

Minutes
NCCC215 Potato Breeding and Genetics Technical Committee
December 8th-9th, 2014
Holiday Inn O'Hare, Rosemont, IL

Monday December 8th

The meeting was called to order by Chair David Douches at 1:00 PM. (see Agenda in Appendix).

Chair requested that each person presenting research provide a short summary to Secretary John Bamberg for the Minutes (see Appendix). Dennis Halterman suggested that participants also submit their formal publications from the past year for inclusion in the minutes.

Each attendee introduced him/herself.

Susie Thompson eulogized colleague Christian Thill, whose untimely death leaves the leadership of the NCCC215-participating UMN breeding program vacant. Elizabeth Hoover from UMN administration was present to dialog about the outlook for filling the position. Comments from the group suggested that aiming to refill the position with an emphasis on standard breeding would be unwise due to difficulty in getting outside grant support, and lack of a vital need for a fourth NC breeding program. An emphasis on basic potato research would be more desirable.

Last year's minutes had been distributed in advance by email. Formal group approval M/S/C.

Report from Administrative Advisor. Douches reports on behalf of Ray Hammerschmidt of MSU. It was noted that meeting minutes should document cooperation of the participants [[see Publications sections in Appendix](#)].

NRSP6 report. This is the inter-regional project at Sturgeon Bay, WI. Project Leader Bamberg noted NRSP6 is up for renewal for FY16-20, and prospects are good for approval at flat funding. On the other hand, there was a substantial permanent funding increase by USDA/ARS starting FY14.

Members and guests present, Institutions, Roster order and Presentation order

FName	LName	Inst	Roster ord	Present ord
Christina	Allen	UW	06	
Maher	Alsahlany	MSU	39	19
John	Bamberg	UW - ARS	16	11
Spencer	Barriball	UMN	25	18

Benoit	Bizimungu	Ag Canada	01	23
Nathan	Butler	MSU	34	16
Grace	Christensen	UW	20	
Mark	Clough	North Carolina State U	02	
Joe	Coombs	MSU	11	15
Walter	DeJong	Cornell	04	
Alfonso	del Rio	UW	10	12
Dave	Douches	MSU	15	14
Jeff	Endelman	UW	23	10
Felix	Enivo	MSU	41	
Curtis	Fredrick	UW	07	01
Caroline	Gray	Colorado State U	30	
Sanjay	Gupta	UMN	26	17
Don	Halseth	Cornell	42	
Dennis	Halteman	UW - ARS	28	03
Andy	Hamernik	UW - ARS	12	
David	Holm	Colorado State U	29	
Emily	Hoover	UMN	32	
Shafiqul	Islam	MSU	40	21
Shelley	Jansky	UW - ARS	31	02
Donna	Kells	MSU	38	
Yuan	Lin	UW	05	04
Saltanat	Mambetovo	MSU	35	
Norma	Manrique-Carpintero	MSU	17	20
Max	Martin	UW	13	
Alicia	Massa	MSU	14	22
Rich	Novy	ARS Aberdeen, ID	36	24
Greg	Porter	University of Maine	37	
Kyle	Rak	UW	08	07
Flor	Rodriguez	CIP	09	
Umesh	Rosyara	UW	24	08
Sagar	Sathuvalli	Oregon State U	27	
Cari	Schmitz	UW	21	09
Lance	Snodgrass	UW	22	06
Greg	Steere	MSU	19	
Susie	Thompson	NDSU	33	13
Craig	Yencho	North Carolina State U	03	
Matt	Zuehlke	MSU	18	

Chairman Douches proposed a discussion of the pending deployment of Simplot Innate technology, but this did not happen during the meeting due to lack of time.

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

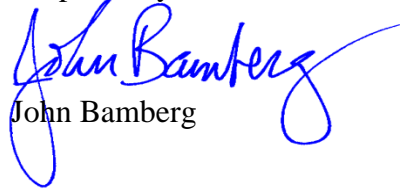
Tuesday, December 9th

Meeting reconvened at 8:00 AM. Presentations continued.

Venue for next meeting was determined to be Dec 7-8, presumably at the same location.
Officers: S. Thompson = Chair, J. Bamberg = Vice Chair, B. Bizimungu = Secretary.

Meeting was adjourned approximately at noon.

Respectfully submitted,


John Bamberg

Appendix 1. Abstracts of presentations

Bethke group

Curtis Frederick

A proposed method to improve phenotyping of processing potatoes is to employ Near Infrared Spectroscopy (NIRS) for specific gravity and sugar concentration measurements. This technology has already been in use in many crop breeding programs for traits that require labor-intensive wet-chemistry analysis. This is because NIRS is a fast, inexpensive method for measurement, its operating costs are low, and only requires under a minute to complete a sample. In order to implement this technology, a calibration curve relating the trait values to the reflectance values of the infrared light would have to be developed. We are in the process of developing this model on a group of 96 individuals from a bi-parental population. Our preliminary results are from dry matter and this data was jackknifed 70:30 on 500 iterations of a Partial Least Squares regression model. The mean R^2 was 0.85 and the mean validation RMSE was < 10% of mean dry matter. These results include multiple sampling methods and are expected to improve when models are created based on sampling types. We expect to run a similar analysis on sugar data as it becomes available. This new technology may be useful for QTL detection in that it can measure more genotypes and allow for larger population sizes. It also has benefits in simple selection programs in that the sugar analysis would require much less resources per sample, thereby allowing more samples throughout the storage season.

Endelman group

Toward genome-wide association studies with the National Chip Processing Trial

Schmitz C, Douches D, Endelman J

Agronomic data collected through the National Chip Processing Trial (NCPT) from 2010 through 2013 at ten locations across the USA lends itself well to genome-wide association study (GWAS). For this project, 182 clones from the NCPT were genotyped with the SolCAP Infinium array, consisting of 8303 SNP markers, and an additional 69 individuals have been SNP genotyped previously. Structure of the SNP-genotyped individuals was examined by inclusion of 221 tetraploid individuals from the SolCAP diversity panel in discriminant analysis of principal components (DAPC). The diversity panel includes all market classes. Clones of the NCPT group into three clusters, as previously observed. Pedigree information is being assembled from breeding records, which is expected to shed more light on the origin of the three chipping potato clusters.

Evaluating culinary properties of fresh market potatoes

Snodgrass L, Endelman J

The cooking type of fresh market potatoes is frequently characterized using an A–D scale, where A is described as “very firm” and D is “very mealy.” Previous research has called into question whether this linear scale can adequately capture the multi-dimensional nature of potato cooking quality. Three key culinary properties that can be measured by human subjects or laboratory instruments are mealiness, hardness, and the extent of sloughing. Fresh market red, russet, and yellow breeding lines from the UW program will be evaluated for these traits during the 2014 storage season. Mealiness will be evaluated by human subjects, hardness by a penetrometer, and sloughing by loss of dry matter after boiling. In preliminary tests with red, yellow, and russet potatoes, there was an inverse relationship between degree of sloughing and hardness (force required for penetration). The red varieties were the hardest and sloughed the least, while the russets were at the other extreme.

Development and application of genome-wide association studies in autotetraploid potato

Rosyara U, Endelman J

Genome-wide association studies (GWAS) are widely used in diploid species to discover causal loci in diversity and breeding populations. The most common statistical method for GWAS is the Q+K mixed model, in which Q and K refer to the structure and kinship matrices, respectively, that are used to control for the effects of population structure. The objectives of this research were to (1) adapt the Q+K methodology for use with bi-allelic, co-dominant markers in autotetraploids, (2) test these models in a diversity panel of 200 potato lines, and (3) make the software available as a user-friendly R package. Unlike earlier approaches to association mapping in autotetraploids, we studied a number of models for gene action, including additive, simplex dominance, and duplex dominance, while employing a faster algorithm that can accommodate larger datasets. Consistent with previous studies, highly significant QTL for tuber shape and eye depth colocalized on chromosome 10 when using an additive model. Under the assumption of complete dominance, the chromosome 10 QTL were not significant, illustrating the influence of the gene model on the results. For most traits, only marginally significant QTL were detected, most likely due to insufficient statistical power. For simulated traits with a heritability of 0.3, the median power was only 0.03. Potential causes for the low power were investigated by varying the population size and marker density in simulated, random-mating autotetraploid populations. The results of the simulation suggest that the size of the diversity panel was the primary limiting factor for statistical power.

Genotyping-by-sequencing of a diploid potato F2 population

Endelman J, Jansky S

Genotyping-by-sequencing (GBS) of multiplexed, restriction-site associated DNA (RAD) libraries is an attractive technology for generating genome-wide markers because of its technical

simplicity and low costs per sample. To investigate its feasibility for potato, a diploid F2 population (*S. tuberosum* DM1-3 x *S. chacoense* M6) was genotyped at 96-plex using the enzyme *EcoT22I*. Using an R-based bioinformatics pipeline to filter the GBS variants, more than 11,000 bi-allelic SNPs were identified. During the curation process, we identified variants in 45 superscaffolds whose linkage group conflicted with the chromosome assignment in the latest version (4.03) of the potato reference genome; further study of these discrepancies may help improve the reference sequence. One indicator of the quality of the curated marker data was that the phase of the F1 parent, which was predicted from the F2 progeny using a Hidden Markov Model, was correct across the entire genome. Another indicator of quality was our ability to map two traits—pigmented skin color (*Stan2*) and yellow flesh color (*CHY2*)—to their known positions on chromosomes 10 and 3, respectively. To guide future research, we used the empirical read depth distribution to simulate GBS libraries at several multiplex levels. For diploid potato, the 96-plex level used in this study appears to offer the best compromise between marker density and cost per sample. For autotetraploid potato, because greater depth is needed to differentiate the three heterozygous genotypes, 48-plex (or lower) is recommended when using *EcoT22I*.

Jansky group

The USDA-ARS Potato Germplasm Enhancement Program in Madison, Wisconsin, is developing five populations of diploid recombinant inbred lines. Self-compatibility in these populations is derived from two sources, *S. chacoense* clone M6 and *S. tuberosum* dihaploid US-W4. F6 populations will be made available for breeding and genetics studies. An unmanned aerial vehicle was tested to evaluate vine development in field trials and is promising as a high-throughput phenotyping tool. The diploid scab resistant clone 4-48 produces 2n pollen and 2n eggs. Some tetraploid offspring from crosses of 4-48 to cultivars produce large smooth tubers with resistance to common scab.

Halterman group

Yu (Monica) Chen – Postdoc

Potato late blight, caused by the oomycete pathogen *Phytophthora infestans*, is one of the most destructive plant diseases. Despite decades of intensive breeding efforts, it remains a big threat to potato production worldwide, because newly evolved pathogen isolates have overcome major resistance genes quickly. The *RB* gene, cloned from the diploid wild potato species *Solanum bulbocastanum*, confers partial resistance to most *P. infestans* isolates through its recognition of the corresponding pathogen effector family IPI-O. IPI-O is a multigene family of effectors. While the majority of IPI-O proteins are recognized by RB to elicit host resistance (e.g. IPI-O1, IPI-O2), some family members are able to elude detection (e.g. IPI-O4). In addition, we have previously shown that the presence of IPI-O4 *in planta* is able to suppress the HR elicited by IPI-O1 in the presence of RB. We have also observed that strains of *P. infestans* containing IPI-O4 are able to cause more disease on *RB* plants compared to strains without IPI-O4. This has led to a hypothesis that the presence of IPI-O4 results in suppression of RB.

Champouret et al. suggested that the absence of IPI-O1 and IPI-O2 in certain strains of *P. infestans* allows them to overcome *RB*. However, these strains also contained IPI-O4, which we believe could also explain the phenotype. The goal of my project is to determine the effect that the presence of IPI-O1 and IPI-O4 has on *P. infestans* virulence. Furthermore, it may provide conclusive evidence that the presence of IPI-O4 *in planta* allows *P. infestans* to overcome *RB* resistance.

In order to assay the effect of expression of IPI-O genes individually, we have stably transformed the susceptible potato cultivar ‘Katahdin’ with IPI-O1 and IPI-O4 separately. We also transformed the potato line K41, which contains the *RB* gene and was developed from the potato-*S. bulbocastanum* hybrid by backcrossing with ‘Katahdin’ three times, with IPI-O4. The transformed plants have been analyzed for the presence or absence of IPI-O genes using PCR and the copy number of the insertion events has been determined using DNA blotting techniques. We are analyzing 10 independent transgenic plants with various copy number of inserted gene for each construct. The effect of IPI-O1 on the ability of *P. infestans* to cause disease symptoms in potato will be assayed using whole plant and detached leaf assays. We expect the overexpression of IPI-O1 to have some visible effect on the virulence of these strains either through more rapid disease progression or increased lesion area. The ability of IPI-O4 to affect *P. infestans* virulence will be assayed in the same way using the wild-type and IPI-O4 transgenic ‘Katahdin’ plants. We will also test the ability of IPI-O4 to confer virulence in the presence of *RB* using the K41 transgenic plants. If the presence of IPI-O4 (and not the absence of IPI-O1 and IPI-O2) is responsible for increased virulence when *RB* is present, we should observe enhanced disease symptoms using strains that lack IPI-O4. We also plan to assay the IPI-O transgenic plants for increased susceptibility to other pathogens, such as potato virus Y, *Phytophthora capsici*, in order to determine whether the activity of IPI-O is specific for virulence in *P. infestans* or whether it has a more general effect on host susceptibility.

Yuan Lin – Postdoc

As one of the most serious potato diseases, potato late blight is caused by the *Phytophthora infestans*. Naturally, some wild potato species have their resistant resources, such as the *RB* gene, from the diploid potato *Solanum bulbocastanum*. *RB* confers partial resistance to most *P. infestans* isolates. The resistance mechanism of *RB* was well known as recognizing pathogen effector family IPI-O specifically. What’s more interesting is the majority of IPI-O proteins are recognized by *RB* to elicit host resistance (e.g. IPI-O1, IPI-O2), however, IPI-O4 blocks recognition of IPI-O1, leading to inactivation of *RB*-mediated programmed cell death, which implied a risk of *RB* mediated resistance being overcome by specific strains of the pathogen. We hypothesize that the presence of IPI-O4 rather than the absence of IPI-O1 results in increased pathogen virulence in the presence of *RB*.

Our previous research suggests an IPI-O and *RB* model based on the interaction behaviors between IPI-O1/4 and the CC domain of *RB* protein. In this model, the CC domain was assumed as a key signal-transferring factor co-functioning with IPI-O1 and 4. This kind of regulation is mostly based on protein-protein interaction or post-translational level, this can lead to a hypothesis that *RB* forms a protein complex within host proteins upon exposure to *P. infestans* IPI-O effectors. We are currently analyzing the *RB* and IPI-O1/4 individual proteins and protein complexes after transient expression in *Nicotiana benthamiana* leaves. This is being accomplished using immunoprecipitation of tagged proteins. Next we will analyze the interacting protein partners of *RB* and IPI-O1/4 individually or cooperatively, which will be helpful in

identifying protein complex components. Also, the post-translational modification of RB protein after recognizing IPI-O1 (active state) or being suppressed by IPI-O4 (inactive state) might be worth digging into.

Austin Meier – PhD student, Plant Breeding and Genetics Program

The potato genome was sequenced in 2011, but potato genomics is in its infancy. With the release of the SolCAP SNP chip, and as additional potato genomes are resequenced, the variation in potato's sequence, and genome structure becomes clearer. Understanding the variation available is useful to breeders and scientist who look to unravel the connection between genotype and phenotype.

C287, a heterozygous diploid hybrid with resistance to *Verticillium* wilt, was sequenced using Illumina's hi-seq, paired ends platform. Using the resulting reads, and a genetic modeling tool known as Pindel, we show the absence of a previously unannotated putative resistance gene when compared to sequenced DM1-3 potato genome. Predicted genetic variation was confirmed using PCR primers designed to amplify designated regions shown to be absent in C287. It is hypothesized that this presence/absence variation may play a role in the resistance of potato species to *Verticillium* wilt.

The use of molecular markers is complicated by the wide genetic variation available in wild potato species, and other less adapted germplasm. Evaluating the usefulness of two CAPS markers previously published that have been shown to predict *Verticillium* wilt resistance. We have found that specificity of these markers can be complicated by the existence of homologous gene clusters, and that continued efforts are needed to develop strategies to deal with structural and sequence variation that exists in wild potato germplasm.

Amilcar Sanchez-Perez – PhD student, Plant Pathology with Amanda Gevens

Survivability and infectivity of oospores generated by mating pairs of Phytophthora infestans collected in Wisconsin

Phytophthora infestans, is a heterothallic oomycete causing late blight of potato and tomato. The pathogen can produce oospores when both mating types A1 and A2 have physical interaction. In the history of late blight in the U.S., *P. infestans* populations have been largely asexual and detection and tracking of clonal lineages has aided in rapid pathotype characterization and prescriptive management. However, in other countries, sexual recombination occurs making for increased strain diversity, soil persistence, and enhanced challenge in disease control. In our study, oospores were produced under controlled laboratory conditions in tomato leaflets by crossing two mating pairs of *P. infestans* collected from Wisconsin, during 2009-2013. US-22 (A2) x US-23 (A1) and US-22 x US-24 (A1). Extracted oospores were then incubated for 5 months under 6 different temperature regimes including one in soil under natural field conditions in central Wisconsin, from Nov to Mar of 2011-12 and 2012-13. The remaining 5 temperatures were controlled in the laboratory and ranged from 22° C to -20° C. Post incubation, the viability of oospores was determined using plasmolysis and vital staining methods. Our results showed that oospores were viable after being exposed to natural field winter conditions with temperatures ranging from 5° C to -10° C at depths from 2 inches to 7 inches. Both viability assessment methods indicated a reduction in percent viability with increased cold conditions. In our assessments of infectivity, we determined that oospores

exposed to different cold temperatures could be a source of inoculum and initiate late blight on tomato leaflets. Oospores incubated at 22°C caused late blight lesions in 9% of tomato leaflets. Averages of 4% of leaflets were infected in the bioassay with soil exposed to winter in field conditions. Oospores could not initiate late blight infection after exposure, in soil to -20°C. Nor were oospores able to initiate disease on potato plantlets emerging from whole seed potatoes planted into oospore-infested soil. We demonstrated the potential for oospores produced by new clonal lineages of *P. infestans* to survive and remain infective after incubation under freezing temperatures in controlled laboratory environments, as well as under field soil conditions during two Wisconsin winters 2011-12 and 2012-13.

Genotypic and Phenotypic Characterization of Phytophthora infestans Collected in Wisconsin during 2014

Phytophthora infestans, the causal agent of late blight of potato and tomato, has been reported in Wisconsin in the last five growing seasons. Twenty nine isolates were collected from seven Wisconsin counties in 2014. Genotypic characterization was performed with *Glucose-6-phosphate isomerase (Gpi)* allozyme locus analysis, mitochondrial haplotyping and genomic assessment with 12 microsatellite markers. Phenotypic characterization included mating type analysis, and sensitivity to the fungicide mefenoxam. *Gpi* allozyme testing revealed alleles 100/111/122 in 23 isolates (clonal lineage US-8) and alleles 100/100 in six isolates (clonal lineage US-23). Isolates belonging to the US-23 clonal lineages, from both potato and tomato tissues, were of the mating type A1 and were sensitive to mefenoxam. The two isolates of the US-8 clonal lineage were both from potato tissues and were of the mating type A2 and were moderate resistance to mefenoxam. Microsatellite analysis did not identify polymorphism within the six isolates of the US-23 or the 23 isolates of the US-8 clonal lineage. All *P. infestans* isolates collected in 2014 were identified as members of the mitochondrial haplotype group Ia. Finding both mating types of *P. infestans* in Wisconsin in 2014 indicated the need for continual disease management to limit the occurrence of opposing mating types in proximity.

Palta group

QTL mapping in tetraploid potato populations for chipping and agronomic traits

Kyle Rak and Jiwan P. Palta, University of Wisconsin-Madison

Two biparental tetraploid potato populations W9817 (n=109) and W10010rus (n=152) have been evaluated for chipping and agronomic traits across three growing and storage seasons. The progeny and parents of these populations have subsequently been genotyped with the SolCAP Illumina Infinium SNP array platform, and evaluation of population structure has determined that the W10010rus population contained 55 individuals which resulted from self-pollination of the female parent Tundra. This group of selfed individuals essentially constitutes a third population for genetic analysis purposes. There were significant differences between the three populations for chip color, yield, tuber number,

and tuber weight. Linkage mapping on the W9817 population reveals a QTL for chip color on chromosome two, and detects an established flower color QTL on chromosome 11. Genome wide association mapping was performed on the W10010rus population as well as both populations combined. The chromosome 11 QTL for flower color was identified in the combined analysis, and QTL for chip color were detected for chip color on chromosome 4 and 7. Within these populations a number of promising clones have also been identified for advancement into breeding trials or as parental material.

Douches group

Title: QTL Analysis of Tuber Dormancy and Apical Dominance in Diploid Potato

Authors: Norma Manrique-Carpintero, Dilson Bisognin, Joseph Coombs, Daniel Zarka, and David Douches

A QTL analysis was done in a segregating diploid population for tuber dormancy and apical dominance. The MSX902 population is a cross between the clone 84SD22 (*S. tuberosum* x *S. chacoense*) and Ber83 (MSA133-57 x *S. berthaultii* PI 498104). Multiple QTL were detected for five traits (Tuber size, tuber number, dormancy, dominance, and dominance type). There was high correlation (0.80 $P < 0.001$) between dormancy and dominance. A QTL on chromosome 02 co-localized for dormancy, dominance, and tuber size. Future analysis will focus on identification of candidate genes.

Title: Genotyping by Sequencing in Diploid and Tetraploid Potato Germplasm/Mapping Populations

Authors: Alicia N. Massa, Norma Manrique-Carpintero, Joseph Coombs, Daniel Zarka, and David Douches

We are exploring the potential of genotyping-by-sequencing (GBS) approaches in potato breeding and genetics. The study was conducted on a set of 190 individual clones from diploid and tetraploid potato germplasm and mapping populations. Over six hundred single nucleotide polymorphisms (SNPs) were discovered across samples. An exploratory data analysis of these SNPs indicated the effect of the number of reads and the amount of missing data on the resultant quantity and quality of the SNP dataset. We further discussed alternative methods for variant calling optimization and suggested different algorithms to increase SNP and genotype calling accuracy.

Title: Assessing the impact of gene replacement and genetic modification methods in a crop species at the whole genome level.

Authors: Nathaniel Butler, Colby Starker, C. Robin Buell, Daniel Voytas, David Douches

Genetic modification using sequence-specific nucleases (SSN) is rapidly being adopted by industry and public institutions to accelerate modern breeding efforts. The lack of data concerning the genome-wide effects of SSN technology in crop species necessitates further investigation and could aid regulatory agencies in decision making. This report demonstrates TALEN and CRISPR/Cas SSN activities in potato cells and the generation of targeted mutations in potato events that are capable of clonal transmission. This information will be used for developing herbicide resistant events that will be used for further investigation.

Title: Potato Fingerprinting Using Genome-wide SNPs

Authors: Joseph Coombs, Daniel Zarka, and David Douches.

With commercial seed production of over 500 different potato varieties and breeding lines in the US and Canada, correctly identifying a particular potato clone is important and can have large economic consequences. Accurate identification of specific potato varieties can be a challenge based on morphological characteristics alone (tuber shape, skin or flesh color, flower color). During the past 25 years, molecular tools such as isozyme electrophoresis and simple sequence repeats (SSRs) have been used to successfully distinguish potato clones. One of the major outcomes from the AFRI/USDA-funded SolCAP project was development of genome-wide, SNP-based markers for potato. The Infinium 8303 Potato SNP Array was used to genotype over 300 North American tetraploid potato varieties and breeding lines (including closely related clones), as well as four tetraploid mapping populations. Tetraploid genotypes were called for 3,702 quality filtered SNPs for all potato samples using the SolCAP custom five cluster calling parameters. Over 1,000 SNP markers uniquely distinguished all tetraploid potato varieties and breeding lines. This demonstrates the power of this marker technology for fingerprinting in potato. The SNP fingerprinting analysis is currently the most accurate and robust method to distinguish potato varieties.

Title: Redesigning Diploid Potato Breeding with Self-compatibility

Authors: Maher Alsahlany and David Douches

There are new opportunities for potato breeding and genetics offered by introducing self-compatibility (SC) to diploid potatoes. We are developing a recurrent selection program to adapt the diploid germplasm (a composite of 5 diploid species) and select for SC as well as cultivated tuber traits. Secondly we are creating a recombinant inbred line (RIL) population in a cross with M6 and we are at the F3 stage. Lastly we have hybridized haploids of Atlantic with bulk pollen of SC lines. Selections were made and we select for SC and backcross to haploid *S. tuberosum*.

Title: 2012-2014 MSU Potato Breeding On-Farm Scab Trials

Authors: David Douches, Joe Coombs, Greg Steere, Matt Zuehlke and Donna Kells

A study was conducted to select for scab resistant chip-processing lines by growing and evaluating in a commercial field with extremely high levels of *Streptomyces scabies*. Single-hill and 12-hill selection in years one and two resulted in 95 selections that were scab resistant and had chip processing potential. In the third year the lines were harvested and graded as two replications of 15-hill plots. Over 24 promising lines were advanced. Some are already in tissue culture and the rest are currently being introduced to tissue culture.

Title: Mapping late blight Resistance in a diploid population of potato

Authors: Shafiqul Islam, Joseph J. Coombs, Norma C. Manrique-Carpintero, William W. Kirk and David S. Douches

Late blight is a devastating disease worldwide. To breed late blight resistant varieties, a mapping population (MSX902) segregating for late blight resistance has been developed by crossing 84SD22 with MSBer83. For phenotyping the population, a detached leaf bio-assay and a field evaluation were conducted using the US23 isolate of *Phytophthora infestans*. Genotyping using a genome-wide set of SNPs markers (8303 SNP array) was accomplished in conjunction with Joinmap 4.1 and mapQTL 6 to map the late blight QTL. The population had 1363 segregating SNPs which gave 98.7% genome coverage. Total map length was 774.7cM. A major QTL for late blight was found on chromosome 10 using the detached leaf bio-assay and field evaluation and minor on chromosome 5 for only field evaluation.

Bamberg Group

Bamberg presented activities of the research arm of the US Potato Genebank. The two potato species native to the USA provide handy collecting research models. We found that a single "Mega-population" of *S. jamesii* at Mesa Verde has most of the AFLP markers in the entire range. Staff continue to research and breed for tuber calcium, Core Collections, "Egg Yolk" style Colombian potatoes, tomatine, Zebra chip resistance, and crossing techniques. Del Rio presented an update of the research project testing frost hardiness under field conditions in the highlands of Peru. The results of the 2013-2014 season are confirming that the selections with cmm bred at USPG had good levels of productivity. These selections recovered very well to frost episodes. This year we also used calcium amendments at planting and the data showed that some of the potato selections and local varieties had 60% increases in the yield.

Spencer Barriball

2014 University of Minnesota potato breeding.

Spencer Barriball

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Brief overview of the Minnesota breeding program was presented and the status of each location was discussed. The research efforts will continue on new variety development for fresh and processing industry, disease resistance screening for PVY and common scab. One hundred fifteen advanced breeding lines and 38 NCRPVT entries were evaluated for yield potential. For common scab screening 115 UM, 38 NCRPVT, 168 NCPT and 32 NFPT entries were evaluated. Entries were evaluated for PVY. Out of 171 germplasm lines 142 lines were found resistant for PVY. Two advanced breeding selections MN10003PLWR-06R and MN10003PLWR-07R for chip processing were discussed.

Benoit Bizimungu

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

The 2014 NCR Trial focussing primarily table stock clones was planted at the Vauxhall Research substation, AB. The trial at Vauxhall comprised a total number of 21 entries from collaborators, including 11 red-skinned, 6 russets and 4 white or yellow-skinned clones. The trial was planted on June 10th and harvested on September 22nd. Yields were relatively better than in 2013, in part due to earlier 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 rainfed 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.

Sanjay Gupta

Inheritance of Biochemical Markers Associated With Cold-Induced Sweetening Resistance in Long Term Cold-Stored Potatoes: A tool For Breeding Programs to Develop New Variety

Sanjay K Gupta

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Processing quality is of paramount importance to the potato industry. The concentration of reducing sugars following long term cold storage is a primary determinant of the acceptability of potato cultivars for processing. Potatoes with excessive amount of reducing sugars produce unacceptably brown to black pigmented processed products, which have an off-taste and higher levels of the carcinogen acrylamide.

Potato breeding is a labor intensive, time consuming and expensive process. In order to compliment the potato breeding programs for early generation selection of promising potato clones, biochemical markers has been developed to predict cold-induced sweetening (CIS) resistance during long term cold storage. These markers are reliable tools for potato breeding programs and have been used to characterize diverse advanced breeding clones from various potato breeding programs across nation as well as the SolCAP mapping population between Premier Russet and Rio Grande Russet. One hundred twenty four breeding clones from PR X RG mapping population were characterized for biochemical markers, Sugar, and sugar end defects. Results showed wide variation in acid invertase activity in mapping population. Most of the clones had enzyme activity between two parents. However, transgressive segregation was observed in segregating population. Similar pattern was observed in terms of reducing sugar accumulation and other parameters. In the segregating population only a small portion of clones had desirable range for processing. In order to have better understanding of the breeding population, all the families in Minnesota Potato Breeding program have been categorized into three main CIS resistance classes based on the biochemical markers. The SolCAP mapping population between Premier Russet and Rio Grande Russet represented Class A⁻ X C⁻. In the year 2013-14 we have established 39 families representing 1124 clones. Out of 39 initial families this year we selected seven families representing different CIS resistance class combinations like MN99380-1Y X MN02696 (Class A⁻XA⁻), MN02696 X NY138 (Class A⁻XA⁺) and Atlantic X NY138 (class B⁺XA⁺) etc. Clones from these families have been evaluated for chip color and sugar before cold storage at 42°F. These clones will be characterized for chip color, sugars and biochemical markers to study the inheritance after 3, 6 and 9th month storage.

The information generated through this collaborative research will increase the efficiency of potato breeding programs to rapidly select clones from large population that are more likely to have the traits desired and save potato industry millions of dollars per year.

Richard Novy

NCCC215 Potato Breeding and Genetics Technical Committee Meeting Mini-Abstract USDA-ARS Potato Breeding and Plant Pathology, Aberdeen, Idaho Rich Novy

Thirty-six entries breeding clones from Aberdeen were entered into advanced agronomic and processing trials in the states of WA, ID, OR, CO, CA, TX, for assessment of their performance relative to industry standards (Western Regional and Tri-State Trials). Five breeding clones from Aberdeen are being considered for release in 2015 as varieties: A02062-1TE, A02507-2LB, A01010-1, A030158-2TE, and A01143-3C; more information regarding these clones was presented in the 'Variety Development' component of the meeting. In addition, research efforts in breeding for resistance to potato leafroll virus, potato virus Y, zebra chip, potato cyst nematode, and potato mop-top virus were also summarized. A summary of our research in breeding for lowered acrylamide was also presented, with A02507-2LB being an example, with an approximate 70-80% reduction in acrylamide content relative to Russet Burbank.

Cooperators	Publication
ARS-Aberdeen and Prosser, Univ. of Idaho, Oregon State U., Washington State U.,	Novy, R.G. , J.L. Whitworth, J.C. Stark, B.A. Charlton, S. Yilma, N.R. Knowles, M.J. Pavek, R.R. Spear, T.L. Brandt, N. Olsen, M. Thornton, and C.R. Brown. 2014. Teton Russet: An Early-Maturing, Dual-Purpose Potato Cultivar Having Higher Protein and Vitamin C Content, Low Asparagine, and Resistances to Common Scab and <i>Fusarium</i> Dry Rot. <i>American Journal of Potato Research</i> 91:380-393.
Researchers from many different institutions contributed book chapters.	Novy, R.G. 2014. Traditional Breeding and Cultivar Development. IN: Navarre, R. and Pavek, M. J. (eds). <i>The Potato: Botany, Production, and Uses</i> . CAB International (CABI), U.K. pp. 272-289.
ARS-Aberdeen and Prosser, Univ. of Idaho, Oregon State U., Washington State U.,	Whitworth, J.L., R.G. Novy , J.C. Stark, S.L. Love, M.K. Thornton, B.A. Charlton, S. Yilma, N.R. Knowles, M.J. Pavek, X. Wang, and J.J. Pavek. 2014. Huckleberry Gold: A Specialty Market Potato Cultivar with Purple-Skin, Yellow-Flesh, High Tuber Antioxidants, and Resistance to Potato Cyst Nematode (H1) and <i>Potato virus X</i> (<i>Nb</i> and <i>Rx1</i>). <i>American Journal of Potato Research</i> . 91:447-458.
University of Idaho and ARS-Aberdeen	Thornton, M.K., R.G. Novy , and J.C. Stark. 2014. Improving phosphorus use efficiency in the future. <i>American Journal of Potato Research</i> . 91:175-179 (Symposium Paper, 2012 Annual Meeting of the Potato Association of America).
University of CA-Riverside, ARS-Aberdeen, and Texas A&M	Diaz-Montano, J., B.G. Vindiola, N. Drew, R.G. Novy , J. C. Miller, and J.T. Trumble. 2014. Resistance of selected potato genotypes to the potato psyllid (Hemiptera: Trioziidae). <i>American Journal of Potato Research</i> . 91:363-367.

Asunta (Susie) Thompson NDSU

Evaluation of Parental Genotypes for Traits Using Marker Assisted Selection

Drs. Rob Sabba and Susie Thompson

Marker assisted selection has associated advantages and disadvantages and few markers are employed on a regular basis in US potato breeding programs. One hundred fort-five parental genotypes used in hybridizing during the winter 2014 were evaluated using several markers. Markers used included the H1 marker for Golden Nematode resistance (Galek et al 2011), Ry_{adg} (Kasia et al 2000) and Ry_{sto} (Song and Schwarzfischer 2008) for PVY resistance, Ve2 (Uribe et al 2014) for Verticillium wilt resistance, and the UGPase marker for cold sweetening resistance (Baldwin et al 2011). Clones varied in their response. Gala, Missoukee, Waneta, several of the Ebt and J lines as well as a handful of NDSU advancing selections and some Chilean clones evaluated with the H1 marker indicated resistance. Eva, King Harry, the Uraguayan lines (as expected) and a few other lines were positive for the Ry_{adg} marker, while J103-K7 and several NDSU selections were positive for the Ry_{sto} marker. The other markers gave incorrect (based on phenotyping) and/or inconsistent results. MAS is fairly simple to use to screen parental genotypes and/or seedling families in order to minimize populations. Evaluations can be conducted during the off-season and are much more rapid than most phenotypic evaluations. Based on our results, as well as comments in the published papers, some markers are specific to genetic background. The NDSU potato breeding program will continue to use several and to evaluate new markers.

From Hybridizing to Release – Cultivar Development for the Northern Plains

In 2014, from 145 parental genotypes, 529 new families were created. In the summer greenhouse 112 seedling families, totaling 24,710 individuals were produced. Fifty six families, totaling about 5,600 genotypes, were evaluated for late blight resistance using a detached leaf assay. In the seedling nursery at Langdon, ND, 34,916 seedlings were planted, representing 240 families segregating for Cold sweetening, late blight, and Colorado Potato Beetle resistance, among many other traits; 442 were retained for evaluation in 2015. Seed maintenance and increase were conducted at Absaraka, ND, and Baker, MN, sites were entered for certification via the North Dakota State Seed Department and Minnesota Department of Agriculture, respectively. Yield and evaluation trials were grown at 8 locations, 3 non-irrigated and 5 irrigated sights from western MN to northwestern ND. Agronomic evaluations were conducted for yield and grade components and quality parameters including incidence of internal defects, specific gravity, chipping/French fry processing, and blackspot and shatter bruise. Many disease screening trials and cultural management related trials are conducted by Team Potato, including evaluations for bacterial ring rot susceptibility and expression, pink rot, Pythium leak, late blight, Verticillium wilt and tuber blemish diseases resistance. Defoliation trials were conducted for

Colorado Potato Beetle feeding at the NPPGA Research Farm. Cultural management trials focused on nutrient management and herbicide tolerance. ND8068-5Russ is a very early selection (about 70 days) with processing potential. Several hybrids of Dakota Russet and Dakota Trailblazer look promising. Chip processing selections ND7519-1, ND7799c-1 and ND8304-2 continue to progress toward release. Red tablestock selections ND4659-1R, ND6002-1R, and AND00272-1R also show potential. The highlight of the year was the release of Dakota Ruby, evaluated as ND8555-8R.

NCCC215 Potato Breeding and Genetics Technical Committee Meeting
Holiday Inn Express at O'Hare, Chicago, Illinois
December 8-9, 2014

Chair: Dave Douches
Vice-chair: Susie Thompson
Secretary: vacant
Tentative Agenda

Dec 8th, Meeting Time: 1PM – 6PM; Refreshments Break: 3PM

1. Welcome, announcements
2. Introduction of members and guests
3. Approval of minutes of the January 2013 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**)
 - Wisconsin
 - North Dakota
 - Minnesota
 - Michigan
 - Alberta
 - Other contributors
 - Open discussion regarding deregulation of Innate Potatoes

6PM -7PM: Mixer

Dec 9th, Meeting Time: 8:00AM – 12:00PM; Refreshments Break 10:30 AM

7. North Central Regional Potato Variety Trial Report (Spencer Bariball)
8. Reports from contributing projects (**Variety Development**)
 - Wisconsin
 - North Dakota
 - Minnesota
 - Michigan
 - Alberta
 - Other contributors
9. New business
10. Date and venue for next year's meeting
11. Election of new officers
12. Adjourn