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Publishing Title:**Phylogenomic Analysis of *Streptococcus sinensis* Hku4^t Reveals a Novel Phylogenetic Group in the Genus *Streptococcus*****Author Block:**

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Abstract Body:

Currently, the genus *Streptococcus* comprised more than 90 species and was divided into 7 major groups, namely anginosus, mitis, salivarius, mutans, bovis, pyogenic and sanguinis. *Streptococcus sinensis* has been discovered by our group from patients with infective endocarditis in Hong Kong in 2002. Subsequently, additional cases reported from worldwide suggested that the bacterium is an emerging pathogen of global importance. Phenotypic profile of *S. sinensis* was similar to members of anginosus, mitis and sanguinis groups. Phylogenetic analyses based on *groEL* gene sequences showed that this species clustered with members of anginosus and sanguinis groups, but 16S rRNA gene sequences revealed that this species branched out from members of anginosus, mitis and sanguinis groups. Thus, the phylogenetic position of this species remained unclear. In this study, a polyphasic approach has been used to determine the taxonomic position of *S. sinensis*. The whole genome sequencing of *S. sinensis* HKU4^T was performed by Illumina Hi-Seq 2500. The draft genome of *S. sinensis* HKU4^T was 2.06 Mb with G+C content of 42.2%. Phylogenomic analyses using the genome sequence of *S. sinensis* HKU4^T and those of 69 *Streptococcus* genomes and 50 ribosomal protein gene sequences from 87 *Streptococcus* genomes showed that *S. sinensis*, together with *S. oligofermentans* and *S. cristatus*, formed a distinct phylogenetic clade. Dendrogram generated from hierarchical cluster analysis of matrix-assisted laser desorption ionization time-of-flight mass spectrometry also formed the same clade. On the basis of these genomic evidences, it is proposed a novel phylogenetic group, “sinensis group”, to include species of *S. sinensis*, *S. oligofermentans* and *S. cristatus*. This study presents the first draft genome of *S. sinensis* and reveals a novel phylogenetic clade in the genus of *Streptococcus*. The findings demonstrate the superior power of phylogenomic analyses to resolve the ambiguities in bacterial taxonomy. Detailed comparative genomic analysis on members belonging to the “sinensis group” and those of the mitis group may illustrate not only the ecology and biology of *S. sinensis* but also pathogenesis of infective endocarditis caused by members of this novel phylogenetic group.

Author Disclosure Block:

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