

A308

Polyphasic Identification of *Tsukamurella* Isolate
Associated with Activated Sludge Foam

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Tsukamurella strain associated with extensive foaming in the aeration basin of activated sludge process was isolated and analyzed with phenotypical, chemotaxonomical and phylogenetical methods. Whole cell sugar pattern of two isolates were pattern A. And the strain contained MK-9(H₀). Then, the almost complete sequences of the 16S rRNA genes (rDNAs) of isolate was determined and compared by using several tree-making algorithms. Strain *Tsukamurella* sp. SCNU5 was distinct from known type strains of genus *Tsukamurella*. BOX1- and REP-PCR pattern confirmed the phylogenetic analysis. Chemical fingerprinting obtained with PyMS also showed the possibility of isolate SCNU5 as novel species. It proposed that presence of the pathogens for chronic lung infections within foams can cause the public health problem as well as render the process inefficient.

A309

Streptomyces Isolate Associated with Activated Sludge Foam

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One Streptomyces strain(SCNU9) was isolated from activated sludge foam, and analyzed with phenotypic and phylogenetic methods. The phenotypic and phylogenetic analysis showed that the strain differ from other *Streptomyces* species. The isolate was identified as cluster 15(*S. chromofuscus*) with probability identification matrix. While, among 50 unit characters more than 10 ones of strain SCNU9 differ from the strains of cluster 15. BOX1- and REP-PCR revealed that the isolate was clearly distinct from strains of that cluster. Otherwise, the number of different nucleotides of 16S rDNA between strain SCNU9 and *S. rutgersensis* which was revealed as the nearest neighbor, phylogenetically, was 30. Moreover, the strains SCNU9 was associated with the foam of sludge, this means the ecological specificity of the isolates. Thus the authors proposed to naming of strain SCNU9 as a novel species.