

## Spatially Resolved Rhizosphere Function for Elucidating Key Controls on Below-ground Nutrient Interactions

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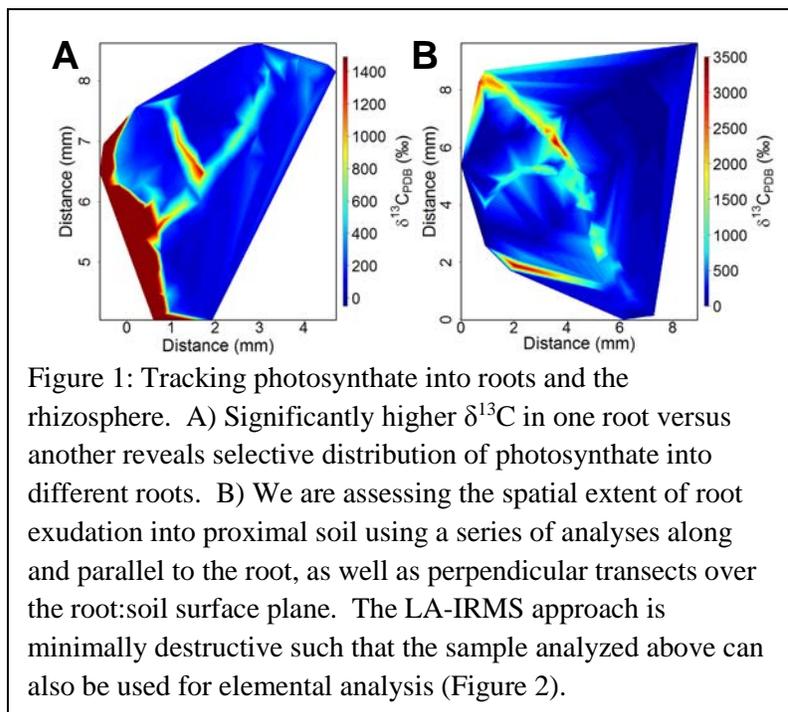
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<http://www.pnl.gov/biology/programs/fsfa/people/moran.stm>

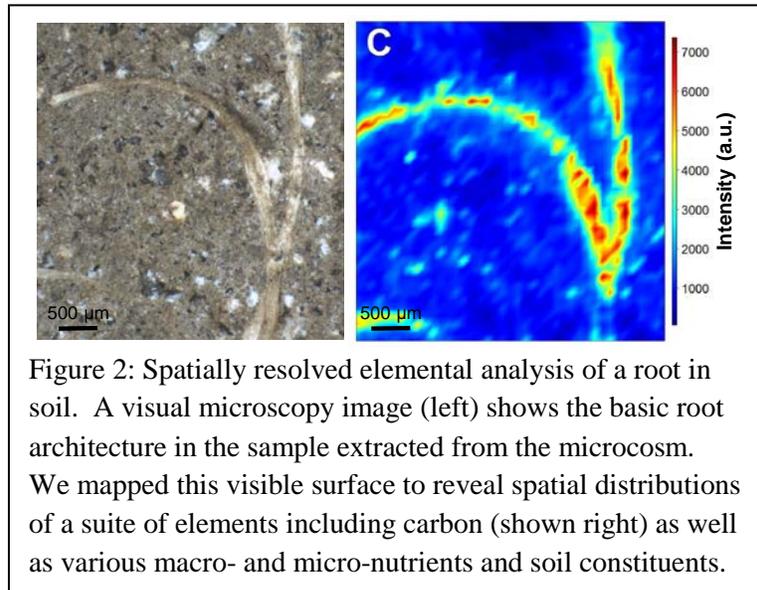
**Project Goals:** This project seeks to elucidate key microbiological and geochemical controls on nutrient exchange through the rhizosphere and the role that spatial organization within the root-rhizosphere-soil continuum plays in nutrient transfer. Spatially-resolved understanding of nutrient exchange across the rhizosphere will identify key variables amenable to manipulation as part of an effective rhizosphere management program targeting enhanced plant productivity. Our aims are directed towards 1) spatially tracking plant-derived organic carbon contributions to soil, 2) identifying key microbial membership distribution within zones of high nutrient transfer, and 3) evaluating whether directed geochemical and/or microbiological modifications can be used to stimulate nutrient exchange to foster improved plant biomass productivity.

The central hypothesis we are testing is that spatially focused regions funnel a disproportionate amount of nutrients to a plant root. Further, we hypothesize that the location of these resulting nutrient exchange hotspots are not stochastically distributed throughout the rhizosphere but, rather, that they are controlled by microenvironmental conditions resulting from a combination of local microbiological communities in conjunction with host soil geochemistry.

To begin testing these hypotheses, we constructed microcosms using switchgrass (variety Cave-in-Rock) and soil harvested from the Kellogg Biological Station (Hickory Corners, MI). We used <sup>13</sup>C-labeled carbon dioxide (CO<sub>2</sub>) to track photosynthetic fixation and subsequent migration of labeled organic compounds through the



roots and into the rhizosphere by applying laser ablation isotope ratio mass spectrometry (LA-IRMS). LA-IRMS allowed us to quantify the amount of  $^{13}\text{C}$ -labeled, recent photosynthate at specific locations harvested from the soil microcosms (Figure 1). We were able to quantify the variable distribution of photosynthate to different roots and identify specific branch points within the root architecture where roots receiving high versus low photosynthate allocations diverged. Spatial analysis of the soil proximal to the roots revealed the extent of root exudation that would be available for microbial activity. We developed a laser induced breakdown spectroscopy (LIBS) technique to enable coupling of the elemental content of the rhizosphere with the localized extent of exudate additions (revealed via LA-IRMS). LIBS permitted suitable spatial resolution to identify the elemental content of distinct mineral grains within the KBS soil and map elemental content over the root:soil interface (Figure 2). We are currently exploring specific regions within the rhizosphere that contain anomalous elemental distributions and highlight a possible expansion of the root influence into the surrounding soil.



To help overcome the high spatial heterogeneity within soil and the rhizosphere, we are developing a proteomics-based method for elucidating the spatial variability of soil and rhizosphere-associated microbial communities from a taxonomic and functional perspective. The preparation technique we are using is non-destructive to enable time series sample analysis and provides spatially-resolved proteomics analysis (approximately 1 mm resolution) suitable for basic community taxonomic identification.

Taken together, our developments are allowing us to spatially track photosynthate from leaves, through the roots, and into the rhizosphere, and subsequently characterize the microbial and elemental composition of specific locations that show enhanced carbon deposition.

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