

CONTACT US	SITE MAP	SEARCH	PRIVACY POLICY	ADVERTISE

Abstract Center . Session List . Search:		Go
--	--	----

Poster: C3 to C4 Post-meeting Workshop

Abs # P70001: Comparative Analysis Of C3 And C4 Leaf Development In Rice, Sorghum And Maize

Presenter: Gandotra, Neeru <u>Contact Presenter</u>

Authors Gandotra, Neeru (A) Tausta, Lori (A) Li, Pinghua (B) Reidel, Edwin (D)

Kebrom, Tesfamichael ^(B) Ponnola, Lalit ^(C) Majeran, Woojciech ^(D) Sun, Qi ^(C) Liu, Peng ^(E) Brutnell, Thomas ^(B) van Wijk, Klaas ^(D) Turgeon, Robert ^(D)

Nelson, Timothy (A)

Affiliations: (A): Yale University

- (B): Boyce Thompson Institute, Cornell University, Ithaca, NY 14853 USA
- (C): Computational Biology Service Unit, Cornell University, Ithaca, NY 14853 USA
- (D): Department of Plant Biology, Cornell University, Ithaca, NY 14853 USA
- (E): Dept of statistics, Iowa state University, Ames Iowa IO 50011 1210

Web Site: http://c3c4.tc.cornell.edu

C4-type plants such as maize, sorghum and several promising biofuel feedstocks possess a set of complex traits that greatly enhance their efficiency of carbon-fixation, water and nitrogen use, and performance in high temperatures and light intensities, in comparison to C3-type plants such as rice. The key C4 traits are (1) specialization and cooperation of two leaf photosynthetic cell types (mesophyll and bundle sheath) for carbon fixation and photosynthesis, (2) enhanced movement of metabolites between cooperating cells, and (3) high density of leaf venation. These C4 traits appear to be regulatory enhancements of features already present in less-efficient C3 plants, but regulated in different patterns. We are comparing several leaf tissues (isolated using Laser capture microdissection) of rice (C3), maize (a moderate C4) and sorghum (an extreme C4 grass). We are surveying the transcriptome, proteome and metabolome along a developmental gradient from immature tissues at leaf base to mature tissues at the leaf tip. This gradient was defined using sinksource transition and cell wall specialization as markers for developmental time points. Two hypotheses will be tested by the comparative analysis of C3 and C4 plant datasets: (1) To produce C4 traits, plants use networks of genes, proteins, and metabolites that are already present in C3 plants, and (2) C4 features are plastic and expressed in a degree that depends on environment and developmental stage. This analysis should identify the regulatory points that are potential targets for the engineering C4 traits in C3 species. Supported by NSF Plant Genome Project DBI 0701736.

Abstract Center . Session List . Search:		Go
--	--	----