**A Path to Durable Biotic and Abiotic Stress Resistance in Rice**

**Jan E. Leach**

**Colorado State University, Ft Collins, CO USA**

**Jan.Leach@colostate.edu**

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Stress tolerance in crops, such as resistance to heat and disease, involves extensive transcriptional reprogramming, leading to changes in the expression patterns of large numbers of genes. Groups of genes related to specific biochemical or physiological processes are often co-activated during stress responses, and the co-expression of many of these genes can enhance stress tolerance. In fact, many of these co-expressed genes underlie quantitative traits (QTL) for stress tolerance. There is considerable overlap in the genes or pathways whose expression is altered in response to different abiotic and biotic stresses, indicating the presence of core responses common to diverse stresses. Stress-induced changes in gene expression are controlled by short sequences in the promoter regions, known as *cis*-regulatory elements (CRE), or by combinations of CREs organized as modules (*cis*-regulatory modules or CRMs). We have shown that conserved CREs and CRMs are found in the promoters of many genes co-activated by a single stress and they are also common to genes co-activated in plants with enhanced tolerance to different stresses, such as heat and disease stresses. This knowledge forms the basis for the concept that molecular markers can be developed based on shared stress-responsive CREs and CRMs, which can then be used to assist in breeding crop plants for simultaneous heat and disease tolerance. Our goal is to enable genome-wide selection of complex traits with a reduced number of markers, allowing for efficient, critical solutions to enhance sustainable food production for a growing global population.