

Neisseria weaveri Andersen *et al.* 1993 is a later heterotypic synonym of *Neisseria weaveri* Holmes *et al.* 1993

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Two species of the genus *Neisseria*, namely *Neisseria weaveri* Andersen *et al.* 1993 and *Neisseria weaveri* Holmes *et al.* 1993, were simultaneously proposed and described in the same volume of *International Journal of Systematic Bacteriology*, and have been maintained as heterotypic homonyms. However, the identical 16S rRNA gene sequence and high (99.1 %) average nucleotide identity (ANI) between the genome sequences of the two type strains implied that these two taxa should be united as a single genomic species. To clarify their taxonomic status, phenotypic properties including enzymic activities and substrate-utilization profiles were investigated. The results demonstrated that the two taxa have no pronounced differences and should constitute a single species. Therefore, the reclassification of *N. weaveri* Andersen *et al.* 1993 as a later heterotypic synonym of *N. weaveri* Holmes *et al.* 1993 is proposed.

Neisseria weaveri Andersen *et al.* 1993 and *Neisseria weaveri* Holmes *et al.* 1993 are homonyms with two different type strains. The two species were described in the same volume of *International Journal of Systematic Bacteriology* (IJSB) (Andersen *et al.*, 1993; Holmes *et al.*, 1993), and erroneously authorized as two validly published names (Validation List no. 47). Moreover, the name *N. weaveri* Andersen *et al.* is illegitimate because *N. weaveri* Holmes *et al.* 1993 has page precedence. Our recent genome-based study revealed that the two type strains are closely related, sharing an average nucleotide identity (ANI) of 99.1 % and 100 % 16S rRNA gene sequence similarity (Yi *et al.*, 2012a). Because an ANI of 95–96 % and a 16S rRNA gene sequence similarity of 98.65 % has been suggested as the substitute for a DNA–DNA hybridization value of 70 %, the accepted threshold value demarcating bacterial species (Auch *et al.*, 2010; Goris *et al.*, 2007; Kim *et al.*, 2014; Konstantinidis & Tiedje, 2005; Richter & Rosselló-Móra, 2009), the values observed for the homonyms clearly indicated that the two taxa constitute a single species. Based on the comparative genomic data, reclassification of *N. weaveri* Andersen *et al.* 1993 was suggested (Yi *et al.*, 2012a). However, the taxonomic proposal was not accompanied by a proper protologue for the united taxon, and thus was only accepted as an opinion and announced in the List of Changes in Taxonomic Opinion no. 16 (Yi *et al.*, 2012b). In this study, we aimed to

resolve the long-standing taxonomic confusion between the two species based upon the previously reported phylogenetic relationship and newly determined phenotypic properties.

The type strains of *N. weaveri* Holmes *et al.* 1993 (LMG 5135^T) and *N. weaveri* Andersen *et al.* 1993 (ATCC 51223^T) were obtained from the respective culture collections and maintained on brain heart infusion agar (BD) at 37 °C. The physiological/biochemical properties were examined using the API NH and API ZYM (bioMérieux) bacterial identification kits according to the manufacturer's instructions. No striking differences were found between the two taxa. The two type strains were distinguishable only by the presence/absence of valine arylamidase; LMG 5135^T was weakly positive while ATCC 51223^T was negative. The results of biochemical and physiological tests are presented in the species description.

Based on the results presented, it is proposed that the two species be united, namely *N. weaveri* Andersen *et al.* 1993 and *N. weaveri* Holmes *et al.* 1993. In accordance with Rules 51b (4) and 24b (2) of the Bacteriological Code (Lapage *et al.*, 1992), *N. weaveri* Andersen *et al.* 1993 should be reclassified as a later heterotypic synonym of *N. weaveri* Holmes *et al.* 1993.

Emended description of *Neisseria weaveri* Holmes *et al.* 1993

The characteristics of this species are as described by Holmes *et al.* (1993), with the following amendments. As determined using the API NH kit, cells produce proline

Abbreviation: ANI, average nucleotide identity.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of *Neisseria weaveri* NCTC 12742^T is KM610326.

arylamidase, but not penicillinase, ornithine decarboxylase, urease, lipase, alkaline phosphatase, γ -glutamyltransferase or β -galactosidase. Cells do not produce indole from tryptophan, or acid from glucose, fructose, maltose or sucrose. As determined using the API ZYM kit, cells produce esterase (C4) and leucine arylamidase, but not alkaline phosphatase, esterase lipase (C8), lipase (C14), cystine arylamidase, trypsin, α -chymotrypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α -galactosidase, β -galactosidase, β -glucuronidase, α -glucosidase, β -glucosidase, *N*-acetyl- β -glucosaminidase, α -mannosidase or α -fucosidase. The reaction for valine arylamidase is variable depending on the strain. The DNA G + C content is 49 mol%.

The type strain is NCTC 12742^T (=LMG 5135^T=CCUG 4007^T=ATCC 51410^T=CIP 103940^T=ISL775/91^T). The GenBank accession numbers for the 16S rRNA gene sequence and whole genome sequence of the type strain are KM610326 and AFWQ00000000, respectively.

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