Burkholderia bannensis sp. nov., an acid-neutralizing bacterium isolated from torpedo grass (Panicum repens) growing in highly acidic swamps

Tomoko Aizawa,1 Pisoot Vijarnsorn,2 Mutsuyasu Nakajima1 and Michio Sunairi1

Correspondence
Tomoko Aizawa
t-aizawa@brs.nihon-u.ac.jp

1Department of Applied Biological Sciences, College of Bioresource Sciences, Nihon University, 1866 Kameino, Fujisawa, Kanagawa 252-0880, Japan
2Banna Experimental Station for Royal Acid Sulfate Soil Improvement Project under Royal Initiatives, Banna, Nakhon Nayok 26110, Thailand

Two strains of acid-neutralizing bacteria, E25T and E21, were isolated from torpedo grass (Panicum repens) growing in highly acidic swamps (pH 2–4) in actual acid sulfate soil areas of Thailand. Cells of the strains were Gram-negative, aerobic, non-spore-forming rods, 0.6–0.8 μm wide and 1.6–2.1 μm long. The strains showed good growth at pH 4.0–8.0 and 17–37°C. The organisms contained ubiquinone Q-8 as the predominant isoprenoid quinone and C16:0, C17:0 cyclo and C18:1ω7c as the major fatty acids. Their fatty acid profiles were similar to those reported for other Burkholderia species. The DNA G+C content of the strains was 65 mol%. On the basis of 16S rRNA gene sequence similarity, the strains were shown to belong to the genus Burkholderia. Although the calculated 16S rRNA gene sequence similarity of E25T to strain E21 and the type strains of Burkholderia unamae, B. tropica, B. sacchari, B. nodosa and B. mimosarum was 100, 98.7, 98.6, 97.4, and 97.3%, respectively, strains E25T and E21 formed a group that was distinct in the phylogenetic tree; the DNA–DNA relatedness of E25T to E21 and B. unamae CIP 107921T, B. tropica LMG 22274T, B. sacchari LMG 19450T, B. nodosa LMG 23741T and B. mimosarum LMG 23256T was 90, 42, 42, 45, and 35%, respectively. The results of physiological and biochemical tests including whole-cell protein pattern analysis allowed phenotypic differentiation of these strains from previously described Burkholderia species. Therefore, strains E25T and E21 represent a novel species, for which the name Burkholderia bannensis sp. nov. is proposed. The type strain is E25T (=NBRC 103871T =BCC 36998T).

Abbreviation: AASS, actual acid sulfate soil.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains E25T and E21 are AB561874 and AB561875.

Three supplementary figures and three supplementary tables are available with the online version of this paper.

Yabuuchi et al. (1992) created the genus Burkholderia by the transfer of seven species from Pseudomonas, with Burkholderia cepacia as the type species. At the time of writing, the genus Burkholderia comprises more than 60 species, occupying a wide range of ecological niches and showing a variety of metabolic activities (Coenye & Vandamme, 2003). During the course of a study to characterize waterweeds adapted to highly acidic aquatic environments (pH 2–4) in actual acid sulfate soils (AASS) in South-East Asia (Aizawa et al., 2008; Sasaki et al., 2008), we have isolated a number of bacteria associated with the waterweeds and reported several novel bacterial species (Aizawa et al., 2007, 2010b, c; Kimoto et al., 2010). In the present study, we characterized two acid-neutralizing bacteria, E25T and E21, isolated from torpedo grass (Panicum repens; see Supplementary Fig. S1, available in IJSEM Online) growing in a highly acidic swamp (pH 2.9) at Banna Experimental Station in Nakhon Nayok Province, Thailand. By a polyphasic approach, including 16S rRNA gene sequence analysis, DNA–DNA hybridization, whole-cell protein analysis, fatty acid methyl ester analysis and phenotypic and biochemical characterization, the strains were shown to be affiliated with the genus Burkholderia. The data obtained suggest that the strains represent a novel species of the genus Burkholderia.

Each P. repens plant was divided into leaves, aerial stems, underwater stems and roots. After gentle washing in excess saline for 1 min to remove loosely attached soil, each part was transferred to fresh saline and shaken vigorously for 15 min; this procedure was repeated three times. The
extracts were combined (to give sample LBM). The LBM sample was transferred to fresh saline and shaken vigorously for 18 h (to give sample TBM). A number of bacteria were isolated from samples LBM and TBM by using one-tenth-strength tryptic soy (1/10 TS) agar plates [3.0 g tryptic soy broth / liter solidified with 15.0 g agar / liter (both from Difco)] at pH 4.0. For preparation of these acidic plates, double-strength medium and 3 % agar solution were autoclaved separately to prevent hydrolysis of the agar and then mixed. Among the isolates, acid-neutralizing bacteria were selected on the basis of neutralization of 1/10 TS liquid medium (pH 4.0), determined by measuring the pH of the culture supernatants after 3 days of cultivation.

Strains E25\textsuperscript{T} and E21 were isolated from TBM samples prepared from a root and an aerial stem, respectively, from the same plant collected in Thailand. Both strains formed round, smooth, convex, pale-yellow colonies with entire margins on 1/10 TS agar plates (pH 4.0). Each showed good growth on these plates at 17–37 °C, with optimum growth at 28–32 °C, but did not grow at 5 or 42 °C. Strains E25\textsuperscript{T} and E21 showed good growth at pH 3–8, with optimum growth at pH 4–7 and no or little growth below pH 2 or above pH 9 when cultured at 30 °C for 5 days. The strains grew well on TS plates (pH 4.0) as on 1/10 TS agar plates (pH 4.0). Growth under anaerobic conditions was determined after 5 days of incubation at 30 °C in an AnaeroPack (Mitsubishi Gas Chemical Co., Ltd). The strains grew well on 1/10 TS plates (pH 4.0) under aerobic conditions but not under anaerobic conditions, indicating that they are aerobes. Cells grown on 1/10 TS agar plates (pH 4.0) were Gram-negative (Ryu, 1938), non-endospore-forming and non-motile. Their morphology was observed by scanning electron microscopy, as described previously (Aizawa et al., 2010b). The cells were irregular rods, 0.6–0.8 \mu m wide and 1.6–2.1 \mu m long, after growth on 1/10 TS agar plates (pH 4.0) at 28 °C for 3 days.

The 16S rRNA genes of the strains were amplified by PCR using universal primers (Tamura & Hatano, 2001), and nearly complete 16S rRNA gene nucleotide sequences were determined. The NCBI BLAST software tool (http://www.ncbi.nlm.nih.gov/blast/Blast.cgi) and the EzTaxon software (Chun et al., 2007) were applied to compare the determined 16S rRNA gene sequences with those of type strains. These sequences showed high similarity to species within the genus Burkholderia. The 16S rRNA gene sequence similarities of strain E25\textsuperscript{T} to strain E21, \textit{Burkholderia unamai} MTI-641\textsuperscript{T}, \textit{B. tropica} Pe8\textsuperscript{T}, \textit{B. sacchari} LMG 19450\textsuperscript{T}, \textit{B. nodosa} Br3437\textsuperscript{T} and \textit{B. mimosarum} PAS44\textsuperscript{T} were 100, 98.7, 98.6, 97.6, 97.4 and 97.3 %, respectively. Phylogenetic relationships of E25\textsuperscript{T} and E21 with closely related species were determined by using MEGA version 4 (Tamura et al., 2007) and the PHYLIP 3.65 package (Felsenstein, 1997) after performing multiple alignments of the data with CLUSTAL_X (Thompson et al., 1997). Evolutionary distances were computed as described previously (Jukes & Cantor, 1969). Phylogenetic trees were reconstructed by using the maximum-parsimony (Kluge & Farris, 1969), maximum-likelihood (Felsenstein, 1981), minimum-evolution (Rzhetsky & Nei, 1992) and neighbour-joining (Saitou & Nei, 1987) methods. The reliabilities of these tree topologies were evaluated by bootstrap analysis with 1000 replicates (Felsenstein, 1985). Phylogenetic trees reconstructed by these four methods were topologically similar and showed that strains E25\textsuperscript{T} and E21 belonged to the genus \textit{Burkholderia}, within which the strains formed a cluster with strains of some \textit{Burkholderia} species isolated from plants and soil: \textit{Burkholderia tuberum} (Vandamme et al., 2002), \textit{B. mimosarum} (Chen et al., 2006) and \textit{B. nodosa} (Chen et al., 2007), isolated from leguminous Mimosa species, \textit{Burkholderia silvatlantica} (Perin et al., 2006), \textit{B. unamai} (Caballero-Mellado et al., 2004) and \textit{B. tropica} (Reis et al., 2004), isolated from maize and sugar cane, \textit{Burkholderia helea} (Aizawa et al., 2010b) and \textit{B. acidipaludis} (Aizawa et al., 2010c), from Chinese water chestnut, \textit{Burkholderia sacchari} (Br{"a}mer et al., 2001), isolated from soil of a sugar cane plantation, and \textit{Burkholderia kururiensis} M130 (Caballero-Mellado et al., 2007), isolated from the root of a rice plant growing in Brazil (Baldani et al., 1997; Weber et al., 1999), as well as \textit{Burkholderia ferrariae} (Valverde et al., 2006), isolated from iron ore. The phylogenetic tree reconstructed by using the neighbour-joining method is shown in Fig. 1. Although the strains showed a high degree of 16S rRNA gene sequence similarity to established species of the genus, they formed a separate line of descent in the phylogenetic cluster of the genus (Fig. 1). Stackebrandt & Goebel (1994) pointed out that a high degree of 16S rRNA gene sequence similarity (97 % or higher) is of limited value for differentiating species, and that DNA–DNA hybridization studies must be performed to determine species affiliation under these conditions.
circumstances. Therefore, we performed DNA–DNA hybridization on these strains and their neighbours on the phylogenetic tree by using the microplate hybridization method (Ezaki et al., 1988, 1989) as described by Tamura et al. (1999). Hybridization was performed at 51 °C for 3 h using a hybridization solution containing 50% deionized formamide, 2 × SSC (1 × SSC is 0.15 M NaCl, 0.015 M trisodium citrate, pH 7.0, 5 × Denhardt’s solution (1 × Denhardt’s solution is 0.02% BSA, 0.02% polyvinylpyrrolidone and 0.02% Ficoll 400), 0.1 mg heat-denatured, sonicated salmon testes DNA ml⁻¹ and 2.5% dextran sulfate. The DNA–DNA relatedness of strain E25T to E21 was 90%, which is higher than the recommended threshold value (70%) for the delineation of genomic species (Wayne et al., 1987). Strain E25T exhibited relatively low levels of DNA–DNA relatedness with respect to B. nodosa LMG 23741T (45%), B. unnamae CIP 107921T (42%), B. tropica LMG 22274T (42%), B. sacchari LMG 19450T (42%) and B. mimosarum LMG 23256T (35%), indicating that strain E25T was not related to them at the species level. These data suggest that strains E25T and E21 represent a novel species of the genus Burkholderia.

Strains E25T and E21 could also be distinguished from closely related species of Burkholderia in the phylogenetic trees (Supplementary Fig. S2) on the basis of physiological characteristics (Supplementary Table S1). All physiological and biochemical experiments were done at least in triplicate using not only strains E25T and E21 but also the type strains of phylogenetically closely related Burkholderia species, B. unnamae CIP 107921T, B. tropica LMG 22274T, B. sacchari LMG 19450T, B. nodosa LMG 23741T and B. mimosarum LMG 23256T. Strains E25T and E21 did not show positive results in acetylene reduction experiments (Burris, 1972) using Winogradsky’s nitrogen-free mineral soft gel medium containing 1% mannitol (Hashidoko et al., 2002), whereas closely related type strains were positive, with the exception of B. acidipaludis SA3T, B. sacchari LMG 19450T, B. kururiensis JCM 10599T, B. tuberum LMG 21444T, B. silvatianna LMG 23149T, B. heleia SA41T and B. ferrariae LMG 23612T. These data showed good agreement with results obtained by 15N2 incorporation assays (Martinez-Aguilar et al., 2008). The nifH PCR assay (Caballero-Mellado et al., 2007) was performed in this study for strains E25T and E21 and also the type strains of phylogenetically closely related Burkholderia species. Interestingly, strains E25T and E21, as well as B. acidipaludis SA3T and B. ferrariae LMG 23612T, gave positive results, whereas B. sacchari LMG 19450T gave a negative result; the results for B. sacchari LMG 19450T and B. ferrariae LMG 23612T were in accordance with a previous report (Caballero-Mellado et al., 2007). Further study might be necessary to determine the diazotrophy of these nifH-positive strains. Strains E25T and E21 could grow in the presence of 1 mM AlCl3 in 0.1% BactoTryptone (Difco) adjusted to pH 3.5 with sulfuric acid.

Standard physiological tests were carried out according to methods described previously (Smibert & Krieg, 1994), Acid production from carbon sources, enzyme activities and resistance to antibiotics were assessed by using the API 50 CH system, API ZYM and API 20 E systems and ATB VET system (bioMérieux), respectively, according to the manufacturers’ instructions. The utilization of various substrates as sole carbon sources was tested by using Biolog GN2 Microplates in accordance with the manufacturer’s instructions. Physiological characteristics that differ between the novel strains and closely related species are summarized in Supplementary Table S1, and physiological diversity within the species is shown in Supplementary Table S2. The DNA G+C content was determined by the method described by Tamaoka & Komagata (1984). The DNA G+C content of strains E25T and E21 was 65 mol%. Cellular fatty acids of the two strains and reference strains were saponified, methylated and extracted as described by Tamura et al. (1994). Fatty acid methyl esters were then analysed by using a Shimadzu model GCMS-QP5050 GC/MS equipped with an SPB-1 column (Supelco). The major fatty acids of both strains grown on 1/10 TS agar plates containing 1% glucose (pH 5.0) at 28 °C for 3 days were C16:0, C17:0 cyclo and C18:1ω7c (Supplementary Table S2); similar patterns were obtained from cells of the type strains of closely related species. Isoprenoid quinones were prepared as described previously (Tamura et al., 1994) and analysed by using a Quattro premier MS coupled to an Acuity UPLC (UPLC/MS/MS; Waters) as described by Aizawa et al. (2010a). The major isoprenoid quinone of the strains was Q-8, as in the case of other species of the genus Burkholderia (Yamada et al., 1982; Zhang et al., 2000; Yang et al., 2006; Valverde et al., 2006; Aizawa et al., 2010b, c).

Whole-cell protein extracts were prepared from strains E25T and E21 and the type strains of several related species and analysed by SDS-PAGE, as described previously (Pot et al., 1994); the results are shown in Supplementary Fig. S3. The newly isolated strains showed a clearly different protein profile from related species of Burkholderia. Since it is well known that bacteria with identical or very similar protein patterns possess high genome similarity (Vandamme et al., 1996), these SDS-PAGE results also support the notion that strains E25T and E21 represent a novel acid-neutralizing Burkholderia species.

Therefore, based on the physiological, biochemical, chemotaxonomic and molecular genetic results described above, strains E25T and E21 represent a novel species of the genus Burkholderia, for which the name Burkholderia bannensis sp. nov. is proposed.

**Description of Burkholderia bannensis sp. nov.**

Burkholderia bannensis (ban.nen’sis. N.L. fem. adj. bannensis pertaining to the Banna region of Nakhon Nayok Province, Thailand, where the first strains were isolated).

Cells are Gram-negative, strictly aerobic, non-spore-forming, non-motile rods (0.6–0.8 × 1.6–2.1 μm). Colonies are smooth, round, convex and pale yellow with entire margins after 3 days of cultivation at 32 °C on 1/10 TS agar plates.
D-mannopyranoside, methyl (pH 4.0). Growth occurs at 17–37 °C, with optimum growth at 28–32 °C. Grows at pH 3–8, with optimum growth at pH 4–6. Positive for hydrolysis of Tweens 20, 40, 60 and 80. Positive for oxidase, catalase, acid and alkaline phosphatases, esterase (C4), esterase lipase (C8), leucine arylamidase, naphthol-AS-BI-phosphohydrolase and reduction of nitrate to nitrite, but negative for hydrolysis of DNA and gelatin, lipase (C14), valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase, α-fucosidase, proteinase, urease, arginine dihydrolase, indole production and reduction of nitrate to N2 (API ZYM, API 20E and API 20NE). Positive for acid production from glycerol, D- and L-arabinose, D-ribose, D-xylene, D-adenitol, D-galactose, D-glucose, D-fructose, D-mannose, L-rhamnose, D-mannitol, D-sorbitol, arbutin, aesculin, cellobiose, maltose, lactose, melibiose, trehalose, gentiobiose, D-lyxose, D- and L-fucose and D-arabitol; negative for acid production from methyl α-D-mannopyranoside, methyl α-D-glucopyranoside, sucrose, inulin, melezitose, raffinose, starch, glycogen and turanose (API 50CH). Positive for utilization of Tweens 40 and 80, N-acetyl-D-glucosamine, adonitol, L-arabinose, D-arabitol, D-fructose, L-fucose, D-galactose, gentiobiose, α-D-glucose, lactulose, D-mannitol, D-mannose, inositol, L-rhamnose, trehalose, pyruvic acid methyl ester, succinic acid mono- and dimethyl ester, cis-aconitic acid, citric acid, D-galacturonic acid, D-gluconic acid, D-gluconaminic acid, D-glucuronic acid, β-hydroxybutyric acid, α-ketoglutaric acid, δ-saccharic acid, succinic acid, succinamic acid, glucuronamide, D-alanine, L-alanyl glycine, L-aspartic acid, glycyl L-glutamic acid, L-histidine, hydroxy-L-proline, L-phenylalanine, L-serine, L-threonine, γ-aminobutyric acid, urocanic acid, thymidine, glyceral, D,L-α-glycerol phosphate and D-glucose 6-phosphate as sole carbon sources; negative for utilization of α-cyclodextrin, glycerol, lactose, melibiose, methyl β-D-glucoside, D-psicose, raffinose, xyitol, α-hydroxybutyric acid, itaconic acid, D-saccharic acid, citric acid and L-α-glycerophosphate (Biolog GN2). Resistant to (μg ml\(^{-1}\)) penicillin (0.25), amoxicillin (4), amoxicillin/clavulanic acid (4/2), oxacillin (2), cephalothin (8), ceperoxazone (4), erythromycin (1), lincomycin (2), pristinamycin (2), tylosin (2), colistin (4), sulfamethizole (100), nitrofurantoin (25), fusidic acid (2) and metronidazole (4); sensitive to (μg ml\(^{-1}\)) streptomycin (8), spectinomycin (64), kanamycin (8), gentamicin (4), apramycin (16), tetracycline (4), doxycycline (4), co-trimoxazole (2/38), flumequin (4), oxolinic acid (2), enrofloxacin (0.5) and rifampicin (4) (ATB VET). The major isoprenoid quinone is Q-8. The predominant cellular fatty acids are C\(_{16:0}\), C\(_{18:1\alpha 7c}\) and C\(_{17:0\alpha cyclo}\). The DNA G+C content of the two known strains is 65 mol%.

The type strain, E25\(^T\) (=NBRC 103871\(^T\) =BCC 36998\(^T\)), and a second strain, E21, were isolated from a root and an aerial stem, respectively, of Panicum repens, an aquatic plant growing luxuriantly in a highly acidic swamp (pH 2.9) in an AASS area in Thailand.

Acknowledgements

We are most grateful to S. Sasaki for giving us the opportunity to conduct this research. We also thank H. Uchiyama for identification of P. repens, D. J. Kang for help in collecting the samples and M. Ohkuma and S. Noda for advice on the acetylene reduction assay. We acknowledge T. Asai, M. Shimizu, K. Kimoto and various other members of our laboratories for their technical assistance and encouragement. We acknowledge P. Rattanawaree at the BCC and K. Suzuki, Y. Nakagawa and Y. Muramatsu at the NBRC for deposit of the isolates and K. Ueda at the Life Science Center for use of instrument facilities, as well as M. Hyoudou-Nakamura, N. Murayama-Akimoto, T. Fujisaki and N. Sekino at the Integrated Technology of Japan.

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References


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