Solanaceae Coordinated Agricultural Project

SolCAP Solanaceae Coordinated Agricultural Advisory Board Meeting		
January 11, 2009	10AM – 11AM Closed Door	The Town and Country Resort, San Diego, CA
Meeting	1st Annual SolCAP Advisory Board Meeting	
Leader	Dr. Glenn Bryan	
Attendees	Glenn Bryan, SCRI Scotland	
	Thomas Osborn, Monsanto	
	Dan Ronis, Frito Lay (Substituting for Bob Hoopes)	
	Debby Lewis, Ohio State Univ.	
	Bob Dietrich, Syngenta (Substituting for Erik Legg)	
	Michael Coe, Cedar Lake Research, SolCAP Assessment	
	Nicholas Wheeler, UC-Davis (Substituting for David Neale)	
	James Giovannoni, Boyce Thompson Institute for Plant Research	
Not Able to Attend	David B. Neale, UC-Davis	
	Charles J. Rivara, California Tomato Research Institute	
	Dani Zamir, The Hebrew University of Jerusalem	
	Caius Rommens, Simplot Company	
	Deana Namuth Covert, University of Nebraska-Lincoln	
	Eric Legg, Syngenta	
SolCAP Advisory Board Discussion with SolCAP Executive Committee and Participants		
11AM (Open Session)	Presenter: Glenn Bryan	
Attendees	Advisory Board (listed above)	
	David Douches, MSU	
	Robin Buell, MSU	
	Allen Van Deynze, UC Davis	
	David Francis, Ohio State Univ.	
	Alexandra Stone, Oregon State Univ.	
	Kelly Zarka, MSU	
	Ed Kaleikau, CSREES-USDA	
	Barbara Liedl, West Virginia State Univ.	
	Jay Scott, Univ. Florida	
	Joan Van Eck, BTI Cornell University	
	Kent McCue, USDA-ARS	
	Hamid Ashrafi, UC-Davis	
	Jan de Haas, HZPC	
	Kaishu Ling, USDA-ARS	

SolCAP Advisory Board Discussion with SolCAP Executive Committee and Participants

Discussion A	

The Advisory board is divided into a Stakeholder Board, a Scientific Board and an Extension Board.

Conclusions	

The Advisory board decided that they would communicate to the Executive Committee as one unit. "The SolCAP Advisory Board"

Discussion B	

The Advisory board felt that the SolCAP project deliverables needs to be revised to include more specific details on each deliverable. For Example: In Obj. 3, a more detailed list of traits is requested as well as inclusion of standardized protocols that will be used uniformly among the participants. It is important that such protocols are developed and agreed upon early in the project (i.e. during 2009).

Conclusions	

Executive Committee members agreed to revise current objectives to include more specific deliverables before seed planting start date. A revised version of the deliverables will be produced and presented to the Advisory Board. Completion date must be before May 2009.

Discussion C	

In regards to SNP analysis what would be criteria for success? For example, in terms of the number of polymorphic markers, what would be deemed a satisfactory outcome for potato and tomato. Clearly the two crops are very different in terms of levels of polymorphism within and among cultivars, potato being highly polymorphic, tomato much less so. These factors potentially impact very significantly on SNP development. For potato finding SNPs in genes is less of an issue but the presence of other SNPs near 'target' SNPs may increase assay failure rate significantly. In tomato the dearth of SNPs among cultivars may make it much harder to obtain useful SNPs in candidate genes. For both crops, but particularly potato, there is a major ascertainment issue in that SNPs developed from sequence data from only a few cultivars may not function well in more diverse material (wide species crosses, crosses involving introgressed resistance genes).

What is your targeted success rate for validated assays?

The criteria needs to be set in place and the analysis should be realistically stated with the intended outcome. In potato, a percentage of assays will fail because of too many SNPs for assay development and in tomato a percentage will fail because of read errors. The SNP calling criteria needs to be set stringently in order to eliminate as many errors as possible.

How many assays will be dedicated for candidate genes? It may be prudent to select more than one SNP per candidate gene, and in potato to develop SNPs that are diagnostic for different SNP haplotypes, if this is possible.

Conclusions	

The tomato success rate was suggested to be 90% but realistically we should consider it 85%.
The potato success rate was suggested to be 85% but realistically we should consider it 80%.

Robin Buell's experience in identifying eSNPs will be used to determine stringent criteria for successful calling of the eSNPs.

The number of assays that will be dedicated for candidate genes has been determined and presented on for tomato but we don't know how many SNPs there are in candidate genes and how many will be polymorphic. In potato, over 100 candidate genes will be selected. This will be examined by looking at the annotation of the potato and tomato ESTs available to date.

Discussion D	

The timeframe for the mapping SNP work:

A deliverable should be constructed that lists the target number of SNPs to map to the genome.

The panel had concerns that there were no plans to include a tomato mapping population in the tomato SNP assay development, and were of the opinion that a suitable tomato reference population be included in the SNP validation phase.

Conclusions	

We have a timeframe for mapping BACs and ESTs to the tomato and potato genomes. The limitation for both of these is the progress of the international potato and tomato genome initiatives. At PAG-09 it was reported that phase I of the tomato sequence will be complete by the end of 2009. Jim Giovannoni is a key scientist involved in the sequencing. The potato genome will be sequenced by 2009 and Robin Buell is a key scientist on this project. We are aware these are "estimates" and "works in progress" but have the informatic capabilities to maximally extract information from available genome sequence data and/or to perform these in an iterative manner.

The deliverables should specifically address the approaches in place to account for some of the contingencies.

The Executive Committee will articulate the approach more specifically in the deliverables to state this is our target number to map and validate.

Currently SolCAP would like to identify 1536 SNPs for tomato and 7600 SNPs in potato.

It was agreed that a mapping population will be used for validating a set of SNPs. For tomato, a mapping a population will be chosen after the first genotyping panel so that maximum number of SNPs can be mapped.

Discussion E	

What is the feasibility of performing association mapping within the timeframe of the project? Are the participants planning to use genome wide or candidate gene approaches? Given their respective biologies it is likely that the former is likely to yield success in tomato, but that candidate gene based approaches may be required in potato, where the extent of LD is somewhat lower.

Conclusions	

Association mapping will most likely be used for developing hypotheses regarding linkages.

A more clear statement of what the deliverables are in Objective 5 is needed so that the focus is not just on association mapping.

Discussion F	

Recipients of awards from the Small Grants program need to be held accountable for specific outcomes and deliverables.

Conclusions	

Generation of conditions for the small grants should be developed which include a deliverable that the recipient must meet. For populations, some standards must be met for the existing phenotypic data.

SolCAP communicated to the community the criteria for prioritizing the genotyping of mapping populations. Some mapping populations are already being developed and phenotyped.

Public and private industry should be eligible for the small grants program as long as they meet the conditions. AFRI program page has USDA-CREES information on private industry involvement.

Discussion F	

Sequence information (genomic, ESTs) for the target crops is currently increasing at a rapid rate, and this situation is likely to continue for a few more years. A specific cut-off point should be applied for use of sequence information for SNP platform design, otherwise the SNP development could be prolonged indefinitely. Of course it will be necessary to 're-design' SNP arrays or OPAs at some point in the future, but continuing accumulation of sequence data should not delay platform development. It is likely (and desirable) that the global tomato and potato genetics research communities will ultimately wish to adopt these marker platforms, perhaps in modified form. There are at least two parallel SNP development efforts in progress for potato, although neither as ambitious as the SOLCAP target. It is important that SOLCAP engages with these other groups to ensure a coordinated development of potato SNP resources that will ultimately improve the cohesiveness of potato mapping efforts worldwide, and that will give SOLCAP partners more visibility globally.

Conclusions	

We need to wait and see what the data shows in order to decide when a desirable stopping point has been reached. Currently, 3000 will be the maximum while 1500 is the current target.

Discussion G	

Is it possible to come up with specific outcomes for workshops?

Conclusions	

Michael Coe will be working on developing surveys for the workshops in order to insure that all the needs and expectations are met. These surveys are being refined specifically for each the tomato community and potato community.