

COMMUNICATIONS TO THE EDITOR

Reclassification as a *Nonomuraea* sp. of the Strain ATCC 39727, Producing the Glycopeptide Antibiotic A40926

The glycopeptide antibiotic A40926 is produced by the actinomycete strain ATCC 39727, originally classified, on the basis of morphology and cell-wall composition, as a member of the genus *Actinomadura*¹⁾. In the last decade, 16S rRNA gene (16S rDNA) sequence-based phylogenetic analysis has been widely applied for classification of bacteria. To this respect, actinomycete taxonomy has been subjected to revisions allowing the clarification of relationships at various taxonomic levels²⁾. In 1990 KROPPESTEDT *et al.*³⁾ proposed the transfer of several *Actinomadura* species to the genus *Microtetraspora* and the taxonomic revision of the two genera. The latter genus, however, has later been emended and several species (namely, all those originally included in the genus *Actinomadura*) transferred to the new genus *Nonomuraea* on the basis of 16S rDNA sequence analysis⁴⁾.

Strain ATCC 39727 is industrially important as the producer of A40926, the precursor of the antibiotic dalbavancin, currently under clinical development⁵⁾. Thus, it was important to classify this strain according to the most recent taxonomy.

Previously, 1147 nt of the 16S rDNA sequence of strain ATCC 39727 were deposited to GenBank (AF135374). Following published procedures⁶⁾, we expanded this sequence to 1460 nt (corresponding to 94.6% of the *E. coli* sequence, accession number AJ582011). Database searches revealed that the most closely related sequences corresponded to the 16S rDNA of several *Nonomuraea* species, all having over 98% identity with that of ATCC 39727. Pairwise comparison with the 16S rDNA sequences of *Actinomadura madurae* DSM 43067^T and *Microtetraspora glauca* DSM 43311^T (type species of these two genera) showed much lower identities, *i.e.* 93.4% and 95.5% respectively.

The 16S rDNA sequence of strain ATCC 39727 was then aligned with the 16S rDNA sequences of the type species of all genera within the suborder *Streptosporangineae*, to which *Actinomadura*, *Microtetraspora* and *Nonomuraea*

belong, as well as with that of several *Nonomuraea* species. The resulting phylogenetic tree (Fig. 1) clearly shows that strain ATCC 39727, together with all the *Nonomuraea* strains, forms a distinct clade within the family *Streptosporangiaceae*. In this tree, the three validly described *Microtetraspora* species form a coherent cluster, clearly distinguished from *Nonomuraea*.

The data from the fatty acid profile are in agreement with this assignment. The major fatty acids of *Actinomadura* spp. are hexadecanoic, 14-methylpentadecanoic (*iso*-16:0) and 10-methyl-octadecanoic acid, while *Nonomuraea* and *Microtetraspora* contain high amounts of *iso*-16:0 with a significant fraction of 10-methyl-heptadecanoic acid (10Me-17)³⁾. In *Microtetraspora* the amount of *iso*-16:0 is more than twice that of 10Me-17, while for *Nonomuraea* the levels of *iso*-16:0 and 10Me-17 are either comparable or the latter is more abundant⁴⁾. The major fatty acid of strain ATCC 39727 is 10Me-17, with a slightly smaller amount of *iso*-16:0⁷⁾.

From the phylogenetic analysis and the fatty acid profiles we can thus conclude that strain ATCC 39727 belongs to the genus *Nonomuraea*.

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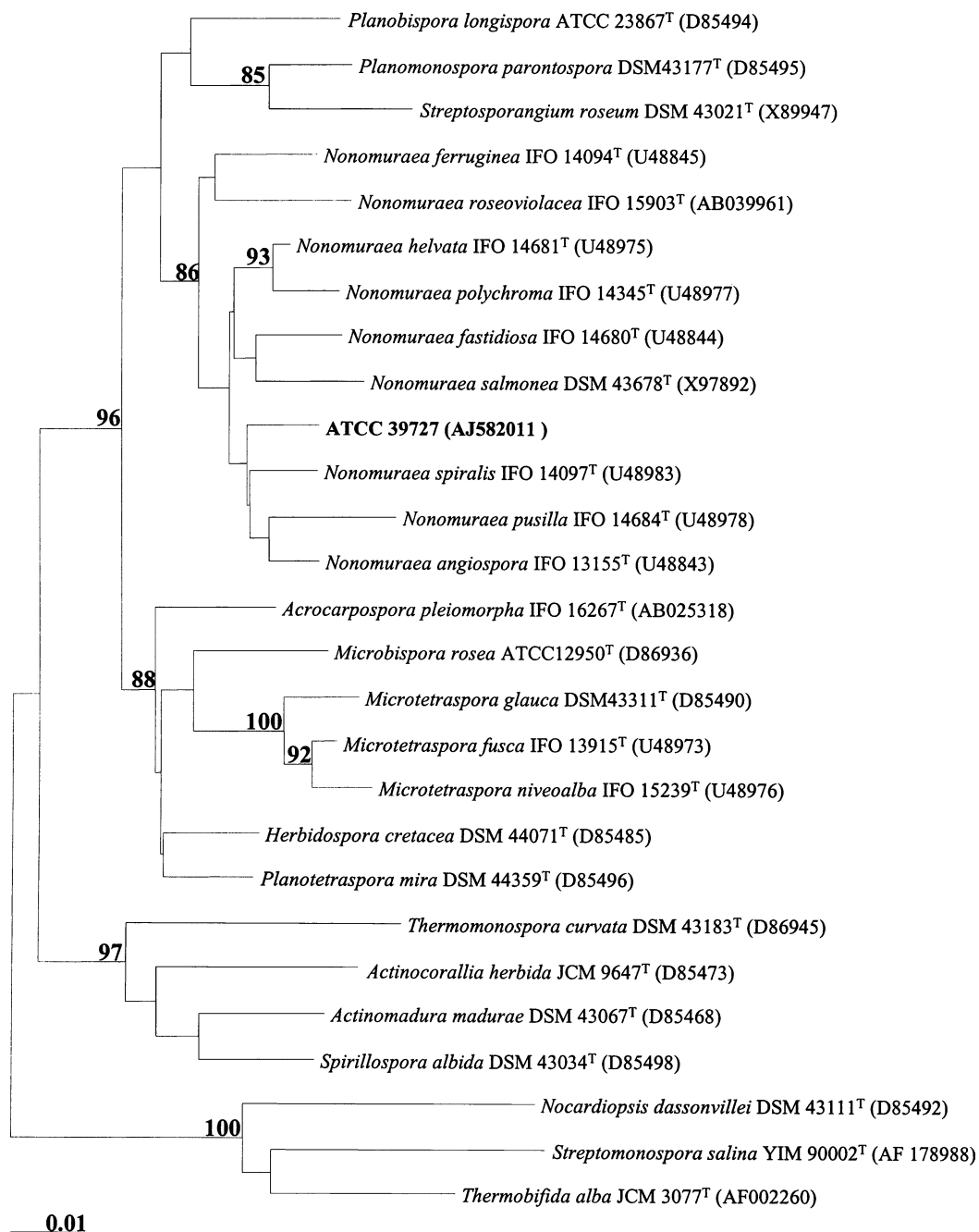
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Fig. 1. Neighbor-Joining tree showing phylogenetic placement of strain ATCC 39727 within the suborder *Streptosporangineae*.



The tree is based on 1440 unambiguously aligned positions within 16S rDNA, and was rooted using the 16S sequence of *Thermobispora bispora* ATCC 19993^T (U58523) as the outgroup. The accession numbers of the corresponding 16S sequences are indicated in parentheses. Numbers at nodes are bootstrap values based on 100 resamplings, only values above 80 are shown. Scale bar: 1 inferred substitution per 100 nucleotides.

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