Panacibacter ginsenosidivorans gen. nov., sp. nov., with ginsenoside converting activity isolated from soil of a ginseng field

Muhammad Zubair Siddiqi, Kang Duk Choi and Wan-Taek Im

1Department of Biotechnology, Hankyoung National University, 327 Chungang-no, Anseong-si, Kyonggi-do 17579, Republic of Korea
2Center for Genetic Information, Graduate School of Bio and Information Technology, Hankyoung National University, 327 Chungang-no, Anseong-si, Kyonggi-do 17579, Republic of Korea
3Chemical Research Department, Green Planet Co. Ltd, Okayama ken, tsushima nishizaka2 chome 5-41-203, Okayama, Japan

A ginsenoside-transforming bacterium, designated Gsoil 1550\(^T\), was isolated from soil of a ginseng field and subjected to a polyphasic taxonomic analysis. Colonies of strain Gsoil 1550\(^T\) were yellow, of low convexity and with regular margin. Cells were long rods, 0.5–1.2 \(\mu\)m wide and 1.6–3 \(\mu\)m long. The isolate grew at 10–37 °C and at pH 5–9 on R2A agar medium; maximum growth occurred at 30 °C and pH 6–7. Phylogenetic study based on the 16S rRNA gene sequence positioned Gsoil 1550\(^T\) in a distinct lineage in the family Chitinophagaceae, sharing 92.5–92.8 % sequence similarity with members of the closely related genera Terrimonas, Paralimonas, Sediminibacterium and Parasegetibacter. Strain Gsoil 1550\(^T\) contained menaquinone MK-7 as the predominant quinone, and iso-C\(_{15:0}\), iso-C\(_{17:0}\), 3-OH, C\(_{16:0}\) and iso-C\(_{15:1}\) G as major fatty acids. The DNA G+C content was 44.6 mol%. Strain Gsoil 1550\(^T\) could be distinguished from other members of the family Chitinophagaceae by a number of chemotaxonomic and phenotypic characteristics. The major polar lipid of strain Gsoil 1550\(^T\) was phosphatidylethanolamine. Based on this polyphasic taxonomic analysis, strain Gsoil 1150\(^T\) represents a novel species within a new genus, for which the name Panacibacter ginsenosidivorans gen. nov., sp. nov. is proposed. The type strain of Panacibacter ginsenosidivorans is Gsoil 1550\(^T\) (=KCTC 12658\(^T\)=JCM 31452\(^T\)).

During screening of ginseng field soil bacteria with \(\beta\)-glucosidase activity, which catalyses the bioconversion of major ginsenosides to minor ginsenosides (Kim et al., 2015), a novel bacterium, designated Gsoil 1550\(^T\), was isolated. Phylogenetic analysis allocated strain Gsoil 1550\(^T\) to the family Chitinophagaceae within the phylum Bacteroidetes. The family Chitinophagaceae was recently described by Kämpfer et al. (2011) with Chitinophaga as the type genus. Members of the Chitinophagaceae are usually non-motile, aerobic or facultatively anaerobic with cells that are often thin rod-shaped. Affiliates of this family contain menaquinone MK-7 as the major quinone. The fatty acid profiles include substantial levels of iso-C\(_{15:0}\), iso-C\(_{17:0}\), 3-OH and iso-C\(_{15:1}\) G. Based on polar lipid analyses, most species of the family possess phosphatidylethanolamine (PE) as the major polar lipid (Siddiqi & Im, 2016a, b; Eder et al., 2015; Albert et al., 2014; Lee et al., 2013; Leandro et al., 2013). At the time of writing, the family Chitinophagaceae contained 33 genera, including the recently described members Cnuella takakiae (Zhao et al., 2014), Arachidicoccus rhizosphaerae (Madhaiyan et al., 2015), Flaviaesturariibacter amylovorans (Kang et al., 2015), Hydrobacter penzbergensis (Eder et al., 2015), Dinghuibacter silviterrae (Lv et al., 2016), Pseudobacter ginsenosidimutans (Siddiqi & Im, 2016a) and Compostibacter hankyongensis (Siddiqi et al., 2016c).

Ginseng soil is good habitat for soil-borne microbial communities. Ginseng plants are able to grow in shade without direct sunlight which is propitious for microbial coloniza-

---

**Abbreviation:** PE, phosphatidylethanolamine.

The GenBank/EMBL/DDJB accession number for the 16S rRNA gene sequence of strain Gsoil 1550\(^T\) is KT950744.

Two supplementary figures are available with the online Supplementary Material.
the rhizosphere region of a ginseng plant (Pocheon Province, Korea). To study the bacterial community and explore for novel strains, soil samples were thoroughly suspended in 0.85% saline water, serially diluted and spread onto R2A agar medium (Difco). The plates were incubated at 30°C for 1 week. Single colonies were purified by subculture. Strain Gsoil 1550T was found among the novel stains isolated, and then it was routinely cultured on R2A agar medium at 30°C and preserved at −80°C in a glycerol suspension (25%, v/v).

The DNA of strain Gsoil 1550T was extracted with a DNA extraction kit (Solgent) and PCR-mediated amplification of the 16S rRNA gene and sequencing of the purified PCR product were carried out according to Kim et al. (2015). Full sequences of the 16S rRNA gene were assembled using SeqMan software (DNASTAR). The 16S rRNA gene sequences of related taxa were obtained from the GenBank database or EzTaxon-e server [http://www.ezbiocloud.net/eztaxon; Kim et al. (2012)]. Multiple alignments were performed via the CLUSTAL X program (Thompson et al., 1997). Gaps were edited in the BioEdit program (Hall, 1999). Evolutionary distances were calculated using the Kimura two-parameter model (Kimura, 1983). Phylogenetic trees were reconstructed by using the neighbour-joining, maximum-likelihood and maximum-parsimony methods (Saitou & Nei, 1987; Fitch, 1971), using the MEGA6 program (Tamura et al., 2013) with bootstrap values based on 1000 replications (Felsenstein, 1985).

The almost-complete 16S rRNA gene sequence of strain Gsoil 1550T (1451 nt) was determined and subjected to comparative analysis. Sequence similarity was determined using the EzTaxon-e server (Kim et al., 2012). Phylogenetic analysis based on 16S rRNA gene sequences showed that the novel isolate represents a member of the family Chitinophagaceae, forming a cluster with the genus Parafilimonas within the family Chitinophagaceae (Fig. 1). All representative species of 31 genera of the family Chitinophagaceae were included in the phylogenetic tree reconstruction. Strain Gsoil 1550T shared 16S rRNA gene sequence similarity of less than 92.8% with type species of the genera Terrimonas, Parafilimonas and Sediminibacterium and other members of the family Chitinophagaceae.

For phenotypic and biochemical tests, strain Gsoil 1550T was routinely cultivated on R2A agar medium. Tests for Gram-staining, oxidase, catalase, and hydrolysis of casein, CM-cellulose, DNA, starch and Tween 80 were performed according to the methods of Smibert & Krieg (1994). Cell morphology was examined by using scanning electron microscopy (Hitachi SU-3500) and phase contrast microscopy (Nikon) with cells grown for 2 days on R2A agar medium at 30°C. Cell motility was determined using the hanging drop method. Optimum growth of strain Gsoil 1550T on different media was evaluated using nutrient agar (NA; Difco), trypticase soy agar (TSA; Difco), Luria–Bertani (LB) agar (Difco) and MacConkey agar (Difco) at 30°C for 7 days. Growth at different temperatures (4, 10, 15, 25, 30, 37, 42°C) and various pH values (pH 4–10 at intervals of 1.0 pH unit) was assessed after 7 days of incubation at 30°C using acetate buffer (pH 4–5.5), phosphate buffer (pH 6–8) and Tris buffer (pH 8.5–10) with final concentration of 50 mM in R2A broth. Salinity (1–6%, w/v, NaCl at intervals of 0.5%) was evaluated after 7 days of incubation at 30°C on R2A agar medium. Production of flexirubin-type pigments was determined by the reversible colour shift to red, purple or brown when yellow or orange colonies are covered with aqueous 20% KOH solution (Fautz & Reichenbach, 1980). Tests in the commercial systems API ZYM, API 20NE and API ID 32 GN (bioMerieux) were generally performed according to the manufacturer’s instructions. The API ZYM test strip was read after 4 h of incubation at 37°C, and the other API strips were examined after 2 days at 30°C. Biotransformation of ginsenosides was carried out as described by Kim et al. (2015).

Cells were Gram-stain-negative, aerobic, non-motile, non-spore-forming long rods (Fig. S1, available in the online Supplementary Material), and colonies of strain Gsoil 1550T grown on R2A agar were circular, convex, opaque and yellow after 48 h of incubation at 30°C. Strain Gsoil 1550T grew well on R2A agar medium and weakly on NA, but did not grow on LB agar (Difco), TSA or MacConkey agar (Difco). The isolate was able to transform ginsenosides Rb1, Rc and Rd completely to ginsenoside F2 after 1 day of incubation at 30°C.

Genomic DNA from the novel isolate was extracted and purified as described by Moore & Dowhan (1995) and enzymatically degraded into nucleosides. The G+C content was then determined as described by Mesbah et al. (1989), using a reversed-phase HPLC system (Younglin). The cellular fatty acid profiles of strain Gsoil 1550T and two reference strains (Parafilimonas terrae KACC 17343T and Filimonas lacunae DSM 21054T) were determined using cells grown on R2A agar for 2 days at 30°C. The cellular fatty acids were saponified, methylated and extracted according to the protocol of the Sherlock Microbial Identification System (MIDI). They were then identified by capillary GLC, using version 6.0 of the Microbial Identification software package (MIDI), the TSBA60 database (Sasser, 1990) and a 6890 chromatograph (Hewlett Packard). Cell biomass of strain Gsoil 1550T for isoprenoid quinone analysis was obtained from culture grown in R2A broth for 2 days at 30°C. Collected cells were lyophilized for 24 h and were extracted with chloroform/methanol (2:1, v/v), evaporated under vacuum and re-extracted in n-hexane/water (1:1, v/v). The crude n-hexane/quinone solution was purified using a Sep-Pak Vac silica cartridge (Waters) and subsequently analysed by HPLC, as previously described (Hiraishi et al., 1996). Strain Gsoil 1550T was investigated for its polar lipid content as described by Minnikin et al. (1984). One hundred milligrams of freeze-dried cells was dissolved in methanol/water (10:1, v/v) and stirred well. Then, 2 ml of petroleum ether was added. After centrifugation at 2000 r.p.m. for 5 min, the upper layer was discarded, and the lipid residues were extracted twice with the first extraction using chloroform/
methanol/water at 90:100:30 (by vol.) and the second extraction step at 50:100:40 (by vol.). Chloroform and 0.3% NaCl (1.3 ml each) solution were added to the combined supernatant, mixed thoroughly and centrifuged. The upper layer was then discarded with a pasture pipette and only the bottom layer was used. Polar lipids were dissolved in chloroform/methanol (2:1, v/v), and the samples were then spotted on the corner of the two-dimensional thin layer chromatograph using TLC Kiesel gel 60F254 (Merck) plates (10×10 cm). The polar lipids were developed in the first direction by using chloroform/methanol/water (65:25:4, by vol.), and in the second direction by chloroform/acetic acid/methanol/water (80:15:12:4, by vol.).

The DNA G+C content of the novel isolate was 44.6 mol%, a value within the range of members of the family Chitinophagaceae. The cellular fatty acid profile of strain Gsoil 1550^T is shown in Table 3 below. The predominant fatty acids of strain Gsoil 1550^T were iso-C_{15:0}, iso-C_{17:0} 3-OH, C_{16:0} and iso-C_{15:1} G. Other members of the family Chitinophagaceae have the same major fatty acids but in different relative proportions. The minor fatty acids were C_{10:0}, C_{12:0}, iso-C_{10:0} and anteiso-C_{11:0}. The presence

**Fig. 1.** Phylogenetic tree reconstructed from a comparative analysis of 16S rRNA gene sequences showing the relationships between strain Gsoil 1550^T and other related genera of the family Chitinophagaceae. The tree was made using the maximum-likelihood method with two-parameter distance matrix and complete deletion. Filled circles indicate generic branches that were also recovered by using the neighbour-joining and maximum-parsimony algorithms. Bootstrap values (expressed as percentages of 1000 replications) greater than 60% are shown at branch points. Bar, 0.05 substitutions per nucleotide position.

http://ij.s.microbiologyresearch.org
of these minor fatty acids differentiated strain Gsoil 1550T from related genera of the family Chitinophagaceae as given in Table 3. The polar lipid profile of strain Gsoil 1550T comprised PE as the major polar lipid. The minor polar lipids were five unidentified polar lipids and two unidentified aminolipids (Fig. S2). On the basis of polar lipid analysis the novel isolate shares the same major polar lipid (PE) with the recently described genera 
Pseudobacter
  (Siddiqi & Im, 2016a), 
Compositibacter
  (Siddiqi et al., 2016c), 
Hydrobacter
  (Eder et al., 2015), 
Parafilimonas
  (Kim et al., 2014), 
Heliimonas
  (Leandro et al., 2013) and Asinibacterium
  (Lee et al., 2013). Strain Gsoil 1550T contained MK-7 as the predominant quinone.

From the results of phylogenetic, phenotypic and chemotaxonomic characteristics, strain Gsoil 1550T could not be assigned to any known taxa. Some phenotypic features (Tables 1 and 2), fatty acid profile (Table 3) and 16S rRNA gene sequences clearly differentiated strain Gsoil 1550T from phylogenetically related, recognized taxa and indicate that it represents a novel species of a new genus in the family Chitinophagaceae, for which the name 
Panacibacter ginsenosidivorans
  gen. nov., sp. nov. is proposed.

Description of 
Panacibacter
  gen. nov.

Panacibacter
  (Panac.i.bi.ca.ter. N.L. n. 
Panax
  the ginseng plant; N.L. masc. n. 
bacter
  rod; N.L. masc. n. 
Panacibacter a rod associated with ginseng).

Cells are Gram-stain-negative, catalase-positive, oxidase-negative, aerobic, long rods. The major respiratory quinone is MK-7. The major fatty acids are iso-C15:0, iso-C17:0 3-OH, iso-C16:0 and C15:1 G. A flexirubin-type pigment is produced. The phenotypic differences from other related genera (identified based on EzTaxon-e results) of the family Chitinophagaceae are summarized in Table 1. Differential phenotypic characteristics from the most closely related genera 
Parafilimonas
  and 
Filimonas
  (based on phylogenetic analysis) are shown in Table 2. Phylogenetically, the genus is affiliated to the family Chitinophagaceae. The type species is 

Panacibacter ginsenosidivorans
  sp. nov.

Description of 
Panacibacter ginsenosidivorans
  sp. nov.

Panacibacter ginsenosidivorans
  (gin.se.no.si.di.vo’rans. N.L. n. 
ginsenosidum
  ginsenoside; L. pres. part. adj. 
vorans eating, devouring; N.L. part. adj. 
ginsenosidivorans ginsenoside-devouring).

Shows the following properties in addition to those given in the genus description. Cells are circular, opaque, yellow, 0.5–1.2 μm wide and 1.6–3 μm long. Growth occurs at 10–37°C and at pH 5–9. Optimum growth occurs at 30 °C and pH 6–7 in the absence of NaCl. Does not hydrolyse 
Tween
  80, starch, casein, xylan, CM-cellulose or DNase. In 
API
  20NE and 
API
  ZYM tests, positive for aesculin hydrolysis, alkaline phosphatase, esterase (C4), β-galactosidase,
Panacibacter ginsenosidimutans gen. nov., sp. nov.

Table 2. Differential phenotypic characteristics between strain Gsoil 1550T and closest related species of the family Chitinophagaceae

Strains: 1, Gsoil 1550T; 2, Parafilimonas terrae KACC 17343T; 3, Filimonas lacunae DSM 21054T. Data presented are from this study except where indicated. All strains are positive for alkaline phosphatase, esterase, leucine arylamidase, valine arylamidase, cystine arylamidase, 1-ramhnoose, sucrose, potassium 5-ketogluconate, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase, α-fucosidase, 4-nitrophenyl-β-D-galactopyranoside, l-arabinose and maltose. Similarly, all strains are negative for lipase, reduction of nitrates, indole production, arginine dihydrolase, urease, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, trisodium citrate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, malic acid and phenylacetic acid. +, Positive; –, negative; ND, no data.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Salinity range for growth (% NaCl, w/v)</td>
<td>0</td>
<td>1.0*</td>
<td>1.0†</td>
</tr>
<tr>
<td>pH range</td>
<td>5–9</td>
<td>5–8*</td>
<td>5–8†</td>
</tr>
<tr>
<td>Enzyme activity:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Esterase lipase</td>
<td>+</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Trypsin</td>
<td>+</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>α-Chymotrypsin</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>β-Glucuronidase</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Utilization of:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D-Mannose</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>N-Acetyl-glucosamine</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Malic acid</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>D-Ribose</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Inositol</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Glycogen</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>D-Glucose</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Salicin</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Melibiose</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>D-Sorbitol</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>L-Histidine</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Potassium 2-ketogluconate</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>l-Proline</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Major polar lipid</td>
<td>PE</td>
<td>PE*</td>
<td>ND</td>
</tr>
</tbody>
</table>

Table 3. Cellular fatty acid profiles of strain Gsoil 1550T and phylogenetically related species of the family Chitinophagaceae

Strains: 1, Gsoil 1550T; 2, Parafilimonas terrae KACC 17343T; 3, Filimonas lacunae DSM 21054T. All data are taken from this study. Results are presented as percentages of the total fatty acids; the major fatty acids (>10%) are in bold type; fatty acids that represent <1% in all strains are omitted. –, Not detected.

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Saturated</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C10:0</td>
<td>1.0</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>C12:0</td>
<td>2.0</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>C14:0</td>
<td>1.3</td>
<td>1.8</td>
<td>1.4</td>
</tr>
<tr>
<td>C16:0</td>
<td>14.3</td>
<td>3.5</td>
<td>12.0</td>
</tr>
<tr>
<td>Branched</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>iso-C15:0</td>
<td>1.0</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>iso-C17:0</td>
<td>1.0</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>anteiso-C11:0</td>
<td>2.6</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>iso-C14:0</td>
<td>–</td>
<td>–</td>
<td>1.0</td>
</tr>
<tr>
<td>iso-C15:0</td>
<td>24.3</td>
<td>41.3</td>
<td>25.8</td>
</tr>
<tr>
<td>iso-C15:0 3-OH</td>
<td>3.7</td>
<td>3.4</td>
<td>2.4</td>
</tr>
<tr>
<td>anteiso-C15:0</td>
<td>–</td>
<td>1.7</td>
<td>1.8</td>
</tr>
<tr>
<td>iso-C16:0</td>
<td>–</td>
<td>–</td>
<td>2.0</td>
</tr>
<tr>
<td>iso-C18:0 3-OH</td>
<td>2.8</td>
<td>1.6</td>
<td>TR</td>
</tr>
<tr>
<td>C16:0 3-OH</td>
<td>3.6</td>
<td>3.6</td>
<td>3.8</td>
</tr>
<tr>
<td>iso-C17:0</td>
<td>–</td>
<td>–</td>
<td>1.6</td>
</tr>
<tr>
<td>iso-C17:0 3-OH</td>
<td>19.8</td>
<td>21.2</td>
<td>16.0</td>
</tr>
<tr>
<td>C17:0 2-OH</td>
<td>2.0</td>
<td>2.4</td>
<td>–</td>
</tr>
<tr>
<td>Unsaturated</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>iso-C15:1 G</td>
<td>17.2</td>
<td>15.7</td>
<td>15.8</td>
</tr>
<tr>
<td>C16:1ω5c</td>
<td>–</td>
<td>–</td>
<td>2.6</td>
</tr>
<tr>
<td>Summed feature*</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3; C16:1ω7c and/or C16:1ω6c</td>
<td>3.2</td>
<td>3.6</td>
<td>10.9</td>
</tr>
</tbody>
</table>

*Summed features represent groups of two or three fatty acids that could not be separated by GLC with the MIDI system.

leucine arylamidase, valine arylamidase, cystine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase activities; negative for nitrate reduction, indole production, lipase dihydrofolate (C14) and urease activities. In API ID 32 GN and API 20NE strips, utilizes various sugars such as l-arabinose, maltose, potassium 5-ketogluconate, sucrose and l-ramhnoose. Does not assimilate itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, 3-hydroxybenzoic acid, L-serine, D-mannitol, L-fucose, propionic acid, capric acid, valeric acid, trisodium citrate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, potassium gluconate, adipic acid or phenylacetic acid. Results of carbon assimilation tests as sole carbon sources (API 20NE and ID 32 GN) and enzyme activities (API ZYM) are given in Table 2. The minor fatty acids are C10:0, C12:0, C14:0, iso-C10:0, iso-C11:0, anteiso-C11:0, iso-C15:0, 3-OH, iso-C16:0, 3-OH, C16:0 3-OH, C17:0 2-OH and summed feature 3 (C16:1ω7c and/or C16:1ω6c). In addition to the major polar lipid (PE), five unidentified polar lipids and two unidentified aminolipids are also present.

The type strain, Gsoil 1550T (=KCTC 12658T=JCM 31452T), was isolated from soil of a ginseng field collected in the Republic of Korea. The DNA G+C content of the type strain is 44.6 mol%.
Acknowledgements

This research was supported by the project on survey and excavation of Korean indigenous species of the National Institute of Biological Resources (NIBR) under the Ministry of Environment and by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (2015R1D1A1A01060255), Republic of Korea.

References


