Mapping Connections between the Genome, Ionome and the Physical Landscape

On Monday, February 2, 2009, David E. Salt (Professor, Horticulture and Landscape Architecture, Purdue University) will present the second of the Spring 2009 Networks and Complex Systems Talk Series. The talk will be from 6:00-7:00 p.m. in SLIS, Wells Library, Room 001. The series organizer is SLIS faculty member Katy Börner.

Abstract:
Understanding how organisms control their ionome or mineral nutrient and trace element composition, could have a significant impact on both plant and human health. Furthermore, associating the genetic determinants that underlie natural ionomics variation, with the landscape of the individuals that carry these genotypes, will provide insight into the genetic basis of adaptation and speciation. We have employed high-throughput mineral nutrient and trace element profiling, using inductively coupled plasma – mass spectrometry (ICP-MS), as a tool to determine the biological significance of connections between an organisms genome and its ionome. Our focus is on genes that control uptake and accumulation of mineral elements, including Ca, K, Mg, P (macronutrients in plant fertilizer), Co, Cu, Fe, Li, Mn, Mo, Ni, Se, Zn, (micronutrients of significance to plant and human health) and As, Cd, Na and Pb (elements causing agricultural or environmental problems). To date we have analyzed the ionome of over 100,000 Arabidopsis plants and 20,000 yeast samples. This includes several Arabidopsis forward genetic screens (Lahner et al., 2003 Nat. Biotechnol. 21:1215), a screen of 360 natural Arabidopsis accession, and a complete analysis of all 5153 strains of the yeast deletion collection (Danku et al., 2009 JAAS (in press)). We have successfully used PCR-based positional cloning, DNA microarray based approaches, QTL and association mapping to identify numerous genes that control the ionome (for example Rus et al., 2006 PLoS Genetics 2(12): e210; Baxter et al., 2008 PLoS Genetics 4(2):e1000004). Association of variation in these genes with the landscape in which these plants naturally grow is starting to reveal the genetic architecture underlying specific adaptations to the environment. We are also finding that specific ionomic “fingerprints” are associated with functionally related sets of genes, and also with the physiological status of the organism (Baxter et al., 2008 PNAS 105: 12081-12086). To maximize the value of this ionomics approach, we have developed a publicly searchable online database containing ionomic information on over 1000,000 samples from over 1500 different experiments (www.ionomicshub.org; Baxter et al., 2007 Plant Physiol 143: 600-611), and the database is being updated regularly.

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