
Timetable of Proposed Experimental Plan

Project Month	Work Performed	Performing Laboratory
1	LCM-microarray optimization group meeting in Ames, IA. Outline project goals, procedures and histological/anatomical terms to all personnel.	Timmermans, Scanlon and Schnable LCM-microarray team.
1-12	Optimize procedures for LCM-microarray of maize SAM.	Timmermans, Scanlon and Schnable LCM-microarray team.
1-12	A) Beta test maize oligo microarrays: compare to cDNA microarrays. B) Determine if oligo microarrays must be supplemented with sequences designed from additional SAM enriched transcripts identified in the maize SAM EST project	Timmermans, Scanlon and Schnable LCM-microarray team.
6-12	Preparation B73 shoot apex cDNA library	Scanlon
6 up to 18*	Maize B73 apex gene discovery project. *Status of gene discovery to be evaluated at 12 months*.	Schnable
18-40	Prepare maize apex-enriched microarrays	Schnable
1-24	Degenerate PCR of maize orthologues of dicot meristem genes	Truman Group
6, 18, 30, 42,	Project group meeting at Maize Genetics Conference	Entire team
3, 15, 27, 39	LCM group users meeting at PAG meeting	M. Scanlon, P. Schnable, M. Timmermans with T. Nelson LCM group and other plant LCM users
1-40	LCM of all samples buttress / above buttress / below buttress - PS LI layer SAM / L2 layer SAM - PS whole SAM / whole seedling (no LCM) -PS whole SAM / mixed RNA (no LCM) - PS narrow sheath SAM / sibling SAM - MS KNOX-on / KNOX-off SAM domains - MS ragged seedling2 SAM / sibling SAM - MS NPA-arrested SAM / unarrested SAM - MS leafbladeless1 SAM / sibling SAM - MT rough sheath2 SAM / sibling SAM- MT adaxial domains / abaxial domains - MT	Schnable (PS), Scanlon (MS) and Timmermans (MT) group

Timetable of Proposed Experimental Plan (continued)		
Project Month	Work Performed	Performing Laboratory
21	Microarrays of LCM-captured samples	Scanlon/Timmermans/Schnable
21	Project group meeting in Ames, IA.	Entire team
22-36	Annotation, literature search, homology search of differentially-expressed genes identified by LCM-microarray analyses	Truman Group
22-36	Identify and select 200 genes for Expression analyses	Entire team
24-48	Expression analyses (Northern analyses, RT-PCR analyses and real time RT-PCR analyses of 200 differentially expressed cDNAs	Scanlon
24-60	Select 20-25 genes for <i>in situ</i> hybridization	Entire team
26-60	Maize <i>in situ</i> hybridization analyses of 20-25 genes	Timmermans
33	Project group meeting at Cold Spring Harbor Laboratory	Entire team
46-48	Research training at ISU, UGA and CSHL (3 students)	Truman State Group