Protein Analysis by Association of Atomic Force Microscopy and Mass Spectrometry

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Aiming the development of analytical methodology oriented for rapid analysis of protein supramolecular systems, this work intends primarily the association between two powerful techniques for protein analysis: atomic force microscopy (AFM) and mass spectrometry (MS). Isolated proteins (the form they are usually examined) give many important information; however, they do not represent the real cell state, characterized by a variety of non-covalent molecular interactions. AFM is a powerful analytical tool for supramolecular systems, allowing proteins complexes systems topography. This work demonstrates AFM and MS association, aiming rapid analysis which a single sample submitted to both analytical tools in similar conditions. Previous studies showed that the off-line coupling of AFM and MS is possible by attaching, on a MALDI plate, the mica surface containing adsorbed analyte molecules previously analyzed by AFM. In this work, we showed that RNAse adsorbed onto mica surface can be identified by PMF method. The AFM-MS method was also used to study a honey bee brain protein complex MRJP1. The AFM image revealed the topography of the complex, while MALDI-MS confirmed that it is a mixture of proteins, and not a single one. The AFM images suggests that the complex could have some kind of hole or pore, however, in order to better interpret the results, the mixture must be separated. The results showed that the association of AFM and MS provides good results especially for smaller proteins, but has some limitations for high mass protein, because the optimal concentrations are different for each instrument.

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