

Metabolic Profiling of Corn (*Zea mays*) Roots by Mid-Infrared Laser Ablation Electrospray Ionization Mass Spectrometry

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Introduction

Meristematic cells have the ability to develop into any cell type within the plant. Cell differentiation is an important process in the development of any multicellular organisms. The comparison of the biochemical profiles of stem cells and differentiated cells in the same tissue could provide understanding of cell differentiation. Laser ablation electrospray ionization (LAESI) mass spectrometry (MS) enables the investigation of these differences by the direct molecular analysis of biological tissues of small cell populations. In this contribution, LAESI-MS is utilized to obtain biochemical profiles of the meristematic region and a proximal region in the root tip of the corn (*Zea mays*) plant at ambient conditions.

Methods

Zea mays seedlings were surface sterilized and germinated in Petri dishes with deionized water in a Percival AR-22L growth chamber under a 14 hour photoperiod. Seven days after germination, the seedling roots were mounted on sterile microscope slides for direct analysis with LAESI-MS. Mid infrared pulses (2.94 μm wavelength) were produced by a Nd:YAG laser pumped OPO operating at 10 Hz repetition rate. The areas of the *Zea mays* tissue were selected for ablation by using a three-axis translation stage for positioning and video microscope for visualization. The ablated neutrals were intercepted by an electrospray plume from a nano-electrospray source and efficiently ionized. The ions generated in the LAESI-MS were analyzed by an orthogonal acceleration time-of-flight mass spectrometer.

Preliminary Data

The roots were analyzed at the root tip, the region containing the meristematic cells, and at an area of the root about 1 cm proximal to the tip. The acquired mass spectra revealed over 100 small metabolites and lipids at each of the sites. Accurate mass measurements, isotope distribution patterns, and a plant-wide metabolomic database search combined with tandem MS enabled the assignment of a subset of these ions to particular compounds. Biochemical profiles of the two regions of *Z. mays* were compared. For example, the peak intensity ratio for monosaccharides (m/z 203.0520 and 219.0262) to disaccharides (m/z 365.0992 and 381.0734) was higher in the proximal root region while the trend reversed in the root tip region. Other ions had higher intensities in the meristematic root tip such as m/z 353.1391, 662.2271, and 760.7172. There were several ions in the root tip found in the high mass region that were not present in the proximal root. Examples of these ions include m/z 1358.3994, 1459.4862, and 1520.5054. Peaks assigned to lipids, such as PC (34:2) at m/z 758.5609 and PC (36:4) at m/z 782.5587, were found to have similar intensities in both analyzed regions. Some ions, such as m/z 282.0798, 383.1057, and 550.6238, had higher intensities in the proximal root rather than the tip. These preliminary results indicate biochemical differences between the meristematic and differentiated cell populations in *Z. mays*, that can help to understand the molecular details of differentiation in plant cells.

Novel Aspect

LAESI-MS reveals metabolic differences in the meristematic and differentiated regions of corn roots.