

Profiling and Analysis of Extracellular Matrix and Related Gene Expression in Human Periodontal Ligament Tissue and Fibroblasts.

著者	NATTAKARN HOSIRILUCK
学位名	博士（歯学）
学位授与機関	北海道医療大学
学位授与年度	令和元年度
学位授与番号	30110甲第325号
URL	http://id.nii.ac.jp/1145/00064834/

Purpose:

Periodontal ligament fibroblasts (PDLFs) are the most abundant cells and have been considered to contribute the regeneration of periodontal ligament (PDL) tissue by producing extracellular matrixes (ECMs) and factors to maintain tissue functions. Our final goal is to regenerate PDL tissue using PDLFs and ECMs. In this study, we identified the profiling of ECM gene expression and analyzed the possible expressing genes that play an important role to regenerate a function of PDL tissue.

Methods:

We isolated the PDL tissues and PDLFs from premolar teeth, which extracted from healthy periodontal status patients for an orthodontic treatment. mRNA expression in PDL tissue and PDLFs were analyzed using CAGE, the cap analysis for gene expression, which is a 2nd generation sequence technique. The gene variations of ECMs were determined by nucleotide sequencing.

Results & Discussion:

Our CAGE data showed that the highly expressed ECM genes in PDL tissue were collagens (mainly type I, III, V, VI, XII), periostin, osteonectin, osteocalcin, asporin, lumican, tenascin N, decorin, osteopontin, fibronectin and osteomodulin. Considering to matrix binding proteins, periostin and osteonectin were the highest expressed genes. They were considered as the bifunctional genes that support PDL tissue structure. In proteoglycans, aspirin and decorin were the highly expressed. These genes play a role to prevent the mineralization and ECM organization in PDL tissues. The ECM gene expression level of PDLFs showed that tenascin N, osteopontin and osteocalcin were the most decreasing ECM genes compared to PDL tissue, due to the environment changes. We found the mixture of osteopontin variant 1 & 2 and periostin variant 1 & 5 & 8 in both PDL tissue and PDLFs. These variations may work together as a controlling genes.

Conclusion:

We identified distinctive gene expression of ECMs in PDL tissue and PDLFs from the profiling. Splicing variation of osteopontin and periostin were identified. These finding may be useful for the regeneration of PDL tissue by reconstructing ECMs and PDLFs.