Oral mucositis: a survey on changes in the proteomic profile

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Objectives. Oral mucositis is the most severe complication of anticancer therapy. It occurs in 40-85% of patients during chemotherapy and radiotherapy but also in patients who have undergone hematopoietic stem cell transplantation. The symptoms for oral mucositis are burning and severe pain oral, spontaneous bleeding, dysphagia, dysarthria and odynophagia; especially pain and burning sensation on swallowing contribute to decreased quality of life for oncologic patients and, in severe cases, may also force the patient to feed parenterally (1). Furthermore, if the mucositis is severe it can lead to partial or complete interruption of radiotherapy before completion of the treatment protocol with consequent worsening of the prognosis (2, 3). Dentists must be familiar with the necessary intervents, in order to help the patient during the course of the treatment and prevent the interruption. Certain measures may help minimize the symptoms associated with oral mucositis; however, further research is required, focusing on lesion prevention prior to treatment initiation. To this end, it has been investigated the salivary proteome of cancer patients who developed oral mucositis, post chemotherapy and/or radiotherapy. In addition, we compared the salivary proteome of the same subjects before developing oral mucositis and immediately after the treatment for the mucositis. The analysis was made with SELDI technology.
Methods. In the current study, 55 saliva samples of patients suffering from different types of cancer were analyzed. The saliva was collected in three times: before the development of mucositis, when it was diagnosed and after the resolution of this pathology. All samples were analyzed by SELDI-TOF/MS analysis. It was possible to create cluster peaks in spectra obtained using BIORAD DataManagerTM software (Ver 3.5).
Results. From this analysis we identified a list of differently expressed mass peaks (clusters). We have selected some significant peaks in a range of values between 3000 m/z 15000 m/z. In particular, five were found to be differentially expressed: 3343, 3486, 3732, 4132 and 4786 m/z. The analysis of the cluster, we evaluated different patterns of peaks in the three groups; some of these were up regulated, as the peak 3732 m/z in samples pre mucositis, and down regulated, such as the 7101 m/z in the samples pre mucositis.
It is noted, moreover, an important increase of the peak 4132 m/z in samples of mucositis.
Conclusions. Oral mucositis is one of the most frequent complications of cancer therapies. It is, therefore, extremely important that the mucositis is prevented whenever possible, or at least treated to reduce its severity and possible complications. Knowing the salivary proteome and its variations in a state of pre mucositis, mucositis and post mucositis can be useful in order to intervene with preventive tools and better therapies. The association of the peaks 3343, 3486, 3732, 4132 and 4786 m / z, in particular the increase in expression of the peak 4132 m / z in samples of mucositis makes us think that it can be used as biomarker of this condition.
Therefore, if these data will be confirmed on a larger series of patients could identify these proteins and study of targeted therapies. Furthermore, it would be helpful to understand whether these variations are associated with a particular chemotherapy and evaluate longer available cancer therapies replacement.

References

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Burning mouth syndrome: the latest research experiences at the school of Milan

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