Reclassification of *Streptomyces flavidofuscus* as a synonym of *Nocardiopsis dassonvillei* subsp. *dassonvillei*

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The genus *Streptomyces* is the largest genus of actinomycetes, containing more than 500 species with validly published names. They are characterized phenotypically by morphology and the presence of a type I cell wall. The genus *Nocardiopsis* was established by Meyer (1976) on the basis of morphological characteristics and the presence of cell-wall type III/C. The genus currently comprises more than 20 species. Members of this taxon are characterized chemotaxonomically by possessing phosphatidylcholine and phosphatidylmethylethanolamine as diagnostic phospholipids, menaquinone (MK)-10 with variable degrees of saturation (Collins et al., 1977), iso-, anteiso- and 10-methyl-branched fatty acids (fatty acid type 3d sensu Lechevalier & Lechevalier, 1970) and mycolic acids. They contain the acetyl type of muramic acid and have a G+C content of 64–69 mol% (Grund & Kropenstedt, 1990).

During the course of quality control studies of the collection of the NITE Biological Resource Center (NBRC), phylogenetic analysis based on 16S rRNA gene sequences of actinomycetes revealed that *Streptomyces flavidofuscus* NBRC 15404T formed a cluster with *Nocardiopsis dassonvillei* and *Nocardiopsis synnemataformans*. Strain NBRC 15404T contained meso-diaminopimelic acid as a cell-wall diamino acid and DNA–DNA hybridization studies also showed that *S. flavidofuscus* NBRC 15404T was a close relative of *N. dassonvillei* subsp. *dassonvillei* NBRC 14626T. Based on chemotaxonomic, phenotypic and genetic analysis of the type strain, *Streptomyces flavidofuscus* should be reclassified as a later heterotypic synonym of *Nocardiopsis dassonvillei* subsp. *dassonvillei*.

Sequence analysis revealed that *S. flavidofuscus* NBRC 15404T was incorporated in a monophyletic cluster with members of the genus *Nocardiopsis* (Fig. 1). The binary similarity value of the 16S rRNA gene sequence of *S. flavidofuscus* NBRC 15404T was 99.5% with *Nocardiopsis dassonvillei* subsp. *dassonvillei* NBRC 14626T. Based on chemotaxonomic, phenotypic and genetic analysis of the type strain, *S. flavidofuscus* has been confirmed by using multiple strains preserved in different culture collections.

Cell-wall amino acids, whole-cell sugars, cellular fatty acids, isoprenoid quinones and DNA base composition were analysed as described previously (Tamura et al., 1994). Freeze-dried cells for chemotaxonomic analyses were prepared from cultures grown in yeast extract-glucose broth [containing (1%) 10 g yeast extract and 10 g D-glucose, pH 7.2] on a rotary shaker at 28 °C for 3 days. The predominant menaquinones were MK-10(H₆) and MK-10(H₈), with MK-10(H₄), MK-9(H₆) and MK-9(H₈) as minor components. The strain contained meso-A₂pm, alanine and glutamic acid in the cell wall and ribose and mannose as whole-cell sugars. The major cellular fatty acids were iso-C₁₆:₀ (50%), 10-methyl C₁₈:₀ (12%) and anteiso-C₁₇:₁ (10%). The DNA G+C content was 71 mol%. The chemotaxonomic characteristics of *S. flavidofuscus* NBRC 15404T were consistent with those of the genus *Nocardiopsis*. 
The microplate hybridization method developed by Ezaki et al. (1988, 1989) was used for the determination of DNA–DNA relatedness. The relatedness values of S. flavidofuscus NBRC 15404T to N. dassonvillei subsp. dassonvillei NBRC 14626T, N. dassonvillei subsp. albirubida NBRC 13392T and N. symnemataformans NBRC 102581T were 81–87, 55–79 and 55–63 %, respectively. N. dassonvillei subsp. albirubida NBRC 13392T exhibited high relatedness (59–73 %) to N. dassonvillei subsp. dassonvillei NBRC 14626T, as reported by Evtushenko et al. (2000). Further, N. symnemataformans NBRC 102581T exhibited 43–61 % relatedness to N. dassonvillei subsp. dassonvillei NBRC 14626T and 53–79 % relatedness to N. dassonvillei subsp. albirubida NBRC 13392T. These species and subspecies are genetically closely related to each other.

The cultural characteristics of S. flavidofuscus NBRC 15404T were similar to those of N. dassonvillei subsp. dassonvillei NBRC 14626T, i.e. they produced a pale-brown soluble pigment in NBRC medium 229, [containing (l-1) 5 g yeast extract, 50 g glycerol, 1 g CaCO3 and 20 g agar, pH 7.3; NBRC catalogue] and developed colourless to pale-brown colonies on NBRC medium 229, yeast extract-starch agar, pH 7.3; NBRC catalogue [ISP 2; Shirling & Gottlieb, 1966]. However, S. flavidofuscus NBRC 15404T differed from N. dassonvillei subsp. dassonvillei NBRC 14626T with regard to the production of a pale-brown soluble pigment on yeast extract-starch, Bennett’s maltose and yeast extract-malt extract agar.

The results of the present study revealed that strain NBRC 15404T, the type strain of S. flavidofuscus, was identified as a strain of N. dassonvillei subsp. dassonvillei. The identity of the 16S rRNA gene sequence of strain NBRC 15404T to that of NRRL B-16366T strongly suggests that this is not merely true for this particular strain but is generalized to the concept of the species. Therefore, the name Streptomyces flavidofuscus Preobrazhenskaya 1986 should be treated as a later heterotypic synonym of Nocardiosis dassonvillei subsp. dassonvillei (Brocq-Rousseau 1904) Meyer 1976.

References


