Proteomic analysis of titanium-cell interaction

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Purpose : This study was performed to determine the effect of different surface dental materials on biologic responses of a human osteoblast-like cell line, MG63 .

Materials and methods : Osteosarcoma cell line(MG63) was cultured in the MEM medium supplemented with fetal bovine serum. MG63 cells were cultured on different surface dental materials such as Smooth, SLA and HA. The morphology and attachment of the cells were examined on different surface dental materials. The attachment of cells were analyzed with a scanning electron microscope (SEM). The cell number on and around the material was counted with a hemocytometer.

To understand the prominent protein expression in the relationship of various titanium surface and osteoblast-like cells, proteomic study based on two-dimensional gel electrophoresis(2DE) and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry(MALDI-TOF MS) was performed.

Results : The appearances of the surfaces observed with SEM were different in the three types of dental substrates. The surface of SLA and HA were shown to be rougher than S. MG63 cells cultured on SLA and HA were cell-matrix interaction.

In all, 10 proteins(10 spots) were identified by matrix-associated laser desorption/ ionization and mass spectrometry, database searching, immunoblotting, running a standard, or a combination of these techniques. The surface propreties of titanium appeared to promote the formation of the specific proteins. In the expression of proteins involved in osseointegration, 10 times up-regulated proteins were Cadherin, Keratin 1, BCL-6 interacting corepressor, Fibroblast growth factor receptor 3 precursor, Insulin-like growth factor in SLA surface and Capping protein(actin filament) muscle Z-line alpha 2, Cell adhesion kinase beta, Collagen, Cadherin-11 precursor (Osteoblast-cadherin) in HA surface.

Summary : It is concluded that the surface of dental materials can influence the expression of the gene and protein in osseointegration. By analyzing the changes in the entire proteome of cells in response to different growth substrates, we may gain a better understanding of the molecular basis of biocompatibility.