

OR-I-5. Specific detection of *Streptococcus pneumoniae* by suppression subtractive hybridization analysis

Sang-Jae Lee*, Yun-Sang Kim, Sung-Hee Pi, Hyung-Keun You,
Hyung-Sik Shin

Department of Periodontology, School of Dentistry, Wonkwang University

Background

Suppression subtractive hybridization was performed to search for the genomic differences between *Streptococcus pneumoniae* KCTC 5080T and the most closely related oral streptococcus, *S. mitis* KCTC 3556T.

Materials and methods

Total of 115 clonal libraries were identified using reverse Southern hybridization and completely sequenced. Of 21 *S. pneumoniae* specific-clones, 7 revealed transporter protein genes and 2 were metabolism genes, one of each gene displayed homology with membrane protein, information protein and miscellaneous protein. Nine had significant similarity with either gene of hypothetical protein or unknown functions.

Results

Subsequently, two oligonucleotide primers for the discrimination of *S. pneumoniae* from "pneumococcus-like" oral streptococci were designed from dexB sequences of the subtracted clone 6, and their specificities were evaluated by PCR using genomic DNAs extracted from 13 *S. pneumoniae* strains and 23 reference streptococci including clinical isolates of *S. mitis* and *S. oralis*. Genomic DNAs purified from all *S. pneumoniae* strains was efficiently detected, whereas there was no amplification with DNA from other streptococci strains tested.

Conclusion

Such an approach to comparative bacterial genomic study can be used to delineate and support the identity of clinical isolates of *S. pneumoniae* and further differentiate from the closely related *S. mitis* and *S. oralis*.