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## Difficult separation of *Haemophilus influenzae* from the closely related but less pathogenic *Haemophilus haemolyticus*: Comparison of 16S rRNA, MLSA and full genomic content

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Non-hemolytic variants of *Haemophilus haemolyticus* are difficult to differentiate from *Haemophilus influenzae*, despite a wide difference in pathogenic potential. We characterized a challenging set of 60 clinical strains by multi-locus sequence analysis (MLSA) and near-full length 16S rRNA gene sequencing. MLSA unambiguously allocated all study strains to either of the two species, while identification by 16S rRNA sequence was inconclusive for three strains. Notably, the two methods yielded conflicting identifications for two strains. Most of the "fuzzy species" strains were *H. influenzae* that had undergone complete deletion of the fucose operon. Such strains, which are untypeable by the *H. influenzae* MLST scheme, have sporadically been reported and predominantly belong to a single branch of *H. influenzae* MLSA phylogenetic group-II. We also found evidence of interspecies recombination between *H. influenzae* and *H. haemolyticus* within the 16S rRNA genes. Full-genome sequences are presently being analyzed.

### Biography

Niels Norskov-Lauritsen is a Senior Consultant and Associate Professor of Clinical Microbiology at Aarhus University Hospital, Denmark. He has completed his Medical education at Aarhus University and received his PhD in Microbiology at the University of Copenhagen, Denmark and his DMSc at the University of Aarhus. He is a Member of the sub-committee on the Taxonomy of Pasteurellaceae under the International Committee on Systematics of Prokaryotes. He is a Principal Investigator at Aarhus University, focusing on cystic fibrosis microbiology, antimicrobial resistance and taxonomy of Pasteurellaceae.

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