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EXPERIMENTAL ARTICLES

Three New Species of Brevibacteria, *Brevibacterium antiquum* sp. nov., *Brevibacterium aurantiacum* sp. nov., and *Brevibacterium permense* sp. nov.

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Abstract—This work deals with the taxonomic study of orange-pigmented bacteria isolated from permafrost sediments, rice plots, and soils contaminated with wastes from the chemical and salt industries that were assigned to the genus *Brevibacterium* on the basis of phenotypic characteristics, as well as of some strains described previously as *Brevibacterium linens.* The study revealed three genomic species, whose members and the type strains of the closest species of *Brevibacterium* had DNA similarity levels between 24 and 59%. The strains of the genomic species differed from each other and from the known species of *Brevibacterium* in some physiological and biochemical characteristics, as well as in the sugar and polyol composition of their teichoic acids. The 16S rDNA sequence analysis confirmed the assignment of the environmental isolates to the genus *Brevibacterium* and showed the phylogenetic distinction of the three genomic species. The results obtained in this study allow three new *Brevibacterium* species to be described: *Brevibacterium antiquum* (type strain VKM Ac-2118^T = UCM Ac-411^T), *Brevibacterium aurantiacum* (type strain VKM Ac-2111^T = NCDO 739^T = ATCC 9175^T), and *Brevibacterium permense* (type strain VKM Ac-2280^T = UCM Ac-413^T).

Key words: actinomycetes, *Brevibacterium*, teichoic acids, 16S rDNA.

The genus *Brevibacterium* includes gram-positive, coryneform bacteria that possess A1γ-type peptidoglycan with *meso*-diaminopimelic acid and respiratory menaquinones MK-8(H_2) and lack mycolic acids [1–3]. The polar lipids of these bacteria contain diphosphatidylglycerol, phosphatidylglycerol, dimannosidediacylglycerol, and phosphatidylinositol (in some strains). The fatty acids are dominated by *anteiso*- and *iso*-branched acids [1–3]. The cell wall teichoic acids of brevibacteria contain glycerol, ribitol, and mannitol [1, 4–6]. The G+C content of DNA is 60–67 mol %. The genus currently comprises nine species [2, 3, 7–11]. The species *B. casei, B. iodinum*, and *B. linens* are commonly isolated from milk and cheese, with *B. linens* being the major component of the cheese microflora. *B. epidermidis* is a typical inhabitant of the human skin, while the species *B. mcbrellneri, B. otitidis, B. paucivorans*, and *B. lutescens* were found in human clinical specimens [1, 7, 9–11].

Among the validly described species of the genus, only the type species *B. linens* produces orange-pigmented colonies. For this reason, orange-pigmented brevibacteria were usually assigned to this species. There is evidence that *B. linens* strains are genetically and phenotypically heterogeneous and form at least two genomic species [1, 5, 12].

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This work deals with the taxonomic study of twelve orange-pigmented strains phenotypically close to *B. linens*, which were isolated from various soils and permafrost sediments.

MATERIALS AND METHODS

Bacterial strains and cultivation conditions. Two of the twelve orange-pigmented strains used in this study (VKM Ac-2118 and VKM Ac-2281) were isolated from 3-million-year-old permafrost sediments on the Kolyma Lowland in Siberia; three strains (VKM Ac-2119, GK-3, and GK-4) were recovered from the soils of rice plots in the Krasnodar region, Russia; and seven strains (VKM Ac-2280, VKM Ac-2279, GK-27, GK-29, GK-30, GK-32, and 49P2) were recovered from soils contaminated with wastes from the chemical and salt industries in Berezniki, Perm oblast, Russia.

A comparative analysis of these strains was carried out by using the following type and reference strains: *B. linens* VKM Ac-2112^T, *B. iodinum* VKM Ac-2106^T, *B. epidermidis* VKM Ac-2108^T, *B. casei* VKM Ac-2114^T, *B. linens* VKM Ac-2111, and "*B. linens*" VKM Ac-2110 = ATCC 9174.

The strains were maintained and cultivated on corynebacterial agar, which contained (g/l) casein peptone, 10; glucose, 5; yeast extract, 5; NaCl, 5; and agar, 20 (pH 7.0).

Morphological and physiological characteristics were studied as described elsewhere [13, 14] and by using the API CORYNE system (Bio Merieux, France).

Chemotaxonomic characteristics. Diaminopimelic acid isomers, mycolic acids, menaquinones, and fatty acids were analyzed as described elsewhere [14]. Teichoic acids were isolated and analyzed as reported by Streshinskaya *et al.* [15].

The polymerase chain reaction of repetitive extragenetic palindrome DNA sequences (REP-PCR) was carried out according to Versalovic *et al.* [16]. The reaction mixture (25 μl) contained 5 μl of 5× buffer (1 M $(NH_4)_2SO_4$, 1 M Tris–HCl, 1 M $MgCl_2$, and 0.5 M EDTA, pH 8.8), 10 vol % DMSO, 50 pM of each primer, 1.25 mM of each dNTP, 2 units *Taq* polymerase (Fermentas, Lithuania), and 50 ng genomic DNA. The primers used were REP1R (5'-IIIICGICGICATCIGGC) and REP2I (5'-ICGICTTATCIGGCCTAC) [16]. PCR was performed with the initial DNA denaturation step at 95°C for 6 min, followed by 30–35 cycles of DNA denaturation at 94°C for 1 min, primer annealing at 40°C for 1 min, and primer extension at 65°C for 8 min. The PCR products were analyzed by electrophoresis in 1.3% agarose gel.

The nucleotide sequence of the 16S rRNA genes. The 16S rRNA genes were amplified by PCR with the universal eubacterial primers 27f and 1525r. The purified PCR products were sequenced by using a Big Dye Terminator Kit (Perkin-Elmer, United States) and an automatic ABI Prism 310 Genetic Analyzer (Perkin-Elmer).

Phylogenetic analysis. The 16S rRNA gene sequences of the strains under study were aligned manually with the aid of the CLUSTAL W program [17]. Evolutionary distances were expressed as the number of nucleotide substitutions per 100 nucleotides [18]. Phylogenetic tree was generated with the TREECON software package [19] and neighbor-joining (NEIGHBOR) algorithm. The topology of the tree was evaluated by the bootstrap analysis of 1000 replications. The nucleotide sequences of the 16S rRNA genes of strains VKM Ac-2118, VKM Ac-2280, and VKM Ac-2119 have been deposited in GenBank under the accession numbers AY243344, AY243343, and AY243345, respectively.

The G+C content of DNA was evaluated from its thermal denaturation temperature [20].

DNA–DNA hybridization. ^{3}H-labeled DNAs were obtained by using deoxy[1',2',5'-^{3}H]CTP and nick translation kit N 5500 (Amersham, United Kingdom). DNA–DNA hydridization was performed by the membrane filter method [21] on 0.2-μm-pore-size nylon-6 filters (Hiiu Kalur, Estonia) under optimal conditions (incubation in 50 vol % formamide at 50°C for 24 h) [22].

RESULTS

All the strains under study were gram-positive, nonspore-forming, nonmotile, irregularly shaped rods morphologically close to the type strain *B. linens* VKM Ac-2112^T. Older cultures (28 to 32 h in age) were dominated by short rods or coccoid cells. The strains grew well on corynebacterial agar at 24°C, producing small (2 to 3 mm in diameter) round colonies, which were first white and then became orange in color. The production of orange pigment(s) in all the strains was induced by light, except that the reference strains "*B. linens*" VKM Ac-2110 and "*B. linens*" VKM Ac-2111 synthesized the pigment(s) both in the light and in the dark.

The strains had chemotaxonomic characteristics typical of the genus *Brevibacterium*: the presence of *meso*-diaminopimelic acid in the cell walls, the presence of MK-8(H_2) as the major menaquinone, and the absence of mycolic acids. The fatty acids of VKM Ac-2119, VKM Ac-2280, VKM Ac-2118, and the type and reference strains of *B. linens* were dominated by *anteiso*-15:0 (46–62%) and *anteiso*-17:0 (26–31%) acids. *Iso*-16:0 and *iso*-17:1 acids amounted to 1.8–8.3 and 1.1–5.7%, respectively. Other fatty acids were minor (0.1–1.3%). The strains VKM Ac-2280 and *B. linens* VKM Ac-2112^T contained squalene in amounts of 1.94 and 5.57%, respectively. The G+C content of the DNA of the isolates varied from 60.1 to 64.3 mol %.

The REP-PCR analysis of the strains (Fig. 1) showed that they formed seven groups. Each of groups

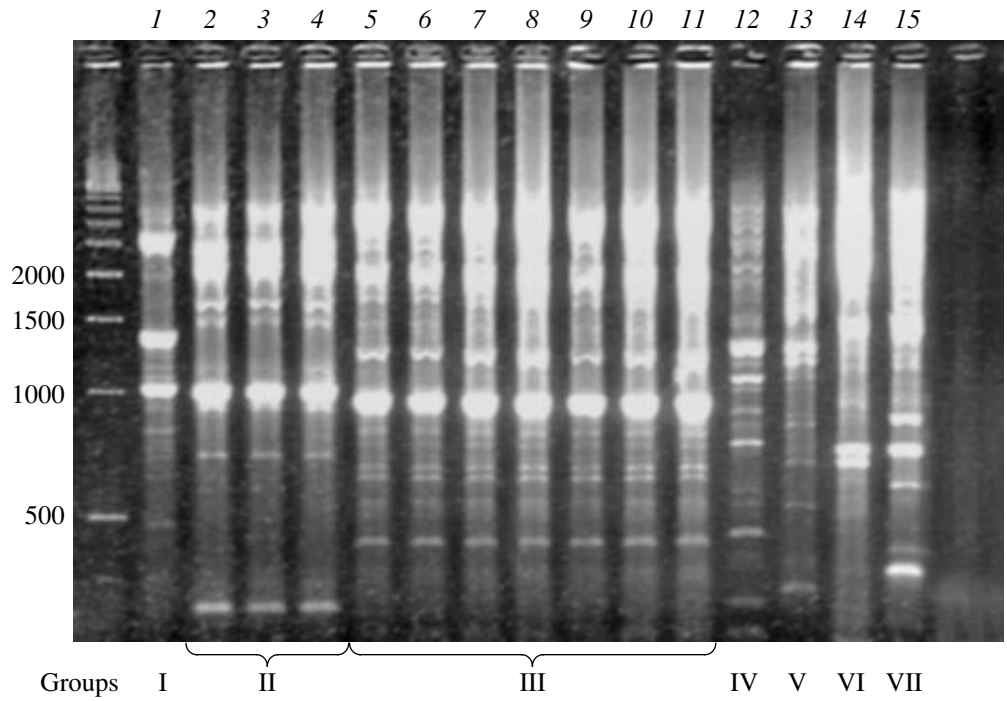

Fig. 1. The REP-PCR analysis of the DNA of orange-pigmented *Brevibacterium* strains. Lanes: (*1*) *B. linens* VKM Ac-2112^T; (*2*) VKM Ac-2119; (*3*) GK-3; (*4*) GK-4; (*5*) VKM Ac-2280; (*6*) VKM Ac-2279; (*7*) GK-27; (*8*) GK-29; (*9*) GK-30; (*10*) GK-32; (*11*) 49P2; (*12*) VKM Ac-2118; (*13*) VKM Ac-2281; (*14*) VKM Ac-2111; (*15*) VKM Ac-2110.

I and IV–VII contained only one strain, whereas group II included three strains (VKM Ac-2119, GK-3, and GK-4) that were isolated from rice plots, and group III comprised seven isolates from the soils of Perm oblast.

To reveal genomic species among *B. linens*-like strains, the DNA of the members of each of the aforementioned groups, as well as of the four type strains of the genus *Brevibacterium*, was hybridized with the [^{3}H]-DNA of strains VKM Ac-2119, VKM Ac-2280, VKM Ac-2118, and VKM Ac-2111 (Table 1). The results obtained showed that only strain VKM Ac-2119 belonged to the genomic species that included the type strain *B. linens* VKM Ac-2112^T (DNA similarity level higher than 70%). The other isolates formed three distinct genomic species; one included strain VKM Ac-2280 isolated from the salt-contaminated soil, the sec-

Table 1. DNA similarity between *Brevibacterium* strains

Strain	Group based on REP-PCR	DNA similarity (%) to			
		VKM Ac-2119	VKM Ac-2280	VKM Ac-2118	VKM Ac-2111
B. linens VKM Ac-2112^T	I	**73**	56	27	31
VKM Ac-2119	II	**100**	32	34	26
VKM Ac-2280	III	33	**100**	35	31
VKM Ac-2118	IV	43	32	**100**	42
VKM Ac-2281	V	–	–	**82**	41
"*B. linens*" VKM Ac-2111	VI	27	27	40	**100**
"*B. linens*" VKM Ac-2110	VII	–	–	39	**75**
B. iodinum VKM Ac-2106^T		39	35	23	24
B. epidermidis VKM Ac-2108^T		41	59	28	28
B. casei VKM Ac-2114^T		31	26	27	27

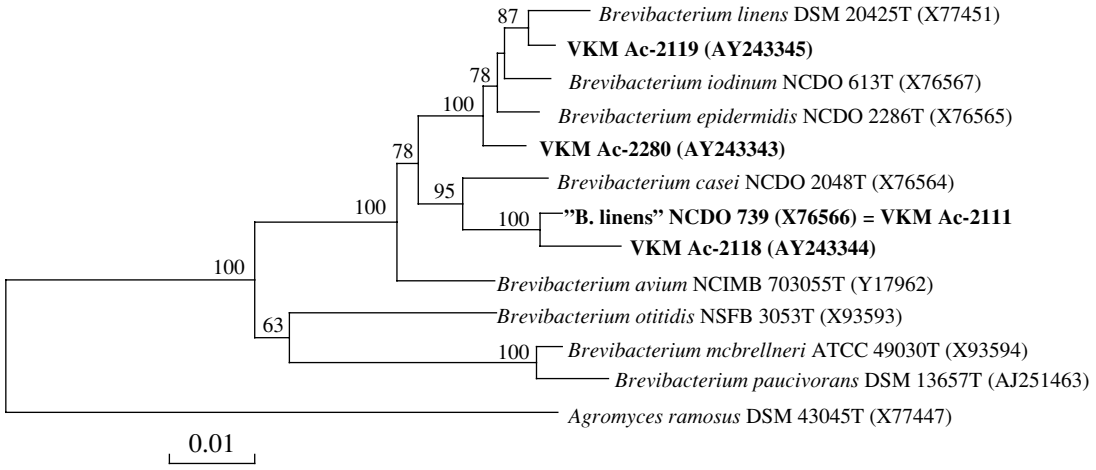

Fig. 2. A phylogenetic tree showing the position of strains VKM Ac-2118, VKM Ac-2119, VKM Ac-2280, and *"Brevibacterium linens"* NCDO 739 based on the 16S rRNA gene sequence analysis with *Agromyces ramosus* DSM 43045^T as an outgroup. Bootstrap values, expressed as a percentage of 1000 replications, are shown at the branching points (the values less than 60% are not shown). The scale bar represents one nucleotide substitution per 100 nucleotides.

ond contained strains VKM Ac-2118 and VKM Ac-2281 isolated from permafrost sediments, and the third genomic species included strains *"B. linens"* VKM Ac-2111 and *"B. linens"* VKM Ac-2110. The DNA similarity of strains *"B. linens"* VKM Ac-2111 and *B. linens* VKM Ac-2112^T was close to the value that was reported earlier by Fiedler *et al.* [5].

For phylogenetic analysis, the almost complete nucleotide sequences of the 16S rRNA genes (1460–1500 bp) of strains VKM Ac-2280, VKM Ac-2118, and VKM Ac-2119 were determined. Relevant data for the strain *"B. linens"* VKM Ac-2111 (NCDO 739) were taken from a public database (http://www.ncbi.nlm.nih.gov). The analysis of 16S rDNA sequences confirmed the assignment of the isolates to the genus *Brevibacterium* and revealed two distinct phylogenetic clusters with bootstrap values of 95 and 100% (Fig. 2). The similarity of the 16S rDNA sequences of strain VKM Ac-2280 and the other members of its cluster (*B. linens* DSM 20425^T, *B. iodinum* NCDO 613^T, and *B. epidermidis* NCDO 2286^T) was 98–98.5%. Strain VKM Ac-2119 was closest to the type strain of *B. linens* (16S rDNA similarity 98.9%). Strains VKM Ac-2111 and VKM Ac-2118 fell into a cluster with *B. casei* NCDO 2048T. The similarity of the 16S rDNA sequences of VKM Ac-2118 and *"B. linens"* NCDO 739 (= VKM Ac-2111) was 98.6%.

To differentiate phenotypically the genomic species that we revealed, the physiological and biochemical characteristics and the composition of the cell wall teichoic acids of the representatives of different genomic species were analyzed (Table 2). All the strains were found to be able to grow in the presence of 15% NaCl and to utilize galactose, glucose, glycerol, mannitol, D-mannose and D-fructose but not D-arabinose, D-arabitol, adonitol, dulcitol, lactose, salicin, sorbitol, fucose, or *meso*-erythritol as carbon sources. The strains produced acids from glucose, galactose, mannose, and fructose but not from melezitose, raffinose, sorbose, trehalose, or inulin. The strains were able to hydrolyze casein but not esculin or starch. All the strains exhibited negative reactions in most of the API CORYNE tests for enzymatic activity, except for pyrazinamidase.

The major sugars and polyols of the cell wall teichoic acids were galactose, glucose, mannose, rhamnose, glycerol, and mannitol in various combinations (Table 2). The teichoic acids of the strains *B. linens* VKM Ac-2112^T, VKM Ac-2119, VKM Ac-2111, and VKM Ac-2110 contained galactose, glucose, and glycerol, while the teichoic acids of the strains VKM Ac-2118 and VKM Ac-2281 contained glucose, glycerol, and mannitol. VKM Ac-2280 contained rhamnose, glycerol, and mannitol in its teichoic acids. The TCA extracts of the cell walls of all the strains also contained amino sugars, which agrees with the data published earlier [1, 4–6].

DISCUSSION

Three isolates (VKM Ac-2119, GK-3, and GK-4) and the type strain *B. linens* VKM Ac-2112^T form one genomic species (Table 1) and show similarity in the major components of their teichoic acids (Table 2). Based on these characteristics, these isolates can currently be identified as belonging to the species *B. linens*. The isolates, however, differ from the type strain of this species in the ability to grow at 37°C, to reduce nitrate, to utilize gluconate and inositol as the carbon sources, and to produce acids from rhamnose and inositol (Table 2).

The study of a greater number of related strains, the evaluation of their DNA similarity to the type strain of *B. linens*, and the finding of additional differentiating

Table 2. The phenotypic characteristics of new isolates and related species of the genus *Brevibacterium* (data of this work and those published in [5, 6, 8, 10])

Characteristic	*B. linens* VKM Ac-2112^T	VKM Ac-2119	VKM Ac-2118	VKM Ac-2281	VKM Ac-2280	"*B. linens*" VKM Ac-2111	"*B. linens*" VKM Ac-2110	*B. iodinum* VKM Ac-2106^T	*B. casei* VKM Ac-2114^T	*B. epidermidis* VKM Ac-2108^T
Color of colonies	Orange	Orange	Orange	Orange	Orange	Orange	Orange	Gray with iodine crystals	Grayish	Yellowish
Dark production of orange pigment	–	–	–		–	+	+	–	–	–
Growth at 37°C	–	+	–	–	+	–	–	+	+	+
Growth at 7°C	–	Poor	+	+	Poor	+	+	Poor	–	+
Nitrate reduction	+	–	–	–	–	+	–	+	V	V
Hydrolysis of										
urea	–	–	+	–	–	–	–	–	–	–
gelatin	+	+	+	+	+	–	+	+	+	+
H_2S production	,	+	–	+	+	+	–	–	+	+
Growth at 18% NaCl	+	+	+	+	+	–	–	–	–	+
Utilization of										
L-arabinose	–	Poor	Poor	–	Poor	–	–	–	–	–
gluconate	–	+	+	+	+	–	–	–	+	+
inositol	–	+	–	–	–	–	–	–	+	–
Acid production from										
inositol	–	+	–	–	–	–	–	–	+	–
mannitol	+	+	–	+	–	–	–	–	–	+
rhamnose	–	+	–	–	–	–	–	–	–	–
salicin	–	–	+	–	+	+	+	–	–	–
sorbitol	–	–	+	+	+	–	–	–	–	–
Teichoic acid constituents:										
galactose	+	+	–	–	–	+	+	–	+	+
glucose	+	+	+	+	–	+	+	+	+	–
mannose	–	–	Traces	Traces	–	Traces	Traces	–	–	–
rhamnose	–	–	–	–	+	–	–	–	–	–
glycerol	+	+	+	+	+	+	+	+	+	+
mannitol	–	–	+	+	+	–	–	+	–	+

Note: The symbols "–," "+," and "V" stand for "no growth," "good growth," and "strain-variable growth," respectively.

characteristics might provide grounds to classify them as subspecies of *B. linens* or separate species.

The other orange-pigmented strains, which fell into three different genomic species and differ from each other and from the known species of brevibacteria in some physiological and biochemical characteristics and the major constituents of the cell wall teichoic acids, are proposed to be classified as three new species: *Brevibacterium antiquum* sp. nov., *Brevibacterium aurantiacum* sp. nov., and *Brevibacterium permense* sp. nov.

The species *B. antiquum* is represented by two strains, VKM Ac-2118^T (type strain) and VKM Ac-2281, isolated from the permafrost sediment samples collected on the Kolyma Lowland. The strains grow well in the presence of 18% NaCl and at 7°C but not at 37°C (Table 2). The strains are able to utilize gluconate but not inositol as the carbon source, produce acids from sorbitol but not from inositol or rhamnose, and hydrolyze gelatin. The nitrate reductase test is negative. The major constituents of the cell wall teichoic acids of these strains are glucose, glycerol, and mannitol. Such a composition of teichoic acids has hitherto been observed only for the species *B. iodinum* [4], which clearly differ from *B. antiquum* in the color of colonies and in the physiological (Table 2) and phylogenetic characteristics (Fig. 2).

Seven strains of the new species *B. permense* (the type strain is VKM Ac-2280^T) isolated from soils contaminated with wastes grow well in the presence of 18% NaCl and at 37°C but slowly at 7°C. They produce H_2S and are unable to reduce nitrate or to utilize inositol as the carbon source. The strains produce acids from salicin and sorbitol but not from inositol, mannitol, or rhamnose. The major constituents of their cell wall teichoic acids are rhamnose, glycerol, and mannitol (Table 2). Such a composition of teichoic acids clearly differentiates *B. permense* from the other orange-pigmented brevibacterial species.

Two strains of the new species *B. aurantiacum*, VKM Ac-2111^T and VKM Ac-2110, differ from the other *Brevibacterium* species in the ability to synthesize orange pigment(s) in the dark and to produce acids from salicin, the inability to grow in the presence of 18% NaCl, and some other properties (Table 2).

The complete descriptions of the three new species of brevibacteria are given below.

Description of *Brevibacterium antiquum* sp. nov. *Brevibacterium antiquum* (an.'ti.qu.um. M. n. adj. *antiquum* ancient). The colonies are white to orange in color, circular, and slightly convex. Orange pigment is produced in the light. Cells are gram-positive, nonmotile, and non-spore-forming. Older cultures are dominated by coccoid cells. Aerobic and oxidase-positive. The optimum growth temperature is 24–26°C. Can grow at 7°C. Is able to utilize L-arabinose (slowly), D-fructose, D-galactose (slowly), D-glucose, glycerol, D-mannitol, D-mannose, and D-xylose as carbon sources for growth in a mineral medium supplemented with 0.05 wt % of yeast extract. D-arabinose, D-arabitol, adonitol, dulcitol, *meso*-erythritol, L-fucose, gluconate, inositol, lactose, D-melibiose, melezitose, raffinose, salicin, and sorbitol are not used as carbon sources in the aforementioned medium. Acids are produced from D-glucose, D-galactose, fructose, mannose, and sorbitol, but not from inositol, inulin, D-mannitol, melezitose, raffinose, sorbose, rhamnose, and trehalose. Is able to hydrolyze gelatin and casein but not esculin or starch. The ability to hydrolyze urea and to produce H_2S is strain-specific. The pyrazinamidase and pyrrolidonyl arylamidase (weak) tests are positive. The β-glucuronidase, β-galactosidase, α-glucosidase, and *N*-acetyl-β-glucosaminidase tests are negative. The ability to produce acids from D-xylose and salicin and the alkaline phosphatase test are strain-variable. Nitrate is not reduced. The Voges–Proskauer and methyl red tests are negative. Is able to grow in the presence of 18% NaCl. The peptidoglycan contains *meso*-diaminopimelic acid. Mycolic acids are absent. The major menaquinone is MK-8(H_2). The cell wall teichoic acids contain glucose, glycerol, and mannitol. The type strain VKM Ac-2118^T (= UCM Ac-411^T) is isolated from 1.8- to 3-million-year-old ancient permafrost sediments located on the Kolyma Lowland, East Siberia, Russia.

Description of *Brevibacterium aurantiacum* sp. nov. *Brevibacterium aurantiacum* (au.ran.ti'a.cum. L.n. *aurantium* specific name of the orange; M.L. neutr. adj. *aurantiacum* orange-colored). The colonies are orange, circular, slightly convex, and glistening. Cells are gram-positive, nonmotile, and non-spore-forming. Older cultures are dominated by coccoid cells. Aerobic and oxidase-positive. The optimum growth temperature is 24–26°C. Can grow at 7°C. Is able to utilize cellobiose (slowly), fructose, D-galactose (slowly), D-glucose, glycerol, D-mannitol, D-mannose (slowly), and D-xylose as carbon sources for growth in a mineral medium supplemented with 0.05 wt % of yeast extract. L- and D-arabinose, D-arabitol, adonitol, dulcitol, *meso*-erythritol, L-fucose, gluconate, inositol, lactose, D-melibiose, raffinose, salicin, sorbitol, and trehalose, as a rule, are not utilized as carbon sources. Acids are produced from galactose, D-glucose, mannose, and salicin, but not from inositol, inulin, D-mannitol, melezitose, raffinose, sorbose, sorbitol, and trehalose. Is able to hydrolyze casein but not esculin, starch, or urea. The abilities to produce acid from fructose and to hydrolyze gelatin are strain-variable. The pyrazinamidase and alkaline phosphatase tests are positive. The pyrrolidonyl arylamidase, β-glucuronidase, β-galactosidase, α-glucosidase, and *N*-acetyl-β-glucosaminidase tests are negative. Nitrate is reduced. The Voges–Proskauer and methyl red tests are negative. H_2S is produced. Is able to grow in the presence of 15% NaCl. The peptidoglycan contains *meso*-diaminopimelic acid. Mycolic acids are absent. The major menaquinone is MK-8(H_2). Contains glycerol teichoic acids. The type

strain VKM Ac-2111^T (= ATCC 9175^T) is isolated from cheese.

Description of *Brevibacterium permense* sp. nov. *Brevibacterium permense* (perm.'ense. M.L. adj. *permense* from Perm, the region of Russia). The colonies are white to orange, circular, slightly convex, and glistening. Orange pigment is produced in the light. Cells are gram-positive, nonmotile, and non-spore-forming. Older cultures are dominated by coccoid cells. Aerobic and oxidase-positive. Growth is good at 37°C and poor at 7°C. The optimum growth temperature is 24°C. Is able to utilize L-arabinose (slowly), cellobiose (slowly), fructose, D-galactose (slowly), D-glucose, gluconate, glycerol, D-mannitol, D-mannose, raffinose (slowly), salicin (slowly), trehalose (slowly), and D-xylose as carbon sources for growth in a mineral medium supplemented with 0.05 wt % of yeast extract. D-arabinose, D-arabitol, adonitol, dulcitol, *meso*-erythritol, L-fucose, inositol, lactose, D-melibiose, raffinose, and sorbitol, as a rule, are not utilized as carbon sources. Acids are produced from D-galactose, D-glucose, fructose, mannose, salicin, and sorbitol, but not from inositol, inulin, D-mannitol, melezitose, raffinose, rhamnose, sorbose, or trehalose. Gelatin and casein but not esculin, starch, or urea are hydrolyzed. The pyrazinamidase and alkaline phosphatase tests are positive. The pyrrolidonyl arylamidase, β-glucuronidase, β-galactosidase, α-glucosidase, and *N*-acetyl-β-glucosaminidase tests are negative. Nitrate is not reduced. The Voges–Proskauer and methyl red tests are negative. H_2S is produced. Is able to grow in the presence of 18% NaCl. The peptidoglycan contains *meso*-diaminopimelic acid. Mycolic acids are absent. The major menaquinone is MK-8(H_2). The cell wall teichoic acids contain rhamnose, glycerol, and mannitol. The type strain VKM Ac-2280^T (= UCM Ac-413^T) is isolated from salt-contaminated soil samples collected in the Perm region of Russia.

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