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TRANSFER OF THE ORGANISM NAMED NEISSERIA
CATARRHALIS TO BRANHAMELLA GEN. NOV.

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ABSTRACT. Neisseria catarrhalis differs from the type species of the genus Neisseria and six other species of this genus. It is proposed that this organism be transferred to Branhamella gen. nov., with the type species Branhamella catarrhalis (Frosch and Kolle) comb. nov. (Basionym Mikrokokkus catarrhalis Frosch and Kolle 1896, 154). Strain Ne 11 (American Type Culture Collection no. 25238) is proposed as the neotype strain.

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Neisseria catarrhalis is a familiar organism. However, both its name and its taxonomic position need to be reviewed. The combination Neisseria catarrhalis (Frosch and Kolle 1896) Holland 1920 has been widely used (2, 5). However, it was not validly published by Holland (6), and apparently the name has not been validly published by any author subsequently. The basionym of the taxon under consideration is Mikrokokkus (sic) catarrhalis Frosch and Kolle in Flügge 1896, 154. Index Bergeyana (6, p. 714) gives this name as validly published, but illegitimate (rule 24b); however, Erwin F. Lessel (personal communication 1969) noted that according to the information given in Index Bergeyana, "catarrhalis" is the earliest available specific epithet, and thus appears to be legitimate.

The species currently named N. catarrhalis differs from the type of the genus Neisseria (N. gonorrhoeae) and from six other species currently placed in the genus Neisseria (9).

A new generic name is proposed, with the transfer of Neisseria catarrhalis to the new genus as its type species. The reasons for this proposal are summarized below.

The base composition and transforming activities of deoxyribonucleic acid (DNA) preparations from representative

strains have revealed high degrees of similarity between each of six species of *Neisseria*: *N. meningitidis*, *N. perflava*, *N. flava*, *N. subflava*, *N. sicca* and *N. flavescens* (9). Moreover, *N. gonorrhoeae* shows close relationships with *N. meningitidis* and *N. perflava* (8, 13, 16). In marked contrast, genetic transformation (specifically, a transfer of information conveying streptomycin resistance) between *N. catarrhalis* and the other species is negligible (9), although high frequencies of transformation occur between various strains of *N. catarrhalis* (10). The bases adenine, thymine, guanine and cytosine are present in about equal proportions in DNA preparations from the seven *Neisseria* species; in contrast, adenine and thymine predominate in the DNA of *N. catarrhalis*. In terms of moles percent guanine + cytosine the values center around 50 for the former, and range from 40-43 for six strains of *N. catarrhalis* (9, 10, 16). In addition, DNA base analyses of sixteen different strains of *N. catarrhalis* have been made in two other laboratories. The moles percent guanine + cytosine of strains studied by Bøvre (4) averaged 41-42, and the range reported by Baumann et al. (1) was 40-44. Catlin and Cunningham (7, 9, 10) considered that the differences of DNA composition and the barrier to successful transfer of genetic information between the organisms indicate that there are few or no homologies of DNA base sequences. Results of determinations of base sequence homologies by DNA hybridization (13, 14) provided confirmatory evidence of this view and of the difference between *N. catarrhalis* and the other *Neisseria* species mentioned above.

The difference of nearly 10% in overall DNA base content and the low degree of DNA homology testify to the magnitude of the hereditary differences between *N. catarrhalis* and the other species of *Neisseria*. It follows that there must be extensive differences of cellular composition or physiology (7, 9, 10, 16). Examples of such differences have been found in recent studies of fatty acid composition (15). Six strains of *N. catarrhalis* produce relatively large amounts of decanoic acid, a fatty acid not detected among a variety of other species of *Neisseria*. Moreover, the respective fatty acid profiles differ (15). Other properties undoubtedly will be found to differ when the appropriate tests are performed.

Various investigators have questioned the inclusion of *N. catarrhalis* in the genus *Neisseria* or have suggested removing it (1, 3, 4, 9, 12, 13, 15). Henriksen and Bøvre (12) felt that it would be acceptable to establish a new genus for *N. catarrhalis*, but preferred to transfer this species to the

genus Moraxella, thereby combining cocci and rods. Baumann et al. (1) considered that the assignment of N. catarrhalis to a new genus would be justified. No new generic name was suggested by any of these authors.

The foregoing evidence, I believe, justifies the transfer of the currently named Neisseria catarrhalis to a new genus. The proposed new genus is Branhamella, named in honor of the late Sara Branham who contributed to our understanding of the neisserias. One species only is proposed, but others may be transferred to Branhamella in the future.

Branhamella gen. nov.

Cocci commonly arranged in pairs with adjacent sides flattened; Gram-negative with a tendency to resist decolorization. No formation of endospores; nonmotile. Growth is aerobic and occurs on customary media lacking blood. Cytochrome oxidase-positive; catalase-positive; nitrates usually reduced; acid not produced from carbohydrates. Deoxy-ribonucleic acid composition: moles percent guanine + cytosine ranges from 40 to about 45. Parasites of mucous membranes of mammals. Differs from Neisseria in DNA base content and fatty acid composition; few or no genetic affinities with Neisseria.

Branhamella is to be included in the family Neisseriaceae Prévot 1933, 119. The type species is Branhamella catarrhalis comb. nov.

Branhamella catarrhalis comb. nov.

Cellular morphology: Gram-negative cocci, commonly 0.6-1.0 μ diameter. Sometimes single, but more often arranged in pairs with adjacent sides flattened; occasionally observed in groups of four as a result of characteristic division in two successive planes at right angles to one another.

Colonies: on blood agar nonhemolytic, white or grayish, small, convex, entire margin later becoming irregular; often friable, sometimes butyrous consistency.

Growth characteristics: Aerobic. Optimum temperature about 37°C but growth occurs at 22°C. In broth often little turbidity, but with a granular sediment and surface ring. Growth occurs on nutrient agar, and in a medium composed of amino acids, mineral salts, biotin, and with lactate or succinate as principal carbon and energy source.

Physiological activities: oxidase reaction positive with dimethyl- and tetramethyl-p-phenylenediamine. No acid from carbohydrates; polysaccharide not produced from

sucrose. Nitrate reduced to nitrite and beyond. Positive tests for catalase, lipase, extracellular deoxyribonuclease. Negative tests for extracellular gelatinase, urea hydrolysis, hydrogen sulfide and indole production.

Cellular fatty acids; include decanoic acid.

DNA base composition: moles percent guanine + cytosine 40-44.

Response to antibiotics: highly susceptible to penicillin (commonly inhibited by 0.1 unit of penicillin G/ml) and many other antibiotics. Commonly resistant to vancomycin at a concentration of 5 µg/ml.

Habitat: mucous membranes of the upper respiratory tract. Strains are occasionally responsible for disease.

The proposed neotype is strain Ne 11 (American Type Culture Collection no. 25238), which has been described by several investigators (1, 3, 4, 9, 10). The brief description of Mikrokokkus catarrhalis given by Frosch and Kolle (11) in 1896 is consistent with the present conception of Branhamella catarrhalis.

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