes**, and **Crenarchaeota** were also detected [24,33,34]. A high abundance of genes associated with spore formation processes, encoding stress proteins and amino acid metabolism, associated with osmoregulation was also discovered. Based on these results, the authors concluded that there was a significant functional diversity of desert bacterial communities [33].

Using the methods of native fluorescence and fatty acid analysis of phospholipids, the number of bacterial cells was found to be 10^7 bacteria per gram of soil [35,36]. Studies of culturable bacteria of this desert are less common, compared to culture-independent methods. A high number of cultured bacteria was shown up to 10^6 colony-forming units per gram (CFU/g) [37].

A study of the number and taxonomic composition of cultured actinomycetes in the soils of this desert revealed the dominance of **Actinoplanes**, **Pilimelia**, and **Streptomyces** genera representatives. The authors noted a high diversity of isolated strains, and the fatty acid methyl ester analysis of isolates indicated a significant proportion of previously undescribed actinomycete species. Extreme effects of external factors were proposed to be the driving force of speciation in desert soils, which leads to the morpho-physiological adaptations of prokaryotes inhibiting them [38].

Community level physiological profile analysis of the microbial complexes (using BIOLOG 96-well Eco-Microplates assimilation test) of soils confined to plants revealed the absence of correlation between the structure and the diversity of bacteria in communities under plant coverage and in soils with no vegetation. A positive correlation between the number of substrates consumed by the bacterial community and the presence and diversity of higher plants growing on that soil was proved. However, bacterial communities confined to areas of the desert lacking vegetation showed active assimilation of amino acids, amines, amides, and various polymers. In addition, representatives of **Sinorhizobium**, **Bacillus**, and **Sphingomonas** genera were isolated and identified in culture grown on selective medium for nitrogen-fixing bacteria [39].

In dry conditions, microbial communities are exposed to different extreme conditions, such as temperature and pH fluctuations, soil moisture shortage, high level of ultraviolet radiation. All of them have a significant impact on microbial communities [17].

Generally, little is known about bacterial communities of arid soils, and previous studies revealed significant taxonomic and functional differences between the bacterial communities of extreme soils and those of temperate zones [24,40]. A high diversity and a high number of cells in bacterial communities of the Mojave Desert soils in situ (i.e., in natural conditions), predominated by **Proteobacteria** and **Actinobacteria** phyla were found. The abundance and diversity of photo- and chemotrophic microorganisms were described predominantly by culture-independent methods. However, heterotrophic community studies are surprisingly rare: only individual groups of culturable bacteria, such as, for example, nitrogen-fixing bacteria and actinomycetes, have been investigated previously. Still, little is known about the bacterial communities of arid soil even though bacterial stress resistance research plays an important role when it comes to extraterrestrial analogue ecosystems in astrobiological context.
In this paper, we studied the aerobic heterotrophic bacterial community and the physiological characteristics of cultured bacteria, isolated from the surface soil sample collected in the central part of the Mojave Desert.

2. Materials and Methods

2.1. Soil Sampling

A single soil sample was collected in the central part of the Mojave Desert in the summer of 2015 in a flat area devoid of vegetation (34°55′39.0″ N 115°45′33.7″ W). The surface soil was taken from 0–3 cm depth with no signs of vegetation and biological soil crust and put into a sterile polypropylene container. The sample was transported and stored at room temperature in an air-dry (natural) condition. Microbiological analyses were performed within one month after the sample collection.

The central region where the sample was taken from is characterized by the most typical climate of this desert: the temperature during the year varies from −10 to 50 °C, the average annual rainfall varies from 30 to 300 mm (arid–semi-arid climate type) [22]. It has been shown that the soil of this desert can be heated up to a temperature of 67 °C [29].

The Mojave tectonic block is a part of the Basin and Range tectonic province, where many asymmetrical basins have been formed during regional extension processes. The central Mojave region was formed during localized extension which occurred between 24 and 18.5 million years ago and produced 40–60 km of extended terrain space [41]. The central Mojave Desert is characterized by a variety of geologic surfaces that includes mountain ranges of diverse rock types, playas, ancient lake deposits, lava flows, sand-dune fields, alluvial fans, and riverbeds. The region of sample studied is underlain by middle Tertiary volcanic rocks, ranging mainly from andesitic to rhyolitic compositions [42].

The sample pH was 7.2. Literature data on the soils of this region indicate the content of organic matter in the range of 0.04–0.1%, total nitrogen content varies from 0.03% to 0.09% [22]. Soil sample texture is found to be sand. Dominance of silica and iron oxide-containing minerals was visually detected and confirmed by polarized light microscopy.

2.2. Epifluorescent Microscopy

The total number of prokaryotes in the samples was determined with epifluorescence microscopy (EFM) with acridine orange dye. Cell desorption was carried out by vortexing using Heidolph Multi Reax vortex for 30 min at 2000 rpm. The preparations were produced in six replicates, fixed by heating, then stained with water solution of acridine orange (1:10,000) for 3 min, washed in still distilled water for 20 min, dried at room temperature, and viewed under the Primo Star (Zeiss, Germany) microscope with fluorescence epi-illumination system (AmScope, Irvine, CA, USA) at 700× magnification for 20 fields of vision for each replication. Cells with green fluorescence were counted. The water used for the dilution preparation was simultaneously examined as control.

The prokaryotic cells number was calculated using the equation \( N = \frac{S_1 \times a \times n}{V \times S_2 \times c} \), where \( N \) is the number of cells per gram of soil; \( S_1 \) is the area of the preparation (\( \mu m^2 \)); \( a \) is the number of cells in the field of view; \( n \) is the dilution index; \( V \) is the volume of the soil suspension drop placed on the glass (mL); \( S_2 \) is the field of view of the microscope (\( \mu m^2 \)); and \( c \) is the sample weight (g) [43].

2.3. Bacteria Culturing and Isolation

Peptone Yeast Glucose (PYG) medium rich in various carbon sources and nutrients (glucose—1 g/L, peptone—2 g/L, yeast extract—1 g/L, tryptone—1 g/L, agar—20 g/L) and modified Czapek (CM) medium (glucose—2 g/L, sucrose—2 g/L, starch—2 g/L, NaNO₃—2 g/L, KH₂PO₄—1 g/L, MgSO₄—0.5 g/L, KCl—0.2 g/L, agar—20 g/L) [44] were used for bacteria cultivating and isolation. Dilutions of the soil sample in sterile 0.01 M phosphate-saline buffer solution (pH 7.4,
0.137 M NaCl, 0.0027M KCl) in tenfold dilution step were plated on the solid nutrient media in three replicates [45].

For the more complete characterization of the cultured bacterial community, culturing was performed at temperatures of 10, 25, and 50 °C (characteristic optima of psychrophilic, mesophilic, and thermophilic bacteria [17]) until the formation of visible macrocolonies was completed (typically for 14 days at 25 and 50 °C and 30 days at 10 °C). Colonies’ morphotypes were distinguished by colour and morphology of the colonies as well as cell morphology. Isolated bacterial strains (Table A1) were deposited to the Astrobiological Collection of Microorganisms of the National Depository Bank of Live Systems “Noah’s Ark” (Available at [46]).

2.4. Amplification and Sequencing of 16S rRNA Genes

For amplification of the 16S rRNA gene, biomass of pure bacterial culture that has been cultured for 2–3 days was subjected to boiling in Tris-EDTA buffer (pH 8.0) which contained 5% Triton X-100, and homogenization by mechanical destruction with sterile glass beads (250–300 µm in diameter) using a Homogenizer Minilys (Bertin Instruments, Montigny-le-Bretonneux, France) at 5000 rpm for 30 s. The resulting homogenate was centrifuged and the resulting supernatant was used as a DNA template for PCR [47].

For amplification of the gene of interest, the primer systems 27 f + Un1492 r [48,49], 63 f + 1387 r [47], 341 f + 805 r [50], and 27 f + 537 r [48,50] were used in order of priority. Amplification process was performed with cell lysate, prepared as described above. If the procedure failed to obtain the PCR product by the first primer system, the next primer system with the same DNA matrix was used and so on until a product that can be used for further sequencing was acquired [45].

The PCR products were purified and sequenced by the Research and Production Company “Evrogen” (Moscow, Russia) using the 1100 r [50], 805 r, or 537 r [51] primers (Table A2). The editing of the nucleotide sequences was carried out using Chromas Lite 2.01 [52]. For alignment, comparison and identification of nucleotide sequences, the Clustal Omega [53] and the BLAST algorithm from the GenBank database [54] were used. The sequences were deposited in GenBank under the accession numbers MK403768—MK403884.

The phylogenetic trees were constructed using MEGA 7 software [55]. Sequences were then aligned using the Clustal Omega online alignment tool [53]. The type material sequences from GenBank were predominantly used for phylogenetic trees construction. Strain identification was based upon phylogenetic analysis and similarity of the sequences with GenBank data.

2.5. Physiological Assays

The resistance spectra of all isolated cultures (121 strains) to various factor influences were obtained by culturing isolates on the same liquid medium that was used to isolate each particular strain from a natural sample; for each of the investigated factors the experiments were conducted in three replicates. To determine resistance to temperature, cultures were incubated in thermostats at temperatures of 2, 4, 10, 25, 37, 45, and 50 °C. Phosphate (KH₂PO₄ + H₃PO₄ final concentration of 100 mM, pH 2–6) and tris-alkaline (Tris + HCl + NaOH final concentration of 100 mM, pH 7–12) buffer systems were used to determine resistance to various pH levels. Bacterial strains’ resistance to presence of salts was determined by aseptic preparation and subsequent dilution of 20% (w/v) stock solutions of NaCl, KCl, NaHCO₃, MgSO₄ to final concentrations of 2, 5, 10, 15, and 20%; the series of magnesium perchlorate concentrations were prepared similarly by diluting a 20% (w/v) sterile stock solution to final concentrations of 0.5, 1, 2, 5, 10, and 15%. Antibiotic resistance was determined on nutrient media containing ampicillin (Amp), cephalaxin (Ceph), chloramphenicol (Chl), tetracycline (Tet), doxycycline (Dox), kanamycin (Kan), or rifampicin (Rif) (Belmed, Russia) with a final concentration of 100 µg/mL. All tests (except for resistance to temperature) were carried out at a temperature of 25 °C [44]. The growth was registered on the tenth day after inoculation for the cultures cultivated at temperatures of 10, 25, 37, 45, and 50 °C; for cultures growing at temperatures of
2 and 4 °C the incubation period was 60 and 30 days, respectively. Growth registering was performed using a Sunrise (Tecan, Menendov, Switzerland) plate photometer at a wavelength $\lambda = 620$ nm: The plates were measured immediately after inoculation and after incubation period. Detailed protocol of physiological assays is described in [44].

2.6. Multisubstrate Testing

To assess the potential metabolic activity of a microbial community, multisubstrate testing (MST) of the soil microbial community was performed [56,57]. The testing was carried out with 47 substrates including sugars, alcohols, amino acids, salts of organic acids, and polymers (all substrates are listed in [43], all tests were performed in two replicates). The soil sample was diluted (1:100) in sterile phosphate saline buffer (pH 7.4) and vortexed for 15 min at 2500 rpm using Heidolph Multi Reax vortex. The mineral particles were precipitated by centrifugation (2000 rpm, 2 min). The hydrogenase activity indicator (triphenyltetrazolium bromide) was added to the supernatant, and after mixing 200 µL aliquot was added to each well of a 96-well plate containing a set of 47 test substrates in two replicates. The plates were incubated at +28 °C for 96 h. After the incubation, the optical density of the solutions was measured photometrically at wavelength $\lambda = 510$ nm using a Sunrise (Tecan, Menendov, Switzerland) plate photometer.

2.7. Data Analysis

Statistical data processing was performed using the Microsoft Office Excel 2011 software package (Redmond, Washington, D.C., USA). For data on cell numbers, confidence intervals of the mean were calculated using Student’s test at $p < 0.05$. When determining the physiological spectra, the results obtained in three replicates was considered a positive reaction. Indices of similarity and biodiversity of microbial communities were calculated according to Chernov and Lysak [58] at genera level of taxonomic affiliation.

3. Results

3.1. Cell Numbers

The total number of prokaryotic cells in the soil sample, obtained by epifluorescence microscopy method, was $(5.8 \pm 1.7) \times 10^8$ cells per gram of soil. Cultured bacteria on PYG medium were detected in the amount of $(8.0 \pm 0.5) \times 10^6$ colony-forming units (CFU) per gram and $(5.5 \pm 0.2) \times 10^6$ CFU/g at 25 °C and 10 °C, respectively. On the CM medium $(8.8 \pm 0.4) \times 10^5$ and $(5.5 \pm 0.2) \times 10^5$ CFU/g were found at 25 °C and 10 °C, respectively (Figure 1). Colony-forming units were not detected after incubation at 50 °C.

![Figure 1](image.png)  
**Figure 1.** Total prokaryotic cells count obtained by epifluorescent microscopy (EFM) and culturable bacteria count on peptone-yeast-glucose (PYG) and Czapek modified (CM) media in the examined soil sample. Error bars are within the standard deviation, $p < 0.05$. 
3.2. Culturable Communities’ Structure

Pigmented forms of microorganisms dominated in all the cultured communities isolated from the sample. In the PYG medium plated communities, which were characterized by a higher cell counts, red-pigmented colonies were predominant and yellow-pigmented colonies were dominant on CM medium (Figure 2). Maximum diversity of colony morphotypes was observed on PYG medium: 61 morphotypes were described in the course of culturing at mesophilic optimum; on CM medium 28 morphotypes were isolated under similar temperature conditions. At low temperature (10 °C), diversity decreased: 22 and 10 colony morphotypes were isolated on PYG and CM media, respectively (Figure S1). In total 121 strains of aerobic heterotrophic bacteria were isolated from the investigated soil sample and subjected to further analysis.

![Proportion of pigmented colonies in the communities studied.](image)

The greatest taxonomic diversity of cultured bacteria was recorded in the microbial community isolated on PYG medium under mesophilic conditions (25 °C). Representatives of 24 genera of bacteria were identified: Agrococcus, Arthrobacter, Bacillus, Brachybacterium, Brevibacterium, Cellulomonas, Geogenia, Janthinobacterium, Kocuria, Labedella, Leucobacter, Massilia, Microbacterium, Micrococcus, Mycetocola, Paracoccus, Planomicrobium, Pseudarthrobacter, Rufibacter, Salinibacterium, and Streptomyces. Bacteria of the species Arthrobacter sp. were dominant and the subdominant positions were occupied by Microbacterium sp., Pseudoarthrobacter sp., and Agrococcus sp. representatives (Figure 3).

Under similar conditions on CM medium, representatives of the genera Agrococcus Arthrobacter, Bacillus, Burkholderia, Cellulomonas, Massilia, Microbacterium, Paracoccus, Pontibacter, Pseudoarthrobacter, Salinibacterium, Sphingomonas, and Streptomyces were identified (listed in descending order of representation degree in the community, Figure 4).

Smaller diversity was observed in the community incubated under low temperature conditions. Bacteria of the genus Planomicrobium were dominant on PYG medium, subdominant positions were represented by species Arthrobacter agilis, and Planomicrobium glaciei, and representatives of Arthrobacter, Pseudarthrobacter, Leucobacter, Microbacterium, Massilia, Micrococcus, Pseudarthrobacter, Rhodococcus, and Sphingomonas genera were minor components of the culturable bacterial community (Figure 5).

On CM medium at low temperature, representatives of the Arthrobacter and Pseudarthrobacter genera accounted for 85% of all colonies cultured under these conditions; representatives of Cellulomonas and Streptomyces were identified as minor components (Figure 6).
Figure 3. Structure of the culturable bacterial community isolated on PYG medium at 25 °C. Hidden percentage corresponds to 1%; the “others” group includes Bacillus sp., Brachybacterium sp., Massilia varians, Microbacterium aurantiacum, and Pseudarthrobacter oxydans represented by 0.5% each.

Figure 4. Structure of the culturable bacterial community isolated on CM medium at 25 °C.
The coefficients of biological diversity, evenness, and similarity of bacterial communities, isolated from the examined site, are presented in Tables 1 and 2. The summarized communities’ diversity data obtained are presented in Table A3. The phylogenetic trees of isolated strains are presented in Supplementary materials Figures S2–S4.

**Table 1.** Ecological indices characterised of cultured communities.

| Index       | PYG 25 °C | PYG 10 °C | CM 25 °C | CM 10 °C |
|-------------|-----------|-----------|----------|----------|
| Shannon index | 3.87      | 2.93      | 3.56     | 1.44     |
| Evenness index | 0.87      | 0.88      | 0.91     | 0.72     |

**Figure 5.** Structure of the culturable bacterial community isolated on PYG medium at 10 °C.

**Figure 6.** Structure of the culturable bacterial community isolated on CM medium at 10 °C.
Table 2. Ecological indices of cultured communities’ similarity.

| Index                        | PYG 25 °C-PYG 10 °C | CM 25 °C-CM 10 °C | PYG 25 °C-CM 25 °C | PYG 10 °C-CM 10 °C |
|------------------------------|---------------------|-------------------|--------------------|--------------------|
| Common genera number         | 8                   | 8                 | 12                 | 3                  |
| Jaccard index                | 0.33                | 0.27              | 0.48               | 0.27               |
| Chekanovskiy–Sørensen index  | 0.50                | 0.42              | 0.65               | 0.43               |
| Sørensen modified index      | 0.55                | 0.42              | 0.57               | 0.34               |

3.3. Multisubstrate Testing

Multisubstrate testing revealed a wide range of substrates suitable for development of the investigated microbial community. The most active substrate assimilation was observed on simple sugars, easily accessible polysaccharides (pullulan, starch, sucrose), lactate, Tween 80, and some amino acids (alanine, glutamine, and proline) (Table 3).

Table 3. Substrate assimilation obtained by multisubstrate testing.

| Most assimilated substrates | Amino acids | Lipid-like substance | Carbohydrates | Alcohol | Salt of carbon acid | Weakly assimilated substrates | Arginine | Amino acid polymer | Salt of carbon acid | Dextran 500 | Xylose |
|-----------------------------|-------------|----------------------|---------------|---------|---------------------|-------------------------------|----------|-------------------|-------------------|-------------|--------|
| Amino acids                 | Arginine    | Arginine             | Asparagine    | Serine  | Asparagine          | Sodium carbonate             | Arginine | Peptone           | Propionate        | Dextran 500 | Xylose |
| Lipid-like substance        | Tween 80    | Tween 80             | Phenylalanine | Serine  | Phenylalanine       | Sodium carbonate             | Arginine | Peptone           | Propionate        | Dextran 500 | Xylose |
| Carbohydrates               | Pullulan    | Pullulan             | Soluble starch| Serine  | Soluble starch      | Sodium carbonate             | Arginine | Peptone           | Propionate        | Dextran 500 | Xylose |
|                             | Sucrose     | Sucrose              | Salt of carbon acid | Serine  | Salt of carbon acid | Sodium carbonate             | Arginine | Peptone           | Propionate        | Dextran 500 | Xylose |
|                             | Arabinose   | Arabinose            | Carbohydrates | Serine  | Carbohydrates       | Sodium carbonate             | Arginine | Peptone           | Propionate        | Dextran 500 | Xylose |
|                             | Glucose     | Glucose              |               |         |                     | Sodium carbonate             | Arginine | Peptone           | Propionate        | Dextran 500 | Xylose |
|                             | Maltose     | Maltose              |               |         |                     | Sodium carbonate             | Arginine | Peptone           | Propionate        | Dextran 500 | Xylose |
| Alcohol                     | Sorbitol    | Sorbitol             |               |         | Sodium carbonate    | Sodium carbonate             | Arginine | Peptone           | Propionate        | Dextran 500 | Xylose |
| Salt of carbon acid         | Lactate     | Lactate              |               |         | Sodium carbonate    | Sodium carbonate             | Arginine | Peptone           | Propionate        | Dextran 500 | Xylose |

3.4. Physiological Assays

Physiological assays were performed for all isolated 121 strains. Strains that were able to metabolize at low temperatures (up to 2 °C) were found to be more common than those that were able to grow at high temperatures. Thermotolerant strains that were able to metabolize at a temperature of 45 °C were found in communities isolated on both media at 25 °C. These strains made up 39% and 10% of the total number of strains in communities cultured on PYG and CM media, respectively. The strains capable to grow at 50 °C were only found in the community isolated on a rich medium at 25 °C, and made up 22% of the total number of isolates under these conditions (Figure 7a,b). Twenty percent of the strains isolated on PYG at 25 °C were able to metabolize at 2 °C and the same percentage was able to grow at 50 °C. At the same time, less than 20% of the community isolated on CM medium under similar conditions were metabolically active at 2 °C and only 10% of the community were able to grow at 45 °C. Higher levels of resistance to low temperatures were detected for strains isolated on CM medium at 10 °C. Amongst all investigated bacteria 10 strains were able to metabolize in extremely wide temperature range (2–4 – 45–50 °C). Detailed characteristics of strain resistance are presented in Table S1.

All of the isolated strains were able to metabolize in the pH range of 6–8. The greatest resistance to pH of the medium was observed in the community isolated on CM medium at 25 °C: more than a half of the isolates were able to metabolize in a medium with pH of 3 and the same percentage was observed for pH of 12. Among communities isolated at 10 °C, the community isolated on CM medium (Figure 7c,d) was also characterized by a higher (by 20% on average) proportion of pH-tolerant strains. The pH range of strains’ metabolic activity was shifted to the alkaline region and ranged from 3–12 pH.
units. Among all investigated bacteria 44 strains were able to metabolize in extremely wide pH range (3–4 – 12 units). Detailed characteristics of strains' resistance are presented in Table S1.

Tests on media with addition of sodium chloride or potassium chloride revealed a moderate halotolerance of all the studied communities. Less than 50% of the strains retained metabolic activity in the presence of 5% NaCl. At the same time, 14% of the community isolated on PYG medium at 25 °C were capable to grow in the presence of 10% sodium chloride and 6% of the same community were able to metabolize on media containing 15% sodium chloride. In addition, almost the same level of resistance was revealed for the communities isolated on CM medium at 10 °C and 25 °C (Figure 7e,f).

Figure 7. Isolated strains resistance to: (a,b)—cultivation temperature; (c,d)—pH of the media; (e,f)—sodium chloride, (g,h)—potassium chloride. Left column: strains isolated on PYG medium; right column—strains isolated on CM medium.
Potassium chloride had a smaller inhibitory effect (on average two times smaller) on the examined communities: 14% of the strains isolated on PYG at 25 °C metabolized in a medium containing 15% of this salt; similarly to sodium chloride resistance, 80% of the strains isolated on CM at 25 °C were resistant to the presence of 2% KCl, and 10% were resistant in 10% solution (Figure 7g,h).

The presence of magnesium sulphate in the medium had a low inhibitory effect on all of the studied communities: 39% and 50% of the strains isolated on PYG medium at 25 °C and 10 °C respectively retained metabolic activity in presence of 20% magnesium sulphate. Seventy-three percent and 60% of the strains isolated on CM medium at 25 °C and 10 °C retained metabolic activity in the same conditions (Figure 8a,b).

Sodium bicarbonate had the highest inhibitory effect among the studied water-soluble salts: few strains resistant to 5% of this salt in the culture medium were detected among the communities isolated on PYG and CM media at 25 °C (9% and 3% of strains, respectively) and among the community isolated on CM at 10 °C (10% of strains) (Figure 9).
The maximum diversity of the community detected on the rich PYG medium under the conditions of this is probably due to the conditions of culturing and intra- and interpopulation interactions between the presence of a single clinical antibiotic.

In the investigated communities, the presence of 10% magnesium perchlorate. The community isolated on PYG at 25 °C was resistant to concentrations of up to 5% of magnesium perchlorate (28% of strains) (Figure 8c,d). Furthermore, higher (on average by 20%) proportion of the strains isolated on CM medium showed high resistance to the presence of this salt in the medium compared to the strains isolated on PYG medium.

The individual ranges of resistance of the isolated strains to physicochemical stress factors are presented in supplementary materials (Table S1).

In general, the investigated communities showed low resistance to the presence of antibiotics—about 20% of isolates in each of the four communities were capable to grow in the presence of a single clinical antibiotic.

High resistance of strains isolated on CM medium at 25 °C to ampicillin, tetracycline, and cephalixin is noteworthy (Figure 8e,f). In all the communities, the strains characterized with multiple antibiotic resistance were found. These strains were related to the genera Bacillus, Agroccocus, Arthrobacter, Leucobacter, Pseudarthrobacter, Planomicrobiun, Massilia, Microbacterium, and Pontibacter (Table S2).

4. Discussion

The total number of prokaryotes and numbers of culturable bacteria revealed in soil studied are in accordance with the previously obtained data for the soils of other regions of the Mojave Desert [32,36,37]. Different cell numbers observed in different regions of the desert could be caused by the high heterogeneity of soil composition and the high heterogeneity of soil resources in this desert, as well as past and current climatic conditions or plant associations which influence bacterial communities [59,60]. At the same time, considering the climatic regime of the studied region, the absence of growth during the isolation of culturable bacteria at high (50 °C) temperature is worth noticing, whereas some strains isolated at lower temperatures (10 °C, 25 °C) were capable of growing at this temperature in axenic culture. This is probably due to the conditions of culturing and intra- and interpopulation interactions between microorganisms, which can complicate the transition from the state of metabolic dormancy to grow under stressful conditions [61–63]. It is notable that the numbers of bacteria cultured at 10 °C and 25 °C were virtually equal. Based on these data, it is possible to assume that there is a high proportion of strains with psychrotolerant properties in the investigated soil, as was previously found for bacteria isolated from the Sahara and the Gibson Desert soils [44].

Lower numbers of CFUs for CM nutrient medium could be explained by lack of vegetation coverage at the sampling site and, as a result, the rareness of plant origin carbon sources (such as starch and sucrose in CM medium) in the soil in situ [39]. In addition, these compounds require preliminary hydrolysis for further assimilation by the cells. However, not all bacteria can produce hydrolytic enzymes for assimilation of these substrates [61].

The predominance of pigmented bacteria in the studied surface soil of the Mojave Desert is not surprising due to the role of pigments in protecting cells from damaging ultraviolet radiation [63,64]. The maximum diversity of the community detected on the rich PYG medium under the conditions of mesophilic temperature optimum indicates a predominantly mesophilic strategy of development for...
the majority of the microbial community studied. Diversity decreases along with decreasing culturing temperatures and limiting of easily available carbon sources and growth factors (such as amino acids and vitamins) in the composition of the nutrient medium. Mesophilic development strategy common for the acquired isolates is probably due to the climatic conditions experienced by the soil sample. The development of psychrotolerant properties could be caused by a high contrast of both diurnal and seasonal temperatures and can be considered to be an adaptive feature under these conditions. The higher biodiversity of cultured bacteria on PYG medium is due to the diversity of carbon sources and the presence of growth factors (such as vitamins and amino acids), which can be used by a larger number of bacteria. The presence of growth factors may also contribute to the reactivation of cells that were in a state of metabolic rest [62].

Representatives of the Actinobacteria phylum were predominant in all of the cultured communities, representatives of the Proteobacteria phylum were the second most common ones, Firmicutes and Bacteriodetes were identified as minor components. The dominance of representatives of Proteobacteria phylum in the edaphic bacterial communities of the Mojave Desert has been shown based on the molecular-genetic tests [21,24]. Simultaneously, the results we obtained reveal the similar structure of bacterial communities in the studied soil of this desert, consistent with culture-independent data published earlier [10,32,33]. The predominance of Actinobacteria in the community is quite natural, considering the fact that many species among them are resistant to desiccation, UV radiation, and other stress effects [22]. Low abundance of representatives of the Firmicutes phylum was previously detected in the Mojave Desert [24]. Among all isolated strains low relative abundance of spore-forming bacteria was observed (seven isolates only), while a high abundance of genes associated with spore formation processes was found in situ by culture-independent methods [33].

The bacteria of genera Arthrobacter, Bacillus, Kocuria, Leucobacter, Massilia, Mycetocola, Microbacterium, Paracoccus, Planonicrobium, Pseudarthrobacter, Rufibacter, Sphingomonas, and Streptomyces were previously isolated from other hot deserts [44,63–65]. Bacteria of the genus Agrococcus were previously cultured from cold deserts [66]. Among the representatives of the genus Brachybacterium several species connected to the root systems of halophilic plants were described and characterized by having plant growth-promoting potential [67]. Members of the genus Plantibacter, which have not been previously isolated from deserts, are also considered to be associated with herbaceous plants [68]. Representatives of the genus Cellulomonas are often isolated from soil [69] with some of them known to be halotolerant species [70]. Bacteria of the genus Pontibacter have been previously isolated from arid soils [71,72].

In this research, bacteria of the genera Janthinobacterium, which were found dominant in the meltwaters of glaciers [73], Salinibacterium, previously found in marine ecosystems and glaciers [74,75], and Labedella were isolated from desert soil for the first time. Noteworthy is the discovery of the bacteria Planonicrobium glaciei in the desert soil. This species was first isolated from glacier, and after that from desert, ecosystems [76]. This allows us to assume that the intracellular mechanisms that determine the resistance and survivability of the species turn out to be adaptive in both cold and hot deserts.

According to community structure diagrams and ecological indices of communities’ similarity, all the obtained communities differ from each other significantly. It indicates that culturing conditions (such as medium composition and cultivation temperature) are the main factors influencing the structure of the communities isolated from studied soil. Nevertheless, the genera represented in all cultured communities are quite similar.

It should be considered that transport of microorganisms by winds is possible [15], which is especially important in case of surface soil sampling. According to this fact, the presence of introduced bacteria could not being excluded. Both culture-dependent and culture-independent methods could not separate indigenous and introduced microorganisms. However, the sampling site is located in the central part of the Mojave Desert, thus minimizing the chance to long distant cell transport from non-desert regions. Thus, even if some of the isolates were not indigenous, they probably were
introduced from the other desert sites. Moreover, virtually all representatives of genera isolated were previously detected in different desert soils. The resistance data obtained also testifies to the high adaptation to the desert conditions and confirms predominantly desert-associated strains were isolated.

Substrates on which the most active development of the examined community was observed, could be produced as metabolites of cyanobacteria [8]. This suggests a functional relationship between the previously shown metabolically active cyanobacterial communities in the studied soil of the Mojave Desert and the heterotrophic community studied by us that exists due to the presence of the primary organic substance of cyanobacterial origin. Based on the aforementioned facts and data on the taxonomic and morphological diversity of isolates, it can be presumed that the culturable bacterial community of the studied site in central Mojave Desert, which is considered to be a Mars analogue site, is functionally differentiated, and is highly adapted to harsh physicochemical conditions. These results are consistent with the data obtained previously in the other regions of this desert [32,33].

The analysis of the resistance of isolates to temperature reveals the thermotolerant properties of communities cultured at 25 °C. The expansion of the range of temperatures suitable for growth occurs mainly in the region of low temperatures, which is probably caused by daily and seasonal temperature fluctuations [19]. The highest resistance was recorded for the community isolated on PYG media at 25 °C, which is probably due to the high number of cells and diversity of this community.

The wide pH ranges in which the metabolic activity is maintained can be explained by contrast temperature conditions and precipitation regimes leading to a change in the solubility of the substances in the soil solution [22]. Higher levels of pH resistance of strains isolated on CM could be caused by their hydrolytic activity, often associated with changes in the pH of the solution [61].

The studied region is characterized by a low content of water-soluble salts [19,20,24], which could mean that the abundance of salts present in the studied sample is low. It explains the moderate general resistance of isolated communities to the presence of sodium chloride or potassium chloride. However, strains with high resistance (up to 15%) to sodium chloride were found. It was previously shown that the same physiological mechanism provides resistance for both desiccation and salinization, which could explains the obtained result [77,78].

High resistance to magnesium sulphate was previously shown for bacterial communities isolated from desert soils [44]. It is probably associated with the assimilation of the components of this salt as elements of mineral nutrition. Low resistance to sodium bicarbonate is associated with the hydrolytic alkaline nature of this salt and its local distribution in the desert in the form of soda lakes. The presence of resistant forms is probably caused by a slight aeolian transfer of sodium bicarbonate and bacteria adapted to its presence, as well as by the formation of this salt in situ during weathering processes [42,44].

High resistance to magnesium perchlorate is particularly important in the astrobiology-oriented review of the obtained results. Maintenance of metabolic activity in vitro in the presence of perchlorates, at concentrations significantly exceeding those found in the regolith of Mars [79], testifies their non-limiting role in the regolith. Resistance to oxidizing agents is also likely due to the physiological adaptation of bacteria to arid conditions [78]. The higher level of resistance of the community isolated on a rich medium (PYG) at 10 °C, compared with the one isolated at 25 °C on the same medium, can be explained by the physiological connection of processes that ensure adaptation to low temperatures and the presence of oxidizers [80]. It has previously been shown that bacterial communities of other desert soils are resistant to high perchlorate concentrations [44].

The highest levels of resistance to physicochemical stress factors were found in representatives of the genera Arthrobacter, Bacillus, Kocuria, Leucobacter, Microbacterium, Planomicrobium, and Pontibacter (Table S1). Representatives of these genera are widely distributed in desert soils and have previously demonstrated high resistance to various types of stress effects [15,17,22,25,44,59,66].

For the representatives of majority genera isolated from soil studied resistance to ionizing and UV radiation was shown ([22,43,81–89] and references therein). It is in accordance with pigmented colonies’ high proportion data and it allows to suggest the presence of high UV- and radioresistance of
the strains studied. Data on the resistance to physicochemical factors combined with the literature data on UV and ionizing radiation resistance could be considered as additional evidence of potential survivability of this bacterial community in Martian-like conditions. UV- and radioresistance of the isolates should be confirmed in further research.

The low resistance of the studied strains to antibiotics suggests that there is no active antibiotics-dependant competition in the communities. It is possible that the communities are realizing a co-metabolism strategy [90], as indirectly confirmed by the results of culturing on PYG medium and MST analysis: they revealed the most intensive growth of a cultured community on peptone containing various oligopeptides, amino acids, and vitamins. A similar result was obtained earlier in the study of the number of antibiotic resistance genes copies in the soils of the Mojave Desert [33]. At the same time, the discovery of a high number of antibiotic-resistant bacteria in the community isolated on CM medium at 25 °C is probably due to the signal role of antibiotics as quorum sensing agents [91,92] for activation of hydrolytic processes in the community. We have not found any previously published data on antibiotic resistance of representatives of Planomicrobium, Salinibacterium, and Labedella genera.

5. Conclusions

Stress effects, such as low water availability, nutrients deficiencies, high levels of solar radiation, and wide temperature fluctuations in the surface soil of the Mojave Desert lead to the formation of physiological survival strategies for prokaryotes existing under these conditions [2,3]. Our study revealed a high diversity (both taxonomic and morphophysiological) of culturable bacteria in the investigated soil. Species typical for various soils, including arid soils, and species that have not been previously isolated from hot arid soils were found in isolated bacterial communities. This suggests that the mechanisms of adaptation to cryo-arid and xero-arid conditions include similar physiological processes and adaptations. The obtained spectra of metabolic activity in the gradients of physicochemical factors indicate predominantly mesophilic and neutrophilic optima of all the studied strains, mostly capable of maintaining metabolic activity in a wide range of conditions, up to extreme ones for individual strains. Extreme resistance levels were identified in bacteria of Arthrobacter, Microbacterium, Bacillus, Planomicrobium, Kocuria, Leucobacter, and Pontibacter genera.

The obtained results, considered together with the data of previous works [25,41,64], testify in favour of viability, functionality, and taxonomical diversity of soil bacterial communities in the central part of the Mojave Desert studied, which is considered as a terrestrial analogue of Martian regolith. The isolated strains require further characterization and description for potential biotechnological applications. Due to the low similarity of the nucleotide sequences of some individual strains to those found in the database, these isolates could be the representatives of undescribed species of culturable bacteria. The most resistant strains that have been found could be used as model objects in further astrobiological studies.

As mentioned earlier, the Mojave Desert has undergone processes similar to those that took place on Mars and formed its current state. The properties of culturable bacterial communities revealed in this study indicate that they have adapted to survive in aggressive changing environmental conditions. Consequently, such communities could be considered as a model for further research of the Martian regolith habitability and the ability of terrestrial bacteria to adapt to extraterrestrial conditions.

Supplementary Materials: The following are available online at http://www.mdpi.com/2076-3263/9/4/166/s1;
Figure S1. Number of colonies’ morphotypes in the communities studied; Figure S2a. Phylogenetic analysis tree of 16S rRNA genes of the strains isolated from the Mojave Desert soil, which were sequenced using 1100r primer; Figure S2b. Phylogenetic analysis subtree of 16S rRNA genes of the strains isolated from the Mojave Desert soil, which were sequenced using 1100 r primer; Figure S2c. Phylogenetic analysis subtree of 16S rRNA genes of the strains isolated from the Mojave Desert soil, which were sequenced using 1100 r primer; Figure S3. Phylogenetic analysis tree of 16S rRNA genes of the strains isolated from the Mojave Desert soil, which were sequenced using 805r primer; Figure S4. Phylogenetic analysis tree of 16S rRNA genes of the strains isolated from the Mojave Desert soil, which were sequenced using 537r primer; Table S1. Physiological characteristics of isolated bacteria, Table S2. Antibiotic resistance spectra of isolated strains.
Author Contributions: A.A.B. and V.S.C. designed the study, all authors performed the study, A.A.B. and V.S.C. prepared draft manuscript, all authors edited and commented on the manuscript.

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Appendix A

Table A1. Taxonomic affiliation of isolated strains.

| Strain–Isolation Conditions–GenBank Accession Number | BLAST Search Results | Taxonomic Affiliation |
|------------------------------------------------------|----------------------|-----------------------|
| KBP.AS.17–PYG 25 °C–MK403789 [MF682005]              | *Pseudarthrobacter siccitolerans* [MF682005]—99.0% | *Pseudarthrobacter siccitolerans* |
|                                                      | *Pseudarthrobacter oxydans* [MF681862]—99.0%     | *Pseudarthrobacter oxydans* |
|                                                      | *Pseudarthrobacter oxydans* [MF681851]—99.0%     | *Pseudarthrobacter oxydans* |
| KBP.AS.62–PYG 25 °C–MK403790 [KX928444]             | *Arthrobacter sp.* [KT944733]—99.5%             | *Arthrobacter sp.* |
|                                                      | *Arthrobacter sp.* [KH507593]—99.5%             | *Arthrobacter sp.* |
| KBP.AS.75–PYG 25 °C–MK403794 [KX928444]             | *Brachybacterium sp.* [MH518254]—99.3%          | *Brachybacterium sp.* |
|                                                      | *Brachybacterium paraconglomeratum* [KY622837]—99.3% | *Brachybacterium paraconglomeratum* |
|                                                      | *Brachybacterium conglobatum* [LH9954811]—99.3% | *Brachybacterium conglobatum* |
|                                                      | *Jannthinobacterium sp.* [KT715033]—98.7%       | *Jannthinobacterium sp.* |
| KBP.AS.105–PYG 25 °C–MK403787 [JF605429]            | *Jannthinobacterium sp.* [JF605404]—98.7%       | *Jannthinobacterium sp.* |
|                                                      | *Arthrobacter sp.* [HM216918]—99.2%             | *Arthrobacter sp.* |
| KBP.AS.160–PYG 25 °C–MK403788 [JN129287]            | Uncultured *Arthrobacter sp.* [JN009621]—99.0% | *Arthrobacter sp.* |
|                                                      | *Arthrobacter agilis* [JN009621]—99.0%          | *Arthrobacter agilis* |
|                                                      | *Microbacterium aurantiacum* [MHT34538]—99.2%   | *Microbacterium aurantiacum* |
| KBP.AS.747–PYG 25 °C–MK403791 [MJ715198]            | *Microbacterium aurantiacum* [MH702463]—99.2%   | *Microbacterium aurantiacum* |


| Strain–Isolation Conditions–GenBank Accession Number | BLAST Search Results | Taxonomic Affiliation |
|----------------------------------------------------|----------------------|-----------------------|
| KBP.AS.748–PYG 25 °C–MK403792                       | *Pseudarthrobacter siccitolerans* [MF682005]—99.22% *Pseudarthrobacter oxydans* [MF681862]—99.2% *Pseudarthrobacter oxydans* [MF681851]—99.2% *Brevibacterium frigoritolerans* [MK318239]—99.9% *Brevibacterium frigoritolerans* [MK318233]—99.9% *Brevibacterium frigoritolerans* [MK318218]—99.9% *Planomicrobium okeanokoites* [KF749386]—99.3% *Planomicrobium okeanokoites* [KF749394]—99.3% *Planomicrobium okeanokoites* [KF749386]—99.3% *Planomicrobium okeanokoites* [KF749394]—99.3% | *Pseudarthrobacter sp.* |
| KBP.AS.749–PYG 25 °C–MK403793                       | *Brevibacterium frigoritolerans* [MK318239]—99.9% *Brevibacterium frigoritolerans* [MK318233]—99.9% *Brevibacterium frigoritolerans* [MK318218]—99.9% *Planomicrobium okeanokoites* [KF749386]—99.3% *Planomicrobium okeanokoites* [KF749394]—99.3% *Planomicrobium okeanokoites* [KF749386]—99.3% *Planomicrobium okeanokoites* [KF749394]—99.3% | *Planomicrobium okeanokoites* |
| KBP.AS.750–PYG 25 °C–MK403795                       | *Planomicrobium okeanokoites* [KF749386]—99.3% *Planomicrobium okeanokoites* [KF749394]—99.3% *Planomicrobium okeanokoites* [KF749386]—99.3% *Planomicrobium okeanokoites* [KF749394]—99.3% | *Planomicrobium okeanokoites* |
| KBP.AS.751–PYG 25 °C–MK403796                       | *Agrococcus sp.* [JX949729]—100% *Agrococcus jenensis* [EF672044]—100% *Agrococcus sp.* [KC702716]—99.5% *Agrococcus sp.* [JX949729]—99.5% *Agrococcus jenensis* [EF672044]—99.4% *Agrococcus sp.* [MG232346]—99.5% | *Agrococcus sp.* |
| KBP.AS.752–PYG 25 °C–MK403797                       | *Agrococcus jenensis* [AJ717350]—99.5% *Agrococcus sp.* [HF954438]—99.5% *Kocuria sp.* [DQ192212]—99.3% *Kocuria sp.* [EF612289]—99.2% *Kocuria sp.* [DQ180950]—99.0% *Planomicrobium glaciei* [KF387709]—100% *Planomicrobium sp.* | *Agrococcus sp.* |
| KBP.AS.753–PYG 25 °C–MK403798                       | *Agrococcus jenensis* [AF717350]—99.5% *Agrococcus sp.* [HF954438]—99.5% *Kocuria sp.* [DQ192212]—99.3% | *Agrococcus sp.* |
| KBP.AS.754–PYG 25 °C–MK403799                       | *Kocuria sp.* [DQ180950]—99.0% | *Kocuria sp.* |
| KBP.AS.755–PYG 25 °C–MK403800                       | *Planomicrobium glaciei* [KF387709]—100% *Planomicrobium glaciei* [HQ232419]—100% | *Planomicrobium glaciei* |
| KBP.AS.756–PYG 25 °C–MK403801                       | *Leucobacter sp.* [KY623368]—99.6% *Leucobacter aridicollis* [KR827428]—99.6% *Leucobacter sp.* [KP152582]—99.6% *Planomicrobium okeanokoites* | *Leucobacter aridicollis* |
| KBP.AS.757–PYG 25 °C–MK403802                       | *Planomicrobium okeanokoites* [KF749386]—99.5% *Planomicrobium okeanokoites* [KU221074]—98.6% | *Planomicrobium okeanokoites* |
| KBP.AS.758–PYG 25 °C–MK403803                       | *Microbacterium esteraromaticum* [GU111572]—98.9% *Microbacterium sp.* | *Microbacterium sp.* |
| Strain–Isolation Conditions–GenBank Accession Number | BLAST Search Results | Taxonomic Affiliation |
|----------------------------------------------------|----------------------|----------------------|
| KBP.AS.759–PYG 25 °C–MK403804                      | *Bacillus pumilus*   | *Bacillus pumilus*   |
|                                                    | [MH910167]—99.9%     |                      |
|                                                    | *Bacillus pumilus*   |                      |
|                                                    | [MH910156]—99.9%     |                      |
|                                                    | *Bacillus pumilus*   |                      |
|                                                    | [MH908782]—99.9%     |                      |
|                                                    | *Microbacterium esteraromaticum* |                  |
|                                                    | [GU111572]—98.9%     |                      |
|                                                    | *Microbacterium sp.* |                      |
| KBP.AS.760–PYG 25 °C–MK403805                      | *Microbacterium sp.* |                      |
|                                                    | [MH231521]—98.2%     |                      |
|                                                    | *Microbacterium sp.* |                      |
|                                                    | [MH231520]—98.2%     |                      |
|                                                    | *Rufibacter sp.*     |                      |
|                                                    | [MH105957]—97.6%     |                      |
|                                                    | *Rufibacter sp.*     |                      |
| KBP.AS.761–PYG 25 °C–MK403806                      | *Microbacterium sp.* |                      |
|                                                    | [MH231521]—98.5%     |                      |
|                                                    | *Microbacterium sp.* |                      |
|                                                    | [MH231520]—98.5%     |                      |
|                                                    | *Massilia niabensis* |                      |
|                                                    | [NR_044571]—98.9%    |                      |
| KBP.AS.762–PYG 25 °C–MK403807                      | *Massilia sp.*       |                      |
|                                                    | [DF9196473]—99.2%    |                      |
|                                                    | *Massilia suwonensis*|                      |
|                                                    | [LN774622]—98.8%     |                      |
|                                                    | *Massilia sp.*       |                      |
|                                                    | [MF990764]—98.2%     |                      |
| KBP.AS.764–PYG 25 °C–MK403809                      | *Bacillus sp.*       |                      |
|                                                    | [EU795022]—97.8%     |                      |
|                                                    | *Massilia alkalitolerans* |                |
|                                                    | [KY010279]—99.7%     |                      |
| KBP.AS.765–PYG 25 °C–MK403810                      | *Massilia alkalitolerans* |            |
|                                                    | [KU510579]—99.7%     |                      |
|                                                    | *Massilia alkalitolerans* |            |
|                                                    | [KP282807]—99.7%     |                      |
|                                                    | *Pseudarthrobacter siccitolerans* |            |
|                                                    | [MF682005]—98.1%     |                      |
| KBP.AS.766–PYG 25 °C–MK403811                      | *Pseudarthrobacter sp.* |            |
|                                                    | *Pseudarthrobacter oxydans* |            |
|                                                    | [MF681862]—98.1%     |                      |
|                                                    | *Pseudarthrobacter oxydans* |            |
|                                                    | [MF681851]—98.1%     |                      |
|                                                    | *Massilia varians*    |                      |
|                                                    | [MF077216]—98.4%     |                      |
| KBP.AS.767–PYG 25 °C–MK403812                      | *Massilia varians*    |                      |
|                                                    | [MF077215]—98.4%     |                      |
|                                                    | *Massilia varians*    |                      |
|                                                    | [MF077214]—98.5%     |                      |
|                                                    | *Planococcus donghaensis* |            |
|                                                    | [LN774491]—100%      |                      |
| KBP.AS.768–PYG 25 °C–MK403813                      | *Planomicrobium sp.*  |                      |
|                                                    | [KF749394]—100%      |                      |
|                                                    | *Planomicrobium sp.*  |                      |
|                                                    | [KF749386]—100%      |                      |
|
Table A1. Cont.

| Strain–Isolation Conditions–GenBank Accession Number | BLAST Search Results | Taxonomic Affiliation |
|------------------------------------------------------|----------------------|----------------------|
| KBP.AS.769–PYG 25 °C–MK403814                        | Microbacterium pseudoresistens [LN890047]—98.9% | Microbacterium pseudoresistens |
|                                                      | Microbacterium pseudoresistens [KF687021]—98.9% | Microbacterium pseudoresistens |
|                                                      | Microbacterium sp. [MH671545]—98.2% | Microbacterium sp. |
|                                                      | Arthrobacter agilis [JX949695]—99.3% | Arthrobacter sp. |
|                                                      | Microbacterium sp. [JF949646]—99.3% | Microbacterium sp. |
| KBP.AS.770–PYG 25 °C–MK403815                        | Arthrobacter sp. | Arthrobacter sp. |
|                                                      | Arthrobacter sp. [KF924209]—99.3% | Arthrobacter sp. |
|                                                      | Arthrobacter sp. [JX949659]—99.3% | Arthrobacter sp. |
|                                                      | Arthrobacter sp. [JX949646]—99.3% | Arthrobacter sp. |
| KBP.AS.771–PYG 25 °C–MK403816                        | Planomicrobium glaciei [MG025800]—100% | Planomicrobium glaciei |
|                                                      | Planomicrobium glaciei [KF387709]—100% | Planomicrobium glaciei |
|                                                      | Planomicrobium sp. [JX949538]—100% | Planomicrobium sp. |
|                                                      | Uncultured bacterium [LC026838]—98.9% | Uncultured bacterium |
|                                                      | Cellulomonas sp. [KP126821]—98.4% | Cellulomonas sp. |
|                                                      | Cellulomonas cellasea [KR922256]—98.4% | Cellulomonas cellasea |
|                                                      | Planomicrobium okeanokoites [KF749394]—99.8% | Planomicrobium okeanokoites |
| kbP.AS.772–PYG 25 °C–MK403817                        | Planomicrobium okeanokoites [KF749386]—99.8% | Planomicrobium okeanokoites |
|                                                      | Planomicrobium okeanokoites [KF724965]—99.8% | Planomicrobium okeanokoites |
|                                                      | Planomicrobium okeanokoites [KF724964]—99.8% | Planomicrobium okeanokoites |
|                                                      | Planomicrobium okeanokoites [KF724965]—99.9% | Planomicrobium okeanokoites |
| kbP.AS.773–PYG 25 °C–MK403818                        | Planomicrobium okeanokoites [KF749394]—99.9% | Planomicrobium okeanokoites |
|                                                      | Planomicrobium okeanokoites [KF749386]—99.9% | Planomicrobium okeanokoites |
|                                                      | Georgenia sp. [EF512742]—99.6% | Georgenia sp. |
|                                                      | Georgenia sp. [AY880044]—99.5% | Georgenia sp. |
|                                                      | Georgenia satyanarayani [NR_117051]—99.5% | Georgenia satyanarayani |
|                                                      | Microbacterium barkeri [MG706019]—98.4% | Microbacterium barkeri |
| kbP.AS.774–PYG 25 °C–MK403819                        | Microbacterium barkeri [MG706019]—98.4% | Microbacterium barkeri |
|                                                      | Microbacterium sp. [KY928100]—98.4% | Microbacterium sp. |
|                                                      | Salinibacterium sp. [MH714650]—99.0% | Salinibacterium sp. |
| kbP.AS.775–PYG 25 °C–MK403820                        | Salinibacterium sp. [MH790149]—99.0% | Salinibacterium sp. |
|                                                      | Salinibacterium sp. [MH299814]—99.0% | Salinibacterium sp. |
| kbP.AS.776–PYG 25 °C–MK403821                        | Salinibacterium sp. [MH299814]—99.0% | Salinibacterium sp. |
|                                                      | Salinibacterium sp. [MH14650]—99.0% | Salinibacterium sp. |
| kbP.AS.777–PYG 25 °C–MK403822                        | Salinibacterium sp. [MH790149]—99.0% | Salinibacterium sp. |
| kbP.AS.778–PYG 25 °C–MK403823                        | Salinibacterium sp. [MH299814]—99.0% | Salinibacterium sp. |
| Strain–Isolation Conditions–GenBank Accession Number | BLAST Search Results | Taxonomic Affiliation |
|-----------------------------------------------------|----------------------|----------------------|
| KBP.AS.779–PYG 25 °C–MK403824                        | *Brevibacterium frigoritolerans* [MK318239]—100% | *Brevibacterium frigoritolerans* |
|                                                     | *Brevibacterium frigoritolerans* [MK318233]—100% | *Brevibacterium frigoritolerans* |
|                                                     | *Brevibacterium frigoritolerans* [MK318218]—100% | *Brevibacterium frigoritolerans* |
|                                                     | *Micrococcus* sp. [JQ229694]—99.3%              | *Micrococcus* sp. |
|                                                     | *Micrococcus* sp. [JQ229689]—99.3%              | *Micrococcus* sp. |
| KBP.AS.780–PYG 25 °C–MK403825                        | *Micrococcus* sp. [KM613156]—99.2%              | *Micrococcus* sp. |
|                                                     | *Kocuria* sp. [KT900591]—98.9%                  | *Kocuria* sp. |
|                                                     | *Kocuria sediminis*                             | *Kocuria sediminis* |
| KBP.AS.781–PYG 25 °C–MK403826                        | [MH178354]—98.85%                               | *Kocuria* sp. |
|                                                     | *Kocuria turfanensis* [MF769333]—98.8%          | *Kocuria* sp. |
|                                                     | *Labedella* sp. [KM253033]—99.2%                | *Labedella* sp. |
|                                                     | *Labedella guwakijensis* [LK021191]—98.2%       | *Labedella* guwakijensis |
|                                                     | *Labedella* sp. [JX276669]—98.2%                | *Labedella* sp. |
| KBP.AS.782–PYG 25 °C–MK403827                        | *Plantibacter flavus* [CP019402]—100%            | *Plantibacter flavus* |
|                                                     | *Plantibacter* sp. [HE662660]—100%              | *Plantibacter* sp. |
|                                                     | *Plantibacter* sp. [HE662693]—100%              | *Plantibacter* sp. |
|                                                     | *Arthrobacter agilis* [KT804924]—99.9%          | *Arthrobacter agilis* |
|                                                     | *Arthrobacter agilis* [MF767263]—99.8%          | *Arthrobacter agilis* |
|                                                     | *Arthrobacter agilis* [KR811202]—99.8%          | *Arthrobacter agilis* |
|                                                     | *Microbacterium esteraromaticum* [GU111572]—99.1% | *Microbacterium esteraromaticum* |
| KBP.AS.785–PYG 25 °C–MK403830                        | *Microbacterium aureliae* [NR152652]—98.6%      | *Microbacterium aureliae* |
|                                                     | *Microbacterium aureliae* [KF793922]—98.6%      | *Microbacterium aureliae* |
|                                                     | *Pseudarthrobacter sicctolerans* [MF682005]—99.0% | *Pseudarthrobacter sicctolerans* |
| KBP.AS.786–PYG 25 °C–MK403831                        | *Pseudarthrobacter oxygenis* [MF681862]—99.0%   | *Pseudarthrobacter oxygenis* |
|                                                     | *Pseudarthrobacter oxygenis* [MF681851]—99.0%   | *Pseudarthrobacter oxygenis* |
|                                                     | Uncultured bacterium [KX507906]—98.2%           | Uncultured bacterium |
| KBP.AS.787–CM 25 °C–MK403832                         | *Massilia niabensis* [IF496256]—98.0%           | *Massilia niabensis* |
|                                                     | *Massilia alkalitolerans* [KY010279]—97.8%      | *Massilia alkalitolerans* |
| KBP.AS.788–CM 25 °C–None                             | Was identified by morphology *Burkholderia* sp. [KU060146]—95.7% | *Burkholderia* sp. |
|                                                      | *Bacillus* sp.                                   | *Bacillus* sp. |
| KBP.AS.789–CM 25 °C–MK403833                         | *Burkholderia* sp. [KU060136]—95.7%             | *Burkholderia* sp. |
|                                                     | *Burkholderia* sp. [KU060135]—95.7%             | *Burkholderia* sp. |
| Strain–Isolation Conditions–GenBank Accession Number | BLAST Search Results | Taxonomic Affiliation |
|------------------------------------------------------|----------------------|----------------------|
| KBP.AS.790–CM 25 °C–MK403834 Cellulomonas hominis [KF817811]—100% Cellulomonas hominis [MF928361]—100% Cellulomonas sp. [LC133615]—100% Cellulomonas sp. [MF82005]—99.5% Pseudarthrobacter sicctolerans [MF681862]—99.5% Pseudarthrobacter oxydans [MF81851]—99.5% Pseudarthrobacter oxydans | Cellulomonas hominis | |
| KBP.AS.791–CM 25 °C–MK403835 Pseudarthrobacter sicctolerans [MF682005]—99.5% Pseudarthrobacter oxydans [MF681862]—99.5% Pseudarthrobacter oxydans [MF681851]—99.5% | Pseudarthrobacter sp. | |
| KBP.AS.792–CM 25 °C–MK403836 Massilia sp. [JQ511858]—100% Massilia sp. [KY635898]—99.6% Massilia sp. [KY635895]—99.6% Uncultured actinobacterium clone [KC994764]—98.8% | Massilia sp. | |
| KBP.AS.793–CM 25 °C–MK403837 Salinibacterium sp. [MH299814]—98.7% Salinibacterium sp. [CP026951]—98.7% Arthrobacter sp. [LN871743]—99.7% Arthrobacter sp. [KU951449]—99.7% | Salinibacterium sp. | |
| KBP.AS.794–CM 25 °C–MK403838 Arthrobacter sp. [L871743]—99.2% Arthrobacter sp. [KJ191079]—99.7% Arthrobacter sp. [KJ91059]—99.8% Arthrobacter sp. [KJ91035]—99.8% Uncultured bacterium clone [K507404]—99.1% Massilia suwonensis [NR116872]—99.1% Massilia sp. [KM187344]—98.8% Mycetocola sp. [MH299815]—98.4% Mycetocola sp. [MH298813]—98.4% Mycetocola sp. [CP026949]—98.4% Arthrobacter agilis [KT804924]—98.9% Arthrobacter agilis [MF767263]—98.8% Arthrobacter agilis [KR811202]—98.8% | Arthrobacter sp. | |
| KBP.AS.795–CM 25 °C–MK403839 Arthrobacter sp. [KU951449]—99.2% Arthrobacter sp. [KJ91079]—99.2% Arthrobacter sp. [KJ91079]—99.8% Arthrobacter sp. [KJ91035]—99.8% Uncultured bacterium clone [K507404]—99.1% Massilia suwonensis [NR116872]—99.1% Massilia sp. [KM187344]—98.8% Mycetocola sp. [MH299815]—98.4% Mycetocola sp. [MH298813]—98.4% Mycetocola sp. [CP026949]—98.4% Arthrobacter agilis [KT804924]—98.9% Arthrobacter agilis [MF767263]—98.8% Arthrobacter agilis [KR811202]—98.8% | Arthrobacter sp. | |
| KBP.AS.816–PYG 25 °C–MK403840 Arthrobacter sp. [KJ191079]—99.2% Arthrobacter sp. [KJ91059]—99.8% Arthrobacter sp. [KJ91035]—99.8% Uncultured bacterium clone [K507404]—99.1% Massilia suwonensis [NR116872]—99.1% Massilia sp. [KM187344]—98.8% Mycetocola sp. [MH299815]—98.4% Mycetocola sp. [MH298813]—98.4% Mycetocola sp. [CP026949]—98.4% Arthrobacter agilis [KT804924]—98.9% Arthrobacter agilis [MF767263]—98.8% Arthrobacter agilis [KR811202]—98.8% | Arthrobacter sp. | |
| KBP.AS.842–PYG 25 °C–MK403841 Arthrobacter sp. [KJ91079]—99.2% Arthrobacter sp. [KJ91079]—99.8% Arthrobacter sp. [KJ91035]—99.8% Uncultured bacterium clone [K507404]—99.1% Massilia suwonensis [NR116872]—99.1% Massilia sp. [KM187344]—98.8% Mycetocola sp. [MH299815]—98.4% Mycetocola sp. [MH298813]—98.4% Mycetocola sp. [CP026949]—98.4% Arthrobacter agilis [KT804924]—98.9% Arthrobacter agilis [MF767263]—98.8% Arthrobacter agilis [KR811202]—98.8% | Arthrobacter agilis | |
| KBP.AS.844–PYG 25 °C–MK403843 Arthrobacter sp. [KJ91079]—99.2% Arthrobacter sp. [KJ91079]—99.8% Arthrobacter sp. [KJ91035]—99.8% Uncultured bacterium clone [K507404]—99.1% Massilia suwonensis [NR116872]—99.1% Massilia sp. [KM187344]—98.8% Mycetocola sp. [MH299815]—98.4% Mycetocola sp. [MH298813]—98.4% Mycetocola sp. [CP026949]—98.4% Arthrobacter agilis [KT804924]—98.9% Arthrobacter agilis [MF767263]—98.8% Arthrobacter agilis [KR811202]—98.8% | Arthrobacter agilis | |
| KBP.AS.845–PYG 25 °C–None Arthrobacter sp. | Streptomyces sp. | |
| KBP.AS.846–PYG 25 °C–MK403844 Arthrobacter pascens [KY880876]—100% Pseudarthrobacter defluvii [KY880845]—100% Arthrobacter sp. | Arthrobacter sp. | |
| Strain–Isolation Conditions–GenBank Accession Number | BLAST Search Results | Taxonomic Affiliation |
|-----------------------------------------------------|----------------------|----------------------|
| KBP.AS.847–CM 25 °C–MK403845                        | Cellulomonas sp. [MH046844]—99.2% Cellulomonas sp. [HM587947]—99.2% Cellulomonas flavigena [KY951360]—99.0% | Cellulomonas sp. |
| KBP.AS.848–PYG 25 °C–MK403846                       | Massilia alkalitolerans [KY010279]—99.6% Uncultured bacterium clone [KU515079]—99.6% Massilia alkalitolerans [KP282807]—99.6% | Massilia sp. |
| KBP.AS.849–PYG 25 °C–MK403847                       | Microbacterium esteraromaticum [GU111572]—98.8% Microbacterium aurantiacum [NR152952]—98.2% Microbacterium aurantiacum [KF793922]—98.2% | Microbacterium sp. |
| KBP.AS.850–PYG 25 °C–MK403848                       | Massilia sp. [MH734560]—99.6% Massilia sp. [KY635898]—99.6% Massilia sp. [KY635895]—99.6% Paracoccus marcusii [MH744726]—99.9% Paracoccus marcusii [MH725412]—99.9% Paracoccus marcusii [MH725411]—99.9% | Massilia sp. |
| KBP.AS.854–CM 25 °C–MK403849                        | Were identified by morphology Arthrobacter crystallopoietes [CP018864]—98.7% Arthrobacter crystallopoietes [CP018863]—98.7% Arthrobacter sp. [KX645729]—98.7% Arthrobacter sulfonivorans [KR233773]—99.9% | Arthrobacter crystallopoietes |
| KBP.AS.855–PYG 25 °C–None                            | Uncultured soil bacterium clone [JX490026]—99.8% Uncultured bacterium clone [KCS54813]—99.7% Uncultured bacterium clone [EU647522]—98.8% | Arthrobacter sp. |
| KBP.AS.858–CM 25 °C–MK403850                        | Sphingomonas xinjiangensis [NR_108386]—98.6% Sphingomonas mucosissima [KM502884]—98.3% Microbacterium paraoxydans [MH819720]—99.9% | Sphingomonas sp. |
| KBP.AS.862–PYG 25 °C–MK403851                        | Uncultured soil bacterium clone [JX490026]—99.8% Uncultured bacterium clone [KCS54813]—99.7% Uncultured bacterium clone [EU647522]—98.8% | Arthrobacter sp. |
| KBP.AS.866–CM 25 °C–MK403852                        | Sphingomonas xinjiangensis [NR_108386]—98.6% Sphingomonas mucosissima [KM502884]—98.3% Microbacterium paraoxydans [MH819720]—99.9% | Sphingomonas sp. |
| KBP.AS.867–PYG 25 °C–MK403853                        | Microbacterium paraoxydans [MH281749]—99.9% Microbacterium sp. [MH558380]—99.9% | Microbacterium paraoxydans |
| Strain–Isolation Conditions–GenBank Accession Number | BLAST Search Results | Taxonomic Affiliation |
|-----------------------------------------------------|----------------------|-----------------------|
| KBP.AS.868–PYG 25 °C–MK403854                        | *Pseudarthrobacter siccitolerans* [MF682005]—99.2% | *Pseudarthrobacter sp.* |
|                                                     | *Pseudarthrobacter oxydans* [MF681862]—99.2% | |
|                                                     | *Pseudarthrobacter oxydans* [MF681851]—99.2% | |
|                                                     | *Kocuria rosea* [KY194315]—98.8% | |
|                                                     | *Kocuria sp.* [KY194287]—98.8% | |
|                                                     | *Kocuria turfanensis* [KY194236]—98.8% | |
|                                                     | *Arthrobacter agilis* [CP024915]—99.1% | |
|                                                     | *Arthrobacter agilis* [MG279727]—99.1% | |
|                                                     | *Arthrobacter sp.* [KJ191029]—99.1% | |
|                                                     | *Salinibacterium sp.* [MH790149]—99.0% | |
|                                                     | *Salinibacterium sp.* [MH299814]—99.0% | |
|                                                     | *Salinibacterium sp.* [CP026951]—99.0% | |
|                                                     | *Streptomyces sp.* [MG930074]—100% | |
|                                                     | *Streptomyces sp.* [MG930073]—100% | |
|                                                     | *Streptomyces atrovirens* [MF662228]—100% | |
|                                                     | *Planomicrobium glaciei* [MG025800]—99.1% | |
|                                                     | *Planomicrobium glaciei* [KY307898]—99.1% | |
|                                                     | Uncultured bacterium clone [KU514918]—99.1% | |
|                                                     | *Sphingomonas xinjiangensis* [NR108386]—98.9% | |
|                                                     | *Sphingomonas mucosissima* [KM502884]—98.6% | |
|                                                     | *Arthrobacter agilis* [MG279728]—99.4% | |
|                                                     | *Arthrobacter agilis* [MF767263]—99.4% | |
|                                                     | *Arthrobacter agilis* [KU884338]—99.4% | |
|                                                     | Uncultured bacterium [KX509715]—99.5% | |
|                                                     | Uncultured bacterium [KX508022]—99.5% | |
|                                                     | *Massilia niabensis* [NR044571]—99.5% | |
|                                                     | *Pseudarthrobacter siccitolerans* [MF682005]—98.5% | |
|                                                     | *Pseudarthrobacter oxydans* [MF681862]—98.5% | |
|                                                     | *Pseudarthrobacter oxydans* [MF681851]—98.5% | |
| KBP.AS.916–PYG 10 °C–MK403859                        | *Pseudarthrobacter sp.* | |
| KBP.AS.926–PYG 10 °C–MK403860                        | *Sphingomonas sp.* | |
| KBP.AS.927–PYG 10 °C–MK403861                        | *Arthrobacter agilis* | |
| KBP.AS.928–PYG 10 °C–MK403862                        | *Massilia sp.* | |
| KBP.AS.929–CM 10 °C–MK403863                        | *Pseudarthrobacter sp.* | |
Table A1. Cont.

| Strain–Isolation Conditions–GenBank Accession Number | BLAST Search Results | Taxonomic Affiliation |
|-----------------------------------------------------|----------------------|----------------------|
| KBP.AS.930–CM 10 °C–MK403864                        | *Pseudarthrobacter siccitolerans* [MF682005]—98.7% *Pseudarthrobacter oxydans* [MF681862]—98.7% *Pseudarthrobacter oxydans* [MF681851]—98.7% | *Pseudarthrobacter sp.* |
| KBP.AS.931–CM 10 °C–MK403865                        | *Arthrobacter boritolerans* [MH828349]—99.7% *Pseudarthrobacter sp.* [MH734752]—99.7% *Arthrobacter sp.* [LC416398]—99.7% | *Arthrobacter sp.* |
| KBP.AS.932–CM 10 °C–MK403866                        | *Pseudarthrobacter sp.* [MG860452]—99.0% *Pseudarthrobacter sp.* [MG860451]—99.0% *Arthrobacter sp.* [LC416398]—99.7% | *Pseudarthrobacter sp.* |
| KBP.AS.936–PYG 10 °C–MK403867                       | *Pseudarthrobacter phenanthrenivorans* [MF077155]—99.8% *Pseudarthrobacter phenanthrenivorans* [MF077155]—99.8% | *Pseudarthrobacter phenanthrenivorans* |
| KBP.AS.937–PYG 10 °C–MK403868                        | *Arthrobacter agilis* [KF876857]—99.9% *Arthrobacter agilis* [KT763365]—99.8% | *Arthrobacter agilis* |
| KBP.AS.938–CM 25 °C–MK403869                        | *Streptomyces sp.* [MG820052]—99.6% *Streptomyces sp.* [MG930074]—99.6% | *Streptomyces sp.* |
| KBP.AS.939–CM 25 °C–MK403870                        | Uncultured bacterium clone [KU515164]—99.0% | *Massilia sp.* |
| KBP.AS.940–CM 25 °C–MK403871                        | Uncultured bacterium clone [KX509026]—98.9% *Massilia sp.* [MG733567]—98.6% | *Microbacterium esteraromaticum* |
| KBP.AS.941–CM 25 °C–MK403872                        | *Pseudarthrobacter siccitolerans* [MF682005]—99.4% *Pseudarthrobacter oxydans* [MF681862]—99.4% *Pseudarthrobacter oxydans* [MF681851]—99.4% | *Pseudarthrobacter sp.* |
| Strain–Isolation Conditions–GenBank Accession Number | BLAST Search Results | Taxonomic Affiliation |
|------------------------------------------------------|----------------------|-----------------------|
| KBP.AS.943–CM 10 °C–MK403873                         |                      | Arthrobacter agilis   |
|                                                      |                      | [JQ684255]—99.8%      |
|                                                      |                      | Arthrobacter agilis   |
|                                                      |                      | [CP024915]—99.7%      |
|                                                      |                      | Arthrobacter agilis   |
|                                                      |                      | [MG279727]—99.7%      |
|                                                      |                      | Microbacterium        |
|                                                      |                      | esteraromaticum       |
|                                                      |                      | strain                |
|                                                      |                      | [GU111572]—99.3%      |
| KBP.AS.947–PYG 10 °C–MK403874                        |                      | Microbacterium sp.    |
|                                                      |                      | [MH231521]—98.5%      |
|                                                      |                      | Microbacterium sp.    |
|                                                      |                      | [MH231520]—98.5%      |
|                                                      |                      | Uncultured Microbacterium sp. |
|                                                      |                      | Clone [MH894291]—99.9% |
|                                                      |                      | Microbacterium sp.    |
|                                                      |                      | [MH813404]—99.9%      |
|                                                      |                      | Microbacterium sp.    |
|                                                      |                      | [MH714660]—99.9%      |
| KBP.AS.954–PYG 10 °C–MK403875                        |                      | Pseudarthrobacter      |
|                                                      |                      | sicicolerans          |
|                                                      |                      | [MF682005]—99.5%      |
|                                                      |                      | Pseudarthrobacter      |
|                                                      |                      | oxydans               |
|                                                      |                      | [MF681862]—99.5%      |
|                                                      |                      | Pseudarthrobacter      |
|                                                      |                      | oxydans               |
|                                                      |                      | [MF681851]—99.5%      |
| KBP.AS.956–PYG 10 °C–MK403877                        |                      | Planomicrobium        |
|                                                      |                      | glaciei               |
|                                                      |                      | [KF387709]—99.9%      |
|                                                      |                      | Planomicrobium sp.    |
|                                                      |                      | [JX949538]—99.9%      |
|                                                      |                      | Planomicrobium sp.    |
|                                                      |                      | [JQ618344]—99.9%      |
|                                                      |                      | Arthrobacter sp.      |
|                                                      |                      | [KX645729]—99.5%      |
|                                                      |                      | Arthrobacter sp.      |
| KBP.AS.957–CM 10 °C–MK403878                         |                      | Arthrobacter sp.      |
|                                                      |                      | [KF889389]—99.5%      |
|                                                      |                      | Arthrobacter crystallopoietes |
|                                                      |                      | [KM257018]—99.5%      |
|                                                      |                      | Arthrobacter sp.      |
|                                                      |                      | [KY173031]—99.6%      |
|                                                      |                      | Arthrobacter sp.      |
|                                                      |                      | [LN614607]—99.6%      |
|                                                      |                      | Arthrobacter oryzae   |
|                                                      |                      | [KC934820]—99.6%      |
| KBP.AS.958–CM 10 °C–MK403879                         |                      | Microbacterium        |
|                                                      |                      | esteraromaticum       |
|                                                      |                      | strain                |
|                                                      |                      | [GU111572]—99.3%      |
|                                                      |                      | Microbacterium sp.    |
|                                                      |                      | [MH231521]—98.6%      |
|                                                      |                      | Microbacterium sp.    |
|                                                      |                      | [MH231520]—98.6%      |
|                                                      |                      | Cellulomonas hominis   |
|                                                      |                      | [KT992126]—99.1%      |
| KBP.AS.960–CM 25 °C–MK403880                         |                      | Microbacterium sp.    |
|                                                      |                      | [MH231521]—98.6%      |
|                                                      |                      | Microbacterium sp.    |
|                                                      |                      | [MH231520]—98.6%      |
|                                                      |                      | Cellulomonas hominis   |
|                                                      |                      | [KT992126]—99.1%      |
| KBP.AS.961–CM 10 °C–MK403881                         |                      | Cellulomonas sp.      |
|                                                      |                      | [Y09658]—99.1%        |
|                                                      |                      | Cellulomonas sp.      |
|                                                      |                      | [MF361869]—98.9%      |
| KBP.AS.962–CM 10 °C–None                             |                      | Was identified by    |
|                                                      |                      | morphology           |
|                                                      |                      | Streptomyces sp.      |
| Strain–Isolation Conditions–GenBank Accession Number | BLAST Search Results | Taxonomic Affiliation |
|-----------------------------------------------------|----------------------|----------------------|
| KBP.AS.963–CM 10 °C–MK403882                        | Arthrobacter agilis  [CP024915]—99.7% Arthrobacter agilis [MG279727]—99.7% | Arthrobacter agilis |
|                                                     | Arthrobacter sp. [KY476520]—99.7% Micrococcus sp. [MH202946]—99.5% | |
| KBP.AS.972–PYG 10 °C–MK403883                        | Micrococcus sp. [AB188213]—99.5% Micrococcus sp. [EF540464]—99.5% | |
|                                                     | Rhodococcus erythropolis [MH285872]—100% | |
| KBP.AS.973–PYG 10 °C–MK403884                        | Rhodococcus sp. [CP034152]—100% Rhodococcus erythropolis [MH251258]—100% | |
|                                                     | Pseudarthrobacter phenanthrenivorans | |
| KBP.AS.1003–PYG 10 °C–MK403768                       | Arthrobacter sp. [LN871743]—100% Arthrobacter sp. [LU951449]—100% | |
|                                                     | Arthrobacter sp. [KR827428]—99.9% Leucobacter aridicollis [KP152582]—99.9% | |
| KBP.AS.1005–PYG 10 °C–MK403769                       | Arthrobacter sp. [KT944733]—100% Arthrobacter sp. [KM507593]—100% | |
|                                                     | Arthrobacter sp. [KM472818]—100% | |
| KBP.AS.1007–PYG 10 °C–MK403770                       | Uncultured bacterium clone [KU514918]—99.3% Planomicrobium sp. [JF411320]—99.0% | |
|                                                     | Planomicrobium gluciae [JX949538]—99.0% Planomicrobium gluciae [MF681862]—99.8% | |
| KBP.AS.1008–PYG 10 °C–MK403771                       | Pseudarthrobacter oxydans [MF681851]—99.8% Planomicrobium gluciae [KF387709]—99.7% | |
|                                                     | Pseudarthrobacter oxydans [MF682005]—99.8% Planomicrobium gluciae [JX949538]—99.7% | |
| KBP.AS.1009–PYG 10 °C–MK403772                       | Pseudarthrobacter oxydans [JF411320]—99.0% Planomicrobium gluciae [MF681862]—99.8% | |
|                                                     | Planomicrobium gluciae [KF387709]—99.7% Planomicrobium gluciae [JX949538]—99.7% | |
| KBP.AS.1010–PYG 10 °C–MK403773                       | Pseudarthrobacter oxydans [MF681851]—99.8% Planomicrobium gluciae [KF387709]—99.7% | |
|                                                     | Pseudarthrobacter oxydans [MF682005]—99.8% Planomicrobium gluciae [JX949538]—99.7% | |
| KBP.AS.1011–PYG 10 °C–MK403774                       | Uncultured soil bacterium clone [DQ248289]—99.3% | |
|                                                     | Arthrobacter sp. [AY238502]—99.3% | |
|                                                     | Arthrobacter sp. | |
| Strain–Isolation Conditions–GenBank Accession Number | BLAST Search Results | Taxonomic Affiliation |
|-----------------------------------------------------|----------------------|----------------------|
| KBP.AS.1012–PYG 10 °C–MK403775                      | *Planococcus donghaensis* [LN774491]—100% *Planonococcus* sp. | *Planonococcus* sp. |
|                                                      | *Planonococcus* okeanokoites [KF749394]—100% *Planonococcus* sp. | *Planonococcus* sp. |
|                                                      | *Planonococcus* okeanokoites [KF724965]—100% *Planonococcus* sp. | *Planonococcus* sp. |
|                                                      | Arthrobacter sp. [KT424968]—100% *Planonococcus* sp. | *Planonococcus* sp. |
| KBP.AS.1021–PYG 10 °C–MK403776                      | [KM036066]—100% Arthrobacter sp. [JN377650]—99.9% *Planonococcus* sp. | *Planonococcus* sp. |
|                                                      | Arthrobacter sp. [LN774491]—100% *Planonococcus* sp. | *Planonococcus* sp. |
| KBP.AS.1024–PYG 10 °C–MK403777                      | *Arthrobacter* sp. [NR_074770]—100% *Arthrobacter* sp. | *Arthrobacter* sp. |
| KBP.AS.1026–CM 25 °C–MK403778                       | Massilia sp. [JQ511857]—98.0% Massilia sp. [JQ511858]—97.8% Agrococcus lahaulensis [KF318382]—99.8% Agrococcus jenensis [EF672044]—99.8% Agrococcus lahaulensis [MF351823]—99.6% Uncultured bacterium clone [DQ125573]—99.5% *Pseudarthrobacter* oxydans [MH304399]—99.3% Arthrobacter sp. [MH714681]—99.3% Pseudarthrobacter siccitolerans [MF682005]—99.9% Pseudarthrobacter oxydans [MF681862]—99.9% Pseudarthrobacter oxydans [MF681851]—99.9% | *Massilia* sp. |
| KBP.AS.1028–CM 25 °C–MK403779                       | Uncultured bacterium clone [DQ125573]—99.5% *Pseudarthrobacter* oxydans [MH304399]—99.3% Arthrobacter sp. [MH714681]—99.3% Pseudarthrobacter siccitolerans [MF682005]—99.9% Pseudarthrobacter oxydans [MF681862]—99.9% Pseudarthrobacter oxydans [MF681851]—99.9% | *Agrococcus* sp. |
| KBP.AS.1029–CM 25 °C–MK403780                       | *Pseudarthrobacter* oxydans [MH304399]—99.3% *Arthrobacter* sp. [MH714681]—99.3% *Pseudarthrobacter* siccitolerans [MF682005]—99.9% *Pseudarthrobacter* oxydans [MF681862]—99.9% *Pseudarthrobacter* oxydans [MF681851]—99.9% | *Arthrobacter* sp. |
| KBP.AS.1030–CM 25 °C–MK403781                       | *Massilia* sp. [MH707216]—99.9% *Massilia* alkalitolerans [KY010279]—99.9% *Massilia* varians [KX784920]—99.9% *Arthrobacter* sp. [KF924209]—99.8% | *Massilia* sp. |
| KBP.AS.1031–CM 25 °C–MK403782                       | *Arthrobacter* sp. [IX949695]—99.8% *Arthrobacter* sp. [IX949646]—99.8% *Microbacterium* sp. [LT601250]—99.5% | *Arthrobacter* sp. |
| KBP.AS.1032–CM 25 °C–MK403783                       | Uncultured bacterium clone [MG805031]—99.5% *Microbacterium* sp. [MF526604]—99.5% | *Microbacterium* sp. |
| KBP.AS.1033–CM 25 °C–MK403784                       | Uncultured bacterium clone [MG805031]—99.5% *Microbacterium* sp. [MF526604]—99.5% | *Microbacterium* sp. |
### Table A1. Cont.

| Strain–Isolation Conditions–GenBank Accession Number | BLAST Search Results | Taxonomic Affiliation |
|-----------------------------------------------------|----------------------|-----------------------|
| KBP.AS.1037–CM 25 °C–MK403785                        | Massilia varians [KC429599]—99.7% | Massilia sp. |
|                                                     | Massilia alkalitolerans [KY010279]—99.6% | |
|                                                     | Massilia alkalitolerans [KP282807]—99.6% | |
|                                                     | Uncultured bacterium clone [KC442649]—87.5% | |
| KBP.AS.1044–CM 25 °C–MK403786                        | Pontibacter sp. [HM579810]—87.5% | Pontibacter sp. |
|                                                     | Pontibacter diazotrophicus [NR_126288]—87.2% | |

Colour highlight indicates strains characterized by 100% sequence similarity.

### Appendix B

#### Table A2. The primers used for 16S rRNA gene amplification and sequencing.

| GenBank Accession Number | Strain | Taxonomic Affiliation | Primers Used for Amplification | Primers Used for Sequencing |
|--------------------------|--------|-----------------------|---------------------------------|-----------------------------|
| MK403789                 | KGP.AS.17 | *Pseudarthrobacter oxydans* | 27 f + Un1492 r 1100 r      | 1100 r                     |
| MK403790                 | KGP.AS.62 | *Arthrobacter sp.*        | 341 f + 805 r 805 r           |                             |
| MK403794                 | KGP.AS.75 | *Brachybacterium sp.*     | 27 f + Un1492 r 1100 r        |                             |
| MK403787                 | KGP.AS.105 | *Janthinobacterium sp.*   | 27 f + Un1492 r 1100 r        |                             |
| MK403788                 | KGP.AS.160 | *Arthrobacter sp.*        | 27 f + Un1492 r 1100 r        |                             |
| MK403791                 | KGP.AS.747 | *Microbacterium aurantiacum* | 27 f + 537 r 537 r           |                             |
| MK403793                 | KGP.AS.749 | *Brevibacterium frigoritolerans* | 27 f + Un1492 r 1100 r       |                             |
| MK403795                 | KGP.AS.750 | *Planomicrobium okeanokoites* | 341 f + 805 r 805 r         |                             |
| MK403796                 | KGP.AS.751 | *Agrococcus sp.*          | 27 f + Un1492 r 1100 r       |                             |
| MK403797                 | KGP.AS.752 | *Agrococcus sp.*          | 27 f + Un1492 r 1100 r       |                             |
| MK403798                 | KGP.AS.753 | *Agrococcus sp.*          | 27 f + 537 r 537 r           |                             |
| MK403799                 | KGP.AS.754 | *Kocuria sp.*            | 27 f + Un1492 r 1100 r       |                             |
| MK403800                 | KGP.AS.755 | *Planomicrobium glaciei*  | 27 f + Un1492 r 1100 r       |                             |
| MK403801                 | KGP.AS.756 | *Leucobacter aridicollis* | 27 f + Un1492 r 1100 r       |                             |
| MK403802                 | KGP.AS.757 | *Planomicrobium okeanokoites* | 341 f + 805 r 805 r         |                             |
| MK403803                 | KGP.AS.758 | *Microbacterium sp.*      | 27 f + Un1492 r 1100 r       |                             |
| MK403804                 | KGP.AS.759 | *Bacillus pumilus*       | 27 f + Un1492 r 1100 r       |                             |
| MK403805                 | KGP.AS.760 | *Microbacterium sp.*      | 27 f + Un1492 r 1100 r       |                             |
| MK403806                 | KGP.AS.761 | *Rafibacter sp.*        | 27 f + 537 r 537 r           |                             |
| MK403807                 | KGP.AS.762 | *Microbacterium sp.*      | 27 f + Un1492 r 1100 r       |                             |
| MK403808                 | KGP.AS.763 | *Massilia sp.*           | 27 f + Un1492 r 1100 r       |                             |
| MK403809                 | KGP.AS.764 | *Bacillus sp.*          | 341 f + 805 r 805 r           |                             |
| MK403810                 | KGP.AS.765 | *Massilia alkalitolerans* | 27 f + Un1492 r 1100 r       |                             |
| MK403811                 | KGP.AS.766 | *Pseudarthrobacter sp.*  | 27 f + Un1492 r 1100 r       |                             |
| MK403812                 | KGP.AS.767 | *Massilia varians*       | 27 f + Un1492r 1100r         |                             |
| MK403813                 | KGP.AS.768 | *Planomicrobium sp.*     | 27 f + Un1492 r 1100r         |                             |
| MK403814                 | KGP.AS.769 | *Microbacterium pseudoresistens* | 27 f + 537 r 537 r       |                             |
| MK403815                 | KGP.AS.770 | *Arthrobacter sp.*      | 27 f + Un1492 r 1100 r       |                             |
| MK403816                 | KGP.AS.771 | *Arthrobacter sp.*       | 27 f + Un1492 r 1100r         |                             |
| MK403817                 | KGP.AS.772 | *Planomicrobium glaciei* | 27 f + Un1492 r 1100r         |                             |
| MK403818                 | KGP.AS.773 | *Cellulomonas sp.*       | 27 f + Un1492 r 1100r         |                             |
| MK403819                 | KGP.AS.774 | *Planomicrobium okeanokoites* | 27 f + Un1492 r 1100r       |                             |
| MK403820                 | KGP.AS.775 | *Planomicrobium okeanokoites* | 27 f + Un1492 r 1100r       |                             |
| MK403821                 | KGP.AS.776 | *Georgenia sp.*         | 27 f + Un1492 r 1100r         |                             |
| MK403822                 | KGP.AS.777 | *Microbacterium bacteri* | 27 f + Un1492 r 1100r         |                             |
| MK403823                 | KGP.AS.778 | *Salinibacterium sp.*   | 27 f + Un1492 r 1100r         |                             |
| MK403824                 | KGP.AS.779 | *Brevibacterium frigoritolerans* | 27 f + Un1492 r 1100r       |                             |
| MK403825                 | KGP.AS.780 | *Micrococcus sp.*        | 27 f + Un1492 r 1100r         |                             |
| MK403826                 | KGP.AS.781 | *Kocuria sp.*           | 27 f + Un1492 r 1100r         |                             |
| MK403827                 | KGP.AS.782 | *Labedella sp.*        | 27 f + Un1492 r 1100r         |                             |
| GenBank Accession Number | Strain | Taxonomic Affiliation | Primers Used for Amplification | Primers Used for Sequencing |
|--------------------------|--------|-----------------------|-------------------------------|-----------------------------|
| MK403828                 | KRP:AS.783 | Plantibacter sp.      | 27 f + 537 r                  | 537 r                       |
| MK403829                 | KRP:AS.784 | Arthrobacter agilis   |                               |                             |
| MK403830                 | KRP:AS.785 | Microbacterium sp.    |                               |                             |
| MK403831                 | KRP:AS.786 | Pseudarthrobacter sp. |                               |                             |
| MK403832                 | KRP:AS.787 | Massilia sp.          |                               |                             |
| MK403833                 | KRP:AS.788 | Bacillus sp.          |                               |                             |
| MK403834                 | KRP:AS.789 | Burkholderia sp.      |                               |                             |
| MK403835                 | KRP:AS.790 | Cellulomonas hominis  |                               |                             |
| MK403836                 | KRP:AS.791 | Pseudarthrobacter sp. |                               |                             |
| MK403837                 | KRP:AS.792 | Massilia sp.          |                               |                             |
| MK403838                 | KRP:AS.793 | Salinisphaeribacter sp.|                             |                             |
| MK403839                 | KRP:AS.794 | Arthrobacter sp.      |                               |                             |
| MK403840                 | KRP:AS.795 | Arthrobacter sp.      |                               |                             |
| MK403841                 | KRP:AS.816 | Arthrobacter sp.      |                               |                             |
| MK403842                 | KRP:AS.821 | Massilia sp.          |                               |                             |
| MK403843                 | KRP:AS.843 | Myctecoloides sp.     |                               |                             |
| MK403844                 | KRP:AS.844 | Arthrobacter agilis   |                               |                             |
| MK403845                 | KRP:AS.848 | Cellulomonas sp.      |                               |                             |
| MK403846                 | KRP:AS.849 | Massilia sp.          |                               |                             |
| MK403847                 | KRP:AS.850 | Microbacterium sp.    |                               |                             |
| MK403848                 | KRP:AS.854 | Paracoccus maracusii  |                               |                             |
| MK403849                 | KRP:AS.855 | Rubribacter sp.       |                               |                             |
| MK403850                 | KRP:AS.856 | Arthrobacter crystallopoietes |             |                             |
| MK403851                 | KRP:AS.862 | Arthrobacter sp.      |                               |                             |
| MK403852                 | KRP:AS.866 | Spingomonas sp.       |                               |                             |
| MK403853                 | KRP:AS.868 | Microbacterium paraoxysmatis |                             |                             |
| MK403854                 | KRP:AS.869 | Pseudarthrobacter sp. |                               |                             |
| MK403855                 | KRP:AS.870 | Kocuria sp.           | 341 f + 805 r                  | 805 r                       |
| MK403856                 | KRP:AS.876 | Arthrobacter agilis   |                               |                             |
| MK403857                 | KRP:AS.877 | Salinisphaeribacter sp.|                               |                             |
| MK403858                 | KRP:AS.899 | Streptomyces sp.      |                               |                             |
| MK403859                 | KRP:AS.915 | Planomicrobium glaciei|                               |                             |
| MK403860                 | KRP:AS.926 | Planomicrobium glaciei|                               |                             |
| MK403861                 | KRP:AS.927 | Arthrobacter agilis   |                               |                             |
| MK403862                 | KRP:AS.928 | Massilia sp.          |                               |                             |
| MK403863                 | KRP:AS.929 | Pseudarthrobacter sp. |                               |                             |
| MK403864                 | KRP:AS.930 | Pseudarthrobacter sp. |                               |                             |
| MK403865                 | KRP:AS.931 | Arthrobacter sp.      |                               |                             |
| MK403866                 | KRP:AS.932 | Pseudarthrobacter sp. |                               |                             |
| MK403867                 | KRP:AS.936 | Pseudarthrobacter sp. |                               |                             |
| MK403868                 | KRP:AS.937 | Pseudarthrobacter sp. |                               |                             |
| MK403869                 | KRP:AS.938 | Pseudarthrobacter sp. |                               |                             |
| MK403870                 | KRP:AS.939 | Pseudarthrobacter sp. |                               |                             |
| MK403871                 | KRP:AS.940 | Pseudarthrobacter sp. |                               |                             |
| MK403872                 | KRP:AS.941 | Pseudarthrobacter sp. |                               |                             |
| MK403873                 | KRP:AS.943 | Arthrobacter agilis   |                               |                             |
| MK403874                 | KRP:AS.947 | Microbacterium sp.    |                               |                             |
| MK403875                 | KRP:AS.954 | Microbacterium sp.    |                               |                             |
| MK403876                 | KRP:AS.955 | Pseudarthrobacter sp. |                               |                             |
| MK403877                 | KRP:AS.956 | Planomicrobium sp.    |                               |                             |
| MK403878                 | KRP:AS.957 | Arthrobacter sp.      |                               |                             |
| MK403879                 | KRP:AS.958 | Arthrobacter sp.      |                               |                             |
| MK403880                 | KRP:AS.960 | Microbacterium sp.    |                               |                             |
| MK403881                 | KRP:AS.961 | Cellulomonas sp.      |                               |                             |
| MK403882                 | KRP:AS.962 | Streptomyces sp.      |                               |                             |
| MK403883                 | KRP:AS.963 | Arthrobacter agilis   |                               |                             |
| MK403884                 | KRP:AS.972 | Micrococcus sp.       |                               |                             |
| MK403885                 | KRP:AS.973 | Rhodococcus erythropolis |                             |                             |
| MK403886                 | KRP:AS.1003 | Arthrobacter sp. |                               |                             |
| MK403887                 | KRP:AS.1005 | Leucobacter arabinos sp. |                             |                             |
| MK403888                 | KRP:AS.1007 | Arthrobacter sp. |                               |                             |
| MK403889                 | KRP:AS.1008 | Planomicrobium glaciei|                               |                             |
| MK403890                 | KRP:AS.1009 | Pseudarthrobacter sp. |                               |                             |
| MK403891                 | KRP:AS.1010 | Planomicrobium glaciei|                               |                             |
| MK403892                 | KRP:AS.1011 | Arthrobacter sp.      |                               |                             |
| MK403893                 | KRP:AS.1012 | Planomicrobium sp.    | 341 f + 805 r                  | 805 r                       |
Table A2. Cont.

| GenBank Accession Number | Strain       | Taxonomic Affiliation           | Primers Used for Amplification | Primers Used for Sequencing |
|--------------------------|--------------|-------------------------------|-------------------------------|----------------------------|
| MK403776                 | KBFAS.1021   | *Arthrobacter agilis*         | 27 f + Un1492 r               | 1100 r                     |
| MK403777                 | KBFAS.1024   | *Arthrobacter* sp.            | 27 f + Un1492 r               | 1100 r                     |
| MK403778                 | KBFAS.1026   | *Massilia* sp.                | 27 f + Un1492 r               | 1100 r                     |
| MK403779                 | KBFAS.1028   | *Agrococcus* sp.              | 27 f + Un1492 r               | 1100 r                     |
| MK403780                 | KBFAS.1029   | *Arthrobacter* sp.            | 27 f + Un1492 r               | 1100 r                     |
| MK403781                 | KBFAS.1030   | *Pseudarthrobacter* sp.       | 27 f + Un1492 r               | 1100 r                     |
| MK403782                 | KBFAS.1031   | *Massilia* sp.                | 27 f + Un1492 r               | 1100 r                     |
| MK403783                 | KBFAS.1032   | *Arthrobacter* sp.            | 27 f + Un1492 r               | 1100 r                     |
| MK403784                 | KBFAS.1033   | *Microbacterium* sp.          | 341 f + 805 r                 | 805 r                      |
| MK403785                 | KBFAS.1037   | *Massilia* sp.                | 27 f + Un1492 r               | 1100 r                     |
| MK403786                 | KBFAS.1044   | *Pontibacter* sp.             | 341 f + 805 r                 | 805 r                      |

Colour highlight indicates strains characterized by 100% sequence similarity.

Appendix C

Table A3. The bacterial genera cultured from the Mojave Desert soil sample on different media. The table summarizes data of community structure diagrams and allows to compare bacterial diversity in a simpler view.

| Brachybacterium | Burkholderia | Cellulomonas |
|-----------------|--------------|--------------|
| Cellulomonas    |              |              |
| Georgenia      |              |              |
| Janthinobacterium |          |              |
| Kocuria        |              |              |
| Leucobacter    | Leucobacter  | Massilia     |
| Massilia       | Microbacterium| Micrococcus |
| Microbacterium |              |              |
| Mycetocella    |              |              |
| Paracoccus     |              |              |
| Planomicrobium | Planomicrobium|          |
| Plantibacter   |              |              |
| Pseudarthrobacter |  Pseudarthrobacter | Rhodococcus |
| Rufibacter     |              |              |
| Salinibacterium| Sphingomonas  | Sphingomonas |
| Streptomyces   |              |              |

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