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Session 2: Expert Speaker, 20 min presentation followed by 10 min Q/A
March 5th at 11:00am CST (9:00am PST, 12:00pm EST, 5:00pm GMT)

Link to Register:

<https://attendee.gotowebinar.com/register/259087085732346370>

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Large-scale, Computational and Empirical UHPLC-MS-SPE-NMR Annotation of Plant Metabolomes

Integrated metabolomics is a revolutionary systems biology tool for understanding plant metabolism and elucidating gene function. Although the vast utility of metabolomics is well documented in the literature, its full scientific promise has not yet been realized due to multiple technical challenges. The number one, grand challenge of metabolomics is the large-scale confident chemical identification of metabolites. To address this challenge, we have developed sophisticated computational and empirical metabolomics tools for the systematic and biological directed annotation of plant metabolomes. This presentation will introduce novel software entitled **Plant Metabolite Annotation Toolbox** (PlantMAT) and a sophisticated UHPLC-MS-SPE-NMR instrumental ensemble that are being used for ‘sequencing’ the first plant metabolomes of the model plant systems *Arabidopsis* and *Medicago truncatula*.

Speaker Details

Dr. Sumner acquired his B.Sc. degree in chemistry with a minor in mathematics in 1989 from Cameron University in Lawton, OK, USA and a Ph.D. in analytical chemistry in 1993 from Oklahoma State University in Stillwater, OK, USA. He then joined Texas A&M University, College Station TX, where he was the Director of the Mass Spectrometry Applications Laboratory and where he later served as the cofounder and Associate Director of the TAMU Laboratory for Biological Mass Spectrometry with Prof. David H Russell. He joined The Noble Foundation in 1999 and has risen to the rank of Professor within the Plant Biology Division.

Dr. Sumner has built a research program focused around the development and integration of large-scale biochemical profiling of plant metabolites, proteins, and transcripts (metabolomics, proteomics and transcriptomics) for the discovery and characterization of the molecular and biochemical components related to plant natural products biosynthesis. He also applies these integrated omics technologies for greater insight into the physiological and biochemical consequences of gene expression and system responses to genetic and environmental perturbations.