

Is the proteomic composition of the salivary pellicle dependent on the substrate material below?

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The use of dental restorative materials is a routine task in clinical dentistry. All orally exposed surfaces are covered with a continuously growing biofilm due to the adsorption of salivary proteins and other macromolecules at the fluid/solid-interface. Each substrate material has different physico-chemical properties supposed to influence the composition of the initial biofilm, termed pellicle. This study aimed at characterizing and comparing the individual pellicle proteome of five subjects formed on six dental restorative materials and natural enamel. Substrate material-specific adsorption patterns were analyzed by comparing the proteomic profiles of the 3-min pellicle and the corresponding saliva. The combination of chemical elution and tandem nano-mass spectrometry resulted in the identification of 1348 different pellicle proteins, out of which 187 to 686 proteins were present in individual 3-min pellicles. Unexpectedly, quantitative analyzes based on the molecular weights, isoelectric points, and molecular functions of the identified proteins yielded in similar distribution patterns independent of the substrate material. Overall similar fold changes were obtained for the major part of commonly enriched or depleted proteins in the 3-min pellicles. These results point to a minor important role of the substrate material on the proteomic composition of the 3-min pellicle.