AN ABSTRACT OF THE DISSERTATION OF

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The cultivated potato (*Solanum tuberosum* L.) is one of the world's most important staple crops, ranked fourth after maize, rice, and wheat. While the potato's success is due largely to its high yield, it also benefits from its broad global acceptance, and its ability to be used by the consumer without prior processing. However, the potato's success as a crop comes despite an array of pathogens that can cause extreme yield losses, and quality defects that can make the potato essentially unmarketable. While they can be costly and at times devastating, the presence of these pathogens creates an enormous opportunity for the genetic improvement of the potato. For every major pathogen in potato, multiple sources of resistance have been identified in landraces or wild potato species that if combined in a suitable potato cultivar, could reduce or eliminate the damage caused by that pathogen. While the utilization of genes from exotic germplasm is far from trivial, advances in genetics, genomics, and phenomics will certainly accelerate this process.

In addition to improved biotic and abiotic stress resistance, a major feat in potato breeding would be to identify an improved system for developing potato clones with superior quantitative traits. The current strategy used to develop new cultivars, which involves planting tens of thousands of seedlings each year from intercrossed heterozygous clones, may be the best strategy for developing new varieties. However, the

difficulty of producing superior potato clones using this strategy has prompted some breeding programs to explore how alternative breeding methods might be applied.

Nine wild potato species were evaluated for their resistance to *Meloidogyne chitwoodi* (the Columbia root-knot nematode, CRKN), which can cause serious damage in potato production systems. Greenhouse screening identified fifteen clones from *S. hougasii*, one clone from *S. bulbocastanum*, and one clone from *S. stenophyllidium*, with moderate to high levels of resistance against three isolates of *M. chitwoodi*. Geographical mapping showed that these newly identified resistance sources are clustered in the states of Jalisco and Michoacán in west-central Mexico. Further, we screened seedlings from nine potato species for their response to Verticillium wilt (*Verticillium dahliae*), a major soil-borne pathogen of potatoes in many regions of the world. Greenhouse screenings identified two clones from *Solanum andreanum* and one clone from *S. bulbocastanum* that had resistance equal to or greater than 'Ranger Russet', the moderately resistant check. These new *V. dahliae* resistance sources have different taxonomic origins from previous *V. dahliae* sources and will expand our *V. dahliae* resistant potato germplasm.

'Castle Russet' is a newly released variety from the Northwest potato variety development program with improved agronomic performance and resistance to *Potato virus Y* (PVY) and Corky ringspot (CRS). A mapping population was developed to study segregation of resistance to PVY and CRS and identify single nucleotide polymorphism (SNP) markers linked to these resistances. SNP genotyping identified that the population phenotyped is in fact a mix of two populations. Molecular mapping of the real population of 49 clones identified 31 SNPs linked to PVY resistance, in addition to the markers STM0003 and YES3-3B, which were previously shown to be linked to Ry_{sto}. A single marker association analysis for CRS identified a major peak in chromosome 9 and two minor peaks in chromosomes 1 and 10. The identified linked SNPs for PVY and CRS need to be validated in a larger population for effective use in marker assisted breeding.

Finally, we investigated crosses between "Russet" and "Chipper" type potato clones (Russet-Chipper crosses), as well as between elite long- day adapted tetraploid clones and clones from an improved population of diploid potatoes derived from Group Phureja and Group Stenotomum (4x-2x crosses) were investigated. In our trials, clones derived from Russet-Chipper crosses had few notable benefits when compared to clones derived from crosses made within the Russet and Chipper groups in our trial. On the other hand, many of the clones derived from 4x-2x crosses clearly out-yielded the highest yielding clones from crosses between elite long-day adapted tetraploid potato clones. While every favorable quality trait measured was present in at least several clones derived from 4x-2x crosses, the frequency of many of these favorable quality traits was lower than was observed in crosses between elite long-day adapted tetraploid potato clones. Therefore, continued selection of parental clones in 4x and 2x populations would likely be required before a high yielding clone with acceptable or superior quality characteristics could be expected from these 4x-2x crosses.

When evaluating the 4x-2x crosses, we found that 61.5% of the resulting clones were triploid, compared to a previously reported frequency of 0.0-7.6%. Tubers of these triploids are generally intermediate between the two parental groups, indicating that there are no pronounced tuber characteristics associated with triploid potato clones. This finding opens the possibility of using triploid potatoes in potato variety development programs and in genetic and genomic studies.

Breeding qualitative and quantitative traits for potatoes in the Columbia basin

by
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I understand that my dissertation will become part of the permanent collection of Oregon State University libraries. My signature below authorizes release of my dissertation to any reader upon request.

Ryan C. Graebner, Author

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CONTRIBUTION OF AUTHORS

Chapter 2. Dr. Brown and Dr. Mojtahedi assisted with the experimental design, and the interpretation of results. Dr. Ingham assisted with the experimental design, and with writing the manuscript. Dr. Hagerty assisted with the nematode extractions and quantifications, and with writing the manuscript. Mr. Quick, Ms. Hamlin, and Ms. Wade assisted with the experimental design, and with maintaining plants during testing. Dr. Bamberg helped select germplasm to evaluate. Dr. Sathuvalli secured the funding and assisted with the experimental design, interpretation of results, and writing the manuscript.

Chapter 3. Dr. Bamberg helped select germplasm to evaluate. Dr. Frost assisted with the experimental design, and with phenotypic evaluations. Dr. Johnson assisted with the selection of isolates to screen. Dr. Hagerty assisted with inoculation preparation and application. Dr. Sathuvalli secured the funding and assisted with the experimental design, interpreting the results, and writing the manuscript.

Chapter 4. Dr. Bali assisted with the genetic characterization of these clones and the mapping of resistance. Dr. Brown assisted with the population development, and the experimental design. Ms. Hamlin and Mr. Quick conducted the phenotypic evaluation for corky ringspot resistance and assisted with the phenotypic evaluation for *Potato virus Y* resistance. Dr. Sathuvalli assisted with all stages of this experiment.

Chapter 5. Mr. Chen assisted with root squashes. Dr. Contreras assisted with flow cytometry and the interpretation of results. Dr. Haynes provided the diploid germplasm and assisted with the experimental design. Dr. Sathuvalli assisted in all stages of this experiment.

Chapter 6. Dr. Haynes provided the diploid germplasm and assisted with the experimental design. Mr. Charlton assisted with the management of potatoes grown in Klamath Falls. Mr. Yilma assisted with crossing the parental clones. Dr. Sathuvalli assisted in all stages of this experiment.

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DEDICATION

This dissertation is dedicated to Christina Heber Hagerty Graebner.

1 Introduction

1.1 Potato's role in global food security

Globally, potato (*Solanum tuberosum* L.) plays an important role in food security. It can be grown in many regions of the world and produces a high yield relative to other major food crops (Food and Agriculture Organization of the United Nations 2016), which does not require pre-consumer processing. Unlike some important staple crops, the potato is high in many vitamins and minerals, including vitamin B-6, vitamin C, potassium, carotenoids, and anthocyanins (Ezekiel et al. 2013; Brown 2008; United States Department of Agriculture Agricultural Research Service 2016), making it especially valuable as part of a healthful, affordable diet.

While these benefits have led to increased potato production and consumption worldwide (Food and Agriculture Organization of the United Nations 2016), potato production still faces significant challenges, particularly those related to pests and diseases, which in many cases can greatly decrease the quality and quantity of tubers harvested. In developing countries, pathogens including viruses, bacteria, and fungi that are transmitted through infected seed tuber pieces are of particular concern, because many developing countries lack the seed production systems capable of providing pathogen-free seed tubers to growers (Jansky et al. 2016). In the United States, *Potato virus Y* (PVY) is commonly present in seed tuber pieces, which can result in substantial yield losses (Nolte et al. 2004). Additionally, *Phytophera infestans*, the causal agent of late blight, can cause dramatic yield losses in some climates, unless genetic resistance or intensive chemical controls are used (Hijmans et al. 2000; Guenthner et al. 2001).

1.2 Potato production in the Columbia Basin of Oregon and Washington

The Columbia Basin growing region of Oregon and Washington is one of the top potato production regions of the United States; together these states produced 29.1% of the country's potatoes in 2016 (National Agricultural Statistics Service 2017a). The majority of potatoes from this region are destined for the French fry industry, although some potatoes are also produced for the potato chip and fresh markets. This region is notable for its high yields, averaging 66.1 metric tons per hectare in Oregon and 70.1 metric tons per hectare in Washington, compared to an average yield of 47.1 metric tons per hectare across the United States and 19.0 metric tons per hectare worldwide (National Agricultural Statistics Service 2017a; Food and Agriculture Organization of the United Nations 2016). These high yields are attributed to a set of environmental factors in this region favorable to potato production, including warm daytime temperatures associated with cool nighttime temperatures that reduce energy loss during nighttime metabolism, a long growing season, sandy loam soils, and ample irrigation from the Columbia River and its tributaries.

‘Russet Burbank’ was the most common potato variety in Oregon and Washington in 2017, with 23.1% of the total acreage planted (National Agricultural Statistics Service 2017b). Following ‘Russet Burbank’ were ‘Ranger Russet’, ‘Umatilla Russet’, and ‘Russet Norkotah’ with 13.8%, 11.6%, and 10.4% of the acreage planted, respectively (National Agricultural Statistics Service 2017b). Of these, ‘Russet Norkotah’ is typically grown as a fresh market russet, while the other three top cultivars go to French fry processing.

Major pathogens of potato in the Columbia Basin include PVY, the Columbia root-knot nematode (CRKN; *Meloidogyne chitwoodi*), Verticillium wilt (VW; *Verticillium dahliae*), *Tobacco rattle virus* (TRV; which incites corky ringspot), and *Potato mop-top virus*. Other pathogens that can at times cause quality defects or yield losses in the Columbia Basin include late blight (*Phytophthora infestans*), zebra chip (*Candidatus* Liberibacter solanacearum), silver scurf (*Helminthosporium solani*), black scurf (*Rhizoctonia solani*), and soft rot and blackleg (*Pectobacterium spp.*).

Potato virus Y is aphid-transmitted and persists when a potato plant is used to produce seed tubers for the following crop (Gray et al. 2010). Foliar symptoms of PVY include mosaic, leaf crinkle, chlorosis and necrosis, and tend to be more severe for the PVY strain PVY^{O} than for other important PVY strains, including PVY^{N}, PVY$^{N\text{-}Wi}$ and PVY^{NTN} (Gray et al. 2010). While PVY is well established in the Columbia Basin (Goodell 1979), the emergence of the strains PVY^{N}, PVY$^{N\text{-}Wi}$ and PVY^{NTN} have complicated the production of virus-free seed, because their mild foliar symptoms often make them more difficult to identify and remove in certified seed programs (Karasev and Gray 2013). Also, the emerging PVY^{NTN} strain is capable of inciting potato tuber necrotic ringspot disease (PTNRD; Figure 1.1), which results in a sunken necrotic ring on the tuber surface, making the tuber unmarketable (Karasev and Gray 2013).

Columbia root knot nematode is a soil-borne nematode that infects potato roots and tubers, as well as the roots of many other crops including carrot, alfalfa and tomatoes (Mojtahedi et al. 1988). While CRKN is not known to cause yield loses in any crop species, it can cause pimple-like bumps at infection sites (Figure 1.2), making these tubers generally unsuitable for fresh markets, and increased sugar concentrations in the surrounding tissue, which browns when fried, making them unsuitable for the French fry and potato chip industries. In the United States, CRKN is most abundant in the Columbia Basin, but is also found in California, Idaho, Colorado, New Mexico, and Texas (Powers et al. 2005), as well as Utah (Griffin and Jensen 1997) and Nevada (Nyczepir et al. 1982). Outside of the United States, CRKN is found in Mexico, Argentina, Belgium, Germany, the Netherlands, Portugal, and South Africa (Powers et al. 2005). Currently, the predominant control methods for CRKN are fumigants and non-fumigant nematicides, as this species' wide host range (Mojtahedi et al. 1988; Wesemael and Moens 2008) limits the effect of crop rotations on this pathogen, and there are no known potato cultivars with genetic resistance to CRKN (Brown et al. 2004).

Verticillium dahliae, (which incites Verticillium wilt, also known as potato early die), is a soil-borne fungus that enters potato roots and tubers, eventually colonizing the plant's vascular tissue (Klosterman et al. 2009). In the vascular tissue, it disrupts water transport, which can lead to wilting and early death of the vine (Johnson and Dung 2010). *V. dahliae* has a wide host range and is able to infect plants from most dicot families, limiting the effect of crop rotations (Powelson and Rowe 1993). *V. dahliae* can also cause vascular discoloration, reducing the tuber’s value (Figure 1.3). As a result, the primary methods used to control *V. dahliae* include fumigation and planting potato cultivars with moderate resistance or tolerance to the pathogen (Berlanger and Powelson 2000).

Tobacco rattle virus (TRV) is vectored by stubby-root nematodes (*Trichodorus spp.* and *Paratrichodorus* spp.; Hafez and Sundararaj 2009; Charleton et al. 2010). In potato, TRV causes corky ringspot disease, which is characterized by necrotic rings in the tuber flesh (Hafez and Sundararaj 2009; Figure 1.4), and can cause 6% to 55% of potatoes an infested field to be unmarketable (Hafez and Sundararaj 2009). Typically, the most effective route to control damage caused by TRV is to control the nematode vector, either through fumigation, the application of non-fumigant nematicides, or by growing alfalfa as a rotation crop (Hafez and Sundararaj 2009; Charlton et al. 2010). While some clones exhibit moderate to strong resistance to TRV, no widely grown russet cultivars have sufficient resistance to completely prevent symptom expression (Hafez and Sundararaj 2009). Additionally, in fields not infested by TRV, the risk of future infestation can be reduced by planting only certified virus-free seed and by limiting possible routes of contamination between fields (Hafez and Sundararaj 2009).

1.3 Progress of germplasm improvement efforts in temperate growing regions

Over the last 100 years, genetic improvement of the potato has lagged behind that of the world's other major crops (Douches et al. 1996; Donmez et al. 2001; Duvick 2005). Some of this is likely because potato is a tetraploid, clonally propagated crop where the breeder has the additional challenge of maintaining heterozygosity across the genome. Progress on several fronts is required to maintain the potato's value as a healthful staple crop.

1.4 Clean introgression of major genes

Only a small proportion of the genetic diversity present in wild potato species was captured when the crop was originally domesticated 10,000 to 13,500 thousand years ago (Spooner et al. 2014), and an even smaller share of this diversity was captured by the clones used to establish modern breeding programs. Valuable traits that have been identified in landraces and wild potato species include cold-induced sweetening resistance (Hamernik et al. 2009), frost tolerance (Hijmans et al. 2003), nutritional attributes (Goyer and Sweek 2011; Brown 2008), desirable flavors (Jansky 2010), pathogen resistance (Jansky 2000), and insect resistance (Pelletier et al. 2011). While the genes controlling these traits are generally favorable, they are often accompanied by alleles from the trait's source such as high glycoalkaloids that can make a clone unmarketable. These traits must be removed by the time-consuming process of introgressing the genes into elite potato germplasm. As an example, one protoplast fusion and five subsequent crosses were required to introduce resistance to *M. chitwoodi* from the wild *S. bulbocastanum* into PA99N82-4, with replicated resistance evaluations at each stage (Brown et al. 2006). PA99N82-4 is a BC_5 clone that approaches suitability for the russet market class. While linked and unlinked alleles can bring unfavorable traits into a potential cultivar, linked alleles likely cause greater problems because they can persist after many cycles of backcrossing, and do not segregate normally in the portion of a population with the trait of interest.

Fortunately, using genetic markers, unfavorable genes that are linked to a gene of interest could theoretically be limited to approximately 1 cm region in two generations, using a method outlined by Young and Tanksley (1989). In the first generation, a mapping population of approximately 200 clones is developed, and characterized with a high-density marker array such as genotyping-by-sequencing (GBS) or single nucleotide polymorphism (SNP) array or even a smaller number of markers flanking the gene's location would be suitable. From this population, the clone with the target gene and the recombination event closest to the target gene is selected, regardless of the clone's other attributes. In the following generation, another approximately 200 clone population is developed using the selected clone; it is again genotyped. This time, the clone with both the target gene and a nearby recombination event on the side of the gene opposite the first recombination event is selected. Through this method, unfavorable genes will be quickly and efficiently be separated from genes of interest, so that the genes can be used freely in variety development programs. New tools and technologies, including GBS and the Potato V3 Infinium Array, with 21,226 SNPs (Neogen, Lansing, MI, USA), can greatly reduce the cost and increase the power of this approach. While genetic markers can be used to accelerate backcrossing when the breeder selects clones that have the trait of interest but not the linked genetic marker, loosely linked markers can also hinder the separation of genes when the breeder selects for clones that have the marker and the trait of interest, as this prevents the separation of the target gene from any alleles positioned between it and the genetic marker.

1.5 Special considerations for pathogen resistance genes

Developing cultivars with pathogen resistance is challenging in potato breeding, as the pathogens have the capacity to evolve in response to host's resistance profile. While a cold-induced sweetening resistant potato cultivar will always be resistant to cold-induced sweetening, the same cannot be said for a cultivar with resistance to *P. infestans* (Goodwin et al. 1995), CRKN (Mojtahedi et al. 2007), or PVY (Karasev and Gray 2013). Strategies to improve the durability of disease resistance include the use of multiple strong resistance genes, which would require a pathogen to overcome each resistance gene simultaneously in order to reproduce (gene pyramiding), and the use of genes that provide resistance to a broad range of isolates of a pathogen, or even to multiple related pathogens (horizontal resistance). While these considerations pose additional challenge to breeders, breeding for pathogen resistance in potato is aided by the abundance of pathogen resistance genes found in potato germplasm. Indeed, many of the major advances in elite potato germplasm are a result of introgressed resistance from landraces and wild potato species. To stay several steps ahead of the pathogen, it is best that the breeder knows not only a clone's resistance status, but also the genes that confer resistance. This, combined with the fact that a clone's disease resistance status can be difficult to measure for many potato pathogens, has led to the widespread development of genetic markers for major pathogen resistance genes (Pineda et al. 1993; Song et al. 2005; Colton et al. 2006; Zhang et al. 2007).

1.6 Improvement of quantitative traits in potatoes

While the introgression of major genes alone has major benefits for potato production, when followed by their successful inclusion in a commercially viable clone, an ideal breeding system would also include a strategy for improving quantitative traits. Traditionally, this has been done by intercrossing heterozygous tetraploid clones which results in populations that typically have a very low percentage of desirable genotypes, due to segregation, inbreeding, and non-additive genetic variance. As a result, large populations of seedlings (10,000-100,000 seedlings) are produced every year for evaluation. Selection in the first field year is carried out on single hills, mainly for tuber appearance, shape, skin type, and to some extent yield and size; 1-5% of the seedlings are retained. Every year following the single hill trial, a smaller number of clones is evaluated in larger plots and in more locations, until it is determined whether any of the clones have the potential for release as cultivars. Consequently, 10 or more years of evaluation are required before a clone can be released as a cultivar. However, this process has had only limited success relative to many other crops, and several alternative strategies have been explored to accelerate the improvement of quantitative traits in potato.

One promising strategy that is being tested in potato is genomic selection, where a training population is used to first predict the effect of every allele, on the basis of large number of genetic markers, and then those markers are used to calculate genomic estimated breeding values for each clone. Early uses of genomic selection have given promising results for chip color and starch content (Sverrisdóttir et al. 2017). However, to our knowledge no breeding programs have selected parents primarily on the basis of genomic selection in variety development efforts or in the selection of clones from those crosses.

Alternatively, some breeding programs have shifted to breeding hybrid potatoes at the diploid level (Lindhout et al. 2011; Jansky et al. 2016). These programs generally envision sets of inbred parental lines that produce consistent, high yielding progeny when crossed with one another. One benefit of this system is that cultivars could be reconstituted from true potato seed in seed production systems though the preferred method would be to grow seed tubers from true potato seed. This technique greatly simplifies the process of providing pathogen-free seed tubers to growers, which would be especially valuable in developing countries that may not have adequate seed certification programs. Another benefit of this system is that by moving to the diploid level, many tools commonly used in plant breeding, including genetic mapping and genomic selection, are more readily implemented. In 2017, ‘Oliver F1’ was the first hybrid potato cultivar produced from true potato seed (Benjo Zaden BV 2017).

A third strategy to improve quantitative traits in potatoes is through identification of genetically distinct groups of potatoes that exhibit hybrid vigor when intercrossed. While this strategy is similar to the diploid hybrid strategy, it emphases the identification and improvement of heterotic groups, but does not attempt to transfer the potato to a diploid crop, or to a crop whose cultivars can be reconstituted from true potato seed. Many studies have shown that crosses between distantly-related groups of potatoes, such as between elite potato clones and clones from Group Andigena, Phureja or Stenotomum, show increased hybrid vigor for yield (Mendiburu and Peloquin 1971; De Jong and Tai 1977; Mendiburu and Peloquin 1977; McHale and Lauer 1981; Carroll and De Maine 1989; Buso et al. 1999). However, most of the clones resulting from these crosses exhibited poor quality traits that were presumably brought in with the unadapted germplasm, and many were later maturing than commercial clones. As a result, few clones have been released from these crosses. Few studies have worked to identify heterotic groups within elite potato germplasm, whether between breeding programs, market classes, or geographic origins of the clones.

While these strategies are being pursued separately at this time, they are not mutually exclusive. For instance, heterotic groups could be used to create single clones or pairs of inbred parents, depending on the relative success of the two strategies, the strength of seed certification systems in the target environment, and the disease profile of the expected cultivar. Additionally, genomic selection could be used to simplify and accelerate the strengthening of heterotic groups. Using conventional methods, reciprocal recurrent selection and similar selection methods could strengthen heterotic groups, which are resource-intensive as they require parental performance to be predicted through the performance of each clone’s progeny. Using genomic selection, the effect of each allele could be calculated by genotyping a large population with a high-density marker array and identifying the loci that only segregated in one of the parental groups. This would allow the portions of the hybrid clone's genome originating from the two parental groups to be analyzed separately. Because only one or two copies of DNA is contributed from each parent, depending on the type of cross and the resulting ploidy levels, the alleles in hybrid clones could be analyzed using the same methods that are used for self-pollinated crops or cross-pollinated diploid crops, respectively.

1.7 Conclusion

In order to accelerate the development of superior potato cultivars, germplasm must be improved in terms of the frequency of beneficial major genes and within a structure that allows the breeder to exploit non-additive genetic variance. While not easy, new genetic resources, new technologies, and a better understanding of potato germplasm will accelerate potato improvement.

In this thesis, I present work that was conducted to identify new sources of resistance to potato pathogens, to better characterize pathogen resistance that was previously identified and introgressed into elite potato germplasm, and to explore how hybrid vigor may be used to improve potato yield. It is my intention that this work will assist breeders in developing cultivars that undergird the potato's role as a leading crop in the Columbia Basin and in the world.

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1.9 Figures

Figure 1.1. Potato necrotic ringspot disease in a potato tuber infected by PVY^{NTN} (image source: http://www.potatovirus.com/).

Figure 1.2. *Meloidogyne chitwoodi* infection on a potato tuber (image source: http://www.inspection.gc.ca/).

Figure 1.3. Vascular discoloration in a potato tuber infected with *Verticillium dahliae* (image source: https://www.extension.umn.edu/).

Figure 1.4. Corky ringspot in potato tuber infected with *Tobacco rattle virus* (image source: http://www.potatogrower.com/).

2 Resistance to *Meloidogyne chitwoodi* identified in wild potato species

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2.1 Abstract

Meloidogyne chitwoodi (Columbia root-knot nematode, CRKN) can cause serious damage in potato production systems. Damage caused by *M. chitwoodi* decreases tuber value in the fresh market and processing industries. Genetic resistance to CRKN was first identified from the wild diploid potato species *Solanum bulbocastanum* accession SB22 and was successfully introgressed into tetraploid potato breeding material. In order to expand the base of genetic resistance, 40 plant accessions from nine wild potato species were screened for their resistance to *M. chitwoodi*. Greenhouse screening identified fifteen clones from *S. hougasii*, one clone from *S. bulbocastanum*, and one clone from *S. stenophyllidium* with moderate to high levels of resistance against three isolates of *M. chitwoodi*. Geographical mapping showed that these resistance sources identified in this and previous studies originated primarily in the states of Jalisco and Michoacán in west-central Mexico. These new sources will be introgressed into elite potato populations to allow the development of potato cultivars with durable resistance to CRKN.

2.2 Introduction

The Columbia root-knot nematode, *Meloidogyne chitwoodi* Golden et al., is a plant parasitic nematode that can reproduce on roots and other underground tissue of a range of economically important crop plants, including potatoes, wheat, corn and alfalfa (Mojtahedi et al. 1988). In the United States, *M. chitwoodi* is most abundant in the Columbia Basin potato growing region of Oregon and Washington, but is also found in California, Idaho, Colorado, New Mexico, and Texas (Powers et al. 2005), as well as Utah (Griffin and Jensen 1997) and Nevada (Nyczepir et al. 1982). Outside of the United

States, *M. chitwoodi* is found in Mexico, Argentina, Belgium, Germany, the Netherlands, Portugal, and South Africa (Powers et al. 2005). The species most closely related to *M. chitwoodi* is *M. fallax* Karssen (false Columbia root-knot nematode), which is found in the Netherlands, Australia, and New Zealand, but which is not known to occur in potato production regions of the United States (Powers et al. 2005).

Meloidogyne chitwoodi emerges from eggs as second-stage juveniles (J2), after undergoing one molt within the egg (Mitkowski and Abawi 2003). Juvenile nematodes enter host roots and tubers, and establish giant cells, which help to support the developing nematodes (Mitkowski and Abawi 2003). In potatoes tubers, pimple-like bumps form at each infection site, dramatically reducing their fresh-market appeal. Adult females lay eggs in the flesh of the tuber where pinhead-sized brown spots later develop. This is further coupled with increased sugar concentrations in the tissue surrounding each infection site, resulting in browning of fried products thus making these tubers unsuitable for the French fry and chip industries. The European Plant Protection Organization has listed *M. chitwoodi* as an A2 pest, recommending that infected plant materials be quarantined by member countries.

The predominant control methods for *M. chitwoodi* are chemical fumigants and non-fumigant nematicides. However, these chemicals have substantial negative aspects, including high cost and health and environmental hazards. Crop rotations can offer some control, but effectiveness is reduced by the nematode’s wide host range and its long persistence in the soil. Considering limited success of crop rotation, genetic resistance to *M. chitwoodi* in elite potato cultivars would provide a valuable tool to growers for controlling this pest.

Two races of *M. chitwoodi* exist in the United States, races 1 and 2, and each infects a unique sets of host plants (Santo and Pinkerton 1985). Both of these races can reproduce on a wide range of crops commonly grown in the Columbia Basin, including potatoes, corn, and wheat (Mojtahedi et al. 1988). A key difference between these races is that race 2 can reproduce on ‘Thor’ alfalfa, while race 2 cannot (Mojtahedi et al. 1994). Of these, race 1 was identified first and is more prevalent in the Columbia Basin, while race 2 is typically found when potatoes are grown in rotation with alfalfa (Mojtahedi et al. 1994).

Host genetic resistance to root-knot nematodes is thought to take advantage of a hypersensitive response (Castagnone-Sereno 2002; Williamson and Kumar 2006). The *Mi* gene in tomato confers resistance to *M. javanica, M. incognita*, and *M. arenaria;* it has been cloned, and found to be a member of the nucleotide binding leucine-rich repeat family of plant resistance genes (Milligan et al. 1998; Vos et al. 1998). In potato, two genes ($R_{Mc1(blb)}$ and $R_{Mctuber(blb)}$) that confer resistance to *M. chitwoodi* are being employed in cultivar development efforts. Both genes were introgressed from the *Solanum bulbocastanum* clone SB22 (PI 275187). $R_{Mc1(blb)}$ confers root resistance to most isolates of race 1 of *M. chitwoodi*, with the exception of WAMCRoza, an isolate that was identified in experimental plots that had been planted repeatedly with clones carrying $R_{Mc1(blb)}$ (Mojtahedi et al. 2007). In the clone CBP-233, a somatic hybrid between SB22 and the *S. tuberosum* clone R4 (PI 203900), necrotic tissue was observed to form in roots around nematode infection sites, suggesting that resistance from $R_{Mc1(blb)}$ is expressed as a hypersensitive response. $R_{Mctuber(blb)}$ confers tuber resistance to both race 1 and race 2 of *M. chitwoodi*. Although root and tuber resistance from SB22 have been successfully introgressed into elite potato germplasm, no cultivars with this resistance have been released.

In addition to root and tuber resistance from SB22, root resistance from *S. hougasii* ($R_{Mc1(hou)}$) and *S. fendleri* ($R_{Mc1(fen)}$) were partially introgressed into elite potato germplasm (Brown et al. 2006 and 2014). Brown et al. (2014) suggested that both of these resistances were identical to $R_{Mc1(blb)}$ based on genetic marker data and the close taxonomic relationship of *S. bulbocastanum*, *S. hougasii*, and *S. fendleri*. To the best of our knowledge, all clones with resistance introgressed from *S. hougasii* and *S. fendleri* have since been lost (Personal communication, Brown 2018).

Resistance to cold temperature root-knot nematode species (*M. chitwoodi*, *M. fallax*, and *M. hapla*) is correlated with that of other cold-temperature species, but not with warm-temperature species (*M. arenaria M. incognita*, and *M. javanica*). The responses of wild potato clones to *M. chitwoodi* and *M. fallax* were particularly similar for clones derived from *S. fendleri* and *S. hougasii* (Janssen et al. 1997). This raises the possibility that $R_{Mc1(hou)}$ and $R_{Mc1(fen)}$ confer resistance to race 1 of *M. chitwoodi* and *M. fallax*, but not race 2 of *M. chitwoodi*. Another study quickly selected for isolates that were virulent on *S. fendleri* clones and found that some of the virulent *M. chitwoodi* isolates also virulent on other resistant clones from *S. fendleri*, *S. bulbocastanum*, *S. hougasii*, and *S. stoloniferum* Schltdl. (Janssen et al. 1998).

While resistance introgressed from SB22 may soon be present in clones that are suitable for release as cultivars in the Pacific Northwest, there is an urgent need to identify additional sources of resistance, especially for root resistance to race 1 isolate WAMCRoza. The objective of this study was to identify new sources of resistance to *M. chitwoodi* for use in breeding, with an emphasis on identifying resistance to the *M. chitwoodi* isolate WAMCRoza.

2.3 Methods

This study consisted of an initial screening of a large number of wild potato seedlings for resistance to *M. chitwoodi* race 1 isolate WAMCRoza, and a replicated evaluation in which putative resistance sources were challenged with races 1 and 2 of *M. chitwoodi*.

2.3.1 Plant material

Forty accessions representing nine wild potato species were selected for initial evaluation of their response to *M. chitwoodi* (Table 2.1), from the NRSP-6 Potato Genebank. When possible, these accessions were chosen to include species and germplasm where resistance had previously been detected. Three checks were used: ‘Rutgers’ tomato, which is susceptible to all races of *M. chitwoodi* (Brown et al. 2014), ‘Vernema’ alfalfa (a differential check), which is resistant to race 1 but susceptible to race 2 (Mojtahedi, Pers. Communication, 2018), and ‘Red Core Chantenay’ carrot (another differential check), which is susceptible to race 1 but resistant to race 2 (Mojtahedi et al 1988). Long-day adapted cultivated potatoes were not included as checks in this experiment, because their tendancy to form tubers under the long photoperiod present in the greenhouses does not resemble the absence of tuber formation under long photoperiods demonstrated by the wild potato

2.3.2 Isolates used

For the initial screening, we used *M. chitwoodi* race 1 isolate WAMCRoza, an isolate of race 1 that is distinguished by its ability to reproduce on roots of potato plants with resistance conferred by $R_{Mc1(blb)}$. For the replicated screening, the following additional isolates were used: WAMC1, an isolate representative of race 1, USA., and WAMC27, an isolate representative of race 2. Each isolate was maintained on 'Rutgers' tomato. Eggs for this experiment were extracted from these 'Rutgers' plants using the same methods used to extract eggs in the initial screening. Egg concentrations were quantified using a nematode counting slide (Chalex, LLC, Park City, Utah, USA), then adjusted to 1,000 eggs/ml.

2.3.3 Initial screening

In the initial screening, we attempted to test 10 seedlings from each of the 40 accessions, although for some accessions low germination and plant mortality resulted in fewer seedlings. In addition, 10 plants of 'Rutgers' tomato and four plants of 'Vernema' alfalfa were used as the susceptible and resistant checks, respectively. Approximately 20 seeds from each accession were soaked in a 0.1% gibberellic acid solution for 24 hours, then placed on a damp paper towel in a covered petri dish and kept moist for one week. The germinated seeds were transferred to 2.54 cm pots, filled with a sterilized mixture of 75% sand and 25% soil and fertilized with 2.0 g Osmocote 14-14-14 Flower and Vegetable Smart-Release Plant Food (The Scotts Company, Marysville, OH, USA) per liter of sand-soil mixture. Twenty-eight days after transplanting, the seedlings were transferred to 10 cm pots, filled with the same mixture of sand, soil, and fertilizer. During the second transplanting, the roots of each plant were inoculated using a pipette with 5,000 eggs of WAMCRoza suspended in water. Plants were then allowed to grow in a greenhouse with 16 hours of artificial lighting per day, and temperatures kept at approximately 24 °C for 56 days, to allow the nematodes enough time to complete two generations in the plant roots. At the end of the 56-day period, the potting soil was rinsed from the roots of each plant, and the roots were shaken at 90 rpm in a solution of 0.6% sodium hypochlorite for 4 min to release the eggs. The resulting solution was strained with a 0.841 mm sieve to remove debris, over a 0.025 mm sieve. The contents in the 0.025 mm sieve were rinsed into a bottle and quantified for egg concentration using a nematode counting slide (Chalex, LLC, Park City, Utah, USA). The initial screening was conducted in five batches to allow the timely harvest and quantification of eggs from each plant at the end of the trial. After the initial evaluation, two replicated evaluations were conducted that had low levels of nematode reproduction and high levels of plant mortality due to extreme greenhouse temperatures. While we did not use these data to confirm resistance, we were able to use these trials to determine that some clones were in fact susceptible and remove them from further evaluation. Data for these evaluations are shown (Appendix A, Supplementary Tables 2.2 and 2.3).

2.3.4 Clone maintenance

At the end of the initial screening for resistance to WACRoza, we attempted to clonally propagate each selected seedling via shoot cuttings, using Dip ‘N’ Grow Rooting Concentrate (Dip ‘N’ Grow, Clackamas, OR, USA) to stimulate root formation. Stem segments of the selected seedlings were surface sterilized by soaking them in 70% ethanol for 1 minute, followed by 0.6% sodium hypochlorite supplemented with three drops TWEEN 20 (Sigma-Aldrich, St. Louis, MO, USA) per 100 ml sodium hypochlorite solution, then in sterile distilled water for 5 minutes. Surface sterilized stem segments were transferred to tissue culture and grown on MS-30 media (Murashige and Skoog 1962) for maintenance.

2.3.5 Replicated evaluation

For the replicated evaluation, each clone identified as resistant in the initial screening was inoculated separately with WAMCRoza, WAMC1, and WAMC27. The transplantation, inoculation, and quantification of resistance for these isolates was carried out on subsequent days, respectively. Each clone was replicated five times for each nematode isolate, although in some cases fewer replicates were used due to low propagation success and plant mortality. The pots for each isolate were placed on separate benches in a greenhouse to avoid cross-contamination. Testing procedures were similar to those of the initial screening, with the following differences: plantlets from tissue cultured cuttings were placed in Greenhouse Mix #3 (Teufel Products Co., Hillsboro, OR, USA) and allowed to grow for 40-60 days before being transplanted into 2 L clay pots filled with a mixture of 84% sand, 10% silt and 6% clay, and fertilized with 2g Tree ‘N’ Vine 12-8-16 Agropell fertilizer (J.R. Simplot Company, Boise, ID, USA) per liter of sand-clay-soil mixture. Plants were inoculated five days after transplanting by pipetting 5,000 nematode eggs per plant into three holes made by inserting a pencil approximately 2.5 centimeters into the soil near the base of each plant.

2.3.6 Characterization of resistant accessions

To better characterize the accessions in which resistance had been detected in the initial test, we planted additional seeds and evaluated 30 seedlings from each of the eight accessions. Each seedling was inoculated with WAMCRoza, and eggs were extracted and counted using the same methods as in the initial screening.

2.3.7 Statistical analysis

All data in this study were transformed using the following transformation:

$$\text{value} = \log_{10}[(\text{no. eggs}/50) + 1]$$

Where “no. eggs” is the total number of nematode eggs extracted from the plant. Geometric mean reproduction values were made by back-transforming the average of the transformed reproduction values. This value was used to calculate a reproduction factor (Rf), defined as the number of eggs extracted divided by the initial number of eggs). To match previous evaluations for *M. chitwoodi* resistance, clones were classified as hosts (Rf > 1.0, corresponding to susceptibility), poor hosts (1.0 > Rf > 0.1, corresponding to moderate resistantance), or non-hosts (RF < 0.1, corresponding to resistance). For the replicated evaluation, an analysis of variance (ANOVA) was run to determine whether clones responded differently to the different nematode races. All statistical tests were conducted using R version 3.2.3 (R Core Team 2005). Tukey tests were used to determine which clones were significantly different from others at $\alpha=0.05$ using the R package "agricolae" (de Mendiburu 2017). For the clone PI545815sph-9mc, only one plant survived the evaluation for isolate WAMC1, so it was excluded from statistical analysis for that isolate.

2.3.8 Relationship of resistance to geographic origin

To investigate a relationship between *M. chitwoodi* resistance and geographic origin, accessions evaluated for *M. chitwoodi* resistance in this or earlier studies were plotted on a map of the southern part of North America.

2.4 Results

2.4.1 Initial screening

In the initial screening, eighteen clones from six accessions were selected from *S. hougasii*, two clones from one accession were selected from *S. bulbocastanum*, two clones from one accession were selected from *S. iopetalum*, one clone from one accession was selected from *S. andreanum*, one clone from one accession was selected from *S. guerreroense*, and one clone from one accession was selected from *S. stenophyllidium*. Further evaluations reduced this panel to fifteen clones from six accessions from *S.* hougasii, one clone from one accession from *S. bulbocastanum*, and one clone from one accession from *S. stenophyllidium*. No clones from *S. boliviense* or *S. stoloniferum* were evaluated for *M. chitwoodi* resistance past the initial screening. Accessions in the initial screening varied widely in their levels of nematode reproduction, with some accessions having close to no *M. chitwoodi* reproduction (Rf=0), and others approaching the susceptibility of 'Rutgers' tomato (Rf>10). The complete results of the initial screening are shown in Appendix A, Supplementary Table 2.1.

2.4.2 Replicated evaluation

Seventeen clones were tested for the replicated evaluation: 15 from *S. hougasii*, one from *S. bulbocastanum*, and one from *S. stenophyllidium*. The ANOVA of the complete set of replicated clones excluding checks showed a significant interaction between clone and nematode isolate ($p<0.001$, Table 2.2), indicating that clones responded differently to different nematode isolates. Within each of the three nematode isolates, significant differences were found among the clones (Table 2.3), as expected. All selected clones displayed significantly greater resistance than ‘Rutgers’ tomato to all isolates of *M. chitwoodi*. These include 15 clones from 6 accessions of *S. hougasii*, one clone of *S. bulbocastanum*, and one clone of *S. stenophyllidium*. However, only eight clones from three accessions were significantly more resistant to WAMCRoza than the ‘Red Core Chantenay’ carrot (the poor host check for race 1), and 11 clones from six accessions were significantly more resistant to MC1 than ‘Red Core Chantenay’ carrot (Table 2.3). No clones were significantly more resistant to WAMC27 than ‘Vernema’ alfalfa (the poor host check for race 2). The complete results for the replicated evaluation are shown in Appendix A, Supplementary Table 2.4.

2.4.3 Characterization of resistant accessions

When additional seedlings from each resistant wild potato accession were evaluated, most of the seedlings tested were poor hosts or non-hosts for WAMCRoza (Figure 2.1). The main exception to this was the *S. stenophyllidium* accession PI 545815, where the reproduction factors ranged from 0 to 3.6, with the majority of seedlings exhibiting intermediate levels of nematode reproduction. Additionally, one seedling from the *S. hougasii* accession PI 558402 had a reproduction factor of 1.1. The detection of additional resistant seedlings suggests resistance genes are present in at a high frequency in these accessions. The complete results for this evaluation are presented in Appendix A, Supplementary Table 2.5.

2.4.4 Geographical Mapping

For the accessions with recorded collection sites, the locations are presented on a geographical map of North and Central America (Figure 2.2 and Appendix A, Supplementary Table 2.6). Resistant and susceptible accessions are shown with different symbols, and accessions evaluated in previous *M. chitwoodi* resistance studies (Brown et al. 1989; Brown et al. 1991; Janssen et al. 1996; Brown et al. 2004) are included. Although at least 46 accessions from South America have also been tested, none have strong resistance to *M. chitwoodi*, and so were excluded from the map. Of the accessions from Mexico and the southwestern United States, resistance clustered in and around the Mexican states of Jalisco and Michoacán, which partly reflects the large number of *S. hougasii* accessions collected in this region. However, the same observation holds true in *S. bulbocastanum*, where accessions from this western region were more likely be resistant than accessions collected in the eastern part of the species' range. The two resistant *S. stenophyllidium* accessions that have been identified originated an area just north of this region.

2.5 Discussion

In this study, we identified strong resistance to all three isolates of *M. chitwoodi*. Fifteen of the 17 resistant clones were from six accessions from *S. hougasii*, while the other two clones were from *S. bulbocastanum* and *S. stenophyllidium*. The abundance of resistant clones from *S. hougasii* was evident in the initial screening, where *S. hougasii* accessions almost always had a lower mean reproduction factor than accessions from other species. The exception to this was the *S. hougasii* accession PI 161727, which was consistently susceptible to WAMCRoza. In addition to differences in genetic resistance between species, *Solanum hougasii* tended be easily propagated from true potato seed and shoot cuttings than other species, which resulted in more resistant clones being maintained from each resistant accession.

For *S. hougasii*, the clones PI239424hou-2mc, PI239424hou-6mc, PI283107hou-5mc, and PI283107hou-9mc were non-hosts for each of the three isolates tested. While not directly tested, it appeared that clones *S. hougasii* clones from the accessions PI

161726, PI 558402, and PI 558422 were substantially more resistant to WAMC1 than WAMCRoza. This is consistent with the hypothesis that the resistance gene $R_{Mc1(hou)}$ (originating from the *S. hougasii* accession PI 161726) is similar or identical to $R_{Mc1(blb)}$ (Brown et al. 2014). However, each of the *S. hougasii* clones tested in the replicated evaluation had moderate to strong resistance to WAMCRoza, indicating that additional resistance genes independent of $R_{Mc1(blb)}$ may be present in this species.

The *S. bulbocastanum* clone PI 255518blb-4mc was a poor host for WAMCRoza, and non-host for WAMC1 and WAMC27. The strong resistance to WAMC1 and WAMC27 of PI 255518blb-4mc was similar to that seen in *S. bulbocastanum* clone SB22. However, moderate resistance of PI255518blb-4mc to WAMCRoza suggests that it has additional resistance that is not present in SB22.

The *S. stenophyllidium* clone PI545815sph-9mc was a non-host for WAMCRoza and a poor host for WAMC27. Like PI255518blb-4mc, the resistance of PI545815sph-9mc to WAMCRoza suggests that it holds resistance to race 1 independent of $R_{Mc1(blb)}$. While *S. stenophyllidium* and *S. bulbocastanum* are in the same nuclear clade (Spooner et al. 2014), morphological differences between the two species suggest that they are not extremely similar and indicating that the resistance found in PI545815sph-9mc and PI255518blb-4mc may not share a common origin.

One recurring concern in breeding for CRKN resistance is the ability of *M. chitwoodi* to overcome host resistance in the field, as has been observed in the lab, through the selection of nematodes able to overcome resistance from *S. hougasii* (Janssen et al. 1998; Mojtahedi et al. 2007; Castagnone-Sereno 2002). One strategy to develop durable resistance is to focus efforts on genes that confer resistance to a wide range of isolates, as these genes likely target attributes that are more central to the nematode's pathogenicity and would likely be more difficult for the nematode to overcome. However, it will be necessary to cross susceptible parents and the selected *S. hougasii* clones that are resistant to multiple *M. chitwoodi* isolates to determine whether they carry any single genes that confer resistance to multiple isolates.

The main challenge with nematode screening is quantification of resistance relative to susceptible checks. This challenge is further complicated by the higher levels of nematode reproduction noticed in ‘Rutgers’ tomato than in other susceptible controls. A conservative approach would be to select only clones that exhibit significantly lower reproduction rates than all of the susceptible controls for a given isolate. The other challenge is correlating *M. chitwoodi* reproduction in pots in the greenhouse to the damage in the field. A more liberal approach would express nematode reproduction relative to ‘Rutgers’ tomato, which is more closely related to potato, and which was shown to have levels of reproduction similar to the more susceptible wild potato clones in the initial screening. If this second more liberal approach were adopted, clones with these genes should be tested in the field early in the introgression process.

Across all of our evaluations, reproduction values varied widely, among plants of each of the checks and among plants of the same clone. We commonly observed a five-fold difference in reproduction among clones from a single accession. This, combined with the high number of trials that gave poor data due to environmental factors (see Appendix A, Supplementary Table 2.1), highlight the difficulties in screening for nematode resistance, and the importance of replication and appropriate statistical methodology for data analysis.

Based on the geographical mapping, it appeared that resistance to *M.* chitwoodi is clustered in and around the Mexican states of Jalisco and Michoacán. Therefore, we propose that accessions in this area are more likely to hold resistance to *M. chitwoodi*, possibly because *M. chitwoodi* or a similar nematode species has been present for a long time and resistance evolved in the wild potato species. This hypothesis is supported by the observation that multiple types of resistance to *M. chitwoodi* are found in this area (including $R_{Mctuber(blb)}$, $R_{Mc1(blb)}$, root resistance to race 2 that was identified in this and earlier studies, and root resistance to WAMCRoza that was identified in this study), while to date no accessions with resistance to *M. chitwoodi* have been found in the entirety of South America. In addition, it is consistent with a report that resistance to *Meloidogyne* species in wild potato accessions is associated with geographic and climatic variables, including precipitation and temperature (Spooner et al. 2009). Thus, we recommend that future screening for resistance to *M. chitwoodi* focus on germplasm from this region.

2.6 Conclusion

We identified *Solanum spp.* clones from eight accessions with high levels of resistance to three key isolates of *M. chitwoodi*. Resistant accessions six accessions from *S. hougasii*, one accession from *S. bulbocastanum*, and one accession from *S. stenophyllidium*. Of the 17 clones with resistance, PI239424hou-2mc, PI239424hou-6mc, PI283107hou-5mc, and PI283107hou-9mc were the only clones that were non-hosts for each of the three nematode isolates tested.

Using these clones, we plan to introgress resistance from these clones into elite potato germplasm. For *S. hougasii*, it should be possible to cross directly to elite tetraploid potatoes (Brown et al. 1991), while genes from *S. bulbocastanum* can be introgressed into elite potato germplasm through protoplast fusion (Austin et al. 1993). For both of these species, continued backcrossing with tetraploid cultivated potatoes after the initial hybridization will eventually result in a tetraploid potato (Brown et al. 2009, Haynes and Qu 2016). To the best of our knowledge, no efforts have been made to hybridize clones from *S. stenophyllidium* with cultivated potatoes, but the steps required for introgression would likely be similar to those for *S. bulbocastanum*. Segregation ratios after sexual recombination in the interspecific hybrids should provide information on the number and locations of the resistance genes in each selected clone. The information on the magnitude and breadth of resistance in these clones will aid in planning future efforts to transfer resistance genes to cultivated potato.

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2.8 Tables

Table 2.1. *Solanum* accessions screened for resistance to *Meloidogyne chitwoodi*.

Species	Origin	Ploidy	EBN*	Number of PIs used
S. iopetalum	Mexico	6x	4	11
S. bulbocastanum	Mexico	2x	1	10
S. hougasii	Mexico	6x	4	8
S. boliviense	Bolivia	2x	2	2
S. guerreroense	Mexico	6x	4	2
S. brevicaule	Bolivia	2x	2	2
S. stenophyllidium	Mexico	2x	1	2
S. stoloniferum	United States	4x	2	2
S. andreanum	Colombia	2x	2	1

*The endosperm balance number (EBN) can be used to predict compatibility between two species. Crosses have the highest chance of success when the parents have the same EBN, or when they have an EBN that differs by a factor of two, and the parent with the lower EBN produces unreduced gametes.

Table 2.2. ANOVA table showing the effect of *Solanum* clones, isolates, and clone × isolate interaction on *Meloidogyne chitwoodi* reproduction, using transformed reproduction values.

	DF	SS	MS	F-value	p-value
Clone	16	31.626	1.977	15.409	<0.001
Isolate	2	33.052	16.526	128.827	<0.001
Clone*Isolate	31	29.267	0.944	7.359	<0.001
Error	187	23.988	0.128		

Table 2.3. Geometric means of reproduction factors (RF = number of eggs extracted/initial number of eggs) and HSD tests for selected wild *Solanum* clones and three checks, against three *M. chitwoodi* isolates. HSD tests were conducted for each nematode isolate separately.

Clone	*M. chitwoodi* Race 1 WAMCRoza		*M. chitwoodi* Race 1 WAMC1		*M. chitwoodi* Race 2 WAMC27	
	Mean RF	*Host Status**	*Mean RF*	*Host Status**	*Mean RF*	*Host status**
PI161726hou-3mc	0.317 (bc)	PH	0.000 (d)	NH	0.123 (bcd)	PH
PI239423hou-1mc	0.063 (bcde)	NH	0.000 (d)	NH	0.290 (bc)	PH
PI239423hou-2mc	0.186 (bc)	PH	0.039 (bcd)	NH	0.563 (b)	PH
PI239423hou-8mc	0.000 (e)	NH	0.000 (d)	NH	0.271 (bc)	PH
PI239423hou-10mc	0.000 (e)	NH	0.001 (d)	NH	0.390 (b)	PH
PI239424hou-2mc	0.000 (e)	NH	0.000 (d)	NH	0.009 (de)	NH
PI239424hou-3mc	0.001 (e)	NH	0.006 (cd)	NH	0.162 (bcd)	PH
PI239424hou-6mc	0.001 (e)	NH	0.003 (cd)	NH	0.020 (cde)	NH
PI239424hou-9mc	0.000 (e)	NH	0.000 (d)	NH	0.331 (bc)	PH
PI255518blb-4mc	0.330 (bc)	PH	0.000 (d)	NH	0.010 (de)	NH
PI283107hou-5mc	0.000 (e)	NH	0.000 (d)	NH	0.062 (bcde)	NH
PI283107hou-6mc	0.109 (bcd)	PH	0.186 (b)	PH	0.337 (bc)	PH
PI283107hou-9mc	0.001 (e)	NH	0.001 (d)	NH	0.087 (bcde)	NH
PI545815sph-9mc	0.033 (cde)	NH	ND		0.372 (bc)	PH
PI558402hou-2mc	0.186 (bc)	PH	0.004 (cd)	NH	0.155 (bcd)	PH
PI558402hou-4mc	0.159 (bcd)	PH	0.017 (cd)	NH	0.108 (bcd)	PH
PI558422hou-2mc	0.622 (b)	PH	0.027 (bcd)	NH	0.121 (bcd)	PH
‘Rutgers’ tomato	20.286 (a)	H	10.254 (a)	H	6.013 (a)	H
‘Vernema’ alfalfa	0.012 (de)	NH	0.000 (d)	NH	0.101 (bcd)	PH
‘Red Core Chantenay’ carrot	0.144 (bcd)	PH	0.062 (bc)	NH	0.000 (e)	NH

*NH –Non-Host (Rf: 0 to 0.1), PH – Poor Host (Rf: 0.1 to 1), H – Host (>1), ND – No Data

2.9 Figures

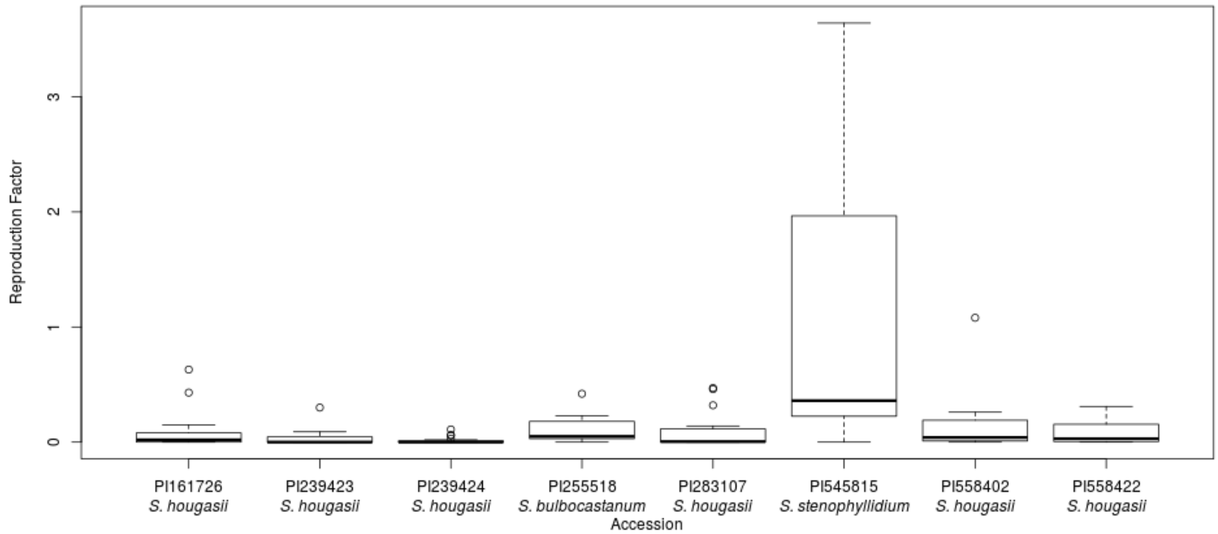

Figure 2.1. Boxplot showing range of WAMCRoza reproduction factors in the eight wild potato accessions with at least one clone resistant to *M. chitwoodi*.

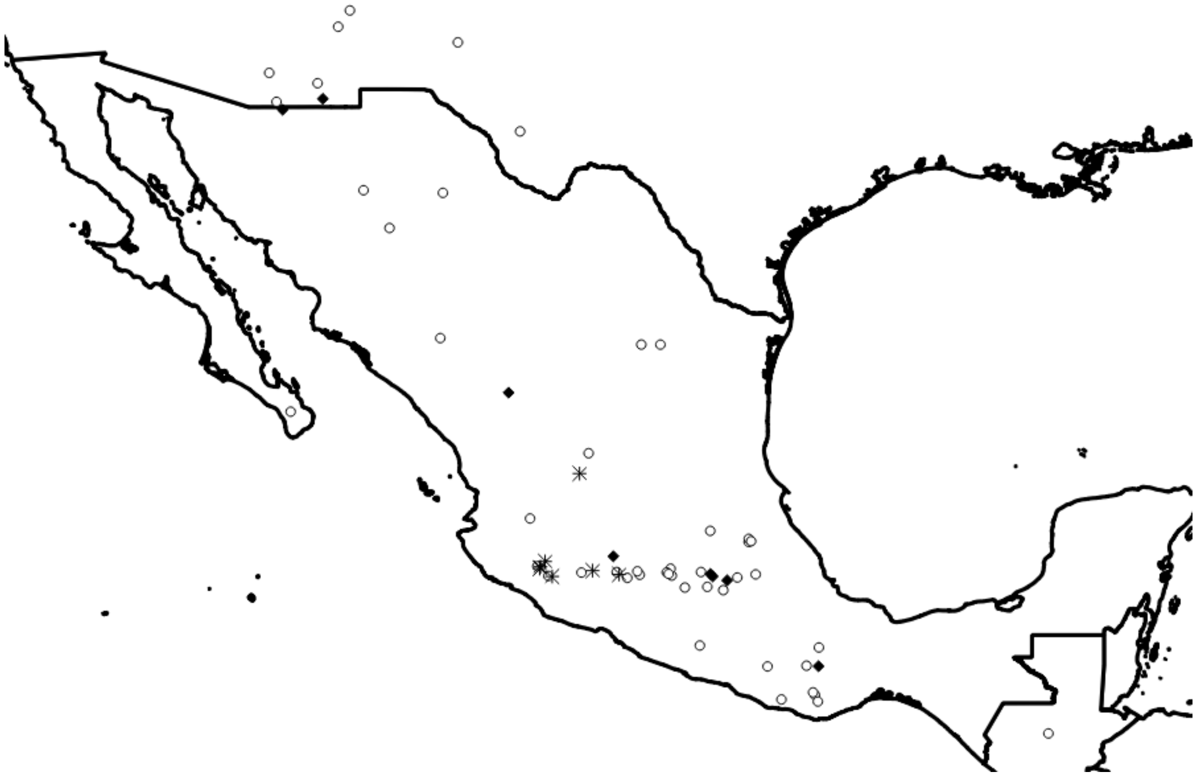

Figure 2.2. Distribution of collection sites of wild potato accessions in Mexico, Guatemala, and the southern United States. Open circles indicate accessions with no detected resistance to *Meloidogyne chitwoodi*, stars indicate resistant accessions detected in this study, and diamonds indicate resistant accessions detected in previous studies.

Figure 2.3. Distribution of collection sites of wild potato accessions in South America. Open circles indicate accessions with no detected resistance to *Meloidogyne chitwoodi*.

3 Response of wild potato species to greenhouse inoculation with *Verticillium dahliae*

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3.1 Abstract

Verticillium dahliae, capable of inciting Verticillium wilt, is a major soil-borne pathogen of potatoes in many regions of the world. While moderate levels of resistance to *V. dahliae* have been identified in cultivated and wild potatoes, there is an urgent need for additional sources that confer strong, unambiguous resistance. To identify novel sources of resistance, we inoculated 80 seedlings from nine wild potato species from North and South America with *V. dahliae* in the greenhouse. Our screening identified two clones of *Solanum andreanum* and one clone of *S. bulbocastanum* that had resistance equal to or greater than 'Ranger Russet', the moderately resistant check. These new sources of *V. dahliae* resistance have different geographic origins and will expand our *V. dahliae* resistant potato germplasm. We plan to introgress these new sources into elite potatoes to develop cultivars with durable resistance to *V. dahliae*.

3.2 Introduction

Verticillium dahliae Kleb., one of the pathogens that can incite Verticillium wilt (VW, commonly called early die), is a major soil-borne fungus of potatoes (*S. tuberosum* L.) and is the most prevalent and damaging *Verticillium* species in the Columbia Basin potato growing region of Oregon and Washington. *Verticillium dahliae* invades potato roots, eventually colonizing the plant's vascular and cortical tissues (Klosterman et al. 2009). This disrupts water transport, and can lead to premature yellowing, wilting and death of the vine (Johnson and Dung 2010). *Verticillium dahliae* produces three types of asexual structures: mycelia, conidia (spores) and microsclerotia. The microsclerotia can persist in the soil for as many as 14 years, making the pathogen difficult to control

(Wilhelm 1955). VW typically causes yield losses of 10-15%, although in some cases losses may reach 30-50% (Johnson and Dung, 2010). *Verticillium dahliae* has been found as a contaminant on many seed potato tubers used to plant commercial fields (Omer et al. 2000), indicating that fields without this pathogen are at high risk of infection. *Verticillium albo-atrum* Reinke and Berthold, another pathogen that commonly causes VW in potatoes, is common in colder potato growing regions, where temperatures rarely exceed 25 °C (Powelson and Rowe 1993). In contrast, *V. dahliae* is favored by the warmer temperatures that predominate in the Columbia Basin, where average daily summer temperatures usually exceed 27 °C (Johnson and Dung, 2010).

Elite potato germplasm includes a moderate level of genetic resistance to *V. dahliae*, but to date, no clone with complete resistance to this pathogen under field conditions has been found (Jansky 2000, Dan et al. 2001, Jansky 2009). The *V. dahliae* resistance that is present in elite potato germplasm appears to be quantitative, with the most important quantitative trait loci that has been mapped explaining 10% and 25% of the phenotypic variance in two populations (Simko et al. 2004).

In exotic potato germplasm, resistance to *V. dahliae* and *V. albo-atrum* has been identified in *S. chacoense* and *S. tuberosum* Group Phureja, and resistance to *V. albo-atrum* has been identified in *S. raphanifolium,* and *S. berthaultii* (Concibido et al. 1994; Lynch et al. 1997). In addition, resistance to *V. dahliae* has been identified in interspecific hybrid clones, with backgrounds including *S. tuberosum*, *S. berthaultii*, *S. brevicaule* and *S. chacoense* (Jansky and Rouse 2000). From crosses between these clones and clones from elite potato germplasm, several interspecific hybrids with resistance to at least one *Verticillium* species have been developed (Jansky and Rouse 2003; Lynch et al. 2004; Frost et al. 2006). However, similar to elite potato germplasm, to date no genes have been found that confer complete resistance to *V. dahliae* in wild potato species, highlighting the need for multiple sources of resistance to this pathogen.

While many crop species are known to have genes that confer moderate but not complete resistance to *V. dahliae*, in tomato, the gene *Ve1* confers complete resistance to race 1 isolates of both *Verticillium* species (Diwan et al. 1999). As a result, this gene is included in most modern commercial tomato varieties. Since its discovery, genes with homology to *Ve1* have been found to confer resistance to *V. dahliae* in a number of other crop species, including mint and cotton (Vining and Davis 2009; Chen et al. 2016).

Verticillium dahliae isolates are typically divided into vegetative compatibility groups (VGCs), where pairs of isolates from different VGCs generally cannot form heterokaryons, making them genetically isolated from each other (Puhalla 1979; Puhalla and Hummel 1983; Dung et al. 2012). In North America, potatoes are most commonly infected by isolates from VCG4A, while isolates from VCG4B and VCG2 are also commonly found associated with potato (Dung et al. 2012). Isolates from VCG4A have been found to be more virulent on potatoes than VCG4B or VCG2 in greenhouse studies (Jaoquim and Rowe 1991; Strausbaugh 1993).

Commercial potatoes are tetraploid, heterozygous clones that require 12 to 16 years from the time initial crosses are made to release of a new variety. Because of its ploidy level and heterozygous nature, efforts to create new potato populations with improved disease resistance traits are slow to yield acceptable varieties. In order to increase the selection efficiency for disease resistance traits, it is important to identify suitable germplasm that carries resistance and has minimal negative effects when crossed with selections carrying desirable commercial traits. To increase breeding efficiency, breeding programs depend on access to germplasm carrying resistance genes and the ability to identify resistant germplasm. To identify new sources of resistance, we screened a panel of wild potato species with two isolates of *V. dahliae* in the greenhouse. The newly identified resistant germplasm will be used to establish an efficient VW resistance breeding program. The moderately resistant ‘Ranger Russet’ served as a benchmark for the level of *V. dahliae* resistance to have a substantial positive impact on potato production.

3.3 Methods

3.3.1 Plant material

Twenty-two accessions from the NRSP-6 Potato Genebank, representing nine wild potato species, were evaluated for their response to *V. dahliae* (Table 3.1). The wild species used in this study represent a group that has received less attention in previous efforts to identify resistance to *Verticillium* species. In addition, cultivars Russet Norkotah and Russet Burbank were used as susceptible controls, and Ranger Russet as a moderately resistant control (Jansky 2009).

3.3.2 Isolates used

For initial screening, we used *V. dahliae* VCG4A isolate 653 that was isolated from a potato tuber in Idaho in 1996 (Dung et al. 2012). For replicated evaluation, in addition to isolate 653, the potential resistant clones identified in the initial screening were inoculated with VCG4B isolate 11-11, which was isolated from a potato tuber in Maine in 1996 (Dung et al. 2012).

3.3.3 Inoculum preparation

For resistance screening, the inoculum was prepared by adding approximately forty 1 cm^2 edge pieces of *V. dahliae* colonies growing on potato dextrose agar to 3 L Czapek-Dox broth prepared according to manufacturer instructions (HiMedia Laboratories, Mumbai, India), in six 1 L Erlenmeyer flasks. The flasks were shaken in the dark at room temperature for 10 days, and then strained through cheesecloth into a large beaker. *V. dahliae* conidia were quantified using a hemocytometer and diluted to a concentration of 1.0×10^6 conidia per mL.

3.3.4 Initial screening

Ten seeds of each accession were placed in a solution of 0.1% gibberellic acid. After 24 hours, the treated seeds were placed on a damp paper towel in a 100 x 15 mm petri dish for five days to promote germination. Germinated seeds were then transferred to 2.5 cm pots containing an autoclaved mixture of 75% sand and 25% soil, fertilized with 2.0 g Osmocote 14-14-14 Flower and Vegetable Smart-Release Plant Food (The Scotts Company, Marysville, OH, USA) per liter sand-soil mixture. At the same time, shoot cuttings of ‘Russet Burbank’ were propagated from tissue culture in the same sand-soil-fertilizer mixture. After 28 days, seedlings were transplanted to larger 10 cm pots with the same sand-soil-fertilizer mixture. During transplantation, the root system of each seedling was inoculated with 3.0×10^7 conidia of isolate 653, suspended in 30 mL water. We tried to inoculate four seedlings per accession, although in some cases, low germination rates meant that fewer accessions were inoculated. The inoculated plants were then grown in a greenhouse with 16 hours of artificial lighting per day. Daytime temperatures kept at 24 °C, and nighttime temperatures at 18 °C. Plant health data were collected weekly beginning five weeks after inoculation. Plant health was scored on a scale of 0-5, where “0” indicated a dead plant, “1” a plant that was barely alive and “5” a healthy plant. After eight weeks, all surviving plants were propagated via shoot cuttings using Dip ‘N’ Grow hormonal rooting concentrate (Dip N Grow Inc, Clackamas, Oregon, United States) diluted to 20X, and were then transferred into tissue culture and maintained on MS30 media (Murashige and Skoog 1962).

3.3.5 Replicated evaluation

Clones that survived the preliminary evaluation and were able to be propagated were subjected to a replicated evaluation. Replicated evaluations were carried out using *V. dahliae* isolates 653 and 11-11. For each isolate, four plants per clone were inoculated with 2.0×10^7 conidia suspended in 20 mL water. Additionally, four plants of each clone were left as uninoculated controls. ‘Russet Norkotah’ and ‘Ranger Russet’ served as the susceptible and moderately resistant controls, respectively. Plants were evaluated using methods similar to the unreplicated evaluation with the following exceptions: plants were propagated from tissue culture 48 days before inoculation; plants were fertilized using Osmocote 19-6-12 Indoor and Outdoor Smart-Release Plant Food (The Scotts Company, Marysville, OH, USA); and weekly plant health notes were recorded beginning one week after inoculation and carried out until eleven weeks post-inoculation. At the end of the evaluation, plant sap was extracted from a 2.5 cm segment of the main stem of each surviving plant using the protocol described by Hoyos et al. (1991) and used to make a 1:10 dilution with sterile water. Two hundred and fifty microliters of the diluted sap solution were plated onto Sorensen’s NP-10 medium (Sorensen et al. 1991) using a spreader bar. The plates were left at room temperature for two weeks. After two weeks, plates were scored on a 1-5 scale, where “5” indicated 0-1 colony forming units (CFU), “4” indicated 2-10 CFU, “3” indicated 11-50 CFU, “2” indicated 51-100 CFU, and “1” indicated >100 CFU. A score of “0” indicated that the plant died before the end of the trial. In addition, the area under the disease scenescence curve was used to quantify plant health, and qPCR was used to quantify *V. dahliae* stem colonization. However, these methods were not as precise, and are reported in Appendix B.

3.3.6 Statistical analysis

The response of each plant in the replicated evaluation to *V. dahliae* was calculated as the sum of the weeks each plant survived (12 if the plant was alive at the end of the trial) plus the score assigned during *V. dahliae* culturing. Significant differences between the responses of clones or isolates, and significant interactions between these two factors were analyzed by ANOVA. An LSD test was used to determine if there were significant differences between the response of each clone, using the R package “agricolae” (de Mendiburu 2017), using a false discovery rate to correct for multiple comparisons. All the statistical analyses were carried out using R version 3.2.3 (R Core Team 2015).

3.4 Results and discussion

3.4.1 Initial screening

A total of 80 clones were evaluated for their response to *V. dahliae*. Of the 80, 19 clones survived the preliminary evaluation, and only eight clones were successfully propagated by shoot cutting (Table 3.2). Of the nine species tested, none of the clones from *S. boliviense, S. brevicaule, S. guerreroense, S. stenophyllidium* or *S. stoloniferum* survived for their response to *V. dahliae* to be quantified. The *S. bulbocastanum* clone PI498011blb-1vd was recorded as being completely dead midway through the screening but was still successfully propagated at the end of the experiment. PI498011blb-1vd is the only clone from *S. bulbocastanum* that was successfully propagated, even though three additional clones survived the initial screening (Table 3.2). The *S. andreanum* accession PI498148 was the only species for which all of the clones that survived initial evaluation were successfully propagated. Of the eight susceptible ‘Russet Burbank’ plants that were inoculated in the initial screening, three survived (Table 3.2). While there was no uninoculated control in the initial screening, in a set of near identical trials conducted at the same time but without *V. dahliae* inoculation, fewer than 25% of the plants died, suggesting that the majority of plant mortality in the initial screening of this study was due to *V. dahliae* infection.

3.4.2 Replicated evaluation

Ten clones, including eight clones from wild potato species, ‘Ranger Russet’ and ‘Russet Norkotah’ were screened for their response to two isolates of *V. dahliae.* Plants from the clone *S. hougasii* PI239423hou-3vd, including uninoculated controls, died soon after transplantation into 10 cm pots. Therefore, this clone was removed from the analysis. Though three out of four of the uninoculated plants of ‘Russet Norkotah’ died before the end of the 12-week trial, we included ‘Russet Norkotah’ as a highly susceptible check in the analysis. Aside from these exceptions, no uninoculated controls died prior to the end of the trial or were found to be infected with *V. dahliae* via culturing.

Both the clone and the isolate had a significant effect on the plant’s response to *V. dahliae* infection ($p<0.001$ and $p=0.008$, respectively), but there was no interaction between potato clone and *V. dahliae* isolate ($p=0.492$; Table 3.3). As a result, data for isolates 653 and 11-11 were pooled for the LSD test (Table 3.4). The LSD test indicated that the clone PI498148-1vd from *S. andreanum* accession exhibited significantly greater resistance than the clones from *S. hougasii* and *S. iopetalum*. However, the increased level of resistance over ‘Ranger Russet’, PI498011blb-1vd, and PI498148-2vd observed in this experiment was not statistically significant (Table 3.4). In addition, the *S. andreanum* clone PI498148-2vd and the *S. bulbocastanum* clone PI498011blb-1vd had significantly greater resistance than the clones from *S. iopetalum*, but the resistance over ‘Ranger Russet’ and the *S. hougasii* clone was not statistically significant. While not always significantly lower in resistance than ‘Ranger Russet’ in this evaluation, the levels of resistance demonstrated by the clones from *S. hougasii* and *S. iopetalum* appeared to be lower than ‘Ranger Russet’, and therefore uninteresting from a breeding perspective.

Clones ranked similarly for 11-11 and 653; for both isolates, the two *S. andreanum* clones, the *S. bulbocastanum* clone, and ‘Ranger Russet’ exhibited greater resistance than the *S. hougasii* clone, the three *S. iopetalum* clones, and ‘Russet Norkotah’.

Solanum andreanum and *S. bulbocastanum* are from nuclear clades 3 and 1, respectively, while the previously identified sources of resistance from *S. chacoense* (Concibido et al. 1994; Lynch et al. 1997), *S. raphanifolium* (Lynch et al. 1997), and *S. berthaultii* (Lynch et al. 1997) are all from nuclear clade 4 (Spooner et al. 2014). Therefore, it is likely that the new sources of resistance presented here include genes that are different from those identified in prior studies. *S. andreanum* PI498148 was collected from Narino, Colombia, while *S. bulbocastanum* PI498011 was collected from Oaxaca, Mexico. While the clones in this study have not been tested for resistance to *V. albo-atrum*, the results from the replicated evaluation suggest that this resistance may be stable against a range of *V. dahliae* isolates.

While isolate 11-11 from VCG4B was more virulent than isolate 653 from VCG4B in this study, it was difficult to draw conclusions from this. It is possible that by using 653 for the initial screening, we selected for clones with improved resistance to this isolate. However, this would not explain why 11-11 was also more virulent on ‘Ranger Russet’. Alternative explanations for this difference include a general difference between these specific isolates, or differences in inoculum preparation between the two isolates.

3.5 Conclusion

Based on our replicated greenhouse evaluations, the level of resistance observed in PI498148adr-1vd, PI498148adr-2vd, and PI498011blb-1vd was similar to that observed in ‘Ranger Russet’. These clones responded similarly to inoculation with isolates from VCG4A and VCG4B, indicating that they may be able to confer resistance to a broad range of the *V. dahlia* isolates found in potato production. As a result, these three clones are of interest in expanding our genetic base for VW resistance breeding. The next step will be to initiate introgression by crossing these three new resistant clones with cultivated potatoes along with studying for inheritance of resistance from these new sources. While the introgression process for clones from *S. andreanum* should be relatively straightforward, the clone from *S. bulbocastanum* would first require protoplast fusion with a cultivated potato. Further, testing these resistant clones against a wider range of *V. dahliae* isolates, and possibly *V. albo-atrum* isolates to determine the breadth of resistance present in each clone could also become a source of valuable information. Early in the introgression process, it will be important to verify that this resistance is expressed under field conditions (Frost et al. 2007). To the best of our knowledge, the two clones from *S. andreanum* are the first clones from this species with confirmed resistance to any pathogen.

3.6 References

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3.7 Tables

Table 3.1. *Solanum* species screened for resistance to *Verticillium dahliae*.

Species	Origin	Ploidy	EBN*
S. andreanum	Columbia	2x	2
S. boliviense	Bolivia	2x	2
S. brevicaule	Bolivia	2x	2
S. bulbocastanum	Mexico	2x	1
S. guerreroense	Mexico	6x	4
S. hougasii	Mexico	6x	4
S. iopetalum	Mexico	6x	4
S. stenophyllidium	Mexico	2x	1
S. stoloniferum	United States	4x	2

*The endosperm balance number (EBN) can be used to predict compatibility between two species. Crosses with greatest chance of success are between parents with the same EBN, or EBNs differing by a factor of two, and the parent with the lower EBN produces unreduced gametes.

Table 3.2. Number of clones tested from each *Solanum* sp. accession for resistance to *Verticillium dahliae* in the initial screening, and the number of clones that survived the screening and were retained for further testing.

Species	Accession	Clones tested	Clones survived	Clones successfully propagated
S. andreanum	PI498148	4	2	2
S. boliviense	PI265861	4	0	0
S. boliviense	PI473361	1	0	0
S. brevicaule	PI545912	4	0	0
S. bulbocastanum	PI243508	4	0	0
S. bulbocastanum	PI243512	4	2	0
S. bulbocastanum	PI275187	4	0	0
S. bulbocastanum	PI498011	4	2	1
S. guerreroense	PI652828	4	0	0
S. hougasii	PI239423	4	2	1
S. hougasii	PI283107	4	2	1
S. iopetalum	PI275181	4	4	1
S. iopetalum	PI275182	4	3	2
S. iopetalum	PI275183	4	1	0
S. iopetalum	PI498022	4	0	0
S. iopetalum	PI498024	3	0	0
S. iopetalum	PI498249	1	0	0
S. iopetalum	PI597682	3	1	0
S. stenophyllidium	PI320265	4	0	0
S. stenophyllidium	PI545815	4	0	0
S. stoloniferum	PI632334	4	0	0
S. stoloniferum	PI643997	4	0	0
S. tuberosum	‘Russet Burbank’	8	3	-

Table 3.3. ANOVA for the replicated evaluation, comparing the response of eight *Solanum* spps. clones inoculated with two *Verticillium dahliae* isolates.

	DF	SS	MS	F-value	p-value
Clone	7	290.250	41.464	6.9348	<0.001
Isolate	1	45.562	45.562	7.6202	0.008
Clone*Isolate	7	38.938	5.562	0.9303	0.492
Error	48	287.000	5.979		

Table 3.4. Means of indexed values describing the response of each clone to inoculation by *Verticillium dahliae* isolates ‘11-11’ and ‘653’, and LSD values for the pooled resistance data. Higher values indicate later plant mortality and lower stem colonization.

	Mean resistance*		
Clone	11-11	653	Pooled
PI498148adr-1vd	14.0	15.8	14.9(a)
PI498148adr-2vd	13.0	16.0	14.5(ab)
PI498011blb-1vd	14.5	13.8	14.1(ab)
‘Ranger Russet’	12.3	14.0	13.1(abc)
PI283107hou-1vd	11.3	12.0	11.6(bcd)
PI275181iop-1vd	10.8	11.3	11.0(cd)
PI275182iop-1vd	8.3	10.3	9.3(d)
‘Russet Norkotah’	8.3	10.3	9.3(d)
PI275182iop-4vd	6.8	11.5	9.1(d)

*Resistance for each clone was calculated as the sum of the number of weeks the plant survived (12 if the plant survived the duration of the trial) plus the 0-5 score assigned during Verticillium culturing (“0” indicates the plant died before the end of the trial, “1” indicates high *V. dahliae* colonization, “5” indicates no detected *V. dahliae* colonization).

4 Evaluation of resistance to *Potato virus Y* and corky ringspot from 'Castle Russet'

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4.1 Abstract

Potato virus Y (PVY) and *Tobacco rattle virus* (which incites corky ringspot; CRS) are both damaging pathogens of potato in the Columbia Basin potato growing region of Oregon and Washington that can be difficult to control using cultural methods. Screening identified 'Castle Russet' to be resistant to both PVY and CRS. In order to study segregation of resistance and identify molecular markers linked to these resistances, we developed a population of 148 clones by crossing 'Castle Russet' with POR08BD1-3. SNP genotyping found that only 49 clones were from these parents, while the other 99 clones originated from an unknown set of parents. Molecular mapping of the 49 clones identified SNPs linked to PVY resistance, in addition to the markers STM0003 and YES3-3B, which were previously found to be linked to resistance from Ry_{sto}. A single marker association analysis for CRS identified a major peak on chromosome 9 and two minor peaks on chromosomes 1 and 10. The SNPs associated with PVY and CRS need to be validated on a bigger population for their effective use in marker assisted breeding.

4.2 Introduction

The Columbia Basin growing region of Oregon and Washington is one of the top potato (*Solanum* tuberosum) production regions of the United States; together these states produced 29.1% of the country's potatoes in 2016 (National Agricultural Statistics Service 2017a). The majority of potatoes from this region are destined for the French fry industry, although some potatoes are also produced for the potato chip and fresh markets. This region is notable for its high yields, averaging 66.1 metric tons per hectare in Oregon and 70.1 metric tons per hectare in Washington, compared to 47.1 metric tons per hectare across the United States and 19.0 metric tons per hectare worldwide (National Agricultural Statistics Service 2017; Food and Agriculture Organization of the United Nations 2016). These high yields are attributed to a set of environmental factors in this region favorable to potato production, including warm daytime temperatures associated with cool nighttime temperatures that reduce energy loss during nighttime metabolism, a long growing season, sandy loam soils, and ample irrigation from the Columbia River and its tributaries. As with most potato growing regions, an array of pathogens can decrease the yield and quality of potatoes in the Columbia Basin, including *Potato virus Y* (PVY), *Tobacco rattle virus* (TRV), the Columbia root-knot nematode (*Meloidogyne chitwoodi*), Verticillium wilt (incited by *Verticillium dahliae* and *V. albo-atrum*), *Potato mop-top virus*, and late blight (incited by *Phytophthora infestans*).

PVY is a plant pathogenic potyvirus that is vectored by aphids and persists when a potato plant is used to produce seed tubers for the following crop (Gray et al. 2010). Foliar symptoms of PVY include mosaic, leaf crinkle, chlorosis and necrosis, and tend to be more severe for the PVY strain PVY^{O} than for other important PVY strains, including PVY^{N}, $PVY^{N\text{-}Wi}$ and PVY^{NTN} (Gray et al. 2010). Yield losses from PVY are reported to be approximately 0.18 t/ha for every 1% of the seed lot that is infected (Nolte et al. 2004). While PVY is well established in the Columbia Basin (Goodell 1979), the emergence of the strains PVY^{N}, $PVY^{N\text{-}Wi}$ and PVY^{NTN} have complicated the production of virus-free seed tubers, because their mild foliar symptoms make the infected plants difficult to identify and rogue in certified seed programs (Karasev and Gray 2013). In addition, the emerging PVY^{NTN} strain is capable of inciting potato tuber necrotic ringspot disease, which results in a sunken necrotic ring on the tuber surface, making the tuber unmarketable (Karasev and Gray 2013). Three sources of extreme genetic resistance to PVY have been identified and introgressed into elite potato germplasm: Ry_{sto} from *S. stoloniferum* (Song et al. 2005), Ry_{adg} from *Solanum tuberosum* group Andigena (Hämäläinen et al. 1997), and Ry_{chc} from *Solanum chacoense* (Sato et al. 2006). Extreme resistance to PVY (conferred by *R* genes) is characterized by a strong reduction of virus reproduction in infected cells, while hypersensitive resistance to PVY (conferred by *Ny* genes) inhibits the virus' spread to new cells (Song et al. 2005). While *Ny* genes are generally strain-specific, *Ry*$_{sto}$, *Ry*$_{adg}$, and *Ry*$_{chc}$ are resistant to all known strains of PVY (Song et al. 2005).

Molecular markers linked to extreme resistance genes *Ry*$_{sto}$ and *Ry*$_{adg}$ have been identified previously (Hämäläinen et al. 1997; Sato et al. 2006) and are being used in marker assisted PVY resistance breeding. Genetic markers linked to *Ry*$_{sto}$ in diverse sets of clones include the STM0003, a simple sequence repeat (SSR) marker on chromosome 12 that was linked to *Ry*$_{sto}$ in an anther-culture derived dihaploid mapping population of 59 clones (Song et al. 2005), and YES3-3A and YES3-3B, sequence tagged site (STS) markers on chromosome 12 that were developed from the amplified fragment length polymorphism (AFLP) marker E+ACC/M+CTC-365, identified in the same dihaploid mapping population (Song and Schwarzfischer 2008). In the initial mapping population, STM0003 and E+ACC/M+CTC-365 co-segregated with *Ry*$_{sto}$ (Song et al. 2005). However, STM0003 was later mapped 2.95 cM away from *Ry*$_{sto}$ in an F1 population of 195 potato clones. YES3-3A, YES3-3B, and E+ACC/M+CTC-365 were not tested in this study (Cernák et al. 2008).

Corky ringspot (CRS) disease, an important disease in the Columbia Basin, is caused by TRV, which is vectored by stubby-root nematodes (*Trichodorus spp.* and *Paratrichodorus* spp.; Hafez and Sundararaj 2009; Charleton et al. 2010). In potato, CRS is characterized by necrotic rings in the tuber flesh (Hafez and Sundararaj 2009), which can cause 6% to 55% of potatoes in an infested field to be unmarketable (Hafez and Sundararaj 2009). Typically, the most effective route to controlling damage caused by TRV is to control the nematode vector, either through fumigation, the application of non-fumigant nematicides, or by growing alfalfa as a rotation crop (Hafez and Sundararaj 2009; Charlton et al. 2010). While some clones exhibit moderate to strong resistance to TRV, no widely-grown russet cultivars have resistance strong enough to prevent symptom expression (Hafez and Sundararaj 2009). Recently, the incidence of CRS in the Columbia Basin has been rising (Personal communication, Brown 2018), increasing the need for strong genetic resistance or other cost-effective control measures.

The Northwest potato variety development program, a collaboration between Oregon State University, Washington State University, the University of Idaho, and the

United States Department of Agriculture, has accelerated its efforts to produce commercially viable potato cultivars with strong genetic resistance to PVY and CRS. The recent releases ‘Payette Russet’ and ‘Castle Russet’ have genetic resistance to PVY from *Ry$_{sto}$*. In addition to PVY resistance, ‘Payette Russet’ also has late blight resistance and cold sweetening resistance (Novy et al. 2017), while ‘Castle Russet’ is also resistant to CRS and PMTV (Personal communication, Sathuvalli 2018).

The objective of this study was to evaluate the segregation of resistance for PVY and CRS from ‘Castle Russet’, and to identify single-nucleotide polymorphism (SNP) markers associated with resistance for use in marker assisted breeding.

4.3 Methods

4.3.1 Plant material

In 2014, a controlled cross was made between PVY and CRS resistant ‘Castle Russet’, and PVY and CRS susceptible selection POR08BD1-3 at USDA-ARS Prosser, to generate 148 seedlings in a progeny designated as POR15V001. ‘Castle Russet’ (POR06V12-3) is a russet-type potato clone with strong resistance to PVY, CRS, and PMTV. Resistance to PVY in ‘Castle Russet’ is conferred by the gene *Ry$_{sto}$*, originally from *S. stoloniferum*. CRS and PMTV resistance in ‘Castle Russet’ are of unknown origin but were likely introgressed from one of the wild potato species in the pedigree of ‘Castle Russet’ (Figure 4.1). POR08BD1-3 is a black dot resistant clone and is highly susceptible to PVY and CRS. Disease inoculations were carried out on 148 clones.

4.3.2 Evaluation for PVY resistance

PVY disease inoculations were carried out in a greenhouse. For each clone, three tuber seed pieces were planted in 10 cm pots separately. Thirty days after planting when the plants were 4 to 6 inches in height, each plant was inoculated with the PVY 40D of strain PVY^{NTN}. To inoculate each plant, carborundum was rubbed on three leaves of each plant. Next, an inoculum mixture consisting of ground infected leaf tissue and 0.03 M potassium phosphate buffer was rubbed on the same three leaves. Thirty-five days after inoculation, three leaf samples above the inoculated leaves were collected from each plant. An ELISA was run on each tissue sample, using an ELISA Reagent Set for *Potato Virus Y* (PVY) (Agdia, Elkhart, IN 46514). Following tissue collection, the inoculated plants were grown for 30 additional days and tubers were harvested from each plant. These tubers were re-grown in a greenhouse for the second round of PVY evaluations, this time using a PathoScreen® Kit for PVY (Agdia, Elkhart, IN 46514) for ELISA testing using the manufacturer's instructions.

For clones where STM0003, YES3-3B, and the measured resistance status did not agree (suggesting an escape or a recombination event), three virus-free mini tubers were planted in the greenhouse and inoculated using the same protocol used for the initial inoculation. Forty days after inoculation, three leaf samples were collected from each plant, and the nine leaves from each clone were bulked. Total nucleic acids were extracted for each bulked sample using a modified Dellaporta extraction (Crosslin and Hamlin 2011). For each sample, the PVY primer s6m (Table 4.1) was amplified by running 25 µL PCR reactions containing 12.5 µL 2x Reaction Mix from the SuperScript^{TM} III One-Step RT System (Invitrogen, Carlsbad, CA, USA), 2.5 µL *Redi*load^{TM} Loading Buffer (Invitrogen, Carlsbad, CA, USA), 0.5 µL of a solution containing 10 µM of both the forward and reverse primers for s6m, 0.5 SuperScript^{TM} III One-Step RT/Platinum^{TM} *Taq* High Fidelity Enzyme Mix, 2 µL extracted total nucleic acids, and 7 µL DEPC water. RT-PCR products were run on a 2% agarose gel at 90 V for 90 minutes. After electrophoresis, gels were shaken in 0.5 µg/mL ethidium bromide for 20 minutes at 50 rpm, then in distilled water for 20 minutes at 50 rpm. Gels were visualized using a Bio-Rad Gel Doc^{TM} XR+ (Bio-Rad Laboratories, Hercules, CA, USA).

In all stages of testing, ELISA absorption values that were more than double the background absorption were interpreted as positive, indicating the presence of PVY. If one sample for a clone was positive at any stage, the clone was assumed to be susceptible.

4.3.3 Evaluation for CRS resistance

Each clone was planted in three 3-hill plots in 2016 and 2017 in fields infested with TRV and its vector, the stubby root nematode at Prosser, WA. At the end of the trial period, tubers from each plot were harvested separately and stored for three months before CRS evaluation. For CRS disease evaluation, up to 20 tubers were cut lengthwise, quartered, and disease appearance (internal browning) were scored on a 0-8 scale based on the number of wedge sides that showed CRS. A disease severity index was calculated for each plot using the following equation:

$$DSI = (\sum S)/(T*8)*100$$

Where "S" is the score each tuber from the plot received, and "T" is the number of tubers scored for that plot. For this analysis, DSIs were averaged across the six plots planted of each clone in 2016 and 2017.

4.3.4 DNA preparation

DNA was extracted from each clone and the parents using a Mag-Bind Plant DNA DS Kit (Omega Bio-Tek, Norcross, GA, USA), using the manufacturer's instructions. Extracted DNA was further purified by precipitation using the following protocol. DNA samples were increased to 270 µL using DEPC water in a 1.5 mL microcentrifuge tube. Next, 30 µL 3 M sodium acetate and 750 µL 100% ethanol were added, mixed thoroughly and then placed in a -80°C freezer for at least 30 minutes. The samples were then centrifuged at 13,000 rpm for 13 minutes at 4°C. The supernatant was discarded, and the pellets were washed twice with 100 percent ethanol. Next, the DNA was reconstituted in 50 µL elution buffer (Omega Bio-Tek, Norcross, GA, USA). Samples were quantified using a NanoDrop™ ND-2000 Spectrophotometer (Thermo Scientific, Waltham, MA, USA), diluted to 25 ng/µL, and stored at -20 °C.

4.3.5 Molecular marker analysis

A total of 400 ng of high quality DNA from each clone was shipped to Geneseek® (Lincoln, NE, USA) for SNP genotyping using the Potato V3 Infinium SNP Array, with 21,226 SNPs. The intensity data obtained from the SNP array was analyzed for SNPs using GenomeStudio v2.0 (Illumina, San Diego, CA, USA) as described by Bali et al. (2017).

For PVY resistance marker analysis, the progeny was evaluated for *Ry_{sto}* linked markers, STM0003 and YES3-3B. PCRs were performed on a 10- µl volume containing 8.5 µl of master mix made from AmpliTaq® Gold with GeneAmp® as per manufacturer instructions (Applied Biosystems, Foster City, CA, USA), 0.4 µL of a solution containing 10 µM of both the forward and reverse primers, and 1.1 µL 25 ng/µL DNA. Primer details including PCR conditions for each primer are presented in Table 4.1. PCR products were separated by electrophoresis on a 2% *w/v* agarose gels (ISC BioExpress, Kaysville, UT) at 90 V for 180 and 400 minutes for STM0003 and YES3-3B, respectively. Gels were stained and visualized using the same methods as described above for the PVY marker s6m.

4.3.6 Determination of population structure

To determine the population structure, a principal component analysis (PCA) was performed from a kinship matrix made using the R package rrBLUP (Endelman et al. 2011). Additionally, pedigree reconstruction software was used to determine the parents of each group (Endelman et al., 2017). Finally, to check for duplicate clones, an R script was written that calculated the percent similarity between genotypes for every possible set of two clones × POR08BD1-3 (excluding loci with missing genotypic data).

4.3.7 Genetic linkage mapping of PVY resistance from Ry_{sto}

After quality filtering, a total of 19,766 SNPs were used in the study. Of these SNPs 1910 SNPs segregated as simplex × nulliplex or simplex × quadriplex and were used in genetic mapping of PVY. Markers STM0003 and YES3-3B along with 1910 SNPs and the resistance phenotype were used to construct a genetic linkage map for the 49 clones from progeny POR15V001 using JoinMap v4.1 (Van Ooijen 2006) as a BC1 population. The clone POR15V001-111 was excluded before constructing the final map, due to excessive missing marker data on chromosome 12.

4.3.8 Association analysis of CRS resistance

7,246 polymorphic SNPs were used to perform a single-QTL association mapping using JMP Genomics (SAS Institute, Cary, NC, USA) for the 48 clones of progeny POR15V001 (POR15V001-102 was excluded prior to analysis, due to missing phenotypic data). Markers were scored as diploids (AA for nulliplex, AB for heterozygous, and BB for quadriplex). A false discovery rate was used to correct for multiple comparisons, using R version 3.2.3 (R Core Team 2015).

4.4 Results

4.4.1 Population structure

A principal component analysis revealed two subgroups from the initial 148 clones: one with 49 clones, and one with 99 clones (Figure 4.2). Pedigree reconstruction software revealed that the group of 49 clones belongs to progeny POR15V001, while the remaining clones are from unknown parents. The pairwise comparison of clones found that some pairs are much more similar to each other than the rest of the population (Figure 4.3), indicating the presence of repeated clones. Using a threshold of 99% similarity, seven putative sets of duplicate clones and two putative sets triplicate clones were identified in this population.

4.4.2 PVY segregation

'Castle Russet' carried PVY resistance from *S. stoloniferum* (Ry_{sto}). A segregation analysis for resistance to PVY from 'Castle Russet' in 49 clones of the progeny POR15V001 confirmed that PVY resistance from 'Castle Russet' is controlled by a dominant allele at a single locus and the resistance was in simplex form. Analysis of closely linked Ry_{sto} markers STM0003 and YES3-3B further confirmed the simplex resistance (Table 4.2). A total of five clones had recombination events between STM0003 and YES3-3B. For two of these clones, the PVY status matched STM0003, and for the other three clones, the resistance status matched YES3-3B. There were no cases where a clone's resistance status did not match either STM0003 or YES3-3B. Surprising, both markers were present in the larger population of unknown parents, and PVY resistance generally segregated with these markers. However, the frequency of resistant clones in this population was higher than that of STM0003 and YES3-3B, and higher than would be expected if a single dominant gene conferred resistance in this population (p=0.002; Table 4.2). In this population, two clones had recombination events between STM0003 and YES3-3B.

4.4.3 Genetic linkage map of PVY resistance from 'Castle Russet'

A genetic linkage map was constructed with PVY linked markers, 1910 SNPs and the resistance phenotype using JoinMap 4.1 (van Ooijen and Voorrips, 2006). The linkage map spanned a distance of 38.2 cM at LOD 5 and included the two previously identified Ry_{sto} linked markers (STM0003 and YES3-3B), the PVY resistance phenotype, and 31 SNP markers (Figure 4.4). Six SNP markers co-segregated with STM0003, and 16 SNP markers co-segregated with YES3-3B. The PVY resistance phenotype was located between STM0003 and YES3-3B at a distance of 4.6 cM and 4.5 cM, respectively. None of the SNP markers included were located between the Ry_{sto} linked markers STM0003 and YES3-3B.

4.4.4 CRS segregation

Segregation analysis of CRS from the 48 clones of progeny POR15V001 revealed that 23 of clones had an average DSI scores that was less than five (Table 4.3). However, there were no natural breaks in average DSI scores, making it difficult to view this as a qualitative trait (Figure 4.5).

The unknown progeny had only four clones with a DSI of less than five (Table 4.3; Figure 4.6), indicating that the strong CRS resistance from 'Castle Russet' was not present in either of the unknown parents.

4.4.5 CRS marker association analysis

A single marker QTL analysis using 7,246 SNPs and the average disease severity index for the 48 clones resulted in a strong "peak" on chromosome 9, where the SNP markers PotVar0105349 and PotVar0108448 explained 61.6% of the phenotypic variance (p<0.0001; Figure 4.7). In addition, on chromosome 10, SNP solcap_snp_c1_12236 explained 30.0% of the phenotypic variance (p=0.0390), and on chromosome 1, SNP PotVar0050687 explained 28.5% of the phenotypic variance (p=0.0396). SNP markers that were significantly associated with CRS disease severity are presented in Table 4.4.

For the SNP markers PotVar0105349 and PotVar0108448, all but three clones with the “ABBB” genotype had an average DSI below 5.0, while all but one clone with the “BBBB” genotype had an average DSI above 5.0 (Figure 4.8). This indicates that a resistance allele is positioned close to these SNP markers that is capable of providing near-complete resistance to CRS in potato.

4.5 Discussion

We found that our initial population of 148 clones was in fact two populations: one population with 49 clones from the cross ‘Castle Russet’ × POR08BD1-3, and one population of 99 clones from a cross between two unknown parents. The possible reasons of progeny mix include mixing of berries from adjacent crosses, mix of seed during seed extraction, or during seedling tuber production. Based on our experience, we suggest performing genotyping first before considering phenotyping on a large data set to save time and money in the event of population errors.

For the population of 49 clones with the parents ‘Castle Russet’ and POR08BD1-3, PVY resistance segregated closely to what would be expected if this trait were controlled by a single dominant gene. PVY resistance for this population was on chromosome 12, 4.6 cM and 4.5 cM from previously the identified markers STM0003 and YES3-3B, respectively, and appeared to be positioned between these two markers. The genetic distance between the resistance and the linked markers observed in our study was slightly larger compared to previous reports (Song et al. 2005; Cernák et al. 2008). This increase in the genetic distance was attributed to the small population size.

CRS resistance appeared to be controlled primarily by a single dominant gene on chromosome 9 and that was capable of reducing disease severity to close to zero. In addition to this locus, significant SNPs on chromosome 1 and 10 may be linked to loci that were able to affect CRS disease severity in clones without the resistance from chromosome 9. Due to the limited size of this population, these results will need to be validated on a larger population.

Detailed genetic analysis of 49 clones found two clones POR15V001-94 and POR15V001-112 of particular value to potato breeders, as they exhibit strong CRS resistance, strong PVY resistance, and apparent recombination events between Ry_{sto} and STM0003 which would help to separate this resistance gene from linkage drag caused by linked alleles from *S. stoloniferum*.

4.6 Conclusion

This study highlights the importance of verifying pedigree information with genetic marker data when the latter is available, as well as checking for duplicate clones. Additionally, with the decreasing cost of genotyping, we recommend that populations be genotyped and checked for errors prior to phenotyping, to avoid the expenditure of unnecessary resources. While the low number of clones that were unique and derived from the cross ‘Castle Russet’ × POR08BD1-3 was not ideal, we were still able to identify the loci and linked SNP markers controlling these two important phenotypes with a reasonable degree of confidence. This relative success was due to the large effects of the alleles conferring resistance in this population, and the high marker density of the Potato V3 Infinium Array that allowed us to identify genetic markers linked closely to these loci. The SNPs identified in this study need to be validated on a larger population and SNPs need to be converted into breeder friendly markers for use in marker-assisted breeding.

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4.8 Tables

Table 4.1. Primers pairs and PCR conditions used to amplify each marker.

Marker	Forward primer	Reverse primer	PCR conditions	Citation
STM0003	5'-GGAGAATCATAACAACCAG-3'	5'-AATTGTAACTCTGTGTGTGTG-3'	95°C 10 min, 40 cycles (95°C 30 s, 52°C 30 s, 72°C 1 min), 72°C 10 min	Song et al. (2005)
YES3-3B	5'-TAACTCAAGCGGAATAACCC-3'	5'-CATGAGATTGCCTTTGGTTA-3'	95°C 10 min, 10 cycles (95°C 40 s, 55°C 40 s, 72°C 1 min), 30 cycles (95°C 40 s, 53°C 40 s, 72°C 1 min), 72°C 10 min	Song and Schwarzfischer (2008)
s6m	5'-GGTGAAGCAAATCATGTCAAC-3'	5'-CATTTGTGCCCAATTGCC-3'	50°C 15 min, 94°C 5 min, 29 cycles (94°C 15 s, 58°C 1 min, 72°C 30 s), 72°C 5 min	Crosslin and Hamlin (2011)

Table 4.2. Segregation of *Potato Virus Y* resistance phenotype and the genetic markers STM0003 and YES3-3B for two populations: POR15V001, and a population with two unknown parents.

Progeny	Marker/Trait	Observed frequency (Present:absent)	Chi square value	P-value
POR15V001	Resistance	28:21	1.00	0.317
	STM0003	27:22	0.51	0.475
	YES3-3B	29:20	1.65	0.199
Unknown	Resistance	65:34	9.71	0.002
	STM0003	49:50	0.01	0.920
	YES3-3B	51:48	0.09	0.764

Table 4.3. Number of clones with an average disease severity index (DSI) for corky ringspot above and below five, for 48 clones from the cross ‘Castle Russet’ × POR08BD1-3, and for 99 clones from the cross between two unknown parents.

Population	Clones with DSI < 5	Clones with DSI > 5
‘Castle Russet’ × POR08BD1-3	23	25
Unknown parents	4	95

Table 4.4. SNP markers significantly associated with corky ringspot disease severity in a population of 49 clones from the cross 'Castle Russet' × POR08BD1-3.

SNP Marker	Chromosome	Position (bp)	Sample size	P-value	% Phenotypic variance explained
PotVar0050687	1	80941052	48	0.0396	28.5
PotVar0072548	9	57005254	47	0.0001	45.4
solcap_snp_c2_20667	9	57072665	47	0.0001	45.4
PotVar0011047	9	57167101	47	0.0001	45.4
solcap_snp_c2_3021	9	58582477	47	<0.0001	56.3
solcap_snp_c2_3007	9	58671679	45	<0.0001	56.0
PotVar0105170	9	58686737	47	<0.0001	56.3
PotVar0105222	9	58687906	45	<0.0001	54.9
PotVar0105228	9	58687944	47	<0.0001	56.3
PotVar0105349	9	58738870	47	<0.0001	61.6
solcap_snp_c2_3073	9	58956854	48	<0.0001	61.1
solcap_snp_c2_2992	9	58997370	46	<0.0001	61.1
PotVar0108720	9	59233052	48	<0.0001	59.5
PotVar0108623	9	59586574	48	<0.0001	59.5
PotVar0108448	9	59677060	47	<0.0001	61.6
solcap_snp_c1_12229	10	59261401	48	0.0396	27.7
solcap_snp_c1_12236	10	59445183	46	0.0390	30.0
PotVar0122870	10	59470538	48	0.0396	27.7
PotVar0122753	10	59562981	48	0.0396	27.7
PotVar0122751	10	59563007	48	0.0396	27.7
PotVar0122709	10	59671177	48	0.0396	27.7
PotVar0122699	10	59671428	48	0.0396	27.7

4.9 Figures

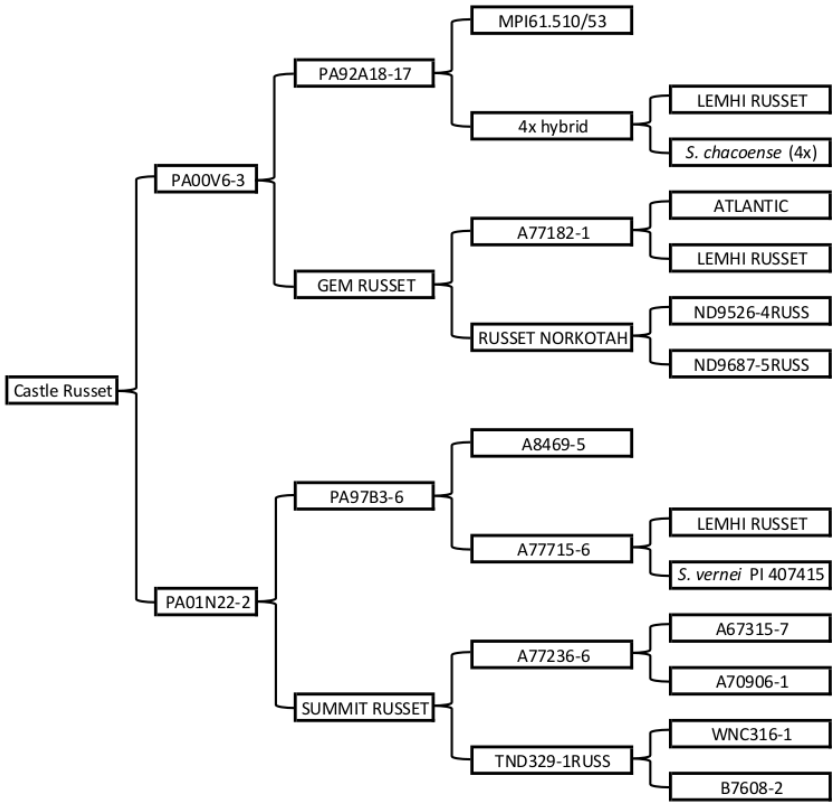

Figure 4.1. Pedigree of ‘Castle Russet’.

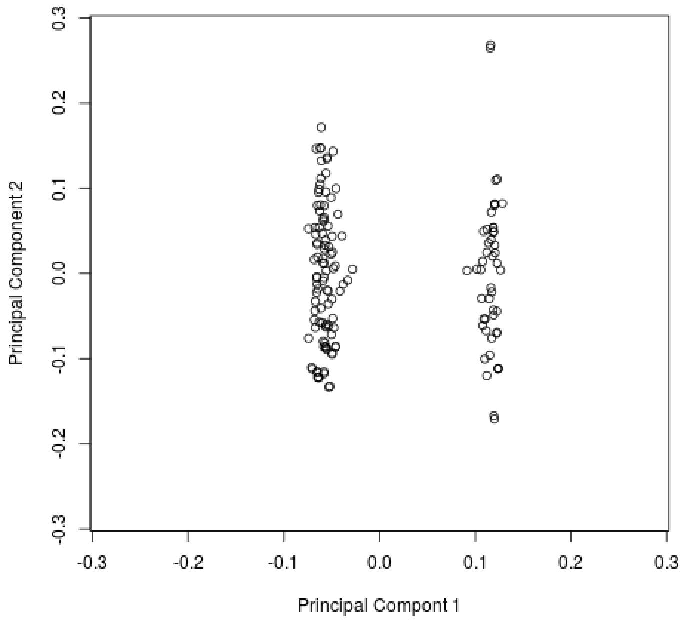

Figure 4.2. Principal component plot of 148 clones made using SNP marker data, showing two clear sub-populations.

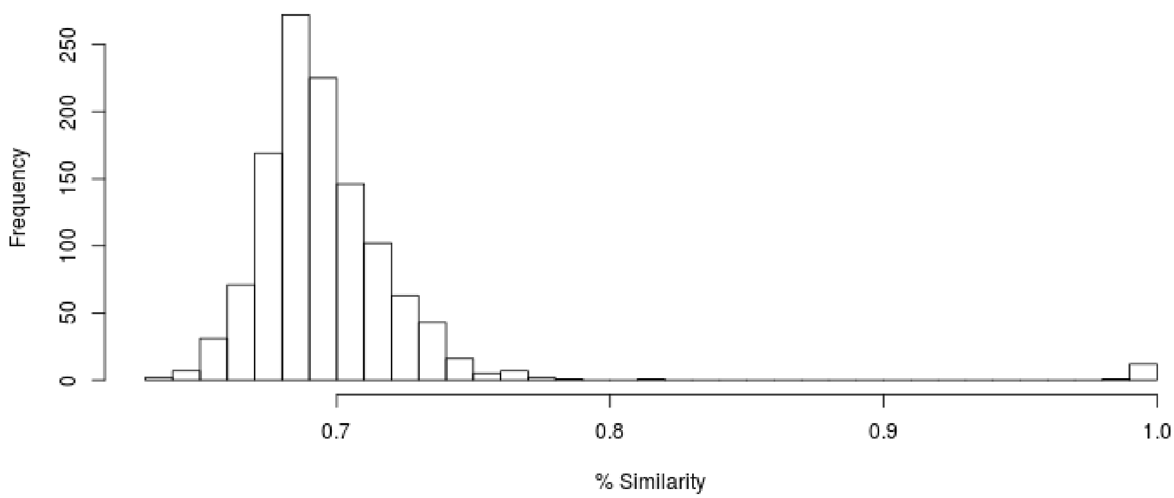

Figure 4.3. Histogram of the % identical loci for every possible pair of the 49 clones from the cross ‘Castle Russet’ × POR08BD1-3.

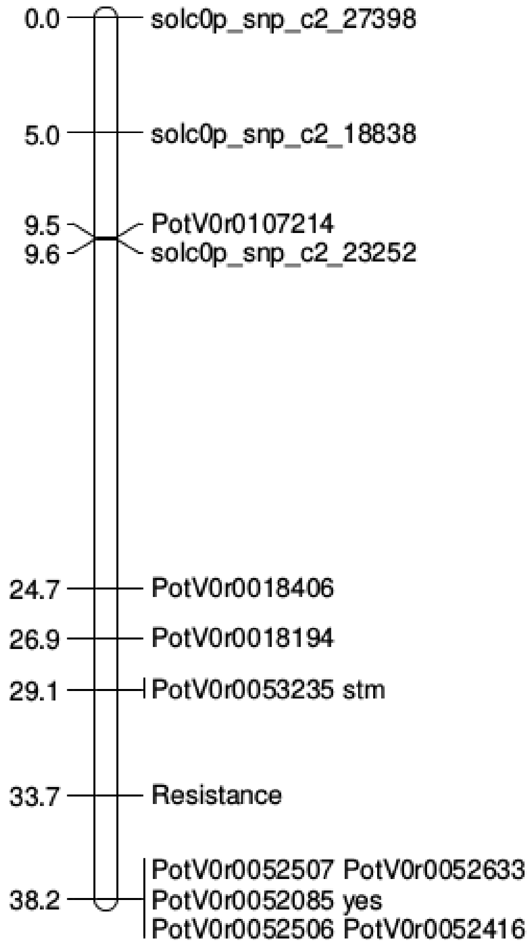

Figure 4.4. Genetic linkage map of the region of chromosome 12 containing the PVY resistance gene *Ry*$_{sto}$.

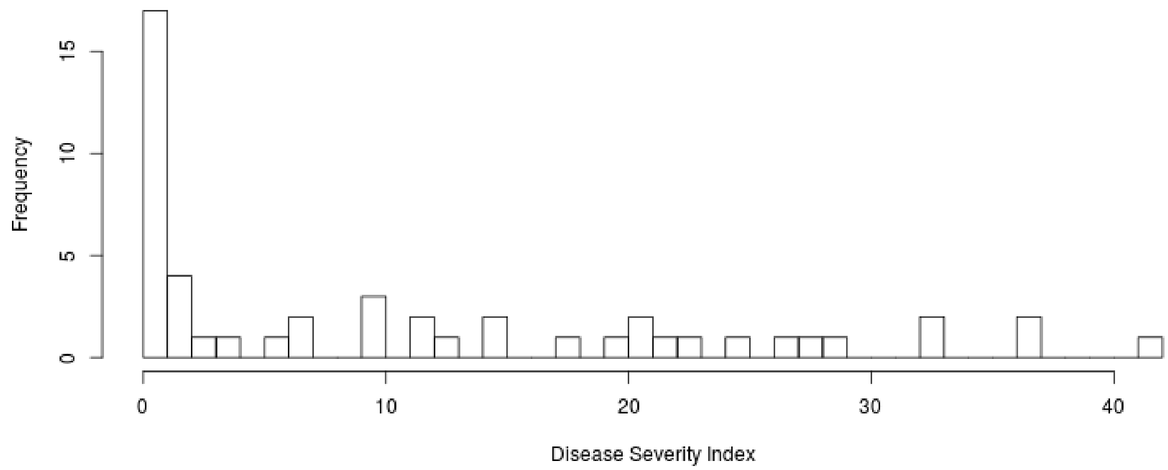

Figure 4.5. Histogram of the mean disease severity index for corky ringspot from two years for the 49 clones from the cross 'Castle Russet' × POR08BD1-3.

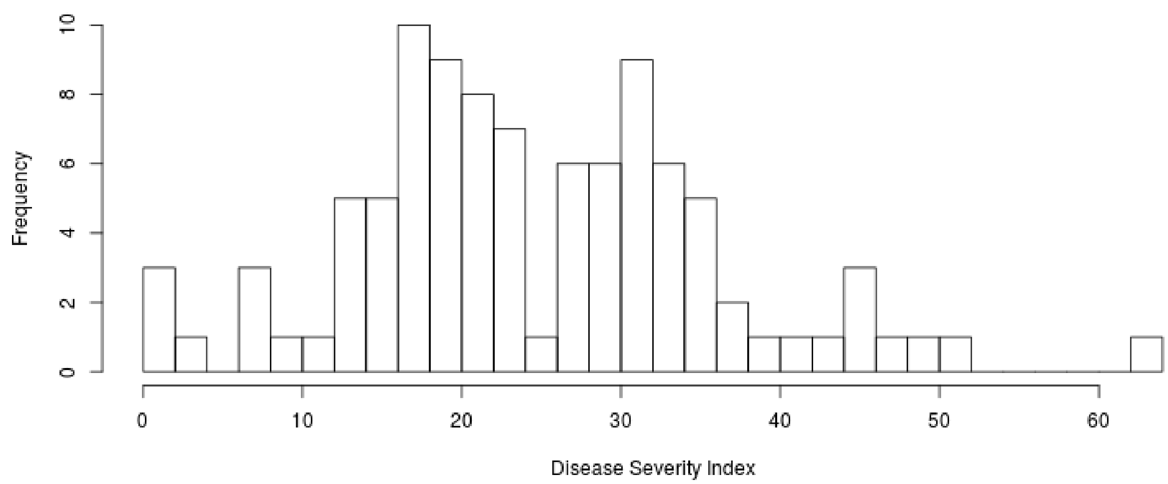

Figure 4.6. Histogram of the mean disease severity index for corky ringspot from two years for the 99 clones from unknown parents.

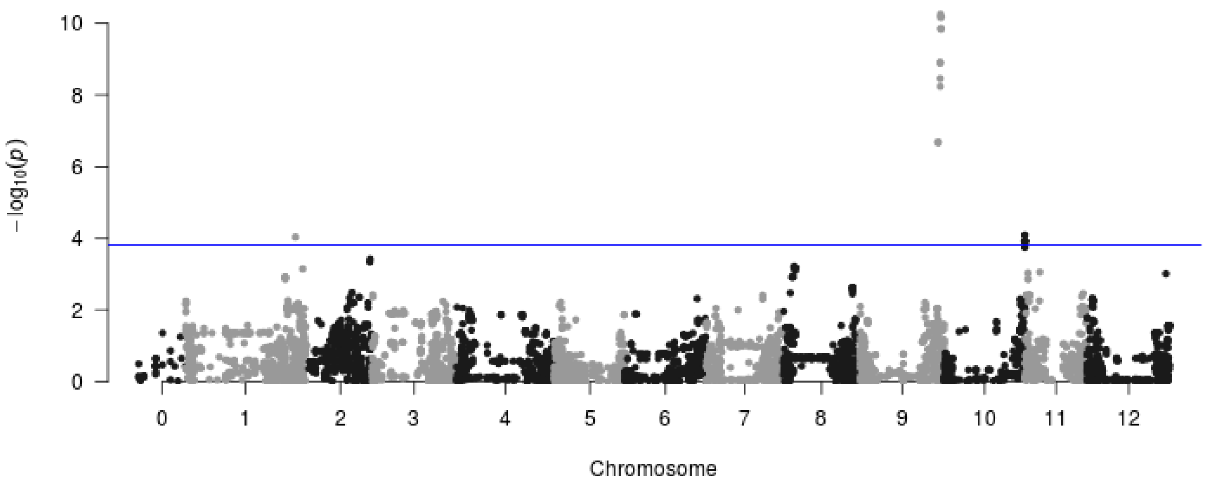

Figure 4.7. Manhattan plot for significance of SNPs with CRS resistance in 49 clones from the cross 'Castle Russet' × POR08BD1-3.

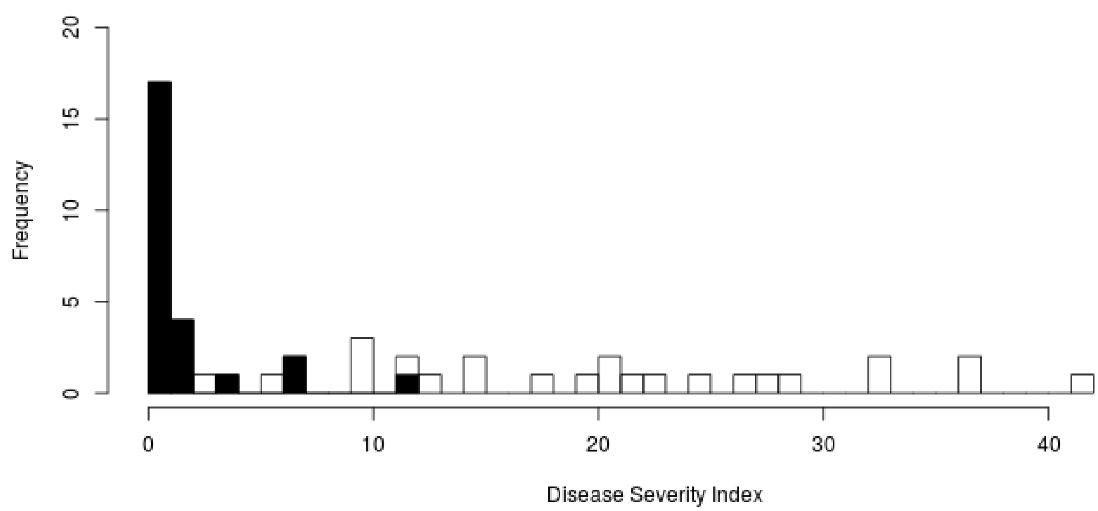

Figure 4.8. Histogram of the mean disease severity index for corky ringspot for 48 clones from the cross 'Castle Russet' × POR08BD1-3, where white indicates clones with the genotype "BBBB" and black indicates clones with the genotype "ABBB" at the loci PotVar0105349 and PotVar0108448. The clone POR15V001-111 was not included in this plot, because its genotypic data was missing at these loci.

5 Identification of a high-frequency of triploid potatoes from tetraploid × diploid crosses

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5.1 Abstract

Conventional wisdom in potato (*Solanum sp.*) breeding holds that a strong triploid block prevents the development of viable triploid seeds from crosses between tetraploid and diploid clones. However, we report that in a recent set of crosses between elite tetraploid potatoes and an improved diploid hybrid population derived from Group Stenotomum and Group Phureja, 61.5% of the resulting clones were found to be triploid. If clones derived from one diploid parent suspected of producing a high frequency of unreduced gametes is excluded, the frequency of triploid clones increases to 74.4%. Tubers of these triploids were generally intermediate in appearance between the two parental groups. Our findings open up the possibility of using triploid potatoes in variety development programs and in genetic and genomic studies.

5.2 Introduction

The term "triploid block" was first used by Marks (1966a) to describe the observation that "...although triploids do occur in the majority of [tetraploid (2n=4x=48) × diploid (2x=2x=24)] crosses, their *frequency* is often far below expectation...”. While this study focused specifically on several sets of crosses between clones of *Solanum chacoense* that were expected to yield a high proportion of triploid clones, this conclusion reflected earlier observations that tetraploid - diploid crosses often resulted in low seed-set. To help explain this and other disparities between the expected and realized ploidy frequencies, Johnston et al. (1980) proposed the endosperm balance number (EBN) hypothesis, which states that for successful endosperm formation, the effective ploidy, determined by EBNs, must be in a 2 maternal:1 paternal ratio. In crosses between clones with the same EBN, this criterion is satisfied through double fertilization. Additionally, in a cross where one of the parents has an EBN half that of another parent, successful endosperm development is expected if a gamete from the lower-EBN parent is unreduced (2n). In North American wild potato species, most diploids are 1EBN, most tetraploids are 2EBN, and all hexaploids are 4EBN, while in South American wild potato species, most diploids are 2EBN, most tetraploids are 4EBN, and all hexaploids are 4EBN (Hanneman 1994).

Since the characterization of the triploid block in potato, numerous studies have produced triploids from crosses between tetraploid (4EBN) and diploid (2EBN) *S. tuberosum* clones. Hanneman and Peloquin (1968) found that up to 7.6% of seeds set were triploids in some tetraploid-diploid crosses and noted that while some diploid parents resulted in a higher seed set, the additional seeds were typically tetraploid, presumably because these clones produced an increased frequency of unreduced gametes. Van Suchtelen (1976) produced a low frequency of triploids and concluded that triploid clones generally resembled their tetraploid siblings in terms of morphology and yield. Finally, de Maine (1994) found that tetraploid Group Tuberosum × diploid Group Phureja crosses could result in 8-71% triploid plants, depending on the tetraploid parent. Despite the moderate to high frequency of triploid plants in these crosses, overall triploid production was consistently low, with plants rarely producing more than a few triploid seeds per fruit.

In addition to crosses where both parents were from *S. tuberosum*, Johnston and Hanneman (1995) found that some Group Andigena clones produced a relatively high number of triploid seeds when pollinated with *S. chacoense* clones, with an average of 17 triploids per fruit for one Group Andigena clone. However, the authors concluded that this trait had a low heritability, which could complicate efforts to replicate this high triploid yield in crosses relevant to variety development efforts.

Marks (1966b) raised an interesting paradox, that while triploid clones are difficult to produce and would therefore constitute a very small proportion of the naturally-occurring seed in cultivated potatoes, triploid clones are relatively abundant in

South American landraces. Marks (1966b) suggests that for this situation to come about, triploids must have some selective advantage over other ploidy levels.

In other crops, triploids are best known for causing seedless fruit, as is often seen in banana (*Musa* spp.), watermelon (*Citrullus lanatus*), and citrus (*Citrus* spp.). However, few traits specifically attributable to triploidy have been reported in the literature. In sugar beet, many commercial European cultivars are triploid hybrids (Sliwinska and Lukasewska 2005), largely as a result of early studies that found that triploid sugar beets (*Beta vulgaris*) had higher root yields than diploid hybrids (Peto and Boyes 1940). However, the reason for this production advantage is not clear (Sliwinska and Lukasewska 2005).

Potato breeding programs across the globe perform various tetraploid × diploid crosses for introgression of biotic and abiotic stress resistance traits from diploid to tetraploid potatoes using unreduced gametes. In an effort to study and quantify the performance of crosses between diploid and tetraploid potato clones for future introgression, we performed a series of crosses using advanced diploid clones and elite tetraploid breeding material. In order to confirm successful cross and ploidy, we conducted flow cytometry to remove any diploids, which would not be expected to contain any DNA from the diploid parents, and therefore be irrelevant to that study. Here we report identification of a high frequency of triploids from tetraploid × diploid crosses made in that study, which were confirmed through somatic chromosome counts and flow cytometry.

5.3 Methods

5.3.1 Plant material

Twelve diploid clones were selected from the cycle four late blight resistant hybrid population derived from group Phureja and group Stenotomum clones and selected for tuberization under long-day growing conditions (described by Haynes 1972, Haynes 1980; Table 5.1. Results from the cycle three population were reported in Haynes et al. 2014). Eighteen elite tetraploid clones from group Tuberosum were selected from clones used in the Oregon State University potato breeding program (Table 5.1). Diploid clones were selected on the basis of disease resistance, tuber shape and dormancy, while tetraploid clones were selected on the basis of superior agronomic traits. In addition to the diploid and tetraploid potatoes, the clones PI 595441 from *S. juzepczukii* and PI 604206 from *S. curtilobum* were included as examples of triploid and pentaploid potatoes, respectively.

5.3.2 Crossing

Plants were grown in a greenhouse in 19 L containers filled with LA4PC (Sun Gro Horticulture H, Agawam, MA USA) potting soil amended with 1 g/L 15-9-12 Osmocote Smart-Release Plant Food Plus Outdoor and Indoor formulation (The Scotts Company, Marysville, OH USA). After planting, plants were irrigated with water supplemented with Jack's Classic No. 4 20-20-20 fertilizer (J.R. Peters Inc., Allentown, PA USA) at a rate of 200 ppm as needed. The greenhouse temperature was set to a daytime temperature of 24 °C and a nighttime temperature of 20 °C, and natural light was supplemented with a combination of metal halide and high-pressure sodium lights on a 20-hour photoperiod. As plants grew, all but 1-2 shoots were snapped off. Occasionally, when a main shoot appeared to be losing vigor, the main shoot was snapped off at the tip, and a lateral shoot was allowed to restore vigor. Plants were staked with bamboo sticks.

Approximately 200 pollinations were attempted, always using the tetraploid clone as the female parent, and the diploid clone as the male parent. Specific combinations of tetraploid and diploid parents crossed were based on pollen and receptive stigma availability at the time of crossing. In general, we attempted to make as many unique crosses as possible.

For pollen collection, anthers were removed from flowers at anthesis, as determined by a black spot at the tip of each anther. Anthers were removed from the flowers, and placed in parchment paper envelopes, and left in the greenhouse for approximately 24 hours. Then, each closed envelope was vibrated using an electric palm sander without sand paper attached. Next, the envelope was opened, and pollen was collected using a knife. Pollen was stored in plastic serum vials in the refrigerator for up to one month.

For pollinations, the petals of unopened flowers were gently removed with tweezers, the flowers were emasculated, and small glassine bags were stapled over each flower before pollination. After 1-2 days, one edge of the glassine bag was cut with scissors, and a very small metal spatula was used to coat the stigma with pollen. After pollination, the cut edges of the glassine bags were stapled and monitored for hybridization success.

5.3.3 Development of triploids

Fruits were collected when they could be easily removed from the plants. After fruits became soft (approximately 30 more days), they were slit open with a scalpel, and seeds were carefully removed and placed on a paper towel to dry. All fruits obtained from tetraploid × diploid crosses had very low seed set. Most fruits had fewer than five seeds and no single fruit had more than twenty seeds. Seeds could typically be found embedded in portions of the placenta that were fleshier than the surrounding tissue. Once the seeds were dry, they were stored in paper envelopes until germination.

Seeds were placed in plastic serum vials with 0.1% gibberellic acid for approximately 24 hours. Then, seeds were placed on damp paper towels in petri dishes that were in turn placed in opaque, humid plastic tote boxes in the greenhouse. The seeds were monitored multiple times per day and moistened with water from a spray bottle as needed. As the cotyledons emerged from the seeds (approximately 7 days), seedlings were transferred to trays of 2.5 cm pots filled with Sun Gro LA4PC Potting Mix. Irrigation water was amended with Jack's Classic No. 4 20-20-20 fertilizer at a rate of 200 ppm.

After three weeks, seedlings were transferred to 2 L pots filled with Greenhouse Mix #3, (Teufel Products Co., Hillsboro, OR, USA), amended with 2g/L 15-9-12 Osmocote Smart-Release Plant Food Plus Outdoor & Indoor formulation (The Scotts Company, Marysville, OH, USA). Approximately 75 days after seedlings were transferred to 2 L pots, mini-tubers were collected from each pot, and stored for later use.

5.3.4 Tuber observation

When enough mini-tubers were produced from the 2 L pots, clones resulting from tetraploid × diploid crosses were planted in four-plant plots in Klamath Falls, Oregon, USA, and when enough seed tubers were available, in additional four-hill plots in Hermiston, Oregon, USA, in 2017. Most of the parents were planted in both locations (clones BD1205-4, BD1244-3, and BD1269-1 were discarded immediately after crossing due to *Potato virus Y* infection). Plots were grown using standard agricultural practices for their respective regions. At the end of the growing season, the tubers were harvested, and checked for tuberization and tuber yields.

5.3.5 Flow cytometry

Fresh leaf tissue samples of each clone derived from tetraploid × diploid crosses, the parents, and the clones PI 595441 and PI 604206 were collected from either pots in the greenhouse or plants in the field. Flow cytometry was conducted using either a CyFlow Ploidy Analyser (Sysmex Corporation, Kobe Japan) or a CyFlow Space flow cytometer system (Sysmex Partec GmbH, Görlitz Germany), with CyStain UV Precise P (Sysmex Corporation, Kobe Japan). Five triploid clones were measured with both methods, to confirm that the different methods did not give substantially different results. Relative fluorescence of *Pisum sativum* 'Ctirad' (8.76 pg/2C; Lattier and Contreras 2017) was used as a standard to determine the genome size of potato samples.

5.3.6 Somatic chromosome counts

Tubers from 3 selected triploid clones (based on flow cytometry results), three diploid parents, one tetraploid parent, and clone 595441 from *S. juzepczukii* were planted in 2 L pots in the greenhouse. After 1-2 weeks, 5-10 quickly growing root tips were collected from each clone at approximately 2:00 pm and placed in 2 mM hydroxyquinoline for three hours in the light at room temperature. Next, root tips were rinsed in distilled water, then fixed in a solution of 75% ethanol and 25% acetic acid for storage of up to several months at 4 °C.

Root tips were treated with the enzyme solution described by Lattier et al. (2017) for one hour in an incubator set to 37 °C. After the enzyme treatment, roots were transferred to a new slide using a pipette. One to two drops of modified Farmer's fixative (3 parts methanol: 1 part glacial acetic acid) were added to the root tip, then root tip cells were separated by tapping the root tip with a metal spatula (Chen et al. 2015). A drop of modified Farmer's solution was added to each corner of the slide, and the solution was immediately lit with a match. Excess liquid was tapped off of the slides, and the slides were allowed to air-dry overnight at 37 °C. Air dried slides were submerged in a 5.7% solution of Giemsa Stain, Modified Solution (Sigma-Aldrich, St. Louis, MO, USA) for 15 minutes, then quickly rinsed in water, and again air-dried overnight at 37 °C. Images were taken using a light microscope at ×200 magnification (Axio Imager A1; Zeiss, Oberkochen, Germany).

5.4 Results

5.4.1 Flow cytometry

The c-values obtained from flow cytometry of the 96 clones obtained from tetraploid × diploid crosses clustered into three peaks corresponding to the diploid, triploid, and tetraploid levels, enabling ploidy values to be assigned to each clone (Figure 5.1). Of these clones, 5 (5.2%) were diploid, 59 (61.5%) were triploid, and 32 (33.5%) were tetraploid (Table 5.2).

Seventeen of the 32 tetraploid clones shared a single diploid parent, BD1205-4. Only one triploid offspring was obtained from this parent. BD1205-4 tended to result in fruits with 5-20 seeds, as opposed to the 1-4 seeds per fruit typical of other tetraploid × diploid crosses. Our results suggest that BD1205-4 produced a high frequency of unreduced gametes, although this cannot be confirmed as we were not successful in maintaining BD1205-4 after crossing. If clones with BD1205-4 as the male parent were excluded from this analysis, 74.4% of the clones resulting from tetraploid × diploid crosses were triploid (Table 5.2).

5.4.2 Root squash

Twenty-four chromosomes were counted in the three diploid parents analyzed, 48 chromosomes were counted in the single tetraploid parent analyzed, and 36 chromosomes were counted in the three triploid clones analyzed (Figures 5.2-5.8). In addition, 36 chromosomes were counted in the *S. juzepczukii* clone PI595441 (Figure 5.9). The ploidy values assigned by flow cytometry reflected the manually counted ploidy values.

5.4.3 Tuber comparison

Each of the 59 triploid clones that were grown in Klamath Falls set tubers, and 44 of the 46 triploid clones that were grown in Hermiston did so. Shapes and sizes of the tubers produced by the triploid potato clones were generally intermediate between the parents, suggesting that there are no consistent morphological characteristics on the whole-plant level specific to triploid potato clones. Examples of eight triploid clones with their parents are shown in Figure 5.10.

The mean tuber yield of triploid clones in Klamath Falls was slightly lower than that of the tetraploid clones derived from the same set of crosses, while in Hermiston, the mean tuber yields of triploid and tetraploid clones were comparable to each other (Table 5.3). In both locations, the average yield of both the triploid and tetraploid clones was lower than that of ‘Russet Burbank’ and ‘Snowden’ (Table 5.3).

5.5 Discussion

While the high proportion of triploid clones obtained in the experiment goes against conventional wisdom, these results do share parallels with several earlier papers that have also reported triploids resulting from tetraploid × diploid crosses (Van Suchtelen 1976; Maine 1994; Hanneman and Peloquin 1968). In particular, Hanneman and Peloquin (1968) observed that for crosses with a higher seed set, the additional seeds were typically tetraploid, similar to what was observed with crosses using the diploid clone BD1205-4 as the male parent in this experiment. Further, our results match the observations made by Van Suchtelen (1976) that the triploid clones generally resemble their tetraploid siblings.

While the identification of triploid clones from tetraploid × diploid crosses was not novel, the frequency of triploid clones relative to tetraploid clones observed in this experiment far exceeds that reported in most prior studies. One possible explanation could be that genetic differences between the clones used in our study compared to those used in the prior experiments either increased the likelihood of triploid formation through a reduction of the triploid block or decreased the likelihood of tetraploid formation through a decreased frequency of unreduced gametes in the male parent. Alternatively, the procedures we used to cross parents and germinate seeds in the experiment may have favored triploid production relative to other experiments; much care was put into germination efforts, allowing for the germination of seeds that appeared to have defects, and in a few cases even the germination of seeds that appeared to have no endosperm. Add discussion on the tuber yield and inform the readers whether it is worth going with Triploid breeding

In regard to variety development efforts, the possibility of triploid potato cultivars poses an interesting intermediate to breeding at the diploid or tetraploid level. However, due to low seed set, any triploid potato variety development effort would require the investment of approximately 100 times the crossing effort to obtain a given number of seeds. Therefore, it would be necessary to demonstrate the clear superiority of triploid potato clones over their diploid and tetraploid counterparts for such a triploid variety development program to be successful. Triploid potatoes are unlikely to serve as parents for germplasm improvement efforts, as they are largely sterile, with some exceptions (Magoon et al. 1962; Van Suchtelen 1976, Johnston and Hanneman 1995).

In addition to variety development, triploid potatoes may contribute to our understanding of the dosage effects of alleles for complex traits. With recent advances in high throughput genome sequencing and chromosome sorting based phased genome sequencing (Yang et al. 2011), production of triploids could contribute to genomic studies in the development of haploid genome sequences and novel genomic regions contributed from the diploid parent.

5.6 References

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5.7 Tables

Table 5.1. Tetraploid and diploid parents used in tetraploid × diploid crosses to measure the frequency of triploid potato clones.

Clone Name	Ploidy
Snowden	4x
Atlantic	4x
EVA	4x
Lamoka	4x
Ivory Crisp	4x
A00710-1VR	4x
AO03123-2	4x
OR01007-3 PVY	4x
ORAYT-9 (PVY)	4x
Castle Russet	4x
Payette Russet	4x
A06866-2PVY adg	4x
A07547-4VR	4x
A08640-2PCN	4x
PALB03016-3	4x
TACNA	4x
BD1202-2	2x
BD1205-4	2x
BD1216-3	2x
BD1222-1	2x
BD1240-6	2x
BD1244-1	2x
BD1244-3	2x
BD1247-3	2x
BD1251-1	2x
BD1253-4	2x
BD1257-5	2x
BD1268-1	2x
BD1269-1	2x

Table 5.2. Number and frequency of triploid potato clones obtained from all tetraploid × diploid crosses in this experiment, and from tetraploid × diploid crosses that did not include the diploid parent BD1205-4.

Cross	Progeny		
	2x	3x	4x
4x × 2x (Including BD1205-4)	5 (5.2%)	59 (61.5%)	32 (33.3%)
4x × 2x (Excluding BD1205-4)	5 (6.4%)	58 (74.4%)	15 (19.2%)

Table 5.3. Mean tuber yields of triploid and tetraploid clones derived from tetraploid × diploid and two commercial cultivars, ‘Russet Burbank’ and ‘Snowden’ in Klamath Falls, OR and Hermiston, OR in 2017.

Clones	Klamath Falls		Hermiston	
	Average Yield (kg/plot)	# Clones	Average Yield (kg/plot)	# Clones
3x clones	3.59	59	3.24	46
4x clones	3.95	32	3.23	26
‘Russet Burbank’	5.82	7	5.58	7
‘Snowden’	5.50	7	5.50	7

5.8 Figures

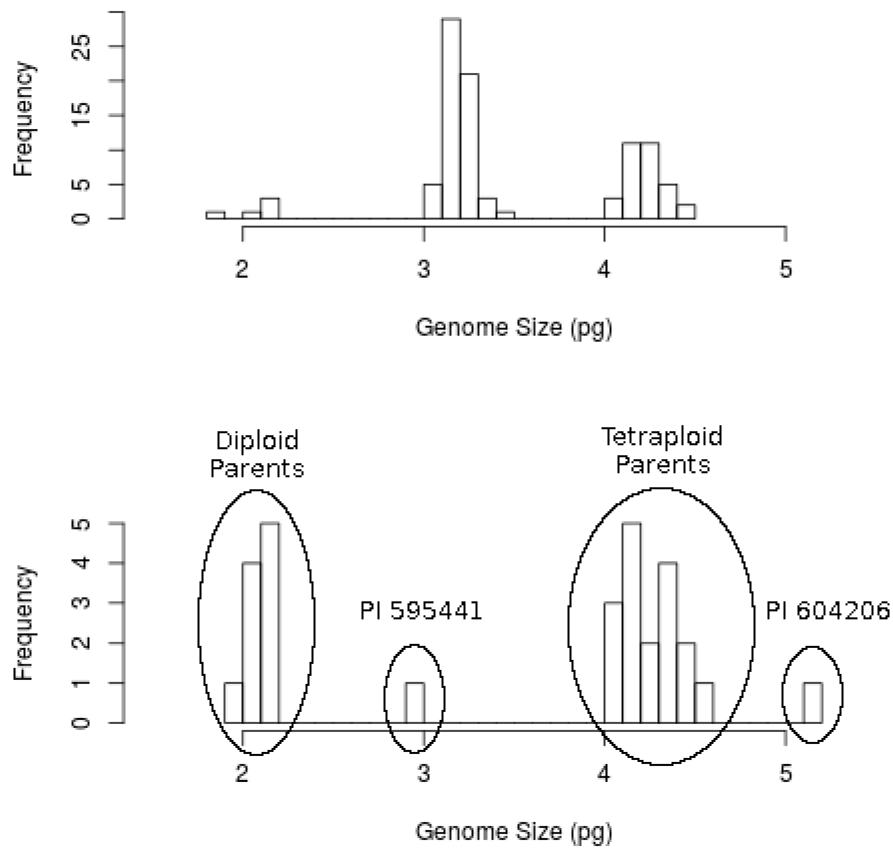

Figure 5.1. a) Estimated genome weights in picograms (pg) of 96 clones from tetraploid × diploid crosses. b) Estimated genome size of parents of tetraploid × diploid crosses, the triploid clone PI 595441 from *S. juzepczukii*, and the pentaploid clone PI 604206 from *S. curtilobum*.

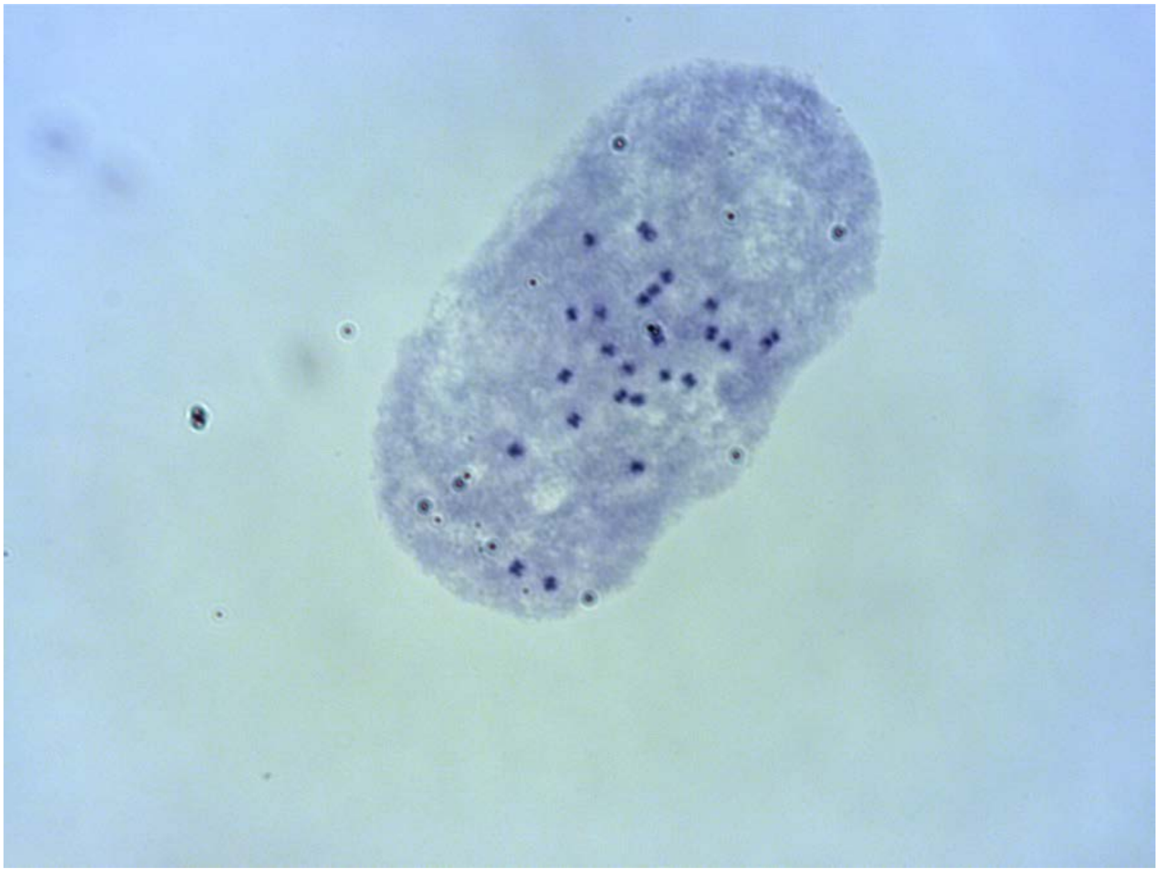

Figure 5.2. Root squashes of the diploid parent BD1222-1 (2n=2x=24; ×200 magnification).

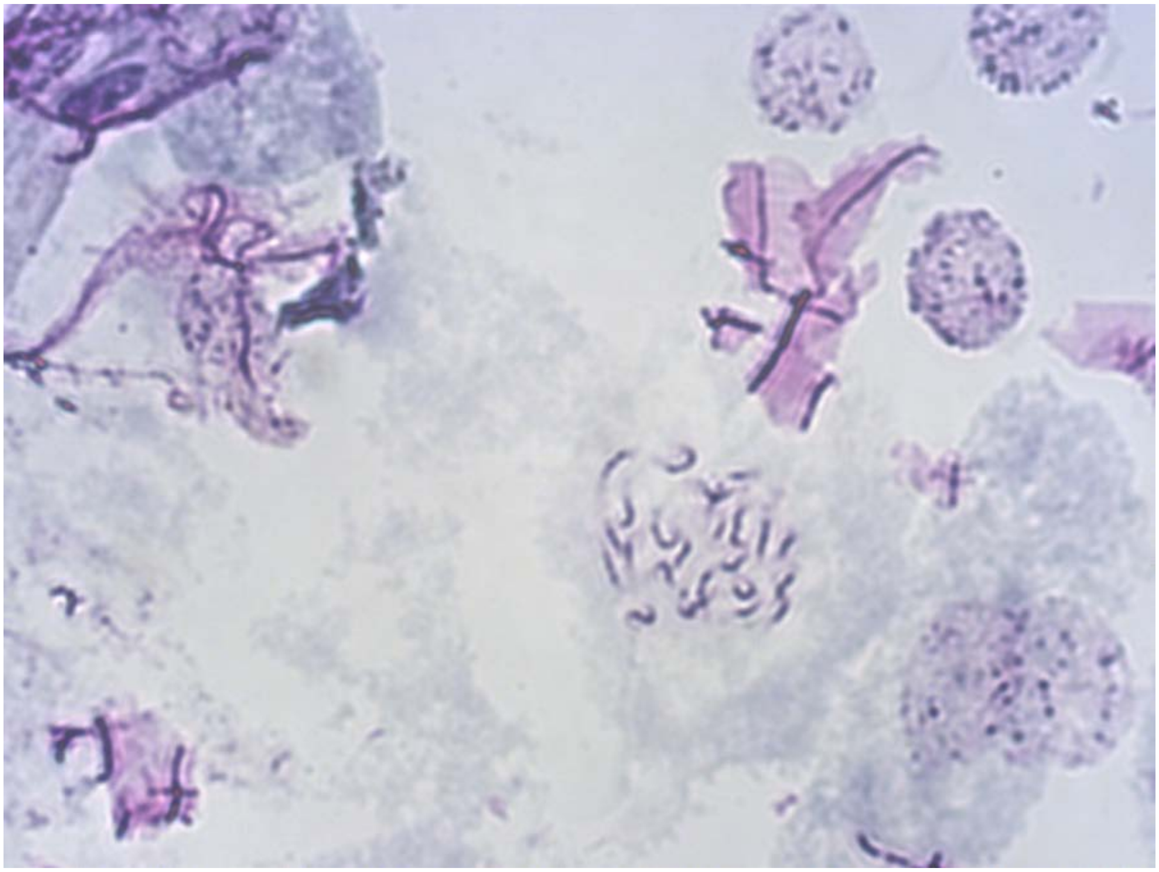

Figure 5.3. Root squashes of the diploid parent BD1240-6 (2n=2x=24; ×200 magnification).

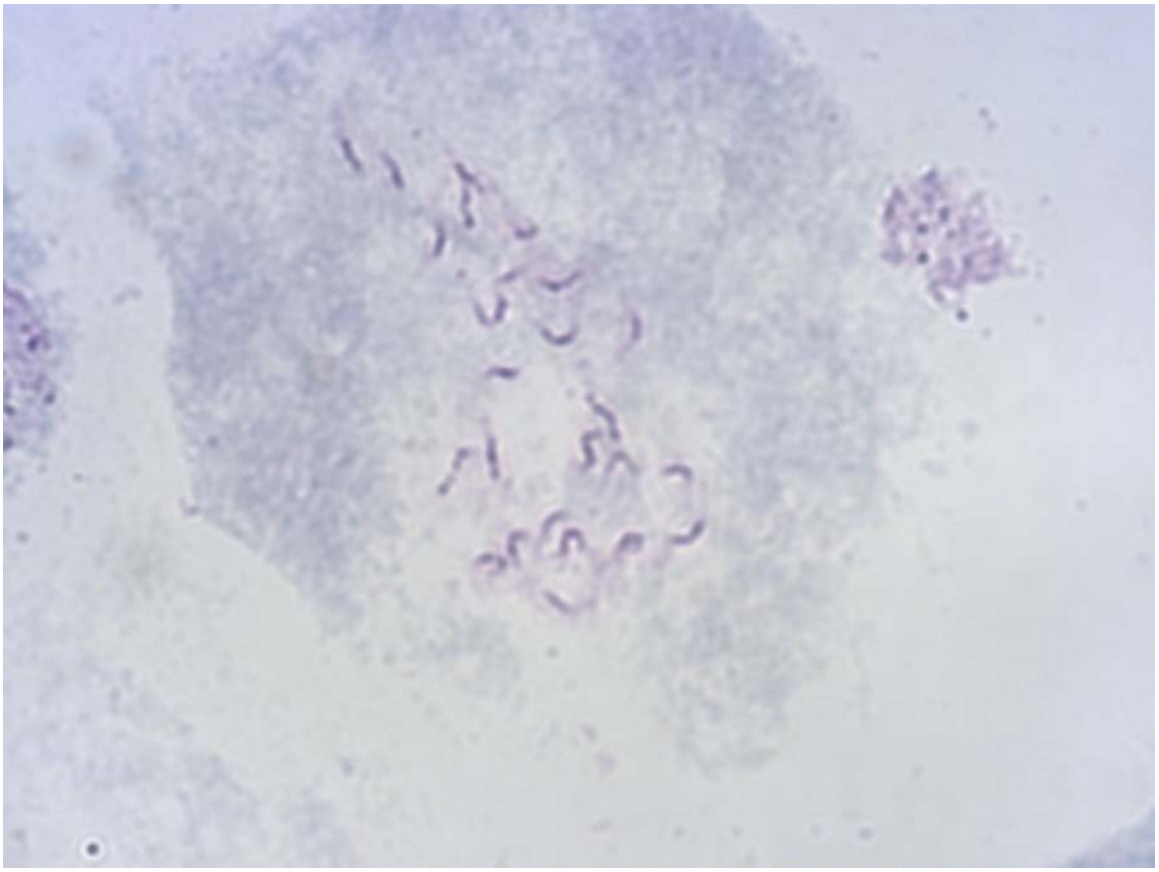

Figure 5.4. Root squashes of the diploid parent BD1268-1 (2n=2x=24; ×200 magnification).

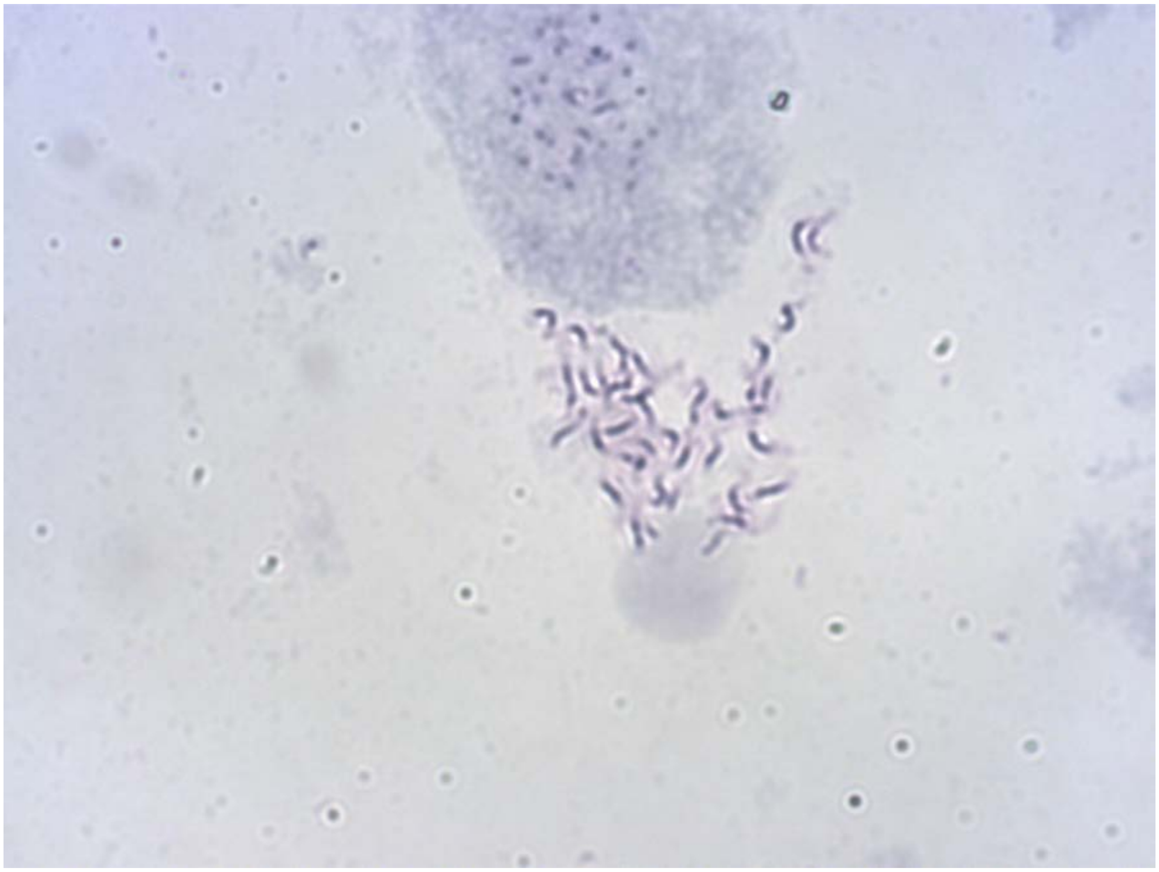

Figure 5.5. Root squashes of the triploid hybrid EP.2.1337 (2n=3x=36; ×200 magnification).

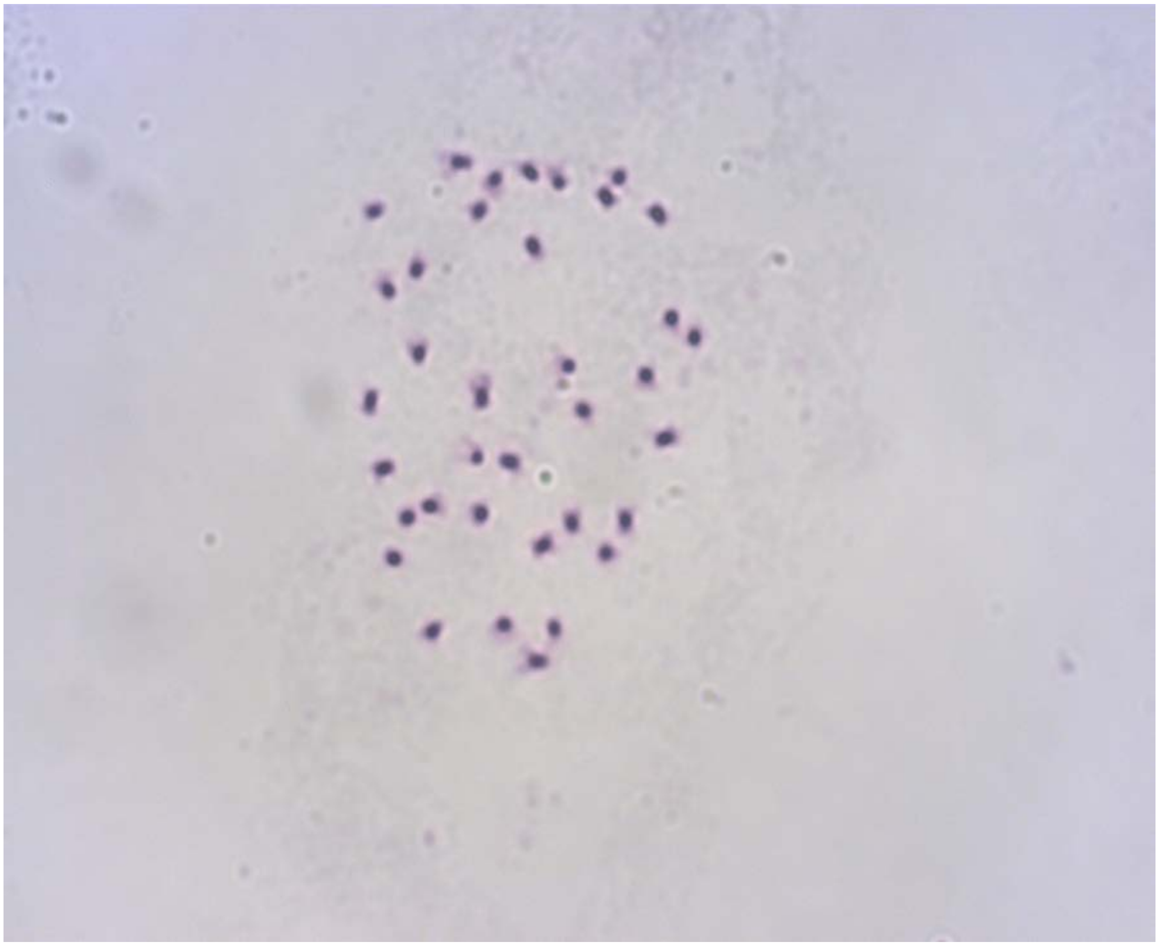

Figure 5.6. Root squashes of the triploid hybrid RP.2.3535 (2n=3x=36; ×200 magnification).

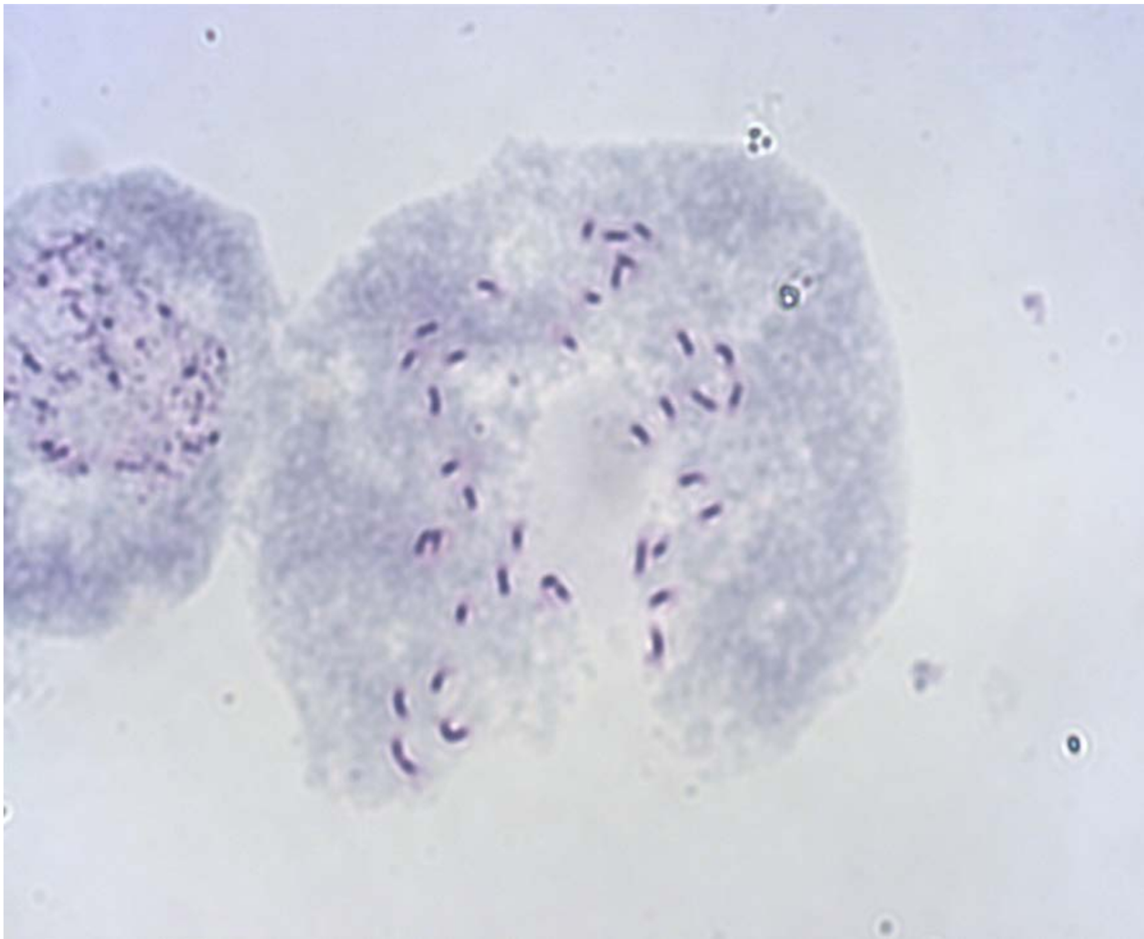

Figure 5.7. Root squashes of triploid hybrid RP.2.3829 (2n=3x=36; ×200 magnification).

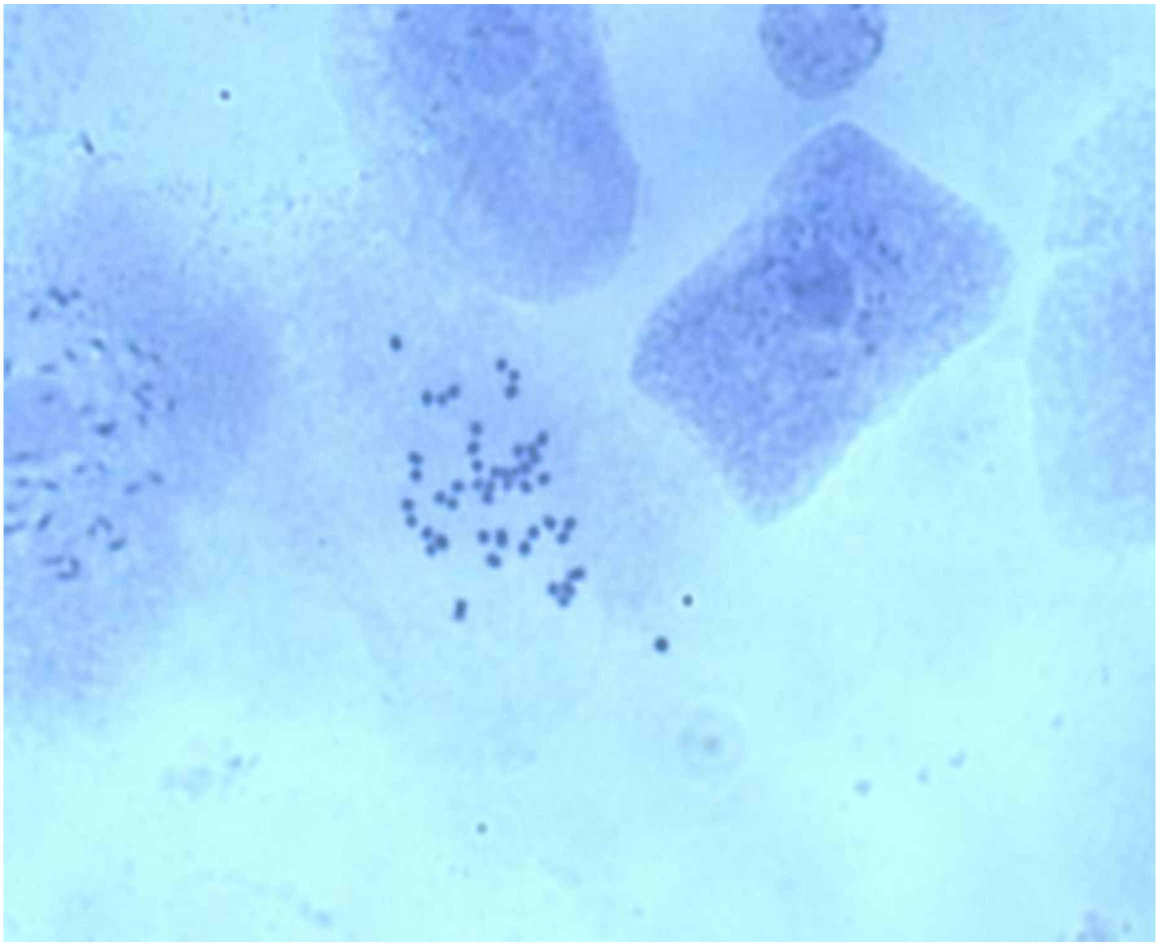

Figure 5.8. Root squashes of the tetraploid parent cv. Eva (2n=4x=48; ×200 magnification).

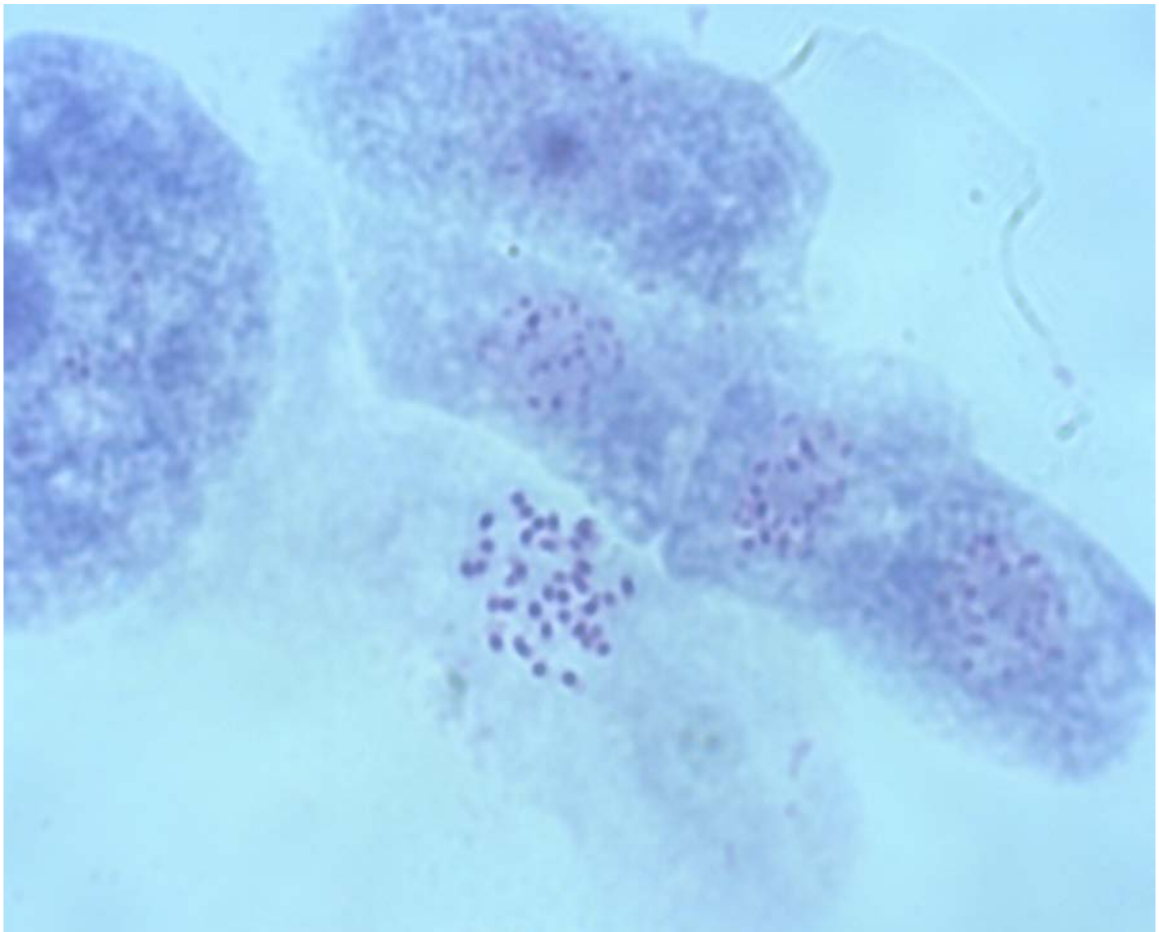

Figure 5.9. Root squashes of the triploid *S. juzepczukii* clone PI 595441 (2n=3x=36; ×200 magnification).

Figure 5.10. Examples of triploids from tetraploid × diploid crosses grown in Hermiston, Oregon, USA. For each row, the clone on the left is the tetraploid parent, the clone on the right is the diploid parent, and the two clones in the center are triploid clones from the cross between the two parents.

6 Evaluation of yield and quality traits in Russet-Chipper and 4x-2x crosses

6.1 Abstract

Genetic improvement of yield in potato has lagged behind that of other major crops over the past century, prompting the search for alternative breeding methods that may accelerate the development of improved cultivars. One strategy that has been proposed is to identify and use heterotic groups to increase the yield and consistency of clones produced by breeding programs. To investigate this approach, hybridizations were made between "Russet" and "Chipper" class elite long-day adapted potato clones, as well as between elite long-day adapted tetraploid clones and clones from an improved diploid population derived from Group Phureja and Group Stenotomum (4x-2x crosses). Field evaluation of random progeny derived from Russet-Chipper crosses had few notable benefits when compared to clones derived from crosses made within the Russet and Chipper groups. However, many of the clones derived from 4x-2x crosses clearly out-yielded the highest yielding clones from crosses between elite long-day adapted tetraploid potato clones. While every favorable quality trait measured was present in at least several clones derived from 4x-2x crosses, the frequency of many of these favorable quality traits was lower than in crosses between elite long-day adapted tetraploid potato clones. Our results suggest that continued selection of parental clones in 4x and 2x populations would likely be required before a high yielding clone with acceptable or superior quality characteristics could be expected from these 4x-2x crosses.

6.2 Introduction

Over the past century, the genetic gains in potato (*Solanum tuberosum* L.) germplasm have lagged behind than that of other major crops, including maize *(Zea mays*), wheat (*Triticum aestivum*), and rice (*Oryza sativa*; Douches et al. 1996; Reilly and Fuglie 1988). This disparity is highlighted by the fact that the more than century-old potato cultivar 'Russet Burbank' is still the most commonly grown potato clone in US, due to its high yield, high specific gravity, low oil absorption, low sugars, long storability, and high recovery of excellent grade French fries (Bethke et al. 2014). This is especially impressive as ‘Burbank’ (the clone that ‘Russet Burbank’ mutated from) was selected from a population of only 23 seedlings, compared to the tens of thousands of seedlings screened by elite potato programs today (Bethke et al. 2014). One strategy that has been proposed as a way to accelerate the development of improved potatoes is to exploit the hybrid vigor that has been observed when some groups of potatoes are crossed with each other. Briefly, "hybrid vigor" or "heterosis" are terms used to describe the tendency for distinct groups of a species (or closely related species) to produce superior offspring when the two groups are crossed with each other.

Little effort has been conducted to identify groups that exhibit hybrid vigor within elite long-day adapted potato germplasm. While in a recent study, Rak and Palta (2015) reported hybrid vigor between chipper-class potato clones (hereafter referred to as “Chippers”) and Russet type potato clones (hereafter referred to as “Russets”), they only compared one F1 family with two Chipper clones as parents with one F1 family with a Russet clone and a third Chipper clone as parents, making it difficult or impossible to attribute the difference observed is due to hybrid vigor between Russets and Chippers, rather than differences in general or specific combining abilities of these parents. However, Rosyara et al. (2016) were able to assign most Chippers and Russets to two distinct groups using genetic data, making hybrid vigor between these groups plausible.

Numerous studies have reported that the yield of clones obtained by crossing elite long-day adapted tetraploid potatoes with potatoes from landraces and some wild species exceeds the mid-parent value, and often exceeds the yield of major cultivars (Mendiburu and Peloquin 1971; Carroll and De Maine 1989). In addition to direct crosses with short-day adapted groups, some studies have crossed elite long-day adapted tetraploid potatoes to the hybrids between elite long-day and short-day adapted potatoes, which resulted in a tetraploid potato with one nearly complete set of genes from the short-day adapted parent (De Jong and Tai 1977; Mendiburu and Peloquin 1977; McHale and Lauer 1981; Buso et al. 1999). The most notable cultivar produced from wide crosses is ‘Yukon Gold’, which was selected by crossing W5279-4 (a hybrid of Group Phureja and haploid ‘Katahdin’) with ‘Norgleam’ (Johnston and Rowberry 1981). The disparity between high yields and a lack of released varieties is most likely due to lower tuber quality that is often seen in these crosses, although the low seed-set of 4x-2x crosses (0.2-34.5 seeds per berry, depending on the cross; Hutten et al. 1994) has likely been a factor. Each of the germplasm groups that have been shown to produce progeny with increased yields when crossed with elite long-day adapted potato germplasm typically forms tubers only under short-day conditions, which makes these parental clones unsuitable for production in long-day growing regions (Mendoza and Haynes 1976; Kittipadukal et al. 2012). While it is difficult to determine exactly how this tuberization response of the parents affects progeny performance, it may be responsible for the later maturity observed in many hybrid clones (McHale and Lauer 1981; Buso et al. 1999).

Several efforts have been initiated to improve the performance of short-day tuberizing potatoes under long day conditions through recurrent selection for variety development purpose. The first effort was based in England, UK starting from a tetraploid population of 3300 seedlings from Group Andigena in 1959 (Simmonds 1966). This program was moved to New York, USA in 1965, and in 2009, this group was reported to be more closely related to Group Chilotanum landraces from south-central Chile rather than to Group Andigena germplasm, presumably due to unintentional hybridization with Group Chilotanum germplasm, followed by a strong rapid selection against the original Andigena clones (Ghislain et al. 2009). A similar program was started in 1962 in Scotland, UK from a diploid population of 1870 seedlings from Group Phureja and Group Stenotomum in 1962 (Carroll 1982), and continued through 1979 (Bradshaw et al. 2006). Along the same lines, in USA, a genetic improvement program was started in 1966 from a diploid population of 60 clones from Group Phureja and Group Stenotomum at North Carolina (Haynes 1972; Haynes and Christ 1999). In 1986, this population was moved to Maine, USA, which was further branched out into two populations: a foliar late blight resistance and high specific gravity (Haynes 2008; Haynes et al. 2014).

Though there has been continuous genetic improvement of potatoes, in order to determine whether hybrid vigor exists between various groups of parents, we made a large number of hybridizations within and between elite Russet clones, elite Chipper clones, and clones from the improved diploid population derived from Group Phureja and Group Stenotomum clones that was initiated in 1966 in North Carolina, USA. Random clones selected from the progenies obtained through the hybridizations were evaluated for their yield and quality traits under field conditions. Agronomic data from clones in these groups was then used to investigate whether crosses between groups held notable advantages relative to crosses made within groups that would enable them to excel in any major market class, with a focus on their utility in the major potato growing regions of Oregon.

6.3 Methods

6.3.1 Selection of parents

Twelve Russet clones were selected from a panel of 264 primarily Russet clones, first based on their agronomic performance in the Columbia Basin growing region of Oregon and Washington, and second on the basis of which clone’s inclusion most increased the diversity of the Russet panel (as measured by expected heterozygosity), using the R package GeneticSubsetter (Graebner et al. 2016) and 23 simple-sequence repeat (SSR) markers (Bali et al. in submission). Six Chipper clones were chosen based primarily on their agronomic performance in the Columbia Basin growing region of Oregon and Washington. Thirteen diploid clones were selected from the cycle IV late blight resistant hybrid population (Haynes et al. 2014), on the basis of eye depth, tuber appearance, specific gravity, and observed tuber diseases. The clones used as parent material for hybridizations between the groups are listed (Table 6.1).

6.3.2 Panel development

A description of the methods used to cross parental clones and to produce mini-tubers from the progeny is available in Chapter 5. In general, efforts were made to make crosses between as many combinations of parents as possible. For 4x-2x crosses, the tetraploid clone was always used as the female parent, and for crosses between Chippers and Russets, no distinction was made between the male and female parents, though the male-sterile clones (including ‘Payette Russet’, ‘Castle Russet’, and ‘Snowden’) were used as females. To limit the number of clones in the panel, no more than five seedlings were kept for each Russet × Russet (RR), Russet × Chipper (RC) and Chipper × Chipper (CC) cross, no more than ten seedlings were kept for Russet x Diploid (RD) and Chipper × Diploid (CD) cross, and no more than two seedlings were kept for each Diploid × Diploid (DD) cross. Mini-tubers of each clone were stored for each of the parents for 7-8 months before being planted in the field. It was previously determined that a majority of progeny obtained from 4x-2x crosses were triploid, using flow cytometry and root squashes (Chapter 5). The number of clones evaluated for each group is presented in Table 6.2. Because the mean performance of unselected progeny in potato is typically inferior to the selected parents (regardless of the cross), we focused on comparisons between progeny of crosses between groups and progeny of crosses within groups, rather than comparisons of progeny with their parental clones.

6.3.3 Progeny evaluation

Every seedling clone retained from various crosses was planted in one 4-hill plot in Klamath Falls, OR, USA in 2017. When there were enough mini-tubers, an additional 4-hill plot was planted in Hermiston, OR in the same year. Not including parent and check clones, a total of 392 and 301 seedling clones were planted in Klamath Falls and Hermiston, respectively (Table 6.2). In each location, most of the parents were planted in two 4-hill plots (the clones ‘Willamette’, BD1205-4, BD1244-3, BD1259-1 and BD1269-1 were not planted due to *Potato virus Y* infection), and the clones ‘Atlantic’, ‘Snowden’, ‘Russet Burbank’, and ‘Russet Norkotah’ were planted in six 4-hill plots as commercial checks. All diploid parents were rogued from the Klamath Falls location mid-way through the 2017 growing season due to virus infection.

The details of crop production management practices are presented in Table 6.3. In Klamath Falls, each plot was separated by a purple marker A02267-5 on either side while in Hermiston, the markers included A02267-5, ‘Ranger Russet’, ‘Atlantic’, or ‘Red LaSoda’. At the end of the trial, the potatoes were hand harvested and stored initially at 12.8 °C for 3 weeks, and later at 8.3 °C until all evaluations were made. The stored potatoes were not treated with any sprout inhibitor.

During the growing season, in-field data was collected for plant maturity. Plant maturity notes were scored based on the percent of the foliage that was still green on August 24, 2017 in Klamath Falls (1634 GDD), and on August 14, 2017 in Hermiston (2105 GDD).

Yield, specific gravity, and tuber length:width ratios were measured on tubers eight weeks after harvest. Specific gravity was measured by the water displacement method. Length:width ratios were measured by taking a picture of at least six tubers for each clone, then taking the median length:width ratio of six tubers, as measured using ImageJ (Abramoff et al. 2004). Similarity scores were given to each clone grown in both locations on a 1-5 scale by comparing pictures of tubers from the two locations, where a “5” indicates that tubers showed no differences between the locations.

Eye depth, tuber uniformity, sprouting, tuber appearance, and tuber acceptability for the French fry and potato chip market classes were rated on a 1-5 scale 16 and 14 weeks after harvest for the Klamath Falls and Hermiston locations, respectively (where a "5" indicates shallow eyes, uniform tubers, no sprouts, good tuber appearance, and acceptable tubers for the French fry and potato chip industries). At the same time, russeting (where a "5" indicates heavy russet skin), tuber shape, skin color, flesh color, and comments were recorded for each plot, although these traits were not included in the analysis.

All data except yield and plant maturity were discarded for plots that produced less than 500 g of tubers.

6.3.4 Statistical analysis

Least significant difference (LSD) tests between each of the three groups derived from within-group crosses (CC, RR, and DD) and each of the three hybrid groups (CR, CD, and RD) were conducted for yield, specific gravity, eye depth, uniformity, sprouting, appearance, length:width ratios, maturity, and similarity using the R package “agricolae” (de Mendiburu 2017), using a false discovery rate to correct for multiple comparisons. “Clone”, “location”, and “group” were included as fixed effects, except for comparisons of tuber similarity between groups, where only “clone” and “group” were included as fixed effects.

For the CC clones, CR clones, and RR clones, correlation coefficients were calculated to describe how the clones from each group correlated between locations for yield, specific gravity, eye depth, uniformity, sprouting, appearance, length:width ratios, and maturity. Separately, correlation coefficients were calculated for all clones derived from 4x-4x crosses (CC, CR, and RR), all clones derived from 4x-2x crosses (CD and RD), and all clones derived from 2x-2x crosses (DD) (CC, CR and RR groups and CD and RD groups were merged for this part of the analysis). The R package “psych” was used to determine whether there was a significant difference between the correlations (Revelle 2017). For each trait, a false discovery rate was used to correct for the multiple comparisons between groups.

To determine top performing clones for four measures (yield, general suitability, suitability for the French fry industry, and suitability for the potato chip industry), best linear unbiased predictor (BLUP) values were made for each clone for yield, specific gravity, eye depth, uniformity, sprouting, appearance, length:width ratios, and maturity. Due to a large difference in variance between 4x-4x crosses, 4x-2x, and 2x-2x crosses for yield and maturity, BLUP values were calculated separately for each of these groups for these traits. BLUP values were determined for each clone using the R package rrBLUP (Endelman 2011), using "clone" as a random effect, and "location" as a fixed effect. To compare each clone’s general suitability, each clone was given an index value based on the following equation:

$$\text{Equation 1: General suitability} = \text{Yield} \times (\text{Eye depth} + 3) \times (\text{Uniformity} + 3) \times (\text{Sprouting} + 3) \times (\text{Appearance} + 3)$$

This equation was chosen due to its ability to balance the yield and quality of clones. “3” was added to each of the quality traits, so that the quality traits would not have an outsized impact on the final index value relative to yield. In addition, to compare each clone’s suitability for the French fry and potato chip industries, each clone was given an index value by multiplying the yield, the dry matter content (as determined by Schippers 1976) and the clone's acceptability for the given market class:

Equation 2: Chipper suitability = Yield × [-2.172 + 2.212 × (Specific gravity)] × (Chipper tuber acceptability)

Equation 3: Russet suitability = Yield × [-2.172 + 2.212 × (Specific gravity)] × (Russet tuber acceptability)

All statistics were conducted in R version 3.2.3 (R Core Team 2005).

6.4 Results

6.4.1 Direct comparison of groups

The mean trait values of RC clones were intermediate between the average values of CC clones and RR clones, with the exception of eye depth. RC clones had slightly deeper eyes than CC or RR clones though not statistically significant (Table 6.4). The mean yield of CD clones was superior to CC clones and DD clones, while the mean yield of RD clones was similar to RR clones and higher than DD clones (Table 6.4). For eye depth, uniformity, sprouting, and appearance, CD and RD clones averaged below CC and RR clones, respectively. The level of similarity between locations for CD clones was comparable to that of CC clones and higher than that of DD clones, while the level of similarity for RD clones was lower than RR clones and comparable to DD clones. For specific gravity trait, CD clones had higher specific gravities than CC clones, and were similar to DD clones, while RD clones had specific gravities that were similar to RR clones and lower than DD clones. The length:width ratios of CD clones were intermediates between CC clones and DD clones, while RD clones had length:width ratios that were similar to RR clones, and lower than DD clones. For plant maturity, CD clones were later maturing than CC clones, and were similar in maturity to DD clones, while RD clones were later maturing than both RR clones and DD clones.

6.4.2 Correlations between locations

For yield, 4x-2x clones had a higher correlation between locations (r=0.672) than either 4x-4x clones (r=0.345, p=0.0027) or 2x-2x clones (r=0.254, p=0.0025). For maturity, 4x-4x clones had a higher correlation between locations (r=0.411) than 2x-2x crosses (r=-0.106; p=0.0005), but 4x-2x clones (r=0.184) were not statistically different from either 4x-4x crosses or 2x-2x crosses (Table 6.5).

For specific gravity, eye depth, uniformity, sprouting, appearance, and length:width ratios, there were no differences in the correlations between groups when comparing 4x-4x clones, 4x-2x clones and 2x-2x clones. No significant differences in correlation between locations were identified for any trait when comparing CC, CR and RR clones (data not shown).

6.4.3 Evaluation of top clones

Of the top 15 yielding clones, all but one (the 11th highest yielding clone) were CD or RD clones (Table 6.6), despite the fact that there were 234% more 4x-4x crosses than there were 4x-2x crosses (Table 6.2). For general suitability, among the top 15 clones, six were CR clones, five were RD clones, two were CD clones, one was a CC clone, and one was a RR clone (Table 6.7). In addition, among the top 15 clones most suitable for the potato chip industry, ten were CR clones, three were CD clones, and two were CC clones (Table 6.8), and for suitability for the French fry industry, eight were RR clones, six were RD clones, and one was a CD clone (Table 6.9).

6.5 Discussion

It is unusual to obtain a high frequency of triploid potato clones from 4x-2x crosses, giving us a valuable opportunity to test the performance of clones obtained from wide crosses that are a different ploidy level than tested in previous crosses. A complete description of the methods used to confirm the ploidy of these clones and a discussion regarding reasons these triploid clones may have been so abundant is presented in Chapter 5.

In this study, CR clones showed few apparent advantages when compared to CC and RR clones. While many of the clones that performed best as Chippers were from group CR (Table 6.8), this is likely because there were 404% more CR clones than CC clones in this analysis (Table 6.2), rather than a result of superior performance of CR clones. The average yields of CR clones were higher than CC clones, but it is unclear if this advantage would be present in all growing regions, or if it is due to hybridization with Russets, which may be better adapted to these specific growing regions. This lack of clear hybrid vigor between Chippers and Russets suggests that breeders must draw from groups outside of elite long-day adapted potato germplasm to maximize the advantages of hybrid vigor.

The most striking advantage of RD and CD clones was yield stability; the yield of these clones across the two tested locations had a correlation coefficient of 0.672, with only one 4-plant plot per location (Table 6.5). This indicates that clones from these wide crosses possess a higher level of yield stability than clones derived from traditional potato crosses. This increase in yield stability would allow any superior clones to be identified with fewer years and locations of evaluations.

Quality traits of 4x-2x clones were generally inferior to 4x-4x clones, most likely due to the expression of unfavorable traits from the diploid parents. One exception to this is specific gravity, where group DD outperformed every other group, presumably because its parents have undergone six cycles of recurrent selection for specific gravity. As a result, CD clones had improved specific gravity relative to CC clones, and RD clones had specific gravity similar to RR clones. One hopeful discovery for RD and CD clones is that every favorable tuber characteristic we measured was present in at least a few of these hybrid clones, including dormancy, russeting, and tuber shape (for Russets and Chippers). Presumably, selection could be conducted in both of the parental groups to decrease the frequency of unfavorable traits in the hybrid clones.

Early in this study, the decision was made to maximize the number of parents used, so that results could accurately reflect the performance of crosses made within and between these parental groups. One consequence of this was that the number of crosses per parent was far too low to make rigorous comparisons of parental performance.

However, an informal analysis of progeny found that for the diploid parents, BD1202-2, BD1240-6, and BD1251-1 did appear to produce better CD and RD clones than the other diploid clones, and for tetraploid parents, ‘Atlantic’ appeared to perform especially well as a parent of CD and RD clones. Superior performance of ‘Atlantic’ is further noticed by the fact that it has been one of the most used parents in various breeding programs.

It is difficult to determine whether triploid or tetraploid CD and RD clones performed better since many of these tetraploids shared a single diploid parent. While each of the top performing CD and RD clones were triploid (Tables 6.6-6.9), overall, there was not a clear difference between clones of these two ploidy levels.

CR clones on average had length:width ratios that were closer to CC clones than RR clones. This was consistent with De Jong and Burns (1993). As a result, our CR clones generally had tuber shapes that were much more suited for the potato chip industry than the French fry industry. Both CD clones and RD clones had length:width ratios that were intermediate between their diploid and tetraploid parents. However, length:width ratios for both of these groups were more similar to the rounder tetraploid parents, suggesting that oblong tubers were more of a recessive trait than a dominant one in this germplasm.

The average maturity of CD and RD clones was later than either the diploid or tetraploid parents. However, it is unclear whether this difference is large enough to be detrimental in potato production. In general, the long growing season of the Columbia Basin region of Oregon and Washington may be more suitable for CD and RD clones than other, shorter-season growing regions.

6.6 Conclusion

Based on this set of crosses, we believe that CR clones hold no notable heterotic advantage over CC and CR clones. However, in some specific circumstances, CR clones may perform better than CC clones when breeding for the potato chip market class. While we noticed some advantages to crossing elite long-day adapted tetraploid potatoes with improved diploids (notably increased yield stability, and some clones with especially high yield), these benefits were generally similar in importance to a decrease in tuber quality seen in many of the CD and RD clones. Based on these parents, we do not feel that the benefits of this set of wide crosses warrants the difficulty of producing 4x-2x true potato seed. Therefore, the utility of these wide crosses to variety development likely depends on the difficulty of selecting better parents in both parental groups.

In our program, we plan to continue to make crosses between the tetraploid and diploid groups evaluated here on a small scale, using 4x-4x and 2x-2x clones from this experiment whose parents appeared to perform better in 4x-2x crosses in this study. If we are able to identify tetraploid and diploid clones from these that are able to consistently produce high-yielding clones with adequate or superior quality, we will likely invest more resources into this line of breeding. In addition, we plan to include Chipper-Russet crosses in future breeding efforts, to try to develop potato clones for the Columbia Basin that are suitable for the potato chip market but have the local adaption that appears to be present in many Russet clones.

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6.8 Tables

Table 6.1. Chipper-type clones, russet-type clones, and clones from an improved population of diploid potatoes derived from Group Phureja and Group Stenotomum used as parents.

Clone	Group	Ploidy	Female parent	Male parent
Snowden	Chipper	4x	Lenape	Wischip
Atlantic	Chipper	4x	Wauseon	Lenape
Eva	Chipper	4x	Steuben	Unknown
Lamoka	Chipper	4x	NY120	NY115
Willamette	Chipper	4x	NDA2031-2	A86463-3
Ivory Crisp	Chipper	4x	ND292-1	A77268-4
AO00710-1	Russet	4x	A92030-5	Liu
AO03123-2	Russet	4x	A98082-17	Premier Russet
OR01007-3	Russet	4x	PA98V2-1	Yagana
ORAYT-9	Russet	4x	A88597-7	A91048-3
Castle Russet	Russet	4x	PA00V6-3	PA01N22-2
Payette Russet	Russet	4x	EGAO9702-2	GemStar Russet
A06866-2	Russet	4x	PA98V1-2	A00715-8
A07547-4	Russet	4x	EGAO9702-2	PALB0303-1
A08640-2	Russet	4x	V15-71	Rio Grande Russet
PALB03016-3	Russet	4x	P00LB5-3	GemStar Russet
Tacna	Russet	4x	720087	386287-1
P2-4	Russet	4x	2-7-4D	Katahdin
BD1202-2	Diploid	2x	BD1002-1	Unknown
BD1205-4	Diploid	2x	BD1005-3	Unknown
BD1222-1	Diploid	2x	BD1022-4	Unknown
BD1240-6	Diploid	2x	BD1040-4	Unknown
BD1244-1	Diploid	2x	BD1044-4	Unknown
BD1244-3	Diploid	2x	BD1044-4	Unknown
BD1247-3	Diploid	2x	BD1047-1	Unknown
BD1251-1	Diploid	2x	BD1051-1	Unknown
BD1253-4	Diploid	2x	BD1053-3	Unknown
BD1257-5	Diploid	2x	BD1057-4	Unknown
BD1259-1	Diploid	2x	BD1059-4	Unknown
BD1268-1	Diploid	2x	BD1068-2	Unknown
BD1269-1	Diploid	2x	BD1069-2	Unknown

Table 6.2. The number of clones evaluated from different hybridizations.*

Group	Clones evaluated in Klamath Falls	Clones evaluated in Hermiston
CC	28	20
CR	113	83
RR	65	47
CD	20	17
RD	68	55
DD	98	79

*Hybrids from Chipper-Chipper (CC), Chipper-Russet (CR), Russet-Russet (RR), Chipper-Diploid (CD), Russet-Diploid (RD), and Diploid-Diploid (DD) crosses planted in Klamath Falls, Oregon and Hermiston, Oregon in 2017.

Table 6.3. Growing conditions for the locations in Klamath Falls, OR, and Hermiston, OR in 2017.

Growing conditions	Klamath Falls, OR	Hermiston, OR
Field coordinates	45.81 °N, 119.29 °W	42.38 °N, 122.00 °W
Planting date	May 23, 2017	April 14, 2017
Vine kill date	September 8, 2017	September 6, 2017
Harvest date	October 5, 2017	September 21, 2017
Vine dill GDD (Base 50°F)	1912	2166
Fertilizer	202-233-336-305 NPKS (kg/ha)	460-101-67-170-27-3.4-2.5 NPKSMgBZn (kg/ha)
Chemical applications	Prowl, Matrix, Outlook, Alias, Luna, Vertisan, Vydate	Vapam, Dual Magnum, Matrix pre-emergence, Outlook, Prowl, Admire, Coragen, Agr-Mek, Echo, Quadris, Ridimil, Omega, Dithane
Vine kill method	Flail Chopped, then Sprayed with Reglone	Cut, beat and roll, Then Sprayed with Reglone
Irrigation	36.3 cm (+ 4.3 cm Rainfall)	77.1 cm (+ 4.1 cm Rainfall)
Plant spacing	23.5 cm	23.5 cm
Space between plots	117.5 cm	117.5 cm
Space between rows	91.4 cm	81.3

Table 6.4. Means and LSD values for nine traits measured on progeny from different hybridizations.*

Group	Yield	Specific gravity	Eye depth	Uniformity	Sprouting	Appearance	Similarity	Length: width	Maturity
CC	2.21(c)	1.076(c)	3.77(a)	3.13(a)	4.00(a)	2.93(a)	3.22(a)	1.12(d)	61.7(c)
CR	3.08(b)	1.077(c)	3.67(a)	3.00(ab)	3.93(a)	2.81(ab)	2.81(b)	1.20(c)	65.3(bc)
RR	3.54(a)	1.079(bc)	3.68(a)	2.93(bc)	3.86(a)	2.70(b)	2.66(bc)	1.49(b)	70.3(b)
CD	3.37(ab)	1.083(ab)	3.31(b)	2.78(cd)	3.11(b)	2.53(c)	3.32(a)	1.23(c)	71.8(ab)
RD	3.50(a)	1.078(bc)	3.40(b)	2.55(e)	2.88(b)	2.34(d)	2.38(d)	1.50(b)	75.8(a)
DD	1.50(d)	1.085(a)	3.43(b)	2.64(de)	2.06©	1.97(e)	2.57(cd)	1.72(a)	68.8(b)

*Chipper-Chipper (CC), Chipper-Russet (CR), Russet-Russet (RR), Chipper-Diploid (CD), Russet-Diploid (RD), and Diploid-Diploid (DD) clones in Hermiston, Oregon and Klamath Falls, Oregon in 2017. Yield was measured in kg/plot. Eye depth, tuber uniformity, sprouting, and tuber appearance were measured on a 1-5 scale, where a "5" indicates shallow eyes, uniform tubers, no sprouts, good tuber appearance, and acceptable tubers. Maturity was measured as % green tissue in each plot late in the growing season.

Table 6.5. Correlation coefficients between Klamath Falls, OR and Hermiston, OR for potato clones from 4x-4x, 4x-2x, and 2x-2x crosses, and letters indicating a significant difference between cross types for each trait.

Trait	4x-4x	4x-2x	2x-2x
Yield	0.345[(b)]	0.672[(a)]	0.254[(b)]
Specific gravity	0.239[(a)]	0.402[(a)]	0.196[(a)]
Eye depth	0.390[(a)]	0.492[(a)]	0.509[(a)]
Uniformity	0.148[(a)]	0.395[(a)]	0.406[(a)]
Sprouting	0.588[(a)]	0.568[(a)]	0.442[(a)]
Appearance	0.314[(a)]	0.340[(a)]	0.339[(a)]
Length:width ratio	0.751[(a)]	0.846[(a)]	0.667[(a)]
Maturity	0.411[(a)]	0.184[(ab)]	-0.106[(b)]

Table 6.6. Top yielding clones obtained from 4x-4x, 4x-2x, and 2x-2x crosses of potato.*

Clone	Yield (kg/plot)	Specific gravity	Eye depth (1-5)	Uniformity (1-5)	Sprouting (1-5)	Appearance (1-5)	Length: width	Maturity (% green)	Chipper tuber acceptability (0-5)	Russet tuber acceptability (0-5)	Female parent	Male parent	Ploidy
RD.2.3829	6.43	1.081	3.35	2.53	1.97	2.50	1.54	71.78	0.15	1.34	PALB03016-3	BD1268-1	3
RD.2.3906	6.40	1.078	3.35	2.27	2.61	2.18	1.29	73.86	0.98	1.15	Tacna	BD1216-3	3
RD.2.3983	5.96	1.074	3.69	2.91	2.18	2.50	1.55	73.86	0.15	1.72	Tacna	BD1251-1	3
RD.2.3976	5.83	1.073	3.18	2.66	2.18	2.18	1.51	76.45	0.15	0.77	Tacna	BD1247-3	3
CD.2.1211	5.67	1.077	2.85	2.79	3.88	2.50	1.34	74.38	0.15	1.91	Atlantic	BD1202-2	3
RD.2.3836	5.60	1.075	3.85	2.27	3.88	2.18	1.55	72.82	0.15	1.34	Tacna	BD1202-2	3
RD.2.3927	5.56	1.076	3.18	2.66	1.55	2.18	1.42	76.45	1.18	0.77	Tacna	BD1240-6	3
RD.2.3661	5.42	1.076	3.54	2.90	2.47	2.73	1.40	73.27	0.26	2.10	ORAYT-9	BD1202-2	3
RD.2.3493	5.38	1.079	3.28	2.72	2.84	2.73	1.49	74.43	0.26	1.80	AO00710-1	BD1205-4	4
RD.2.3752	5.35	1.077	3.69	2.79	1.97	2.18	1.58	71.78	0.15	0.21	A06866-2	BD1205-4	4
R.2.3066	4.97	1.076	3.69	2.66	4.30	2.34	1.15	75.07	1.39	0.77	Tacna	AO00710-1	4
RD.2.3955	4.91	1.074	3.35	2.40	2.61	2.18	1.26	72.30	0.15	1.53	Tacna	BD1247-3	3
RD.2.3521	4.89	1.080	3.52	2.79	2.61	2.18	1.44	74.89	0.15	0.96	AO00710-1	BD1205-4	4
CD.2.1225	4.72	1.083	3.69	2.91	2.82	2.66	1.15	74.89	2.01	0.21	Atlantic	BD1222-1	3
RD.2.3570	4.71	1.080	3.01	2.27	2.82	2.18	1.35	78.01	0.15	1.34	AO00710-1	BD1268-1	4

* In all traits scored 1-5 or 0-5, “5” indicates the preferable state.

Table 6.7. Top clones obtained from crosses of potato, as judged by "general suitability" obtained from 4x-4x, 4x-2x, and 2x-2x crosses of potato.*

Clone	Yield (kg/plot)	Specific gravity	Eye depth (1-5)	Uniformity (1-5)	Sprouting (1-5)	Appearance (1-5)	Length: width	Maturity (% green)	Chipper tuber acceptability (0-5)	Russet tuber acceptability (0-5)	General suitability	Female	Male	Ploidy
C.2.1134	3.91	1.082	3.85	3.30	4.30	3.30	1.07	64.37	2.83	0.21	7779.01	Eva	Willamette	4
CR.2.1610	4.54	1.075	3.35	2.91	4.52	2.82	1.16	65.56	2.83	0.96	7456.14	Eva	AO00710-1	4
R.2.3066	4.97	1.076	3.69	2.66	4.30	2.34	1.15	75.07	1.39	0.77	7332.65	Tacna	AO00710-1	4
CR.2.1666	4.29	1.076	3.69	3.04	3.88	3.14	1.14	77.45	2.83	0.21	7317.52	Eva	PALB03016-3	4
CD.2.1211	5.67	1.077	2.85	2.79	3.88	2.50	1.34	74.38	0.15	1.91	7252.52	Atlantic	BD1202-2	3
RD.2.3836	5.60	1.075	3.85	2.27	3.88	2.18	1.55	72.82	0.15	1.34	7195.73	Tacna	BD1202-2	3
CD.2.1337	4.61	1.080	3.35	2.79	4.09	2.82	1.33	71.27	0.15	1.72	6992.87	Eva	BD1240-6	3
RC.2.3234	4.22	1.077	3.18	2.91	4.52	2.98	1.16	70.32	2.63	0.21	6932.17	OR01007-3	Lamoka	4
CR.2.1400	4.22	1.078	3.69	2.79	4.30	2.66	1.29	56.04	1.39	1.15	6750.91	Atlantic	AO00710-1	4
RD.2.3983	5.96	1.074	3.69	2.91	2.18	2.50	1.55	73.86	0.15	1.72	6714.79	Tacna	BD1251-1	3
RD.2.3549	4.11	1.080	3.69	2.79	4.09	2.82	1.42	74.89	0.15	2.67	6562.06	AO00710-1	BD1244-1	3
RD.2.3661	5.42	1.076	3.54	2.90	2.47	2.73	1.40	73.27	0.26	2.10	6561.34	ORAYT-9	BD1202-2	3
RC.2.3283	3.33	1.082	3.69	3.17	4.73	3.14	1.15	66.75	2.42	0.21	6528.76	Payette Russet	Lamoka	4
CR.2.1435	3.65	1.081	3.69	2.91	4.30	3.14	1.18	71.51	2.63	0.21	6483.27	Atlantic	BD1216-3	4
RD.2.3493	5.38	1.079	3.28	2.72	2.84	2.73	1.49	74.43	0.26	1.80	6479.62	AO00710-1	BD1205-4	4

*In all traits scored 1-5 or 0-5, "5" indicates the preferable state. For "general suitability", higher scores indicate clones with higher yields and quality traits. "General suitability" was calculated using Equation 1.

Table 6.8. Top clones obtained from crosses of potato, as judged by “chipper suitability” obtained from 4x-4x, 4x-2x, and 2x-2x crosses of potato. For “chipper suitability”, higher scores indicate clones that have higher yields and tuber traits more acceptable for the potato chip market.*

Clone	Yield (kg/plot)	Specific gravity	Eye depth (1-5)	Uniformity (1-5)	Sprouting (1-5)	Appearance (1-5)	Length: width	Maturity (% green)	Chipper tuber acceptability (0-5)	Russet tuber acceptability (0-5)	Chipper suitability	Female	Male	Ploidy
CR.2.1610	4.54	1.075	3.35	2.91	4.52	2.82	1.16	65.56	2.83	0.96	2.64	Eva	AO00710-1	4
CR.2.1666	4.29	1.076	3.69	3.04	3.88	3.14	1.14	77.45	2.83	0.21	2.54	Eva	PALB03016-3	4
C.2.1134	3.91	1.082	3.85	3.30	4.30	3.30	1.07	64.37	2.83	0.21	2.45	Eva	Willamette	4
RC.2.3234	4.22	1.077	3.18	2.91	4.52	2.98	1.16	70.32	2.63	0.21	2.34	OR01007-3	Lamoka	4
CR.2.1883	4.45	1.078	3.18	3.04	2.82	2.66	1.14	57.23	2.42	0.96	2.29	Ivory Crisp	PALB03016-3	4
CR.2.1491	4.07	1.078	3.35	2.79	3.88	2.82	1.11	59.61	2.63	0.21	2.27	Snowden	AO00710-1	4
CR.2.1729	3.93	1.075	3.52	2.91	3.88	2.98	1.12	64.37	2.63	0.21	2.14	Willamette	AO00710-1	4
CD.2.1246	4.46	1.080	3.35	2.79	2.82	2.50	1.14	72.30	2.21	0.21	2.14	Atlantic	BD1240-6	3
CD.2.1225	4.72	1.083	3.69	2.91	2.82	2.66	1.15	74.89	2.01	0.21	2.13	Atlantic	BD1222-1	3
CR.2.1435	3.65	1.081	3.69	2.91	4.30	3.14	1.18	71.51	2.63	0.21	2.11	Atlantic	AO03123-2	4
RC.2.3136	3.68	1.080	3.35	3.04	2.40	2.66	1.04	67.94	2.63	0.21	2.09	AO00710-1	Lamoka	4
C.2.1043	3.29	1.076	3.69	3.17	3.88	2.82	1.04	70.32	3.04	0.21	2.09	Snowden	Lamoka	4
CD.2.1232	4.34	1.080	3.18	2.91	2.40	2.50	1.14	70.75	2.21	0.21	2.09	Atlantic	BD1240-6	3
CR.2.1603	3.85	1.075	3.85	2.91	4.30	2.66	1.31	65.56	2.63	0.96	2.08	Eva	AO00710-1	4
RC.2.3416	3.55	1.074	3.52	3.04	4.52	2.98	1.01	66.75	2.83	0.21	2.05	Tacna	Willamette	4

*In all traits scored 1-5 or 0-5, “5” indicates the preferable state. For “chipper suitability”, higher scores indicate clones that have higher yields and tuber traits more acceptable for the potato chip market. “Chipper suitability” was calculated using Equation 2.

Table 6.9. Top clones obtained from crosses of potato, as judged by "russet suitability" obtained from 4x-4x, 4x-2x, and 2x-2x crosses of potato. For "russet suitability", higher scores indicate clones that have higher yields and tuber traits more acceptable for the French fry market. *

Clone	Yield (kg/plot)	Specific gravity	Eye depth (1-5)	Uniformity (1-5)	Sprouting (1-5)	Appearance (1-5)	Length: width	Maturity (% green)	Chipper tuber acceptability (0-5)	Russet tuber acceptability (0-5)	Russet suitability	Female	Male	Ploidy
RD.2.3661	5.42	1.076	3.54	2.90	2.47	2.73	1.40	73.27	0.26	2.10	2.38	ORAYT-9	BD1202-2	3
RD.2.3549	4.11	1.080	3.69	2.79	4.09	2.82	1.42	74.89	0.15	2.67	2.37	AO00710-1	BD1244-1	3
R.2.2842	4.48	1.078	3.52	3.04	3.24	2.82	1.53	70.32	0.15	2.48	2.36	ORAYT-9	PALB03016-3	4
CD.2.1211	5.67	1.077	2.85	2.79	3.88	2.50	1.34	74.38	0.15	1.91	2.27	Atlantic	BD1202-2	3
R.2.2758	3.77	1.083	3.85	3.17	3.67	2.98	1.92	70.32	0.15	2.67	2.24	AO03123-2	PALB03016-3	4
RD.2.3983	5.96	1.074	3.69	2.91	2.18	2.50	1.55	73.86	0.15	1.72	2.09	Tacna	BD1251-1	3
RD.2.3493	5.38	1.079	3.28	2.72	2.84	2.73	1.49	74.43	0.26	1.80	2.08	AO00710-1	BD1205-4	4
R.2.2996	3.53	1.079	3.35	3.04	3.88	2.82	1.63	73.89	0.15	2.67	2.04	A08640-2	AO00710-1	4
R.2.2863	3.72	1.080	3.52	2.91	4.30	2.82	1.63	65.56	0.15	2.48	2.01	Castle Russet	PALB03016-3	4
RD.2.3794	4.25	1.082	3.35	2.66	2.61	2.50	1.40	72.30	0.15	2.10	1.98	A08640-2	BD1268-1	4
R.2.3073	4.36	1.077	3.35	2.53	4.09	2.50	1.75	75.07	0.15	2.10	1.92	Tacna	AO00710-1	4
R.2.2744	3.68	1.077	3.52	2.91	4.52	2.66	1.85	66.75	0.15	2.48	1.92	AO03123-2	PALB03016-3	4
R.2.2772	3.71	1.078	3.79	2.90	4.31	2.73	1.75	63.39	0.26	2.41	1.91	OR01007-3	AO00710-1	4
RD.2.3829	6.43	1.081	3.35	2.53	1.97	2.50	1.54	71.78	0.15	1.34	1.90	PALB03016-3	BD1268-1	3
R.2.3059	4.57	1.080	3.18	2.66	2.82	2.66	1.39	67.94	0.15	1.91	1.89	A08640-2	PALB03016-3	4

* In all traits scored 1-5 or 0-5, "5" indicates the preferable state. For "russet suitability", higher scores indicate clones that have higher yields and tuber traits more acceptable for the potato chip market. "Russet suitability" was calculated using Equation 3.

7 Conclusions

The cultivated potato (*Solanum tuberosum* L.) is one of the world's most important staple crops, ranked fourth after maize, rice, and wheat. While the potato's success is due largely to its high yield, it also benefits from its broad global acceptance, and its ability to be used by the consumer without prior processing. However, the potato's success as a crop comes despite an array of pathogens that can cause extreme yield losses, and quality defects that can make the potato essentially unmarketable. While they can be costly, and at times devastating, the presence of these pathogens creates an enormous opportunity for the genetic improvement of the potato. For every major pathogen in potato, multiple sources of resistance have been identified in landraces or wild potato species that if combined in a suitable potato cultivar, could reduce or eliminate the damage caused for that pathogen. While the utilization of genes from exotic germplasm is far from trivial, advances in genetics, genomics and phenomics will certainly accelerate this process.

In this study, I report the identification of new sources of resistance to Columbia root knot nematode (CRKN; *Meloidogyne chitwoodi)* and Verticillium wilt (VW; *Verticillium dahlia*) as well as efforts to identify and map genes from 'Castle Russet' conferring resistance to *Potato virus Y* (PVY) and Corky ringspot caused by *Tobacco rattle virus* and vectored by stubby root nematode. In addition, we evaluated clones selected at random from a group of tetraploid and diploid potato crosses to identify groups of potatoes that exhibit hybrid vigor for yield and quality traits.

New sources of resistance for *M. chitwoodi* identified include clones from *S. hougasii*, *S. bulbocastanum,* and *S. stenophyllidium*. Levels of resistance in these clones tended to be moderately high to absolutely no reproduction of nematodes. For *V. dahliae*, new sources of resistance were identified in *S. andreanum* and *S. bulbocastanum*. Levels of resistance to *V. dahliae* appeared to be moderate, with clones generally showing signs and symptoms that were slightly less severe than those observed for 'Ranger Russet' (the moderately resistant check).

The next step will be to begin introgressing these newly identified resistance genes into elite potato germplasm. Based on the endosperm balance numbers, *S. hougasii* and *S. andreanum* should be directly crossable with elite tetraploid potatoes while *S. bulbocastanum* and *S. stenophyllidium* are not considered to be sexually compatible with elite tetraploid potatoes, and in order for successful introgression, they will likely need to put through somatic hybridization (protoplast fusion). For all of these species, continued backcrossing with tetraploid cultivated potatoes after the initial introgression process will eventually result in a tetraploid potato with improved agronomic performance (Brown et al. 2009, Haynes and Qu 2016). Early in the introgression process, segregation of resistance should be determined to understand the number of genes that confer each source of resistance. Additionally, these clones should be tested against a wide range of isolates for their respective pathogens in greenhouse as well as in field conditions.

‘Castle Russet’ was recently released from the Northwest potato variety development program with resistance to PVY, CRS and *Potato mop-top virus* along with good agronomic traits. In this study, we planned on identifying single nucleotide polymorphism (SNP) markers linked to PVY and CRS resistance. Unfortunately, our efforts were hindered by the fact that the majority of the clones in a biparental population were not from the intended cross (Castle Russet x POR08BD1-3). Though our true population was only 49 clones, we were able to successfully map PVY and CRS resistance using traditional genetic mapping and single marker QTL analysis. Further, we identified the loci controlling resistance to PVY and TRV with a reasonable degree of confidence. Despite these challenges, we were able to identify the loci controlling resistance to PVY and CRS with a reasonable degree of confidence. Our results identified 22 SNPs that were closely linked to PVY resistance at 4.5-4.6 cM and 14 SNPs that were closely associated with CRS. Further validation of these markers is essential to confirm which of these SNPs are closely linked to these resistances for future use in marker assisted breeding. As phenotyping is expensive and takes a great deal of time, for larger population for PVY and CRS, with the decreasing cost of genotyping, we recommend that populations are genotyped and checked for these errors prior to phenotyping.

The relative success of mapping and identification of linked markers was due both to the large effects of the alleles conferring resistance in the population and the high marker density of the Potato V3 Infinium Array (22K), which allowed us to identify genetic markers linked very closely to these phenotypes. Segregation of resistance for CRS, and associated set of SNPs on chromosome 9, support the hypothesis that CRS resistance from 'Castle Russet' is conferred by a single dominant gene, giving a basis for future efforts to map this gene. In addition, we were able to identify two clones that held strong resistance to PVY and CRS, as well as a recombination event positioned very closely to Ry_{sto}, which may have separated PVY resistance from some linkage drag. Therefore, these clones could be valuable parents in future variety development efforts.

In an effort to understand hybrid vigor, a wide range of hybridizations were made between elite chipper potatoes, elite russet potatoes, and an improved population of diploid potatoes. Based on this set of crosses, we did not find evidence that chipper-russet hybrids benefited significantly from hybrid vigor, as the yield of these clones was generally intermediate to the yields of crosses made within each group. However, clones derived from chipper-russet crosses did appear to be generally suitable for the chip industry and may serve as a way to leverage the local adaptation many russet clones have in the Columbia Basin when breeding new chip class potatoes. In addition, we found notable advantages when crossing elite long-day adapted tetraploid potatoes with improved diploid population notably for increased yield and yield stability. However, these benefits were generally similar in importance to a decrease in tuber quality seen in many of the chipper x diploid and russet x diploid clones. Therefore, we don't feel that benefits of wide crosses warrant the difficulty of producing 4x-2x true potato seed for this set of clones. That being said, all of the desired quality traits, including russeting, dormancy, and uniformity, were present in at least some of the 4x-2x hybrids, suggesting that these wide crosses could be valuable if better parents could be selected from these parental groups.

In our evaluation of 4x-2x crosses, we conducted flow cytometry on the progeny to identify and remove any accidental diploid clones (any diploid clones would likely be haploids of the tetraploid parents, and therefore irrelevant to the study). However, we were surprised to identify clones from these crosses as triploids, rather than tetraploids: up to 74.4%. This is in contrast to previous studies, which have reported a frequency of 0-7% triploids from these types of crosses. While we are unsure of the exact reasons for this difference in triploid frequency, there are many possible reasons including continuous crossing of diploid clones that produce low seed set, greenhouse conditions and embryo rescue of the low number of seeds obtained from the crosses. Nevertheless, the high frequency of triploids identified in this study gave us an opportunity to evaluate a large number of triploid potato clones under field conditions. While we were not able to detect strong differences in yield or quality between tetraploid and triploid clones derived from 4x-2x crosses in this study, all of the best performing 4x-2x hybrids were triploid, indicating that the triploid clones are at least on par with their tetraploid siblings, and possibly better.

Genetic resistance to pathogens and pests is likely the best method potato breeders have to improve yield and contribute to food security, while improving profitability for producers. The work conducted here, to identify new sources of genetic resistance, and to better characterize resistance that was previously introgressed into elite potato germplasm, will play an important role in developing improved cultivars for the Pacific Northwest potato industry and beyond. Along with biotic and abiotic stress resistance, improved agronomic performance including high yield and good processing quality is essential for successful release of new varieties. As a tetraploid and highly heterozygous, alternative potato breeding strategies are essential for successful breeding program, possibly including wide crosses, diploid hybrid breeding, genomic selection, or a yet unthought-of strategy. While a proof of concept has not been achieved for any of these strategies (which would come in the form of a clearly superior potato cultivar), their potential benefits to potato breeders makes it critical that each of these strategies is pursued, especially when new tools and genetic resources become available.

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Appendix A. Supplemental tables

Supplementary Table 2.1. *Meloidogyne chitwoodi* reproduction data for the initial screening (chapter 2). “Rep” indicates the seedling number within the clone, “Batch” indicates which batch of evaluations the seedling was screened in, and “Eggs Extracted” indicates the total number of *M. chitwoodi* eggs that were screened at the end of the evaluation.

Clone	Accession	Species	Rep	Batch	Eggs extracted
PI558402hou-1mc	PI558402	*S. hougasii*	1	1	200
PI558402hou-2mc	PI558402	*S. hougasii*	2	1	80
PI558402hou-3mc	PI558402	*S. hougasii*	3	1	80
PI558402hou-4mc	PI558402	*S. hougasii*	4	1	0
PI558402hou-5mc	PI558402	*S. hougasii*	5	1	40
PI558402hou-6mc	PI558402	*S. hougasii*	6	1	160
PI558402hou-7mc	PI558402	*S. hougasii*	7	1	80
PI558402hou-8mc	PI558402	*S. hougasii*	8	1	0
PI558402hou-9mc	PI558402	*S. hougasii*	9	1	0
PI558402hou-10mc	PI558402	*S. hougasii*	10	1	320
PI275184blb-1mc	PI275184	*S. bulbocastanum*	1	1	7120
PI275184blb-2mc	PI275184	*S. bulbocastanum*	2	1	2360
PI275184blb-3mc	PI275184	*S. bulbocastanum*	3	1	9525
PI275184blb-4mc	PI275184	*S. bulbocastanum*	4	1	11880
PI275184blb-5mc	PI275184	*S. bulbocastanum*	5	1	1880
PI275184blb-6mc	PI275184	*S. bulbocastanum*	6	1	240
PI275184blb-7mc	PI275184	*S. bulbocastanum*	7	1	1640
PI275184blb-8mc	PI275184	*S. bulbocastanum*	8	1	960
PI275184blb-9mc	PI275184	*S. bulbocastanum*	9	1	1720
PI275184blb-10mc	PI275184	*S. bulbocastanum*	10	1	1280
PI275182iop-1mc	PI275182	*S. iopetalum*	1	1	14440
PI275182iop-2mc	PI275182	*S. iopetalum*	2	1	2200
PI275182iop-3mc	PI275182	*S. iopetalum*	3	1	8720
PI275182iop-4mc	PI275182	*S. iopetalum*	4	1	8800
PI275182iop-5mc	PI275182	*S. iopetalum*	5	1	360
PI275182iop-6mc	PI275182	*S. iopetalum*	6	1	2160
PI275182iop-7mc	PI275182	*S. iopetalum*	7	1	4640
PI275182iop-8mc	PI275182	*S. iopetalum*	8	1	2160
PI275182iop-9mc	PI275182	*S. iopetalum*	9	1	1120
PI275182iop-10mc	PI275182	*S. iopetalum*	10	1	680
PI243505blb-1mc	PI243505	*S. bulbocastanum*	1	1	360
PI243505blb-2mc	PI243505	*S. bulbocastanum*	2	1	2880
PI243505blb-3mc	PI243505	*S. bulbocastanum*	3	1	1040
PI243505blb-4mc	PI243505	*S. bulbocastanum*	4	1	2040
PI243505blb-5mc	PI243505	*S. bulbocastanum*	5	1	160
PI243505blb-6mc	PI243505	*S. bulbocastanum*	6	1	560

Supplementary Table 2.1 (Continued)

PI243505blb-7mc	PI243505	*S. bulbocastanum*	7	1	1520
PI243505blb-8mc	PI243505	*S. bulbocastanum*	8	1	2360
PI243505blb-9mc	PI243505	*S. bulbocastanum*	9	1	400
PI243505blb-10mc	PI243505	*S. bulbocastanum*	10	1	3280
PI597682iop-1mc	PI597682	*S. iopetalum*	1	1	10840
PI597682iop-2mc	PI597682	*S. iopetalum*	2	1	1320
PI597682iop-3mc	PI597682	*S. iopetalum*	3	1	1080
PI597682iop-4mc	PI597682	*S. iopetalum*	4	1	2200
Rutgers	Rutgers	Tomato	1	1	800
Rutgers	Rutgers	Tomato	2	1	3920
Rutgers	Rutgers	Tomato	3	1	12280
Rutgers	Rutgers	Tomato	4	1	240
Rutgers	Rutgers	Tomato	5	1	4080
Rutgers	Rutgers	Tomato	6	1	440
Rutgers	Rutgers	Tomato	7	1	7600
Rutgers	Rutgers	Tomato	8	1	760
Rutgers	Rutgers	Tomato	9	1	9000
Rutgers	Rutgers	Tomato	10	1	2920
Vernema	Vernema	Alfalfa	1	1	0
Vernema	Vernema	Alfalfa	2	1	0
Vernema	Vernema	Alfalfa	3	1	0
Vernema	Vernema	Alfalfa	4	1	0
PI498148adr-1mc	PI498148	*S. andreanum*	1	2	73500
PI498149adr-2mc	PI498149	*S. andreanum*	2	2	850
PI498150adr-3mc	PI498150	*S. andreanum*	3	2	133600
PI498151adr-4mc	PI498151	*S. andreanum*	4	2	109800
PI498152adr-5mc	PI498152	*S. andreanum*	5	2	128400
PI498153adr-6mc	PI498153	*S. andreanum*	6	2	70400
PI498154adr-7mc	PI498154	*S. andreanum*	7	2	84800
PI498155adr-8mc	PI498155	*S. andreanum*	8	2	8050
PI498156adr-9mc	PI498156	*S. andreanum*	9	2	86000
PI498157adr-10mc	PI498157	*S. andreanum*	10	2	38400
PI243508blb-1mc	PI243508	*S. bulbocastanum*	1	2	14100
PI243508blb-4mc	PI243508	*S. bulbocastanum*	4	2	77200
PI243508blb-7mc	PI243508	*S. bulbocastanum*	7	2	5600
PI243508blb-8mc	PI243508	*S. bulbocastanum*	8	2	4350
PI243508blb-10mc	PI243508	*S. bulbocastanum*	10	2	1100
PI275196blb-1mc	PI275196	*S. bulbocastanum*	1	2	81800
PI275196blb-2mc	PI275196	*S. bulbocastanum*	2	2	9950
PI275196blb-3mc	PI275196	*S. bulbocastanum*	3	2	56600
PI275196blb-4mc	PI275196	*S. bulbocastanum*	4	2	124800
PI275196blb-5mc	PI275196	*S. bulbocastanum*	5	2	60300
PI275196blb-6mc	PI275196	*S. bulbocastanum*	6	2	12400
PI275196blb-7mc	PI275196	*S. bulbocastanum*	7	2	44800
PI275196blb-8mc	PI275196	*S. bulbocastanum*	8	2	26500

Supplementary Table 2.1 (Continued)

PI275196blb-9mc	PI275196	*S. bulbocastanum*	9	2	46000
PI275196blb-10mc	PI275196	*S. bulbocastanum*	10	2	11100
PI347757blb-2mc	PI347757	*S. bulbocastanum*	2	2	12300
PI347757blb-3mc	PI347757	*S. bulbocastanum*	3	2	15300
PI347757blb-4mc	PI347757	*S. bulbocastanum*	4	2	14700
PI347757blb-6mc	PI347757	*S. bulbocastanum*	6	2	20000
PI347757blb-7mc	PI347757	*S. bulbocastanum*	7	2	8350
PI347757blb-9mc	PI347757	*S. bulbocastanum*	9	2	2300
PI347757blb-10mc	PI347757	*S. bulbocastanum*	10	2	3000
PI161730grr-1mc	PI161730	*S. guerreroense*	1	2	34000
PI161730grr-2mc	PI161730	*S. guerreroense*	2	2	36200
PI161730grr-3mc	PI161730	*S. guerreroense*	3	2	39000
PI161730grr-5mc	PI161730	*S. guerreroense*	5	2	147400
PI161730grr-6mc	PI161730	*S. guerreroense*	6	2	38900
PI161730grr-8mc	PI161730	*S. guerreroense*	8	2	34100
PI161730grr-9mc	PI161730	*S. guerreroense*	9	2	850
PI161730grr-10mc	PI161730	*S. guerreroense*	10	2	103800
PI653828grr-4mc	PI653828	*S. guerreroense*	4	2	66600
PI653828grr-5mc	PI653828	*S. guerreroense*	5	2	73400
PI653828grr-7mc	PI653828	*S. guerreroense*	7	2	350
PI653828grr-8mc	PI653828	*S. guerreroense*	8	2	95700
PI653828grr-9mc	PI653828	*S. guerreroense*	9	2	86000
PI558405iop-1mc	PI558405	*S. iopetalum*	1	2	196000
PI558405iop-2mc	PI558405	*S. iopetalum*	2	2	213600
PI558405iop-3mc	PI558405	*S. iopetalum*	3	2	119400
PI558405iop-4mc	PI558405	*S. iopetalum*	4	2	104700
PI558405iop-5mc	PI558405	*S. iopetalum*	5	2	204200
PI558405iop-6mc	PI558405	*S. iopetalum*	6	2	27500
PI558405iop-7mc	PI558405	*S. iopetalum*	7	2	52800
PI558405iop-8mc	PI558405	*S. iopetalum*	8	2	17900
PI558405iop-9mc	PI558405	*S. iopetalum*	9	2	106200
PI558405iop-10mc	PI558405	*S. iopetalum*	10	2	80500
PI604099iop-1mc	PI604099	*S. iopetalum*	1	2	11600
PI604099iop-2mc	PI604099	*S. iopetalum*	2	2	104600
PI604099iop-3mc	PI604099	*S. iopetalum*	3	2	28100
PI604099iop-4mc	PI604099	*S. iopetalum*	4	2	28100
PI604099iop-5mc	PI604099	*S. iopetalum*	5	2	5600
PI604099iop-6mc	PI604099	*S. iopetalum*	6	2	5850
PI604099iop-7mc	PI604099	*S. iopetalum*	7	2	49000
PI604099iop-8mc	PI604099	*S. iopetalum*	8	2	11600
PI604099iop-9mc	PI604099	*S. iopetalum*	9	2	6750
PI643997sto-6mc	PI643997	*S. stoloniferum*	6	2	98600
Rutgers	Rutgers	Tomato	1	2	210800
Rutgers	Rutgers	Tomato	2	2	216400
Rutgers	Rutgers	Tomato	3	2	170400

Supplementary Table 2.1 (Continued)

Rutgers	Rutgers	Tomato	4	2	319800
Rutgers	Rutgers	Tomato	5	2	302800
Rutgers	Rutgers	Tomato	6	2	231600
Rutgers	Rutgers	Tomato	7	2	225280
Rutgers	Rutgers	Tomato	8	2	112100
Rutgers	Rutgers	Tomato	9	2	65600
Rutgers	Rutgers	Tomato	10	2	352200
Vernema	Vernema	Alfalfa	1	2	0
Vernema	Vernema	Alfalfa	2	2	0
Vernema	Vernema	Alfalfa	3	2	400
Vernema	Vernema	Alfalfa	4	2	0
PI243512blb-1mc	PI243512	*S. bulbocastanum*	1	3	2200
PI243512blb-4mc	PI243512	*S. bulbocastanum*	4	3	8000
PI243512blb-5mc	PI243512	*S. bulbocastanum*	5	3	33400
PI243512blb-6mc	PI243512	*S. bulbocastanum*	6	3	35600
PI243512blb-7mc	PI243512	*S. bulbocastanum*	7	3	2500
PI243512blb-8mc	PI243512	*S. bulbocastanum*	8	3	5500
PI243512blb-10mc	PI243512	*S. bulbocastanum*	10	3	2300
PI275187blb-2mc	PI275187	*S. bulbocastanum*	2	3	2850
PI275187blb-3mc	PI275187	*S. bulbocastanum*	3	3	3050
PI275187blb-6mc	PI275187	*S. bulbocastanum*	6	3	1400
PI275187blb-8mc	PI275187	*S. bulbocastanum*	8	3	6800
PI275187blb-9mc	PI275187	*S. bulbocastanum*	9	3	33400
PI161727hou-1mc	PI161727	*S. hougasii*	1	3	22800
PI161727hou-2mc	PI161727	*S. hougasii*	2	3	34200
PI161727hou-3mc	PI161727	*S. hougasii*	3	3	64200
PI161727hou-4mc	PI161727	*S. hougasii*	4	3	11000
PI161727hou-5mc	PI161727	*S. hougasii*	5	3	20400
PI161727hou-6mc	PI161727	*S. hougasii*	6	3	9700
PI161727hou-7mc	PI161727	*S. hougasii*	7	3	16900
PI161727hou-8mc	PI161727	*S. hougasii*	8	3	39400
PI161727hou-9mc	PI161727	*S. hougasii*	9	3	11000
PI161727hou-10mc	PI161727	*S. hougasii*	10	3	27600
PI239423hou-1mc	PI239423	*S. hougasii*	1	3	50
PI239423hou-2mc	PI239423	*S. hougasii*	2	3	500
PI239423hou-3mc	PI239423	*S. hougasii*	3	3	13800
PI239423hou-4mc	PI239423	*S. hougasii*	4	3	50
PI239423hou-6mc	PI239423	*S. hougasii*	6	3	4650
PI239423hou-7mc	PI239423	*S. hougasii*	7	3	0
PI239423hou-8mc	PI239423	*S. hougasii*	8	3	100
PI239423hou-9mc	PI239423	*S. hougasii*	9	3	5400
PI239423hou-10mc	PI239423	*S. hougasii*	10	3	0
PI243344iop-1mc	PI243344	*S. iopetalum*	1	3	7000
PI243344iop-2mc	PI243344	*S. iopetalum*	2	3	1000
PI243344iop-4mc	PI243344	*S. iopetalum*	4	3	6000

Supplementary Table 2.1 (Continued)

PI243344iop-5mc	PI243344	*S. iopetalum*	5	3	10900
PI243344iop-6mc	PI243344	*S. iopetalum*	6	3	2700
PI243344iop-7mc	PI243344	*S. iopetalum*	7	3	10900
PI243344iop-8mc	PI243344	*S. iopetalum*	8	3	1600
PI243344iop-9mc	PI243344	*S. iopetalum*	9	3	3350
PI243344iop-10mc	PI243344	*S. iopetalum*	10	3	7600
PI545771iop-2mc	PI545771	*S. iopetalum*	2	3	2100
PI545771iop-4mc	PI545771	*S. iopetalum*	4	3	750
PI545771iop-6mc	PI545771	*S. iopetalum*	6	3	16500
PI545771iop-8mc	PI545771	*S. iopetalum*	8	3	3200
PI604098iop-1mc	PI604098	*S. iopetalum*	1	3	20000
PI604098iop-2mc	PI604098	*S. iopetalum*	2	3	2150
PI604098iop-3mc	PI604098	*S. iopetalum*	3	3	46400
PI604098iop-4mc	PI604098	*S. iopetalum*	4	3	1050
PI604098iop-5mc	PI604098	*S. iopetalum*	5	3	3150
PI604098iop-6mc	PI604098	*S. iopetalum*	6	3	6000
PI604098iop-7mc	PI604098	*S. iopetalum*	7	3	23200
PI604098iop-9mc	PI604098	*S. iopetalum*	9	3	2850
PI604098iop-10mc	PI604098	*S. iopetalum*	10	3	22100
PI607859iop-1mc	PI607859	*S. iopetalum*	1	3	11500
PI607859iop-2mc	PI607859	*S. iopetalum*	2	3	17400
PI607859iop-3mc	PI607859	*S. iopetalum*	3	3	15300
PI607859iop-4mc	PI607859	*S. iopetalum*	4	3	28600
PI607859iop-5mc	PI607859	*S. iopetalum*	5	3	40000
PI607859iop-6mc	PI607859	*S. iopetalum*	6	3	2650
PI607859iop-7mc	PI607859	*S. iopetalum*	7	3	17800
PI607859iop-8mc	PI607859	*S. iopetalum*	8	3	20000
PI607859iop-9mc	PI607859	*S. iopetalum*	9	3	36600
PI607859iop-10mc	PI607859	*S. iopetalum*	10	3	54400
PI320265sph-1mc	PI320265	*S. stenophyllidium*	1	3	12000
PI320265sph-3mc	PI320265	*S. stenophyllidium*	3	3	17300
Rutgers	Rutgers	Tomato	1	3	187400
Rutgers	Rutgers	Tomato	2	3	103400
Rutgers	Rutgers	Tomato	3	3	129200
Rutgers	Rutgers	Tomato	4	3	106800
Rutgers	Rutgers	Tomato	5	3	117400
Rutgers	Rutgers	Tomato	6	3	138800
Rutgers	Rutgers	Tomato	7	3	100600
Rutgers	Rutgers	Tomato	8	3	103800
Rutgers	Rutgers	Tomato	9	3	155200
Rutgers	Rutgers	Tomato	10	3	199800
Vernema	Vernema	Alfalfa	1	3	1400
Vernema	Vernema	Alfalfa	2	3	0
Vernema	Vernema	Alfalfa	3	3	0
Vernema	Vernema	Alfalfa	4	3	0

Supplementary Table 2.1 (Continued)

PI310975blv-1mc	PI310975	*S. boliviense*	1	4	3100
PI310975blv-2mc	PI310975	*S. boliviense*	2	4	21000
PI310975blv-4mc	PI310975	*S. boliviense*	4	4	9300
PI310975blv-5mc	PI310975	*S. boliviense*	5	4	3600
PI310975blv-6mc	PI310975	*S. boliviense*	6	4	3900
PI310975blv-7mc	PI310975	*S. boliviense*	7	4	5200
PI310975blv-9mc	PI310975	*S. boliviense*	9	4	48200
PI310975blv-10mc	PI310975	*S. boliviense*	10	4	12200
PI473504brc-1mc	PI473504	*S. brevicaule*	1	4	4400
PI473504brc-2mc	PI473504	*S. brevicaule*	2	4	12600
PI473504brc-3mc	PI473504	*S. brevicaule*	3	4	32200
PI473504brc-4mc	PI473504	*S. brevicaule*	4	4	27600
PI473504brc-5mc	PI473504	*S. brevicaule*	5	4	38600
PI473504brc-6mc	PI473504	*S. brevicaule*	6	4	31400
PI473504brc-7mc	PI473504	*S. brevicaule*	7	4	78400
PI473504brc-9mc	PI473504	*S. brevicaule*	9	4	20300
PI473504brc-10mc	PI473504	*S. brevicaule*	10	4	12600
PI255518blb-1mc	PI255518	*S. bulbocastanum*	1	4	41600
PI255518blb-3mc	PI255518	*S. bulbocastanum*	3	4	2700
PI255518blb-4mc	PI255518	*S. bulbocastanum*	4	4	3750
PI498224blb-2mc	PI498224	*S. bulbocastanum*	2	4	71000
PI498224blb-3mc	PI498224	*S. bulbocastanum*	3	4	39600
PI498224blb-4mc	PI498224	*S. bulbocastanum*	4	4	23400
PI498224blb-6mc	PI498224	*S. bulbocastanum*	6	4	29800
PI498224blb-7mc	PI498224	*S. bulbocastanum*	7	4	13400
PI498224blb-8mc	PI498224	*S. bulbocastanum*	8	4	20800
PI498224blb-9mc	PI498224	*S. bulbocastanum*	9	4	29400
PI239424hou-2mc	PI239424	*S. hougasii*	2	4	50
PI239424hou-3mc	PI239424	*S. hougasii*	3	4	0
PI239424hou-4mc	PI239424	*S. hougasii*	4	4	100
PI239424hou-5mc	PI239424	*S. hougasii*	5	4	50
PI239424hou-6mc	PI239424	*S. hougasii*	6	4	0
PI239424hou-7mc	PI239424	*S. hougasii*	7	4	0
PI239424hou-8mc	PI239424	*S. hougasii*	8	4	100
PI239424hou-9mc	PI239424	*S. hougasii*	9	4	0
PI239424hou-10mc	PI239424	*S. hougasii*	10	4	50
PI275181iop-1mc	PI275181	*S. iopetalum*	1	4	3450
PI275181iop-2mc	PI275181	*S. iopetalum*	2	4	3200
PI558417iop-1mc	PI558417	*S. iopetalum*	1	4	23200
PI558417iop-2mc	PI558417	*S. iopetalum*	2	4	32400
PI558417iop-3mc	PI558417	*S. iopetalum*	3	4	3100
PI558417iop-4mc	PI558417	*S. iopetalum*	4	4	38400
PI558417iop-5mc	PI558417	*S. iopetalum*	5	4	33400
PI558417iop-6mc	PI558417	*S. iopetalum*	6	4	8100
PI558417iop-7mc	PI558417	*S. iopetalum*	7	4	13100

Supplementary Table 2.1 (Continued)

PI558417iop-9mc	PI558417	*S. iopetalum*	9	4	38000
PI558417iop-10mc	PI558417	*S. iopetalum*	10	4	101200
PI545815sph-1mc	PI545815	*S. stenophyllidium*	1	4	44600
PI545815sph-2mc	PI545815	*S. stenophyllidium*	2	4	71200
PI545815sph-3mc	PI545815	*S. stenophyllidium*	3	4	1650
PI545815sph-4mc	PI545815	*S. stenophyllidium*	4	4	28000
PI545815sph-5mc	PI545815	*S. stenophyllidium*	5	4	13100
PI545815sph-6mc	PI545815	*S. stenophyllidium*	6	4	4550
PI545815sph-7mc	PI545815	*S. stenophyllidium*	7	4	8300
PI545815sph-9mc	PI545815	*S. stenophyllidium*	9	4	300
PI545815sph-10mc	PI545815	*S. stenophyllidium*	10	4	14100
Rutgers	Rutgers	Tomato	1	4	100800
Rutgers	Rutgers	Tomato	2	4	128600
Rutgers	Rutgers	Tomato	3	4	56600
Rutgers	Rutgers	Tomato	4	4	106600
Rutgers	Rutgers	Tomato	5	4	42400
Rutgers	Rutgers	Tomato	6	4	58600
Rutgers	Rutgers	Tomato	7	4	92200
Rutgers	Rutgers	Tomato	8	4	88600
Rutgers	Rutgers	Tomato	9	4	102000
Rutgers	Rutgers	Tomato	10	4	104000
Vernema	Vernema	Alfalfa	1	4	0
Vernema	Vernema	Alfalfa	2	4	50
Vernema	Vernema	Alfalfa	3	4	50
Vernema	Vernema	Alfalfa	4	4	0
PI265861blv-1mc	PI265861	*S. boliviense*	1	5	0
PI265861blv-2mc	PI265861	*S. boliviense*	2	5	9600
PI265861blv-4mc	PI265861	*S. boliviense*	4	5	8800
PI265861blv-7mc	PI265861	*S. boliviense*	7	5	29800
PI265861blv-8mc	PI265861	*S. boliviense*	8	5	13600
PI265861blv-9mc	PI265861	*S. boliviense*	9	5	18200
PI265861blv-10mc	PI265861	*S. boliviense*	10	5	17300
PI545912brc-1mc	PI545912	*S. brevicaule*	1	5	19100
PI545912brc-2mc	PI545912	*S. brevicaule*	2	5	44800
PI545912brc-3mc	PI545912	*S. brevicaule*	3	5	75400
PI545912brc-4mc	PI545912	*S. brevicaule*	4	5	16800
PI545912brc-5mc	PI545912	*S. brevicaule*	5	5	12600
PI545912brc-6mc	PI545912	*S. brevicaule*	6	5	22800
PI545912brc-7mc	PI545912	*S. brevicaule*	7	5	63000
PI545912brc-8mc	PI545912	*S. brevicaule*	8	5	78200
PI545912brc-9mc	PI545912	*S. brevicaule*	9	5	40600
PI545912brc-10mc	PI545912	*S. brevicaule*	10	5	103000
PI498011blb-1mc	PI498011	*S. bulbocastanum*	1	5	3900
PI498011blb-3mc	PI498011	*S. bulbocastanum*	3	5	2000
PI498011blb-4mc	PI498011	*S. bulbocastanum*	4	5	5500

Supplementary Table 2.1 (Continued)

PI498011blb-6mc	PI498011	*S. bulbocastanum*	6	5	13500
PI498011blb-7mc	PI498011	*S. bulbocastanum*	7	5	20000
PI498011blb-8mc	PI498011	*S. bulbocastanum*	8	5	7700
PI498011blb-9mc	PI498011	*S. bulbocastanum*	9	5	1600
PI498011blb-10mc	PI498011	*S. bulbocastanum*	10	5	34800
PI161174hou-1mc	PI161174	*S. hougasii*	1	5	2300
PI161174hou-2mc	PI161174	*S. hougasii*	2	5	700
PI161174hou-5mc	PI161174	*S. hougasii*	5	5	1850
PI161174hou-8mc	PI161174	*S. hougasii*	8	5	1300
PI161174hou-9mc	PI161174	*S. hougasii*	9	5	5800
PI161174hou-10mc	PI161174	*S. hougasii*	10	5	6400
PI161726hou-1mc	PI161726	*S. hougasii*	1	5	1900
PI161726hou-2mc	PI161726	*S. hougasii*	2	5	50
PI161726hou-3mc	PI161726	*S. hougasii*	3	5	100
PI161726hou-4mc	PI161726	*S. hougasii*	4	5	200
PI161726hou-7mc	PI161726	*S. hougasii*	7	5	350
PI161726hou-8mc	PI161726	*S. hougasii*	8	5	400
PI558422hou-1mc	PI558422	*S. hougasii*	1	5	500
PI558422hou-2mc	PI558422	*S. hougasii*	2	5	150
PI558422hou-5mc	PI558422	*S. hougasii*	5	5	450
PI558422hou-6mc	PI558422	*S. hougasii*	6	5	550
PI558422hou-7mc	PI558422	*S. hougasii*	7	5	600
PI283107hou-2mc	PI283107	*S. hougasii*	2	5	6100
PI283107hou-5mc	PI283107	*S. hougasii*	5	5	0
PI283107hou-6mc	PI283107	*S. hougasii*	6	5	250
PI283107hou-7mc	PI283107	*S. hougasii*	7	5	0
PI283107hou-9mc	PI283107	*S. hougasii*	9	5	0
PI275183iop-1mc	PI275183	*S. iopetalum*	1	5	5100
PI275183iop-2mc	PI275183	*S. iopetalum*	2	5	2400
PI275183iop-3mc	PI275183	*S. iopetalum*	3	5	9400
PI632334sto-3mc	PI632334	*S. stoloniferum*	3	5	16200
PI632334sto-4mc	PI632334	*S. stoloniferum*	4	5	21200
PI632334sto-7mc	PI632334	*S. stoloniferum*	7	5	36600
Rutgers	Rutgers	Tomato	2	5	34400
Rutgers	Rutgers	Tomato	3	5	73200
Rutgers	Rutgers	Tomato	4	5	81000
Rutgers	Rutgers	Tomato	5	5	119400
Rutgers	Rutgers	Tomato	6	5	133600
Rutgers	Rutgers	Tomato	7	5	107600
Rutgers	Rutgers	Tomato	8	5	164600
Rutgers	Rutgers	Tomato	9	5	234000
Rutgers	Rutgers	Tomato	10	5	120400
Vernema	Vernema	Alfalfa	1	5	0
Vernema	Vernema	Alfalfa	2	5	0
Vernema	Vernema	Alfalfa	3	5	1150

Supplementary Table 2.1 (Continued)

Vernema	Vernema	Alfalfa	4	5	550

Supplementary Table 2.2. *Meloidogyne chitwoodi* reproduction data for the first unsuccessful evaluation following the initial screening.

Clone	Species	Rep	WAMC1 eggs extracted	WAMC27 eggs extracted
PI161726hou-2mc	*S. hougasii*	1		
PI161726hou-2mc	*S. hougasii*	2		
PI161726hou-2mc	*S. hougasii*	3		
PI161726hou-3mc	*S. hougasii*	1	100	100
PI161726hou-3mc	*S. hougasii*	2	100	
PI161726hou-3mc	*S. hougasii*	3		
PI239423hou-1mc	*S. hougasii*	1	0	
PI239423hou-1mc	*S. hougasii*	2	250	
PI239423hou-1mc	*S. hougasii*	3	50	
PI239423hou-2mc	*S. hougasii*	1	3400	
PI239423hou-2mc	*S. hougasii*	2	5450	
PI239423hou-2mc	*S. hougasii*	3	3550	
PI239423hou-4mc	*S. hougasii*	1	150	
PI239423hou-4mc	*S. hougasii*	2		
PI239423hou-4mc	*S. hougasii*	3		
PI239423hou-8mc	*S. hougasii*	1	850	
PI239423hou-8mc	*S. hougasii*	2	550	
PI239423hou-8mc	*S. hougasii*	3		
PI239423hou-10mc	*S. hougasii*	1	100	1700
PI239423hou-10mc	*S. hougasii*	2	400	
PI239423hou-10mc	*S. hougasii*	3	200	
PI239423hou-9mc	*S. hougasii*	3	2500	
PI239424hou-2mc	*S. hougasii*	1	50	550
PI239424hou-2mc	*S. hougasii*	2	0	
PI239424hou-2mc	*S. hougasii*	3		
PI239424hou-3mc	*S. hougasii*	1	450	12000
PI239424hou-3mc	*S. hougasii*	2	100	
PI239424hou-3mc	*S. hougasii*	3	300	
PI239424hou-6mc	*S. hougasii*	1	1700	50
PI239424hou-6mc	*S. hougasii*	2	200	
PI239424hou-6mc	*S. hougasii*	3	4100	
PI239424hou-9mc	*S. hougasii*	1	150	4200
PI239424hou-9mc	*S. hougasii*	2	50	
PI239424hou-9mc	*S. hougasii*	3	200	
PI255518blb-3mc	*S. bulbocastanum*	1		0
PI255518blb-3mc	*S. bulbocastanum*	2		150
PI255518blb-3mc	*S. bulbocastanum*	3		
PI255518blb-4mc	*S. bulbocastanum*	1	150	
PI255518blb-4mc	*S. bulbocastanum*	2	750	
PI255518blb-4mc	*S. bulbocastanum*	3	450	
PI275181iop-1mc	*S. iopetalum*	1	1000	13100

Supplementary Table 2.2 (Continued)

PI275181iop-1mc	*S. iopetalum*	2	2500	10600
PI275181iop-1mc	*S. iopetalum*	3		16300
PI275181iop-2mc	*S. iopetalum*	1	3950	6600
PI275181iop-2mc	*S. iopetalum*	2	3800	
PI275181iop-2mc	*S. iopetalum*	3		
PI283107hou-5mc	*S. hougasii*	1	300	
PI283107hou-5mc	*S. hougasii*	2		
PI283107hou-5mc	*S. hougasii*	3		
PI283107hou-6mc	*S. hougasii*	1		
PI283107hou-6mc	*S. hougasii*	2		
PI283107hou-6mc	*S. hougasii*	3		
PI283107hou-9mc	*S. hougasii*	1	150	1000
PI283107hou-9mc	*S. hougasii*	2		3150
PI283107hou-9mc	*S. hougasii*	3		
PI498148adr-2mc	*S. andreanum*	1	30300	
PI498148adr-2mc	*S. andreanum*	2	39800	
PI498148adr-2mc	*S. andreanum*	3	102800	
PI545815sph-9mc	*S. stenophyllidium*	1	1750	
PI545815sph-9mc	*S. stenophyllidium*	2	1350	
PI545815sph-9mc	*S. stenophyllidium*	3	1500	
PI558402hou-2mc	*S. hougasii*	1	6800	
PI558402hou-2mc	*S. hougasii*	2		
PI558402hou-2mc	*S. hougasii*	3		
PI558402hou-4mc	*S. hougasii*	1		
PI558402hou-4mc	*S. hougasii*	2		
PI558402hou-4mc	*S. hougasii*	3		
PI558422hou-2mc	*S. hougasii*	1	1600	
PI558422hou-2mc	*S. hougasii*	2	16800	
PI558422hou-2mc	*S. hougasii*	3	1550	
PI653828grr-7mc	*S. guerreroense*	1		
PI653828grr-7mc	*S. guerreroense*	2		
PI653828grr-7mc	*S. guerreroense*	3		
Rutgers	Tomato	1	60200	35200
Rutgers	Tomato	2	29400	10900
Rutgers	Tomato	3	68000	32400
Rutgers	Tomato	4		49000
Vernema	Alfalfa	1	50	300
Vernema	Alfalfa	2	50	1550
Vernema	Alfalfa	3	0	150
Vernema	Alfalfa	4	0	700
Stephens	Wheat	1	1050	
Stephens	Wheat	2	9400	
Stephens	Wheat	3	5000	
Stephens	Wheat	4	7900	
Red Core	Carrot	1	550	

Supplementary Table 2.2 (Continued)

Red Core	Carrot	2	750	
Red Core	Carrot	3	50	
Red Core	Carrot	4	13500	

Supplementary Table 2.3. *Meloidogyne chitwoodi* reproduction data for the second unsuccessful evaluation following the initial screening.

Accession	Species	Rep	WAMCRoza eggs extracted	WAMC1 eggs extracted
PI161726hou-3mc	*S. hougasii*	1	0	
PI161726hou-3mc	*S. hougasii*	2	0	0
PI161726hou-3mc	*S. hougasii*	3	0	
PI239423hou-1mc	*S. hougasii*	1		0
PI239423hou-1mc	*S. hougasii*	2	0	0
PI239423hou-1mc	*S. hougasii*	3		
PI239423hou-2mc	*S. hougasii*	1	0	0
PI239423hou-2mc	*S. hougasii*	2	0	
PI239423hou-2mc	*S. hougasii*	3	0	
PI239423hou-8mc	*S. hougasii*	1	0	300
PI239423hou-8mc	*S. hougasii*	2	0	0
PI239423hou-8mc	*S. hougasii*	3	0	0
PI239423hou-10mc	*S. hougasii*	1	0	0
PI239423hou-10mc	*S. hougasii*	2	0	0
PI239423hou-10mc	*S. hougasii*	3		0
PI239424hou-2mc	*S. hougasii*	1	0	0
PI239424hou-2mc	*S. hougasii*	2		0
PI239424hou-2mc	*S. hougasii*	3		100
PI239424hou-3mc	*S. hougasii*	1	0	0
PI239424hou-3mc	*S. hougasii*	2	100	0
PI239424hou-3mc	*S. hougasii*	3		
PI239424hou-6mc	*S. hougasii*	1	0	0
PI239424hou-6mc	*S. hougasii*	2	0	0
PI239424hou-6mc	*S. hougasii*	3		0
PI239424hou-9mc	*S. hougasii*	1	0	0
PI239424hou-9mc	*S. hougasii*	2	0	0
PI239424hou-9mc	*S. hougasii*	3		0
PI255518blb-1mc	*S. bulbocastanum*	1	800	0
PI255518blb-1mc	*S. bulbocastanum*	2		
PI255518blb-1mc	*S. bulbocastanum*	3	100	
PI255518blb-4mc	*S. bulbocastanum*	1	800	0
PI255518blb-4mc	*S. bulbocastanum*	2	0	
PI255518blb-4mc	*S. bulbocastanum*	3		
PI283107hou-5mc	*S. hougasii*	1	0	0
PI283107hou-5mc	*S. hougasii*	2	0	0
PI283107hou-5mc	*S. hougasii*	3	100	0
PI283107hou-6mc	*S. hougasii*	1	0	400
PI283107hou-6mc	*S. hougasii*	2	0	0
PI283107hou-6mc	*S. hougasii*	3	0	
PI283107hou-9mc	*S. hougasii*	1	0	0
PI283107hou-9mc	*S. hougasii*	2	0	0

Supplementary Table 2.3 (Continued)

PI283107hou-9mc	*S. hougasii*	3	0	0
PI545815sph-9mc	*S. stenophyllidium*	1	0	
PI545815sph-9mc	*S. stenophyllidium*	2		
PI545815sph-9mc	*S. stenophyllidium*	3		
PI558402hou-2mc	*S. hougasii*	1	200	0
PI558402hou-2mc	*S. hougasii*	2	0	100
PI558402hou-2mc	*S. hougasii*	3	0	0
PI558402hou-4mc	*S. hougasii*	1	600	0
PI558402hou-4mc	*S. hougasii*	2	500	200
PI558402hou-4mc	*S. hougasii*	3		200
PI558422hou-2mc	*S. hougasii*	1	300	0
PI558422hou-2mc	*S. hougasii*	2	400	
PI558422hou-2mc	*S. hougasii*	3	0	0
PI652828grr-7mc	*S. guerreroense*	1	600	0
PI652828grr-7mc	*S. guerreroense*	2	3300	1600
PI652828grr-7mc	*S. guerreroense*	3	2000	500
Rutgers	Tomato	1	4300	0
Rutgers	Tomato	2	1400	9400
Rutgers	Tomato	3	1700	7600
Rutgers	Tomato	4	400	11600
Rutgers	Tomato	5	5200	1500
Rutgers	Tomato	6	6800	5600
Rutgers	Tomato	7	2300	10100
Rutgers	Tomato	8	2300	3500
Rutgers	Tomato	9	6100	12900
Rutgers	Tomato	10	1700	4100
Vernema	Alfalfa	1	0	0
Vernema	Alfalfa	2	0	0
Vernema	Alfalfa	3	0	0

Supplementary Table 2.4. *Meloidogyne chitwoodi* reproduction data for the replicated evaluation, for three isolates of *M. chitwoodi*.

Clone	Species	Rep	WAMCRoza eggs extracted	WAMC1 eggs extracted	WAMC27 eggs extracted
PI161726hou-3mc	*S. hougasii*	1	2900	0	750
PI161726hou-3mc	*S. hougasii*	2	1700	0	650
PI161726hou-3mc	*S. hougasii*	3	1450	0	2650
PI161726hou-3mc	*S. hougasii*	4	6000	0	1650
PI161726hou-3mc	*S. hougasii*	5	200	0	0
PI239423hou-1mc	*S. hougasii*	1	200	0	1900
PI239423hou-1mc	*S. hougasii*	2	400	0	550
PI239423hou-1mc	*S. hougasii*	3	200	0	1300
PI239423hou-1mc	*S. hougasii*	4	200	0	2500
PI239423hou-1mc	*S. hougasii*	5	900	0	1850
PI239423hou-2mc	*S. hougasii*	1	1500	400	1250
PI239423hou-2mc	*S. hougasii*	2	750	450	5300
PI239423hou-2mc	*S. hougasii*	3	350	1500	4850
PI239423hou-2mc	*S. hougasii*	4	1850	0	1400
PI239423hou-2mc	*S. hougasii*	5	900	0	3850
PI239423hou-8mc	*S. hougasii*	1	0	0	750
PI239423hou-8mc	*S. hougasii*	2	0	0	1000
PI239423hou-8mc	*S. hougasii*	3	0	0	1600
PI239423hou-8mc	*S. hougasii*	4	0	0	1600
PI239423hou-8mc	*S. hougasii*	5	0	0	2350
PI239423hou-10mc	*S. hougasii*	1	0	0	3500
PI239423hou-10mc	*S. hougasii*	2	0	50	3000
PI239423hou-10mc	*S. hougasii*	3	0	0	1750
PI239423hou-10mc	*S. hougasii*	4	0	0	700
PI239423hou-10mc	*S. hougasii*	5	Missing	0	2150
PI239424hou-2mc	*S. hougasii*	1	0	0	0
PI239424hou-2mc	*S. hougasii*	2	0	0	150
PI239424hou-2mc	*S. hougasii*	3	0	0	0
PI239424hou-2mc	*S. hougasii*	4	0	0	0
PI239424hou-2mc	*S. hougasii*	5	0	0	300
PI239424hou-3mc	*S. hougasii*	1	0	150	2100
PI239424hou-3mc	*S. hougasii*	2	0	100	950
PI239424hou-3mc	*S. hougasii*	3	0	0	400
PI239424hou-3mc	*S. hougasii*	4	50	0	1350
PI239424hou-3mc	*S. hougasii*	5	0	0	300
PI239424hou-6mc	*S. hougasii*	1	0	0	100
PI239424hou-6mc	*S. hougasii*	2	50	0	0
PI239424hou-6mc	*S. hougasii*	3	0	50	50
PI239424hou-6mc	*S. hougasii*	4	0	50	450
PI239424hou-6mc	*S. hougasii*	5	0	0	150
PI239424hou-9mc	*S. hougasii*	1	0	0	1950
PI239424hou-9mc	*S. hougasii*	2	0	0	1400
PI239424hou-9mc	*S. hougasii*	3	0	0	1400

Supplementary Table 2.4 (Continued)

PI239424hou-9mc	*S. hougasii*	4	0	0	5700
PI239424hou-9mc	*S. hougasii*	5	0	0	550
PI255518blb-4mc	*S. bulbocastanum*	1	18200	0	200
PI255518blb-4mc	*S. bulbocastanum*	2	250	0	0
PI255518blb-4mc	*S. bulbocastanum*	3	850	0	0
PI255518blb-4mc	*S. bulbocastanum*	4	Missing	Missing	100
PI255518blb-4mc	*S. bulbocastanum*	5	Missing	Missing	Missing
PI283107hou-5mc	*S. hougasii*	1	0	0	200
PI283107hou-5mc	*S. hougasii*	2	0	0	700
PI283107hou-5mc	*S. hougasii*	3	0	0	200
PI283107hou-5mc	*S. hougasii*	4	0	0	800
PI283107hou-5mc	*S. hougasii*	5	0	0	100
PI283107hou-6mc	*S. hougasii*	1	400	850	200
PI283107hou-6mc	*S. hougasii*	2	550	300	3500
PI283107hou-6mc	*S. hougasii*	3	150	750	600
PI283107hou-6mc	*S. hougasii*	4	450	4700	4250
PI283107hou-6mc	*S. hougasii*	5	2700	700	6250
PI283107hou-9mc	*S. hougasii*	1	0	0	800
PI283107hou-9mc	*S. hougasii*	2	50	50	350
PI283107hou-9mc	*S. hougasii*	3	0	0	250
PI283107hou-9mc	*S. hougasii*	4	0	0	500
PI283107hou-9mc	*S. hougasii*	5	0	0	Missing
PI545815sph-9mc	*S. stenophyllidium*	1	0	0	950
PI545815sph-9mc	*S. stenophyllidium*	2	1250	Missing	3050
PI545815sph-9mc	*S. stenophyllidium*	3	100	Missing	2200
PI545815sph-9mc	*S. stenophyllidium*	4	Missing	Missing	Missing
PI545815sph-9mc	*S. stenophyllidium*	5	Missing	Missing	Missing
PI558402hou-2mc	*S. hougasii*	1	1900	50	1300
PI558402hou-2mc	*S. hougasii*	2	300	0	1550
PI558402hou-2mc	*S. hougasii*	3	1800	0	1050
PI558402hou-2mc	*S. hougasii*	4	250	100	600
PI558402hou-2mc	*S. hougasii*	5	2350	0	200
PI558402hou-4mc	*S. hougasii*	1	2450	250	1450
PI558402hou-4mc	*S. hougasii*	2	3200	250	600
PI558402hou-4mc	*S. hougasii*	3	100	150	150
PI558402hou-4mc	*S. hougasii*	4	100	0	150
PI558402hou-4mc	*S. hougasii*	5	2300	0	1750
PI558422hou-2mc	*S. hougasii*	1	8400	0	850
PI558422hou-2mc	*S. hougasii*	2	1300	0	650
PI558422hou-2mc	*S. hougasii*	3	6700	1750	50
PI558422hou-2mc	*S. hougasii*	4	4050	200	Missing
PI558422hou-2mc	*S. hougasii*	5	950	Missing	2900
Rutgers	Tomato	1	136800	87200	40400
Rutgers	Tomato	2	150400	85600	37600
Rutgers	Tomato	3	264000	59600	46000
Rutgers	Tomato	4	76000	28000	13000
Rutgers	Tomato	5	50800	49600	58000
Rutgers	Tomato	6	37200	67200	10000

Supplementary Table 2.4 (Continued)

Rutgers	Tomato	7	138000	22400	42000
Rutgers	Tomato	8	104000	Missing	Missing
Vernema	Alfalfa	1	0	0	0
Vernema	Alfalfa	2	0	0	0
Vernema	Alfalfa	3	0	0	950
Vernema	Alfalfa	4	0	0	1500
Vernema	Alfalfa	5	2400	0	13600
Red Core	Carrot	1	2200	2050	0
Red Core	Carrot	2	50	200	0
Red Core	Carrot	3	1750	50	0
Red Core	Carrot	4	1850	2300	0
Red Core	Carrot	5	300	0	0

Supplementary Table 2.5. *Meloidogyne chitwoodi* reproduction data for the final characterization of resistant accessions.

Accession	Clone Number	Total eggs extracted
PI161726	11	100
PI161726	14	150
PI161726	16	400
PI161726	17	0
PI161726	18	250
PI161726	19	2150
PI161726	20	750
PI161726	21	0
PI161726	22	3150
PI161726	23	550
PI161726	24	0
PI161726	25	50
PI161726	27	0
PI161726	29	100
PI161726	32	0
PI161726	33	0
PI161726	34	0
PI239423	13	150
PI239423	14	350
PI239423	17	50
PI239423	19	300
PI239423	22	450
PI239423	25	0
PI239423	27	0
PI239423	28	0
PI239423	30	0
PI239423	32	0
PI239423	33	1500
PI239423	35	0
PI239423	36	50
PI239423	38	0
PI239423	39	0
PI239424	11	50
PI239424	12	300
PI239424	13	150
PI239424	16	0
PI239424	17	0
PI239424	18	0
PI239424	19	0
PI239424	20	0
PI239424	21	50
PI239424	24	100
PI239424	26	300
PI239424	27	0

Supplementary Table 2.5 (Continued)

PI239424	28	0
PI239424	29	0
PI239424	31	0
PI239424	32	550
PI239424	33	0
PI239424	34	0
PI239424	35	0
PI239424	36	50
PI239424	39	0
PI255518	12	400
PI255518	13	250
PI255518	14	300
PI255518	15	900
PI255518	16	200
PI255518	17	0
PI255518	18	2100
PI255518	20	1150
PI255518	22	0
PI255518	23	1050
PI255518	24	250
PI255518	25	150
PI255518	27	150
PI283107	11	0
PI283107	12	600
PI283107	14	0
PI283107	15	0
PI283107	17	0
PI283107	19	550
PI283107	20	2350
PI283107	21	2300
PI283107	24	0
PI283107	25	0
PI283107	26	50
PI283107	27	0
PI283107	30	0
PI283107	33	0
PI283107	34	1600
PI283107	35	700
PI283107	37	150
PI283107	38	0
PI283107	39	50
PI283107	40	50
PI545815	11	0
PI545815	13	18200
PI545815	16	17000
PI545815	18	800
PI545815	19	1800
PI545815	22	2650

Supplementary Table 2.5 (Continued)

PI545815	28	1450
PI558402	13	300
PI558402	14	200
PI558402	15	100
PI558402	17	5400
PI558402	18	1050
PI558402	19	1300
PI558402	20	1000
PI558402	21	100
PI558402	26	50
PI558402	29	900
PI558402	30	0
PI558402	32	0
PI558402	33	50
PI558402	35	0
PI558402	40	250
PI558422	11	150
PI558422	14	1150
PI558422	15	0
PI558422	16	150
PI558422	18	400
PI558422	19	1550
PI558422	20	700
PI558422	21	0
PI558422	22	100
PI558422	26	50
PI558422	29	0
PI558422	34	850

Supplementary Table 2.6. Collection locations and *Meloidogyne chitwoodi* resistance status for accessions used to make Figure 2.2.

Accession	Species	Ploidy	Latitude	Longitude	Host status
PI161173	*S. verrucosum*	2	19.28	-101.36	Susceptible
PI161174	*S. hougasii*	6	19.4	-101.6	Susceptible
PI161686	*S. demissum*	6	19.37	-98.07	Susceptible
PI161726	*S. hougasii*	6	19.55	-103.63	Resistant
PI161727	*S. hougasii*	6	19.55	-103.63	Susceptible
PI161730	*S. guerreroense*	6	17.55	-99.5	Susceptible
PI186560	*S. hjertingii*	4	25.25	-100.51	Susceptible
PI210034	*S. boliviense*	2	-19.55	-65.4	Susceptible
PI210043	*S. candolleanum*	2	-11.27	-75.58	Susceptible
PI230459	*S. iopetalum*	6	19.34	-100.22	Susceptible
PI239423	*S. hougasii*	6	19.47	-102.25	Resistant
PI243344	*S. iopetalum*	6	20.2	-98.25	Susceptible
PI243350	*S. agrimonifolium*	4	15.3	-90.57	Susceptible
PI243505	*S. bulbocastanum*	2	19.35	-99.2	Resistant
PI243508	*S. bulbocastanum*	2	19.22	-98.8	Resistant
PI243512	*S. bulbocastanum*	2	18.97	-98.9	Susceptible
PI247322	*S. colombianum*	4	2.21	-76.2	Susceptible
PI251063	*S. stoloniferum*	4	25.25	-101	Susceptible
PI251721	*S. iopetalum*	6	19.33	-103.38	Susceptible
PI255518	*S. bulbocastanum*	2	19.7	-103.47	Resistant
PI265861	*S. boliviense*	2	-19.13	-64.9	Susceptible
PI265863	*S. candolleanum*	2	-15.5	-70.02	Susceptible
PI265865	*S. candolleanum*	2	-17.37	-67.15	Susceptible
PI275162	*S. stoloniferum*	4	31.54	-109.16	Resistant
PI275165	*S. stoloniferum*	4	31.26	-110.19	Resistant
PI275181	*S. iopetalum*	6	20.25	-98.22	Susceptible
PI275182	*S. iopetalum*	6	20.25	-98.22	Susceptible
PI275183	*S. iopetalum*	6	16.2833	-96.55	Susceptible
PI275184	*S. bulbocastanum*	2	19.35	-99.2	Resistant
PI275187	*S. bulbocastanum*	2	19.83	-101.72	Resistant
PI275194	*S. bulbocastanum*	2	17.02	-96.46	Resistant
PI275196	*S. bulbocastanum*	2	17.5	-96.45	Susceptible
PI275198	*S. bulbocastanum*	2	19.43	-99.47	Susceptible
PI275199	*S. bulbocastanum*	2	19.29	-98.54	Susceptible
PI283076	*S. gandarillasii*	2	-18.4	-65.1	Susceptible
PI283089	*S. boliviense*	2	-26.33	-66.3	Susceptible
PI283107	*S. hougasii*	6	19.4	-101.6	Resistant
PI310927	*S. berthaultii*	2	-17.4	-66.15	Susceptible
PI310928	*S. boliviense*	2	-19.0333	-65.2833	Susceptible
PI320265	*S. stenophyllidium*	2	29.1333	-106.0833	Susceptible
PI320269	*S. commersonii*	2	-28.23	-53.55	Susceptible
PI320343	*S. stoloniferum*	4	19.42	-101.07	Susceptible

Supplementary Table 2.6 (Continued)

PI338615	*S. mochiquense*	2	-11.21	-77.23	Susceptible
PI347757	*S. bulbocastanum*	2	19.5167	-100.25	Susceptible
PI442697	*S. candolleanum*	2	-13.39	-73.28	Susceptible
PI472874	*S. infundibuliforme*	2	-23.08	-65.06	Susceptible
PI472995	*S. brevicaule*	2	-22.43	-65.12	Susceptible
PI473011	*S. brevicaule*	2	-23.47	-65.33	Susceptible
PI473061	*S. brevicaule*	2	-24.19	-66.06	Susceptible
PI473067	*S. brevicaule*	2	-24.45	-65.44	Susceptible
PI473124	*S. boliviense*	2	-22.27	-66.11	Susceptible
PI473201	*S. neorossii*	2	-22.15	-65.02	Susceptible
PI473220	*S. berthaultii*	2	-25.11	-65.48	Susceptible
PI473351	*S. lignicaule*	2	-13.26	-71.51	Susceptible
PI473361	*S. boliviense*	2	-16.3695	-69.2214	Susceptible
PI473504	*S. brevicaule*	2	-17.7167	-66.2333	Susceptible
PI473509	*S. acaule*	4	-26.47	-65.45	Susceptible
PI497997	*S. stoloniferum*	4	28.2333	-107.45	Susceptible
PI498000	*S. stoloniferum*	4	25.4167	-106.15	Susceptible
PI498011	*S. bulbocastanum*	2	17.0333	-96.7667	Susceptible
PI498022	*S. iopetalum*	6	20.4833	-99.2333	Susceptible
PI498024	*S. iopetalum*	6	16.35	-96.6	Susceptible
PI498075	*S. berthaultii*	2	-19.32	-65.16	Susceptible
PI498093	*S. brevicaule*	2	-18.6333	-64.15	Susceptible
PI498109	*S. berthaultii*	2	-17.34	-66.23	Susceptible
PI498114	*S. brevicaule*	2	-17.19	-66.22	Susceptible
PI498136	*S. candolleanum*	2	-17.23	-66.1	Susceptible
PI498148	*S. andreanum*	2	1.2167	-77.2833	Susceptible
PI498224	*S. bulbocastanum*	2	19.4	-100.35	Susceptible
PI498238	*S. stoloniferum*	4	29.2	-108.1167	Susceptible
PI498249	*S. iopetalum*	6	17.0135	-97.7659	Susceptible
PI498250	*S. schenckii*	6	16.17	-97.41	Susceptible
PI498357	*S. kurtzianum*	2	-27.43	-66.55	Susceptible
PI545771	*S. iopetalum*	6	19.0333	-99.8833	Susceptible
PI545815	*S. stenophyllidium*	2	21.95	-102.5833	Resistant
PI545912	*S. brevicaule*	2	-17.7167	-65.1	Susceptible
PI558396	*S. stoloniferum*	4	23.5333	-109.9833	Susceptible
PI558402	*S. hougasii*	6	19.5667	-103.5833	Resistant
PI558405	*S. iopetalum*	6	19.4167	-102.5333	Susceptible
PI558417	*S. iopetalum*	6	19.3833	-100.3	Susceptible
PI558422	*S. hougasii*	6	19.3167	-103.2833	Resistant
PI558484	*S. stoloniferum*	4	20.8	-103.85	Susceptible
PI564025	*S. stoloniferum*	4	31.4333	-110.3167	Susceptible
PI564037	*S. stoloniferum*	4	32.9833	-105.7	Susceptible
PI564039	*S. stoloniferum*	4	33.3833	-108.7667	Susceptible
PI564041	*S. stoloniferum*	4	33.8	-108.4667	Susceptible
PI595781	*S. stoloniferum*	4	30.7058	-104.1053	Susceptible

Supplementary Table 2.6 (Continued)

PI597682	*S. iopetalum*	6	19.0507	-99.3088	Susceptible
PI607859	*S. iopetalum*	6	16.1161	-96.4767	Susceptible
PI632334	*S. stoloniferum*	4	31.9181	-109.2736	Susceptible
PI643997	*S. stoloniferum*	4	32.2033	-110.5331	Susceptible
VSA 182	*S. stipuloideum*	2	-17.03	-67.18	Susceptible
VSAH 185	*S. tuberosum*	4	-18.2	-67.36	Susceptible
VSLC 138	*S. boliviense*	2	-17.4	-66.32	Susceptible
VSOA 86	*S. candolleanum*	2	-15.37	-68.56	Susceptible
EBS 2942	*S. stoloniferum*	4	19.42	-101.07	Susceptible
HAM 9	*S. brevicaule*	2	-18.14	-66.29	Susceptible
HAM 65	*S. brevicaule*	2	-19.13	-65.5	Susceptible
HAM 72	*S. boliviense*	2	-19.32	-65.43	Susceptible
HAM 102	*S. brevicaule*	2	-19.27	-65.49	Susceptible
HAM 126	*S. chacoense*	2	-19.18	-64.27	Susceptible
HAM 188	*S. acaule*	4	-21.38	-65.03	Susceptible
HAM 209	*S. boliviense*	2	-19.38	-65.17	Susceptible
HHA 6523	*S. brevicaule*	2	-18.42	-64.12	Susceptible
HHLs 1287 x 1471	*S. stenophyllidium*	2	24.02	-104.4	Resistant
HHLs 1475 x 1473	*S. stoloniferum*	4	22.47	-102.35	Susceptible
OKA 4917	*S. brevicaule*	2	-25.1	-65.52	Susceptible

Supplementary Table 3.1. Plant health score at weeks 1-11 of the replicated experiment in chapter 3 for plants inoculated with isolates “11-11” or “653” of *V. dahliae*, or left uninoculated as a control. Plants were given a 0-5 score, where “5” indicated a healthy plant, and “0” indicated a dead plant.

Entry	Clone	Treatment	Rep	Week 1 score	Week 2 score	Week 3 score	Week 4 score	Week 5 score	Week 6 score	Week 7 score	Week 8 score	Week 9 score	Week 10 score	Week 11 score
1	PI239423hou-3v	1- 11-11	C	3.5	3	2	2	0	0	0	0	0	0	0
2	PI275181iop-1v	2- 653	C	5	5	5	5	4.5	4.5	4	4.5	4	2	0
3	PI239423hou-3v	3- Control	A	4	3	3.5	2	2	0	0	0	0	0	0
4	PI239423hou-3v	3- Control	B	4	3	1.5	0	2	0	0	0	0	0	0
5	PI498148adr-2v	1- 11-11	D	4.5	5	4	4.5	5	5	5	5	5	4.5	4.5
6	PI498011blb-1v	3- Control	B	5	4.5	3.5	3.5	4	3	4	3.5	3.5	3.5	4
7	PI283107hou-1v	1- 11-11	D	5	4.5	4.5	5	5	4	5	2.5	1	1.5	1.5
8	PI498148adr-2v	2- 653	D	5	5	5	5	5	4.5	5	5	5	5	5
9	PI498148adr-1v	2- 653	A	5	5	4.5	5	5	4.5	3.5	4	4.5	4.5	0
10	PI275182iop-4v	1- 11-11	D	5	2.5	4	4	4	3.5	3	0	0	0	0
11	PI275181iop-1v	1- 11-11	D	5	4.5	4	4	4.5	4.5	4	5	4	4	3
12	PI275182iop-1v	2- 653	C	5	4.5	4.5	5	4.5	4	4	0	0	0	0
13	PI239423hou-3v	2- 653	C	4	2.5	2	2	0	0	0	0	0	0	0
14	PI275181iop-1v	3- Control	A	5	5	4.5	4.5	5	4.5	5	5	5	4.5	4
15	PI275181iop-1v	3- Control	B	5	5	4.5	4.5	4	4	4	4	4	4	3
16	Ranger Russet	3- Control	C	5	5	4.5	4.5	5	4.5	4.5	4	4	4	3.5
17	PI283107hou-1v	3- Control	C	4.5	5	5	4.5	5	4	5	4.5	5	4	3
18	PI498011blb-1v	1- 11-11	D	5	4	4	4	4.5	4	4.5	5	4.5	4.5	4
19	PI498011blb-1v	1- 11-11	B	5	4.5	3	3	5	4.5	5	5	4.5	4	2
20	PI498148adr-1v	2- 653	D	5	5	5	5	5	4.5	5	5	5	5	5
21	PI498148adr-2v	3- Control	C	5	5	5	5	5	4.5	4.5	3.5	4.5	5	4.5
22	PI275181iop-1v	1- 11-11	B	4.5	4.5	4	4	4.5	4	1	0	0	0	0

Supplementary Table 3.1 (Continued)

23	PI275182iop-4v	1- 11-11	C	5	2.5	3.5	3.5	3	3.5	0	0	0	0	0
24	Ranger Russet	1- 11-11	C	5	5	4.5	4.5	4.5	4.5	3.5	0	0	0	0
25	PI275181iop-1v	3- Control	D	5	4	4	4	4.5	4.5	4.5	4.5	4.5	4.5	4
26	PI498011blb-1v	2- 653	B	5	4	3	3	4	3.5	4	4.5	4	4	3.5
27	PI283107hou-1v	2- 653	C	5	5	4.5	5	5	3	4.5	5	3.5	1.5	0
28	PI498011blb-1v	3- Control	D	5	5	3.5	3	4.5	4	4.5	4	3.5	3.5	3.5
29	PI275182iop-1v	3- Control	D	5	5	4.5	4.5	4	4	4	4	4.5	5	4
30	PI275181iop-1v	2- 653	B	5	5	5	5	4.5	4.5	4.5	5	4.5	2	0
31	Russet Norkota	2- 653	B	5	5	4.5	4	4	3.5	3.5	0	0	0	0
32	Ranger Russet	3- Control	D	5	5	5	5	5	5	4.5	4.5	3	4	4
33	PI275182iop-4v	1- 11-11	A	5	4.5	4.5	4	2.5	0	0	0	0	0	0
34	PI239423hou-3v	2- 653	D	3	2	2.5	3	2	0	0	0	0	0	0
35	PI275182iop-1v	1- 11-11	C	5	5	4.5	4.5	3	0	0	0	0	0	0
36	PI498011blb-1v	2- 653	A	5	3.5	4	3.5	3	3	3	4.5	0	0	0
37	PI239423hou-3v	3- Control	D	4	2.5	2	2	2	0	0	0	0	0	0
38	PI283107hou-1v	3- Control	D	5	5	5	5	3.5	4.5	4	4.5	3	3	4
39	PI275182iop-4v	3- Control	D	5	4.5	4.5	4.5	2.5	4	3	3.5	4	4.5	4
40	Ranger Russet	3- Control	B	5	5	4.5	4.5	4	4.5	4	4	3	4	4
41	PI498148adr-1v	1- 11-11	D	5	5	5	5	4	4	4.5	4.5	4	5	4.5
42	PI275182iop-1v	1- 11-11	A	5	5	4.5	5	4.5	4.5	1	0	0	0	0
43	PI275182iop-1v	2- 653	A	5	4.5	5	5	4.5	5	5	5	3.5	0	0
44	PI275182iop-4v	2- 653	A	5	4	4.5	4	3	3	3	3	2	0	0
45	PI498148adr-1v	3- Control	A	5	5	4.5	5	4.5	4.5	4.5	3.5	4.5	5	4.5
46	PI239423hou-3v	2- 653	A	3.5	2.5	1.5	2	0	0	0	0	0	0	0
47	PI275182iop-1v	3- Control	A	5	4.5	5	4	3	4	3	3.5	4.5	5	5
48	Russet Norkota	2- 653	D	4.5	5	4.5	4.5	3	0	0	0	0	0	0

Supplementary Table 3.1 (Continued)

49	PI498011blb-1v	3- Control	A	4.5	5	5	4.5	4.5	4.5	4.5	4.5	4	5	5
50	Ranger Russet	1- 11-11	B	5	4.5	5	5	4.5	4.5	3	4.5	2	0	0
51	PI275182iop-4v	2- 653	C	5	3.5	4	3.5	2.5	4	3	3.5	3.5	3.5	1.5
52	Ranger Russet	2- 653	D	5	4.5	4	4.5	4.5	4.5	4	3	0	0	0
53	Russet Norkota	3- Control	A	5	5	4	4	3	3.5	2.5	0	0	0	0
54	PI275182iop-1v	1- 11-11	D	5	4.5	5	4.5	4.5	4.5	4	4	3.5	0	0
55	PI498148adr-2v	1- 11-11	B	5	5	4.5	5	4.5	4.5	4	4.5	4.5	5	4
56	PI498148adr-2v	2- 653	C	5	5	5	5	4.5	4.5	4.5	5	5	5	5
57	Ranger Russet	1- 11-11	D	5	5	4.5	4.5	4.5	4	4	4	3	4	3
58	PI498011blb-1v	2- 653	C	4.5	4	4.5	4	4.5	4.5	5	5	5	5	5
59	PI275181iop-1v	1- 11-11	A	5	3.5	4	4	3.5	4.5	3	5	3	0	0
60	PI498148adr-1v	1- 11-11	B	5	4	3	3.5	3	4.5	4	5	4.5	3	3
61	PI283107hou-1v	2- 653	D	5	5	4	3	3.5	4.5	3	5	4	1	0
62	PI498148adr-1v	1- 11-11	A	5	5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	5	4.5
63	PI275182iop-1v	3- Control	B	5	5	5	5	4.5	4.5	4	4	4	5	4
64	Ranger Russet	2- 653	A	5	5	4.5	4.5	4	4	4	4	3.5	3.5	3
65	PI275182iop-4v	2- 653	B	5	4.5	4.5	4	3	4	3	3	3	3.5	3
66	PI275181iop-1v	1- 11-11	C	5	4	4.5	4	4	4	4	3	3.5	0	0
67	PI498148adr-2v	3- Control	A	5	5	4.5	4.5	4.5	4	4.5	4.5	4.5	5	4.5
68	Ranger Russet	2- 653	C	4.5	4.5	4	4.5	3.5	4.5	4.5	5	5	5	4
69	PI275182iop-1v	2- 653	D	5	5	4.5	4.5	4	3.5	5	5	3.5	0	0
70	PI275181iop-1v	2- 653	D	5	5	5	5	5	5	5	5	4.5	4.5	4
71	PI239423hou-3v	3- Control	C	2.5	0	0	0	0	0	0	0	0	0	0
72	PI275182iop-4v	1- 11-11	B	5	4	3.5	4	2.5	0	0	0	0	0	0
73	PI283107hou-1v	3- Control	A	5	4.5	4.5	5	4	5	5	5	5	4	4
74	PI275182iop-1v	2- 653	B	5	5	4.5	5	5	5	4.5	4	4.5	5	4.5

Supplementary Table 3.1 (Continued)

75	PI275182iop-4v	2- 653	D	5	4.5	4.5	4	3.5	4.5	3	3	2	2	0
76	PI239423hou-3v	2- 653	B	3.5	2	2	2	0	0	0	0	0	0	0
77	PI498148adr-1v	3- Control	D	5	5	4.5	4.5	4.5	5	5	5	4.5	4.5	4.5
78	Russet Norkota	1- 11-11	B	5	4	4	4	3.5	3.5	3	0	0	0	0
79	PI275182iop-4v	3- Control	B	5	4.5	3.5	4	4	3.5	3.5	3	2.5	3	3
80	PI498011blb-1v	3- Control	C	5	5	3.5	3	3	3.5	3.5	3.5	4	3.5	3.5
81	PI275181iop-1v	3- Control	C	5	4.5	4.5	4	4	4.5	5	4	4	4.5	4
82	PI498148adr-1v	2- 653	C	5	4.5	4.5	4.5	5	4.5	4.5	5	4.5	5	5
83	PI498148adr-2v	3- Control	B	5	4.5	5	5	5	4.5	4.5	5	4.5	4.5	4.5
84	PI283107hou-1v	1- 11-11	C	5	4.5	5	4.5	5	4	4	0	0	0	0
85	PI498011blb-1v	1- 11-11	C	5	4	3	3	2	5	5	5	5	5	5
86	PI498148adr-2v	1- 11-11	A	5	5	5	5	5	4.5	5	5	5	5	4.5
87	PI498148adr-1v	3- Control	B	5	5	5	5	5	4.5	5	5	4.5	5	4.5
88	PI498148adr-2v	3- Control	D	5	5	5	4	4.5	4.5	4.5	5	4	4.5	4.5
89	PI498148adr-1v	1- 11-11	C	5	4.5	4.5	4.5	4.5	4.5	4.5	4	4	4	4
90	Ranger Russet	1- 11-11	A	4.5	4.5	4	4.5	4.5	3.5	3.5	4	3	3	4
91	PI283107hou-1v	2- 653	B	5	5	4.5	3	4.5	5	4.5	4	4	4	4
92	PI498148adr-2v	2- 653	A	5	4.5	5	5	5	5	5	5	5	5	5
93	Russet Norkota	1- 11-11	C	5	5	5	4.5	3.5	3.5	2.5	2.5	0	0	0
94	PI239423hou-3v	1- 11-11	D	2.5	2	2	2	2	0	0	0	0	0	0
95	PI275181iop-1v	2- 653	A	5	5	4.5	4	4	4.5	5	4.5	4.5	0	0
96	Ranger Russet	2- 653	B	5	5	4.5	5	4.5	4.5	4.5	4.5	4	4	4
97	Russet Norkota	1- 11-11	D	4.5	4.5	5	4	3.5	3	3	0	0	0	0
98	Russet Norkota	3- Control	D	4.5	4.5	4.5	4.5	4.5	4.5	4.5	5	5	5	4
99	PI498148adr-1v	2- 653	B	5	4.5	4.5	5	4.5	4.5	5	5	4.5	5	5
100	PI283107hou-1v	1- 11-11	A	5	5	3.5	3	4	3.5	4	4.5	4.5	4	3.5

Supplementary Table 3.1 (Continued)

101	PI498011blb-1v	1- 11-11	A	5	5	3.5	3.5	3	3.5	3.5	4	2.5	1	1
102	PI283107hou-1v	2- 653	A	5	5	5	4.5	4.5	4	5	4	4.5	4	3
103	PI239423hou-3v	1- 11-11	B	3	2	0	0	0	0	0	0	0	0	0
104	Russet Norkota	2- 653	C	5	4.5	4.5	5	5	5	4.5	4.5	3.5	0	0
105	Russet Norkota	1- 11-11	A	4.5	5	4	4.5	3	2	2	0	0	0	0
106	Ranger Russet	3- Control	A	5	5	4.5	4.5	4.5	4.5	4.5	4.5	3	3	3
107	Russet Norkota	3- Control	C	4.5	4	4	3.5	3.5	3.5	3.5	4	3.5	3	3
108	PI275182iop-4v	3- Control	C	5	4.5	4.5	4	3	4	3	4	3	3	4
109	PI283107hou-1v	3- Control	B	5	5	5	5	4.5	5	5	5	4	3.5	4.5
110	PI498148adr-1v	3- Control	C	5	5	5	5	5	5	4.5	4.5	4.5	4	5
111	PI498011blb-1v	2- 653	D	5	4.5	3	3	3	3.5	3.5	3	2.5	2	1
112	PI275182iop-1v	3- Control	C	5	5	5	4.5	4.5	4	4	4	4.5	4	4.5
113	PI275182iop-4v	3- Control	A	5	5	3.5	4	4	4	4	4	4	3.5	3
114	Russet Norkota	3- Control	B	5	4	4.5	5	4	3.5	3	3.5	3.5	2.5	2.5
115	PI239423hou-3v	1- 11-11	A	2	0	0	0	0	0	0	0	0	0	0
116	PI283107hou-1v	1- 11-11	B	5	5	3.5	4.5	4.5	4.5	4	4.5	4.5	3.5	1.5
117	PI498148adr-2v	1- 11-11	C	5	5	4.5	5	5	4.5	4.5	5	4.5	5	4.5
118	Russet Norkota	2- 653	A	4	4.5	4	4	4	4.5	4	4	4	4	4.5
119	PI498148adr-2v	2- 653	B	5	5	4.5	5	4	4.5	4.5	4.5	4	5	5
120	PI275182iop-1v	1- 11-11	B	5	5	4	4	4.5	4	3.5	4.5	4.5	0	0

Supplementary Table 3.2. Results of *V. dahliae* culturing and qPCR, when analyses were conducted. *Verticillium dahliae* cultures were rated on a 1-5 scale, where lower values indicated higher *V. dahliae* stem colonization. Results of qPCR evaluation are expressed in CT values, where lower values indicate that *V. dahliae* and housekeeping sequences were detected during earlier stages of qPCR. For qPCR, each sample was evaluated in triplicate for both *V. dahliae* and housekeeping primer sequences.

Entry	Clone	Treatment	Replicate	*V. dahliae* Culture Rating	*V. dahliae* CT rep 1	*V. dahliae* CT rep 2	*V. dahliae* CT rep 3	Housekeeping CT rep 1	Housekeeping CT rep 2	Housekeeping CT rep 3
1	PI239423hou-3v	1- 11-11	C							
2	PI275181iop-1v	2- 653	C		30.6	31.1	32.5	33.7	36.0	38.3
3	PI239423hou-3v	3- Control	A							
4	PI239423hou-3v	3- Control	B							
5	PI498148adr-2v	1- 11-11	D	*1*	31.8	32.5	33.5	38.7	40.0	32.3
6	PI498011blb-1v	3- Control	B	*5*	35.3	40.0	40.0	39.8	40.0	40.0
7	PI283107hou-1v	1- 11-11	D		24.0	24.6	24.9	30.8	30.1	29.8
8	PI498148adr-2v	2- 653	D	*5*	33.1	36.0	34.0	30.8	30.4	30.6
9	PI498148adr-1v	2- 653	A	*1*	30.7	31.2	31.4	28.5	28.9	40.0
10	PI275182iop-4v	1- 11-11	D		27.0	27.1	26.7	29.7	27.6	27.2
11	PI275181iop-1v	1- 11-11	D	*3*	34.8	40.0	40.0	29.7	28.7	30.7
12	PI275182iop-1v	2- 653	C		27.5	27.6	28.1	30.3	28.5	30.8
13	PI239423hou-3v	2- 653	C							
14	PI275181iop-1v	3- Control	A	*5*	40.0	35.2	36.8	31.7	29.8	27.9
15	PI275181iop-1v	3- Control	B	*5*	40.0	40.0	34.6	30.5	30.0	29.3
16	Ranger Russet	3- Control	C	*5*						
17	PI283107hou-1v	3- Control	C	*5*	31.9	32.1	32.3	27.5	27.6	26.9
18	PI498011blb-1v	1- 11-11	D	*4*	34.3	35.8	35.6	40.0	40.0	40.0
19	PI498011blb-1v	1- 11-11	B	*1*	31.7	33.5	35.9	40.0	40.0	38.0
20	PI498148adr-1v	2- 653	D	*5*	35.6	34.8	35.4	29.5	27.7	28.2
21	PI498148adr-2v	3- Control	C	*5*	31.6	33.7	33.8	28.5	28.3	28.1
22	PI275181iop-1v	1- 11-11	B		25.9	26.7	26.9	30.6	29.9	30.4
23	PI275182iop-4v	1- 11-11	C		34.6	33.7	33.5	28.2	27.7	34.9
24	Ranger Russet	1- 11-11	C		21.4	21.8	21.3	29.5	29.4	29.5

Supplementary Table 3.2 (Continued)

25	PI275181iop-1v	3- Control	D	*5*	34.7	34.8	35.8	29.2	27.5	27.9
26	PI498011blb-1v	2- 653	B	*5*	40.0	40.0	40.0	37.5	36.2	34.9
27	PI283107hou-1v	2- 653	C		29.2	28.7	29.5	30.3	29.2	27.5
28	PI498011blb-1v	3- Control	D	*5*						
29	PI275182iop-1v	3- Control	D	*5*	40.0	40.0	37.3	28.6	28.3	28.6
30	PI275181iop-1v	2- 653	B		37.0	32.2	33.7	30.5	31.6	30.8
31	Russet Norkota	2- 653	B		24.2	24.4	24.5	35.6	36.0	34.6
32	Ranger Russet	3- Control	D	*5*	33.0	33.2	35.3	27.1	28.1	27.0
33	PI275182iop-4v	1- 11-11	A		26.3	26.6	26.7	28.8	27.8	27.7
34	PI239423hou-3v	2- 653	D							
35	PI275182iop-1v	1- 11-11	C		27.1	28.3	27.7	28.0	28.5	28.0
36	PI498011blb-1v	2- 653	A		22.7	24.2	24.7	37.0	36.5	38.1
37	PI239423hou-3v	3- Control	D							
38	PI283107hou-1v	3- Control	D	*5*	36.7	36.4	35.9	28.8	29.7	31.1
39	PI275182iop-4v	3- Control	D	*5*	33.3	35.3	40.0	28.3	28.3	28.3
40	Ranger Russet	3- Control	B	*5*	40.0	40.0	40.0	26.8	26.3	26.2
41	PI498148adr-1v	1- 11-11	D	*5*	34.3	40.0	34.0	28.7	28.3	28.8
42	PI275182iop-1v	1- 11-11	A							
43	PI275182iop-1v	2- 653	A		32.7	33.1	34.6	32.9	31.6	30.8
44	PI275182iop-4v	2- 653	A		26.9	28.5	28.3	26.8	26.4	26.7
45	PI498148adr-1v	3- Control	A	*5*	33.6	32.7	34.7	27.5	27.9	27.5
46	PI239423hou-3v	2- 653	A							
47	PI275182iop-1v	3- Control	A	*5*	40.0	40.0	40.0	29.3	28.5	28.8
48	Russet Norkota	2- 653	D		24.8	25.8	26.1	32.4	32.6	32.9
49	PI498011blb-1v	3- Control	A	*5*	36.6	40.0	34.7	40.0	38.1	36.2
50	Ranger Russet	1- 11-11	B		29.6	31.0	30.9	25.0	26.5	26.1
51	PI275182iop-4v	2- 653	C	*1*	32.7	33.0	33.6	27.8	27.0	27.8
52	Ranger Russet	2- 653	D							
53	Russet Norkota	3- Control	A		33.6	36.1	36.1	33.2	32.0	33.7
54	PI275182iop-1v	1- 11-11	D							

Supplementary Table 3.2 (Continued)

55	PI498148adr-2v	1- 11-11	B	*1*	32.5	33.6	33.1	28.9	27.9	27.1
56	PI498148adr-2v	2- 653	C	*1*	36.0	33.1	34.3	30.0	30.1	29.1
57	Ranger Russet	1- 11-11	D	*2*						
58	PI498011blb-1v	2- 653	C	*5*	40.0	40.0	40.0	36.2	36.8	36.0
59	PI275181iop-1v	1- 11-11	A		29.0	28.8	30.2	26.7	26.3	25.4
60	PI498148adr-1v	1- 11-11	B	*1*	26.5	27.9	28.4	27.2	27.2	27.1
61	PI283107hou-1v	2- 653	D		31.1	30.2	32.1	29.2	29.2	28.6
62	PI498148adr-1v	1- 11-11	A	*1*	30.7	30.8	30.5	27.0	26.8	27.0
63	PI275182iop-1v	3- Control	B	*5*	33.2	40.0	33.8	28.5	29.1	29.3
64	Ranger Russet	2- 653	A	*5*	33.1	33.3	32.2	26.7	26.0	25.7
65	PI275182iop-4v	2- 653	B		31.4	33.2	32.5	26.5	28.6	27.5
66	PI275181iop-1v	1- 11-11	C		25.3	26.8	27.9	26.3	26.0	26.7
67	PI498148adr-2v	3- Control	A	*5*	40.0	40.0	40.0	28.6	28.0	27.9
68	Ranger Russet	2- 653	C	*5*	40.0	35.5	40.0	25.8	25.6	25.8
69	PI275182iop-1v	2- 653	D		30.6	30.2	31.0	30.3	29.2	28.6
70	PI275181iop-1v	2- 653	D	*1*	34.5	34.1	34.5	28.2	28.7	28.3
71	PI239423hou-3v	3- Control	C							
72	PI275182iop-4v	1- 11-11	B		25.4	25.3	26.2	27.5	27.3	26.2
73	PI283107hou-1v	3- Control	A	*5*	34.6	40.0	33.9	26.9	26.7	26.8
74	PI275182iop-1v	2- 653	B	*1*	34.4	32.8	32.3	28.9	28.4	27.8
75	PI275182iop-4v	2- 653	D		32.2	31.6	31.5	25.5	25.9	25.9
76	PI239423hou-3v	2- 653	B							
77	PI498148adr-1v	3- Control	D	*5*	37.9	35.1	40.0	26.9	26.9	27.2
78	Russet Norkota	1- 11-11	B		25.7	25.4	25.2	35.8	32.5	33.9
79	PI275182iop-4v	3- Control	B	*5*	30.8	31.7	34.1	26.5	28.1	27.7
80	PI498011blb-1v	3- Control	C	*5*						
81	PI275181iop-1v	3- Control	C	*5*	40.0	40.0	40.0	28.1	27.8	27.7
82	PI498148adr-1v	2- 653	C	*5*	37.7	40.0	40.0	28.0	27.5	28.0
83	PI498148adr-2v	3- Control	B	*5*	40.0	36.2	40.0	26.4	27.1	26.8
84	PI283107hou-1v	1- 11-11	C							

Supplementary Table 3.2 (Continued)

85	PI498011blb-1v	1- 11-11	C	*5*						
86	PI498148adr-2v	1- 11-11	A	*1*	40.0	40.0	40.0	29.0	28.6	27.7
87	PI498148adr-1v	3- Control	B	*5*	40.0	34.9	40.0	27.1	27.7	27.2
88	PI498148adr-2v	3- Control	D	*5*	32.8	31.4	32.0	27.2	27.2	26.4
89	PI498148adr-1v	1- 11-11	C	*1*	29.6	32.7	30.7	26.9	27.0	27.2
90	Ranger Russet	1- 11-11	A	*5*	33.9	32.5	32.1	26.9	26.3	25.9
91	PI283107hou-1v	2- 653	B	*1*	34.1	35.7	34.0	26.8	27.0	27.0
92	PI498148adr-2v	2- 653	A	*5*	26.9	31.9	31.3	26.6	26.0	26.7
93	Russet Norkota	1- 11-11	C		22.6	23.2	23.3	25.0	24.9	25.0
94	PI239423hou-3v	1- 11-11	D							
95	PI275181iop-1v	2- 653	A		27.0	27.9	28.2	25.6	26.9	26.8
96	Ranger Russet	2- 653	B	*1*	35.3	34.1	40.0	27.1	26.7	27.1
97	Russet Norkota	1- 11-11	D		23.6	25.0	24.8	32.4	31.7	32.8
98	Russet Norkota	3- Control	D		40.0	40.0	40.0	26.7	27.4	27.1
99	PI498148adr-1v	2- 653	B	*5*	33.5	33.9	33.9	28.8	28.6	26.5
100	PI283107hou-1v	1- 11-11	A	*1*						
101	PI498011blb-1v	1- 11-11	A		30.0	30.9	29.1	31.6	34.0	32.5
102	PI283107hou-1v	2- 653	A	*1*						
103	PI239423hou-3v	1- 11-11	B							
104	Russet Norkota	2- 653	C		36.0	40.0	32.5	32.4	31.9	32.8
105	Russet Norkota	1- 11-11	A		20.9	21.7	21.4	29.9	30.1	30.2
106	Ranger Russet	3- Control	A	*5*	40.0	40.0	40.0	26.3	25.8	25.4
107	Russet Norkota	3- Control	C	*5*	40.0	40.0	40.0	25.6	25.4	25.4
108	PI275182iop-4v	3- Control	C	*5*	40.0	40.0	40.0	30.8	30.4	28.9
109	PI283107hou-1v	3- Control	B	*5*	40.0	40.0	40.0	26.2	25.6	25.8
110	PI498148adr-1v	3- Control	C	*5*	30.6	32.2	31.2	27.3	29.3	29.0
111	PI498011blb-1v	2- 653	D							
112	PI275182iop-1v	3- Control	C	*5*	40.0	40.0	40.0	30.4	28.8	29.3
113	PI275182iop-4v	3- Control	A	*5*	40.0	40.0	40.0	30.3	30.4	28.9
114	Russet Norkota	3- Control	B		34.5	40.0	40.0	25.3	25.6	24.9

Supplementary Table 3.2 (Continued)

115	PI239423hou-3v	1- 11-11	A							
116	PI283107hou-1v	1- 11-11	B							
117	PI498148adr-2v	1- 11-11	C	*1*	34.3	40.0	40.0	28.2	27.7	26.0
118	Russet Norkota	2- 653	A	*5*	35.1	40.0	33.8	25.2	26.2	25.4
119	PI498148adr-2v	2- 653	B	*5*	40.0	40.0	40.0	26.7	27.1	26.2
120	PI275182iop-1v	1- 11-11	B		29.5	30.6	31.3	27.1	27.2	28.0

Supplementary Table 4.1. Presence of STM0003 and YES3-3B alleles indicating *Potato virus Y* (PVY) PVY resistance, PVY resistance phenotype, and corky ringspot resistance phenotype in a population of 49 potato clones used in chapter 4.

Entry	STM0003	YES3-3B	PVY resistance status	Corky ringspot disease severity index
POR15V001-8	1	1	R	28.4
POR15V001-14	1	1	R	9.7
POR15V001-17	0	0	S	0.2
POR15V001-18	1	1	R	19.3
POR15V001-19	0	1	S	11.8
POR15V001-20	1	1	R	0.0
POR15V001-21	0	0	S	32.3
POR15V001-23	1	1	R	12.6
POR15V001-26	0	0	S	1.0
POR15V001-28	1	1	R	0.0
POR15V001-33	1	1	R	2.0
POR15V001-38	0	0	S	3.3
POR15V001-51	1	1	R	36.9
POR15V001-54	1	1	R	5.9
POR15V001-60	0	0	S	0.5
POR15V001-61	1	1	R	17.7
POR15V001-65	1	1	R	20.3
POR15V001-68	1	1	R	1.5
POR15V001-69	1	1	R	36.2
POR15V001-73	0	0	S	0.3
POR15V001-74	1	1	R	20.5
POR15V001-75	0	0	S	1.6

Supplementary Table 4.1 (Continued)

POR15V001-76	0	0	S	0.2
POR15V001-86	0	0	S	21.3
POR15V001-89	1	1	R	11.1
POR15V001-91	1	1	R	41.4
POR15V001-93	1	1	R	24.3
POR15V001-94	0	1	R	0.0
POR15V001-96	0	0	S	0.0
POR15V001-99	0	1	S	14.1
POR15V001-102	0	0	S	26.7
POR15V001-104	1	1	R	0.0
POR15V001-107	0	0	S	0.6
POR15V001-109	0	0	S	9.2
POR15V001-110	1	1	R	6.5
POR15V001-111	1	0	S	14.1
POR15V001-112	0	1	R	0.4
POR15V001-113	1	1	R	0.4
POR15V001-114	1	1	R	1.7
POR15V001-115	1	1	R	22.3
POR15V001-122	1	1	R	0.2
POR15V001-124	0	0	S	0.1
POR15V001-126	0	0	S	32.8
POR15V001-129	1	1	R	6.9
POR15V001-132	1	1	R	27.7
POR15V001-137	0	0	S	0.2
POR15V001-140	1	1	R	9.4
POR15V001-142	0	0	S	0.0

Supplementary Table 4.1 (Continued)

POR15V001-143	0	0	S	0.0

Supplementary Table 5.1. Clones produced from each tetraploid × diploid combination, with the number of triploid clones produced from that cross in parentheses.

		Male Parent												
		BD1202-2	BD1205-4	BD1216-3	BD1222-1	BD1240-6	BD1244-1	BD1244-3	BD1247-3	BD1251-1	BD1253-4	BD1257-5	BD1268-1	BD1269-1
Female Parent	Snowden	3(2)	1(0)	1(1)			1(1)	1(1)						
	Atlantic	1(1)	1(0)		1(1)	3(2)		1(0)					1(1)	
	EVA		1(0)			1(1)					1(0)			
	Lamoka		2(0)					1(1)			1(1)			
	Ivory Crisp							2(0)						
	A00710-1		8(1)	1(0)	1(1)	1(0)	1(1)		1(1)		1(1)		2(1)	
	AO03123-2					1(0)	1(1)		2(2)	1(1)				1(0)
	OR01007-3				1(1)			1(1)				1(1)	1(0)	
	ORAYT-9	1(1)					1(1)		1(1)		3(2)	1(1)		
	Castle Russet						1(1)				2(2)			
	Payette Russet					1(1)								
	A06866-2	1(0)									1(0)			
	A07547-4						1(1)		2(2)		1(1)			
	A08640-2							1(1)					1(0)	
	PALB03016-3							1(1)			1(1)	1(0)	2(2)	
	Tacna	1(0)	5(0)	7(5)		1(1)	1(1)	1(1)	4(3)	1(1)		1(0)		

Supplementary Table 6.1. Clones used to evaluate ploidy frequencies of tetraploid × diploid crosses in chapter 5, and to test for hybrid vigor between groups in chapter 6.

Clone	Group	Female parent	Male parent	Genome size (pg)	Ploidy
C.2.1001	CC	Atlantic	Lamoka		
C.2.1008	CC	Atlantic	Lamoka		
C.2.1015	CC	Atlantic	Lamoka		
C.2.1022	CC	Atlantic	Lamoka		
C.2.1029	CC	Atlantic	Lamoka		
C.2.1036	CC	Snowden	Lamoka		
C.2.1043	CC	Snowden	Lamoka		
C.2.1050	CC	Snowden	Lamoka		
C.2.1057	CC	Snowden	Lamoka		
C.2.1064	CC	Snowden	Lamoka		
C.2.1071	CC	Eva	Lamoka		
C.2.1078	CC	Eva	Lamoka		
C.2.1085	CC	Eva	Lamoka		
C.2.1092	CC	Eva	Lamoka		
C.2.1099	CC	Eva	Lamoka		
C.2.1106	CC	Eva	Willamette		
C.2.1113	CC	Eva	Willamette		
C.2.1120	CC	Eva	Willamette		
C.2.1127	CC	Eva	Willamette		
C.2.1134	CC	Eva	Willamette		
C.2.1141	CC	Willamette	Lamoka		
C.2.1148	CC	Willamette	Lamoka		
C.2.1155	CC	Willamette	Lamoka		
C.2.1162	CC	Willamette	Lamoka		
C.2.1169	CC	Willamette	Lamoka		
C.2.1176	CC	Ivory Crisp	Lamoka		
C.2.1183	CC	Ivory Crisp	Lamoka		
C.2.1190	CC	Ivory Crisp	Lamoka		
C.2.1197	CC	Ivory Crisp	Lamoka		
C.2.1204	CC	Ivory Crisp	Lamoka		
CD.2.1211	CD	Atlantic	BD1202-2	3.14	3
CD.2.1218	CD	Atlantic	BD1205-4	4.28	4
CD.2.1225	CD	Atlantic	BD1222-1	3.24	3
CD.2.1232	CD	Atlantic	BD1240-6	3.17	3
CD.2.1239	CD	Atlantic	BD1240-6	2.18	2
CD.2.1246	CD	Atlantic	BD1240-6	3.21	3
CD.2.1253	CD	Atlantic	BD1244-3	4.20	4
CD.2.1260	CD	Atlantic	BD1268-1	3.18	3
CD.2.1267	CD	Snowden	BD1202-2	3.14	3
CD.2.1274	CD	Snowden	BD1202-2	3.09	3
CD.2.1281	CD	Snowden	BD1202-2	4.45	4
CD.2.1288	CD	Snowden	BD1205-4	4.03	4

Supplementary Table 6.1

CD.2.1295	CD	Snowden	P.1.1743	3.19	3
CD.2.1302	CD	Snowden	BD1222-1		
CD.2.1309	CD	Snowden	BD1240-6		
CD.2.1316	CD	Snowden	BD1244-1	3.19	3
CD.2.1323	CD	Snowden	BD1244-3	3.28	3
CD.2.1330	CD	Eva	BD1205-4	4.21	4
CD.2.1337	CD	Eva	BD1240-6	3.29	3
CD.2.1344	CD	Eva	BD1253-4	4.30	4
CD.2.1351	CD	Lamoka	BD1205-4	4.36	4
CD.2.1358	CD	Lamoka	BD1205-4	4.43	4
CD.2.1365	CD	Lamoka	BD1244-3	3.22	3
CD.2.1372	CD	Lamoka	BD1253-4	3.18	3
CD.2.1379	CD	Ivory Crisp	BD1244-3	2.04	2
CD.2.1386	CD	Ivory Crisp	BD1244-3	2.13	2
CR.2.1393	CR	Atlantic	AO00710-1		
CR.2.1400	CR	Atlantic	AO00710-1		
CR.2.1407	CR	Atlantic	AO00710-1		
CR.2.1414	CR	Atlantic	AO00710-1		
CR.2.1421	CR	Atlantic	AO00710-1		
CR.2.1428	CR	Atlantic	AO03123-2		
CR.2.1435	CR	Atlantic	AO03123-2		
CR.2.1442	CR	Atlantic	AO03123-2		
CR.2.1449	CR	Atlantic	AO03123-2		
CR.2.1456	CR	Atlantic	PALB03016-3		
CR.2.1463	CR	Atlantic	PALB03016-3		
CR.2.1470	CR	Atlantic	PALB03016-3		
CR.2.1477	CR	Atlantic	PALB03016-3		
CR.2.1484	CR	Atlantic	PALB03016-3		
CR.2.1491	CR	Snowden	AO00710-1		
CR.2.1498	CR	Snowden	AO00710-1		
CR.2.1505	CR	Snowden	AO00710-1		
CR.2.1512	CR	Snowden	AO00710-1		
CR.2.1519	CR	Snowden	AO00710-1		
CR.2.1526	CR	Snowden	AO00710-1		
CR.2.1533	CR	Snowden	A06866-2		
CR.2.1540	CR	Snowden	A06866-2		
CR.2.1547	CR	Snowden	A06866-2		
CR.2.1554	CR	Snowden	A06866-2		
CR.2.1561	CR	Snowden	PALB03016-3		
CR.2.1568	CR	Snowden	PALB03016-3		
CR.2.1575	CR	Snowden	PALB03016-3		
CR.2.1582	CR	Snowden	PALB03016-3		
CR.2.1589	CR	Snowden	PALB03016-3		
CR.2.1596	CR	Eva	AO00710-1		
CR.2.1603	CR	Eva	AO00710-1		

Supplementary Table 6.1

CR.2.1610	CR	Eva	AO00710-1		
CR.2.1617	CR	Eva	A06866-2		
CR.2.1624	CR	Eva	A06866-2		
CR.2.1631	CR	Eva	A06866-2		
CR.2.1638	CR	Eva	A06866-2		
CR.2.1645	CR	Eva	A06866-2		
CR.2.1652	CR	Eva	PALB03016-3		
CR.2.1659	CR	Eva	PALB03016-3		
CR.2.1666	CR	Eva	PALB03016-3		
CR.2.1673	CR	Eva	PALB03016-3		
CR.2.1680	CR	Eva	PALB03016-3		
CR.2.1687	CR	Lamoka	PALB03016-3		
CR.2.1694	CR	Lamoka	PALB03016-3		
CR.2.1701	CR	Lamoka	PALB03016-3		
CR.2.1708	CR	Lamoka	PALB03016-3		
CR.2.1715	CR	Lamoka	PALB03016-3		
CR.2.1722	CR	Willamette	AO00710-1		
CR.2.1729	CR	Willamette	AO00710-1		
CR.2.1736	CR	Willamette	AO00710-1		
CR.2.1743	CR	Willamette	AO00710-1		
CR.2.1750	CR	Willamette	AO00710-1		
CR.2.1757	CR	Willamette	A06866-2		
CR.2.1764	CR	Willamette	A06866-2		
CR.2.1771	CR	Willamette	A06866-2		
CR.2.1778	CR	Willamette	A06866-2		
CR.2.1785	CR	Willamette	PALB03016-3		
CR.2.1792	CR	Willamette	PALB03016-3		
CR.2.1799	CR	Willamette	PALB03016-3		
CR.2.1806	CR	Willamette	PALB03016-3		
CR.2.1813	CR	Ivory Crisp	AO00710-1		
CR.2.1820	CR	Ivory Crisp	AO00710-1		
CR.2.1827	CR	Ivory Crisp	AO00710-1		
CR.2.1834	CR	Ivory Crisp	AO00710-1		
CR.2.1841	CR	Ivory Crisp	AO00710-1		
CR.2.1848	CR	Ivory Crisp	A06866-2		
CR.2.1855	CR	Ivory Crisp	A06866-2		
CR.2.1862	CR	Ivory Crisp	A06866-2		
CR.2.1869	CR	Ivory Crisp	PALB03016-3		
CR.2.1876	CR	Ivory Crisp	PALB03016-3		
CR.2.1883	CR	Ivory Crisp	PALB03016-3		
CR.2.1890	CR	Ivory Crisp	PALB03016-3		
CR.2.1897	CR	Ivory Crisp	PALB03016-3		
D.2.1904	DD	BD1202-2	BD1205-4		
D.2.1911	DD	BD1202-2	BD1205-4		
D.2.1918	DD	BD1202-2	P.1.1743		

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D.2.1925	DD	BD1202-2	P.1.1743		
D.2.1932	DD	BD1202-2	BD1222-1		
D.2.1939	DD	BD1202-2	BD1244-1		
D.2.1946	DD	BD1202-2	BD1244-1		
D.2.1953	DD	BD1202-2	BD1244-3		
D.2.1960	DD	BD1202-2	BD1244-3		
D.2.1967	DD	BD1202-2	BD1247-3		
D.2.1974	DD	BD1202-2	BD1247-3		
D.2.1981	DD	BD1202-2	BD1251-1		
D.2.1988	DD	BD1202-2	BD1251-1		
D.2.1995	DD	BD1202-2	BD1253-4		
D.2.2002	DD	BD1202-2	BD1253-4		
D.2.2009	DD	BD1202-2	P.1.1977		
D.2.2016	DD	BD1202-2	BD1257-5		
D.2.2023	DD	BD1202-2	BD1257-5		
D.2.2030	DD	BD1202-2	BD1268-1		
D.2.2037	DD	BD1202-2	BD1268-1		
D.2.2044	DD	BD1205-4	P.1.1743		
D.2.2051	DD	BD1205-4	BD1222-1		
D.2.2058	DD	BD1205-4	BD1222-1		
D.2.2065	DD	BD1205-4	BD1240-6		
D.2.2072	DD	BD1205-4	BD1240-6		
D.2.2079	DD	BD1205-4	BD1244-1		
D.2.2086	DD	BD1205-4	BD1244-1		
D.2.2093	DD	BD1205-4	BD1244-3		
D.2.2100	DD	BD1205-4	BD1244-3		
D.2.2107	DD	BD1205-4	BD1247-3		
D.2.2114	DD	BD1205-4	BD1247-3		
D.2.2121	DD	BD1205-4	BD1251-1		
D.2.2128	DD	BD1205-4	BD1253-4		
D.2.2135	DD	BD1205-4	BD1253-4		
D.2.2142	DD	BD1205-4	BD1257-5		
D.2.2149	DD	BD1205-4	BD1257-5		
D.2.2156	DD	BD1205-4	BD1268-1		
D.2.2163	DD	BD1205-4	BD1268-1		
D.2.2170	DD	P.1.1743	BD1240-6		
D.2.2177	DD	P.1.1743	BD1240-6		
D.2.2184	DD	P.1.1743	BD1244-1		
D.2.2191	DD	P.1.1743	BD1244-1		
D.2.2198	DD	P.1.1743	BD1244-3		
D.2.2205	DD	P.1.1743	BD1244-3		
D.2.2212	DD	P.1.1743	BD1268-1		
D.2.2219	DD	BD1222-1	P.1.1743		
D.2.2226	DD	BD1222-1	P.1.1743		
D.2.2233	DD	BD1222-1	BD1244-1		

Supplementary Table 6.1

D.2.2240	DD	BD1222-1	BD1244-1		
D.2.2247	DD	BD1222-1	BD1244-3		
D.2.2254	DD	BD1222-1	BD1244-3		
D.2.2261	DD	BD1222-1	BD1247-3		
D.2.2268	DD	BD1222-1	BD1247-3		
D.2.2275	DD	BD1222-1	BD1251-1		
D.2.2282	DD	BD1222-1	BD1251-1		
D.2.2289	DD	BD1222-1	BD1253-4		
D.2.2296	DD	BD1222-1	BD1257-5		
D.2.2303	DD	BD1222-1	BD1257-5		
D.2.2310	DD	BD1222-1	BD1268-1		
D.2.2317	DD	BD1222-1	BD1268-1		
D.2.2324	DD	BD1240-6	BD1202-2		
D.2.2331	DD	BD1240-6	BD1202-2		
D.2.2338	DD	BD1240-6	BD1222-1		
D.2.2345	DD	BD1240-6	BD1222-1		
D.2.2352	DD	BD1240-6	BD1244-3		
D.2.2359	DD	BD1240-6	BD1244-3		
D.2.2366	DD	BD1240-6	BD1247-3		
D.2.2373	DD	BD1240-6	BD1247-3		
D.2.2380	DD	BD1240-6	BD1251-1		
D.2.2387	DD	BD1240-6	BD1253-4		
D.2.2394	DD	BD1240-6	BD1253-4		
D.2.2401	DD	BD1240-6	BD1257-5		
D.2.2408	DD	BD1240-6	BD1257-5		
D.2.2415	DD	BD1240-6	BD1268-1		
D.2.2422	DD	BD1244-1	BD1240-6		
D.2.2429	DD	BD1244-1	BD1240-6		
D.2.2436	DD	BD1244-1	BD1244-3		
D.2.2443	DD	BD1244-1	BD1244-3		
D.2.2450	DD	BD1244-1	BD1247-3		
D.2.2457	DD	BD1244-1	BD1247-3		
D.2.2464	DD	BD1244-1	BD1257-5		
D.2.2471	DD	BD1244-1	BD1268-1		
D.2.2478	DD	BD1244-1	BD1268-1		
D.2.2485	DD	BD1244-1	BD1268-1		
D.2.2492	DD	BD1244-3	BD1247-3		
D.2.2499	DD	BD1244-3	BD1247-3		
D.2.2506	DD	BD1244-3	BD1251-1		
D.2.2513	DD	BD1244-3	BD1253-4		
D.2.2520	DD	BD1244-3	BD1253-4		
D.2.2527	DD	BD1244-3	BD1257-5		
D.2.2534	DD	BD1244-3	BD1257-5		
D.2.2541	DD	BD1247-3	BD1251-1		
D.2.2548	DD	BD1247-3	BD1251-1		

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D.2.2555	DD	BD1247-3	BD1257-5		
D.2.2562	DD	BD1247-3	BD1257-5		
D.2.2569	DD	BD1253-4	BD1244-1		
D.2.2576	DD	BD1253-4	BD1244-1		
D.2.2583	DD	BD1253-4	BD1257-5		
D.2.2590	DD	BD1253-4	BD1257-5		
D.2.2597	DD	BD1253-4	BD1268-1		
D.2.2604	DD	BD1253-4	BD1268-1		
D.2.2611	DD	BD1257-5	BD1251-1		
D.2.2618	DD	BD1257-5	BD1251-1		
D.2.2625	DD	BD1257-5	BD1268-1		
D.2.2632	DD	BD1257-5	BD1268-1		
D.2.2639	DD	BD1268-1	BD1244-3		
D.2.2646	DD	BD1268-1	BD1244-3		
D.2.2653	DD	BD1268-1	BD1257-5		
D.2.2660	DD	BD1268-1	BD1257-5		
R.2.2667	RR	AO00710-1	A06866-2		
R.2.2674	RR	AO00710-1	A06866-2		
R.2.2681	RR	AO00710-1	A06866-2		
R.2.2688	RR	AO00710-1	A06866-2		
R.2.2695	RR	AO00710-1	A06866-2		
R.2.2702	RR	AO00710-1	PALB03016-3		
R.2.2709	RR	AO00710-1	PALB03016-3		
R.2.2716	RR	AO00710-1	PALB03016-3		
R.2.2723	RR	AO00710-1	PALB03016-3		
R.2.2730	RR	AO00710-1	PALB03016-3		
R.2.2737	RR	AO03123-2	PALB03016-3		
R.2.2744	RR	AO03123-2	PALB03016-3		
R.2.2751	RR	AO03123-2	PALB03016-3		
R.2.2758	RR	AO03123-2	PALB03016-3		
R.2.2765	RR	OR01007-3	AO00710-1		
R.2.2772	RR	OR01007-3	AO00710-1		
R.2.2779	RR	OR01007-3	PALB03016-3		
R.2.2786	RR	OR01007-3	PALB03016-3		
R.2.2793	RR	OR01007-3	PALB03016-3		
R.2.2800	RR	OR01007-3	PALB03016-3		
R.2.2807	RR	ORAYT-9	AO00710-1		
R.2.2814	RR	ORAYT-9	AO00710-1		
R.2.2821	RR	ORAYT-9	AO00710-1		
R.2.2828	RR	ORAYT-9	PALB03016-3		
R.2.2835	RR	ORAYT-9	PALB03016-3		
R.2.2842	RR	ORAYT-9	PALB03016-3		
R.2.2849	RR	ORAYT-9	PALB03016-3		
R.2.2856	RR	ORAYT-9	PALB03016-3		
R.2.2863	RR	Castle Russet	PALB03016-3		

Supplementary Table 6.1

R.2.2870	RR	Castle Russet	PALB03016-3		
R.2.2877	RR	Castle Russet	PALB03016-3		
R.2.2884	RR	Castle Russet	PALB03016-3		
R.2.2891	RR	Payette Russet	AO00710-1		
R.2.2898	RR	Payette Russet	AO00710-1		
R.2.2905	RR	Payette Russet	AO00710-1		
R.2.2912	RR	Payette Russet	AO00710-1		
R.2.2919	RR	Payette Russet	AO00710-1		
R.2.2926	RR	Payette Russet	PALB03016-3		
R.2.2933	RR	Payette Russet	PALB03016-3		
R.2.2940	RR	Payette Russet	PALB03016-3		
R.2.2947	RR	Payette Russet	PALB03016-3		
R.2.2954	RR	Payette Russet	PALB03016-3		
R.2.2961	RR	A06866-2	PALB03016-3		
R.2.2968	RR	A06866-2	PALB03016-3		
R.2.2975	RR	A06866-2	PALB03016-3		
R.2.2982	RR	A06866-2	PALB03016-3		
R.2.2989	RR	A06866-2	PALB03016-3		
R.2.2996	RR	A08640-2	AO00710-1		
R.2.3003	RR	A08640-2	AO00710-1		
R.2.3010	RR	A08640-2	AO00710-1		
R.2.3017	RR	A08640-2	AO00710-1		
R.2.3024	RR	A08640-2	AO00710-1		
R.2.3031	RR	A08640-2	PALB03016-3		
R.2.3038	RR	A08640-2	PALB03016-3		
R.2.3045	RR	A08640-2	PALB03016-3		
R.2.3052	RR	A08640-2	PALB03016-3		
R.2.3059	RR	A08640-2	PALB03016-3		
R.2.3066	RR	Tacna	AO00710-1		
R.2.3073	RR	Tacna	AO00710-1		
R.2.3080	RR	Tacna	AO00710-1		
R.2.3087	RR	Tacna	AO00710-1		
R.2.3094	RR	Tacna	PALB03016-3		
R.2.3101	RR	Tacna	PALB03016-3		
R.2.3108	RR	Tacna	PALB03016-3		
R.2.3115	RR	Tacna	PALB03016-3		
R.2.3122	RR	Tacna	PALB03016-3		
R.2.3129	RR	P2-4	PALB03016-3		
RC.2.3136	RC	AO00710-1	Lamoka		
RC.2.3143	RC	AO00710-1	Lamoka		
RC.2.3150	RC	AO00710-1	Lamoka		
RC.2.3157	RC	AO00710-1	Lamoka		
RC.2.3164	RC	AO00710-1	Lamoka		
RC.2.3171	RC	AO03123-2	Lamoka		
RC.2.3178	RC	AO03123-2	Lamoka		

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RC.2.3185	RC	AO03123-2	Lamoka		
RC.2.3192	RC	AO03123-2	Lamoka		
RC.2.3199	RC	AO03123-2	Lamoka		
RC.2.3206	RC	OR01007-3	Lamoka		
RC.2.3213	RC	OR01007-3	Lamoka		
RC.2.3220	RC	OR01007-3	Lamoka		
RC.2.3227	RC	OR01007-3	Lamoka		
RC.2.3234	RC	OR01007-3	Lamoka		
RC.2.3241	RC	Castle Russet	Lamoka		
RC.2.3248	RC	Castle Russet	Lamoka		
RC.2.3255	RC	Castle Russet	Lamoka		
RC.2.3262	RC	Castle Russet	Lamoka		
RC.2.3269	RC	Castle Russet	Lamoka		
RC.2.3276	RC	Payette Russet	Lamoka		
RC.2.3283	RC	Payette Russet	Lamoka		
RC.2.3290	RC	Payette Russet	Lamoka		
RC.2.3297	RC	Payette Russet	Lamoka		
RC.2.3304	RC	A06866-2	Lamoka		
RC.2.3311	RC	A06866-2	Lamoka		
RC.2.3318	RC	A06866-2	Lamoka		
RC.2.3325	RC	A06866-2	Lamoka		
RC.2.3332	RC	A06866-2	Lamoka		
RC.2.3339	RC	A08640-2	Lamoka		
RC.2.3346	RC	A08640-2	Lamoka		
RC.2.3353	RC	A08640-2	Lamoka		
RC.2.3360	RC	A08640-2	Lamoka		
RC.2.3367	RC	A08640-2	Lamoka		
RC.2.3374	RC	Tacna	Lamoka		
RC.2.3381	RC	Tacna	Lamoka		
RC.2.3388	RC	Tacna	Lamoka		
RC.2.3395	RC	Tacna	Lamoka		
RC.2.3402	RC	Tacna	Willamette		
RC.2.3409	RC	Tacna	Willamette		
RC.2.3416	RC	Tacna	Willamette		
RC.2.3423	RC	Tacna	Ivory Crisp		
RC.2.3430	RC	Tacna	Ivory Crisp		
RC.2.3437	RC	Tacna	Ivory Crisp		
RC.2.3444	RC	Tacna	Ivory Crisp		
RC.2.3451	RC	Tacna	Ivory Crisp		
RC.2.3458	RC	P2-4	Ivory Crisp		
RD.2.3465	RD	AO00710-1	BD1202-2		
RD.2.3472	RD	AO00710-1	BD1205-4	3.18	3
RD.2.3479	RD	AO00710-1	BD1205-4	4.24	4
RD.2.3486	RD	AO00710-1	BD1205-4	4.26	4
RD.2.3493	RD	AO00710-1	BD1205-4	4.08	4

Supplementary Table 6.1

RD.2.3500	RD	AO00710-1	BD1205-4	4.19	4
RD.2.3507	RD	AO00710-1	BD1205-4	4.22	4
RD.2.3514	RD	AO00710-1	BD1205-4	4.11	4
RD.2.3521	RD	AO00710-1	BD1205-4	4.22	4
RD.2.3528	RD	AO00710-1	P.1.1743	4.19	4
RD.2.3535	RD	AO00710-1	BD1222-1	3.16	3
RD.2.3542	RD	AO00710-1	BD1240-6	2.14	2
RD.2.3549	RD	AO00710-1	BD1244-1	3.22	3
RD.2.3556	RD	AO00710-1	BD1247-3	3.20	3
RD.2.3563	RD	AO00710-1	BD1253-4	3.22	3
RD.2.3570	RD	AO00710-1	BD1268-1	4.10	4
RD.2.3577	RD	AO00710-1	BD1268-1	3.36	3
RD.2.3584	RD	AO03123-2	BD1240-6	4.35	4
RD.2.3591	RD	AO03123-2	BD1244-1	3.24	3
RD.2.3598	RD	AO03123-2	BD1247-3	3.18	3
RD.2.3605	RD	AO03123-2	BD1247-3	3.20	3
RD.2.3612	RD	AO03123-2	BD1251-1	3.32	3
RD.2.3619	RD	AO03123-2	BD1269-1	3.21	3
RD.2.3626	RD	OR01007-3	P.1.1743		
RD.2.3633	RD	OR01007-3	BD1222-1	3.11	3
RD.2.3640	RD	OR01007-3	BD1244-3	3.09	3
RD.2.3647	RD	OR01007-3	BD1257-5	3.13	3
RD.2.3654	RD	OR01007-3	BD1268-1	4.27	4
RD.2.3661	RD	ORAYT-9	BD1202-2	3.23	3
RD.2.3668	RD	ORAYT-9	BD1240-6		
RD.2.3675	RD	ORAYT-9	BD1244-1	3.17	3
RD.2.3682	RD	ORAYT-9	BD1247-3	3.25	3
RD.2.3689	RD	ORAYT-9	BD1253-4	1.85	2
RD.2.3696	RD	ORAYT-9	BD1253-4	3.29	3
RD.2.3703	RD	ORAYT-9	BD1253-4	3.23	3
RD.2.3710	RD	ORAYT-9	BD1257-5	3.12	3
RD.2.3717	RD	Castle Russet	BD1244-1	3.19	3
RD.2.3724	RD	Castle Russet	BD1253-4	3.03	3
RD.2.3731	RD	Castle Russet	BD1253-4	3.04	3
RD.2.3738	RD	Payette Russet	BD1240-6	3.10	3
RD.2.3745	RD	A06866-2	BD1202-2	4.36	4
RD.2.3752	RD	A06866-2	BD1253-4	4.23	4
RD.2.3759	RD	A07547-4	BD1244-1	3.14	3
RD.2.3766	RD	A07547-4	BD1247-3	3.20	3
RD.2.3773	RD	A07547-4	BD1247-3	3.30	3
RD.2.3780	RD	A07547-4	BD1253-4	3.19	3
RD.2.3787	RD	A08640-2	BD1244-3	3.42	3
RD.2.3794	RD	A08640-2	BD1268-1	4.22	4
RD.2.3801	RD	PALB03016-3	BD1244-3	3.14	3
RD.2.3808	RD	PALB03016-3	BD1253-4	3.12	3

Supplementary Table 6.1

RD.2.3815	RD	PALB03016-3	BD1257-5	4.17	4
RD.2.3822	RD	PALB03016-3	BD1268-1	3.23	3
RD.2.3829	RD	PALB03016-3	BD1268-1	3.28	3
RD.2.3836	RD	Tacna	BD1202-2	3.24	3
RD.2.3843	RD	Tacna	BD1205-4	4.12	4
RD.2.3850	RD	Tacna	BD1205-4	4.19	4
RD.2.3857	RD	Tacna	BD1205-4	4.18	4
RD.2.3864	RD	Tacna	BD1205-4	4.13	4
RD.2.3871	RD	Tacna	BD1205-4	4.17	4
RD.2.3878	RD	Tacna	P.1.1743	3.25	3
RD.2.3885	RD	Tacna	P.1.1743	3.11	3
RD.2.3892	RD	Tacna	P.1.1743	3.14	3
RD.2.3899	RD	Tacna	P.1.1743	4.25	4
RD.2.3906	RD	Tacna	P.1.1743	3.16	3
RD.2.3913	RD	Tacna	P.1.1743	4.36	4
RD.2.3920	RD	Tacna	P.1.1743	3.18	3
RD.2.3927	RD	Tacna	BD1240-6	3.20	3
RD.2.3934	RD	Tacna	BD1244-1	3.14	3
RD.2.3941	RD	Tacna	BD1244-3	3.10	3
RD.2.3948	RD	Tacna	BD1247-3	3.11	3
RD.2.3955	RD	Tacna	BD1247-3	3.22	3
RD.2.3962	RD	Tacna	BD1247-3		
RD.2.3969	RD	Tacna	BD1247-3	4.22	4
RD.2.3976	RD	Tacna	BD1247-3	3.16	3
RD.2.3983	RD	Tacna	BD1251-1	3.21	3
RD.2.3990	RD	Tacna	BD1257-5	4.16	4
RD.2.3997	RD	Tacna	Unknown	3.21	3

Supplementary Table 6.2. Phenotypes of clones grown in Klamath Falls, OR in 2017 to evaluate groups for hybrid vigor in chapter 6. In all traits scored 1-5 or 0-5, “5” indicates the preferable state. For “chipper suitability” and “russet suitability”, higher scores indicate clones that have higher yields and tuber traits more acceptable for the potato chip market. “Chipper suitability” and “russet suitability” were calculated using Equations 2 and 3 in chapter 6.

Plot	Clone	% Green (8-24-17)	Yield (kg/plot)	Specific gravity	Russeting (1-5)	Skin color	Flesh color	Shape	Eye depth (1-5)	Uniform (1-5)	Sprouting (1-5)	Appearance (1-5)	Length:width	Chipper suitability (0-5)	Russet suitability (0-5)	Comments
1	D.2.1988	100	1.0	1.070	1.5	buff pink	white cream	long fing	3	2.5	3	2	2.425			knobs, pointy, flat butt end
2	D.2.2289	95	2.4	1.089	1	yellow	yellow	oval	3.5	2.5	2	2.5	1.293			pointy, baby, bottle
3	C.2.1155	100	2.1	1.083	2	buff	white	comp	3.5	2.5	4.5	3	1.026	3		FBE, flat, sticky
4	RD.2.3710	95	1.5	1.096	1	buff pink	yellow	oval blocky	3	2	3.5	2	1.335			irregular, bottle, greening, pointy
5	CR.2.1687	90	3.1	1.074	2.5	tan	white	comp round	3.5	3	4.5	3	1.174	3		**hollow heart**, greening
6	Eva	95	2.1	1.069	1.5	buff	white	round oblong	3.5	3	4.5	3	1.269	3		greening
7	C.2.1064		0.0													
8	ORAYT-9	85	7.6	1.072	3.5	tan	cream	oval oblong blocky	3	2.5	4.5	3	1.554		3	bottle
9	R.2.3087	90	2.8	1.061	2.5	buff tan	white	round	3.5	1	4.5	1	1.220	1		**growth cracks**, **greening**, scab, ugly
10	CR.2.1652	95	0.9	1.074	1	buff pink	white	round	4	3.5	4	2	1.099			ugly skin, sticky
11	Snowden	85	5.1	1.075	2.5	buff tan	white	comp round	3	3	4.5	3	1.035	3		deep eyes, FBE, sticky, greening
12	RC.2.3325	55	6.2	1.081	2	buff tan	white	round comp	3.5	3.5	4.5	3.5	1.141	3.5		
13	R.2.3080	95	3.0	1.083	1.5	buff yellow	cream yellow	round oval	4	3.5	4.5	3	1.413		2.5	short, skinning, greening
14	RC.2.3143	95	2.1	1.086	1.5	buff	white	round	3.5	3	4.5	3	1.076	3		greening, lenticels, short
15	D.2.2373	90	1.6	1.113	1	yellow	yellow	round oval	3.5	2.5	3	2	1.573			pointy, bottle
16	R.2.2779	100	4.0	1.077	2.5	buff tan	white	oblong	4	3	3.5	2.5	1.397	2.5	2.5	flat, typy, rhizoc
17	CR.2.1750	95	2.7	1.077	1.5	buff	white	round	3.5	3	4.5	2.5	1.217	3		bottle, rot, short, skinning
18	RC.2.3374	100	3.3	1.065	2	buff	white	comp oblong	4	2.5	4	3	1.063	3		hollow heart, skinning, flat
19	C.2.1071	85	2.4	1.074	2	buff tan	white	round	4	2.5	4	2.5	1.254	3		greening, flat, rot, slightly irregular
20	C.2.1043	95	3.6	1.080	2.5	buff tan	white	round oblong	4	3.5	4.5	3	1.062	3.5		skinning, flat
21	R.2.2975		2.4	1.079	2.5	buff tan	white	long oblong	4	3	4.5	3	1.659		3	shatter, sticky
22	D.2.2408	95	1.7	1.081	1	yellow	yellow	oval	3.5	2	1.5	1.5	1.391			shriveled, pointy, bottle, greening
23	RC.2.3206	85	1.7	1.078	1.5	buff	white	long oval	4	2.5	4.5	2.5	1.401		2	bottle, pointy, short

Supplementary Table 6.2 (Continued)

24	CR.2.1645		1.5	1.068	1.5	buff	white	round	3.5	3	5	3	1.225	2.5		pear, bottle, short, greening
25	C.2.1106	90	0.8	1.076	1.5	buff	white	round	3.5	3	4.5	3	1.112	2		rhizoc, greening
26	C.2.1183		0.6	1.051	1.5	buff yellow	cream white	oval round	3.5	3	4	2.5	1.880			bottle, pointy, bumpy skin
27	D.2.2044	95	1.2	1.115	1	orange yellow	orange yellow	oval	3	3	2.5	2	1.851			bottle, pointy, knobs, shriveled
28	RC.2.3262	90	4.1	1.081	2	buff	white	long oblong	3.5	3	4.5	2.5	1.650		3	skinning, knobs, rhizoc, flay, typy
29	D.2.2401	100	1.4	1.084	1.5	champaign	yellow	round	2.5	1.5	1.5	1	1.324			bottle, pointy, irregular, rot
30	D.2.2107	95	1.4	1.089	1	yellow	dark yellow	long fing	3	1.5	2.5	1	2.105			end rot, pointy, curvy, greening
31	RD.2.3598	80	3.4	1.080	2	buff yellow	yellow	oval oblong	3.5	3	3.5	2.5	1.339		2	rot, bottle, pear, greening
32	CR.2.1519	85	4.3	1.074	2	buff tan	yellow	oval oblong	3.5	2.5	4.5	3	1.221		2.5	pointy, XL
33	D.2.2422	85	0.6	1.078	1.5	buff yellow	cream yellow	oval	3.5	2	2.5	1.5	1.482			bottle, multiple eyes at butt end, patchy, rot, ugly
34	CR.2.1624	70	2.0	1.079	1.5	buff	white	oval oblong	3.5	3	4	3	1.318		2.5	short, bottle
35	D.2.2254	70	1.0	1.099	1.5	maroon red	yellow w/ red	long fing	3	2.5	2.5	1.5	1.931			ugly flesh, dumbbell, bottle, multiple buds on butt end, landrace type
36	R.2.3094	80	1.7	1.085	1.5	buff	cream white	comp round	4	3.5	4.5	2.5	1.024	3		FBE, flat
37	D.2.1995	90	2.7	1.086	1	yellow w/ pink	yellow	long fing	2.5	2.5	2.5	2.5	2.720			bottle, curvy, pointy
38	R.2.3108	100	1.5	1.072	1.5	buff	white	round comp	4	2.5	3.5	2	1.133	2		flat, short, skinning
39	CR.2.1610	85	5.7	1.072	2	buff	white	round	3	3	5	3	1.118	3.5		FBE, deep eyes, blocky
40	CR.2.1554	85	1.7	1.076	2.5	buff tan	yellow	round	4	3	3	3	1.301		1.5	short, flaky, greening
41	R.2.2835	65	4.8	1.075	2.5	tan	white	round	3	3.5	3.5	3	1.100	3		greening, FBE
42	BD1247-3		0.0													
43	CR.2.1778	80	3.2	1.077	1.5	buff	white	round oblong	3.5	3	4.5	3	1.182	3		skinning, greening, FBE, button
44	R.2.2947	80	2.1	1.070	3	buff tan	white	long oval	4	3	4.5	3	0.990		3	bottle, pointy, typy
45	R.2.3010	75	5.4	1.077	2.5	buff tan	white	oblong round	3.5	3.5	5	3	1.003	3		hollow heart, deep eyes, shatter, greening
46	C.2.1022	75	2.4	1.077	2	buff tan	white	round comp	3.5	3	4	3	1.121	3		sticky, FBE, greening
47	POR06V12-3	85	2.9	1.083	4.5	buff tan	white	oval oblong	3.5	3	4.5	3	1.711		3	heavy russet, pointy, sticky
48	D.2.2471	90	3.0	1.110	1.5	buff pink	yellow	long oval	3	1	2	1.5	1.851			cracky skin, **knobs**, dumbbell, pointy, bottle, bulged eyes
49	Atlantic	65	4.6	1.084	2.5	tan	white	round oblong	3	2.5	4	2.5	1.112	3		FBE, deep eyes, flaky, rot, greening
50	R.2.2849	85	2.1	1.085	3	tan	white	oval long	3.5	2.5	4	2	1.428		2	skinning, pointy, **short**, hollow heart
51	D.2.2058		0.3	1.078	1.5	champaign	yellow	round oval	3.5	2.5	3.5	2	1.567			pointy, button, bottle

Supplementary Table 6.2 (Continued)

52	CR.2.1589	40	1.4	1.071	3	tan buff	white	round	4	2	5	1	1.210	1	1	ugly, cracky skin, scaby, greening, hollow heart
53	D.2.2555	95	0.7	1.096	1	orange yellow	dark yellow	round oval	4	3	4	2	1.357			short, button, chain, skinning
54	D.2.2100	95	0.8	1.098	1.5	buff pink	cream yellow	long fing	3.5	2.5	4	2	2.761			end rot, pointy
55	D.2.2436	100	0.9	1.066	1	yellow	cream yellow	long fing	3.5	2.5	3.5	2	2.237			**end rot**, bottle, pointy, knobs
56	CR.2.1638	90	4.4	1.084	2	buff	white	oblong round	3.5	3	4.5	3	1.191	3	2.5	sticky, greening, skinning, lenticels
57	RD.2.3836	80	6.5	1.068	1.5	buff	white	long	4.5	1.5	4	1.5	1.490		1.5	**knobs**, **growth cracks**, button, **bulging eyes**, greening
58	R.2.2912	90	3.5	1.080	2.5	buff	white	oval	3.5	2.5	4.5	2.5	1.360	2	2	**hollow heart**, scab, pointy, button
59	OR01007-3	85	4.4	1.077	2.5	buff	white	long	4	3	4.5	3	2.036		3	thin, curvy, greening
60	RC.2.3241	30	2.1	1.079	2.5	buff tan	white	oval oblong	3.5	3	4.5	3	1.352		2.5	short, typy
61	BD1257-5		0.0													
62	CR.2.1631	30	3.7	1.073	2	buff yellow	yellow	oval oblong	3.5	3	4.5	2.5	1.323	2.5	2.5	pear, skinning, bottle
63	D.2.2240	90	0.7	1.094	1	yellow	yellow	long fing oval	4	3	2.5	2.5	1.480			cracky skin, pointy
64	RD.2.3661	85	6.7	1.075	2.5	buff yellow	yellow	oval oblong	3.5	3	2.5	3	1.400		3	blocky, sticky, pointy
65	CR.2.1491	65	5.2	1.083	2.5	buff yellow tan	white	round	3.5	3	4.5	3	1.082	3.5		greening, flaky, sticky
66	R.2.3073	95	3.6	1.077	2.5	buff tan	yellow	oblong blocky	4	2.5	4.5	3	1.580		3	growth cracks, knobs, sticky, XXL
67	D.2.1904	95	1.7	1.099	1	light red	white	oval round	3.5	2.5	2	2	1.615			shriveled, pointy, bottle
68	RD.2.3976	95	6.2	1.067	1.5	yellow	yellow	oval oblong	3	2.5	2.5	2	1.615			deep eyes, bottle, greening, irregular
69	D.2.2009	60	2.2	1.095	1.5	maroon	yellow	long fing	3.5	3	3	2.5	1.791			cracky skin, greening, pointy
70	RD.2.3493	95	6.6	1.091	1.5	buff pink	yellow	long oblong	3	2.5	3	3	1.505		2.5	pointy, short
71	RD.2.3920	50	2.6	1.085	1.5	peach red	yellow w/ red	oval round	3.5	2.5	2.5	2	1.620			pointy, bottle, sl. Irregular, unattractive
72	D.2.2660	95	2.0	1.093	1.5	champaign	yellow	round oval	3.5	2	1.5	2	1.346			pointy, sticky, bottle, shriveled
73	RD.2.3983	85	6.6	1.070	1.5	buff	white	long oval	3.5	3	2	2.5	1.416		2	greening, thin, pointy, bottle
74	R.2.2891	100	0.8	1.068	1.5	buff	white	round	3.5	2	5	2.5	1.194		1.5	greening, bottle, IPS
75	D.2.2506	95	2.5	1.084	1.5	buff	white cream	oval	3.5	2.5	2.5	2	1.658			pointy, bottle, greening
76	CR.2.1666	90	6.3	1.082	2.5	buff tan	white	comp round	4	3.5	5	3.5	1.201	3.5		flat, bottle, greening
77	CD.2.1316	90	2.8	1.091	2	buff	white	oval oblong	2.5	3	2.5	3	1.230		3	deep eyes, sticky, interesting

Supplementary Table 6.2 (Continued)

78	Russet Burbank	85	5.4	1.071	3	buff tan	white	long	3	2.5	5	3	1.675		3	pointy, knobs, curvy
79	RC.2.3395	70	2.5	1.079	1.5	buff tan	cream white	rounded oval	3.5	3	4	3	1.341	3	2.5	short, greening, pointy, button
80	RC.2.3185	90	1.4	1.094	2	buff	white	round oval	3.5	3	4.5	2.5	1.223	2	2	bottle,, pointy, short, greening
81	RD.2.3752	80	7.4	1.072	1.5	yellow	yellow	oval	4	2.5	2.5	2	1.739			greening, **knobs**, rhizoc, irregular
82	RC.2.3402	100	4.5	1.080	2	buff	white	oval oblong	4	3	4.5	3	1.259	2.5	2.5	flat, bottle, skinning
83	C.2.1169	85	1.3	1.078	1.5	buff	cream yellow	round oval	4	3	5	3	1.409	2.5		skinning, short, knobs, small bumps
84	CR.2.1841	55	7.2	1.079	1.5	buff	yellow	round	4	2.5	4.5	3	1.568	2.5		irregular, curvy, greening, pointy
85	CR.2.1827	95	3.3	1.089	2	buff	white cream	round	4	3	4.5	2.5	1.209	3		greening, bottle, skinning
86	Russet Burbank	85	6.1	1.077	3.5	tan	white	long	3.5	1.5	5	1.5	1.724		1	**knobs**, bottle, bulged eyes, hollow heart, ugly
87	RC.2.3290	65	3.4	1.084	2.5	buff	white	oval round	4	3	4.5	3	1.370	2.5		greening, sticky, flat
88	RD.2.3780	85	3.0	1.083	2	buff	white	oblong long	3.5	3	4	3	1.420		3	rot, sticky, pointy
89	D.2.2170	100	2.3	1.084	1	yellow	yellow	round	3	2.5	2	3	1.028			pink eyes, **button**, multiple eyes at butt end
90	RD.2.3815	90	1.5	1.079	1.5	purple red	yellow w/ purple	round oval	3.5	2.5	2.5	2	1.362			sticky, bottle, pear (try chipping?)
91	POR06V12-3	85	3.8	1.083	4.5	tan brown	white	long oval	4	3.5	4.5	3	1.776		3.5	heavy russet, sticky
92	BD1240-6		0.0													
93	A08640-2	75	2.8	1.077	2.5	buff	cream white	oval oblong	3.5	3	4.5	3	1.331	2.5	2.5	short, greening
94	R.2.2870	60	3.1	1.081	4	tan	white	long	3.5	3	4.5	3	1.754		3	typy, rhizoc, flaky
95	CR.2.1442	90	3.5	1.086	2.5	buff tan	white	oblong round	3.5	3	4	3	1.233		3	short
96	D.2.2163	90	1.5	1.101	1.5	buff pink	cream yellow	long fing	2.5	3.5	4.5	3	2.092			end rot, pointy, bottle
97	CR.2.1701	70	6.0	1.082	2.5	buff tan	white	oval oblong	3.5	2.5	4.5	2	1.222		2.5	pointy, sticky, short
98	C.2.1134	85	3.0	1.091	1.5	buff	white	round	4	3.5	4.5	3.5	1.010	3		FBE, sticky, greening
99	RD.2.3794	85	4.6	1.093	2.5	buff tan	white	oval oblong	3.5	2.5	3	2.5	1.381		2.5	typy, shatter, flaky, flat
100	RD.2.3843	90	3.0	1.092	1.5	buff tan	white cream	long oval	4	2	3.5	2	1.350		2.5	bottle, curvy, pointy
101	RD.2.3927	90	6.3	1.074	2	buff	cream white	round oblong	3.5	3	1.5	2.5	1.374	2.5		bottle, greening, thin
102	D.2.2023	90	2.8	1.093	1.5	maroon red	yellow	oval	4	3	2	3	1.351			**hollow heart**, cracky skin, pointy
103	CR.2.1722	90	2.8	1.082	2	buff tan	white	round	3	3	5	3	1.045	3		growth cracks, sticky, FBE
104	R.2.2709	90	2.2	1.075	3	tan	white	oblong	4	2.5	5	2.5	1.407	2.5	2.5	bottle, pointy, skinning
105	CR.2.1694	90	3.1	1.079	2	buff	white	oblong	3.5	2.5	3	2	1.214		2	thin, **short**

Supplementary Table 6.2 (Continued)

106	RD.2.3500	95	4.7	1.084	1.5	buff w/ pink	yellow	long oval	2.5	2.5	4	3	1.343		2.5	pointy, **growth cracks**, bottle, pear, greening
107	RD.2.3507	85	4.6	1.086	2	champaign	yellow	round	2.5	3	2.5	2.5	1.236	2.5		deep eyes, button, growth cracks
108	RD.2.3829	80	7.4	1.083	3	purple brown	cream white	long oblong	3.5	2.5	2	2	1.391		1.5	scab, hollow heart, pointy, curvy, purple, VD
109	Snowden	90	9.2	1.083	3.5	buff tan	white	comp round	3	3.5	4.5	3.5	0.963	3.5		sticky, FBE
110	R.2.2884	95	5.3	1.076	4	brown	white	long oblong	3.5	3	4	3	1.897		3.5	flat, pointy, sl. Irregular
111	R.2.3031	45	4.0	1.088	3	buff tan	white	oblong blocky	3	3	5	3	1.517	2.5	3	FBE, short
112	A08640-2	50	3.2	1.073	2.5	buff tan	yellow	oblong round	3	3.5	4.5	3	1.166	3.5		flaky, sticky
113	D.2.1967	95	4.7	1.079	1.5	pink red	yellow	long oval	2.5	2.5	1.5	2	1.440			end rot, squishy, shriveled, curvy, button
114	C.2.1001	90	3.8	1.097	2	buff	white	round	3	2.5	3	2.5	0.969	3		deep eyes, sticky, sl. Irregular
115	R.2.3129	80	1.3	1.067	1.5	buff	white	oval oblong	2.5	3.5	5	3.5	1.364		2	deep eyes, pointy, pear, **short**
116	CD.2.1337	85	3.8	1.094	1.5	buff	cream white	oval	3.5	2.5	4	2.5			2	button, pear, curvy, **short**
117	R.2.3038	60	4.6	1.083	3	tan	cream yellow	round	3	3	2	2.5	1.119	3		FBE, flaky skin, sticky
118	RD.2.3731	85	2.5	1.087	2	buff tan	white	(check photo)	2	2	4	2.4	1.340		2	short, irregular russet, round
119	CD.2.1246	90	4.7	1.087	2	buff	white	round oblong	3	3	3.5	3	1.176	3		skinning, shatter, dumbbell
120	R.2.3101	70	1.3	1.082	2	buff yellow	white	round oval	3	2.5	3	2	1.333	2.5		pointy, bottle, pear
121	C.2.1099	95	2.6	1.074	2	buff	white	oval oblong	4	2.5	4.5	2.5	1.513	2.5	3	skinning, greening, pointy
122	RD.2.3479	95	2.2	1.089	2	pink buff	yellow	oval	4	2.5	3.5	2	1.396			pear, pointy
123	CR.2.1463	95	0.9	1.084	2.5	buff	white	oblong	3.5	2.5	4.5	3	1.406		2.5	pointy, sticky
124	D.2.2184	90	2.0	1.109	1.5	maroon	yellow w/ pink	long fing	3	3.5	2.5	2.5	2.031			bottle, button, multiple eyes at butt end, ugly, flesh discoloration
125	RD.2.3682	80	1.4	1.073	2	buff	white	round oblong	3.5	2.5	3	2	1.205		2	round, short,greening
126	Atlantic	65	6.0	1.094	2.5	buff tan	white	round comp	3	3	4	3	1.066	3		bulging eyes, greening, FBE, sticky, flaky
127	RC.2.3276	75	3.4	1.085	2	buff tan	white	oval round	3.5	2	4.5	2.5	1.559		2.5	short, pear, button, sticky, pink eyes
128	RC.2.3409	85	3.8	1.090	2	buff tan	white	round	3.5	3.5	4.5	3	0.992	3.5		greening, flaky skin
129	D.2.2415	95	2.1	1.089	1	buff w/ pink	cream yellow	oval long	3.5	2.5	1.5	2	2.149			bottle, pear, button, end rot, sticky, curvy
130	D.2.2219	90	1.4	1.134	1	yellow	dark yellow	round oval	3.5	2	2	1	1.313			rodent damage, greening, shriveled, pointy

Supplementary Table 6.2 (Continued)

131	Snowden	75	2.6	1.089	2.5	yellow buff tan	cream white	round comp	3	3	4.5	3	0.984	3		FBE, greening, flaky skin, sticky
132	R.2.2842	80	3.3	1.076	2.5	buff tan	white	long oblong	3	3.5	3.5	3	1.625		3	processing only, deep eyes, shatter
133	D.2.2618	85	2.3	1.071	1.5	yellow	yellow	long oval	3.5	3	1.5	2.5	1.267			greening, short, round
134	A07547-4	80	3.9	1.070	2.5	buff tan	white	long oval blocky	3.5	3	4	3	1.609		3	pointy, bottle, round
135	CD.2.1274	95	4.0	1.087	3	buff yellow tan	yellow	long oblong	3	3.5	3.5	3	1.496		3	deep eyes, short, sticky
136	D.2.2296	70	1.8	1.080	1	champaign yellow	yellow	oval	4	3.5	2	3	1.377			button, pointy, nice, shriveled
137	D.2.1960	95	2.0	1.077	1	red	yellow	long fing	3.5	3	1.5	2.5	1.830			shriveled, pointy, curvy
138	R.2.2821	85	3.8	1.076	2	buff tan	cream white	oval oblong	3.5	3	4.5	2.5	1.241		3	skinning, greening, round, button, typy
139	D.2.2156	95	2.6	1.097	1.5	champaign	yellow	round	3	2.5	2	2.5	1.206			pointy, bottle, shriveled, ting
140	D.2.2450	100	2.7	1.089	1	yellow	dark yellow	long fing	3.5	3	2.5	3.5	2.475			fingerling, pointy, curvy
141	Russet Norkota	75	5.1	1.070	3.5	tan	white	long oblong	3.5	3.5	5	3.5	1.849		3.5	pointy, sl, curvy, typy
142	R.2.2982	40	2.3	1.094	1.5	buff	white	oblong	4	3	4	2.5	1.411		2.5	typy, pear, flat
143	RC.2.3192	75	3.4	1.089	2.5	buff	white cream	oval oblong	4	3.5	4.5	3	1.382		2.5	short, flat, pointy, greening
144	D.2.2513	85	1.0	1.106	1.5	yellow	yellow cream	long oval	3	2.5	2	2.5	1.767			growth cracks, pointy, shriveled
145	RD.2.3759	90	1.5	1.090	2	buff	white	long	2.5	3	4.5	3	1.553		2	**short**, pointy
146	RD.2.3773	80	3.5	1.082	2	buff yellow	yellow	long	3.5	2	3	3	1.973		3	pointy, thin
147	RC.2.3157	90	3.5	1.080	3	buff tan	cream yellow	round oblong	4	3.5	4	3	1.219	3		skinning, sticky
148	D.2.2394	90	3.8	1.112	1.5	buff yellow	yellow	oval	3.5	2.5	2	2	1.392		1.5	pointy, greening, button, pear
149	CD.2.1351	60	3.1	1.097	2	red	yellow w/ pink	round	3.5	3	3.5	3	1.277			button, sticky, cracky skin, hollow heart
150	CR.2.1757	85	4.0	1.074	1.5	buff yellow	yellow	oval oblong	4	3	4.5	3	1.140	2.5	2.5	growth cracks, curvy
151	R.2.2758	80	5.2	1.087	2	buff	white	long	4	3.5	4.5	3	2.068		3.5	thin, typy, scab, nice
152	Russet Burbank	85	6.2	1.076	3	tan	white	long	3.5	2.5	5	2	1.576		2.5	growth cracks, knobs, curvy, bottle
153	RC.2.3318	75	4.4	1.093	2	buff w/ pink	cream yellow	oblong round	3	3	4	2.5	1.160	2.5		sticky, IBS
154	Eva	90	1.4	1.079	1.5	buff	white	round	4	3	5	3	1.110	3		skinning, lenticels
155	D.2.2590	95	1.9	1.105	1.5	red	dark yellow	long oval	3.5	3	1.5	2	1.367			end rot, shriveled, pointy
156	CR.2.1449	90	0.2	1.077	1.5	buff	white	round	4	2	4.5	1.5	1.208	1		skinning, pear
157	CR.2.1806	85	1.9	1.093	1.5	buff	white	oval	4	2.5	4	2	1.524		2	round, **short**, skinning, translucent end
158	R.2.2989	80	4.7	1.087	3	tan	white	oblong long	4	3	4.5	3	1.475		3	typy, flat, sl. Irregular

Supplementary Table 6.2 (Continued)

159	RD.2.3563	90	1.6	1.087	1.5	buff	yellow	round	3.5	2.5	4.5	2.5	1.178	2		skinning, shriveled, pear, bottle
160	RD.2.3584	95	3.2	1.087	1.5	yellow buff	yellow		2.5	4	4	2	1.353		2	**greening**, knobs, pointy
161	RC.2.3311	95	1.4	1.090	1.5	yellow	yellow	oval	4	2.5	3.5	2.5	1.609			pointy, bottle, curvy, skinning
162	C.2.1127	90	2.6	1.078	2	buff tan	white cream	round	3.5	3.5	5	3	0.924	3.5		FBE, sticky, greening
163	R.2.2688	80	4.1	1.084	2.5	buff yellow	yellow	oval long blocky	3	2	4.5	2.5	1.396		2.5	pear, round, skinning
164	R.2.2933	90	5.1	1.089	2	buff tan	white	long oval	3.5	2.5	3.5	2	1.350		2.5	skinning, shriveled, shatter
165	D.2.2114	90	1.5	1.110	2	peach red	yellow	oval long	4	3	2	2.5	1.827			pointy, curvy, good flesh
166	Snowden	60	1.5	1.098	2.5	buff tan yellow	cream	round	3	3	4.5	3	0.976	3		sticky, FBE, flaky
167	D.2.2499	95	2.2	1.102	1.5	buff pink	cream white	oval round	3	2	1.5	1.5	1.703			bottle, pointy, button, ugly
168	RD.2.3633	75	1.7	1.093	1.5	buff yellow	yellow	oval long	4	2.5	3.5	2.5	1.666		2	short, bottle, button, lenticels, shriveled
169	P2-4	85	5.6	1.076	2	buff w/ purple	white	oval oblong	4	2.5	5	2.5	1.586		2	**bulgy eyes**, pointy, pear, curvy, greening
170	RD.2.3857	90	3.0	1.085	1.5	champaign	yellow	round	3.5	2	1.5	2	1.004			chain, button, dumbbell, irregular
171	CD.2.1260	90	4.3	1.083	2	rusty red	white w/ pink	round	3	1	2	1	1.184			scab, growth cracks, irregular, knobs, button, cracky skin, ugly
172	RD.2.3486	95	4.1	1.084	1.5	buff pink	yellow	round	3.5	3.5	3	2.5	1.559			bottle, pointy, sl. Irregular
173	C.2.1085	40	1.2	1.086	2	buff	white	round	4	3	2.5	2	1.070	2		pointy, pear, short, sticky
174	R.2.3066	95	7.7	1.082	2	buff tan	yellow	oblong long	4	2	4.5	1.5	1.216		1.5	XXXL, **growth cracks**, **knobs**, greening, sticky
175	RC.2.3269	55	2.6	1.080	2.5	tan	white	oval	3.5	2.5	4	2	1.731		2.5	bottle, pear, pointy, short
176	D.2.1925	90	0.0													
177	C.2.1078	85	1.8	1.097	2	buff	white	round	4	2.5	4.5	2.5	1.097	3		sticky, short, shatter bruise
178	CD.2.1295		0.6	1.086	2.5	buff tan	yellow	oval long	4	3	5	3	1.657		3	2 tubers, nice
179	D.2.2093	90	1.4	1.100	1	champaign	dark yellow	oval	3.5	2	2	2.5	1.556			pointy, shriveled
180	A06866-2	75	3.9	1.107	2.5	buff	yellow	round oval	4	3	3.5	3	1.383		2.5	twins, pointy, flat
181	D.2.2030	95	1.7	1.104	1.5	red	cream white w/ purple	long	3.5	3	2	1.5	1.729			knobs, button, rot, pointy, bottle, cracky skin
182	Snowden	75	5.3	1.085	2.5	buff tan	white	round comp	3	3	4.5	3	1.046	3		flaky, deep eyes, FBE, greening, sticky
183	CD.2.1379	90	2.0	1.104	1	yellow	yellow	oval	3	2.5	1.5	2.5	1.203			pointy, bottle, curvy
184	Ivory Crisp	75	4.5	1.080	2	buff tan	white	round	3.5	2.5	4.5	2.5	0.932	2.5		FBE, sticky, greening, XL
185	D.2.2646	90	2.0	1.116	1.5	light red w/ buff	cream	long fing	3	2	3.5	2	3.124			**end rot**, cracky skin, curvy
186	CR.2.1890	85	1.8	1.085	2.5	tan	white	round	3.5	3	4.5	3	0.961	2.5		**short**, sticky

Supplementary Table 6.2 (Continued)

187	D.2.2639	90	1.1	1.102	2	buff pink	cream yellow	oval	3.5	2.5	2	1.5	1.467			cracky skin, pointy, button, shriveled
188	D.2.2352	95	1.2	1.100	1.5	red buff	yellow	oval	4	3.5	2.5	2	1.420			skinning, patchy, rot
189	D.2.2016	95	2.0	1.088	1	orange yellow	yellow	long blocky	3	2.5	2	2	1.650			irregular, pointy, curvy
190	AO03123-2	95	1.5	1.074	2.5	buff tan	white	long	3.5	2.5	5	2.5	1.734		2.5	short, sticky
191	RD.2.3528	95	4.8	1.086	2	buff red	yellow	oval round blocky	2.5	2	4	1.5	1.315			rodent damage, deep eyes, button, pointy, hollow heart
192	C.2.1176	90	0.7	1.079	2	buff w/ pink	white	round oval	3.5	1.5	2	2.5	1.080	1.5		bottle, short
193	CR.2.1708	35	1.2	1.103	2	buff tan	white	round	4	3	4	2.5	1.054	2		short, shriveled, rot
194	D.2.1939	80	2.1	1.104	1.5	red	yellow	long fing	3.5	2.5	2.5	2.5	2.753			purple discoloration in flesh, curvy, pointy, cracky
195	D.2.2520	95	1.8	1.078	1.5	red	yellow w/ pink	long fing	3.5	2.5	2.5	2	1.872			curvy, pointy, cracky skin
196	C.2.1120	85	2.4	1.088	2	buff tan	white	round	4	3	3.5	3	1.085	3		greening, short
197	D.2.1918	95	2.3	1.090	1.5	red	yellow	long fing	2	3	2.5	2	3.289			landrace type, too many eyes, curvy, snaky
198	R.2.2863	80	4.0	1.091	5	dark brown	white	long oblong	3.5	3	5	3	1.511		3.5	heavy russet, pointy
199	CR.2.1505	90	1.0	1.076									1.072			SEVERE MIX
200	R.2.3122	95	1.8	1.089	2	buff	white	oval	3.5	2.5	4	2.5	1.557		2.5	pointy, bottle
201	CR.2.1407	95	0.5	1.082	2	buff w/ pink	white	oval	3.5	2.5	4.5	2	1.293		1	**short**, greening
202	D.2.2002	95	1.2	1.095	1.5	yellow w/ pink	yellow cream	oval long	3	3	2	2.5	1.826			greening, squishy
203	CR.2.1428	85	1.0	1.086	2.5	buff tan	white	oval oblong	3.5	3	3.5	2	1.316		2	**short**, cracky skin
204	RC.2.3367	85	0.6	1.069	2	buff	cream yellow	round oval	4	2.5	3.5	2	1.266		2	squishy, **short**
205	RD.2.3808	85	1.5	1.094	2	buff	white	round oval	3.5	2.5	4	3	1.337	2		short, bottle, pear
206	RD.2.3675	95	1.5	1.075	1.5	buff	white cream	oval	3.5	3	3.5	2.5	1.349		2.5	**short**, typy, skinny
207	Ivory Crisp	85	1.3	1.072	1.5	buff tan	cream yellow	round	3.5	3	3	3	1.013	3		greening, FBE
208	BD1251-1		0.0													
209	AO00710-1	90	1.2	1.080	3.5	tan	yellow	long oblong	4	3	5	3	1.520		3	pointy, button
210	R.2.2877	75	1.8	1.082	2.5	buff w/ pink	white	oval oblong	4	3.5	4.5	2.5	1.755		3	typy, greening, **IPSB, skinning**
211	D.2.2324		0.6	1.053	1.5	light red	yellow w/ pink	long fing	3.5	2	1.5	1	1.697			rot, pointy, curvy, ugly flesh
212	RD.2.3605	95	1.8	1.090	2	buff tan	yellow	oval oblong	4	2.5	4	2.5	1.555		1.5	hollow heart, **IPS**, greening, rot
213	RD.2.3885	85	4.2	1.075	1.5	champaign red	yellow w/ red	long	2.5	2.5	4.5	2.5	3.094			bottle, pointy, curvy

Supplementary Table 6.2 (Continued)

214	CR.2.1834	80	2.2	1.086	1.5	buff	cream yellow	round	3.5	3	5	3	1.060	3		skinning, pointy
215	BD1268-1		0.0													
216	D.2.2072	70	2.1	1.117	1.5	buff yellow	cream yellow	oval	4	2	2	1.5	1.689			pointy, button, bottle
217	D.2.2653	95	1.9	1.104	1.5	orange yellow	dark yellow	oval oblong	3.5	2.5	2.5	2	1.363			squishy, pointy, cracky
218	R.2.2996	90	3.2	1.086	2.5	buff	white	long oval	3.5	3	4.5	3	1.603		3	pointy, bottle, pear
219	CD.2.1344	85	4.8	1.078	2	buff yellow	yellow	oval oblong	4	3	4.5	2.5	1.344		2.5	short, flat, greening, bottle
220	CD.2.1225	90	4.5	1.099	2	buff	yellow	round	3.5	3	3.5	3	1.211	2.5		greening, bottle, pointy
221	A06866-2	90	4.0	1.097	2	buff yellow	yellow	long	4	3	4.5	3	1.541		2.5	**hollow heart**, **greening**, typy
222	RD.2.3738		0.2	1.095									2.904		1	one tuber
223	D.2.1953	85	0.4	1.115	1.5	maroon red	yellow w/ maroon	long fing	3.5	3	4.5	1.5	2.184			pointy, bottly, ugly flesh
224	CR.2.1764	95	2.3	1.092	1.5	buff	cream white	round	4	3	4.5	3	1.213	3		greening, pointy
225	D.2.2310	90	2.2	1.099	1.5	buff yellow	yellow	oval	3.5	2.5	1.5	1.5	1.642			squishy, bottle, pointy
226	RD.2.3465	90	0.2	1.087									1.284			SEVERE MIX
227	CR.2.1659	85	3.6	1.090	2	buff tan	white	long oblong	3.5	2.5	4.5	3	1.640		2	skinning, bottle, flat
228	Russet Norkota	80	5.5	1.073	4	brown	cream white	oval oblong	3.5	3.5	5	3	1.865		3	knobs, typy, curvy
229	R.2.2814	75	6.6	1.095	2	buff	white	long oval	4.5	2.5	4.5	2.5	1.546		2.5	bulging eyes, pointy, curvy, greening
230	D.2.2317	80	2.2	1.099	1.5	light red	yellow	long fing	3.5	3	2.5	2.5	1.955			pointy, cracky, skin, bottle
231	CR.2.1596	85	3.7	1.093	2.5	buff tan	yellow	oval	3.5	3	5	2.5	1.440		2.5	pointy, pear, short, greening
232	R.2.3024	90	1.5	1.095	2.5	buff tan	cream yellow	oval	4	3	4.5	3	1.411	2		dumbbell, pointy, **short**
233	RD.2.3913	95	5.1	1.095	1	red yellow	yellow	round	2.5	2	2.5	2	1.067			bottle, pointy, irregular
234	Russet Burbank	85	4.2	1.077	3	tan	white	long oval	3.5	2.5	5	2.5	1.431		3	typy, pointy, short
235	R.2.3017	80	1.2	1.088	2	buff	white	oval	4	3.5	4.5	2.5	1.489		2.5	pointy, pear, short
236	RD.2.3766	100	1.8	1.082	2	buff yellow	yellow	oval blocky	2.5	2	4.5	3	1.386		2.5	blocky, deep eyes, curvy, pointy
237	P.1.1743		0.0										1.451			
238	D.2.2464	85	1.6	1.100	1.5	yellow	yellow	long fing	2.5	2.5	3	2	1.891			hollow heart, pointy, dumbbell, flaky
239	Snowden	80	4.8	1.088	2.5	buff tan	white cream	round comp	3	3.5	4.5	3.5	1.057	3.5		greening, FBE, sticky
240	BD1268-1		0.0													
241	AO03123-2	80	3.3	1.085	2.5	tan	white	long oblong	4	3	5	3	1.674		3	sticky
242	C.2.1197	70	1.4	1.091	2	buff	white cream	comp round	3.5	3	4	3.5	1.142	3		flat, skinning, greening

Supplementary File Table 6.2 (Continued)

243	D.2.1974	90	2.0	1.105	2	buff	yellow	oval	3.5	3	1.5	2	1.475		2	shriveled, hollow heart, short
244	CD.2.1288	90	2.5	1.099	1.5	yellow	yellow	round	3.5	3	4.5	3	1.065			**hollow heart**, sticky
245	RC.2.3423	70	3.8	1.081	1.5	buff	white	round comp	3.5	2.5	3	2.5	1.022	2.5		skinning, squishy, flat
246	R.2.2674	90	4.7	1.089	2.5	buff tan	yellow	oval oblong	4	3.5	4	3	1.400	2.5	3	blocky, squishy, pear
247	RD.2.3549	85	2.8	1.096	3	tan	cream white	oval oblong	4	2.5	4.5	3	1.401		3	bulging eyes, sticky, greening
248	RD.2.3535	95	4.5	1.076	2	buff tan	yellow	oval oblong	4	3.5	3	3	1.404		3	pointy, button, bottle
249	CR.2.1729	80	6.2	1.076	2.5	buff tan	cream yellow	comp round	3.5	3	4	3.5	1.080	3		greening, flat, XL
250	Payette Russet	90	1.8	1.085	3.5	tan	yellow	long oval	3.5	3	5	3	1.657		3	curvy, bottle, pear
251	CR.2.1526	75	2.9	1.082	1.5	yellow	yellow	round oval	4	2.5	4.5	2.5	1.453	3		skinning, squishy, pear
252	D.2.2198	80	4.1	1.110	1.5	orange yellow	dark yellow	long fing	3.5	3	3.5	2.5	1.968			cracky, pointy, bottle
253	R.2.2681	50	2.8	1.091	2	buff tan	cream white	long oval	4	3.5	4.5	2.5	1.614		3	typy, pointy, thin
254	BD1202-2		0.0		1.5	maroon red	yellow	long oval	3.5	2.5	3	2	2.276			pointy, knobs, bottle, multiple eyes at butt end
255	CR.2.1862	85	2.9	1.075	2	buff	white	round oblong	3	2.5	4.5	2.5	1.355	2.5	2.5	deep eyes, sticky
256	RC.2.3339	80	3.0	1.075	2.5	buff tan	cream yellow	round oblong	4	3	3	2.5	1.300	2.5		short, greening, sticky
257	CR.2.1883	85	6.5	1.084	2.5	tan buff	white	round	2.5	3.5	2.5	2.5	1.137	2.5		bottle, flat, shatter
258	D.2.2086	90	0.5	1.164	2	red	yellow w/ red	oval	3.5	2.5	1.5	1	1.333			squishy, ugly flesh, bottle
259	Atlantic	85	6.8	1.088	2.5	buff tan	white	round	3	2.5	4	3	1.023	3		hollow heart, flaky, sticky, FBE
260	CR.2.1897	85	5.7	1.085	2.5	tan	white	round oval blocky	3	3	3	2.5	1.302		2.5	IPS, irregular, FBE
261	RC.2.3381	75	1.8	1.071	2	buff	white	round	4	3	3.5	2.5	1.245	2.5		greening, short
262	R.2.2786	90	4.5	1.089	2	buff tan	white	long	4	2.5	4	2	2.040		2	**lenticels**, squishy, snaky, x long, skinning
263	D.2.2128	90	1.5	1.104	1.5	yellow	dark yellow	oval	4	3	2	2.5	1.221			pointy
264	R.2.2716	90	2.0	1.116	2	buff	white	oval oblong	3.5	3	5	3	1.478		2.5	short, pointy, bottle
265	RD.2.3591	90	2.8	1.091	2.5	buff tan	white	long oval	3	3	4.5	3	1.706		3	sticky, deep eyes, short
266	BD1257-5		0.0													
267	CR.2.1855		0.0										1.329			1 tuber
268	BD1202-2		0.0													
269	CR.2.1603	75	3.5	1.067	2	buff	white	round oblong	4	2.5	4.5	2.5	1.215	2.5	2	round, skinning, IBS
270	CD.2.1358	95	3.0	1.078	2	champaign red	yellow	round comp	3.5	3	3.5	3	1.136			dumbbell, sticky
271	RD.2.3864	85	3.2	1.079	1.5	buff pink	yellow	round oval	3.5	2.5	2.5	2	1.222			bottle, pear, growth cracks, alligator skin

Supplementary Table 6.2 (Continued)

272	RC.2.3346	30	1.6	1.080	2.5	buff tan	white	round	4	3	5	3	1.094	3		skinning, greening, sticky
273	RC.2.3451	90	4.9	1.094	2	buff	white	round oblong	4	3	2.5	2.5	0.998	2.5		skinning, flaky
274	RD.2.3969	85	1.9	1.058	1.5	yellow	yellow	long oval	4.5	2.5	2	2.5	1.718		2	bulgy eyes, greening, sl. Irregular, button, knobs
275	R.2.3003	85	3.0	1.080	1.5	buff	cream yellow	long	4	2.5	4.5	2.5	1.845		2.5	**knobs**, greening, skinning
276	CR.2.1785	90	1.6	1.062	1.5	buff tan	white	round	3.5	2	5	1.5	1.112	1		bottle, dumbbell, growth cracks, irregular
277	R.2.2961	90	3.0	1.084	2.5	tan brown	yellow cream	round oval	4	2.5	4	2	1.314	2.5		**IBS**, skinning, ugly skin
278	RC.2.3199	85	2.6	1.087	1.5	buff	white	round	4	3	4	3	1.392	2.5		greening, pointy
279	D.2.2338	95	2.3	1.079	1	yellow	buff yellow	oval	3.5	2.5	2	2	1.448			pointy, bottle, sticky
280	RD.2.3472	80	4.3	1.088	1.5	buff pink	yellow	long	3.5	2	2	2	1.705		2	rot, bottle, skinning, squishy
281	R.2.2968	90	2.6	1.083	2	buff yellow	yellow	oval	3.5	3	4	3	1.599		2.5	short, flat, button, pointy
282	D.2.2611	90	0.6	1.125	1	buff yellow	yellow	oval	3.5	2.5	2	2	1.372			pointy, bottle, greening
283	D.2.2562	85	1.9	1.095	1	orange yellow	yellow	round oval	3	2.5	2	2	1.619			bottle, pointy, greening, squishy
284	RD.2.3647	90	1.4	1.093	2	buff pink	yellow	oval long	4	3.5	4.5	2.5	1.900		2.5	thin, shriveled, button
285	R.2.2800	85	2.6	1.070	2	buff	white	long	4	2	3.5	2	1.925		1.5	thin, squishy, button, curvy, bottle
286	CR.2.1715	85	0.7	1.091	2.5	buff	white	oval	3.5	3	3.5	3	1.419		1.5	short
287	P2-4	85	4.5	1.077	2	buff	white	oval long	5	2.5	5	2	1.725		2	**bulging eyes**, bointy, bottle, button
288	Russet Norkota		0.0													
289	Atlantic	75	8.0	1.090	2.5	buff tan	white	round oblong	3	2.5	4	2.5	1.042	2		**hollow heart**, deep eyes, sticky, greening
290	D.2.2212		1.3	1.120	1.5	maroon red	orange yellow	long fing	2.5	3	2.5	2.5	2.028			curvy, pointy, bottle
291	AO00710-1	90	2.1	1.092	4	brown	yellow	round oval	4	2.5	5	2	1.283		2.5	round, pointy, sticky
292	RD.2.3934	90	5.3	1.077	1.5	buff	white	long	3	2	2.5	2	1.876		2	bottle, pointy, end rot, curvy
293	CR.2.1582	75	6.1	1.082	3	buff tan	white	oblong long blocky	3.5	3	3	3			3	deep eyes, greening, flaky
294	D.2.2366	85	2.0	1.090	1	yellow	yellow	oval round	3.5	3	2.5	2	1.568			greening, sticky, squishy
295	D.2.2492	90	2.2	1.098	1.5	champaign	yellow	long fing	4.5	2.5	2	1.5	2.329			hollow heart, bottle, pointy, button
296	C.2.1113	75	2.4	1.070	2	buff	white	round	4	3	4.5	3	1.107	2.5		short
297	R.2.3045	80	3.7	1.084	3	buff tan	white	long oblong	3	3	2	2.5	1.513		2.5	greening, flat, flaky
298	D.2.2457	90	1.6	1.096	1.5	buff yellow	cream white	oval	4	3	1	1.5	1.750			greening, pointy, shriveled, button
299	RD.2.3724	80	3.8	1.094	1.5	buff yellow	yellow	oval oblong	3.5	3	4	3	1.617		2.5	sticky, squishy, thin
300	BD1222-1		0.0													

Supplementary Table 6.2 (Continued)

301	RC.2.3304	40	1.1	1.075	2	buff	white	round	4	3	5	2.5	1.231	2.5		sticky, short
302	Snowden	80	3.7	1.083	2.5	yellow buff tan	cream white	round	3	3	4	3	1.013	3		deep eyes, FBE, greening, sticky, flaky
303	D.2.2268	90	1.9	1.116	1	yellow	yellow	oval	3.5	3	2	2.5				pointy, short
304	RD.2.3745	90	5.5	1.094	1.5	buff yellow	yellow	long	4	2.5	3.5	3	1.726		2.5	knobs, pointy
305	BD1244-1		0.0													
306	C.2.1036	95	4.6	1.110	2	buff	white	round	4	3	4	3	1.107	3		cracky, greening, sticky
307	RC.2.3388	85	5.1	1.091	2	buff	white	round comp	4	3	3	2	1.263	2.5		dumbbell, chain, button, flat
308	D.2.2359	95	1.8	1.107	1	buff	white cream	oval	4	3	1.5	2	1.478			pointy, squishy
309	C.2.1050	80	0.9	1.066	3.5	brown	white	round	3.5	3.5	5	1	0.962	1.5		scab, heavy cracky skin, ugly
310	D.2.2142	100	1.4	1.100	1.5	light red	orange yellow	oval	3	2.5	1.5	1.5	1.406			pointy, button, too small
311	D.2.2065	95	1.2	1.103	1.5	red	white	oval	3.5	3	1.5	2	1.320			bottle, pointy, squishy
312	ORAYT-9	85	5.8	1.070	3	buff tan	white	long	3.5	2.5	4.5	2.5	1.529		2.5	knobs, patchy russet, sticky
313	D.2.2247	90	1.8	1.106	1	yellow	dark yellow	long fing	3	3	2	2	1.519			
314	C.2.1015	70	2.4	1.083	2	buff	white	comp round	3.5	3	3	2.5	1.092	2.5		greening, flat
315	R.2.2807	90	3.0	1.080	2.5	tan	yellow	oval oblong	4	3	4.5	3	1.290	3	2.5	round, lenticels
316	CR.2.1512	85	4.8	1.086	2	buff	cream white	oval oblong	3	2.5	4.5	2.5	1.299	2.5		greeniing, skinning, deep eyes, irregular
317	Snowden	85	6.8	1.089	2.5	buff tan	white cream	round oblong comp	3	3	4	3	1.007	3		deep eyes, FBE, sticky, greening
318	R.2.2856	80	6.0	1.088	3	buff tan	white	long oblong	3	3.5	4	3	1.637		3	
319	D.2.2037	90	1.3	1.099	1.5	maroon red	yellow w/ pink	long fing	2.5	2.5	2	2				pointy, bottle, ugly flesh
320	R.2.2695	90	3.1	1.099	1.5	yellow buff	yellow	long	4	3	4.5	3.5	1.705		3	typy, pointy
321	CR.2.1421	85	4.1	1.091	1.5	buff	yellow	oval round	3.5	3	4.5	3	1.216	2	2	greening, **growth cracks**, pear
322	RD.2.3717	80	3.4	1.092	1.5	buff tan	white	oval oblong	3.5	3	4.5	3	1.500	2.5		typy, short, sticky
323	Atlantic	85	4.5	1.089	2.5	buff tan	white	round comp	4	3.5	4.5	3.5	1.016	3.5		**hollow heart**, FBE, sticky
324	BD1247-3		0.0													
325	CR.2.1617	85	2.3	1.071	1.5	yellow buff	cream	round	4	3.5	5	3.5	1.280			sl. flat
326	RD.2.3801	85	2.4	1.092	2.5	tan	white	long oval	4	2.5	4	2	1.605		2	pointy, bottle, short
327	R.2.2905	95	4.6	1.075	3	tan	white	oval oblong	4	2.5	4.5	2	1.499		2.5	bottle, pointy, curvy, skinning
328	C.2.1057	65	1.2	1.078	2.5	buff tan	white	round comp	4	3	5	3	1.099	2.5		flat, short, sticky
329	D.2.2429	90	2.3	1.107	1	buff	white cream	oval	4	2.5	1.5	2	1.776			pointy, bottle, shriveled, button

Supplementary Table 6.2 (Continued)

330	CD.2.1330	90	4.5	1.092	1.5	buff	yellow	oblong round	3	3	3	2.5	1.341	2.5		deep eyes, greening, blocky
331	R.2.2730	85	2.6	1.080	2.5	tan	cream yellow	round	3.5	3	5	2.5	1.121	2.5		growth cracks, sticky, button
332	RC.2.3234	90	6.6	1.087	2.5	buff tan	white cream	comp	3	3	4.5	3	1.106	2.5		FBE, flat, lenticels, hollow heart
333	CD.2.1253	90	3.5	1.086	1.5	champaign red	yellow w/ purple	round	3.5	1.5	3.5	1.5	1.239			knobs, **chain**, growth cracks, button
334	RC.2.3416	95	2.6	1.070	2.5	buff	white	round comp	3.5	3	4.5	3	1.019	3		flat, sticky, flaky
335	RD.2.3941	90	3.5	1.082	1	buff	white	long oval	3.5	2	2	2.5	2.113		1.5	bottle, dumbbell, button, pointy
336	RD.2.3871	90	4.8	1.083	1.5	buff pink	yellow	long oval	3.5	2.5	2	2.5	1.472		2.5	pointy, bottle
337	CR.2.1743	100	0.7	1.079	2	buff	white	round	3.5	3	5	2	1.097			pointy, sticky
338	D.2.2443	80	2.6	1.078	1.5	light red	yellow w/ pink	long fing	4	3	4.5	3	2.844			ugly flesh, curvy
339	RC.2.3227	90	3.7	1.085	2	buff	white	round comp	3.5	3	4.5	2.5	1.033	2.5		growth cracks, compressed, greening, lenticels
340	CR.2.1561	90	0.1										1.311			3 tubers
341	R.2.2772	80	4.9	1.085	3.5	buff tan	yellow	long oval	4	3	5	3	1.840		3.5	pointy, bottle
342	RC.2.3437	85	2.4	1.075	2	buff	white	oval long	3.5	3	4.5	3	1.460		3	bottle, pointy
343	C.2.1148	90	2.7	1.090	2.5	buff tan	white	round comp	4	3.5	4.5	3	1.012	2.5		hollow heart, greening, sticky, short
344	D.2.2282	85	2.2	1.087	1	yellow	dark yellow	oval	4	3.5	2	2.5	1.524			pointy, green, shriveled
345	Atlantic	80	4.9	1.083	2.5	buff tan	white	round	3	3	3.5	3	1.035	3		hollow heart, FBE, greening, flaky
346	CD.2.1281	75	2.2	1.085	2.5	rusty red	yellow	round	3.5	3	3.5	1.5	1.115			cracky skin, greening
347	PALB03016-3	90	4.7	1.078	4	tan brown	white	oblong long	3.5	3	3.5	3.5	1.353		2	**hollow heart**, sticky, heavy russet
348	D.2.2261	85	1.2	1.096	1	yellow	yellow	oval	4	3	1.5	2	1.505			pointy, green, shriveled tubers, multiple eyes at butt end
349	RD.2.3514	95	4.6	1.089	2	buff pink	yellow	oval round	3.5	2.5	3	2	1.425		2	pointy, sticky, bottle
350	CR.2.1575	80	3.0	1.086	2.5	buff tan	cream white	comp round	3	3	2.5	3	0.972	3		FBE, flat, short
351	Payette Russet	95	2.4	1.075	3.5	tan	white	oval long	4	3	4.5	3	1.203		2.5	curvy, bottle, round
352	RC.2.3255	90	1.4	1.089	1.5	buff	white	long oval	3	3	4.5	3	1.136		2	**short**, greening, sticky
353	CD.2.1211	95	6.6	1.080	2.5	buff tan	white	long oval	2	3	4.5	2.5	1.376		2.5	**hollow heart**, bottle, pointy
354	RC.2.3360	85	0.9	1.092	2	buff	cream yellow	comp round	3.5	3	4.5	3	0.955	3		short
355	Lamoka	80	3.4	1.087	2	buff	white cream	oblong round	3.5	3.5	4.5	3	0.977	3		FBE, flaky skin, greening
356	BD1240-6		0.0													

Supplementary Table 6.2 (Continued)

357	D.2.2583	95	2.0	1.096	1	yellow	dark yellow	oval	3.5	3	2	2.5	1.173			bottle, button, pointy, shriveled
358	R.2.2723	100	2.1	1.074	2.5	buff	white cream	long oblong	3	3	4.5	3	1.583		2.5	pointy, button, knobs
359	D.2.2331	90	2.1	1.095	1	yellow	yellow	long oval	3.5	2.5	2	2.5	2.089			pointy, bottle, knobs, greening
360	RC.2.3213	95	3.9	1.081	1.5	buff	white	comp round	4	3	5	3	1.186	3		scab, sticky, flat
361	RD.2.3556	80	0.6	1.101	1.5	buff	white	round	3.5	3	3.5	3	1.136			shriveled, lenticels
362	BD1253-4		0.0													
363	RD.2.3948	95	3.9	1.087	1.5	buff	white	round	4	3	4.5	3	1.231	3		greening, bottle, pear
364	CD.2.1323	90	1.7	1.079	1.5	buff w/ pink	yellow	round	3	3.5	3.5	2.5	1.292		2.5	short, sticky
365	RC.2.3248	75	2.8	1.089	3	tan	white	round oblong	4	3	4	3	1.221	3		flat, sticky
366	C.2.1204	65	0.3		1.5	buff	white	round	4	3	3.5	3	1.150			pointy, bottle
367	RD.2.3899	90	5.5	1.079	2	yellow w/ pink	yellow	round	2.5	2.5	3.5	3	1.225			pointy, blocky, bulging eyes, button, bottle
368	RC.2.3136	70	5.0	1.077	2	buff tan	white	comp round	3.5	3.5	2.5	3	0.986	3		greening, skinning, flat
369	R.2.2898	70	2.5	1.087	3.5	tan brown	yellow	oval long	4	3	5	2.5	1.214		2.5	**round**, greening, hollow heart
370	R.2.2737	80	3.5	1.067	3	buff tan	white	oval long	4	3.5	4	3	1.618		3	hollow heart, pointy, pear, skinning
371	R.2.2940	80	4.4	1.090	3	buff tan	white	oval oblong	4	3	4.5	2.5	1.430		2.5	flat, pointy, bottle
372	BD1253-4		0.2	1.074	1	buff yellow	cream yellow	oval	3.5	3	1	1.5	1.413			shriveled
373	RD.2.3521	85	5.8	1.095	1.5	pink w/ buff	yellow	oval	3.5	2.5	2.5	2	1.223		2	pointy, bottle, pear
374	D.2.2121	85	1.1	1.081	1.5	red	yellow	oval	3.5	2.5	2	2	1.544			pointy, bottle, button
375	RC.2.3444	85	4.8	1.069	1.5	buff	white	round comp	4	3	4	3	1.009	3		greening, flat, squishy
376	RD.2.3822	85	4.2	1.097	2	buff w/ pink	white	long oval	4	2.5	2.5	2	1.465		1.5	**hollow heart**, ugly, skin
377	D.2.2303	80	0.5	1.096	1	red	yellow w/ red	round	3	3.5	2	2.5	1.160			button
378	C.2.1092	85	1.7	1.066	2	buff	white	round comp	4	3	4.5	3	0.988	2.5		short, shriveled, rot, lenticels
379	CR.2.1435	80	3.9	1.087	3	buff tan	white	oblong round	4	3	4.5	3.5	1.218	2.5		sticky, **hollow heart**
380	D.2.2478	85	1.0	1.100	3	rusty red	cream yellow	long oval	3.5	3	2	1	2.181			pointy, button, bottle
381	RD.2.3892	95	4.1	1.084	1.5	yellow w/ pink	yellow	round	3	2.5	2.5	2	1.145			XL, dotty russet, FBE
382	RC.2.3178	85	2.4	1.082	2	buff	white	oval oblong	4	3.5	5	3	1.716		3	short, greening, typy

Supplementary Table 6.2 (Continued)

383	CR.2.1876	90	4.5	1.077	2.5	buff w/ pink	white	oval oblong	3.5	2.5	2	2.5	1.151	2.5		bottle, sticky, sl. Irregular
384	D.2.2534	100	1.2	1.085	1	yellow	dark yellow	oval	3.5	3	1.5	2	1.463			greening, pointy
385	RC.2.3430	90	2.4	1.066	1.5	buff	white	round	4	3	3	2	1.160			baby, squishy
386	Lamoka	80	6.2	1.087	2	buff	white	round	3.5	3	4.5	3	1.039	3		growth cracks, sticky, greening
387	Russet Burbank	85	6.2	1.075	3.5	tan buff	white	long oval	3.5	3	5	2.5	1.562		2.5	hollow heart, typy
388	RD.2.3703	95	5.3	1.087	1.5	yellow buff	yellow	oval round	4	3	2.5	2.5	1.415			skinning, greening, button
389	CR.2.1673	85	5.5	1.070	2	buff	white	oblong long	3.5	3.5	4.5	3	1.322		2.5	scab, **hollow heart**, shatter bruise
390	RD.2.3654	95	2.4	1.085	2	rusty red	white	long	5	1.5	4	1	2.561			bulging eyes, knobs, cracky skin
391	CD.2.1372	85	1.5	1.085	2	buff	yellow	oval oblong	4	3	3	2.5	1.364		2.5	greening, skinning
392	PALB03016-3	85	4.0	1.080	2.5	buff tan	white	oval oblong	3.5	3	3.5	3	1.616		2.5	hollow heart, short, pointy
393	Atlantic	90	6.5	1.086	2.5	buff tan	white	round oblong	3	3	3.5	3	0.975	3		greening, FBE, flaky
394	OR01007-3	95	4.3	1.080	2	buff	white	long	4	3	4.5	2.5	1.805		3	shriveled
395	D.2.2569	90	0.7	1.082	1	yellow	dark yellow	oval round	4	3.5	3.5	2.5	1.491			dumbbell
396	D.2.2548	95	2.2	1.078	1.5	yellow	yellow	oval	3.5	2.5	2.5	2.5	1.621			pointy, squishy
397	Russet Norkota	80	5.5	1.067	3.5	tan buff	white	oval oblong	3.5	3.5	5	3	1.947		3.5	pointy, typy
398	CR.2.1470	85	2.2	1.088	2.5	buff tan	white	oval oblong	3.5	3	2.5	2	1.185		2	short, round
399	R.2.2751	70	5.2	1.080	3	buff tan	white	round	3.5	3	2.5	3	1.228	2.5		pointy, pear
400	Tacna	90	5.8	1.070	2.5	buff tan	white	comp oblong	4	2.5	2.5	2	1.335		2	greening, skinning, flat
401	D.2.2135	100	1.5	1.091	1	buff pink	cream white	round oval	3.5	3	2.5	2.5	1.415			pointy, too small
402	RD.2.3577	85	3.3	1.093	3.5	purple brown	cream white	oval long	3.5	3	4	3	2.018		2.5	pointy, bottle, cracky skin, twins
403	CR.2.1540	80	1.4	1.089	2	buff tan	white	oval oblong	4	2.5	4.5	3	1.150		2	short, greening
404	C.2.1190	90	0.6	1.071	2	buff tan	white cream	round	3.5	3.5	4.5	3	1.083	2		short, skinning
405	RC.2.3458	80	1.9	1.054	2	buff	white	round	3.5	3	4.5	3	1.163	2.5		bottle, short
406	D.2.1981	90	1.5	1.070	1	buff yellow	white	round oval	3.5	2	2	2.5	1.525			irregular size, greening, pointy
407	RD.2.3619	90	4.1	1.083	1.5	yellow	yellow	oval oblong	3	2	4.5	2	1.386		2	curvy, cracky, round
408	CR.2.1414	85	1.7	1.073	1.5	yellow	yellow	round	4	2.5	3.5	2	1.006			growth cracks, greening, lenticels, squishy
409	RC.2.3332	85	3.8	1.084	2	buff	white cream	oval oblong	3.5	2.5	4	2	1.344		2	pointy, bottle, pear, irregular, pink skin, cracky, button
410	Tacna	95	6.3	1.072	2	buff	white	round oblong	4	3	2	2	1.387	2.5		skinning, button, greening, bottle
411	R.2.2744	80	4.4	1.083	3	buff	white	long oval	3.5	3	4.5	2.5	1.968		3	curvy, pointy, sticky
412	C.2.1162	85	3.0	1.078	2	buff	white	round	4	3	3	3	1.228	3		greening, flaky, sticky

Supplementary Table 6.2 (Continued)

413	BD1244-1		0.0													
414	CR.2.1736	85	3.1	1.069	2	buff	white	oval round	4	2.5	5	2.5	1.103	2.5		**growth cracks**, greening
415	D.2.2275	90	3.9	1.074	1	yellow	yellow	round	3.5	3	2.5	2.5	1.277			pointy
416	R.2.3052	80	1.4	1.084	3	buff tan	white	oval	4	3.5	4.5	3	1.783			short, thin, pointy
417	D.2.2597	85	0.9	1.092	1	orange yellow w/ pink	yellow	long oval fing	3	2.5	2	2	1.968			pointy, knobs, curvy
418	D.2.2345	90	1.4	1.085	1.5	yellow w/ pink	yellow	oval	3.5	2.5	1.5	2	1.354			greening, pointy, squishy
419	CR.2.1393	85	4.1	1.087	2.5	tan	yellow	oval oblong	3.5	2.5	4.5	2.5	1.383		2.5	pointy, bottle, pear, short
420	Russet Norkota	85	0.0													
421	Russet Norkota	75	4.4	1.067	3.5	brown	white	long oblong	3.5	3.5	5	3.5	2.006		3	typy, sticky, curvy
422	Snowden	80	6.2	1.091	2.5	buff tan	cream white	round	3	3	4.5	3	1.008	3		hollow heart, greening, sticky, FBE
423	CR.2.1547	90	3.4	1.075	2	buff tan	cream yellow	round comp	3.5	3	3.5	2.5	0.939	2.5		sticky, greening
424	CR.2.1848	85	3.3	1.085	1.5	buff	white	round	4	2.5	4.5	2.5	1.150	2.5		bottle. sl. Irregular
425	RD.2.3990	95	3.1	1.072	2	yellow buff	yellow	oval oblong	3	2	2	1.5	1.524		2	pointy, button, bottle, pear, short
426	D.2.2604	100	1.8	1.087	1.5	buff pink	white	round oval	3.5	3	2	2	1.385			pointy, cracky, squishy
427	RD.2.3570	95	5.7	1.088	1.5	pink buff	white	oval oblong	3	1.5	3	2	1.471		1.5	growth cracks, bulging eyes, bottle, flat, irregular
428	D.2.1946	95	2.8	1.088	2	red	yellow w/ pink	oval	3	2	2	1.5	1.359			rusty, cracky, bottle
429	CR.2.1533	90	3.3	1.077	2	buff	white	round oblong	4	3.5	3.5	3	1.095	2.5		short, greening
430	RD.2.3878	85	4.1	1.080	1	yellow w/ pink	yellow	oval long	2.5	2.5	4.5	3	1.235			greening, button, deep eyes, multiple eyes at butt end
431	R.2.2954	80	2.5	1.084	2.5	buff	white	oval	4	3.5	4.5	3	2.016		2	short, pear, bottle, button
432	D.2.2051	100	1.5	1.094	1.5	light red	yellow w/ red	oval	3.5	3	2.5	2	1.638			bottle, button, squishy, rusty
433	R.2.2793	85	3.5	1.074	1.5	buff	white cream	long oval	4	3.5	4.5	2	1.615		2	thin, pear, **lenticels**, squishy, green
434	CR.2.1869	80	6.0	1.084	2	buff	cream white	round	4	3	2.5	2.5	1.205	2.5		skinning, flat, bottle, pear
435	Russet Burbank	90	5.7	1.074	3	tan buff	white	long oval	3	3.5	5	3	1.475		3	knobs, typy
436	CD.2.1267	85	2.9	1.100	2.5	buff yellow tan	yellow	long oblong	3	3	3.5	3	1.338		2.5	sticky, greening, short
437	CR.2.1568	80	3.4	1.095	2.5	buff tan	white	round oblong	4	3	3	2.5	1.155	2.5		**hollow heart**, slaky
438	C.2.1029	50	2.1	1.076	2.5	buff tan	white	round	3.5	3	4	2.5	1.029	2		sticky, scaby skin, short
439	R.2.2926	75	2.0	1.099	2	buff	white	oval	4	3.5	5	3	2.119		2	bottle, pear, pointy

Supplementary Table 6.2 (Continued)

440	RD.2.3850	80	2.8	1.083	2	buff yellow	yellow	long oblong	3.5	1.5	3.5	2	1.123		1.5	hollow heart, knobs, sticky, greening, ugly, growth cracks
441	CR.2.1456	55	3.1	1.079	2.5	buff tan	white	round	4	3	3.5	3.5	1.102	3		**hollow heart**, flaky
442	D.2.1932	85	2.3	1.085	1.5	red	yellow w/ pink	oval	3	3	2	2	1.645			button, pointy, curvy
443	CR.2.1799	85	3.3	1.081	3.5	tan buff	white	round	3.5	3.5	4.5	3	1.061	3		heavy russeting, raised eyebrows
444	RC.2.3164	80	6.8	1.089	1.5	buff yellow	yellow	round oblong	4	3	4	2.5	1.269	2.5		hollow heart, skinning, flat
445	P.1.1743		0.0													
446	D.2.2205	85	4.2	1.108	1	maroon w/ yellow	orange yellow	round	2.5	2.5	2	2	1.078			deep eyes, sticky, multiple eyes at butt end, irregular
447	CD.2.1232	80	4.6	1.093	2.5	buff	white	round oblong	3	3	2.5	3	1.167	3		deep eyes, button
448	D.2.2541	90	2.5	1.082	1	buff	cream	long fing	4	3.5	3.5	3	1.922			fingerling, pointy, growth cracks, irregular
449	Atlantic	85	6.7	1.094	2.5	buff tan	white	round	3.5	3	4.5	3	1.066	3.5		greening, FBE, sticky, flaky
450	CD.2.1365	90	3.5	1.099	2	champaign red	cream white	round	3	3	4.5	3	1.318			sticky, sl. Irregular
451	CR.2.1477	95	3.1	1.092	2.5	buff tan	white	round	3.5	2.5	3	2.5	1.100	2.5		sticky, sl. Irregular
452	R.2.2702	85	2.8	1.074	3	buff tan	white	oval oblong	4	2.5	4.5	2.5	1.338		2.5	flat, shattered, irregular
453	RD.2.3787	95	4.2	1.071	1.5	buff w/ pink	cream w/ pink	long oblong	3	3	3	2.5	1.356		2	cracky skin, growth cracks, ugly flesh
454	R.2.3059	80	5.9	1.082	2.5	buff tan	white	long oblong	3	3	3.5	3	1.333		2	**hollow heart**, blocky
455	R.2.2667	75	4.4	1.073	2	buff	yellow	oval	4	3	4.5	3	1.592		2	bottke, **pear**, button, greening
456	CR.2.1498	90	3.3	1.082	2	yellow buff	yellow	round oval	4	3	4.5	3	1.052	2.5	2	pointy, short
457	D.2.2527	80	2.2	1.095	1	champaign	yellow	oval	3.5	3.5	2	2	1.554			pointy, bottle
458	A07547-4	75	4.3	1.077	3	buff tan	white	long oval	3.5	3	4.5	3	1.473		3	sl. round, button
459	D.2.2233	85	2.1	1.075	1	yellow	yellow	long fing	4	3	2	3	1.680			pointy, shriveled, knobs, greening
460	RC.2.3150	85	2.0	1.074	1.5	buff	cream yellow	round	3.5	3.5	4.5	2.5	1.231	2.5		skinning, bottle, pointy
461	RD.2.3955	90	4.6	1.075	2.5	buff yellow	yellow	oval round	3.5	2	2.5	2.5	1.205		2	short, round, curvy, knobs, greening
462	CR.2.1813	85	2.5	1.097	2	buff	white	round	3.5	3	5	3	1.216	3		flat, pear shape
463	BD1251-1		0.0													
464	CR.2.1792	90	4.5	1.074	2.5	buff	white	round	3	3	5	3	1.197	2.5		**hollow heart**, deep eyes, FBE, knobs
465	RD.2.3906	85	7.8	1.086	1.5	buff tan	yellow	oblong round	3	2	3	2.5	1.103	2	1.5	irregular, sticky, bottle
466	D.2.2387	75	2.3	1.081	1	buff	cream yellow	oval	3.5	3	2.5	2.5	1.336			pointy, bottle

Supplementary Table 6.2 (Continued)

467	Russet Burbank	85	7.0	1.075	3	buff tan	white	long	3.5	2.5	5	2.5	1.881		3	bulged eyes, knobs
468	R.2.3115	85	3.0	1.074	2.5	buff tan	white	oval oblong	4	3	3	2.5	1.300		2.5	typy, squishy, thin, bottle
469	BD1222-1		0.0													
470	RC.2.3283	85	4.9	1.089	2.5	buff tan	white	round	3.5	3.5	5	3.5	1.154	3		flat, sticky
471	CR.2.1680	80	5.5	1.072	2	buff tan	white	oblong round	3.5	2.5	4.5	2.5	1.265	2	2	squishy, sticky, button
472	R.2.2828	80	3.2	1.094	2	buff tan	white	long	3.5	3	3.5	2	1.732		2.5	**thin**, skinning, short
473	CR.2.1400	75	6.1	1.083	2	buff tan	yellow	oblong long	4	3	5	2.5	1.311		2.5	FBE, hollow heart, growth cracks
474	RD.2.3668		0.0													
475	RD.2.3696		1.1	1.068	1.5	buff	yellow	long oval	2.5	2.5	5	3	1.684		2	pointy, bottle, button
476	CD.2.1302		0.0													
477	RD.2.3962		0.9	1.053	2	buff yellow	white	oblong long	2.5	2.5	4.5	3			2	greening, button, irregular
478	RD.2.3997		5.1	1.078	1.5	buff yellow	cream yellow	long	3.5	1.5	2	1.5	2.236		1	curvy, snaky, dumbbell, knobs, skinning, **irregular**
479	RD.2.3612		0.3	1.050	1.5	buff	white	round	3	-	4.5	2.5	1.210	2.5		greening, few tubers
480	RD.2.3626		0.1										0.943			1 tuber
481	CD.2.1218		2.7	1.101	2	pink buff	yellow	round	3	3	3.5	3	1.043	2.5		deep eyes, FBE, sticky
482	RD.2.3689		0.2	1.024	1	buff	white	long fing	4	4	4.4	4	2.734			pointy, low yield, nice
483	CD.2.1309		0.0													

Supplementary Table 6.3. Phenotypes of clones grown in Hermiston, OR in 2017 to evaluate groups for hybrid vigor in chapter 6. In all traits scored 1-5 or 0-5, “5” indicates the preferable state. For “chipper suitability” and “russet suitability”, higher scores indicate clones that have higher yields and tuber traits more acceptable for the potato chip market. “Chipper suitability” and “russet suitability” were calculated using Equations 2 and 3 in chapter 6.

Plot	Clone	Percent green (8-14-17)	Yield (kg/plot)	Specific gravity	Russeting	Skin color	Flesh color	Shape	Eye depth	Uniform	Sprouting	Length:width	Appearance	Chip suitability	Russet suitability	Comments
1	R.2.2835	70	4.0	1.083	2	buff	white	round oval	3	2	2	1.148	2.5	2		bottle, pointy, knobs
2	Snowden	80	7.0	1.063	2.5	buff	white	round oblong	2.5	3	2.5	1.087	3	2.5		flat, compressed
3	Russet Norkota	65	4.1	1.074	3.5	buff tan	white	oval oblong	3.5	3.5	3	2.032	3.5		3	typy
4	D.2.2037	90	0.7	1.061	1.5	red	yellow	long fing	2.5	3	2.5	2.492	2.5			knobs, curvy
5	R.2.3073	80	7.6	1.069	2.5	buff tan	cream	oblong long	2.5	2	4	2.005	2		2	severe six (discard yield data) deep eyes, bottle, sticky
6	D.2.2387	60	1.4	1.094	1	buff yellow	cream	round oval	3	3	2	1.464	1.5			chain, rot, shriveled, ugly
7	BD1257-5	60	2.6	1.078	1	yellow	yellow	round oval	3.5	2.5	1.5	1.369	1.5			pointy, chain
8	C.2.1078	85	1.9	1.076	1.5	buff	white	comp round	4	3.5	5	1.237	3.5	3		growth cracks, sticky, lenticels
9	Atlantic	75	9.4	1.076	2.5	buff tan	white	comp round	3	3	2.5	1.025	3.5	3		flaky, greening, FBE
10	D.2.2296	20	0.5	1.058	1	pink yellow	yellow	round	4	3.5	1	1.369	1.5			shriveled, pointy, tiny
11	RC.2.3136	75	3.5	1.089	2.5	buff	white	round comp	3	3	2	0.989	2.5	3		FBE, scab
12	CR.2.1435	80	4.5	1.089	3	buff	white	comp	3.5	3	4.5	1.074	3.5	3.5		sticky, lenticels, greening, XL
13	CD.2.1281	65	1.0	1.054	2	purple red	yellow	round	3	3	2	1.085	2.5			bulging eyes, sticky
14	R.2.2975	65	3.0	1.078	2.5	buff	white	oval oblong	4	2.5	3	1.390	3			curvy, pointy
15	RD.2.3598	90	2.2	1.070	1.5	buff yellow	cream yellow	round	3.5	3	2.5	1.139	3			bottle, pointy, shriveled
16	Atlantic	80	6.5	1.075	2.5	buff tan	white	comp	3	3	2.5	1.042	3	3		FBE, greening
17	D.2.2268	60	2.1	1.082	1	yellow	yellow	round oval	4	3.5	2.5	1.319	1.5			silver scurf, shriveled, rot, hard
18	R.2.2996	80	4.8	1.077	2	buff	white	long	3	3.5	3.5	1.705	3		3.5	curvy, growth cracks
19	RC.2.3269	0	0.9	1.070	2.5	buff	white	oval	4	4	3	1.613	3.5			pointy, typy
20	D.2.2443	0	0.2	1.162	1	light red	yellow w/ red	long fingerling	3.5	3.5	2	2.784	1.5			
21	RD.2.3787	20	2.6	1.063	1	buff pink	light yellow	long	3	3.5	1.5	1.743	2.5		2	growth cracks, bottle
22	CR.2.1589	20	3.2	1.074	3.5	buff tan	white	round oblong	3.5	3	4.5	1.417	3		2	flaky, short, knobs
23	C.2.1099	55	4.1	1.054	2	buff	white	round comp	4	3	4.5	1.263	3	2.5		bottle, pointy, sticky
24	RD.2.3675	35	2.8	1.076	1.5	buff	cream yellow	oval long	3.5	3	1.5	1.296	2.5		2	button, bottle, lenticels
25	D.2.1988	5	0.4	1.032	1	light pink	white	long fing	3	3	2.5	1.918	2			flat butt end
26	RD.2.3815	75	3.4	1.069	3.5	brown purple	yellow w/ purple	round oval	3.5	3	2	1.446	1.5		1.5	bottle, chain, dumbbell, skinning

Supplementary Table 6.3 (Continued)

27	P.1.1743	45	0.9	1.087	1	pink w/ yellow	orange yellow	round	3	2	1.5	1.453	1.5			curvy, silver scurf, bottle, dark flesh
28	Atlantic	35	7.8	1.069	2.5	buff tan	white	comp round	3.5	3.5	2.5	0.939	3	3		skinning, sticky, greening, chain
29	CD.2.1344	70	3.0	1.050	1.5	buff yellow	yellow	round oval	4	2.5	2.5	1.313	3		1.5	greening, bottle, pointy
30	CD.2.1267	80	1.8	1.072	2	buff yellow	dark yellow	long	3	2	3	1.383	2		2	bottle, **knobs**, dumbbell
31	A06866-2	25	4.0	1.071	1.5	buff	yellow	round oval	4	3	2	1.502	3	2	2.5	pointy, scab, greening
32	D.2.2436	15	0.2	1.432	1	yellow	yellow	long fing	3.5	NA	4	2.609	3			1 tuber
33	CD.2.1295	0	0.0													
34	CR.2.1743	30	0.5	1.107	2	buff tan	white	round	4	3.5	4.5	1.018	1.5			shriveled, dark patches, ugly
35	RD.2.3731	25	0.7	1.052	1	buff	yellow	round	4	3.5	4.5	1.220	3.5			
36	Payette Russet	65	3.0	1.086	4	tan	white	oval	4	3.5	5	1.308	3		2.5	short, skinning
37	CD.2.1274	85	0.9	1.090	2	buff yellow	yellow	oblong long	3.5	3	3	1.443	3		2	bulging eyes, bottle, knobs
38	Atlantic	50	8.6	1.078	2.5	buff tan	white	comp round	3	3.5	3	1.013	3.5	3.5		flaky, FBE, sticky
39	PALB03016-3	75	7.9	1.094	3.5	buff tan	white	long	3	2.5	2	1.429	3.5		3	deep eyes, button, chain, sticky
40	RD.2.3752	50	4.3	1.074	1	buff yellow	yellow	oval oblong	3.5	3	1	1.460	2			pointy, tiny, large, shriveled
41	CR.2.1799	30	2.9	1.096	3.5	buff tan	white	r	3.5	4	4.5	0.996	3.5	2.5		short, sticky, small
42	R.2.3108	85	5.8	1.086	2	buff	white	comp oblong	4	3	2.5	1.147	2.5	2		flat, bottle, greening, chain
43	C.2.1155	75	3.5	1.073	1.5	buff	white	round	4	3.5	3.5	1.081	3	3		sticky, bottle, skinning
44	RC.2.3409	80	2.3	1.075	2	buff	white	round	4	3.5	4	1.129	3	3		bottle, greening
45	R.2.2751	40	5.8	1.065	3	buff tan	white	round	4	3	2	1.145	3		2	**chain**, short, greening
46	D.2.1925	40	1.1	1.070	1	red	yellow	oval long	3	2	1.5	1.581	1			bottle, pointy, chain, rot
47	Atlantic	0	8.5	1.090	2.5	buff tan	white	comp round	3	3.5	3	1.091	3.5	3		greening, FBE, sticky
48	CR.2.1470	10	1.7	1.087	2.5	buff	white	round	3.5	3	2.5	0.995	2.5		1.5	short, round, greening, patchy russet
49	BD1244-1	60	0.8	1.075	1	buff yellow	cream	oval fing	4	3.5	2	1.868	2.5			pointy, silver scurf
50	RC.2.3339	60	5.0	1.077	2	buff yellow	yellow	round oblong	4	3.5	4	1.124	3.5	3.5		shriveled, sticky
51	CR.2.1778	40	3.3	1.070	1.5	buff	white	comp round	4	3.5	4	1.096	3.5	3		scab, flat
52	Snowden	40	8.4	1.073	2.5	buff tan	white	round comp	3.5	3	3	1.032	3	3		flaky, FBE, sticky
53	D.2.2492	50	0.7	1.057	1	orange yellow	dark yellow	long fing	4	3	1.5	1.804	2			shriveled, pointy, scurf
54	RC.2.3325	5	1.0	1.069	1.5	buff	white	round	4	3.5	4	0.989	3	1		short, sticky
55	CD.2.1225	70	5.6	1.088	2	buff yellow	yellow	comp round	4	3	2	1.017	2.5	2		short, flaky
56	CR.2.1554	10	0.6	1.066	2.5	buff w/purple	cream	round	4	3.5	4.5	0.988	2			pointy, cracky skin
57	RC.2.3311	60	2.8	1.077	1.5	buff	yellow	oval oblong	4	3.5	2.5	1.315	2.5		2.5	skinning, soft, flat, typy
58	BD1222-1	65	1.3	1.087	1	yellow	dark yellow	round oval	4	3	1.5	1.282	2			shriveled
59	RD.2.3983	65	6.6	1.060	2	buff	white	oval	4	3	2	1.724	2.5			bottle, curvy, pointy

Supplementary Table 6.3 (Continued)

60	BD1202-2	5	2.9	1.537	1	light red	yellow	long	3	2	1.5	1.610	1.5			silver scurf, dumbbell, bottle, bulging eyes, irregular, ugly
61	CR.2.1596	40	3.2	1.081	2	buff yellow	yellow	round oblong	3.5	3.5	5	1.200	3.5	3		bottle, pointy
62	OR01007-3	75	3.7	1.070	2	buff	white	long oblong	4	3.5	4.5	1.465	2.5		2.5	growth cracks, curvy, bottle, lenticels, bulging eyes
63	D.2.2317	35	1.0	1.046	1	orange yellow	yellow	long fing	3.5	2.5	2	1.848	2			silver scurf, shriveled, pointy
64	D.2.1946	5	0.8	1.058	1.5	light red	yellow	round oval	3.5	3	2	1.523	2.5			scurf, shriveled, chain, dumbbell
65	RD.2.3878	35	0.4	1.011	1	yellow w/ pink	yellow	round	3	3.5	3.5	1.104	3			
66	R.2.3122	75	8.0	1.062	2	buff	white	long	3.5	2.5	3	1.498	2.5		2	bottle, chain, shriveled, ugly
67	Ivory Crisp	50	4.3	1.069	2.5	buff tan	white	round	3.5	3.5	3.5	1.059	3	3		XL, tuber worm, skinning
68	RC.2.3283	55	2.3	1.088	2.5	buff	white	round	4	3.5	5	1.067	3.5	2.5		FBE, sticky, short, button
69	CR.2.1645	10	2.1	1.059	1.5	buff	white	round	4	3	4	1.131	2.5	2.5		bottle, FBE, sticky, short
70	Tacna	85	6.5	1.046	2	buff	white	oblong long	4	2.5	2	1.159	2		2	chain, bottle, button, sticky
71	R.2.2709	85	3.0	1.077	4.5	brown	white	round oblong	4	3	5	1.181	3	2.5	2.5	chain, sticky, skinning, short
72	RD.2.3913	95	3.3	1.078	1	pink yellow	yellow	round	2.5	2	2.5	1.132	1.5			chain, bottle, button, irregular, knobs, bulging eyes
73	D.2.2016	5	1.2	1.077	1	buff yellow	yellow	oval	3	3	2	1.696	2.5			pointy, silver scurf, curvy
74	D.2.2240	50	0.7	1.073	1	yellow	yellow	oval	4	3.5	2.5	1.552	2.5			silver scurf
75	RD.2.3836	60	5.8	1.071	1.5	buff	white	long oblong	3.5	2	4	1.634	2.5		1.5	skinning, dumbbell, knobs, bottle, irregular, hard
76	D.2.2415	50	1.9	1.097	1	buff light pink	white	oval round	3.5	3	1.5	1.642	2			bottle, pointy, curvy, silver scurf, shriveled
77	CR.2.1624	55	7.0	1.080	1.5	buff	white	comp	3.5	2.5	3.5	1.256	2.5	2	1.5	shriveled, chain, flat, dumbbell
78	RD.2.3941	90	2.7	1.066	1.5	buff	white	oval	3.5	1.5	2	1.565	2		1.5	pointy, triangle, dumbbell, curvy
79	BD1253-4	60	1.4	1.077	1	buff	yellow	oval	4	2.5	2	1.496	2			sprouts, pointy, irregular
80	D.2.2072	65	0.4	1.039	1	buff yellow	cream	oval	3.5	3	2	1.568	1			shriviled, pointy, tiny
81	RD.2.3549	75	5.8	1.069	3.5	tan	white	oval oblong	3.5	3	4	1.442	3		3.5	button, skinning,sticky, typy
82	RD.2.3885	85	2.6	1.052	1	yellow w/ pink and purple	light yellow	long	2.5	2.5	2.5	3.376	2			landrace type, bulgy eyes, curvy, very long, novelty
83	D.2.2660	35	0.7	1.070	1	yellow	yellow	oval	3.5	2.5	1.5	1.675	2			shriveled, pointy, sticky
84	D.2.2065	5	0.7	1.094	1	light red	white	oval	4	3	1.5	1.551	2			shriveled, pointy, ugly
85	C.2.1169	55	2.0	1.061	1.5	buff	cream white	round	4	3	4	1.294	3	2.5		skinning
86	RD.2.3955	45	6.0	1.055	2	buff yellow	yellow	long oblong	3	2	2.5	1.264	1.5		1.5	bottle, chain, knobs, button, ugly

Supplementary Table 6.3 (Continued)

87	CR.2.1708	5	0.1	1.094	1	buff	white	round	4	3.5	4.5	1.064	3.5			
88	R.2.2786	60	4.6	1.076	2	buff	white	long	4	2.5	4.5	2.159	2		2	thgin, long, greening, bottle, curvy, **lenticels**
89	CR.2.1652	0	0.4	1.030	1.5	buff pink	white	round	3.5	3.5	4	0.926	3			rhizoc, pink splash
90	CR.2.1841	0	1.4	1.062	1.5	buff yellow	yellow	comp round	4	3	4.5	1.021	3	2.5		growth cracks, sticky
91	CR.2.1533	40	1.0	1.056	2	buff	white	round	3.5	3	2.5	1.004	3	2		short
92	RD.2.3850	25	1.5	1.057	1.5	buff yellow	yellow	round	4	3	1.5	1.018	2			lenticels, dumbbell
93	R.2.3024	50	3.7	1.066	3.5	tan	cream	oval oblong	4	3	4.5	1.488	3		2	bottle, short, flaky
94	D.2.1960	30	1.3	1.048	1.5	red	yellow	oval	3.5	3	1.5	1.858	2			shriveled, pointy, bottle
95	CD.2.1316	35	4.7	1.069	1.5	buff yellow	white	round	2.5	3	1.5	1.097	2			greening, irregular, deep eyes
96	RD.2.3920	60	1.3	1.086	1	light orange yellow	yellow	oval fing	3.5	3	2	1.528	2			bottle, pointy, curvy
97	CR.2.1456	50	2.9	1.084	4	buff tan	white	round oval	4	3.5	3.5	1.277	3		2	short, flaky, chain
98	RC.2.3185	15	1.2	1.059	1.5	buff	white	oval oblong	4	3	4.5	1.227	2.5		1.5	short, skinning, rhizoc
99	D.2.2107	40	0.1	1.128	1	orange yellow	orange yellow	oval fing	4	3	3	1.910	1			rotten, pointy, ugly, shriveled
100	BD1251-1	45	1.2	1.062	1	buff yellow	yellow	oval round	4	3.5	2	1.390	2.5			shriveled, scab, pointy
101	D.2.2289	40	2.0	1.065	1	yellow	yellow	oval pointy	4	2	1	1.429	1.5			chain, shriveled, bottle
102	OR01007-3	20	3.4	1.070	1.5	buff	white	long	4	2.5	5	2.095	2.5		2.5	lenticels, curvy, pointy
103	AO03123-2	50	1.8	1.067	3	buff tan	white	oval oblong	3.5	3.5	4.5	1.592	4		3.5	
104	D.2.2548	45	0.8	1.085	1	yellow	yellow	oval	4	2	1.5	1.700	1.5			shriveled, pointy, bulgy
105	D.2.2254	55	0.1	1.136	1	red	yellow	oval	3.5	1	1	1.738	1			sticky, chain, rot
106	RC.2.3248	60	2.6	1.089	3	buff tan	white	round	4	3	2.5	1.077	3	2		
107	BD1257-5	65	1.6	1.097	1	yellow	dark yellow	oval	3	3	1	1.472	1			shriveled, chain
108	CR.2.1407	80	2.5	1.079	1.5	buff	white	round oval	3.5	3	3	1.363	3		2.5	
109	R.2.2744	60	4.2	1.064	2.5	buff	white	long	3.5	3	5	1.833	3		3	curvy, sticky
110	D.2.2093	15	0.6	1.055	1	light red	orange yellow	fingerling	4	1.5	1	2.354	1			rot, chain, ugly
111	R.2.3045	30	4.7	1.091	3	buff	white	oblong long	4	3.5	1.5	1.332	3.5		3	
112	BD1251-1	70	1.1	1.050	1	buff yellow	yellow	oval pointy	3.5	2	1	1.641	1.5			bottle, chain
113	R.2.2982	60	2.3	1.081	1.5	buff	white	oblong	4	3	2	1.587	3		2.5	curvy, flat
114	RD.2.3829	50	7.0	1.093	1.5	brown purple	white	oblong	3	2	1.5	1.717	3		1.5	
115	RD.2.3563	60	1.2	1.048	1	buff yellow	yellow	oblong oval	4	2	2.5	1.242	2.5			
116	RD.2.3843	20	0.9	1.088	1	buff	white	oval long	3.5	2.5	1.5	1.454	2.5		1.5	
117	R.2.2863	55	4.7	1.079	5	brown	white	oblong long	3.5	3	4	1.801	3		2.5	chain, bottle, heavy russet
118	RD.2.3724	40	2.1	1.075	1	buff	yellow	oval	3.5	3.5	3.5	1.377	2.5			knobs, chain, sticky
119	D.2.2212	40	2.4	1.080	1	red	dark yellow	long	2	2	3	1.744	2			chain, pointy, bottle, ugly
120	BD1247-3	30	1.6	1.088	1	buff yellow	dark yellow	oval	3.5	2	3	1.377	1			shriveled, hard, chain, ugly
121	RD.2.3703	90	1.6	1.059	1	buff	yellow	oval	3.5	2.5	1.5	1.366	2			green, shriveled
122	RD.2.3710	80	1.2	1.078	1	buff	yellow	oval	3.5	2.5	2	1.275	2			chain, irregular, bottle
123	D.2.2261	75	0.6	1.095	1	yellow	yellow	oval	3.5	2	2.5	1.522	1			rot, tiny, shriveled

Supplementary Table 6.3 (Continued)

124	C.2.1036	75	1.8	1.085	1.5	buff	white	round	4	3.5	3.5	1.164	3.5	2.5		
125	RC.2.3451	50	1.5	1.050	2	buff	white	round comp	3.5	3.5	1.5	0.978	3	3		
126	Russet Burbank	70	4.8	1.067	3	buff tan	white	oblong long	3	3.5	4.5	1.954	3.5		3.5	bottle, rhizoc, pointy
127	CD.2.1232	40	4.6	1.076	2	buff	white	round comp	3	3	2	1.044	2	2		bottle, flat
128	Snowden	40	6.6	1.068	2	buff	white	comp round	3	3	2.5	1.013	3	3		FBE, sticky
129	Russet Burbank	60	7.9	1.075	3	buff tan	white	long	3	2.5	4.5	1.748	3		2.5	curvy, folded, bottle, pointy, knobs, chain
130	BD1222-1	35	3.1	1.083	1	yellow	yellow	Round-oval	4	3	1.5	1.370	2.5			shriveled, chain, pointy
131	D.2.2142	45	0.8	1.093	1.5	peach	dark yellow	oblong oval	3.5	1	1.5	1.923	1			stem end rot, curvy, pointy, chain
132	CR.2.1631	50	4.0	1.063	1.5	buff	cream	round oblong	3.5	2.5	4.5	1.341	3	2	2.5	
133	RC.2.3241	15	1.3	1.072	3.5	buff tan	white	round oblong	4	3	4.5	1.289	3		1.5	short, bulgy
134	R.2.2793	45	2.1	1.066	2.5	buff	white	oval	4	3.5	4	1.647	2.5		2	lenticels, bottle
135	D.2.2359	10	1.2	1.066	1	buff	cream yellow	oval pointy	4	3.5	1	1.561	1			stem end rot, vascular discoloration, ugly
136	CD.2.1323	25	3.2	1.071	2	buff	yellow	oval oblong	4	1.5	2	1.380	1		1.5	knobs, bulged eyes, irregular, greening
137	Russet Norkota	10	5.8	1.056	3.5	buff tan	white	oval oblong	3.5	3.5	4	1.805	3.5		3.5	typy, pointy
138	RC.2.3304	15	0.6	1.062	1	buff white	white	round	4	3.5	4.5	1.157	3.5	2.5		
139	A08640-2	55	1.2	1.064	1.5	buff	cream	round	3.5	3	5	1.291	3.5		2.5	curvy, tuber worm, early
140	R.2.2884	75	2.9	1.063	4	tan	white	oblong long	3	3	2.5	1.518	2.5		2.5	
141	D.2.2366	45	0.8	1.083	1	yellow	dark yellow	round oval	3.5	2.5	3	1.695	2.5			knobs, irregular, silver scurf
142	R.2.3038	0	3.0	1.097	3	buff tan	cream white	round oblong	3.5	3.5	2	1.243	3		2	blocky, dumbbell
143	CR.2.1617	0	1.0	1.066	1.5	buff	cream	round	4	3.5	5	1.171	4	1.5		
144	CR.2.1491	45	4.9	1.069	2	buff	white	comp round	3	2.5	3.5	1.064	3	2.5		FBE, sticky, knobs
145	CD.2.1260	60	4.4	1.086	2	buff pink	white	round oblong	3.5	2.5	1.5	1.129	2	1.5	2	growth cracks, chain, lenticels
146	RD.2.3906	65	6.5	1.069	1	buff yellow	yellow	oval long	3.5	1.5	2	1.448	1.5		1	bottle, pointy, greening
147	CR.2.1687	25	1.7	1.080	2	buff tan	white	round	3.5	2.5	2	1.173	2.5	2		
148	Russet Burbank	50	6.0	1.068	3	buff tan	white	long pointy	3	3	4.5	1.659	3.5		3	pointy, curvy, bottle
149	CR.2.1442	20	2.3	1.071	2	buff	white	round oblong	3.5	3.5	2.5	1.352	3.5		2.5	
150	CR.2.1659	80	6.6	1.062	1.5	buff	white	oblong long	3	2.5	4.5	1.672	2.5		2	flat, curvy, pointy, bottle
151	D.2.2604	20	0.9	1.061	1	buff	white	round oval	3.5	3	1.5	1.459	2			button, short, shriveled, silver scurf
152	R.2.2695	60	3.5	1.069	2	buff yellow	cream yellow	oval	3.5	2	3	1.444	3		2.5	bottle, curvy, pointy
153	PALB03016-3	35	5.4	1.080	3	buff tan	white	oblong long	4	3	4	1.624	3		2.5	bottle, pointy, flat
154	D.2.2450	70	1.2	1.067	1.5	yellow	dark yellow	long fingerling	4	2.5	2.5	2.045	3			pointy, shriveled, dumbbell, curvy

Supplementary Table 6.3 (Continued)

155	CR.2.1526	65	4.9	1.071	1.5	buff	cream yellow	round comp	3.5	3	4.5	1.142	3	3		bottle
156	D.2.2534	60	3.6	1.067	1	yellow	dark yellow	fing	4	2	1.5	1.841	1.5			chain, pointy, shriveled, ugly, VD
157	RC.2.3416	45	5.4	1.062	2	buff	white	round	3.5	3.5	5	0.904	3.5	3.5		sticky, pointy, FBE
158	D.2.2002	30	2.5	1.064	1	yellow	cream yellow	oval long	3	2.5	1	2.119	2			knobs, curvy, pointy
159	CD.2.1358	80	2.3	1.078	1.5	buff pink	yellow	round	3.5	3.5	2	1.001	3	2		silver scurf, dumbbell, pointy
160	D.2.2282	70	1.6	1.043	1	yellow	orange yellow	round oval	3.5	2.5	1.5	1.603	2.5			
161	D.2.1981	40	1.4	1.070	1	buff	white	oval round	3.5	2	1.5	1.377	1.5			button, chain, sticky, bottle
162	RC.2.3444	55	5.3	1.063	2	buff	white	comp	4	3	2	1.013	3	2.5		
163	BD1240-6	60	1.9	1.071	1	buff yellow	yellow	oval long	3.5	2.5	1.5	1.507	2			silver scurf, pointy, bottle, ugly
164	R.2.2821	45	3.4	1.087	1.5	buff	cream white	round oval	3.5	3	5	1.163	3.5		2	sticky, pointy, short
165	R.2.2849	90	3.3	1.086	2.5	buff tan	white	oval oblong	4	3.5	3.5	1.505	3		2.5	sticky, button, short
166	C.2.1085	0	2.0	1.079	1.5	buff	white	round	4	3.5	3	1.054	2.5	2.5		
167	RD.2.3773	85	2.3	1.061	1	buff yellow	cream yellow	long	4	3	2.5	2.053	2.5			folded, curvy, pointy
168	CR.2.1505	90	3.6	1.086	2.5	buff tan	white	round	3.5	3.5	4.5	1.051	3.5	3.5		greening, shory
169	CR.2.1722	85	1.6	1.087	1.5	buff	white	round	3.5	4	5	1.076	3.5	3.5		alligator skin, greening, lenticels
170	CR.2.1848	75	4.8	1.063	1.5	buff	white	comp round	3.5	3.5	2.5	0.965	3	3		bottle
171	D.2.2121	75	1.4	1.094	1	buff pink	light yellow	round oval	3.5	2	1.5	1.783	1.5			pointy, short, shriveled
172	R.2.3115	75	3.9	1.072	3	tan	white	oval	3.5	2	1.5	1.735	2		1.5	sticky, pointy, irregular, chain
173	Atlantic	65	8.1	1.074	2.5	buff	white	comp round	3	3.5	2	1.074	3	3		FBE
174	D.2.2345	75	0.5	1.067	1	buff yellow	yellow	round oval	4	3	1.5	1.436	1.5			hard, shriveled, VD
175	CD.2.1288	80	1.6	1.077	1.5	buff	yellow	round	3.5	3	3.5	0.952	3	2.5		growth cracks
176	R.2.3129	5	0.8	1.045	2	buff	white	oval	2.5	3.5	5	1.510	3		2.5	
177	RD.2.3738	0	0.2	1.173	2	buff	white	round	4	3.5	4.5	1.001	4	3.5		greening, lenticels
178	RD.2.3899	70	4.5	1.079	2	pink tan	yellow	oval oblong	2.5	2	2	1.471	2.5		2	button, pointy, greening, pointy, dumbbell
179	CR.2.1855	0	0.4	1.063	1.5	buff	cream	round	3	3.5	2	1.035	3.5	2		
180	ORAYT-9	20	2.6	1.056	3	buff tan	white	oval oblong	3	3.5	3.5	1.738	3		3	skinning, lenticels
181	C.2.1127	55	4.2	1.056	2	buff	white	round	3.5	3	5	1.085	3.5	3.5		greening, FBE
182	Russet Norkota	0	4.0	1.062	3.5	tan	white	oval oblong	3.5	3.5	4	1.704	3		3.5	tuber worm, alligator, typy
183	C.2.1176	5	2.7	1.064	1	buff	white	round	3.5	4	4	0.985	4	4		
184	BD1202-2	30	3.0	1.087	1	light red	yellow	oval	3	1.5	1.5	1.658	1			pointy, silver scurf, ugly
185	C.2.1162	15	1.7	1.072	1.5	buff	white	round	4	3.5	3	1.021	3	2.5		silver scurf
186	Snowden	30	5.7	1.064	2.5	buff tan	white	round oblong	2.5	3	2	0.917	3	3		FBE, sticky

Supplementary Table 6.3 (Continued)

187	Castle Russet	35	4.9	1.074	4.5	brown tan	white	oval oblong	3.5	3	4.5	1.668	3.5		3	sticky, heavy russet
188	Russet Burbank	90	4.7	1.073	3	buff tan	white	long	3	2.5	5	1.680	3		3	bottle, dumbbell, knobs
189	Eva	85	8.9	1.071	1.5	buff	white	round oblong	3	3	4.5	1.163	3.5	3.5		skinning, greening, shriveled, bottle
190	Russet Norkota	15	4.8	1.062	3.5	tan	white	oval oblong	3.5	3.5	4	1.674	3.5	3.5		pointy, curvy
191	ORAYT-9	75	3.3	1.073	3	buff tan	white	oval oblong	3	2.5	4.5	1.550	3		3	growth cracks, short
192	D.2.2429	70	2.5	1.066	1	buff	white	oval fing	4	2.5	1	1.936	1.5			pointy, shriveled, silver scurf
193	CR.2.1638	75	3.4	1.073	1.5	buff	white	round comp	3	3	2.5	1.085	3	3		button, flat
194	D.2.2422	70	0.4	1.052	1	buff	white	round oval	3.5	3	2	1.306	1			shriveled, hard, VD
195	D.2.2555	10	0.4	1.121	1	orange yellow	yellow	round oval	3.5	3.5	2	1.521	2			shriveled, pointy, rot
196	Russet Burbank	60	6.8	1.071	3	buff tan	white	long	3	2.5	4.5	1.807	2.5		2.5	curvy, bottle, button, button, irregular
197	CR.2.1869	5	1.5	1.070	2	buff	white	oval oblong	3.5	2.5	2	1.222	2		1.5	button, irregular, pointy, short
198	CR.2.1540	30	1.6	1.075	1.5	buff	white	round	3.5	3	5	1.089	3	2		silver scurf, greening
199	CR.2.1568	40	0.1	1.051	2	buff	white	round	4	3.5	4	1.031	3	2		
200	RD.2.3969	0	0.1	1.046	1	yellow	yellow	round	4	3.5	1	0.946	2	1.5		greening, scab, pointy, shriveled
201	D.2.2275	55	4.1	1.075	1	buff yellow	yellow	round oval	3.5	3	3.5	1.424	3			shriveled, baby, chain
202	BD1247-3	60	2.9	1.092	1.5	yellow	yellow	round oval	3.5	2.5	2	1.429	1.5			shriveled, irregular
203	D.2.2562	65	1.2	1.067	1	orange yellow	yellow	round oval	3.5	2.5	2	1.363	1.5			silver scurf, shriveled, pointy, bottle
204	Snowden	50	8.6	1.070	2.5	buff tan	white	comp round	3	3	2.5	0.987	3	3		FBE, sticky, flat, flaky
205	D.2.2198	60	1.0	1.108	1	orange yellow	dark yellow	long fing	3.5	2.5	2.5	2.091	2.5			dumbbell, too many tiny, pointy
206	R.2.3087	40	3.2	1.045	2	buff	white	round	2.5	3	2	1.232	2	2		**knobs**, bottle
207	BD1268-1	15	1.6	1.081	1	buff	white	oval	3.5	3	2	1.476	2			pointy, bottle, shriviled
208	R.2.3066	80	6.0	1.058	2.5	buff	yellow	round	3.5	3	4.5	1.006	3	3		rot, VD, pointy
209	D.2.2058	80	0.2	1.116	1	yellow	yellow	round oval	4	2.5	2	1.533	2			chain, shriveled, dumbbell
210	RD.2.3619	70	3.5	1.073	1.5	yellow	cream yellow	round	3.5	2.5	2.5	1.309	2			pink eyes,
211	BD1253-4	5	0.8	1.046	1	yellow	yellow	round oval	3.5	2	2	1.449	1.5			knobs, pointy, bottle, shriveled
212	D.2.1974	75	1.9	1.074	1	buff yellow	yellow	round oval	3.5	2	1.5	1.410	1.5			scab, shriveled, chain, button, greening
213	RD.2.3521	75	4.8	1.073	1	buff pink	yellow	oval	3.5	3	2.5	1.671	2			growth cracks, cracky skin, greening, pointy
214	D.2.2352	15	0.7	1.043	1	buff pink	yellow	round	4	3	2	1.448	1.5			baby, pointy, bottle, shriveled
215	RC.2.3388	75	1.6	1.049	1.5	buff	white	round comp	4	2.5	2.5	1.143	2.5	2		flat, skinning, too short

Supplementary Table 6.3 (Continued)

216	D.2.1995	15	1.1	1.071	1	yellow	yellow	long oval	3	2.5	1.5	1.683	2		2	pointy, shriveled
217	R.2.2989	15	2.7	1.074	3.5	tan	white	oval oblong	4	3	3.5	1.318	2.5	2.5	3	flat, pointy, knobs
218	D.2.2373	75	2.7	1.086	1	yellow	yellow	oval	3	1.5	2	1.528	1			pointy, bottle, button, chain, shriveled, ugly
219	P2-4	90	8.5	1.059	2	buff	white	oval long	4	2.5	3.5	1.718	2.5		2	chain, bulgy eyes, pointy
220	D.2.1918	45	1.0	1.068	1	red	yellow	long fing	3	3	2	2.379	2.5			pointy, few yellow tubers
221	RD.2.3871	55	4.1	1.064	1.5	yellow	yellow	round oval	4	2	1.5	1.310	1.5			irregular size, chain, bottle, pointy
222	D.2.2184	60	1.5	1.060	2	red	yellow	long fing	5	3	4	2.117	2			silver scurf, bulgy, knobs, landrace
223	CD.2.1211	60	5.9	1.066	2	buff	white	round oval	3	2.5	3.5	1.292	2.5		2	deep eyes, greening, short, round
224	R.2.2968	75	5.1	1.074	2	buff	cream	long oblong	4	2.5	2	1.516	2		1.5	flat, bottle, button, curvy
225	RD.2.3472	60	4.3	1.076	1	buff pink	yellow	oval	3.5	2.5	3.5	1.477	2		2	pointy, curvy, bottle
226	AO03123-2	55	3.6	1.071	3	buff tan	white	oval oblong	3.5	3	4.5	1.767	3		3.5	twins, curvy, typy
227	CR.2.1715	40	0.6	1.069	2.5	buff	white	oval	3.5	3.5	3.5	1.397	3		1	sticky
228	C.2.1001	55	3.8	1.073	1	buff	white	round comp	3	3	4	0.942	3	3		FBE, sticky
229	RD.2.3766	40	1.3	1.059	1.5	buff yellow	yellow	long	3	1	4.5	1.515	2			folded, curvy, rhizoc
230	RC.2.3199	35	2.3	1.071	1.5	buff	white	comp round	3	3.5	3	1.006	3	3		greening, short
231	RD.2.3500	65	4.8	1.080	1.5	buff w/ pink	yellow	long	3	3	2.5	2.062	2.5		2	growth cracks, rhizoc, knobs
232	RC.2.3206	45	2.2	1.058	1.5	buff	white	long	4	2	4.5	1.770	1.5		1.5	sticky, shriveled, curvy, patchy, dumbbell, ugly
233	D.2.2324	70	2.6	1.055	1.5	buff pink	cream	long	3	2	1	1.493	1			shriveled, scurf, hard, chain
234	RC.2.3157	0	2.0	1.066	3	tan	yellow	round comp	4	3	2.5	0.987	3	3		skinning, sticky, short, scab
235	D.2.2128	25	0.5	1.056	1	orange yellow	orange yellow	oval	4	3	1.5	1.567	1.5			shriveled, pointy, bottle
236	Payette Russet	60	1.0	1.079	3.5	tan	white	round oval	4	3	4.5	1.175	3		2	short, sticky, skinning
237	RD.2.3892	70	3.6	1.057	1	yellow w/ pink	yellow	round	3.5	2	1	0.941	1.5			chain, dumbbell, bottle, irregular, shriveled
238	RD.2.3528	55	5.0	1.089	2	buff w/ pink	yellow	oval round	2.5	2	2.5	1.537	2		2	patchy russet, irregular skin colors
239	D.2.1939	70	0.5	1.054	1.5	buff pink	yellow	long fing	3	2.5	2.5	2.186	2			pointy, bottle, button
240	D.2.2205	10	0.8	1.077	1.5	red w/ orange	orange yellow	long fing	3	1.5	2.5	2.004	1			end rot, knobs, shriveled, ugly, landrace type
241	C.2.1057	0	1.0	1.074	2.5	buff tan	white	comp	4	3.5	3	1.106	3	2.5		short, sticky
242	CR.2.1603	60	5.7	1.069	2	buff	white	round comp	4	3.5	4.5	1.368	3	3.5		**lenticels**, sticky, flat
243	Lamoka	45	2.8	1.069	2	buff	white	round	3.5	3	4.5	0.993	3	3		skinning, sticky, FBE
244	CD.2.1253	50	3.1	1.092	1	buff pink	cream yellow	round	3.5	2	2	1.087	2.5			**chain**, growth cracks, sticky
245	CR.2.1785	70	3.0	1.070	2.5	buff tan	white	round	3.5	1.5	4	1.103	1.5	1.5		**growth cracks**, folded tubers, scab, skinning
246	RC.2.3234	65	4.0	1.064	2	buff	white	comp oblong	3	3	5	1.149	3.5	3.5		sticky, FBE, **lenticels**

Supplementary Table 6.3 (Continued)

247	A08640-2	10	2.8	1.071	2.5	buff	white	comp oblong	3.5	3.5	4.5	1.259	3.5	3.5		greening, cracky skin, flaky, sticky
248	A07547-4	25	4.3	1.053	3.5	buff tan	white	blocky oval oblong	4	3	4	1.484	3		3	curvy, pointy, patchy
249	Ivory Crisp	60	4.9	1.065	2	buff	white	round comp	3.5	3	4.5	1.048	3	3.5		growth cracks, sticky, FBE
250	D.2.2471	55	0.7	1.075	1.5	buff pink	yellow	long fing	2.5	1.5	2	1.933	1.5			bottle, knobs, rot, dumbbell
251	R.2.3094	55	2.4	1.077	1.5	buff	white	round comp	4	3.5	4	1.102	3	3		bottle, short, lenticels
252	CR.2.1729	50	3.3	1.063	2.5	buff tan	yellow	round	3.5	3	4	1.072	3	3		dumbbell, bottle, sticky
253	C.2.1113	60	0.8	1.068	1.5	buff	white	round	4	3.5	4.5	1.146	3.5			button, tuber worm
254	BD1240-6	65	1.5	1.066	1	yellow	yellow	oval	4	2	1.5	1.519	1.5			bottle, pointy, dumbbell, curvy, shriveled
255	RD.2.3486	75	2.6	1.071	1.5	yellow	yellow	round oval	3.5	3	4	1.444	3.5			pointy, bottle, folded tubers
256	CR.2.1400	20	4.5	1.072	2	buff yellow	cream yellow	round oblong	3.5	2.5	4	1.233	3	3		folded, deep eyes, sticky
257	Snowden	40	7.3	1.073	2.5	tan	white	comp oblong	3	3	2.5	1.012	3	3		greening, sticky, FBE
258	BD1244-1	30	0.2	1.023	1	buff yellow	white	long oval	3.5	3	2.5	1.567	2.5			pointy, bottle
259	C.2.1022	10	4.7	1.068	2.5	buff tan	white	round	4	3	3.5	0.885	2.5	2.5		sticky, FBE, patchy, cracky, greening
260	CD.2.1330	50	2.9	1.071	1.5	buff yellow	yellow	round	3.5	3	3.5	1.151	2.5			sticky, irregular
261	Snowden	55	6.2	1.055	2.5	tan	white	comp round	3	3	2.5	1.020	3	3		sticky, FBE, flaky
262	CR.2.1680	20	2.6	1.068	2.5	buff tan	white	oval oblong	3.5	3	4.5	1.347	3		2	short, bottle, thin
263	R.2.2702	25	5.3	1.079	3	tan	white	round oblong	3	2	4.5	1.470	2.5	2	2	sticky, deep eyes, cracky, bottle
264	BD1268-1	40	1.1	1.081	1.5	buff	white	oval	3.5	2.5	2	1.763	2			bottle, pointy, rot, knobs
265	R.2.2814	85	3.3	1.068	1.5	buff	white	oval oblong	4	3	3.5	1.710	3		2.5	greening, button, bointy
266	CR.2.1519	75	4.6	1.054	2.5	buff	cream yellow	round	3	2	4	1.458	3	3		bottle, irregular, greening
267	RC.2.3255	50	3.0	1.074	2.5	buff tan	white	oval oblong	3.5	2.5	2.5	1.244	2		2	rot, growth cracks, thin, irregular, knobs
268	R.2.2870	5	0.4	1.062	3	buff tan	white	long oblong	3.5	3	4.5	1.934	3.5		3	typy, slightly thin
269	R.2.2898	75	1.9	1.075	4	brown tan	yellow	round oval	4	3	5	1.221	3		2.5	scab, skinning, short
270	D.2.2338	70	0.8	1.064	1	yellow	yellow	oval	3.5	3	2.5	1.547	2.5			bottle, pointy, shriveled
271	RD.2.3514	95	3.3	1.080	1.5	buff pink	yellow	oval oblong	3.5	3	2.5	1.385	3		2	pointy, short
272	R.2.2856	35	2.1	1.069	3	tan	white	round oblong	3.5	3	3.5	1.249	3	3		blocky, pointy, sticky
273	D.2.2009	0	1.2	1.053	1.5	buff light red	yellow	oval	3.5	3	2	1.883	2			scurf, pointy, tiny tubers
274	RD.2.3535	85	2.5	1.051	1	buff yellow	yellow	oval	3.5	3	4	1.470	3			bottle, irregular
275	CR.2.1876	70	4.4	1.073	2.5	buff	white	comp oblong	3.5	2.5	3	1.154	3	3		flat, FBE
276	CR.2.1421	70	5.4	1.070	2	buff	cream yellow	round	3.5	3	3	1.106	3	3		sticky, chain, skinning
277	RC.2.3423	20	2.0	1.061	1.5	buff	white	comp round	3.5	3	2	0.968	3	3		skinning, flat
278	CR.2.1736	40	1.5	1.072	2	buff	cream	round	4	3	4.5	1.143	2.5	2		growth cracks, greening, scab, bottle

Supplementary Table 6.3 (Continued)

279	CR.2.1694	50	2.4	1.067	2.5	buff tan	white	oval	4	3	2.5	1.319	3		2	short, small tubers, cracky
280	RD.2.3794	50	4.4	1.088	3	buff tan	white	oblong long	3	2.5	2	1.422	2.5		2.5	pointy, irregular, bottle
281	Lamoka	70	6.3	1.078	2	buff	white	round comp	3.5	3	3.5	1.018	3		3.5	FBE, skinning, greening
282	R.2.3080	75	4.3	1.068	1.5	buff yellow	yellow	oval oblong	4	2.5	2.5	1.745	2		2	bottle, patchy, shriveled, short
283	D.2.2233	95	2.5	1.055	1	yellow	yellow	oval	3	2.5	2	1.728	2			shriveled, too many tiny, pointy, rot
284	D.2.2401	80	0.3	1.152	1	yellow	yellow	oval	4	1	2	1.633	1			rot, pointy, ugly
285	C.2.1071	60	4.2	1.077	2	buff	white	round comp	4	3	3.5	1.175	3	3		skinning, greening, slightly flat
286	D.2.2023	55	2.4	1.092	2	pink	yellow	oval	4	2.5	1.5	1.500	1.5			shriveled, scurf, rot, chain
287	P.1.1743	60	0.8	1.098	1	yellow w/ red	orange yellow	oval	2.5	2	2.5	1.632	2.5			pointy, scurf, slightly irregular
288	C.2.1092	0	1.4	1.062	1.5	buff	cream white	comp round	3.5	3	4	1.053	3	3		greening, shatter bruise, sticky
289	RD.2.3717	5	2.4	1.092	2.5	buff tan	cream white	oval oblong	4	3	3.5	1.412	3		2	chain, short, sticky
290	Russet Burbank	10	4.5	1.070	3.5	tan	white	long	3	2.5	4.5	1.863	2.5		2.5	bottle, curvy, button
291	Russet Norkota	0	3.1	1.062	3.5	brown tan	white	oval oblong	3.5	3	3.5	1.905	3		3	typy, skinning, tuber worm
292	RC.2.3402	80	3.8	1.078	1.5	buff	white	round oblong	4	3	3.5	1.199	3	3		skinning, sticky, some small
293	RD.2.3577	65	3.8	1.075	3	brown purple	cream white	long	4	2	2.5	2.037	2		1.5	curvy, bottle, dumbbell, irregular
294	C.2.1183	0	0.0	#N/A												
295	CD.2.1337	40	6.0	1.074	1	buff	white	oval oblong	3	3	4.5	1.299	3.5		2	bottle, dumbbell, pointy
296	D.2.2457	65	2.8	1.053	1	buff yellow	cream white	oval	4	2	1.5	1.490	1.5			shriveled, end rot, pointy, ugly
297	Russet Burbank	10	4.5	1.058	3	buff tan	white	long	3.5	3	4.5	1.875	3		3	chain, knobs, dumbbell, bottle
298	CR.2.1477	85	4.9	1.072	2.5	tan	white	round	3.5	2	3	1.087	2.5	2.5		bottle, button, lenticels
299	CD.2.1246	45	4.8	1.078	2	buff	white	round	3.5	2.5	2	1.033	2	2		chain, button, shriveled, sticky
300	R.2.2716	50	2.1	1.068	1.5	buff	white	oval oblong	4	2.5	4.5	1.664	2		2	**lenticels**, round, shriveled, pointy, bottle
301	C.2.1134	45	6.5	1.087	1.5	buff	white	round	4	4	4.5	1.038	4	3.5		greening
302	D.2.2527	30	1.3	1.115	1	orange yellow	yellow	round oval	3.5	3	1.5	1.691	1.5			pointy, silver scurf, scriveled
303	RC.2.3381	45	6.4	1.056	2	buff	white	oblong round	4	3.5	2	1.095	3	3		greening
304	Eva	70	6.1	1.072	1.5	buff	white	oblong round	4	3.5	5	1.126	3	3		greening, folded, shriveled
305	R.2.2940	20	3.3	1.086	3	buff tan	white	round	4	3.5	3.5	1.289	3.5	2	2	short, pointy, shriveled
306	RC.2.3374	75	5.6	1.057	1	buff	white	comp round	4	2.5	2	1.111	2.5	2.5		skinning, short
307	RD.2.3927	85	6.0	1.068	1.5	buff	white	oval long	2.5	2	1	1.462	1.5		1.5	bottle, pointy, flat
308	R.2.2842	75	8.4	1.079	2.5	buff	white	oblong	4	3	3	1.472	3		3	flat, knobs
309	R.2.2758	75	3.7	1.095	2.5	buff	white	oval oblong	4	3.5	3	1.894	3.5		3	bottle, dumbbell, knobs

Supplementary Table 6.3 (Continued)

310	CD.2.1379	10	1.0	1.091	1	yellow	yellow	round oval	3.5	3	1.5	1.222	2			pointy, shriveled
311	D.2.2478	50	0.4	1.103	2	buff red	cream white	oval fing	4	3.5	1.5	2.032	1.5			shriveled, dumbbell, hard
312	R.2.3101	40	3.1	1.078	2.5	buff tan	white	round oval	3.5	3.5	3.5	1.415	3		2.5	greening, short
313	RC.2.3276	5	1.3	1.071	1.5	buff	white	round oblong	3.5	3	5	1.201	3	1		skinning, pink eye
314	RC.2.3430	5	1.3	1.065	1	buff	white	round	4	3	1.5	1.426	2	1.5		short, dumbbell, green
315	Atlantic	75	10.0	1.085	2	buff	white	round comp	3.5	2.5	3.5	1.006	3.5	3		flaky, sticky, FBE
316	RC.2.3213	75	3.7	1.077	1.5	buff	white	round	3.5	3.5	5	1.103	3.5	3		small, short, flat, sticky
317	RD.2.3976	80	6.7	1.056	1.5	buff yellow	yellow	oval	3	2.5	1.5	1.419	2		1.5	knobs, bulged eyes, pointy, curvy
318	RD.2.3654	70	3.6	1.083	1.5	buff red	white	long	4	1	3.5	2.791	1		1	**knobs**, too long, ornamental
319	R.2.3031	0	4.8	1.071	2.5	buff	yellow	oblong	3.5	3	2	1.168	3		2	flat, tuber worm, alligator
320	CR.2.1883	15	5.1	1.070	2.5	buff	white	round oblong	3.5	3	3	1.064	3	3	2	bottle
321	RD.2.3808	70	0.9	1.055	1.5	buff	white	round oval	4	2.5	2	1.186	2	1		lenticels, pointy, sticky
322	Russet Norkota	5	6.5	1.065	3.5	tan	white	oblong long	3.5	3	3.5	1.841	3		3	typy, curvy, bottle, greening
323	RD.2.3948	70	2.1	1.058	1.5	buff	white	round	4	3	2.5	1.208	2.5	1		bottle, pointy, dumbbell
324	CR.2.1463	60	3.5	1.082	2	buff	white	round	4	3.5	3.5	1.001	3	2.5		short, green
325	D.2.2170	75	1.1	1.077	1	buff yellow	yellow	round	3	3	2.5	1.112	1			chain, irregular, hard, **button**
326	CR.2.1393	40	3.2	1.063	3	buff tan	yellow	round oval	4	3.5	5	1.312	3.5		2.5	short, pointy, lenticels
327	C.2.1204	5	0.2	1.031	1	buff yellow	yellow	round	4	3.5	2.5	1.148	1.5			knobs, chain
328	RD.2.3479	85	7.3	1.094	1.5	buff orange	yellow	long	4	3.5	2.5	1.668	3		3	knobs, greening
329	R.2.3003	75	3.4	1.073	1.5	buff	cream	oblong long	4	3.5	5	1.653	3.5		3	pointy, curvy, growth cracks
330	RD.2.3934	60	3.9	1.054	1.5	buff	white	long	3	2	1.5	1.998	1.5		1.5	pointy, greening, curvy, folded
331	RD.2.3556	70	0.7	1.078	1.5	buff	white	round oval	3.5	3.5	3	1.339	2.5			shriveled
332	A07547-4	40	5.0	1.053	2.5	buff tan	white	oval oblong	3.5	3	4	1.503	3.5		3	short, bottle, sticky
333	E.1.3	10	6.0	1.075	2.5	buff tan	white	round comp	3	3	1.5	1.000	2.5	3		greening, FBE, sticky
334	P2-4	30	6.7	1.068	2	buff	white	oval long	3.5	1.5	4.5	1.489	1.5		2	**knobs**, bulge, button, curvy
335	Tacna	75	7.1	1.033	1.5	buff	white	round oval	3.5	2	1.5	1.356	1.5		1.5	translucent ends, sticky, pointy, moist tubers, bottle
336	RD.2.3759	0	0.0	#N/A												
337	R.2.2828	30	1.0	1.088	2.5	buff	white	oval oblong	4	2.5	2	1.755	2.5		2	dumbbell, short, curvy
338	D.2.2100	0	0.3	1.061	1	buff	light yellow	fing	4	3.5	2	3.391	2			pointy, shriveled, low yield
339	A06866-2	25	5.3	1.075	2	buff	cream yellow	oblong long	4	3	2	1.491	3		3	button, curvy
340	D.2.1967	5	1.4	1.057	1.5	buff orange	yellow	oval	3.5	3	1.5	1.744	1			shriveled, pointy, ugly
341	R.2.3052	30	2.4	1.088	2	buff	white	long oval	4	2.5	4	1.719	3		2	dumbbell, bottle
342	D.2.2051	0	0.0	#N/A												

Supplementary Table 6.3 (Continued)

343	R.2.2737	85	4.1	1.065	2.5	buff	white	long oblong	4	3	3.5	1.684	3		2.5	bottle, **knobs**, curvy, lenticels
344	D.2.2331	50	1.5	1.072	1	yellow	yellow	long fing	2.5	3	2	2.848	3.5			bottle, pointy, curvy
345	D.2.1932	25	1.6	1.061	1.5	light red	orange yellow	oval	3	3	1.5	1.451	1.5			lenticels, pointy, knobs, greening
346	D.2.2310	25	3.3	1.069	1	buff yellow	yellow	oval	3.5	2.5	1	1.684	1.5			pointy, shriveled, rot, ugly
347	R.2.2688	20	2.5	1.067	2	buff yellow	yellow	oblong	4	3.5	2.5	1.353	3		2.5	bottle, pointy
348	CR.2.1582	35	4.7	1.086	2.5	buff	yellow	round oblong	3.5	3.5	2.5	1.130	3	3		sticky, greening
349	RD.2.3507	85	1.9	1.078	1	buff yellow	dark yellow	round oval	3	3	2	1.355	2.5			pink eyes, pointy
350	D.2.2646	65	0.7	1.101	1	buff pink	cream yellow	long fing	3.5	2	1.5	2.802	1			shriveled, stem end rot
351	D.2.2247	70	0.3	1.057	1	orange yellow	orange yellow	long fing	3.5	3	1.5	1.981	1.5			rot, hard, shriveled
352	CR.2.1806	65	0.8	1.061	1.5	buff	white	round	3.5	3	3	1.083	2.5	1.5		lenticels, short
353	CR.2.1764	70	1.7	1.067	1.5	buff	white	round oblong	4	3.5	3	0.976	3	2.5		lenticels, short
354	RC.2.3192	50	1.9	1.079	1.5	buff	white	oval	4	3.5	5	1.588	3.5		1.5	short, pointy
355	RC.2.3143	40	0.7	1.052	1	buff	white	round	4	3.5	5	1.079	3	1.5		lenticels, skinning
356	D.2.1953	0	0.0	#N/A												
357	CR.2.1610	50	6.2	1.063	1.5	buff	white	round oblong	3.5	3	4.5	1.130	3	3	2	rhizoc, lenticels, FBE
358	AO00710-1	65	10.9	1.063	4.5	brown tan	cream yellow	long oval	4	2.5	4.5	1.651	2		1.5	shriveled, lenticels, folded, VD
359	D.2.2135	10	0.1	1.313	1	buff pink	cream	oval	3.5	4	1.5	1.229	1.5			tiny, shriveled, hard
360	D.2.2597	20	1.0	1.044	1	buff pink	yellow	long fing	3	1.5	1	2.306	1.5			pointy, knobs, curvy, short
361	RD.2.3745	75	3.3	1.071	1	buff yellow	yellow	oval oblong	3.5	3	2	1.277	2.5		1	bottle, irregular, sticky, greening
362	R.2.3059	65	6.2	1.082	3	buff tan	white	oval oblong	3	2	2	1.438	2.5		2.5	**knobs**, button, pointy
363	RD.2.3990	75	2.8	1.058	1.5	buff yellow	yellow	round oval	4	3.5	1	1.449	1.5			rhizoc, shriveled, ugly
364	R.2.2730	45	1.6	1.071	1.5	buff	cream	comp oblong	4	3.5	4.5	1.191	2.5	2.5		lenticels, cracky skin, scab
365	D.2.2219	60	1.4	1.075	1	orange yellow	orange yellow	round oval	3.5	3	1.5	1.380	1.5			shriveled, pointy, hard
366	C.2.1043	60	3.4	1.064	2.5	buff tan	white	comp	3.5	3.5	3.5	0.919	3	3.5		skinning, sticky
367	R.2.2933	90	5.0	1.077	2	buff	white	round oval	3.5	3	2	1.400	3		1.5	bottle, pointy, short
368	CR.2.1666	95	4.7	1.062	2	buff	white	round comp	3.5	3	3	1.001	3.5	3		button, sticky
369	AO00710-1	70	2.3	1.069	4.5	brown tan	cream yellow	oval oblong	3.5	3.5	5	1.425	3.5		3.5	alligator, heavy russet, pointy, sticky
370	CR.2.1673	10	4.8	1.060	2	buff	white	oval oblong	4	3.5	2.5	1.495	3		2.5	bottle, short
371	RC.2.3227	90	4.7	1.062	1.5	buff	white	oval oblong	4	3.5	4.5	1.387	3		2.5	short, lenticels
372	D.2.2086	70	0.9	1.075	1	light red	dark yellow	oval	4	3	1	1.380	1			shriveled, pointy, short, chain, sticky
373	D.2.2583	5	0.7	1.017	1.5	buff yellow	yellow	oval	3.5	3.5	2	1.353	2			pointy, shriveled, rot
374	D.2.2618	55	1.3	1.053	1	buff yellow	yellow	oval	3.5	3	2	1.466	2.5			shriveled, curvy

Supplementary Table 6.3 (Continued)

375	Castle Russet	75	4.1	1.091	4.5	brown	white	oval oblong	3.5	3.5	4	1.313	3.5		3	heavy russet, sticky
376	D.2.2114	50	1.5	1.070	1	buff pink	yellow	oval	3.5	3	1	2.227	1.5			shriveled, hard, silver scurf
377	CR.2.1498	30	4.1	1.078	2	buff	cream	round	4	3.5	3.5	1.041	3	2		lenticels, shriveled
378	RD.2.3591	85	3.9	1.080	1.5	buff	white	long	2.5	3.5	4	1.873	3.5		2.5	greening, deep eyes
379	Atlantic	5	6.2	1.074	2.5	buff tan	white	round comp	3	3.5	2	1.197	3	3		FBE, flaky, sticky
380	E.1.3	20	7.8	1.072	2.5	buff tan	white	comp round	3	3	2.5	1.138	3	3		FBE, flat, greening
381	RD.2.3570	95	4.4	1.079	2	buff pink	white	round oblong	2.5	2	2.5	1.218	2		1.5	button, curvy, bottle, greening
382	C.2.1148	15	1.8	1.064	1.5	buff	white	round	3.5	3.5	4	1.174	3	3		lenticels, skinning
383	CD.2.1239	15	1.7	1.056	2	buff tan	white	brown	3.5	3	4.5	1.004	3.5	2		tuber worm
384	CD.2.1386	10	0.9	1.084	1	yellow	yellow	oval fing	4	3	1	1.790	1.5			shriveled, pointy
385	RD.2.3542	0	0.0	#N/A												

Appendix B. Supplemental analysis of *Verticillium dahliae* infection using qPCR and the area under the senescence progress curve

Introduction

In addition to culturing *V. dahliae*, we used the area under the disease senescence curve (AUSPC) and quantitative polymerase chain reaction (qPCR) to evaluate *V. dahliae* colonization of plant stems. AUDSC data was generally very similar for the inoculated and uninoculated plants, indicating that this metric was more suitable for measuring general plant health than *V. dahliae* progress. qPCR was judged to be less reliable than Verticillium culturing for two reasons. First, during extraction of DNA from plant stems, several samples were lost when wells broke, leading to missing data points. Second, qPCR samples detected low levels of *V. dahliae* DNA in uninoculated control plants, which may have been the result of contamination rather than incidental inoculation. As a result, this data was removed from the main analysis. Despite these concerns, the qPCR data did correlate fairly well with scores derived from the visual evaluations and the Verticillium culturing (r=0.677).

Methods

AUDSC

To calculate AUSPC, the sum of the area between the senescence progress (Supplementary Table 3.1) and a score of "5" (a healthy plant) was calculated using the following the equation described by Simko and Piepho (2012).

qPCR

At the same time as sap was extracted from each plant at the end of the replicated trial for Verticillium culturing, the lowest 2.5 cm segment of each plant stem was stored in a 96-well sample collection plate, and frozen at -80°C until DNA could be extracted. DNA was extracted from samples using a Mag-Bind Plant DNA DS Kit (Omega Bio-

Tek), using manufacturer instructions. After extraction, DNA samples were diluted to a concentration of 3ng/µl with DEPC treated water.

qPCR was conducted in triplicate in QuantStudio 3 Real-Time PCR System (Applied Biosystems) using PowerUp SYBR Green Master Mix (Thermo Scientific) with 3 ng DNA and 200 nM of each of the primers VertBt-F and VertBT-R (Modified from Atallah et al. 2007). In addition, qPCR was conducted in triplicate with the primers PotAct-F and PotAct-R (for *act* gene in potato). To produce a standard curve, the following amplification was used: 2 min at 50°C, then 2 min at 95°C, then 40 cycles of 95°C for 1 s and 60°C for 35 sec. At the end of the 40 cycles, a melt curve analysis was used to ensure that the correct target sequences were amplified (data not shown). Average cycle threshold (Ct) values of the three technical replicates were used to approximate *V. dahliae* colonization of the stem tissue for each plant. If the plant was dead and qPCR was not conducted, the plant was arbitrarily given a Ct value of 20, indicating a high level of *V. dahliae* infection.

Statistical analysis

ANOVA and LSD tests were conducted for the qPCR data using the same methods as in the main analysis. In addition, qPCR values were correlated with the indexed values in the main analysis, and broad-sense heritability values were calculated for the visual evaluations, the Verticillium culturing, the indexed scores used in the main analysis, and the qPCR Ct values.

Results

AUSPC values were very similar for the inoculated an uninoculated clones, indicating that this was not a suitable metric to quantify *V. dahliae* resistance in these clones. However, for all clones except PI498149adr-2v (which was scored as one of the most resistant clones in the main analysis), the AUSPC was higher for the inoculated clones than the uninoculated clones, indicating this metric was still able to detect the effects of *V. dahliae* infection.

The ANOVA of the qPCR data confirmed that there was a significant difference between clones in this analysis (Supplementary Table 3.3). However, the corresponding LSD test was not able to determine which clones were significantly different from each other using only the qPCR data (Supplementary Table 3.4). The correlation between the qPCR values and the index values used in the main analysis was 0.677 (Supplementary Figure 3.1). Broad-sense heritabilities were 0.664 for the visual evaluations, 0.706 for the Verticillium culturing, 0.768 for the indexed values used in the main analysis, and 0.479 for the qPCR data.

Discussion

In this experiment, AUSPC was not an effective measure of *V. dahliae* resistance, presumably due to a general difficulty in distinguishing *V. dahliae* symptoms from general plant health, as well as a wide variation in plant health between these species under greenhouse conditions.

The precision of the qPCR data was much lower than that of either the visual evaluations or the visual evaluations or the Verticillium culturing. However, the success of both Verticillium culturing and qPCR is partially dependent on the abilities of the researchers conducting the experiments. Therefore, the relative success of these techniques may change from lab to lab.

References

Atallah ZK, Bae J, Jansky SH, Rouse DI, Stevenson WR (2007) Multiplex real-time quantitative PCR to detect and quantify *Verticillium dahliae* colonization in potato lines that differ in response to Verticillium Wilt. *Phytopathology* 97: 865-872.

Simko I, Piepho HP (2012) The area under the disease progress stairs: calculation, advantage, and application. *Phytopathology* 102: 381-389.

Tables

Supplementary Table 3.2. Mean AUDCC values for clones infected with isolates “653” or “11-11” of *Verticillium dahlia*e, and for uninoculated controls.

Clone	Mean AUDSC (inoculated clones)	Mean AUDSC (uninoculated clones)
PI275182iop-4v	23.8	19.8
Russet Norkotah	21.5	19.0
PI275182iop-1v	15.8	12.6
PI498011blb-1v	12.2	11.4
PI275181iop-1v	12.0	10.0
Ranger Russet	11.6	9.9
PI283107hou-1v	11.2	9.1
PI498148adr-1v	4.9	4.1
PI498148adr-2v	2	2.5

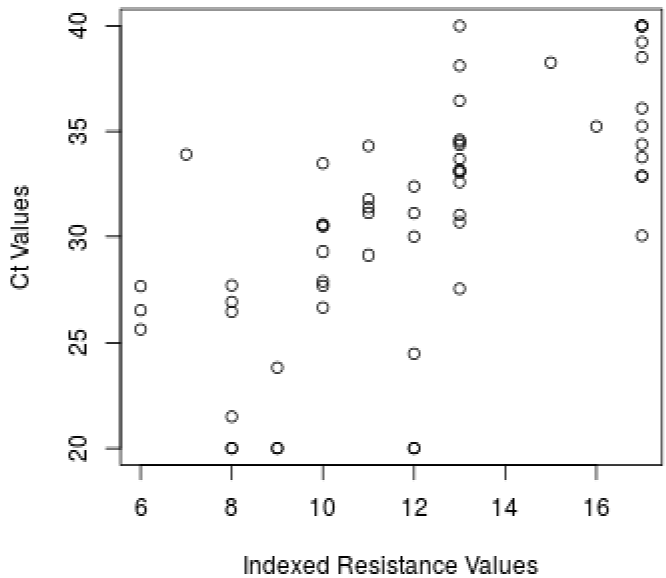
Supplementary Table 3.3. ANOVA for *Verticillium dahliae* infection using qPCR data.

	DF	SS	MS	F-value	p-value
Clone	7	399.25	57.036	2.2654	0.046
Isolate	1	138.83	138.834	5.5143	0.023
Clone*Isolate	7	186.16	26.594	1.0563	0.407
Error	44	1107.79	25.177		

Supplementary Table 3.4. LSD values for *Verticillium dahliae* infection for qPCR data.

Clone	Mean CT Value
PI498148adr-2vd	35.3(a)
PI498148adr-1vd	33.1(a)
PI498011blb-1vd	31.8(a)
PI275181iop-1vd	31.1(a)
Ranger Russet	30.4(a)
PI275182iop-4vd	29.8(a)
PI275182iop-1vd	27.9(a)
PI283107hou-1vd	26.6(a)

Figures



Supplementary Figure 3.1. Correlation between qPCR data and indexed values from main experiment.

Appendix C. Protocols used

Marker Amplificication Protocol

(DNA extraction conducted Mag-Bind Plant DNA DS Kit according to manufacturer instructions)

DNA precipitation (to increase purity)

1. Transfer DNA to a micro-centrifuge tube.
2. Bring the volume to 270 µl with DEPC water.
3. Add 30 µl 3M sodium acetate.
4. Add 750 µl 100% ethanol.
5. Mix thoroughly by turning tubes over on themselves.
6. Put in -80 °C freezer for at least 30 minutes- ideally overnight.
7. Centrifuge at 13,000 rpm for 13 minutes at 4 °C.
8. Slowly pour out liquid, leaving a small clear DNA pellet.
9. Add 400 µl chilled 70% ethanol and mix by turning tubes over on themselves.
10. Centrifuge at 13,000 rpm for 5 minutes at 4C.
11. Carefully pour out liquid.
12. Repeat steps 9-11.
13. Turn tubes upside down on a paper towel, until all liquid drips out (approximately 5 minutes).
14. Place tubes under hood, leave there until no more ethanol smell (about 15 minutes).
15. Add 50 µl elution buffer.

Primer Dilution (to 10 µM)

1. Add 10 µl water per nmol primer.
2. Vortex, let sit at room temperature for 5 minutes, then centrifuge.
3. Mix 10% forward primer, 10% reverse primer, 80% H2O, vortex, and centrifuge.

PCR Protocol

1. Mix 8.5 µl master mix made from AmpliTaq® Gold with GeneAmp, 0.4 µl 10 µM primer mixture, and 1.1 µl 25 ng/µl DNA.
2. Spin mixture.
3. PCR- modify PCR conditions for specific primers.

Gel Protocol

1. Mix 6.4 g agarose with 320 ml TE buffer in a 500 ml Erlenmeyer flask.
2. Microwave for 90 seconds, mix flask, and repeat until liquid boils.
3. Place flask in a tray of water on a stir plate for 5 minutes, to allow the mixture to cool down.
4. Pour contents of flask into a gel caster tray and position the combs as required..
6. After gels have cooled, use immediately, or store in TE buffer for later use.

Electrophoresis Protocol

1. Add 5 µl dye into each PCR cell (containing 10 µl PCR product).
2. Spin tubes.
3. Load contents of PCR cells into gels.
4. Put 5 µl ladders into empty cells adjacent to samples
5. Run at 90 V for 90-400 minutes, depending on the expected fragment size, and the expected difference between fragments. DNA moves from black to red.
6. Shake gel in 0.5 µg/ml ethidium bromide for 20 minutes.
7. Shake gel in water for 20 minutes.
8. Use imager as per instructions.

Root Squash Protocol

Fix Root Tips

1. Collect 1 cm root tips of quickly growing roots at 2:00 pm (young plants work best).
2. Place root tips in 2 mM hydroxyquinoline for 3 hours.
3. Rinse root tips with distilled water.
4. Store root tips in a mixture of 3 ethanol:1 acetic acid, for up to several months.

5 (optional). After 2 days, transfer to 70% ethanol for storage for years.

Squash root cells on slide

1. Move root tips through three distilled water baths, 5 minutes per bath.
2. Place 2mm tips of each root in an enzyme solution (Lattier et al. 2017), and let sit at 37 °C for 30 minutes.
3. Move each tip to a slide with a pipette or a razor blade, 1-2 tips per slide.
4. Add 1-2 drop 3 methanol:1 acetic acid.
5. Lightly smash root tip with a metal spatula spread the mixture on the slide by tapping (in this project a large paper clip with one end flattened with a hammer was used instead of a metal spatula). Add drops as needed to prevent drying.
6. Light the surface of the slide with a lighter.
7. Tap off excess drops.
8. Let the slide sit for one hour to overnight at 37 °C.

Stain root cells

1. Mix 3 mL Giemsa stain per 50 mL water.
2. Scoop oil off top of the stain mixture with Kimwipe.
3. Soak slides in the stain solution for 15 minutes.
4. Rinse slide in distilled water and let dry at 37 °C.

Meloidogyne chitwoodi extraction protocol

1. Remove each plant from its pot and place it in a bowl with water. Gently shake the roots to separate them from the soil.
2. Move the roots to another bowl with water and swirl the roots to remove more soil. Continue to move the roots to bowls of fresh water until the roots are clean. If necessary, cut the root systems into pieces no larger than 5 cm across so that all of the soil can be removed.
3. Add the roots to a 500 ml container, and add 0.5% sodium hypochlorite to the container until the roots are covered.
4. Place the container on shaker at approximately 90 rpm for 3 minutes (or shake by hand).
5. Pour the resulting mixture through a size 20 sieve over a size 500 sieve. Nematode eggs will collect in the size 500 sieve.
6. Rinse contents of size 500 sieve into a beaker/vial.

Verticillium dahliae inoculum preparation protocol

1. Transferred edges of six potato dextrose agar plates previously infected with *V. dahliae* into 3 l autoclaved Czapec Dox broth in Erlenmeyer flasks in a sterile environment. Plug opening of the flasks with sterile cotton, and cover with sterile aluminum foil.
2. Shake flasks at 25 °C in the dark for ten days.
3. Strain *V. dahliae* conidia from broth using a cheesecloth, and dilute conidia with deionized water.
4. Quantify *V. dahliae* conidia with a hemocytometer, then dilute to the desired concentration.

Verticillium dahliae culturing protocol

1. Cut stems at base, break off leaves and side shoots, and brush off dirt.
2. If the main shoot is alive, cut a 2.5 cm stem segment, soak it in 0.5% sodium hypochlorite solution for 3 minutes, then transfer it to water.
3. Dry off stem segment w/ paper towel, then crush stem. Wipe crushing equipment with ethanol between crushes.
4. Pipette 30 µl sap. If necessary, fold crushed stem, and re-crush. Put sap in 100 µl distilled water, then pipette up and down to mix.
5. Spread sap over the media described by Hoyos et al. (1991) in a petri dish with a spreader bar. Wait until colonies form to count *V. dahliae* colony forming units. Colony appearance may depend on *V. dahliae* isolate.

Potato crossing protocol

Pollen collection

1. Remove approximately 20 newly opened flowers from the clone intended to be used as a male parent.

2. Remove anthers from the flowers and place them in a labeled parchment paper pouch with a tweezer. Dip the tweezers in ethanol and wipe them off between clones reduce pollen contamination.

3. Place the pouches in a dry place with natural light for approximately 24 hours.

4. Release the pollen from the anthers by touching an edge of the pouches with an electric sander.

5. Open the pouches and transfer the pollen to a plastic serum vial by gently scraping it up with a knife. Use the pollen fresh, or store in a refrigerator for up to one month.

Emasculation and pollination

1. Select potato buds that are expected to open in 1-2 days.

2. Carefully separate the petals with a pair of tweezers and remove each anther by bending it away from the style.

3. Place a small glassine bag (approximately 4 cm × 4 cm) over the flower. To fasten bag, fold the open end of the bag over on itself and staple shut, so that flower’s pedicel goes through the bag’s only opening, on a corner.

4. One to three days after emasculation, cut the end of the glassine bag opposite the folded stapled edge with a pair of scissors. Coat the stigma by dipping it in a scoop of pollen. If pollen does not adhere to the stigma, the flower will not be ready for pollination for another 1-2 days. Staple the cut end of the glassine bag closed. If the pollination is successful, fruit will begin to form in one week, and will be ready for harvest in approximately one month.