Minutes

**NCCC215 Potato Breeding and Genetics Technical Committee**

December 7th-8th, 2015

Holiday Inn O'Hare, Rosemont, IL

**Monday December 7th**

The meeting was called to order by Chair Susie (Asunta) Thompson at 1:00 PM. (see Agenda in Appendix 2). Some participants, including the Secretary were delayed due weather.

Each attendee introduced him/herself.

Approval of minutes of the December 2014 meeting: Last year's minutes had been distributed in advance by email. Minutes of the December 2014 meeting and agenda were formally approved.

Report from Administrative Advisor : Comments of administrative advisor (Ray Hammerschmidt, MSU) – NIMMS system is being upgraded. Our project is up for renewal next fall. Some items to include should be collaborative grants (whether within the region or amongst others).

NRSP6 report: This is the inter-regional multi-state genebank project at Sturgeon Bay, WI. Project Leader Bamberg indicated this funding source for the genebank was renewed for another 5 year term, FY16-20. One potentially revolutionary advance is the offer of Pepsico, CIP, and Chinese collaborators to genotype most items in the collection and return the data for free use.

Diploid potato breeding initiative: Shelley Jansky presented a report of the meeting held in June in Madison. Momentum has continued, including a white paper submitted to Crop Science. Discussion continued around building a research base without taking away from tetraploid cultivar development and the need to develop input.

Reports from contributing projects: Abstracts are presented in Appendix 1.

**Members and guests present and Institutions**

|  |  |  |
| --- | --- | --- |
| FName | LName | Inst |
| Maher | Alsahlany | MSU |
| John | Bamberg | UW - ARS |
| Spencer | Barriball | UMN |
| Benoit | Bizimungu | Ag Canada |
| Nathan | Butler | MSU |
| Grace | Christensen | UW |
| Mark | Clough | North Carolina State U |
| Joe | Coombs | MSU |
| Walter | DeJong | Cornell |
| Alfonso | del Rio | UW |
| Dave | Douches | MSU |
| Jeff | Endelman | UW |
| Curtis | Fredrick | UW |
| Dennis | Halteman | UW - ARS |
| Andy | Hamernik | UW - ARS |
| David | Holm | Colorado State U |
| Shafiqul | Islam | MSU |
| Shelley | Jansky | UW - ARS |
| Yuan | Lin | UW |
| Norma | Manrique-Carpintero | MSU |
| Alicia | Massa | MSU |
| Rich | Novy | ARS Aberdeen, ID |
| Greg | Porter | University of Maine |
| Sagar | Sathuvalli | Oregon State U |
| Cari | Schmitz | UW |
| Lance | Snodgrass | UW |
| Greg | Steere | MSU |
| Susie | Thompson | NDSU |
| Craig | Yencho | North Carolina State U |
| Matt | Zuehlke | MSU |
| Creighon | Miller | TAMU |
| Trina | Zavislan | Colorado State U |
| Chen | Zhang | MSU |
| Kate | McGlew | MSU |
| Ryan | Graebner | Oregon State U |
| Schuyler | Smith | UW |
| Jeff | Koyn | TAMU |
| David | Hannapel | IASTATE U |
| Swathi | Nadakuduti | MSU |
| Susan | Otieno | MSU |
| Haiyan | Jia | PEPSICO |
| Tom | Michaels | UMN |
| Rosa | Lozano | UMN |
| Tim | Kazmierczak | ARS USDA |
| Arun | Kuman | UW |
| Monica | Chen | UW |
| Henry | Castleberry |  |

Wine and cheese mixer at 5:50 ended the Monday session, with dinner "on your own".

**Tuesday, December 8th**

Meeting reconvened at 8:00 AM. Presentations continued.

Venue for next meeting was determined to be Dec 5-6, 2016 at the same venue.

Officers: J. Bamberg = Chair, B. Bizimungu = Vice Chair, Jeff Endelman = Secretary.

Meeting was adjourned approximately at noon.

Respectfully submitted,

B. Bizimungu

**Appendix 1.** Abstracts of research presentations

**Shelley Jansky and Andy Hamernik**

**USDA-ARS and Department of Horticulture, UW-Madison**

**Recombinant inbred line (RIL) development.** We are generating four recombinant inbred line (RIL) populations from crosses between the *S. chacoense* inbred line M6 and diploid clones. A fifth RIL population is being generated using a dominant self-compatibility gene from the cultivated diploid US-W4.

**Creation of a diploid inbred *S. tuberosum* clone.** As we approach completion of the RIL populations, our next plan is to create introgression lines. This will require a homozygous cultivated diploid that carries a dominant self-incompatibility inhibitor. Toward this end, we have self-pollinated US-W4 and currently have 12 S4 plants in the greenhouse, five of which are flowering. To begin IL development, we will cross a US-W4 S6 clone with M6 and a *S. verrucosum* clone and then backcross to the S6 inbred.

**DM1-3 x M6 F2 phenotyping and genotyping.** This true F2 population of 211 clones is segregating for many traits, including male fertility, self-compatibility, 2n egg production, glandular trichome density, vine vigor and stolon production; tuber amylose content and pH; and tuber skin color, flesh color, dormancy, size, shape and dry matter content. In collaboration with Jeff Endelman and Dave Douches, we have mapped 10 genes using SolCAP SNP markers.

**New phenotyping methods**. We are initiating research using a hand-held thermal infra-red imager to evaluate Verticillium wilt resistance in field plots.

**National Verticillium wilt trial.** Three trials were planted on May 5, 2015. Each consisted of three replications of five-hill units of 50 cultivars and advanced selections from the U.S. potato breeding programs. Symptom, sap and dried stem data have been collected and will be made available to cooperators.

**David J. Hannapel**

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NCCC215 Summary Dec. 7, 2015

Email: [djh@iastate.edu](mailto:djh@iastate.edu)

**Front-loaded and doubled-down: The signaling network of tuberization**

**Summary.** Under optimum conditions, tuberization is activated by a signal(s) that arises from the leaf and moves down into stolon tips to induce tuber formation. Our current understanding of tuber development envisions a finely tuned process of cell growth in the stolon meristem that is tightly regulated both spatially and temporally. Three major signals have been identified: *St*CDF1 in the leaf for earliness (Kloosterman et al., 2013) and *StBEL5* RNA and *St*SP6A protein as mobile signals arising from the leaf (Hannapel, 2013). *St*CDF1 is a transcriptional regulator that controls plant maturity and mediates the onset of tuberization by down-regulating the repressive activity of *St*CONSTANS. *St*SP6A is a transcriptional co-regulator, whereas *St*BEL5 is a transcription factor (TF) that is transported as mRNA to stolons where it is translated and functional (Banerjee et al., 2006). During this process, *St*BEL5 front-loads activity in the leaf through the transcriptional induction of both *StCDF1* and *StSP6A* (Sharma et al., 2016). Localization of the signal into stolons is regulated by transport of the mobile protein, *St*SP6A, and the full-length mRNA of *StBEL5* through the sieve element system. RNA-binding proteins protect and mobilize the *StBEL5* transcript (Cho et al., 2015). Amplification of the signals occurs in stolons, where *St*BEL5 in tandem with its Knox partner induces transcription of both *StSP6A* and *StBEL5*. Site mutagenesis in tandem TTGAC motifs, (specific for the StBEL5/Knox complex) located in the upstream sequence of both *StBEL5* and *StSP6A* suppressed the SD-induced activity of their promoters in young tubers (Lin et al., 2013; Sharma et al., 2016).

Through its transcriptional activity in conjunction with a Knox partner, *St*BEL5 front-loads the tuber signals, *St*SP6A and *St*CDF1, in the leaf and then follows this with a doubling-down of the two key tuber signals, *St*SP6A and *St*BEL5, in stolons during the onset of tuber formation. Yeast two-hybrid assays suggest that StSP6A and StBEL5 interact and that both are critical components of a novel tuber activation complex. In summary, the current model for the tuber-signaling pathway exhibits several unique features:

1) StBEL5 induces transcription of the FT ortholog, StSP6A, and the gene for earliness, StCDF1. In both cases, SP6A activity is enhanced.

2) Full-length *StBEL5* mRNA moves through the sieve-element system from leaf to stolon.

3) Specific RNA-binding proteins facilitate this long-distance transport of mRNA.

4) There are two mobile signals that mediate tuber formation: *St*BEL5 and *St*SP6A.

5) Suppression of *St*BEL5 shuts down tuber formation.

In this evolving model, *St*BEL5 is positioned upstream of an intricate regulatory network involving hormonal pathways and transcriptional regulators that controls the onset of tuber formation. In its role as a TF, *St*BEL5 functions to directly activate tuberization, and at the same time, to amplify other indispensable signals in the pathway.

References

**Banerjee AK, Lin T, Hannapel, DJ** (2009) Untranslated regions of a mobile transcript mediate RNA metabolism. *Plant Physiol* 151:1831-1843.

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Chen, H, Banerjee, A. K, and Hannapel, D. J. 2004. The tandem complex of BEL and KNOX partners is required for transcriptional repression of *ga20ox1*. *Plant J* 38: 276-284.

**Cho SK, Sharma P, Butler NM, Kang IH, Shah S, Rao AG,** Hannapel DJ (2015) Polypyrimidine tract-binding proteins of potato mediate tuberization through an interaction with *StBEL5* RNA. *J Expt Bot* 66: 6835-6847.

**Hannapel DJ** 2013. A perspective on photoperiodic phloem-mobile signals that control development. Front Plant Sci 4: 295.

**Kloosterman B, Abelenda JA, Gomez MdM, Oortwijn M, de Boer JM, Kowitwanich K, Horvath BM, van Eck HJ, Smaczniak C, Prat S, Visser RG, Bachem CW** (2013) Naturally occurring allele diversity allows potato cultivation in northern latitudes. Nature 495: 246-250

**Lin T, Sharma P, Gonzalez D, Viola I, Hannapel DJ** (2013) The impact of the long-distance transport of a *BEL1*-like mRNA on development. *Plant Physiol* 161: 760-772.

**Sharma P, Lin T, Hannapel DJ** (2016) Targets of the *St*BEL5 transcription factor include the FT ortholog *St*SP6A. *Plant Physiol* (Jan. issue).

**David Douches**

**MSU Potato Breeding and Genetics Report:** We use a combination of conventional breeding and biotech approaches to develop and improve potato germplasm for variety development. We emphasize scab, late blight and PVY resistance. Field trials are used to help us characterize the advanced and early generation lines for their late blight and scab reaction. DNA markers help us select for PVY virus resistance. We have a number of promising chip processing advanced selections that are scab resistant. A few also combine late blight and PVY resistance with the scab resistance. The same holds for our table selections. All lines are brought into tissue culture and we use cryotherapy to remove virus. We also have a greenhouse certified and dedicated to mini-tuber certified seed production of MSU advanced selections and new varieties.

**Maher Alsahlany**

**Diploid potato breeding with self-compatibility:** How does recurrent selection effect on adapting SC germplasm for photoperiod, keeping genetic diversity in population, and reducing genetic load? Opportunity to select best lines from each cycle to produce new recombination inbred line (RIL) population.

**Alicia N Massa**

**Linkage analysis and QTL mapping in tetraploid potato:** We are developing a SNP-based linkage map for the parents of the PRRG (Premier Russet × Rio Grande) mapping population. A preliminary data analysis using these maps identified quantitative trait loci and candidate SNPs for key agronomic and tuber quality traits, including reducing sugars, specific gravity, growth habit, and plant maturity. These candidate SNPs are of interest and are the focus of further marker development.

**Chen Zhang**

***eIF4E-*mediated Potato Resistance against *Potato Virus Y* in Susceptible Potato Varieties:**

The translation initiation factor 4E (*eIF4E*) has been implicated in naturally-occurring resistance to the Potato Virus Y (PVY) determined by the *pot-1* locus in tomato. Some of the susceptible potato varieties were selected to be transformed with the tomato *pot-1* gene. Transgenic potato lines have been screened for PVY resistance in a greenhouse setting with artificial inoculation, as well as in the field with naturally-spreading PVY. Among all the tested transgenic lines, Classic Russet and MSE149-5Y with this transgene demonstrated complete resistance against PVY in both greenhouse and field. In contrast, the symptomless carriers, Russet Norkotah and Silverton Russet, displayed moderate resistance to PVY.

**Swathi Nadkumar**

The specificity of genome editing reagents such as TALENs and CRISPR/cas systems to induce double stranded breaks is questionable, since un-intended cleavage activities else where in the genome are previously reported. GUIDE-seq method has been developed for genome-wide unbiased identification of these off-target cleavages enabled by sequencing to evaluate the utility of these reagents for genome editing.

**Felix Enciso**

**Genomic approximations to improve pathogen resistance in tetraploid potato:** A pipeline was developed to perform a Genome Wide Association Analysis in a tetraploid potato population. Late blight and scab resistance were measured during 6 years and all records were corrected using the best linear unbiased prediction method. Potato lines were genotyped and 4859 SNPs were identified, generating a filtered genotype file coded for a tetraploid additive model. Processed phenotypic and genotypic files were used to generated the GWAS using a generalized least square model for both traits. Three and five SNPs were significant associated for late blight ad scab resistance respectively. These markers are located on genes previously reported for their role in plant disease resistance.

**Norma C. Manrique-Carpintero**

**Improved Genetic Map DRH Population:** The density of the DRH population genetic map was improved by increasing the population size from 96 to 190 individuals. The additional 94 individuals were genotyped with the Infinium Potato Array version 2. In that specific sub-set 3196 segregating markers were identified compared to 1948 from previous array version. Comparison of maps allowed identifying that besides more segregating markers, some were located in gap positions of the previous map as expected. We also present an update of the results of development of a monoploid line of *Solanum tuberosum* Group Tuberosum.

**Shafiqul Islam**

**Combined PVY and PLRV resistance in advanced tetraploid potato breeding germplasm:** PVY and PLRV are worldwide concern in potato. They reduce tuber yield significantly by giving necrotic symptom in tuber. Aphids are main vector to carry them to potato plants. Current objective is to combine PVY (*Ryadg*) and PLRV (*Rlagd*) resistance in a single line with good agronomic traits. Current developed progeny is MSCC725 from the cross between MSR061-01 and MSAA731-01. In here, the parent, MSR061-01 was PVY resistance and the grandparent, Alca Tarma was PLRV resistance. The population MSCC725 was planted in field and in large pot in summer 2015 for evaluation of tuber and vine maturity. During vegetative stage, young leaf tissues were collected to isolate DNA. Using these DNA, lines were screened by first with PVY marker, RYSC3 and then PLRV marker, SCAR for them which had positive PVY band. Total line was 438 from where 208 lines were PVY positive and 93 lines were PLRV positive from 208 PVY positive lines. Their segregation ratios were 47.5% and 20.2%, respectively. Tuber weight, tuber appearance and vine maturity were normally distributed except tuber number. Tuber numbers were right skewed distribution. This population was selected population, not a random. It meant tuber number were associated with major disease PVY and PLRV resistance QTL. All the 93 PVY and PLRV positive lines were clustered hierarchically and they fell in one major cluster including parent, MSR061-01 and grandparent, Alca Tarma.

**Kathleen McGlew**

**Genetic Marker Testing for MSU Potato Breeding Program**

Using PCR to test potato varieties for some of the most important potato diseases is a useful tool in potato breeding, specifically at Michigan State University. Some of the main markers that are used at MSU include: *RYSC3*, a PVY resistance marker; *IPM4*, a PVX resistance marker; *TG689*, a golden nematode resistance marker; and RB, a Late Blight resistance marker*.* Over the past half-decade, much of the MSU program germplasm has been tested for disease resistance with the confirmation of several important disease-resistant parents and lines. These include: MSW027-1 (Eva x MSQ176-05), MSW242-5Y (NY121x Malinche), MSX380-3 (NY121x MSM246-B), MSX540-4 (MSR061-1 x NY139), MSR061-1 (W1201 x NY121), and MSM182-1 (Stirling x NY121). Additionally, we tested for disease resistant markers in second year tubers. Based on our PVY resistance marker testing, we planted out the 45% of the 700 first year tubers that were positive for PVY resistance in the summer of 2015. This allowed for a prioritization of the space in the field and in tissue culture for lines that were disease resistant and allowed for earlier, more informed decisions in variety selection.

*Benoit Bizimungu*

**Agriculture and Agri-Food Canada, Potato Research Centre, Fredericton, NB**

The 2015 NCR Trial focusing primarily table stock clones was planted at the Vauxhall Research substation, AB. The trial at Vauxhall comprised a total number of 12 entries from collaborators, including 7 russets and 5 white or yellow-skinned clones, in addition to standard check varieties. The trial was planted on June 14th and harvested on August 26th. Yields were relatively lower than previous year, in part due to late planting. A complete report was sent to NCR Trial collaborators.

The national potato breeding program focusses on the production of French fry, chip, fresh market and specialty varieties which are adapted to production under rain-fed conditions in eastern Canada and to production under irrigation in western Canada. Duplicates of early generation material are grown each year at the Benton Ridge Substation, NB and at the Vauxhall Research Substation, AB. Advanced selections resulting from both streams are evaluated in national adaptation trials. Superior clones with commercial potential are offered to industry under an Accelerated Release Program where companies may evaluate clones on a non-exclusive basis for two years before requesting rights for exclusive evaluation and a licence for commercialization. Further information is available on-line at:[www.agr.gc.ca/potato-cultivars](http://www.agr.gc.ca/potato-cultivars).

**L. Snodgrass, J. Endelman**

Dept. Horticulture, University of Wisconsin, Madison, WI 53706

**Agronomic and culinary evaluation of elite fresh market potato germplasm**

The goal of this study was to measure the agronomic and culinary properties of elite fresh market breeding lines. The agronomic properties, which included total yield, tubers per plant, tuber size distribution, tuber disease incidence, and the incidence of internal defects, were measured with a replicated complete block design at two commercial locations and one research station in Wisconsin. The multi-environment trial structure enabled a comparison of the broad-sense heritability for each location as well as the genetic correlation between sites, estimated using a multivariate mixed model. The culinary traits, which included two different analytical measurements of texture and the results of a human sensory panel, were only evaluated for tubers from one location due to their labor-intensive nature. Results from the first year showed that, except for disease incidence, the heritability of the agronomic traits was consistently high (> 0.7). The genetic correlation between sites was high for some traits, such as tubers per plant (> 0.8), but was more variable and lower for yield. This research has helped identify several breeding lines with superior agronomic and culinary properties as candidates for variety release.

**C. Schmitz Carley, J. Endelman**

Dept. Horticulture, University of Wisconsin, Madison, WI 53706

**Allelic Dosage Scoring for Tetraploids**

Accurate tetraploid allelic dosage calls are important for genome-wide association studies (GWAS) on diverse collections of tetraploid potato germplasm, such as entries from the National Chip Processing Trial (NCPT). A few shortcomings of the published methods for allelic dosage assignment for tetraploid samples have been identified. Clustering samples into allelic dosage groups via mixture models can result in difficulties in identifying small membership clusters and in separating close heterozygous clusters. We propose a new two-step process by which a model is trained with several bi-parental families, and those resulting genotype calls are then used to inform a prediction phase. The prediction phase can be used to make genotype calls for diverse clones.

**J. Bamberg, A. del Rio, T. Kazmierczak**

US Potato Genebank, Sturgeon Bay, WI 54235

**Genebank research update**

The genebank group was represented by Bamberg and Kazmierczak from Sturgeon Bay and del Rio from Madison. Del Rio began by describing cooperative breeding with physiologist Jiwan Palta of Madison and Peruvian cooperators on the Altiplano in Puno province of Peru. Some selections from populations bred at Sturgeon Bay are being released as new cultivars with superior yield, quality and frost resistance. Bamberg then presented the latest studies on the USA native potato species *S. jamesii*. In addition to several useful traits, this year significant tuber freezing resistance was discovered-- otherwise unknown in potato. This year the first *jamesii* hybrids with *tuberosum* were successfully made. It was found that the mega-population at Mesa Verde contains nearly all the known genetic diversity for the species, and staff have joined forces with Utah anthropologists to explore the possibility of human intervention. Bamberg mentioned that the small Colombian *Criolla* egg-yolk style specialty potatoes the group has been evaluating might combine two consumer-recognized qualities, "baby red" and (Yukon) "gold" if produced in a form with red skin. Finally, Kazmierczak presented experiences in brewing beer from potato juice, and projections of the significant positive impact on national nutrition and demand for potato if beer was sourced from potato rather than grain. These topics and others are fully reported on the genebank website, http://www.ars-grin.gov/nr6/.

**Publications**

Bamberg, J., Moehninsi, R. Navarre, and J. Suriano. 2015. Variation for Tuber Greening in the Diploid Wild Potato *Solanum microdontum*. American Journal of Potato Research 92:435-443.

Hardigan, M., J Bamberg, C Robin Buell and D Douches. 2015. Taxonomy and genetic differentiation among wild and cultivated germplasm of Solanum sect. Petota. The Plant Genome. 8:1:16.

**Appendix 2-Agenda**

**NCCC215 Potato Breeding and Genetics Technical Committee Meeting**

**Holiday Inn Express at O’Hare, Chicago, Illinois**

**December 7-8, 2015**

**Chair: Susie Thompson**

**Vice-chair: John Bamberg**

**Secretary: Benoit Mizimungu**

***Dec 7th, Meeting Time: 1PM – 6PM***; *Refreshments Break: 3PM*

1. Welcome, announcements

2. Introduction of members and guests

3. Approval of minutes of the December 2014 meeting

4. Comments of administrative advisor (Ray Hammerschmidt, MSU)

5. NRSP-6 update (John Bamberg)

6. Reports from contributing projects (**Potato Breeding and Genetics Research**)

* Alberta
* Michigan
* Minnesota
* North Dakota
* Wisconsin
* Other contributors

*6PM -7PM: Mixer*

***Dec 8th****,* ***Meeting Time: 8:00AM – 12:00PM***; Refreshments Break 10:00 AM

7. North Central Regional Potato Variety Trial Report (Jeff Endelman)

8. Reports from contributing projects (**Variety Development**)

* Alberta (Benoit Bizimungu)
* Michigan (Dave Douches)
* Minnesota (Tom Michaels)
* North Dakota (Susie Thompson)
* Wisconsin (Jeff Endelman)
* Other contributors (ID, CO, etc.)

9. New business

10. Date and venue for next year’s meeting

11. Election of new officers

12. Adjourn