High quality draft genome sequence of the type strain of *Pseudomonas lutea* OK2\textsuperscript{T}, a phosphate-solubilizing rhizospheric bacterium

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**Abstract**

*Pseudomonas lutea* OK2\textsuperscript{T} (=LMG 21974\textsuperscript{T}, CECT 5822\textsuperscript{T}) is the type strain of the species and was isolated from the rhizosphere of grass growing in Spain in 2003 based on its phosphate-solubilizing capacity. In order to identify the functional significance of phosphate solubilization in *Pseudomonas* Plant growth promoting rhizobacteria, we describe here the phenotypic characteristics of strain OK2\textsuperscript{T} along with its high-quality draft genome sequence, its annotation, and analysis. The genome is comprised of 5,647,497 bp with 60.15 % G + C content. The sequence includes 4,846 protein-coding genes and 95 RNA genes.

**Keywords:** Pseudomonad, Phosphate-solubilizing, Plant growth promoting rhizobacteria (PGPR), Biofertilizer

**Abbreviations:** HGAP, Hierarchical genome assembly process; IMG-ER, Integrated microbial genomes-expert review; KO, Kyoto encyclopedia of genes and genomes Orthology; PGAP, Prokaryotic genome annotation pipeline; PGPR, Plant growth-promoting rhizobacteria; RAST, Rapid annotation using subsystems technology; SMRT, Single molecule real-time

**Introduction**

Phosphorus, one of the major essential macronutrients for plant growth and development, is usually found in insufficient quantities in soil because of its low solubility and fixation [1, 2]. Since phosphorus deficiency in agricultural soil is limits plant growth, the release bound phosphorus from soils by microbes is an important aspect that can be used to improve soil fertility for increasing crop yields [2].

Phosphate-solubilizing microorganisms, a group of soil microorganisms capable of converting insoluble phosphate to soluble forms, have received attention as efficient bio-fertilizers for enhancing the phosphate availability for plants [3]. As one of the representative phosphate-solubilizing bacteria [4], rhizosphere-colonizing pseudomonads are of interest owing to the benefits they offer to plants. Besides increasing the phosphate accessibility, they promote plant development by facilitating direct and indirect plant growth promotion through the production of phytohormones and enzymes or through the suppression of soil-borne diseases by inducing systemic resistance in the plants [5–7].

*Pseudomonas lutea* OK2\textsuperscript{T} (=LMG 21974\textsuperscript{T}, CECT 5822\textsuperscript{T}) with insoluble phosphate-solubilizing activity was isolated from the rhizosphere of grass growing in northern Spain [8]. Characteristics of the whole genome sequence and a brief summary of the phenotype for this type strain are presented in this study.

**Organism information**

**Classification and features**

A 16S rRNA gene sequence of *P. lutea* OK2\textsuperscript{T} was compared to those of other type strains of the genus *Pseudomonas* using BLAST on NCBI [9]. The 16S rRNA gene sequence showed highest similarity (99 % identity) to that of *P. graminis* DSM 11363\textsuperscript{T} [10], followed by similarity to the 16S rRNA gene sequence of *P. rhizosphaerae* IHS\textsuperscript{T} (98 % identity) [11], *P. protegens* CHA0\textsuperscript{T} (98 % identity)
[12, 13], *P. rhodesiae* CIP 104664T (97% identity) [14], and *P. argentinensis* CH01T (97% identity) [15]. Species showing full-length 16S rRNA gene sequences in BLAST analysis were considered for further phylogenetic analyses. A phylogenetic tree was constructed using the neighbor-joining method [16], and the bootstrap value was set as 1,000 times random replicate sampling. The consensus phylogenetic neighborhood of *P. lutea* OK2T within the genus *Pseudomonas* is shown in Fig. 1.

*P. lutea* OK2T is a motile, strictly aerobic, non-spore forming, gram-negative bacterium that belongs to the family *Pseudomonadaceae* of the class *Gammaproteobacteria* [8]. The cells are rod-shaped with a diameter of approximately 0.75 μm and a length of 1.2–1.6 μm (Fig. 2). The strain produces yellow, translucent, circular convex colonies of 1–2 mm diameter on plates containing YED-P medium (per liter: 7.0 g of glucose, 3.0 g of yeast extract, 3.0 g of bicalcium phosphate, and 17.0 g of agar) within 2 days at 25 °C [8]. *P. lutea* OK2T is capable of oxidizing glucose in media containing ammonium nitrate as a nitrogen source and hydrolyzes aesculin [8]. Further, it can utilize galactose, ribose, mannose, glycerol, D-fructose, D-xylene, D-/L-arabinose, D-/L-arabitol, D-/L-fucose, L-lyxose, melibiose, inositol, mannitol, adonitol, xylitol, caprate, malate, gluconate, 2-ketogluconate, and citrate as sole carbon sources, but cannot utilize maltose, lactose, sucrose, trehalose, cellobiose, starch, glycogen, inulin, sorbitol, D-tagatose, D-raffinose, L-xylene, L-sorbose, L-rhamnose, N-acetylglucosamine, salicin, and...
erythritol [8]. Unlike other pseudomonads, the strain OK2\textsuperscript{T} does not produce fluorescent pigments [8].

**Chemotaxonomic data**

The important non-polar fatty acids present in *P. lutea* OK2\textsuperscript{T} include hexadecenoic acid (16:1, 39.0 %), hexadecanoic acid (16:0, 29.0 %), and octadecenoic acid (18:1, 18.6 %). In addition, the strain OK2\textsuperscript{T} has hydroxy fatty acids such as 3-hydroxydodecanoic acid (3-OH 12:0, 3.3 %), 2-hydroxydodecanoic acid (2-OH 12:0, 2.7 %), and 3-hydroxydecanoic acid (3-OH 10:0, 2.4 %) [8]. The whole-cell fatty acid profile of this strain is similar to that observed in other representative strains of the genus *Pseudomonas*, such as *P. graminis* [10] and *P. rhizosphaerae* [11]. The general characteristics of the strain are summarized in Table 1.

**Genome sequencing information**

**Genome project history**

*P. lutea* OK2\textsuperscript{T} was selected as a novel-phosphate solubilizing strain for the genome-sequencing project of agriculturally useful microbes undertaken at Kyungpook National University. Genome sequencing was performed in September 2014, and the results of the Whole Genome Shotgun project have been deposited at DDBJ/EMBL/GenBank under the accession number JRMB00000000. The version described in this study is the first version, indicated as JRMB00000000.1. The information obtained from the genome sequencing project is registered on the Genome Online Database [17] with the GOLD Project ID Gp0107463. A summary of this information and its association with the Minimum Information about a Genome Sequence (MIGS) version 2.0 compliance [18] are presented in Table 2.

**Growth conditions and genomic DNA preparation**

The strain was cultured in tryptic soy broth (Difco Laboratories Inc., Detroit, MI) at 30 °C on a rotary shaker at 200 rpm. Genomic DNA was isolated using a QIAamp\textsuperscript{TM} DNA Mini Kit (Qiagen, Valencia, CA) according to the manufacturer’s standard protocol. The quantity and purity of the extracted genomic DNA were assessed using a Picodrop Microliter UV/Vis Spectrophotometer (Thermo Fisher Scientific Inc., Waltham, MA) and Qubit\textsuperscript{TM} 2.0 Fluorometer (Fisher Scientific Inc., Pittsburgh, PA), respectively.

**Genome sequencing and assembly**

The isolated genomic DNA of *P. lutea* OK2\textsuperscript{T} was sequenced using the SMRT DNA sequencing platform and the Pacific Biosciences RS II sequencer with P4 polymerase-C2 sequencing chemistry (Pacific Biosciences, Menlo Park, CA) [19]. After shearing the genomic DNA, a 10-kb insert SMRT-bell library was prepared and loaded on two SMRT cells. During the 90 min of movie time, 654,270,150 read bases were generated from 300,584 reads. All the obtained bases were filtered to remove any reads shorter than 100 bp or those having accuracy values less than 0.8. Subsequently, 461,880,761 nucleotides were obtained from 116,562 reads, with a read quality of 0.843. These bases were assembled *de novo* using the RS HGAP assembly protocol version 3.3 on the SMRT analysis platform version 2.2.0 [20]. The HGAP analysis yielded five contigs corresponding to five scaffolds, with a 67.58-fold coverage. The maximum contig length and N50 contig length were identical: 2,839,280 bp. The total length of the *P. lutea* OK2\textsuperscript{T} genome was found to be 5,647,497 bp.

**Genome annotation**

The protein coding sequences were determined using the NCBI PGAP version 2.8 (rev. 447021) [21]. Additional gene prediction and functional annotation analyses were performed on the RAST server [22] and IMG-ER pipeline, respectively, by the Department of Energy-Joint Genome Institute [23].

**Genome properties**

The average G + C content of the genome was 60.15 %. The genome was predicted to encode 4,941 genes including 4,846 protein-coding genes and 95 RNA genes (24 rRNAs, 70 tRNAs, and 1 ncRNA). Putative functions were assigned to 4,102 of the protein-coding genes, and 3,507 genes (approximately 70.98 %) were assigned to the COG functional categories. The most abundant COG category was "Amino acid transport and metabolism" (10.36 %), followed by "General function prediction only" (8.71 %), "Transcription" (8.34 %), and "Signal transduction mechanisms" (6.52 %). The category for "Mobilome: prophages, transposons" (0.92 %) was also
### Table 1 Classification and general features of *Pseudomonas lutea* OK2<sup>T</sup> [18]

| MIGS ID | Property               | Term                                                                 | Evidence code<sup>a</sup> |
|---------|------------------------|----------------------------------------------------------------------|---------------------------|
|         | Classification         | Domain *Bacteria*                                                     | TAS [64]                  |
|         |                        | Phylum *Proteobacteria*                                              | TAS [65]                  |
|         |                        | Class *Gammaproteobacteria*                                          | TAS [66, 67]              |
|         |                        | Order *Pseudomonadales*                                              | TAS [47, 68, 69]          |
|         |                        | Family *Pseudomonadaceae*                                            | TAS [47, 70]              |
|         |                        | Genus *Pseudomonas*                                                  | TAS [47, 71–73]           |
|         |                        | Species *Pseudomonas lutea*                                          | TAS [8]                   |
|         |                        | Type strain OK2<sup>T</sup> (=LMG 21974<sup>T</sup>, CECT 5822<sup>T</sup>) | TAS [8]                   |
| MIGS-6  | Gram stain             | Negative                                                             | TAS [8, 74]               |
| MIGS-6.3| Cell shape             | Rod-shaped                                                           | TAS [8, 74]               |
| MIGS-11 | Motility               | Motile                                                               | TAS [8, 74]               |
| MIGS-12 | Sporulation            | None                                                                 | TAS [8, 74]               |
| MIGS-13 | Temperature range      | Mesophilic                                                           | NAS                       |
|         | Optimum temperature    | 25°C                                                                 | TAS [8]                   |
|         | pH range               | 7.0–7.5                                                              | NAS                       |
| MIGS-14 | Carbon source          | Heterotrophic                                                        | TAS [75]                  |
| MIGS-6  | Habitat                | Soil                                                                  | TAS [8]                   |
| MIGS-6.3| Salinity               | Not reported                                                          |                           |
| MIGS-22 | Oxygen requirement     | Aerobic                                                              | TAS [8, 74]               |
| MIGS-15 | Biotic relationships   | Free living                                                          | NAS                       |
| MIGS-14 | Pathogenicity          | Non-pathogen                                                         |                           |
| MIGS-4  | Geographic location    | Spain; northern Spain                                                | TAS [8]                   |
| MIGS-5  | Sample collection      | 2003                                                                 | NAS                       |
| MIGS-4.1| Latitude               | Not reported                                                          |                           |
| MIGS-4.2| Longitude              | Not reported                                                          |                           |
| MIGS-4.4| Altitude               | Not reported                                                          |                           |

<sup>a</sup>Evidence codes - IDA: Inferred from Direct Assay; TAS: Traceable Author Statement (i.e., a direct report exists in the literature); NAS: Non-traceable Author Statement (i.e., not directly observed for the living, isolated sample, but based on a generally accepted property for the species, or anecdotal evidence). These evidence codes are from the Gene Ontology project [76].

### Table 2 Project information

| MIGS ID | Property               | Term                                                                 |
|---------|------------------------|----------------------------------------------------------------------|
| MIGS-31 | Finishing quality      | Draft                                                               |
| MIGS-28 | Libraries used         | 10-kb SMRT-bell library                                             |
| MIGS-29 | Sequencing platforms   | PacBio RS II                                                        |
| MIGS-31.2| Fold coverage          | 67.58 ×                                                             |
| MIGS-30 | Assemblers             | RS HGAP Assembly Protocol [20] in SMRT analysis pipeline v.2.2.0   |
| MIGS-32 | Gene calling method    | NCBI Prokaryotic Genome Annotation Pipeline [77]; GeneMarkS+ [78]  |
|         | Locus Tag              | LT42                                                                |
|         | Genbank ID             | JRMB000000000                                                        |
|         | Genbank Date of Release| September 29, 2014                                                   |
|         | GOLD ID                | Gp0107463                                                           |
|         | BIOPROJECT             | PRJNA261881                                                         |
| MIGS-13 | Source material identifier | LMG 21974<sup>T</sup>, CECT 5822<sup>T</sup>                      |
|         | Project relevance      | Agriculture                                                          |
classified with functional genes for transposase (LT42_00515, LT42_05870, LT42_07855, LT42_10965, LT42_14240, LT42_14330, LT42_18595, LT42_19270, LT42_21870, LT42_21925), integrase (LT42_17205), terminase (LT42_06460, LT42_17145, LT42_17150), and plasmid stabilization protein (LT42_19025, LT42_24175). The genome statistics of strain OK2\textsuperscript{T} are presented in Table 3 and Fig. 3. The gene distribution within the COG functional categories is presented in Table 4.

**Table 3** Genome statistics

| Attribute                          | Value     | % of Total |
|-----------------------------------|-----------|------------|
| Genome size (bp)                  | 5,647,497 | 100.00     |
| DNA coding (bp)                   | 4,778,153 | 84.61      |
| DNA G + C (bp)                    | 3,397,087 | 60.15      |
| DNA scaffolds                      | 5         | 100.00     |
| Total genes                        | 4,941     | 100.00     |
| Protein coding genes              | 4,846     | 98.08      |
| RNA genes                          | 95        | 1.92       |
| Pseudo genes                      | 239       | 4.84       |
| Genes in internal clusters        | 1,402     | 26.64      |
| Genes with function prediction    | 4,102     | 83.02      |
| Genes assigned to COGs            | 3,507     | 70.98      |
| Genes with Pfam domains           | 4,026     | 81.48      |
| Genes with signal peptides        | 485       | 9.82       |
| Genes with transmembrane helices  | 1,026     | 20.77      |
| CRISPR repeats                    | 0         | 0.00       |

**Table 4** Number of genes associated with general COG functional categories

| Code | Value | % age | Description                                           |
|------|-------|-------|------------------------------------------------------|
| J    | 231   | 5.75  | Translation, ribosomal structure and biogenesis      |
| A    | 1     | 0.02  | RNA processing and modification                      |
| K    | 335   | 8.34  | Transcription                                         |
| L    | 121   | 3.01  | Replication, recombination and repair                |
| B    | 2     | 0.05  | Chromatin structure and dynamics                      |
| D    | 34    | 0.85  | Cell cycle control, Cell division, chromosome partitioning |
| V    | 73    | 1.82  | Defense mechanisms                                    |
| T    | 262   | 6.52  | Signal transduction mechanisms                        |
| M    | 228   | 5.68  | Cell wall/membrane biogenesis                         |
| N    | 133   | 3.31  | Cell motility                                         |
| U    | 97    | 2.41  | Intracellular trafficking and secretion               |
| O    | 152   | 3.78  | Posttranslational modification, protein turnover, chaperones |
| C    | 248   | 6.17  | Energy production and conversion                      |
| G    | 256   | 6.37  | Carbohydrate transport and metabolism                 |
| E    | 416   | 10.36 | Amino acid transport and metabolism                   |
| F    | 85    | 2.12  | Nucleotide transport and metabolism                   |
| H    | 198   | 4.93  | Coenzyme transport and metabolism                     |
| I    | 182   | 4.53  | Lipid transport and metabolism                        |
| P    | 234   | 5.83  | Inorganic ion transport and metabolism                |
| Q    | 98    | 2.44  | Secondary metabolites biosynthesis, transport and catabolism |
| R    | 350   | 8.71  | General function prediction only                      |
| S    | 212   | 5.28  | Function unknown                                      |
| -    | 1434  | 29.02 | Not in COGs                                           |

The total is based on the total number of protein coding genes in the genome.

**Insights from the genome sequence**

Microorganisms that show phosphate-solubilizing activity are generally known to be involved in either of the following two biochemical mechanisms: production of organic acids for the acidification of external surroundings for plants and production of enzymes for direct solubilization [24, 25]. Genes encoding functional enzymes with these biochemical properties were predicted using the KO database via IMG-ER pipeline [26, 27]. The genome of *P. lutea* OK2\textsuperscript{T} was annotated with several genes involved in phosphate solubilization. For example, *ldhA* (D-lactate dehydrogenase, KO:K03778) and *icd* (isocitrate dehydrogenase, KO:K00031) were found to be involved in the production of organic acids, and *phoD* (alkaline phosphatase D, KO:K01113) was involved in direct phosphate solubilization. Direct oxidation of glucose to gluconic acid by a periplasmic membrane-bound glucose dehydrogenase is also known to be one of the major metabolic steps for phosphate solubilization in pseudomonads [6]. In relation to this process, the *gcd*
Table 5 Putative genes related to functional enzymes for potential PGPR effects predicted from the genome sequence of *Pseudomonas lutea* OK2

| Function ID | Name |
|-------------|------|
| KO:K01113 | alkaline phosphatase D [EC:3.1.3.1] (phoD) |
| KO:K03778* | D-lactate dehydrogenase [EC:1.1.1.28] (ldhA)* |
| KO:K0031 | isocitrate dehydrogenase [EC:1.1.1.42] (icd) |
| KO:K01647 | citrate synthase [EC:2.3.3.1] (gltA) |
| KO:K01177 | quinoprotein glucose dehydrogenase [EC:1.1.5.2] (gcpD) |

**Antibiotic resistance**

| KO:K17836* | beta-lactamase class A (penicillinase) [EC:3.5.2.6] (penP)* |
| KO:K08218 | MFS transporter, PAT family, beta-lactamase induction signal transducer AmpG (ampG) |
| KO:K03806 | beta-lactamase expression regulator, N-acetyl-anhydromuramyl-L-alanine amidase AmpD protein (ampD) |
| KO:K03807 | Membrane protein required for beta-lactamase induction, AmpE protein (ampE) |
| KO:K05365 | penicillin-binding protein 1B [EC:2.4.1.129 3.4.-.-] (mrcB) |
| KO:K05366 | penicillin-binding protein 1A [EC:2.4.1.-3.4.-.-] (mrcA) |
| KO:K05367 | penicillin-binding protein 1C [EC:2.4.1.-] (pnpC) |
| KO:K05515 | penicillin-binding protein 2 (mraA) |
| KO:K07522 | MFS transporter, DHA1 family, bicyclomycin/chloramphenicol resistance protein (bcr) |
| KO:K08223 | MFS transporter, FSR family, fosmidomycin resistance protein (fsr) |
| KO:K05595* | multiple antibiotic resistance protein (marC)* |
| KO:K18138 | multidrug efflux pump (acrB, mexB, adeI, smeE, mtrD, cmeB) |
| KO:K07799 | putative multidrug efflux transporter MdtA (mdtA) |
| KO:K07788 | RND superfamily, multidrug transport protein MdtB (mdtB) |
| KO:K07789 | RND superfamily, multidrug transport protein MdtC (mdtC) |

**Toxins**

| KO:K11068 | membrane damaging toxins Type II toxin, pore-forming toxin hemolysin III (hlyIII) |

**Metal ion resistance**

| KO:K02713 | copper chaperone |
| KO:K07245 | putative copper resistance protein D (pcoD) |
| KO:K07665 | two-component system, OmpR family, copper resistance phosphate regulon response regulator CusR (cush) |
| KO:K06189 | magnesium and cobalt transporter (corC) |
| KO:K0870| nickel/cobalt exporter (corA)* |
| KO:K06213 | magnesium transporter (mgtE) |
| KO:K16074 | zinc transporter (zntB) |
| KO:K16081 | zinc transport system substrate-binding protein (znuA) |
| KO:K09816 | zinc transport system permease protein (znuB) |
| KO:K09823 | Fur family transcriptional regulator, zinc uptake regulator (zur) |
| KO:K03893 | arsenical pump membrane protein (arsB) |
| KO:K11811* | arsenical resistance protein ArsH (arsH)* |

**Siderophore**

| KO:K02362 | enterochelin synthetase component D [EC:2.7.8.-] (entD) |
| KO:K16090 | catecholate siderophore receptor (fus) |
gene coding for a cofactor pyrroloquinoline quinone-dependent glucose dehydrogenase (=quinoprotein glucose dehydrogenase, KO:K00117) was revealed (Table 5). Phosphate solubilization is normally a complex phenomenon depending on conditions such as bacterial, nutritional, physiological, and growth variations [2]. Given that phosphate solubilization can occur through various microbial processes/mechanisms [28], the predicted genes on the genome being described could compositely contribute to this activity.

*P. lutea OK2* is also expected to possess functional traits related to plant growth promotion [29–32]. As shown in Table 5, genes coding for functional enzymes with various PGPR effects such as “antibiotic resistance”, “metal ion resistance”, “toxin production”, “siderophore production”, “attachment and colonization in the plant rhizosphere”, and “plant hormone auxin production” were revealed. Although *nif* gene clusters involved in nitrogen-fixing activity were not found in the strain

### Table 5 Putative genes related to functional enzymes for potential PGPR effects predicted from the genome sequence of *Pseudomonas lutea* OK2 (Continued)

| Attachment and colonization in the plant rhizosphere | secretion system |
| --- | --- |
| KO:K04095* | KO:K03196*, KO3198*, KO3199*, KO3200*, KO3203*, KO3204*, KO3205* |
| KO:K06596* | KO:K11891*, K11892*, K11893*, K11894*, K11895*, K11896*, K11900*, K11901* |
| KO:K08086, K02280 | KO:K11903*, K11904* |
| KO:K02655, K02656, K02662, K02663, K02664, K02665, K02666, K02671, K02672, K02673, K02674, K02676, K02650*, K02652, K02653 | KO:K11905* |
| KO:K02657, K02658 | KO:K11906*, K11907*, K11910* |
| KO:K02659, K02660, K02669, K02670* | Plant hormone auxin biosynthesis |

*Based on the function profiles obtained from the KO database [25, 26], under the IMG-ER pipeline [23]

*Predicted only in the genome sequence of *P. lutea* OK2 (IMG Genome ID 2593339262) upon comparison with the complete genome sequence of *P. rhizosphaerae* IH5 (=DSM 16299T, IMG Genome ID 2593339263) [34]

### Table 6 Average nucleotide identity of the genome sequence of different *Pseudomonas* species with that of OK2

| Strain | Average Nucleotide Identity (%) |
| --- | --- |
| *Pseudomonas syringae* ATCC 19310T | 77.31 |
| *Pseudomonas kilonensis* S20-20T | 76.96 |
| *Pseudomonas protegens* CHAO | 76.86 |
| *Pseudomonas veronii* CIP 104663T | 76.72 |
| *Pseudomonas libanensis* CIP 105460T | 76.48 |
| *Pseudomonas fluorescens* CCM 2115T | 76.45 |
| *Pseudomonas syxantha* IAM 12356T | 76.39 |
| *Pseudomonas rhizosphaerae* IHS5T | 76.39 |
| *Pseudomonas putida* IAM 1236T | 75.59 |
| *Pseudomonas monteilii* CIP 1048883T | 75.39 |
| *Pseudomonas stutzeri* ATCC 17588T | 73.85 |
OK2T, a gene encoding for the nitrogen-fixation protein NifU (KO:K04488) was identified [33].

Within the genus *Pseudomonas sensu stricto*, *P. lutea* OK2T is presented as a group phylogenetically closest to *P. graminis* DSM 11363T [10] and *P. rhizosphaerae* IHS5T [11] (shown in Fig. 1). The majority of the genes in *P. lutea* OK2T were predicted based on the genome of *P. rhizosphaerae* IHS5T (=DSM 16299T, IMG Genome ID 2593339263) [34]. However, genes such as *ldhA* (D-lactate dehydrogenase, KO:K03778), *penP* (beta-lactamase class A, KO:K17836), *marC* (multiple antibiotic resistance protein, KO:K05595), *rcnA* (nickel/cobalt exporter, KO:K08970), *arsH* (arsenical resistance protein ArsH, KO:K11811), *fic* (cell filamentation protein, KO:K04095), and *chpA* (chemosensory pili system protein ChpA, KO:K06596) and the gene clusters coding for enzymes with type IV secretion systems were only annotated in OK2T. Furthermore, pertinent gene clusters for type VI secretion systems, known as a complex multicomponent secretion machine, with bacterial competitions [35–37] were only predicted in the strain OK2T. The type VI secretion system may be related to possible features of bacterial motility/adaptation/competition in the strain. Although the strain *P. graminis* DSM 11363T had similar general features and biochemical properties as strain OK2T, its genome sequence is not yet available.

Average Nucleotide Identity calculations [38] were used to compare the genomes of *P. lutea* OK2T and other sequenced *Pseudomonas* species (Table 6). The strain was found to be most closely related to *Pseudomonas syringae* ATCC 19310T (77.31 % identity), followed by *Pseudomonas kilonensis* 520-20T (76.96 % identity). These values are under the acceptable range of species cutoff values of 95–96 % [39], indicating that *P. lutea* OK2T is different from other sequenced *Pseudomonas* species.

**Conclusions**

We presented here the first genome sequence of *P. lutea* OK2T, a phosphate-solubilizing bacterium isolated from the rhizosphere of grass in northern Spain [8]. This study showed that *P. lutea* OK2T has potential traits including phosphate-solubilizing capability, making it as an effective pseudomonad-PGPR.

Considering a variety of complex conditions that occur in rhizospheres [40], the environmental adaptability of PGPR in *in situ* rhizosphere became an important factor for improved plant growth-promoting capacity. In addition, initial studies focusing on the functional properties of PGPR [31, 32] have led to interest in the comparative analyses of pan-/core-genomes of these bacteria, which are of ecological importance for elucidating the fundamental genotypic features of PGPR under diverse rhizosphere conditions [41, 42]. The genetic information obtained for *P. lutea* OK2T will improve our understanding of the genetic basis of phosphate-solubilizing pseudomonad-PGPR activities and further provide insights into the practical applications of the strain as a biocontrol agent in the field of agriculture.

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**Authors’ contributions**

YK performed the genomic sequencing, genomic analyses, phenotypic characterization of the bacterium, and drafted the manuscript. GP performed the genomic analyses and drafted the manuscript. JHS conceived the study, participated in its design and coordination, and drafted the manuscript. All the authors have read and approved the final manuscript.

**Competing interests**

The authors declare that they have no competing interests.

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