**Niabella beijingensis** sp. nov. and **Thermomonas beijingensis** sp. nov., two bacteria from constructed wetland

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**Abstract**

Two Gram-stain-negative, aerobic, non-motile and rod-shaped bacterial strains designated 3A5MI-3T and RSS-23T were isolated from the Dragon-shaped Wetland System in Beijing Olympic Park, PR China. Strain 3A5MI-3T grew at 15–45 °C, pH 5.0–9.0 and with 0–2 % NaCl (w/v), and strain RSS-23T grew at 15–40 °C, pH 5.5–9.0 and with 0–1 % NaCl (w/v). Phylogenetic analyses of 16S rRNA gene sequences revealed that strains 3A5MI-3T and RSS-23T were members of Bacteroidetes and Proteobacteria, respectively. Phylogenetically closest relatives of strains 3A5MI-3T and RSS-23T were *Niabella pedocola* R384T and *Thermomonas aquatica* SY21T, respectively. The cells of strain 3A5MI-3T contained menaquinone MK-7 and phosphatidylethanolamine, and the major cellular fatty acids were composed of iso-C15:0 3-OH, iso-C15:0 3-0Hc and/or iso-C16:0 3-OH, C14:0 and summed feature 3 (C16:1ω7c/C16:1ω6c). Strain RSS-23T contained ubiquinone Q-8 and diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine, two unknown phospholipids and an unknown lipid, and its major cellular fatty acids were iso-C15:0 3-OH, iso-C16:0 3-0Hc, iso-C17:0 3-OH and summed feature 3 (C16:1ω7c/C16:1ω6c). DNA sequencing resulted in 6.59 Mb for the strain 3A5MI-3 genome and 2.79 Mb for the strain RSS-23 genome. The calculated G+C molar contents for strains 3A5MI-3T and RSS-23T were 47.07 and 61.21 mol%, respectively. According to phenotypic and phylogenetic characteristics, strains 3A5MI-3T and RSS-23T represent novel species of the genera *Niabella* and *Thermomonas* for which the names *Niabella beijingensis* sp. nov. and *Thermomonas beijingensis* sp. nov. are proposed. The type strain for *N. beijingensis* sp. nov. is 3A5MI-3T (=CGMCC 1.17737T=KCTC 82817T). The type strain for *T. beijingensis* sp. nov. is RSS-23T (=CGMCC 1.17738T=KCTC 82820T).

**DATA SUMMARY**

The newly sequenced data included in this work are deposited under the nucleotide accession numbers: MZ919349 and MZ920050 and under the Bioproject accession numbers JAIQDI000000000, JAJNEC000000000 and JAIQDJ000000000 at a public domain server in the National Center for Biotechnology Information (NCBI) database.

All supporting data, code and protocols have been provided within the article or through supplementary data files. A supplementary table and further supplementary files can be found at: https://doi.org/10.6084/m9.figshare.18220907.v1 [1].

Although members of the genera *Niabella* and *Thermomonas* are often isolated from similar environmental samples [2–5], they belong to the Bacteroidetes and Proteobacteria, respectively. The genus *Niabella* is a member of the family Chitinophagaceae. Cells of *Niabella* species are Gram-stain-negative, aerobic, non-flagellated and short rods. Since the genus *Niabella* was firstly described...
by Kim et al. [6], 11 specific names have been validly published [2, 3, 6–13] (https://lpsn.dsmz.de/genus/niabella). The names of ‘Niabella terrae’ [14] and ‘Niabella thaonhiensis’ [15] were proposed but have not been validated at the time of this writing.

The constructed wetland system, also called the Dragon-shaped Wetland, located in the central area of the Beijing Olympic Park area (40° 0.2′ N and 116° 22.28′ E), is the largest urban artificial water system in Asia. The water in the Dragon-shaped Water System comes mainly from the Beijing Qinghe Water Reclamation Plant, and the entire water system has a complete circulation system. Sludge samples from the Dragon-shaped Wetland water system were collected, and were serially diluted with 0.85% NaCl (w/v) and plated onto Reasoner’s 2A (R2A) agar (Difco). The isolates, designated as 3A5MI-3T and RSS-23T, were obtained after incubation for 3 days at 30 °C and were routinely stored at −80 °C as suspensions in R2A broth supplemented with 20% (v/v) glycerol.

Genomic DNA was extracted with a commercial TIANamp Bacteria DNA Kit, and 16S rRNA genes were amplified by PCR with universal bacterial primers 27 F and 1492R [20], which was also used for sequencing the PCR product. The almost-complete Genomic DNA was extracted with a commercial TIANamp Bacteria DNA Kit, and 16S rRNA genes were amplified by PCR with both have the chitinase gene in their genome, neither of them can use chitin. Trypsin-like serine proteases were found in the (Fig. 2a) and RSS-23 T (Fig. 2b).
Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences, showing the phylogenetic position of strains 3A5MI-3\(^T\) (a) and RSS-23\(^T\) (b) among closely related taxa. GenBank accession numbers are given in parentheses. Numbers at nodes indicate the percentage of 1000 bootstrap replicates yielding this topology; only values >50% are shown. Filled circles indicate nodes recovered by all three treeing methods (neighbour-joining, maximum-likelihood and maximum-parsimony). *Chitinophaga pinensis* NBRC 18968\(^T\) and *Citrobacter bitternis* SKKU-TP7\(^T\) were used as outgroups.
strain 3A5MI-3^T genome but not in strain *N. pedocola* JCM31011^T*, which corresponds to APIZYM trypsin activity for strain 3A5MI-3^T but not for *N. pedocola* JCM31011^T*. Comparing the genomes of strain 3A5MI-3^T and *N. pedocola* JCM31011^T*, we found that the specific genes detected in strain 3A5MI-3^T were as follows: four genes encoding lipopolysaccharide biosynthesis protein, three genes encoding biotin synthase, three genes encoding CRISPR-associated protein Cas1, two genes encoding 2-dehydropantoate 2-reductase, one gene encoding bifunctional NAD(P)H-nitrite reductase/anaerobic dehydrogenase, two genes encoding arabinogalactan endo-1,4-beta-galactosidase, three genes encoding TDP-4-oxo-6-deoxy-d-glucose aminotransferase, one gene encoding zinc-binding alcohol dehydrogenase family protein, three genes encoding 3-phytase, three genes encoding alpha-glucuronidase and one gene encoding Alg9-like mannosyltransferase family protein. The accession numbers of the sequences in the database relating to the specific or characteristic (marked in yellow) genes of strain 3A5MI-3^T and *N. pedocola* JCM31011^T* are provided as supplementary material. The ANI value between strains 3A5MI-3^T and *N. pedocola* JCM31011^T* was calculated using ChunLab’s online ANI Calculator [28]. We performed genome sequencing of *N. pedocola* JCM31011^T* and its GenBank/EMBL/DDBJ accession number is JAJNEC000000000. The ANI result was 77.48%, below the 95% inter-species threshold [30].
**Table 1. Phenotypic characteristics that differentiate strain 3A5MI-3' from the phylogenetically closely related strains of the genus Niabella**

Strains: 1, 3A5MI-3'; 2, *N. pedocola* JCM 31011'; 3, *N. aquatica* JCM 30952' [2]; 4, *N. aurantiaca* DSM 17617' [6]; 5, *N. ginsengisoli* JCM 15444' [3]; 6, *N. ginsenosidivorans* JCM 18199' [13]; 7, *N. hibiscisoli* KACC 18857' [10]; 8, *N. hirudinis* DSM 25812' [9]; 9, *N. soli* DSM 19437' [12]; 10, *N. terrae* JCM 19502' [14]; 11, *N. thaohniensis* JCM 18864' [15]; 12, *N. yanshanensis* KACC 14980' [11]; 13, *N. drilacis* DSM25812' [9]; 14, *N. tibetensis* CCTCC AB 209167' [7]. +, Positive; −, negative; w, weakly positive. The data of strain 3A5MI-3' and *N. pedocola* JCM 31011' were taken from the current study, others were taken from the published literature.

| Characteristic                     | 1   | 2   | 3   | 4   | 5   | 6   | 7   | 8   | 9   | 10  | 11  | 12  | 13  | 14  |
|-----------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Source of isolation               | Sludge | Soil | Water | Soil | Soil | Compost | Soil | Leeches | Soil | Soil | Soil | Soybean rhizosphere | Leeches | Soil |
| pH range for growth               | 5–9 | 5.5–10.5 | 5–9 | 5–8 | 6–8 | 4.5–10 | 5–8 | 4.5–10.5 | 5–8 | 5–8.5 | 6.5–11 | 6–10 | 4.5–10.5 | 5–8 |
| Temperature range for growth (°C) | 15–45 | 15–40 | 10–37 | 10–35 | 5–35 | 18–42 | 4–40 | 15–30 | 15–35 | 15–35 | 15–37 | 15–35 | 15–30 | 15–34 |
| Catalase/oxidase                  | −/+ | −/w | +/− | +/− | +/+ | +/+ | −/+ | +/+ | +/+ | −/+ | +/+ | −/+ | +/+ | +/+
| Gelatin hydrolysis               | +   | −   | −   | +   | −   | +   | −   | −   | +   | −   | +   | −   | +   | +   |
| Assimilation tests (API 20NE and Biolog GENII): | | | | | | | | | | | | | | |
| d-Glucose                         | −   | +   | +   | +   | +   | +   | −   | +   | +   | +   | +   | +   | +   | +   |
| d-Mannitol                        | −   | −   | −   | −   | −   | −   | −   | +   | +   | −   | −   | −   | −   | −   |
| l-Fucose                          | w   | −   | +   | −   | +   | +   | +   | −   | −   | +   | −   | −   | −   | −   |
| l-Serine                          | +   | −   | +   | +   | −   | −   | −   | −   | −   | −   | −   | −   | −   | −   |
| l-Alanine                         | w   | −   | −   | −   | −   | −   | −   | +   | −   | −   | −   | −   | +   | −   |
| Enzyme activities (API ZYM):      | | | | | | | | | | | | | | |
| Cystine arylamidase               | w   | +   | +   | −   | +   | +   | −   | −   | −   | w   | +   | +   | +   | +   |
| Trypsin                           | w   | −   | −   | −   | −   | +   | +   | w   | −   | +   | −   | +   | w   | −   |
dDDH was performed with genome sequences of strains 3A5MI-3^T and *N. pedocola* JCM 31011^T using the Genome-to-Genome Distance Calculator [29]. The estimated dDDH value was 19.50%, which was below the standard value generally recommended for species differentiation.

The genome of strain RSS-23^T contained also three contigs, and the total length is 2.79 Mb, encoding 2575 genes. The calculated genomic DNA G+C content of strain RSS-23^T was 61.21 mol%. The genome of strain RSS-23^T carries 58 ncRNA genes, including six rRNA genes (5S, 16S, 23S), 49 tRNA genes and three sRNA genes. The KEGG functional category distribution revealed that large numbers of genes in the genome of strain RSS-23^T belonged to the metabolism (53%), genetic information processing (16%), environmental information processing (14%), cellular processes (8%). Annotated with the RefSeq NR database, the genomes of strain RSS-23^T harboured 61 genes encoding phosphatase, six genes encoding glucosidase, four genes encoding glycosyl hydrolase, 27 genes encoding glycosyl transferase and 11 genes encoding polysaccharide biosynthesis protein. APIZYM positive enzyme genes such as alkaline phosphatase, acid phosphatase and α-glucosidase were also found in the genome. Comparing the genomes of strains RSS-23^T and *T. fusca* DSM 15424^T, we found that the specific genes contained in strain RSS-23^T are as follows: three genes encoding aminotransferase class I/II, six genes encoding chloride channel protein, three genes encoding penicillin acylase, three genes encoding UDP-glucose 4-epimerase, three genes encoding UDP-N-acetylglucosamine 2-epimerase and three genes encoding carbonate dehydratase. The accession numbers of the sequences on the database relating to the specific or characteristic (marked in yellow) genes of strain RSS-23^T and *T. fusca* DSM 15424^T are provided as supplementary files. The ANI values between strain RSS-23^T and *T. fusca* DSM 15424^T or *T. aquatica* SY21^T were 78.10 and 76.11%, respectively, which were below the 95% inter-species threshold [30]. The estimated dDDH values of strain RSS-23^T to *T. fusca* DSM 15424^T and *T. aquatica* SY21^T were 25.20 and 20.90 %, respectively, which were below the standard value generally recommended for species differentiation.

The morphology and size of cells grown on R2A agar at 30 °C for 2 days were observed by using transmission electron microscopy (JEM-1400, JEOL), and motility was observed with light microscopy. Gram-staining was performed according to Hucker [31].

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**Table 2. Phenotypic characteristics that differentiate strain RSS-23^T from the phylogenetically closely related species of the genus Thermomonas**

Strains: 1. RSS-23^T; 2. *T. fusca* DSM 15424^T [18]; 3. *T. aquatica* KCTC 62191^T [4]; 4. *T. carbonis* KCTC 42013^T [17]; 5. *T. brevis* DSM 15422^T [18]; 6. *T. haemolytica* DSM 13605^T [16]; 7. *T. koreensis* KCTC 12540^T [5]; 8. *T. hydrothermalis* DSM 14834^T [19]. +, Positive; −, negative; w, weakly positive/sensitive.

The data of strain RSS-23^T and *T. fusca* DSM 15424^T were taken from the current study, others were taken from the published literature.

| Characteristic | 1       | 2       | 3       | 4       | 5       | 6       | 7       | 8       |
|---------------|---------|---------|---------|---------|---------|---------|---------|---------|
| Colony colour on R2A agar | Cream   | Beige   | Cream   | Yellow  | Beige   | Cream   | Beige   | Cream   |
| Cell shape    | Ovoid rod| Rod     | Rod     | Ovoid rod| Rod     | Rod     | Rod     | Rod     |
| Nitrate reduction | +       | +       | −       | −       | +       | +       | −       | −       |
| Optimum growth temperature (°C) | 30      | 28–37   | 28      | 28      | 28–37   | 37–50   | 37      | 50      |
| Motility      | −       | +       | −       | −       | +       | +       | +       | −       |
| Aesculin hydrolysis | +       | −       | −       | +       | +       | −       | +       | +       |
| Gelatin hydrolysis | +       | +       | −       | −       | +       | −       | +       | +       |
| Assimilation tests (API 20NE and Biolog): | | | | | | | | |
| D-Glucose | +       | −       | +       | −       | +       | −       | +       | +       |
| Malose | +       | −       | +       | w       | +       | −       | +       | +       |
| D-Mannitol | −       | −       | +       | +       | −       | −       | −       | −       |
| N-Acetylglucosamine | +       | −       | w       | +       | +       | −       | −       | −       |
| D-Mannose | −       | −       | +       | −       | +       | −       | −       | −       |
| L-Proline | +       | +       | +       | +       | −       | +       | +       | +       |
| Enzyme activities (API ZYM): | | | | | | | | |
| Trypsin | +       | +       | +       | w       | +       | −       | −       | −       |
| β-Glucosidase | +       | −       | +       | −       | +       | −       | −       | +       |
| Cystine arylamidase | +       | +       | +       | w       | +       | +       | +       | −       |
| Chymotrypsin | +       | +       | −       | w       | −       | +       | −       | +       |
| Lipase (C14) | −       | −       | −       | −       | −       | −       | −       | −       |
Table 3. Cellular fatty acid composition (% of total) of strain 3A5MI-3T and closely related species of the genus Niabella

Strains: 1, 3A5MI-3T; 2, N. pedocola JCM 31011\textsuperscript{T} [8]; 3, N. aquatica JCM 30952\textsuperscript{T} [2]; 4, N. aurantiaca DSM 17617\textsuperscript{T} [6]; 5, N. ginsengisoli JCM 15444\textsuperscript{T} [3]; 6, N. ginsenosidivorans JCM 18199\textsuperscript{T} [13]; 7, N. hibiscioli KACC 18857\textsuperscript{T} [10]; 8, N. hirudinis DSM 25812\textsuperscript{T} [9]; 9, N. soli DSM 19437\textsuperscript{T} [12]; 10, 'N. terrae' JCM 19502\textsuperscript{T} [14]; 11, 'N. thaonhiensis' JCM 18864\textsuperscript{T} [15]; 12, N. yanshanensis KACC 14980\textsuperscript{T} [11]; 13, N. drilacis DSM 25812\textsuperscript{T} [9]; 14, N. tibetensis CCTCC AB 209167\textsuperscript{T} [7]. −, Not detected or <0.1%. The data of strain 3A5MI-3T and N. pedocola JCM 31011\textsuperscript{T} were taken from the current study, others were taken from the published literature.

| Fatty acid | 1  | 2  | 3  | 4  | 5  | 6  | 7  | 8  | 9  | 10 | 11 | 12 | 13 | 14 |
|------------|----|----|----|----|----|----|----|----|----|----|----|----|----|----|
| Saturated: |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| iso-C\textsubscript{15:0} | 40.6 | 40.9 | 40.4 | 33.7 | 32.8 | 42.0 | 27.5 | 52.4 | 29.2 | 38.9 | 36.7 | 39.4 | 39.4 | 40.8 | 41.3 |
| anteiso-C\textsubscript{15:0} | 1.9 | 1.2 | 0.9 | 1.6 | – | 0.7 | 0.6 | – | 1.2 | 3.8 | 0.9 | – | 0.7 | 0.9 |
| C\textsubscript{16:0} | 5.5 | 5.9 | 2.2 | 3.5 | 7.9 | 2.1 | 13.3 | 2.9 | 6.8 | 2.6 | 3.6 | 4.3 | 3.2 | 3.4 |
| Unsaturated: |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| iso-C\textsubscript{15:1} G* | 19.0 | 32.2 | 23.4 | 22.3 | 36.4 | 15.9 | 20.3 | 16.6 | 18.4 | 20.3 | 20.8 | 30.5 | 20.5 | 14.9 |
| anteiso-C\textsubscript{15:1} | 1.1 | 1.0 | – | – | – | – | – | – | – | – | – | – | – | – |
| Hydroxy: |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
| iso-C\textsubscript{16:0} 3OH | 1.7 | 2.1 | 2.8 | 2.9 | 3.7 | 2.9 | 3.0 | 3.8 | 2.2 | 3.0 | 2.6 | 3.2 | – | 2.4 |
| iso-C\textsubscript{17:0} 3OH | 1.1 | – | – | – | – | 0.7 | – | – | – | 2.2 | – | – | – | 0.7 |
| C\textsubscript{18:0} 3OH | 2.4 | – | 1.8 | 2.4 | – | 1.2 | 1.8 | 1.9 | 2.2 | 1.8 | 2.9 | 1.4 | 3.5 | 3.3 |
| iso-C\textsubscript{17:1} 3OH | 11.4 | 7.6 | 13.9 | 15.5 | 9.5 | 16.4 | 10.7 | 9.7 | 11.8 | 12.9 | 9.1 | 7.7 | 9.2 | – |
| Summed feature 3† | 7.1 | 5.2 | 12.5 | 10.6 | 3.5 | 14.4 | 8.8 | 5.2 | 11.1 | 5.3 | 15 | 7.8 | 10.7 | 16.0 |

*iso-C\textsubscript{15:1} G should correspond to either iso-C\textsubscript{15:0} \textit{ω6c} and/or iso-C\textsubscript{15:0} \textit{ω7c}. The double bond position indicated by a capital letter is unknown.
†Summed features are fatty acids that cannot be resolved reliably from another fatty acid using the chromatographic conditions chosen. The MIDI system groups these fatty acids together as one feature with a single percentage of the total. Summed feature 3 comprised C\textsubscript{16:1} \textit{ω7c}/C\textsubscript{16:1} \textit{ω6c}.
Growth was measured at temperatures of 16, 20, 30, 37, 40, 45, 50, 60, 65 and 70 °C. Anaerobic growth was examined in R2A broth without oxygen, and using L-cysteine (1 g l\(^{-1}\) ) to consume residual oxygen and resazurin (1 mg l\(^{-1}\) ) as a redox indicator.

Salt tolerance was investigated by supplementing NaCl concentrations of 0, 1, 2, 3, 4 and 5.0 % (w/v) to R2A broth. The effect of pH (at pH 5.0, 6.0, 7.0, 8.0 and 9.0) was tested in R2A broth using phosphate buffer (for pH 5.0–7.0) and Tris buffer (for pH 8.0–9.0). Catalase activity was determined using a 3 % (v/v) hydrogen peroxide solution. Oxidation of N,N,N′,N′-tetramethyl-p-phenylenediamine dihydrochloride was used to check oxidase activity [32]. Monosaccharide, disaccharide and polysaccharide utilization was tested with the following compounds and basic inorganic salt at concentration of 1 g l\(^{-1}\) : starch, cellulose, chitin, xylan, agar, fructose, galactose, mannose, xylose, arabinose, glucose, maltose, cellobiose, trehalose, sucrose and sorbose.

Bacterial cells grown in R2A were collected and washed three times with basic inorganic salt medium, inoculated at 1 % (v/v), and cultivated for 2 days. Other physiological and biochemical analyses were carried out by using the API ZYM, API 20NE and Biolog GEN III systems, according to the manufacturers’ instructions. Cells of strains 3A5MI-3 T and RSS-23 T were Gram-negative, aerobic, non-motile and short rod-shaped (Fig. S3). The distinctive physiological characteristics of strains 3A5MI-3 T and RSS-23 T are listed in Tables 1 and 2, respectively.

The cellular fatty acids were determined using cells grown on R2A agar for 2 days at 30 °C with the standard MIDI protocol (Sherlock Microbial Identification System, version 6.0B) and analysed with a gas chromatograph (GC6890, Agilent) [33]. The extraction, purification and analysis of quinones were carried out according to the methods of Collins et al. [34]. The total lipids were extracted using chloroform and methanol, followed by thin-plate biphasic chromatography to identify each lipid component [35].

Strain 3A5MI-3 T contained aliphatic saturated fatty acid (iso-C\(_{15:0}\)) as its predominant cellular fatty acid that accounted for about half of total fatty acids, followed by iso-C\(_{15:1\omega6c}\) and/or iso-C\(_{15:1\omega5c}\), iso-C\(_{17:0}\) 3-OH and summed feature 3 (C\(_{16:1\omega7c}/C_{16:1\omega6c}\)). The composition of the fatty acids is shown in Table 3. The major cytochrome was determined to be MK-7, as previously reported.
for described members of the genus \textit{Niabella}. The polar lipid profile of strain 3A5MI-3\textsuperscript{T} contained phosphatidylethanolamine and three unknown lipids (Fig. S4a).

Strain RSS-23\textsuperscript{T} also contained aliphatic saturated fatty acid (iso-C\textsubscript{15} : 0) as its predominant cellular fatty acid, which accounted for about one third of total fatty acids. The fatty acid profiles are shown in Table 4. The major isoprenoid quinone was determined to be Q-8, as previously reported for members of the genus \textit{Thermomonas}. The polar lipid profile contained diphasphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine, two unknown phospholipids and an unknown lipid (Fig. S4b).

Based on the phylogenetic and phenotypic characteristics, we conclude that strains 3A5MI-3\textsuperscript{T} and RSS-23\textsuperscript{T} represent novel species of the genera \textit{Niabella} and \textit{Thermomonas}, respectively, for which the names \textit{Niabella beijingensis} sp. nov. and \textit{Thermomonas beijingensis} sp. nov. are proposed.

\section*{DESCRIPTION OF \textit{NIABELLA BEIJINGENSIS} SP. NOV.}

\textit{Niabella beijingensis} (bei.jing.en'sis. N.L. fem. adj. beijingensis, pertaining to Beijing, the geographical origin of the type strain).

Cells are Gram-stain-negative, strictly aerobic, non-motile and short rod-shaped (Fig. S3a). Colonies are convex, circular, smooth and edges were regular after incubation on R2A broth for 2 days at 30°C. The strain can grow in a wide range of temperature (16–45°C) and pH (5.0–9.0), and the range of NaCl tolerance is 0–2% (w/v) NaCl. Optimal growth at 30°C, pH 7.0 and with 1% NaCl (w/v). Oxidase and catalase activities are positive and negative, respectively. According to the API 20NE system, nitrate cannot be reduced to nitrite. Positive for aesculin ferric citrate, gelatin, 4-nitrophenyl-\textbeta-N-galactopyranoside, \textgamma-glucose, \textalpha;-arabinose, \textdelta;-mannose, \textalpha;-galactosaminidase, \textalpha;-mannosidase and \textalpha;-fucosidase. Esterase lipase (C8), cystine arylamidase and trypsin are weak; and esterase (C4), lipase (C14), \textalpha;-chymotrypsin and \textbeta;-glucuronidase are negative (API ZYM).

\textit{Thermomonas} sp. nov. are proposed.

The polar lipid profile of strain 3A5MI-3\textsuperscript{T} contained phosphatidylethanolamine and three unknown lipids. The G+C content of the type strain is 47.07 mol%.

The type strain, 3A5MI-3\textsuperscript{T} (=CGMCC 1.17737\textsuperscript{T}=KCTC 82817\textsuperscript{T}), was isolated from constructed wetland sludge from Beijing, PR China.

\section*{DESCRIPTION OF \textit{THERMOMONAS BEIJINGENSIS} SP. NOV.}

\textit{Thermomonas beijingensis} (bei.jing.en'sis. N.L. fem. adj. beijingensis, pertaining to Beijing, the geographical origin of the type strain).

Cells are Gram-stain-negative, aerobic, non-motile and rod-shaped. Colonies are convex, circular, smooth and edges are regular after incubation on R2A broth for 2 days at 30°C. The strain can grow in a wide range of temperature (16–45°C) and pH (5.0–9.0). The range of NaCl tolerance is 0–1% NaCl (w/v). Optimal growth at 30°C, pH 7.0 and with 1% NaCl (w/v). Oxidase and catalase activities are positive and negative, respectively. According to the API 20NE system, nitrate cannot be reduced to nitrite. Positive for aesculin ferric citrate, gelatin, 4-nitrophenyl-\textbeta-N-galactopyranoside, \textalpha;-glucose, \textalpha;-arabinose, \textdelta;-mannose, \textalpha;-galactosaminidase, \textalpha;-mannosidase and \textalpha;-fucosidase. Esterase lipase (C8), cystine arylamidase and trypsin are weak; and esterase (C4), lipase (C14), \textalpha;-chymotrypsin and \textbeta;-glucuronidase are negative (API ZYM).

Carbon sources utilized include dextrin, maltose, cellobiose, gentiobiose, sucrose, stachyose, maltose, trehalose, cellobiose, turanose, raffinose, lactose, melibiose, \textbeta;-mannose, \textbeta;-fructose, \textdelta;-galactosamine, gelatin, glycy-\textgamma-l-proline, \textalpha;-alanine, \textalpha;-arginine, \textalpha;-aspartic acid, \textalpha;-glutamic acid, \textalpha;-serine, methyl pyruvate, xylan and cellulose. No utilization of 3-methyl glucose, \textalpha;-fucose, inosine, \textdelta;-sorbitol, \textdelta;-arabitol, \textalpha;-inositol, \textdelta;-fructose-6-PO\textsubscript{4}, \textalpha;-serine, \textalpha;-arginine, \textalpha;-pyrogulatamic acid, mucic acid, quinic acid, \textdelta;-saccharic acid, \textbeta;-hydroxy-phenylacetic acid, \textdelta;-lactic acid methyl ester, \textalpha;-keto-glutaric acid, \textdelta;-malic acid, \textdelta;-malic acid, bromo-succinic acid, \textgamma;-amino-butyric acid, \textbeta;-hydroxy-\textdelta;/\textbeta;-butyric acid, \textalpha;-keto-butyrilic acid, propionic acid, formic acid and chitin (Biolog GEN\textsuperscript{III} and cultivation examinations).

The predominant cellular fatty acids are iso-C\textsubscript{15} : 0, iso-C\textsubscript{17} : 0\textsubscript{3-OH} and/or iso-C\textsubscript{17} : 0\textsubscript{3-OH} and summed feature 3 (C\textsubscript{16} : 1\textsubscript{ω7c/C\textsubscript{16} : 1\textsubscript{ω6c}}). Contains cytoquinone MK-7 as respiratory quinone. The polar lipid profile contains phosphatidylethanolamine and three unknown lipids. The G+C content of the type strain is 47.07 mol%.

The type strain, 3A5MI-3\textsuperscript{T} (=CGMCC 1.17737\textsuperscript{T}=KCTC 82817\textsuperscript{T}), was isolated from constructed wetland sludge from Beijing, PR China.
Twin 40, α-hydroxy-butyric acid, β-hydroxy-3,6-butyric acid, α-keto-butyric acid, acetoacetic acid, propionic acid, acetic acid, d-arabino-β-d-glucosamine, d-glucose-6-PO4, d-aspartic acid and pectin. No growth occurs on trehalose, sucrose, stachyose, raffinose, lactose, melibiose, methyl β-d-glucoside, β-salicylic, N-acetyl-β-d-mannosamine, β-d-glucose, β-d-mannose, β-d-galactose, β-methyl glucose, d-fucose, L-fucose, L-rhamnose, inosine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-serine, L-histidine, L-prolylglutamic acid, D-galactaric acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, glucuronamide, mucic acid, quinic acid, L-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, glucuronamide, mucic acid, quinic acid, L-galacturonic acid, D-lactic acid methyl ester, L-lactic acid, citric acid, α-keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic acid, γ-aminobutyric acid, formic acid, cellulose, and chitin (Biolog GENIII and cultivation examinations). The predominant cellular fatty acids are iso-C15:0, iso-C17:1ω7c, 10-methyl iso-C15:0, 10-methyl iso-C17:1ω7c, 3-OH and summed feature 3 (C16:1ω7c, C16:1ω6c). The major isoprenoid quinone is Q-8. The polar lipid profile contains diphasitidyglycerol, phosphatidylglycerol, phosphatidylethanolamine, two unknown phospholipids and an unknown lipid.

The type strain, RSS-23T (＝CGMCC 1.17738T＝KCTC 82820T), was isolated from soil of the Dragon-shaped Wetland System in Beijing Olympic Park, PR China. The DNA G+C content of the type strain is 61.21 mol%.

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**Conflicts of interest**

The authors declare that there are no conflicts of interest.

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