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学位論文名	Multilocus Sequence Typing of <i>Streptococcus mutans</i> (<i>Streptococcus mutans</i> における Multilocus Sequence Typing 法の構築)
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論文内容の要旨

Streptococcus mutans is the major pathogen of dental caries, and occasionally causes bacteremia and infective endocarditis. *S. mutans* strains have been classified into four serotypes (*c*, *e*, *f*, and *k*) based upon the chemical composition of the serotype-specific polysaccharide. Although serotyping has been widely used to differentiate *S. mutans*, this method has limited discriminatory power to reveal the genetic relationship of strains within the same serotypes. Moreover, little is known about the *S. mutans* population, including the clonal relationships among strains of *S. mutans*, in relation to the particular clones that cause systemic diseases. To address this issue, a multilocus sequence typing (MLST) scheme for *S. mutans* has been developed. Eight housekeeping gene fragments (*tkt*, *glnA*, *gltA*, *glk*, *aroE*, *gyrA*, *murI*, and *lepC*) were sequenced from each of 102 *S. mutans* oral or blood strains isolated from Japanese or Finnish. The number of alleles per locus was between 14 and 23, thus the theoretical potential to distinguish more than 1.2×10^{10} different STs was provided by this highly discriminatory system. Based upon this method, 92 STs were identified from the 102 strains, indicating that *S. mutans* contains a diverse population. The serotype *c* strains were widely distributed in the dendrogram, whereas the serotype *e*, *f*, and *k* strains were differentiated into clonal complexes. Therefore, we conclude that the ancestral strain of *S. mutans* is serotype *c*. No clonal complex was observed among strains isolated from blood. However, the distribution of the collagen-binding protein gene (*cnm*), one of infective endocarditis potential virulence factors, was clearly evident. In conclusion, the superior discriminatory capacity of this MLST scheme for *S. mutans* may have important practical implications

論文審査の結果の要旨

本研究は、う蝕の主要な病原細菌である *Streptococcus mutans* に Multilocus Sequence Typing (MLST) 法を適用し、その分類法を確立したものである。本研究の成果は、新たに確立した MLST 法が *S. mutans* の比較進化解析

を含めた分子レベルでの分析を可能とただけでなく、臨床分離株の伝播様式の解明、類縁性の推定にも応用できることを示したものである。

以上のことから、本研究は *S. mutans* の病原性に関する研究を、分子遺伝学的に系統立てて遂行する上で重要な手法を確立したものであり、博士（歯学）の学位授与に値するものと認める。