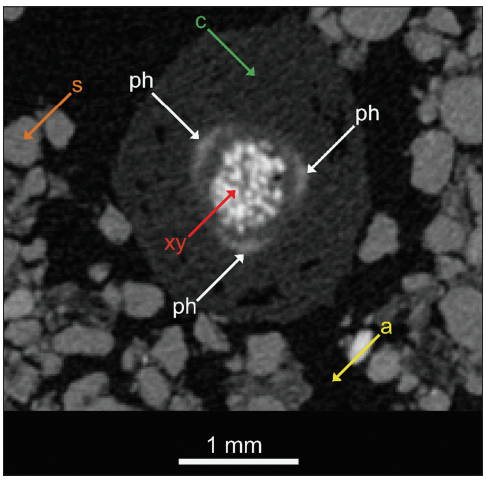
Highlights from Microscopy AND Microanalysis

Biological Applications

The Application of Contrast Media for In Vivo Feature Enhancement In X-Ray Computed Tomography of Soil-Grown Plant Roots by SD Keyes, NJ Gostling, JH Cheung, T Roose, I Sinclair, and A Marchant, *Microsc Microanal* 23(3) (2017) 538–52

Use of iodinated contrast media is a mature and fundamental approach within modern medical imaging. By introducing radiopaque media to the human body, the often-poor native contrast between different tissues can be greatly enhanced. X-ray computed tomography (XCT) is increasingly being applied to study plant root systems and their interaction with soil. These studies are often complicated by the poor contrast observed between different root and soil structures. As a result, the image analysis of XCT data in plant imaging studies is highly user-dependent and time-consuming. Here we document the use of two iodinated contrast media to perfuse living, soil-grown samples of *Pisum sativum* and describe the resulting contrast enhancement in XCT data. Over a range of applied concentrations, substantial contrast enhancement was observed within the root vasculature, allowing the xylem bundle and phloem poles to be distinguished. The intricate 3D vasculature of undisturbed rhizobial root nodules was also elucidated in a number of cases. The non-ionic iopamidol provided better contrast than Gastografin, with fewer apparent osmotoxic effects.

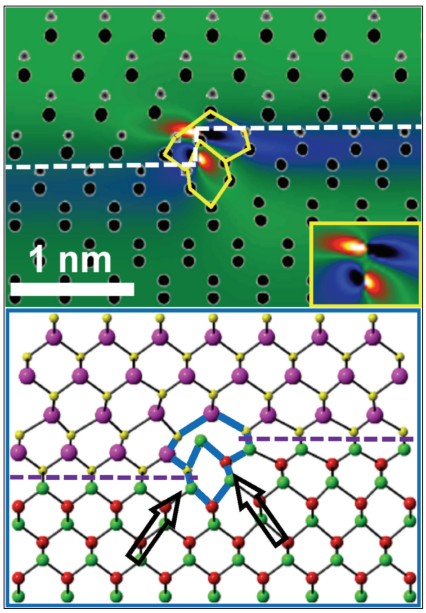


Digital slice through a 3D XCT seminal root volume of *Pisum sativum* with aerial tissue perfused with iopamidol for 24 h prior to imaging. Substantial contrast is seen in xylem (xy) and phloem (ph) versus the cortical tissue (c). Soil minerals (s) and air-filled pores (a) are indicated. In un-perfused samples, the entire root cross section appears as (c).

Materials Applications

The Relationship Between Atomic Structure and Strain Distribution of Misfit Dislocation Cores at Cubic Heteroepitaxial Interfaces by C Wen, *Microsc Microanl* 23(3) (2017) 449–59

Atomic structure and strain distribution of misfit dislocation (MD) cores were separately studied. They should be closely related because atomic reconstructions are frequently caused by the strong strain fields around MD cores, and the positions of the maximum lattice distortions can be given by the corresponding strain distribution map. This paper reports the relationship between atomic structure and strain distribution of MD cores at the AlSb/GaAs (001) cubic zincblende interface using simulated projected potential and aberration-corrected high-resolution electron microscopy (HREM) images in combination with the geometric phase analysis technique. The results show that strain distributions can be used to determine the MD type (a Lomer, a 60°, or a 60° pair dislocation) and reveal the atomic structure characteristics of the MD cores, such as left displacements, atomic steps, and symmetrical Lomer dislocation reconstruction (see figure). Strain maps should be measured from optimum-defocus images or restored structure images. Image distortion caused by contrast transfer function modulation and other factors must be considered.



ε_{yy} strain distribution map of an MD core at a AlSb/GaAs (001) interface. Bottom panel shows the [110] projected structure model.

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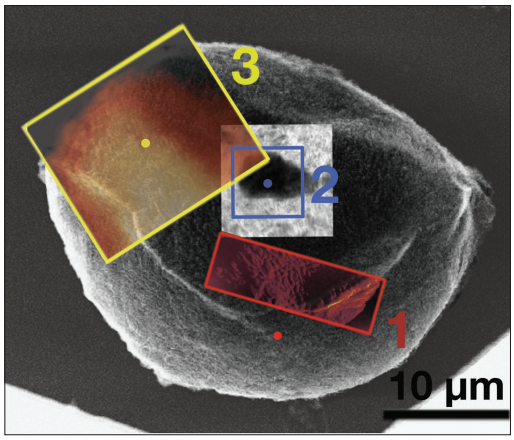
Microscopy AND Microanalysis

Techniques and Biological Applications

Measuring the Autocorrelation Function of Nanoscale Three-Dimensional Density Distribution in Individual Cells Using Scanning Transmission Electron Microscopy, Atomic Force Microscopy, and a New Deconvolution Algorithm by Y Li, D Zhang, I Capoglu, KA Hujsak, D Damania, LS Cherkezyan, EW Roth, R Bleher, J Wu, H Subramanian, VP Dravid, and V Backman, *Microsc Microanal* 23(3) (2017) 661–67

Biological processes are highly dependent on the nanoscale architecture of the cellular components. Statistical measures, such as the autocorrelation function (ACF) of the 3D mass–density distribution, are widely used to quantify cellular nanostructures. Conventional electron tomography to characterize the 3D mass–density distribution, from which ACF can be calculated, has been inadequate for thick biological structures because of the inverse relation between voxel resolution and total reconstructed volume. We have developed a robust method to calculate the ACF of the 3D mass—density distribution without tomography. Assuming the biological mass–density distribution is isotropic, our method allows for accurate ACF calculation of the 3D mass–density distribution with a single projection image from scanning transmission electron microscopy and a thickness map from atomic force microscopy. Here, we present validation of the ACF reconstruction algorithm and its application to calculate the ACF of the 3D distribution of mass–density of a human buccal cell nucleus. This method may provide important insights into architectural changes that accompany cellular processes.



STEM HAADF and AFM measurements were taken from the cell nucleus (region 2). The co-localization was achieved by scanning a feature on the SE image (region 1) to locate the AFM tip (red dot), which was then offset to the center of the nucleus (blue dot). A background (region 3) was measured for AFM thickness calibration.