

Summary of Solanaceae Coordinating Meetings

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Abstract

A *Solanaceae* Coordinated Agricultural Project planning meeting was held during the Solanaceae 2006 conference in Madison, Wisconsin, in order to organize a community of researchers for “translational genomics”, the adaptation of information derived from genome technologies for crop improvement. This meeting continued a planning process that was initiated during the 2005 American Society of Horticultural Sciences workshop “Translational Genomics of Vegetable Crops”, and continued at the University of California, Davis, in November 2005 and the Plant and Animal Genome conference in January 2006. The goal is to create an inclusive community consisting of applied and basic, private and public researchers combined with participation of commodity groups, growers, and end users focused on leveraging genome resources for improvement of Solanaceous crops. The meeting participants: breeders, genomics scientists, commodity stakeholder groups and end users, felt that focusing the SolCAP on both fresh and processed commodities from the three major Solanaceous vegetable crops (potato, pepper and tomato) would offer both breadth and challenge. Priorities were systematically defined for traits and tools that would benefit more than one commodity in the Solanaceae. A consensus from the community was to emphasize candidate gene approaches that are low risk, high priority, high impact and cross-commodity. The community defined clear goals for traits: 1) detailed investigation of the carbohydrate/sugar metabolism pathways; 2) increasing the levels and/or bioavailability of ascorbic acid /Vitamin C. A roundtable discussion on tools developed an extensive list and gave high priority to the following: 1) need for a centralized phenotyping facility and database; 2) access to genotyping platforms 3) breeder friendly analysis tools and centralized database for markers 4) markers useful in breeding germplasm 5) development of standard genotyping panels. A committee was formed to take a lead in each of the topic areas. Information on SolCAP can be found at <http://www.oardc.ohio-state.edu/tomato/SOLCAP.htm>.

SUMMARY

A planning meeting for Solanaceae translational genomics was held during the Solanaceae 2006 conference in Madison, Wisconsin. This meeting continued a planning process that was initiated during the 2005 American Society of Horticultural Sciences workshop “Translational Genomics of Vegetable Crops”, and continued at the University of California, Davis, in November 2005 and the Plant and Animal Genome conference in San Diego in January 2006. The goal of this process is to organize a community of researchers for “translational genomics”, the adaptation of information derived from genome technologies for crop improvement. Models for organizing translational research are now emerging. One example, the USDA/NRI Coordinated Agricultural Project (CAP)

program, currently offers \$4-5 million competitive funding to coordinate research and tool development while maximizing cooperation and minimizing redundancy. The applied plant genomics CAPs were initiated to bring together scientists and stakeholders with a shared vision and plan to facilitate translation of basic discoveries and technology. The goal is to create an inclusive community consisting of applied and basic, private and public researchers combined with participation of commodity groups, growers, and end users. “Translational” research that makes use of genome sequencing information requires that we think about agricultural research from the point of view of taxonomic groups and DNA sequence homology rather than traditional commodity boundaries. To maximize the use of resources, a research community must be willing to work beyond the traditional commodity divisions.

The goal of the process is to organize the Solanaceae community, seek input and define the goals of a Solanaceae CAP (SolCAP). The planning meetings have been attended by breeders, genomics scientists, commodity stakeholder groups and end users working with a diversity of solanaceous crops. Both public and private sectors were represented. A topic of discussion was the scope of a CAP focused on the Solanaceae. Models for translational genomics that have been funded by the USDA CAP program have focused on single commodities. The Solanaceae offer an opportunity to transcend commodity boundaries, but there is a need to balance goals that are generalized for several commodities while providing sufficient resources to accomplish specific goals with impact. It has been suggested that comparative genomics efforts could extend tools developed in tomato and potato to the Asterid clade. At the same time the diversity of commodities within the family Solanaceae will make it difficult to affect applied goals with any impact unless the SolCAP is focused. Participants in the planning process felt that focusing the SolCAP on both fresh and processed commodities from the three major solanaceous vegetable crops (potato, pepper and tomato) would offer both breadth and challenge.

Presentations were made to introduce the CAP concept, report on introductory meetings held on the subject for potato and vegetable crops in summer 2005, summarize the current resources for translational genomics in the three principal commodities and summarize the current use of markers in breeding these vegetables. These presentations were followed by facilitated discussions on traits and tools that are of high priority for each commodity. Priorities were then systematically defined for traits and tools that would benefit more than one commodity in the Solanaceae. Based upon these discussions, some clear directions emerged that would be widely supported by the community of researchers working with the vegetable Solanaceae. With regard to traits, an extensive list was developed that included:

1. Nutrient content.
2. Processing quality.
3. Disease and insect resistance.
4. Agronomic characteristics and yield.

Traits were initially listed for each commodity and priority was subsequently given to those that would benefit at least two species. A consensus from the community was to emphasize candidate gene approaches that are low risk, high priority, high impact and cross-commodity. Traits that the group felt could provide a focus for a SolCAP proposal include carbohydrate/ sugar metabolism, resistance to *Phytophthora* and viruses, and

calcium as it relates to post harvest quality. Although *Phytophthora* (late blight) is a serious problem in all three crops, it was recognized by the group that several resources are already being developed for this trait. Detailed investigation of the carbohydrate/sugar metabolism pathways would be supported by the potato processing industry, constituting 60% of potato utilization, and by both the fresh market and processing tomato industry. Sugar metabolism is not a high priority in pepper, though commercial breeders often practice selection for sugar content. Increasing the levels and/or bioavailability of ascorbic acid / Vitamin C, which is both a nutrient and antioxidant, was also considered to be important for many solanaceous crops. During discussion of candidate genes it was noted that resources for translational genomics should include information on promoter sequences, and not just the open reading frames. By the time SolCAP would be funded, significant potato and tomato genome sequence data are expected to be available and this will have an influence on the ultimate strategies used. Efforts by EU SOL (the European Union effort in translational genomics) in carbohydrate / sugar metabolism may also be leveraged in SolCAP.

Similar to the discussion on traits, the roundtable discussion on tools developed an extensive list. Common threads in the tools discussion were:

1. Need for a centralized phenotyping facility and database
2. Access to genotyping platforms
3. Breeder friendly analysis tools and centralized database for markers
4. Markers useful in breeding germplasm
5. Development of standard genotyping panels

Central Phenotyping Facility

Facilities would be identified and supported to standardize data collection and create a central database to prevent duplication of efforts and reduce costs. A priority would be given for traits that are expensive to measure and cross commodity boundaries, such as detailed characterization and quantification of carbohydrates and sugars.

Access to Common Genotyping Platforms

Access to genotyping platforms was identified by the community as important for collecting and standardizing data in breeding programs. It is recognized that no single platform will serve all needs. For example, one platform may be size polymorphism-based for SSR and INDEL markers, while others may be microarray- and SNP-based. Deep sequencing of select genes (such as those related to carbohydrate metabolism) across well-defined panels representing historically important germplasm, elite breeding material, and parents of mapping populations was identified as an important goal. To that effect, access to sequencing as a genotyping and SNP discovery platform was also identified as a priority.

Breeder-Friendly Analysis Tools

Common and centralized phenotyping and genotyping facilities will help standardize datasets and help populate and/or extend a common database with consistent allele calling. Bioinformatics expertise and database management is needed for the applied breeding community. Of particular importance to breeders was the need for current genomics tools and databases (like SGN) to be extended to become “breeder friendly” tools able to quickly select markers, view polymorphisms and develop a central

database and nomenclature for phenotypes. A central database for phenotypes and common nomenclature will enable QTL analyses and association studies across populations. TIGR and SGN could play an important role in the development of these databases. This type of service would benefit the smaller sized breeding efforts in the private and public sector. Training would be delivered through a series of workshops that would be held in a central location or regionally. Extension and education efforts are important to the SolCAP structure.

Markers in Breeding Germplasm

High-throughput, robust markers that can be used in elite germplasm as well as mapping populations are needed by the community. Indeed, an important legacy of SolCAP would be the development of high throughput, robust and user-friendly markers for breeding germplasm in commodities, specifically, potato, tomato and pepper. Many of the stakeholders put a priority on markers related to quality traits.

Standard Germplasm Panels

The stakeholders agreed that standard panels should be developed that represent a balance between relevant breeding lines and broad genetic-based germplasm to survey the allelic diversity for important traits and develop pertinent markers. Standardized platforms and germplasm may be used in exploring association mapping strategies within the commodities and examining domestication events (i.e. which genes came under selection).

Based on the above input, the stakeholders agreed that a deep-sequencing and genotyping strategy of genes and promoters related to carbohydrate metabolism would have the highest priority. Developing a common database and formats for collecting phenotypes, genotypes and a base set of germplasm on a complex trait important across *solanaceous* species will lay the foundation to pursue many other traits and germplasm. Some of the stakeholders are also involved in the EU SOL project. Activities of the SolCAP will be coordinated to leverage the EU SOL project. For example, with central genotyping facilities, a breeder could send populations in for genotyping. These populations could be segregating for any traits deemed important to breeding. The phenotyping would be done by the breeder. With a central genotyping facility, SolCAP would free breeders to focus more on phenotype and less on technology development. Developing accessible and user-friendly analysis tools for translational genomics will make genomics information accessible to the breeding community.

An important component of the SolCAP will be extension and training to ensure the community is familiar with analytical tools and resources developed. The training will take the form of workshops for bioinformatics and database access and/or management. Workshops for marker development and utilization would also be valuable to the community. Again, these workshops would be a deliverable from SolCAP that would benefit the Solanaceae community and bridge the gap between genomics and applied breeding efforts in the private and public sectors.

During the planning meeting held at the Plant and Animal Genome conference, draft proposals for target genes and germplasm panels were discussed. Volunteers to coordinate specific tasks aimed at developing individual trait and tool modules for the SolCAP infrastructure were identified for each goal.

At the Solanaceae Genomics conference in Madison WI, July 2006, David Douches was named the Project Director; an executive committee and overseeing

stakeholder and science advisory boards were outlined, as well as team leaders for each of the above mentioned goals. A small-sub grants program was also discussed. The workshop (<http://www.horticulture.wisc.edu/PAA-Solanaceae/>) highlighting current resources for translational genomics in Solanaceae worldwide was attended by over 100 people. Information on SolCAP can be found at <http://www.oardc.ohio-state.edu/tomato/SOLCAP.htm>.

An emerging objective of the SolCAP is to develop an infrastructure that allows applied programs to leverage the many genomic resources being developed for improvement of solanaceous crops. The organization of applied scientists will in-turn foster new collaborations among public and private breeders and genomic scientists. The successful funding of a CAP through the USDA in the future should not be considered the sole benefit of organizing. Any organizational structure that improves access to technology, resources, and methods for applied plant research will benefit public and private sector research, growers and end-users.

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