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# Chryseobacterium ginsengiterrae sp. nov., a bacterium with ginsenoside converting activity isolated from soil of a ginseng field

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## **Objectives**

A Gram-negative, aerobic, non-motile, yellow-pigmented, rod-shaped bacterium, designated strain DCY70<sup>T</sup>, was isolated from the soil of a ginseng field in South Korea.

Strain DCY70<sup>T</sup> was grown well at 25 - 30 °C and pH 6.0 - 6.5 in R2A broth. On the basis of 16S rRNA gene sequence similarity data, strain DCY70<sup>T</sup> was shown to belong to the family Flavobacteriaceae and was most closely related to T(97.5%), PSD1-4<sup>T</sup>(97.1%) and CTM<sup>T</sup>(96.8%).

The G+C conten to the genomic DNA of strain DCY $70^{T}$  was 36.1mol%. The predominant quinone was MK-6(90.9%) and MK-7(9.15%) supported the affiliation of strain DCY $66^{T}$  to the genus The result so physiological and biochemical tests were enabled strain DCY $66^{T}$  to be differentiated genotypically and phenotypically from recognized species of the genus. The isolate there for erepresent sanovelspecies, for which the name sp.nov. isproposed. The type strain is DCY $70^{T}$ .

#### Materials and Methods

The strain DCY70<sup>T</sup> was isolated from oilo faginseng fieldin South Korea. R2A agar, tryptic soy broth, macconkey and nutrient broth were purchased from Difco. The 60 F-254 Silica gel plate (Merck) was used for thin-layer chromatography (TLC).

The 16S rRNA gene sequence of strain DCY70<sup>T</sup> was amplified from the chromosomalDNA using universal bacteriaprimer set27F, 518Fand1492R,(Lane,1991) and comparis on with other *Chryseobacter* species were measure dusing the EzTaxonserver (Chun*etal.*,2007). The G+C content was determined by HPLC (Mesbah et al., 1989). Isoprenoid quinones were analyzed by HPLC as described by Collins (1985)

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### Results

The 16S rRNA gene sequence of strain DCY70<sup>T</sup> was compared with existing sequences from the public databases using the EzTaxonserverv.2.1(Chung*etal.*,2007) place the new isolatein the genus *Chryseobacterium*. The sequence similarity values to recognized members of the genus *Chryseobacterium* were as follows:  $^{T}$  (97.5%), Chryseobacterium soldanellicola PSD1- $^{4}$ (97.1%) and CTM<sup>T</sup>(96.8%).

Strain DCY70<sup>T</sup> was showed positive for alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, acid phosphatase naphtol-AS-BI-phosphohydrolase,  $\beta$  - glucosidase, N - acetyl -  $\beta$  - glucosaminidase, and weakly positive for,  $\alpha$  - chymotrypsin and,  $\alpha$  - glucosidase and negative for lipase (C14),  $\alpha$  - galactosidase,  $\beta$  - galactosidase,  $\beta$  - glucuronidase,  $\alpha$  - glucosidase,  $\alpha$  - mannosidase and  $\alpha$  - fucosidase. The DNA G+C content of strain DCY70<sup>T</sup> was 36mol%(HPLC), which is similar to other *Chryseobacter*species(Vandamme *et al.,* 1994). The predominant quinone was MK-6 (90.9%) and MK-7 (9.15%). Strain DCY70T was converted ginsenoside Rb1 into F2 and compound K