

MALDI IMAGING MASS SPECTROMETRY AS A COMPLEMENTARY TOOL IN
THE CHARACTERIZATION OF *VIGNA UNGUICULATA* SEED PROTEINS

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The recent expansion of the field of plant proteomics has been crucial to the identification of target proteins implicated in plant development and interactions with the environment. However, much of the proteomic work has been based upon the identification of proteins derived from total protein extraction protocols that homogenize the plant tissue, consequently losing the protein tissue distribution. In order to recapture the protein *in situ* expression pattern, we have combined two methodologies: the classical proteomic approach to characterize the total protein content in a germinating seed of *Vigna unguiculata* and the application of MALDI imaging mass spectrometry to localize the proteins within the seed by means of direct molecular ion detection. MALDI imaging offers the possibility of generating spatial snapshots of a particular physiological state whereby the local expression of proteins of known molecular mass can be followed. In this work, *V. unguiculata* seeds were cultured in water for a period of five days and sectioned on a daily basis. An imprint of each section was generated on PVDF membranes which were placed on a MALDI plate for the direct acquisition of the mass spectra. Our results demonstrate that the expression pattern of known protease inhibitors and thionins could be followed through the entire germination period.

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