EARLY GENERATION SELECTION FOR COLD CHIPPING IN POTATO GENOTYPES DEVELOPED BY CONVENTIONAL TETRAPLOID BREEDING AND BY INTERSPECIFIC AND INTERPLOIDY HYBRIDIZATIONS

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DAVID L. ESPLIN

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DR. CHRISTIAN A. THILL

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Abstract

A potato cultivar with the cold chipping (CC) trait accumulates less reducing sugars during cold (4C) storage and can therefore produce light colored chips with reduced acrylamide levels directly from storage. Cold chipping cultivars could reduce the losses and costs associated with most potato storage regimes. Development of CC cultivars using sexual polyploidization (SP) coupled with early generation selection (EGS) may accelerate the development of CC cultivars by increasing genetic variation, reducing new parent development time, and reducing population sizes necessary in potato breeding programs.

The objectives of this research were to determine the variance and genetic gains that result from EGS for CC on tubers derived from seedling transplants or greenhouse-grown tubers using populations developed from 2x-2x, 2x-4x, 4x-2x, and 4x-4x matings. Agronomic and horticultural traits were also evaluated for selected genotypes.

Cold chipping was evaluated after 3 and 6 months cold (4C) storage. Chips were made by frying a 1 mm thick slice from the center of one longitudinally cut tuber per genotype in 185C vegetable oil until bubbling ceased. Chip color scores were visually evaluated using a standard color scale ranging from 1 to 10 with a score of 4 or less considered acceptable. Total and marketable yield, specific gravity, general tuber appearance, eye depth, sprouting, skin and flesh color, tuber shape, and maturity were evaluated for selected genotypes.

Large variances, high frequencies of acceptably chipping genotypes, and excellent mean color scores were observed in all 4 mating types. Positive genetic gains resulted from EGS for CC but were reduced by genotype by environment interactions.

This illustrates the importance of testing genotypes over multiple locations and storage durations as a part of developing CC varieties.

Greater genetic gains from early generation selection may result by using SP with germplasm that has excellent CC coupled with superior agronomic and horticultural trait performance. The excellent performance of the 2x-2x matings in this research suggests that combining EGS with bilateral sexual polyploidization for CC may increase the probability of selecting a tetraploid CC genotype with cultivar potential if accurate and efficient methods of separating the resulting diploid and tetraploid progeny can be utilized.

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Dedication

For Ciana Fielding Esplin

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Potato Processing and Storage

Potatoes are produced worldwide in widely divergent climates and elevations. In 2009, more than 7.2 billion hundred-weight (cwt) or 329 million metric tons of potatoes were produced (FAO 2010). Worldwide production is primarily in the industrialized countries of the northern hemisphere, but rapid increases in acreage and yield in developing countries has occurred in the last 50 years (Niederhauser 1993). In 2006, an estimated 14 percent of the total world potato crop was processed (Keijbets 2008). Processing capacity has increased rapidly, especially in China and India.

Potato growers in the U.S. produced 431 million cwt (6.2 % of world total) on 1.0 million acres during the 2009 season with a value of 3.5 billion dollars at the farm-gate and billions of dollars more in value-added sales of potato products such as potato chips and french fries (NASS 2011). About 256 million cwt (59 %) of the total U.S. production of potatoes was used for processed products, with potato chip and shoestring product processing accounting for 42.9 million cwt or about 17 percent of that total (NASS 2011).

U.S. potato production is predominately located in the northern states with a fall-harvested crop. The northern U.S. offers less disease and insect pressure, less heat stress, and better storage climates than the more southern states (Hijmans 2001). The Midwestern states including Minnesota, Michigan, Wisconsin, and North Dakota produced about 20 percent of the total U.S. production (NASS 2011). Minnesota

produced 20.7 million cwt of potatoes on 45,000 acres in 2009 worth approximately 147 million dollars (NASS 2011).

The utilization of fresh potatoes in the U.S. has shrunk to 42 pounds from a peak of 81 pounds per person in the 1960's (ERS 2011). The consumption of processed potatoes increased dramatically as the consumption of fresh potatoes declined. Currently, 86 pounds of processed potatoes are consumed annually per capita. An average of 55 pounds is from frozen products, 17 pounds from chips, and 14 pounds from dehydrated products (ERS 2011).

Industry consolidation has led to increased efficiencies and fewer players in the domestic and international processing markets (Keijbets 2008). For example, the 400 plants that processed 20 million cwt of chipping potatoes in 1960 were reduced to 92 plants processing 67 million cwt in 2006 (Lucier and Dettmann 2008). Similar trends have been observed in other potato processing markets. Because the potato processing industry is "mature" fewer new products are being developed, but products are being altered to decrease the salt and fat content and increase the nutritional content. The new processed products that are introduced emphasize convenience, indulgence, and wellness demands and shifting ethnic demographics of the population (MSU 2011). Also, convenience or value added products such as pre-peeled and pre-cooked potatoes as well as innovated coating and cuts of french fries are being well received by consumers (Keijbets 2008). The future of processing may include increased sustainability of production practices and cultivars, altered starch properties, and reduced acrylamide.

The shelf- life of a bag of potato chips is approximately 4 to 6 weeks, therefore processors need a constant supply of raw potatoes to make potato chips (Brewer et al.

1990; Smith 1987). To meet the year-round demand, much of the fall crop is put into long term storage for use in the winter months until spring and summer crops from the southern U.S. are available for chipping (Brewer et al. 1990). The main goals of long-term storage are to control disease and sprouting, minimize shrinkage, and maintain processing quality until the tubers are required by the processor (Knowles et al. 2009). Storability of potatoes is determined by many factors including cultivar, diseases, tuber integrity, maturity (physical and chemical), storage conditions, and storage duration (Rastovski 1987; Sowokinos 2001b). Storage regimes that include several weeks of warmer storage before (preconditioning) and after (reconditioning) the long-term storage temperatures are established have been helpful to meet the primary goals of storage but have variable efficacy depending on cultivar and storage duration (Knowles et al. 2009). Conditioning also requires additional storage management and cost for the grower. Only a few potato varieties are considered acceptable to be used for long-term storage to meet the high quality demands of processors and marketers, because of the large differences in storage performance (Christiansen and Laerke 2003).

Despite the use of varieties that store well and optimization of storage regimes, every year a large and valuable portion of the stored crop is lost during storage. In 2009, the USDA reported that 29.1 million cwt or 6.7 percent of the total U.S. production was lost due to shrinkage, disease, and other postharvest loss factors (NASS 2011). This represents an annual loss of over 200 million dollars. The common causes of postharvest storage losses include respiration, sprouting, changes in chemical composition of the tuber flesh, spreading of disease, damage from extreme temperatures, and shrinkage (Rastovski 1987). A major factor contributing to the postharvest potato loss problem is

the relatively warm storage (approximately 10C) typically practiced in commercial potato storage facilities (Rastovski 1987). The temperatures chosen usually reflect a compromise between the competing goals of minimizing pathogen development, prolonging dormancy, and maintaining low carbohydrate levels to optimize product color during processing (Knowles et al. 2009). To avoid sprouting in the relatively warm storage temperatures, Chlorpropham (known as CIPC or isopropyl N-(3-chlorophenyl) carbamate), or other postharvest chemicals are applied to the tubers in storage (Kleinkopf et al. 2003). CIPC stops sprout growth by interfering with spindle formation during active mitosis, therefore stopping cellular division (Vaughn and Lehnen 1991).

Potato cultivars that tolerate lower storage temperatures without increased reducing sugars or that can be processed directly without the need for conditioning would have many benefits for growers and processors. These include extended marketability of the crop as the grower can hold the crop for a longer period of time in order to obtain a higher price. Cold storage also reduces the high costs of heating and humidifying storage facilities and simultaneously reduces the need for expensive and potentially dangerous dormancy maintaining chemicals (Christiansen and Laerke 2003; Thill and Peloquin 1995). Finally, cold storage maintains the overall tuber weight through reduced respiration and reduced disease prevalence (Ewing 1974; Sowokinos 2001b). The biggest drawback of cold storage for most currently available cultivars is the sharp accumulation of reducing sugars that occurs in tubers stored in cold conditions. This phenomenon is known as cold-induced sweetening (CIS) (Sowokinos 2001b).

Cold-Induced Sweetening

During normal tuber respiration, starch is enzymatically converted to energy though the normal metabolic pathways of glycolysis and mitochondrial respiration in tubers (Ap Rees et al. 1981). Some starch is converted in an alternative pathway to glucose intermediates and sucrose. These carbohydrates are then metabolized to the reducing sugars glucose and fructose in an irreversible process known as hexogenesis. The rate of conversion to reducing sugars is increased dramatically during cold stress conditions such as cold temperature storage (Sowokinos 2001b). The mechanisms responsible for this observed increase are not fully understood at the molecular level but likely include changes of hormonal levels, structures of cellular membranes, enzyme activities, and concentration changes to key ions, substrates, or enzymes (Sowokinos 1990). Sweetening may provide the adaptive advantage of increased cold-hardiness for the plant (Ap Rees et al. 1981).

Reducing sugars in the tubers react during processing with free amino acids in a non-enzymatic Maillard reaction that produces dark-colored, bitter-tasting processed potato products. These products are not acceptable to consumers and are high in acrylamide, a neurotoxin and potential carcinogen (Smith 1987; Mottram et al. 2002; Shallenberger et al. 1959). The amount of reducing sugars required to initiate this chemical reaction is very low, with a threshold level for acceptable chip colors at 0.25 mg of glucose per gram of tuber (Douches and Jastrzebski 1993). Such a low level of reducing sugars is difficult to maintain over a 6-8 month storage season even in conventional storage temperatures (Smith 1987). Colder storage temperature and newly developed and untested varieties are considered too risky to be considered for most

processors because product color is the most important trait that determines acceptability of a cultivar for processing. Product color is the primary market limiting trait because a processor will reject raw potatoes that may be superior in all traits but produce unacceptable color (Thill and Peloquin 1995; Sowokinos 2001b). In the U.S., processing plants annually reject approximately 15% of potatoes due to high reducing sugar levels (Sowokinos 2001b).

The two most important enzymes involved in CIS are uridine diphosphoglucose pyrophosphorylase (UGPase: E.C. 2.7.7.9) and acid invertase (AcInv: E.C. 3.2.1.26) (Katsube et al. 1990; Zhou et al. 1994). UGPase is found in excess in potato tubers and exerts control of the sweetening pathway by controlling the formation of uridine-5'-diphosphoglucose (UDP-Glc) which is the first committed step of the sweetening pathway and the rate limiting substrate for sucrose production (Sowokinos 2001b). Vacuolar AcInv catalyzes the final step in hexogenesis (Richardson et al. 1990; Davies et al. 1989). Vacuolar AcInv hydrolyzes sucrose into glucose and fructose in an approximate 1:1 ratio at a rate that increases as the storage temperature decreases (Isla et al. 1992; Zrenner et al. 1996; Zhou et al. 1994). The rate of accumulation is variable and dependent on the cultivar, storage temperatures, and storage duration.

Two alleles of UGPase (UgpA and UgpB) correlate to cold sensitivity of potato varieties (Sowokinos 2001a). Cold-resistant varieties such as 'Snowden' had an UgpA: UgpB ratio of 4:0 or 3:1 and cold-sensitive varieties had a ratio of 1:3 or 0:4. Three of the five isozymes of UGPase are found only in association with UgpB in cold sensitive varieties. The biochemical basis for the variation of sugar accumulation may be explained by the differences in kinetics of the isozymes. Therefore, under cold storage temperatures

cultivars with an efficient form of UGPase may accumulate reducing sugars more quickly than cultivars with a less efficient form (Sowokinos 2001b). These results also suggest that UGPase has the potential to serve as a genetic marker for cold-sweetening resistance in potato breeding populations at either the allele or isozyme level (Sowokinos 2001a).

The importance of AcInv in CIS was convincingly demonstrated recently by researchers who prevented CIS by suppressing the vacuolar acid invertase gene (*VInv*) using genetically transformed plants (Bhaskar et al. 2010). For effective CIS prevention, they found that suppression of approximately 90% or greater was required. To get that level of suppression the researchers combined three RNAi constructs that targeted different regions of the *VInv* gene. Of the 150 RNAi lines they created, only 23 lines had 90 percent or more AcInv suppression (Bhaskar et al. 2010). One very important finding of their research was that naturally occurring, heritable variation for *VInv* gene expression measured using real-time PCR exists in the wild potato species *Solanum raphanifolium*. That species was also among those identified as having the ability to produce acceptable potato chip color from 2C storage (Hamernik 1998). They also showed transmission of the low expression levels of *VInv* to the progeny of a cross between *S. raphanifolium* and a haploid-species hybrid of *S. tuberosum* and *S. chacoense* (Bhaskar et al. 2010). These results are encouraging for potato breeders who are interested in developing cold chipping cultivars without the regulatory challenges of genetic engineering.

The demand for cultivars with lower reducing sugars has increased dramatically recently because potato processing companies such as Simplot and Frito-Lay, as well as retailers such as McDonald's are scrambling to reduce acrylamide levels following a lawsuit filed by the Attorney General of California in 2005 that would require potato

products with high levels of acrylamide to be labeled as potentially carcinogenic (Anonymous 2005). Despite the scientific debates about the potential risk to human health, if the levels of acrylamide are not reduced soon, retailers may be forced to label their potato products as potentially carcinogenic (Wilkins 2011; Pelucchi et al. 2003). While heat regulation, moisture management, blanching, or treatments with organic acids or asparaginase during processing may provide methods of reducing acrylamide formation in current processing varieties, the development of new varieties that naturally produce less acrylamide during processing is essential. If transgenic varieties become acceptable to the regulators or to the general public, reduction of asparagine via transgenic potato varieties has been shown to reduce acrylamide (Rommens et al. 2008). Until then, developing varieties with lower reducing sugar levels commonly found in wild species germplasm would provide a powerful method of reducing acrylamide development (Claus et al. 2008; McCann et al. 2010).

The challenge to the potato industry caused by the concerns of acrylamide may help potato breeders overcome the reluctance of processors to accept new cultivars and replace cultivars such as the 100-year old 'Russet Burbank' that has been the industry standard for decades (Burton 1989). Acrylamide and the threat of labeling requirements may actually be the catalyst for processors to trial new varieties more vigorously. Currently, two major projects backed by the U.S. Potato board, state potato organizations and processors such as Simplot, McCain Foods, Frito Lay, and H.J. Heinz are testing the most promising new clones available in national trials in order to identify a variety that produces lower acrylamide levels for chipping and french fries (Wilkins 2011). Studies of

acrylamide and asparagine in wild related species indicate excellent potential for improving new cultivars using potato breeding (McCann et al. 2010; Bhaskar et al. 2010).

Potato Genetics and Biodiversity

Evolution and Diversity

The evolution of potatoes probably occurred in the mountain altiplano of the Andes around Lake Titicaca at 2-3000 meter elevation. That geographic area is a center of diversity for cultivated potato, and may also be a center of origin (Burton 1989; Hawkes 1990). The systems of parallel mountain ranges and valleys in that region and the wide variation for moisture, temperature, and sunlight in that region would have provided the perfect evolutionary environment for the development of a wide variety of potato species (Hawkes 1994). The process of evolution would have been enhanced by the genetic variability, large population sizes, and the large degree of dominance and epistasis associated with the potato (Hancock 2004). Potato speciation occurred as barriers to reproduction such as endosperm balance number (EBN), self-incompatibility, endosperm failure, and unreduced (2n) gametes developed and interacted in geographical and ecological isolation (Carputo et al. 2003; Hancock 2004). Potato speciation is unmatched by any other crop with more than 180 tuber-bearing species found at elevations ranging from sea-level to 4500 meters and latitudes from Southern Chile to the Southwestern United States (Hawkes 1990; Spooner and Bamberg 1994).

The gametophytic self incompatibility (GSI) system of potato probably evolved as out-crossing increased the likelihood of survival (Clark and Kao 1994). The general mechanism of incompatibility is pollen tube death caused by S-RNase that degrades the

ribosomal RNA of the pollen tube as it moves down the style (Richman and Kohn 2000; Lord and Russell 2002). Both a receptor specific model and a receptor non-specific model have been suggested to explain the process that occurs as S-RNases interact with the pollen tube and destroy those with alleles identical to the style (Lord and Russell 2002; Wheeler et al. 2001). Two hypervariable regions of the S-RNase alleles along with modifier genes control the specificity of the GSI system (Cruz-Garcia et al. 2003). Sporophytic incompatibility does not seem to apply in potatoes (Hanneman 1999; de Nettencourt 1997).

The EBN hypothesis was developed to explain certain cross-ability differences that are not explained by ploidy. It is an important evolutionary mechanism because it determines the success or failure of interspecific or interploidy crosses (Carputo et al. 2003). An EBN number is considered an "effective ploidy" and values range from 1-4 with assignment based on actual crossing success with reference species. Typically, diploid species are 1 or 2 EBN, triploids are 2 EBN, tetraploids are 2 or 4 EBN, and hexaploids are 4 EBN (Carputo et al. 2003). Successful crosses have a 2:1 ratio (maternal to paternal) of the EBN in the endosperm (Johnston et al. 1980). Simply stated a viable cross is likely if the EBNs of the parents match and other crossing barriers are absent (Hanneman 1999). For example, a cross between a pair of 4 EBN tetraploid genotypes will be successful because the endosperm consists of 2 maternal nuclei and 1 paternal nucleus that meet the required 2:1 ratio. A haploid of a tetraploid 4 EBN species has an effective EBN of 2 and can be crossed with species that have 2 EBN to create haploid-species hybrids. The mechanism underlying the EBN hypothesis is not currently

known but two studies reviewed by Carputo et al. (2003) suggest that additive gene action with either 2 or 3 loci determines EBN.

2n gametes and EBN are especially important mechanisms in the evolution of polyploid potato species such as *Solanum tuberosum*. Polyploidization of diploids can occur through somatic doubling or sexual polyploidization. 2n gametes lead to sexual polyploidization that maximizes the heterozygosity and genetic diversity essential in potatoes while EBN allows continued gene flow to occur despite the change in ploidy (Carputo et al. 2003).

Ancestry and Domestication

A better understanding of the ancestral background of cultivated potato is important to help understand and improve breeding techniques (Peloquin and Ortiz 1992). The morphological, cytoplasmic, and molecular evidence of ancestry is complicated and does not lead to simple conclusions about which species are the most likely candidates (Hancock 2004). Hawkes (1990) claims that *S. tubersosum* ssp. *tuberosum* developed from four wild species S. *acaule, S. sparsipilum, S. leptophyes,* and *S. megistacrolobum* based primarily on morphological evidence. According to this theory, *S. leptophyes* evolved to form *S. stenotomum* which is a diploid cultivated variety. Subsequently, *S. stenotomum* hybridized with *S. sparsipilum* to form the amphipolyploid *S. tuberosum* ssp. *Andigena*. *S. tuberosum* ssp. *andigena* then evolved to form ssp. *tuberosum* when humans took it to the long-day environments of southern Chile before the Spanish conquest. A study by Cribb and Hawkes (1986) found that a cross of *S. stenotomum* and *S. sparsipilum* that was treated with colchicine resulted in an

allopolyploid that was very similar to *S. tuberosum*. Further evidence for this theory was a study that showed selection for long days on a population of *S. tubersosum* ssp. *andigena* resulted in morphologies similar to *S. tubersosum* ssp. *tuberosum* that have been called 'neo-tuberosum' and used in potato breeding (Simmonds 1995). A recent paper questions the purity of the development of neo-tuberosum based on microsatellite and plastid DNA markers suggesting that an unintended hybridization to *S. tubersosum* ssp. *tuberosum* occurred as it was developed. The marker data shows that neo-tuberosum is more closely related to the cultivated *S. tubersosum* ssp. *tuberosum* germplasm than it is to the *S. tubersosum* ssp. *andigena* germplasm (Ghislain et al. 2009).

Alternative hypotheses of the development of *S. tuberosum* include a study by Debner et al. (1990) that show phylogenetic relationships based on RFLP markers, suggesting that *S. canasense* rather than *S. sparsipilum* was a parent. Grun (1990) suggests that a currently unknown parent with "cytoplasmic sterility factors encoded in mitochondria or plastids having a distinctive type of DNA" acted as the female parent. Volkov et al. (2001) cites 5S rRNA nucleotide sequence homology as evidence to reject the Hawkes hypothesis in favor of *S. phureja* and *S. spegazzinii* as the ancestral parents of *S. tubersosum* ssp. *tuberosum*. Ugent (1970) was probably accurate when he suggested that because of the frequency of interspecific hybridization and the diversity of tetraploid cultivars that there were "a number of independently acting, but genetically interconnected, lines of evolution that were simultaneously involved."

Domestication of potato probably occurred sometime after 11,000 B.C. (Grun 1990; Hawkes 1990). Domestication had three main stages: domestication of diploid species in South America, emergence of cultivated tetraploid species in South America,

and tetraploid species evolution to long-day growing conditions and subsequent worldwide dispersal and utilization (Bradshaw and MacKay 1994). Specific archaeological evidence of domestication has been found dating from 8000 years ago (Hoopes and Plaisted 1987; Hawkes 1990). The lack of written records or potato fossils reduces our ability to gain an understanding of precisely when or how potato was domesticated (Dodds 1965). It is not until 1 A.D. that hard evidence of potato cultivation in the form of ceramics depicting potatoes have been identified (Hawkes 1990). During the same period of time that potatoes were domesticated, South American peoples domesticated a great number of valuable crops including maize (*Zea mays* L.), quinoa (*Chenopodium quinoa* Wild.), and other tubers such as oca (*Oxalis tuberosa* Molina), ulluco (*Ullucus tuberoses* Caldas), and mashua (*Tropaeolum tuberosum* Ruiz and Pavon) (Dodds 1965).

Domestication resulted in cultivated potatoes that have historically been classified into seven species including three diploids (*Solanum Phureja, Solanum Stenotomum, Solanum ajanhuiri*), two triploids (*Solanum chaucha, Solanum juzepczukii*), one tetraploid with two subspecies (*Solanum tuberosum* ssp. *tuberosum* and *Solanum tuberosum* ssp. *andigena*), and one pentaploid (*Solanum curtilobum*) (Hawkes 1990). Most of these cultivated potato species are still grown in the Lake Titicaca region. *Solanum tuberosum* ssp. *tuberosum* is the cultivated species of worldwide distribution.

Solanum taxonomy has been changing in the last few years based on molecular markers. The species designations listed above are being challenged and changed. These changes are slowly becoming the standard for researchers and breeders (Spooner and Bamberg 1994; Huaman and Spooner 2002). This dissertation will continue with the

older designations to avoid the errors and confusion of converting to the new and still changing system.

Cytogenetics

The 48 chromosomes of cultivated potato (*Solanum tuberosum* L.) are very small and difficult to visualize under the light microscope. Most researchers agree that the basic chromosome number for the genus *Solanum* is 12 (Wilkinson 1994). The evidence supporting this hypothesis includes: loss of the strong self-incompatibility of 24 chromosome potato when increased to 48 chromosomes, secondary associations reported between heterochromatic regions that were not homologous chromosomes, infrequent secondary balance between triploid and diploid or tetraploid, and finally most other Solanaceae genera have the chromosome base number of x=12. However, Grun (1990) cites the high frequency of unreduced gametes as possible evidence of an ancestral tetraploid with base chromosome number of x = 6.

Diploid potatoes have 24 chromosomes that undergo normal bivalent pairing. Most are obligate out-breeders that have a strong GSI system (Wheeler et al. 2001). Most diploid potato species can naturally produce some tetraploid progeny through 2n gametes. The GSI system is overcome upon polyploidization so that tetraploid genotypes are typically self-compatible but undergo severe inbreeding depression upon selfing (Hancock 2004; MacKay 1987).

Tetraploid potatoes have 48 chromosomes with a mean frequency of quadrivalent pairing during meiosis dependent on the cultivar. Howard (1970) showed a range of 1.37 quadrivalents per cell for an andigena cultivar ‘C.P.C. 1384’ to 4.40 quadrivalents per

cell in ‘Chippewa’. Due to its tetrasomic inheritance for some traits, some researchers consider cultivated potato an autotetraploid or a ‘functional’ autotetraploid (Douches and Jastrzebski 1993; Hancock 2004). However, Peloquin (1989a) argues that the term ‘tetrasomic polyploidy’ is a better reflection of the tetrasomic inheritance, cytological pairing, and the lack of evolutionary knowledge about the species.

The genetic diversity in wild species related to cultivated potato is probably broader than for any other crop (Hawkes 1990). Potato breeders and geneticists have found valuable variation for yield, maturity, specific gravity, disease resistances, cold chipping, and many other traits (Spooner and Bamberg 1994; Hayes and Thill 2002a; Zlesak and Thill 2002; Hamernik 1998; Hanneman 1989). Utilizing wild species has proven challenging for tetraploid potato breeding because 70 percent of the species are diploid and most are not adapted to tuberize in the long-day length climates common in commercial potato production regions (Hermundstad and Peloquin 1986; Hanneman 1989). Nevertheless, germplasm incorporation from wild species is relatively simple compared to other crops (Serquen 1994). Methods of incorporation include bridge crosses (Dionne 1963; Dinu 2005), direct hybridization and backcrossing with *S. tuberosum* (Stalker 1980), chromosome doubling (Howard 1970), pollen mixtures, chemical treatments (Stalker 1980), and ploidy manipulation using haploid x species breeding methods (Peloquin et al. 1989b; Ortiz 1998). The haploid x species methods have been especially useful in evaluating wild species traits in a genetic combination that will tuberize in long-day Northern hemisphere climates (Jansky and Peloquin 2006).

Potato Breeding and Variety Development

Potato breeding is expensive and has a relatively low profit potential. The costs are high because it is a heavy underground crop that requires large and expensive equipment to plant, harvest, haul, store, and evaluate. Also, cross-pollination, seed extraction, sowing, transplanting and selection are time-intensive manual operations (Bradshaw and MacKay 1994). Additional costs result from the challenges of breeding a crop that is highly heterozygous, frequently male sterile, difficult to propagate quickly and maintain virus-free, challenging to store in the short term, and nearly impossible to archive in the long term (Howard 1978).

The biggest advantage in breeding potatoes compared to sexually reproduced crops is that every hybrid genotype can be kept true to type by vegetative propagation (Howard 1978). In practice, selections are made in the F1 populations and carried through to become cultivars. Other advantages of potato breeding include the amount of related germplasm with traits of interest, the relative ease of making wide crosses, and the availability of haploid induction and unreduced gametes that allow for ploidy manipulations (Howard 1978; Ortiz 1998).

The glacial shifts in cultivar usage in the potato industry lead to low profitability for private research and breeding companies. Leading cultivars in crops such as tomatoes typically shift and change every 4 to 7 years, but the number one variety in potatoes, ‘Russet Burbank’ is nearly 100 years old (Burton 1989). Potato variety usage has not changed regularly because of the excellent traits of the current varieties, the cultivar preferences of processors and retailers, and the potentially unlimited lifetime of a potato variety as they can be freed of virus degradation using meristem culture techniques

(Howard 1978). Also, variety changes may be more difficult for potato processors because their products are typically derived directly from a single cultivar rather than blending as would be common for other processed products such as tomato paste. Therefore, it is not possible to include a small amount of an experimental variety without substantial risks to the processor. In general, the potato processing industry has not been willing to accept those risks in order to support the development of new varieties. This led to reduced profits for potato breeding and shift from private for-profit potato breeding companies to public non-profit breeding programs over the last 120 years (Hoopes and Plaisted 1987). Only one major private company, Frito-Lay, Inc. continues to develop potatoes varieties.

History

The systematic and scientific methods of potato breeding are relatively recent efforts compared with the conscious and unconscious methods of ancient farmers (Howard 1970). The first indications of systematic potato breeding occurred in the mid 1700's as an effort to build varieties that were not susceptible to the 'curl' disease which likely described symptoms of the viruses now known as PLRV and PVY (Salaman 1985). The early breeding efforts depended on self-pollinated seed rather than controlled crosses. Early breeders include Paterson who developed 'The Rock' and 'Victoria' and Reverend Goodrich who developed 'Garnet Chili' which became the ancestor of most modern cultivars (Burton 1989; Plaisted and Hoopes 1989; van Berloo et al. 2007). T.A. Knight outlined and used systematic, controlled cross-pollination methods for potato

starting in 1807, but the methods did not become widespread until the twentieth century (Burton 1989).

The Mendelian revolution has done less to advance progress in potato breeding than many other crops because the tetraploid nature of potato was not discovered until the late 1930s and because of the complexity of breeding a tetraploid crop species that experiences severe inbreeding depression (Tarn et al. 1992; Bradshaw and MacKay 1994). Modern potato breeders typically still use the basic empirical methods that T.A. Knight pioneered, with an increased intensity and scale (Bradshaw and MacKay 1994). Very few of the cultivars that are developed by potato breeders are successfully introduced into the commercial market (Douches et al. 1996). This may partly explain the results of a study that showed cultural practices rather than cultivar or genetic improvements have contributed more to the 6-fold increase in field yield from 1920 to 1989. In comparison, 60-90 percent of the yield improvement for crops such as maize are attributable to genetic improvement (Douches et al. 1996).

Potato Breeding Methods

Potato breeding programs typically use a tetraploid breeding method based on phenotypic recurrent selection that cycles every 5-9 years (Bradshaw and MacKay 1994; Douches et al. 1996). The inbreeding depression inherent in potato and the high levels of heterozygosity required to maximize yield and other important traits make other breeding and selection methods difficult to implement (Ross 1985; Brown 1990). Potato breeding is a long term process with the time to develop a cultivar requiring at least 5 general steps in a minimum of 16 years (Tai and Young 1984). The first step is to evaluate potential

parents (years 1-2), single plant and small plot selections in early clonal generations (years 3-5), larger plot evaluations and selections in later clonal generations (years 6-7), evaluations of advanced genotypes in multiple years and locations (years 8-12), and grower evaluations and cultivar release (years 13-16).

The many desirable traits and characteristics required of a new cultivar make it virtually impossible to find one genotype that encompasses all desirable traits (Hoopes and Plaisted 1987). The chances of developing a new cultivar are estimated at between 1 in a million and 1 in a trillion (Bradshaw and MacKay 1994; Hoopes and Plaisted 1987). Douches and Jastrzebski (1993) divided the most important traits into three complexes; yield and adaptation, resistance to pests and diseases, and quality. The most important traits include yield, high dry matter (as measured by specific gravity -- 1.080 or higher), uniformity, no internal or external defects, quality, eye appeal, resistance to mechanical damage, disease and pest resistances (Bradshaw and MacKay 1994). Tarn et al. (1992) counted 18 fresh and processing traits, 23 pest and disease resistances, and "numerous" agronomic traits required for the perfect cultivar. Therefore, potato breeders must select "less imperfect" genotypes that perform as well as established cultivars in most locations and better in some locations (Bradshaw and MacKay 1994).

Conventional modern breeding programs may screen more than 100,000 seedling genotypes per year for merit and lack of defects (Bradshaw and MacKay 1994; Douches and Jastrzebski 1993). Each year the number of lines evaluated is reduced dramatically and the number of plants per line is increased. In the AgCanada program 99 percent of the lines evaluated are eliminated by the 3rd clonal year of evaluations (Tarn et al. 1992). Because of the dramatic elimination of genotypes, the success of a breeding program is

dependent upon selections done in the first 3 years of testing (Tai and Young 1984). Breeders typically rely on visual selection in the earliest populations because it is a quick and efficient phenotypic evaluation. However, visual selection alone may result in the loss of valuable genotypes especially for non-visual traits such as processing color (Maris 1966; Brown et al. 1987; Anderson and Howard 1981) and for traits with moderate heritability estimates (Tai 1975).

Selection is influenced by many factors including selection intensity, heritability of the trait, genotype by environment interaction, and genetic variation available for selection (Tai and Young 1984). The genetic variation of the population is dependent upon the parents used to make the cross. Genetic variation is highest in an unselected population and drops as the population is subjected to multiple rounds of selection. Selection intensity is a measure of the proportion of the individuals kept for further testing and their trait superiority compared to the unselected population (Falconer and Mackay 1996). Heritability is an estimate of the genetic variation available for phenotypic based selection (Fairbanks and Anderson 1999) and predicts the potential effectiveness of selection (Falconer and Mackay 1996). Heritability estimates can be reduced due to a narrow genetic base and broadened with increased genetic diversity. Broad sense heritability estimates, defined as the genetic variation (Vg) divided by the phenotypic variation (Vp), are appropriate for clonal crops because genetic variation among genotypes includes additive, dominance, and epistatic genetic effects (Hayes 2002). The effectiveness of selection can be reduced by non-heritable variation such as large genotype-by-environment interactions and the use of small experimental units grown under atypical production (Tai and Young 1984).

The earliest opportunity for selection occurs in the first year after botanical seeds are produced. Seedlings can either be transplanted to the field to produce field grown tubers or kept in the greenhouse to produce mini-tubers (Tarn et al. 1992; Bradshaw and MacKay 1994). Selection on field grown tubers from seedlings that were transplanted to the field may be effective if applied with low intensity thresholds and for traits such as stolon length, defects, maturity, and vigor (Tai and Young 1984; Neele et al. 1988). Improvements for yield, morphological, and most agronomic traits have not been successful using early generation selection (EGS) with Brown et al. (1987) concluding that selection for yield on seedling tubers was equivalent to random selection. However, selection for potato chip color in early generations has been shown to be effective (Thill and Peloquin 1995; Hayes and Thill 2003). Selections based on family means of agronomic traits were repeatable over multiple years and can be useful to identify superior crosses and parents (Clulow and Bradshaw 1994). Early generation selection on field grown tubers is typically inefficient because plants are spaced wider than normal, seed piece sizes are not uniform, and selection preferences vary by breeder (Tai 1975; Davies and Johnston 1974). The effectiveness of EGS on greenhouse grown tubers for overall merit in the first year has been found inefficient and would have eliminated valuable genotypes (Anderson and Howard 1981). However, on a population level rather than an individual level, selection for specific gravity and reducing sugar content was effective and correlated well to field grown tubers (Neele and Louwes 1989). Selections in the greenhouse must be made with care because of differences between field tubers and greenhouse grown tubers for important traits such as cold sweetening (Pathirana et al. 2008).

Tetraploid potato breeding as typically practiced is challenged by the narrow genetic base of tetraploid potato, biological complications inherent in the potato, labor expenses, tetrasomic inheritance, and reduced germplasm sources (Douches and Jastrzebski 1993). The genetic base of cultivated potatoes is so narrow that many commonly used commercial varieties are equivalent to full or half-siblings (Mendoza and Haynes 1974b). Tetrasomic inheritance is challenging because it is often difficult to understand and control the genetic basis of a trait due to the complexity of polyploid segregation ratios that increase the frequency of heterozygosity, break up favorable epistatic interactions, and reduce the probability of selecting superior individuals (Douches and Jastrzebski 1993). Inherent biological factors that further complicate breeding include cytoplasmic male sterility, gametophytic incompatibility, and inbreeding depression that make it more difficult to accumulate favorable alleles at the tetraploid level (Douches and Jastrzebski 1993; Burton 1989). Important traits such as yield are predominantly controlled by non-additive genetic effects that are disrupted during meiosis and hybridization of closely related clones (Mendiburu and Peloquin 1977b; Mendoza and Haynes 1974a). Additionally, the amount of labor required to plant, harvest, and evaluate a heavy crop like potatoes is significant; therefore the large populations required to successfully obtain a cultivar are cost prohibitive. Finally, an estimated 70 percent of wild species diversity is at the diploid level and is not directly accessible for tetraploid breeding primarily due to ploidy and EBN difference (Hawkes 1990). The modified analytical breeding scheme developed by Chase (1963) and modified by Mendiburu and Peloquin (1977b) using 2n gametes allows access to that

germplasm (Figure 1).

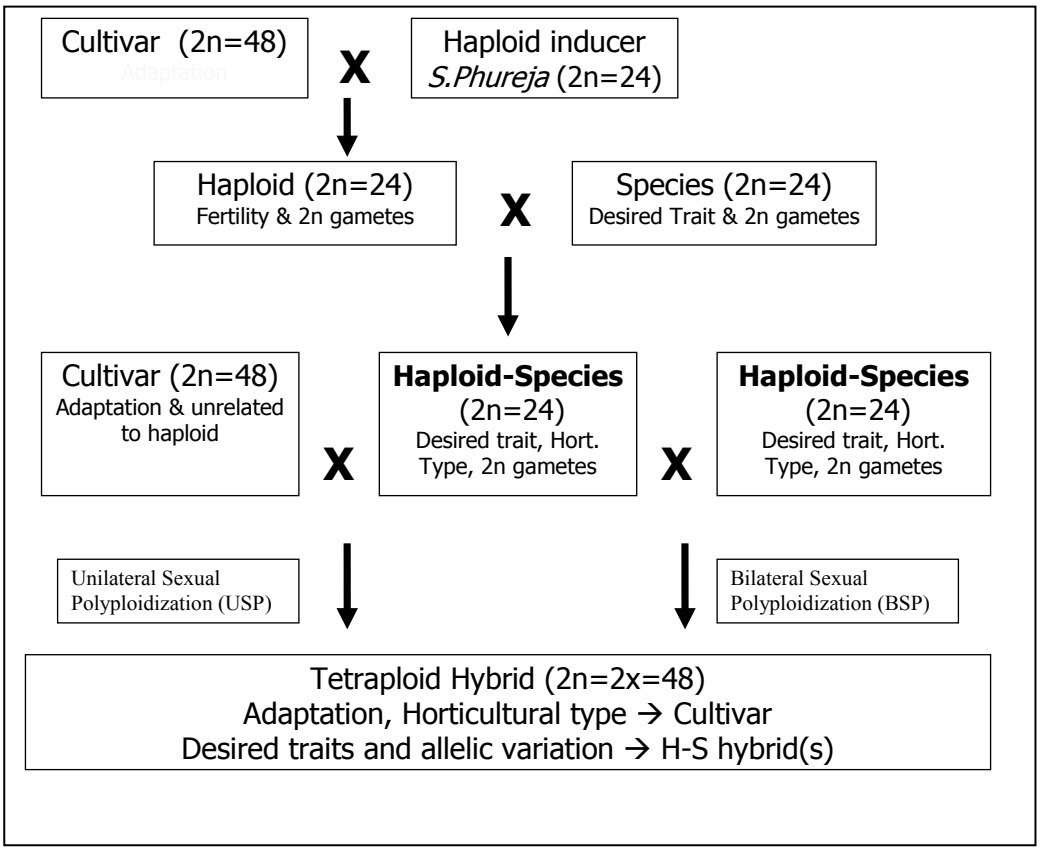

Figure 1. *The modified analytical breeding scheme including haploidization, haploid-species hybridization, and sexual polyploidization (adapted from Peloquin and Ortiz (1992).*

The modified analytical scheme, also known as breeding via ploidy manipulations, avoids many of the challenges of tetraploid breeding and makes it easier to access, evaluate, control, and utilize wild species germplasm (Bradshaw and MacKay 1994; Ortiz 1998).The breeding scheme is a three step process of ploidy reduction, breeding with wild and/or cultivated diploid germplasm at the diploid level, and ploidy increase using 2n gametes (Peloquin 1983; Peloquin et al. 1989b).

The ploidy reduction step extracts a haploid (2n=2x =24) from *S. tuberosum* (2n=4x=48) cultivars and breeding lines (Hougas and Peloquin 1958; Peloquin and Hougas 1959). Haploids are most commonly extracted using an interspecific-interploidy 4x x 2x cross where the cultivar is the tetraploid and the pollinator is a specific clone of the diploid *Solanum phureja* (Peloquin et al. 1996). The haploid develops because both gametes from the diploid pollinator unite with the polar nuclei forming a hexaploid endosperm leaving the unfertilized egg to develop into an embryo parthenogenetically (Peloquin et al. 1996). The resulting haploids have chromosomes from *Phureja* in the endosperm but not in the embryo. The frequency of haploid induction is variable depending on "pollinator effects" (Hougas et al. 1964) that are most likely due to endosperm effects (Peloquin et al. 1996). Hougas and Peloquin (1960) found that the haploids were compatible in crosses to many diploid potato species. This allows the breeder to develop parents at the diploid level. The benefits of breeding at the diploid level include more accurate segregation ratio interpretation, ease of selecting polygenetic traits, reduced populations and number of seedlings to obtain a desired progeny, reduced chromosome exchange and the related occurrence of undesirable traits, increased 2n gamete availability, and the ease of utilizing the 70 percent of wild species that are diploid for traits of interest (Watanabe et al. 1995; Ross 1985). However, breeding efforts at the diploid level have been hampered by large amounts of nonadditive variance, especially for yield (Hanneman 1999). Haploid *S. tuberosum* crossed to wild species also known as Haploid-Species (H-S) hybrids can capture traits of interest in wild or cultivated diploid species and tuberize under long day conditions allowing them to be

evaluated for tuber traits in potato growing regions of the northern hemisphere (Hermundstad and Peloquin 1986).

The step to increase ploidy can be accomplished by sexual polyploidization (SP) using 2n gametes from one parent in a unilateral sexual polyploid (USP) or with 2n gametes from both parents in a bilateral sexual polyploid (BSP) (Mendiburu and Peloquin 1977a). The ploidy of the progeny that result from a BSP cross must be evaluated to distinguish diploid and tetraploid plants. Chromosome counting is the only way to unequivocally determine the ploidy number of a potato genotype (Hanneman and Peloquin 1968). But, the time and skill required to obtain accurate counts is extensive and not practical for large populations developed via bilateral sexual polyploidization (Bamberg and Hanneman 1991). Alternative methods of estimating ploidy include leaf and leaflet morphological characteristics (Pehu et al. 1987), pollen diameter measurements (Bamberg and Hanneman 1991), flow cytometry (Uijtewaal 1987; Owen et al. 1988) stomatal guard cell length (Barrino and Powell 1988), and stomatal guard cell chloroplast counts (Frandsen 1968; Subova et al. 1997; Hutten et al. 1995). Each alternative method has benefits and detriments. The accuracy and speed of flow cytometry for ploidy determination is unmatched but the equipment required is very expensive and the data analysis is complex. Leaf and leaflet morphology is very quick and simple to measure or visually estimate, but the correlations to ploidy are not as high. Chloroplast density in stomatal guard cells, which is closely correlated to the sporophytic ploidy, is much faster than root tip squashes to count chromosomes, and is simple and inexpensive. The best option for accuracy and efficiency is to measure multiple characteristics in order of increasing complexity. For example, Pehu et al. (1987) found

that a combination of 4 characteristics, anther length, leaflet width, corolla width, and chloroplast counts dramatically reduce the number of genotypes for which chromosome counting needed to be performed without reducing the accuracy of the results.

Progeny from a USP cross are almost exclusively tetraploid because of the strong triploid block that occurs due to endosperm failure from developmental abnormalities associated with the pentaploid chromosome number of the endosperm (Peloquin et al. 1989b; Johnston et al. 1980). Typically, more than 90 percent of progeny from 4x-2x or 2x-4x crosses are tetraploid (Hanneman and Peloquin 1968).

Regardless of the type of polyploidization, unreduced gametes are an essential component of the analytical breeding method because they are an effective way to transmit the diversity from the diploid to the tetraploid level (Peloquin et al. 1999). Use of 2n gametes has proven to be far superior to colchicine for polyploidization in potatoes and other crops due to the increase in allelic diversity, maximization of heterozygosity and epitasis that is transmitted to the progeny (Ramanna and Jacobsen 2003; Peloquin et al. 1989b). Meiotic mutants that produce 2n gametes are widespread in potato. Parallel spindles (ps) generate 2n pollen by a mechanism genetically equivalent to First Division Restitution (FDR) (Mok and Peloquin 1975). The recessive trait (ps/ps) shows variable expressivity and incomplete penetrance that may result in a mixture of n and 2n gametes (Ortiz 1998). Parallel spindles occurs regularly in typical cultivated and wild potato species, and is the primary mechanism of 2n gamete production in potato (Peloquin et al. 1989b; Mok and Peloquin 1975). Parallel spindles transmits an estimated 80 percent of the heterozygosity and a large proportion of the epistasis of the 2x parent to the tetraploid progeny (Peloquin 1983). These estimates were confirmed by molecular marker analysis

(Barone et al. 1995). FDR increases the potential for yield performance by transmitting more of the non-additive variation that is essential for high yield compared with typical products of meiosis (Hutten et al. 1994; De Jong and Tai 1977; Concilio and Peloquin 1986; Buso et al. 1999; De Jong and Tai 1991).

Omission of second division (os) after a normal first division generates 2n eggs most frequently in potato (Werner and Peloquin 1987). 2n eggs developed from os are genetically equivalent to second division restitution (SDR) (Stelly and Peloquin 1986) and transmit about 40 percent of the diploid heterozygosity to the resulting progeny (Peloquin 1983; Barone et al. 1995). The combination of 2n SDR eggs and 2n FDR pollen can result in highly heterotic 4x progeny.

Many traits of interest in the wild species become accessible using H-S hybrids including: high yield, disease resistance, high specific gravity, high tuber set, improved nutritional factors, and cold chipping (Hale et al. 2001; Hamernik 1998; Hanneman 1994, 1996; Spooner and Bamberg 1994; Jansky and Peloquin 2006; Bae et al. 2008; Zlesak and Thill 2002). These traits can be accessed with relative ease because 2n gametes are widespread in H-S hybrids (Watanabe and Peloquin 1991). The effect of utilizing more species to generate H-S hybrids would result in a broader genetic base of cultivated potato and likely allow true genetic improvements to be made (Bradshaw and MacKay 1994; Douches et al. 1996; Hayes and Thill 2003).

The benefits of breeding using ploidy manipulations also include the potential to accelerate cultivar development without yield and quality losses as well as increasing the efficiency of breeding when compared to tetraploid breeding (Peloquin and Ortiz 1992; Ortiz 1998). The increase in efficiency is due to the transfer of more heterozygosity and

epistatic interactions essential in potatoes without the loss of genetic variation and high performance for traits of interest such as specific gravity and chip color (Peloquin et al. 1989b; Thill and Peloquin 1995). The increased frequency of valuable alleles may increase the genetic variation vital for selection and allow for reduced breeding population sizes without reducing the number of superior genotypes selected from those populations (Hayes 2002; Thill 1994). It is essential to remember that using ploidy manipulation to increase allelic diversity must be coupled with the use of high yielding, adapted germplasm in order to be successful (Hermundstad and Peloquin 1986).

Many examples are found in the literature of breeding success utilizing these methods including the release of two cultivars, Krantz and Yukon Gold that were both developed from 4x-2x matings (Johnston and Rowberry 1981; Ortiz 1998). Both cultivars have *Solanum phureja* and a haploid of the cultivar Katahdin (USW1) in their ancestry. 'Krantz' also has the wild species *Solanum raphanifolium* and *Solanum spegazzinii* in its genetic background (van Berloo et al. 2007). Ploidy manipulations have also led to improvements for both total and marketable yield, total tuber solids, disease resistance, low reducing sugars, and acceptable chip color (Peloquin et al. 1989b; Frost et al. 2006; Thill 1994; Hayes and Thill 2003; Hermundstad and Peloquin 1986; Zlesak and Thill 2002). Tetraploid progeny of 2x-2x crosses (BSP) had better yield and specific gravity than 4x check cultivars and better yield, vine maturity, and tuber size than the 2x progeny (Hutten et al. 1995; Ortiz 1998; Peloquin and Ortiz 1992). Many researchers have shown mid- and high-parent heterosis for tuber yield in 4x-2x crosses (Darmo and Peloquin 1990; Peloquin and Ortiz 1992; Werner and Peloquin 1991; Buso et al. 1999). The yield of these crosses was found to be high and stable over many environments (Darmo and

Peloquin 1990; Buso et al. 2003) and selection for specific gravity was also efficient in early generations (Concilio and Peloquin 1987). On a family basis the 4x-2x families had better vigor, maturity, yield, general tuber appearance, and uniformity than 4x-4x families and better yield and vigor than the 4x parents (Peloquin et al. 1989b; Buso et al. 2000a). The 4x-2x families also had a higher frequency of superior genotypes (Buso et al. 1999), higher combined yield and general tuber appearance (GTA) (Concilio and Peloquin 1991), increased yield, specific gravity, and chip color (Darmo and Peloquin 1990), and efficiency of cultivar development (Peloquin et al. 1989b) . The value of 4x-2x breeding is demonstrated by the programs that continue to use it, including the University of Minnesota, AgCanada, University of Naples, Chinese National Academy, and private breeders in Germany & the Netherlands as well as the large Polish potato breeding program (Jansky and Peloquin 2006). The Polish program reported that 4x-2x breeding is 5 times more effective than conventional 4x-4x breeding.

Breeding for Cold Chipping

The ideal chipping cultivar is characterized as a smooth white potato that is round but blocky in shape, approximately 8 cm in diameter, free from physiological defects, with high specific gravity (above 1.080), acceptable plant appearance, and uniformity across all traits, and which produces light colored chips directly from the field or from storage (Douches et al. 1996; Smith 1987). The shape and size are important to processors because of mechanized slicing requirements of chip production. High specific gravity is a very important trait to processors because it directly affects chip yield in the

factory. Cultivars with higher specific gravity yield more chips per pound of raw potatoes and absorb less oil, therefore saving the processors money (Smith 1987).

Chipping cultivar development is an important objective of many potato breeding programs. 'Norchip' was released in 1968 as the first cultivar specifically bred for chipping (Douches et al. 1996). Cold chipping (CC) or the ability to make light colored potato products directly from cold storage (4C) is an important focus for potato breeders (Douches and Jastrzebski 1993; Love et al. 1998). A cultivar with cold chipping capacity would have the benefits of reduced shrinkage and tuber degradation in storage, reduced dependence on sprout inhibitors and other agro-chemicals, and increased marketability (Sowokinos 2001b). In addition, cold chipping cultivars would accumulate lower levels of reducing sugars during storage and acrylamide during processing (Claus et al. 2008; Bhaskar et al. 2010).

Cold chipping is a very complex trait affected by multiple alleles on multiple chromosomes at both the diploid and tetraploid levels (Chen et al. 2001; Li et al. 2008). Several researchers have suggested a two locus model for cold chipping on the tetraploid level with recessive alleles at each locus with epistatic effects (Ehlenfeldt and Johansen 1989; Accatino 1973). Thill and Peloquin (1994) proposed a three locus model for diploid potatoes with one dominant allele required at each locus.

Breeding work for cold chipping was first reported in 1962 with a single genotype that produced light colored chips after cold storage (Hyde and Walkof 1962). Lauer and Shaw (1970) reported 2 clones with CC. A 2x clone that chipped with good color after storage at 3.3C was reported in 1973 (Accatino 1973). In the 1990's, twenty-five wild species with cold chipping in temperatures down to 2C were reported (Hanneman 1993,

1996). Thill and Peloquin (1994) found 11 clones with 25% *S. tarijense* that had cold chipping, and Hammernick (1998) reported on haploid-species hybrids with cold chipping at temperatures as low as 2C. *Solanum raphanifolium* that has recently been associated with reduced vacuolar AcInv activity (Bhaskar et al. 2010) was identified as producing excellent cold chipping clones in a haploid-species hybrid (Oltmans and Novy 2002a).

'ND860-2' was the first chipping variety that could be stored under 10C (7.2C). 'Snowden', a popular chipping cultivar, is approximately equal to the storage capabilities of 'ND860-2' (Douches and Jastrzebski 1993). Newer cultivars such as 'White Pearl' and 'Dakota Diamond' have been released recently and are touted to produce light colored chips directly from colder storage temperatures. These may be the first commercial cultivars to have the cold chipping trait (Groza et al. 2006; Thompson et al. 2008).

Chip color is often assessed in the third or fourth year after the pollination was made and after several rounds of visual selection for cultivar potential (Louwes and Neele 1987; Thill and Peloquin 1995). Many cold chipping genotypes are lost by this system due to genetic drift and the inefficiencies of visual selection. The feasibility of cold chipping selection in early generations was demonstrated by Thill and Peloquin (1995), who successfully selected for cold chipping genotypes in the first clonal year on tubers stored for 6 months at 4C followed by 2 weeks of reconditioning. In the following year adequate levels of trait variation for specific gravity and field yield remained in the selections retained for cold chipping performance. Good x good crosses between unrelated parents produce the best progeny (Thill 1994; Pereira et al. 1994). The reliability of screening for cold chipping on a single chip sample per genotype was

confirmed by Chavez (2005). The benefits of this breeding method were to objectively measure cold chipping in the first year which allowed good clones to be identified more quickly and utilized as parents or replanted the next season in multiple-hill plots for further evaluation (Thill and Peloquin 1995). The effectiveness of early identification of clones to be used as parents is demonstrated in the second chapter of this dissertation by a much higher than expected frequency of acceptable chipping clones resulting from 4x-4x matings of parents that had been selected for cold chipping performance two to three years prior to this research.

Immediate selection for the objective cold chipping trait in early generations provides an alternative to the subjective visual selection practices currently used and has the potential to reduce the breeding cycle by four years by identifying good parents earlier in the breeding cycle. Breeding population sizes can be reduced quickly by starting in the early generations with cold chipping and in later years selecting for traits with lower heritability estimates such as yield that also need larger samples sizes for efficient evaluation (Thill and Peloquin 1995).

Sexual polyploidization and early generation selection for cold chipping was effective using 4x-2x and 2x-4x crosses (Hayes and Thill 2002b; Hayes and Thill 2002c). Hayes and Thill (2003) found significant genetic gains from early generation selection for cold chipping from a population developed using 4x-4x matings and suggested that future research should use favorable alleles for cold chipping from wild Solanum species with sexual polyploidization to increase the genetic variation and potential genetic gain in a population.

One reason for the success of selection based on such small sample sizes is the high heritability of the cold chipping trait, which has been estimated between 0.77 (Accatino 1973) and 0.88 (Jakuczun and Zimnoch-Guzowska 2004), although Oltmans and Novy (2002a) calculated a heritability estimate for cold chipping of 0.45. The discrepancy may be due to the genotype-by-environment or genotype-by-storage-duration interactions that have been shown to be common in cold chipping research (Pereira et al. 1994; Tai and Coleman 1999; Ewing et al. 1981; Loiselle et al. 1989) and typically reduce genetic gains for cold chipping (Hayes and Thill 2003). These interactions illustrate the need for breeders to test breeding lines over multiple locations and storage durations as an important part of developing cold chipping varieties (Thill 1994; Hayes and Thill 2003).

Conclusion

The value and importance of developing cold chipping cultivars to take advantage of the benefits of cold storage and reduce acrylamide accumulation is clear from the literature. Breeders that access wild diploid germplasm as discussed in this dissertation may be able to develop high yielding, stable, and widely adapted cold chipping cultivars more efficiently.

The focus of this research was to evaluate the variation and potential genetic gains for cold chipping from populations developed from 2x-2x, 2x-4x, 4x-2x, and 4x-4x matings. The progeny of these matings were grown as greenhouse-grown seedlings or field-grown seedling transplants to examine the feasibility and potential genetic gains of selecting for cold chipping in the earliest possible generations. Additional data was generated to better understand the yield, tuber appearance, specific gravity, and other

important agronomic and horticultural traits in addition to the chip color of selected progeny.

Chapter 1: Genetic gain for cold chipping in *S. tuberosum* using greenhouse-grown seedling tubers generated from matings of diploid and tetraploid parents.

Introduction

Color in processed potato products, such as potato chips, is an important market limiting trait because a cultivar may be superior for every trait but will still be rejected by the processor if it does not produce market-acceptable light-colored products (Smith 1987; Thill and Peloquin 1995). Reducing sugars in the tubers react during processing with free amino acids in a non-enzymatic Maillard reaction that produces dark-colored, bitter-tasting products that contain the potentially carcinogenic compound acrylamide and are not acceptable to consumers (Marque and Anon 1986; Mottram et al. 2002). Reducing sugar levels accumulate as the starch in the tuber is converted to sugars. The level of reducing sugar accumulation primarily determines processed potato product color (Marque and Anon 1986). In the United States, processing plants annually reject approximately 15% of potatoes due to high reducing sugar levels (Sowokinos 2001b). Under cold temperature stress, the conversion process increases in a process known as cold-induced sweetening (CIS) that is controlled by the enzymes uridine diphosphate glucose pyrophosphorylase (UGPase) and vacuolar acid invertase (AcInv) (Sowokinos 2001b; Bhaskar et al. 2010).

Commercial storage practices routinely utilize relatively warm storage temperatures above 7.5C in association with sprout inhibiting agrochemicals to extend storage life and resist CIS (Rastovski 1987). Unfortunately, these temperatures increase storage costs and tuber losses especially over long-term storage regimes and thereby

reducing crop marketability (Knowles et al. 2009; Thill and Peloquin 1995). In 2009, 6.7 percent of the crop valued at approximately 200 million dollars was lost due to post-harvest factors (NASS 2011). Cold storage conditions reduce overall potato losses but require careful management to maintain acceptable processing color and quality (Sowokinos and Preston 1988; Amrein et al. 2003).

Cultivars that can be processed directly from cold (4C) storage are considered to have the cold chipping (CC) trait (Thill 1994). Cold chipping is an important objective for potato breeders (Douches and Jastrzebski 1993). A cold chipping cultivar would allow growers and processors to take advantage of the benefits of reduced tuber shrinkage and degradation in storage, reduced dependence on sprout inhibitors and other agro-chemicals, and reduced storage costs (Sowokinos 2001b; Knowles et al. 2009). In addition, cold chipping cultivars would have lower acrylamide levels due to lower levels of accumulated reducing sugars (Bhaskar et al. 2010; Pedreschi 2007).

In a potato breeding program, selection efficiency is critical because population sizes following sexual hybridizations are reduced by 99 percent in the first three years (Tai and Young 1984). The earliest opportunity for selection occurs in the first year after botanical seeds are produced. Seedlings can either be transplanted to the field to produce seedling tubers or kept in the greenhouse to produce greenhouse-grown tubers (Tarn et al. 1992; Bradshaw and MacKay 1994). Selection on field grown tubers from seedlings may be effective if applied with low intensity thresholds and for traits such as stolon length, defects, maturity, and vigor (Tai and Young 1984; Neele et al. 1988). The effectiveness of early generation selection (EGS) on greenhouse-grown tubers (GGT) for overall merit was inefficient and would have eliminated valuable genotypes due to performance

differences between the field and the greenhouse environments (Anderson and Howard 1981; Pathirana et al. 2008; Neele and Louwes 1989). Family based selection for important traits such chip color and dry matter content have been recommended when using greenhouse-grown tubers to reduce incorrect selection (Neele and Louwes 1989). However, individual selection for chip color and glucose content using greenhouse-grown tubers was found to be an effective approach (Louwes and Neele 1987; Xiong et al. 2002).

Breeders typically wait to evaluate chipping ability until at least the second year of the breeding process, but selection for chip color in earlier generations has been shown to be effective (Neele and Louwes 1989; Thill and Peloquin 1995; Hayes and Thill 2003). Thill and Peloquin (1995) successfully selected for cold chipping in the first field year by retaining genotypes that produced light colored potato chips. The benefits of this breeding method were to objectively measure cold chipping in the first year, allowing good clones to be identified and utilized as parents or replanted the next season for further evaluation (Thill and Peloquin 1995). Hayes and Thill (2003) found significant genetic gains for cold chipping from a population developed using 4x-4x matings. They suggested that future research should use favorable alleles for cold chipping from wild *Solanum* species to increase the genetic variation and therefore potential genetic gain in a population. Many wild potato species are diploid (2x), and can be utilized by breeders working at the tetraploid level (4x) through sexual polyploidization (SP) using 2n gametes (Peloquin et al. 1989b). Previous research has shown that SP, especially 4x-2x matings, tend to result in superior breeding success compared to 4x-4x matings for many important breeding objectives such as tuber yield and percent solids (Buso et al. 2000a).

The objectives of this research were 1) to determine the variation for cold chipping in a population developed using 2x-4x, 4x-2x and 4x-4x matings propagated in the greenhouse and 2) to compare the genetic gain for cold chipping, as measured by response to selection that resulted from early generation selection on greenhouse-grown tubers.

Materials and Methods

A population of 103 families was developed by mating 60 diploid and tetraploid parents of good and poor chipping ability from breeding materials and commercial cultivars. The sexual polyploid (SP) group included 30 families developed from 2x-4x matings and 57 families from 4x-2x families. The 4x-4x group included 16 families developed from 4x-4x matings and represents the conventional approach for breeding for cold chipping. All of the progeny from the 2x-4x and 4x-2x matings were considered to have developed via sexual polyploidization and therefore to be tetraploid due to the strong triploid block typically observed in potato research (Peloquin et al. 1989b; Hanneman and Peloquin 1968). The resulting botanical seed was sown in seeding flats at the University of Minnesota greenhouses at St. Paul, MN on September 2, 2002 and transplanted into standard greenhouse flats with 24 individual cells each measuring 9cm x 6 ½ cm. On January 18, 2003, after more than 120 days of growth, all seedling tubers from up to 24 genotypes per family were harvested, maintained clonally, and placed into cold 4C storage for 3 months. Potato chips were made by frying a 1 mm thick slice from the center of one longitudinally cut tuber per genotype in 185C vegetable oil until bubbling ceased. Color scores were visually evaluated using a standard color scale that ranged from 1 to 10 with a score of 4 or less considered acceptable. Genotypes that had a

score of 4 or less were considered part of the retained selection group while those that had a score of 5 or more were considered part of the discarded selection group. Both groups were planted in the spring of 2003 for further evaluations.

In 2003, family plots of single-hill clonally maintained genotypes were established from those clones grown in 2002, provided that a seedling tuber remained for planting. Each family plot was randomized and planted in field plots at Morris, MN on May 20, 2003 with 0.91 m between rows and 0.91 m between plants. The family plots included genotypes from both the retained and discarded selection groups carefully identified and maintained clonally. A red-skinned clone was placed every six hills within the family plot as a marker to help ensure greater accuracy during harvest. After over 120 days of growth, all genotypes were harvested on October 14th and 15th, with up to five tubers per genotype collected into a clonally labeled bag. Harvested tubers were placed in 4C storage at the United States Department of Agriculture Potato Research Worksite (USDA-PRW), East Grand Forks, MN. Chips were made and evaluated directly from storage after 3 months, following the same protocol used above.

Selection differential (**S**), selection intensity (**I**), expected response (**E**) and selection response (**R**) were calculated on the 2002 chip color data following the analysis of Hayes and Thill (2003) which was based on Falconer and MacKay (1996).

S = 2002 discarded group mean – 2002 retained group mean

I = **S** / progeny group phenotypic variance

R = 2003 discarded group mean – 2003 retained group mean

E = **I** * heritability * Progeny group phenotypic standard deviation

The heritability used to calculate the expected response (**E**) was estimated at 0.77 by Accatino (1973). A nested analysis of variance (ANOVA) was generated with families nested within progeny group. The percentages of acceptably chipping genotypes were compared using a 99% confidence interval based on exact binomial distributions. Correlations were calculated to measure dependence between chip colors and genotypes from different years. Statistical analysis was conducted using SAS Statistical Software Version 9.1.1 (SAS Institute Inc., Cary, NC, USA).

Results

In 2002, 109 cold chipping genotypes were identified from the 987 genotypes evaluated (Table 1). The overall population chip color score mean was 6.70 and the variance was 2.48. The SP group had a mean chip color score of 6.69 and 4x-4x group had a mean chip color score of 6.71. The SP group had twice as many genotypes that were cold chipping, although the percentage of acceptably chipping genotypes was not different between the SP and 4x-4x groups.

In 2003, 763 genotypes were re-evaluated from the field grown tubers. Fifty-three genotypes had acceptable chip color scores. The mean chip scores from the 4x-4x and SP groups were similar but statistically different and the variances were very similar. The frequency of acceptably chipping genotypes was not different, although the actual number of cold chipping genotypes was again higher in the SP progeny group. The variances and number of genotypes with acceptable chip color scores was much lower in 2003 compared to 2002 (Table 1). Analysis of variance (ANOVA) showed that the families nested within progeny groups were significant sources of variation for chip color with probability values less than 0.05 in both 2002 and 2003 (Table 2).

Within the SP progeny group, 77 cold chipping genotypes were retained with acceptable chip color and 539 were placed in the discarded group (Table 3). The 4x-4x progeny group had 32 retained and 339 discarded group clones. Selection differential, selection intensity, and expected response to selection were calculated for the SP and 4x-4x groups using the 2002 chip color data. The SP group had a selection differential of 3.47, a selection intensity of 1.26 and an expected response of 1.61. The 4x-4x group had a selection differential of 3.38 selection intensity of 1.66, and an expected response of 1.82.

In 2003 the discarded and retained selection groups from each progeny group were re-evaluated in the field (Table 4). The mean chip color score of the retained SP group was 6.32 while the mean score of the discarded group was 6.84. Similarly, the 4x-4x retained mean chip color score was 6.54 and the discarded was 6.92. Observed response to selection was calculated to be 0.52 for the SP progeny group and 0.38 for the 4x-4x progeny group. A 99 percent confidence interval was estimated at 0.03 to 1.02 for the SP progeny group and -0.34 to 1.09 for the 4x-4x progeny group. Potato chip color correlation between the clones chipped in 2002 and 2003 was low (0.22) but significantly different than zero.

Discussion

Cold chipping is a complex trait controlled by many genes in a quantitative manner (Douches and Jastrzebski 1993; Thill and Peloquin 1994). The high frequencies of cold chipping genotypes observed in this population coupled with the reasonable chip color score means, large ranges, and high variances in both 2002 and 2003 indicate good potential for improvement for cold chipping (Table 1). The chip color score differences

between progeny groups (SP and 4x-4x) and the families nested within progeny groups in this experiment was significant (Table 2).

The 2002 chip color score means were lower than normal resulting in lower calculated selection differentials, selection intensities, and expected responses for the experiment (Table 3). The slightly lower selection intensity and expected response values from the SP group were likely due to the higher genetic variation associated with the group.

The responses to clonal selection that resulted from both the SP and 4x-4x matings selected in the greenhouse and then grown in the field were typically positive and greater than zero (Table 4). Though the responses were lower than expected, they indicate a positive improvement for reduced chip color scores and were similar to what Hayes and Thill (2003) observed from 4x-4x matings re-evaluated in multiple locations. The SP progeny group response was higher than the 4x-4x group but this difference was not statistically significant at the 99 percent confidence level.

As expected, sexual polyploidization led to an increased level of variation in the SP progeny group versus the 4x-4x progeny group (Table 1). However, this increased variance did not translate to a significantly increased response to selection in this experiment. An explanation for this surprising result is the low correlation coefficient calculated between the 2002 and 2003 data. Also, the overall lower variance and percentage of acceptable genotypes in 2003 may have been a contributing factor. These factors were likely caused by the genotype by environmental influences on potato chip color that is well documented in the literature (Tai and Coleman 1999; Sowokinos 2001b; Hayes and Thill 2003). However, Hayes and Thill (2002c) showed similarly low

correlations between chip color scores in a 4x-4x population across two years of evaluation using field-grown tuber, but still demonstrated responses to selection that usually were greater than the ones found here. Even without a dramatic response to selection it is important to note that the integration of species germplasm adds diversity and heterozygosity for other traits without reducing the potential for cold chipping (Thill and Peloquin 1995).

The use of greenhouse-grown tubers in the selection population may have resulted in incorrect selection decisions that led to reduced responses to selection. The effectiveness of using greenhouse-grown tubers for selection depends on the trait of interest. Indeed, selection for overall merit is so inefficient that it has been calculated to be equivalent to random selection (Anderson and Howard 1981; Brown et al. 1984). However, selection for chip color and glucose content was reported to be effective (Louwes and Neele 1987; Xiong et al. 2002). The low selection responses in this research may be due to differences in CIS responses between field tubers and greenhouse-grown tubers that have been reported in the time since this research was concluded (Pathirana et al. 2008). One 4x-4x family (No. 208) in this research illustrates this phenomenon because it performed poorly when grown in the greenhouse in 2002, producing no acceptable chipping genotypes from the 20 clones tested and a mean chip color score of 7.5. In 2003, family 208 was one of the best chipping families with 7 of the 18 clones tested as chipping acceptably directly from cold storage and a mean family chip color score of 5.4.

To help reduce the number of incorrect selection decisions that result from high environmental variation associated with greenhouse-grown tubers, Neele and Louwes

(1989) recommended using family means rather than individual genotype values to select for chip color and dry matter content in greenhouse-grown tuber populations. In this research, discarding the bottom 25 percent of the families based on 2002 chip color scores would have resulted in the loss of 23 percent of the clones that were acceptable in 2003. This suggests that family mean selection would also have been less effective in these populations. However, if family 208 was removed from the data, family mean selections that discarded the worst 25 percent of the families that chipped poorly would have resulted in only losing 11 percent of the clones that turned out to chip acceptably in 2003.

The value of a single family like number 208 in this research is an important reminder that making progress for the development of cold chipping cultivars requires superior germplasm, heterozygosity, allelic diversity, and high genetic variances regardless of the type of matings utilized. Thus, the high variance that SP populations can provide must be coupled with excellent trait performance to be utilized effectively for cultivar development (Hermundstad and Peloquin 1986). The use of high performing H-S hybrids can increase allelic diversity, heterozygosity, and genetic variance without reducing the frequency of cold chipping. Further research should compare 4x-4x and SP populations that combine superior cold chipping performance as well as agronomic and horticultural performance with high genetic variance. Finally, selection for cold chipping from populations developed using 2x-2x matings may be valuable especially if a rapid method such as flow cytometry can be utilized to sort diploid and tetraploid progeny.

Table 1. Potato chip color means, variances, and frequency of acceptably chipping genotypes of the sexual polyploid (SP) and 4x-4x progeny groups grown in 2002 and 2003 and chipped after three months storage at 4C.

	2002 Chip Color						2003 Chip Color					
Progeny Group	No. of Progeny	Mean[1]	Variance	No. ≤ 4	%	99% CI[2]	No. of Progeny	Mean[1]	Variance	No. ≤ 4	%	99% CI[2]
SP	616	6.69[a]	2.75	77	12.5	9-16	475	6.77[a]	1.85	31	6.5	4-10
4x-4x	371	6.71[b]	2.04	32	8.6	6-13	288	6.88[b]	1.80	22	7.6	4-13
Total	987	6.70	2.48	109	11.0	9-13	763	6.82	1.84	53	6.9	5-9

[1] Chip color was scored on a 1-10 scale, chip colors≤ 4 are industry acceptable, Mean chip color scores with different letters indicate a significant difference between means.

[2] Confidence interval of the percent of genotypes with scores ≤ 4 at the 99 percent level.

Table 2. Mean squares, degrees of freedom, and probability values for the nested analysis of variance of potato chip color[1] after 3 months storage at 4C for the SP and 4x-4x progeny groups[2] in 2002 and 2003.

	2002 chip color			2003 chip color		
Source	df	MS	p-value	df	MS	p-value
Progeny Groups	1	9.10	0.0152	1	15.69	0.0004
Family(Progeny group)	102	10.65	<0.0001	84	6.56	<0.0001
Error	883	1.54		677	1.25	

[1] Chip color was scored on a 1-10 scale, chip colors $\leq$ 4 are industry acceptable.
[2] Progeny groups include the 4x-4x and the sexual polyploids (SP).

Table 3. Potato chip color means, selection differentials, selection intensities, and expected responses of the SP and 4x × 4x progeny groups grown in the greenhouse and chipped after three months storage at 4C in 2002.

Selection group[1]	No. of progeny	Mean[2]	Selection Differential[3]	Selection Intensity[4]	Expected response[5]
SP					
Retained	77	3.65	3.47	1.26	1.61
Discarded	539	7.12			
4x-4x					
Retained	32	3.63	3.38	1.66	1.82
Discarded	339	7.01			

[1]Selection group determined by the 2002 three month cold chipping evaluations: chip colors ≤ 4 were retained and >4 were discarded.
[2]Chip color was scored on a 1-10 scale, chip colors≤ 4 are industry acceptable.
[3]Selection differential = discarded group mean – retained group mean.
[4]Selection intensity = selection differential/phenotypic standard deviation.
[5]Expected response = selection intensity*phenotypic standard deviation*heritability (heritability estimated by Accatino at 0.77).

Table 4. Number of progeny, potato chip color means, responses to selection, and 99 percent confidence intervals for the responses after evaluation of SP and 4x × 4x progeny groups grown in field plots and stored at 4C for three months in 2003.

Selection group[1]	No. of progeny	Mean	Response[2]	99 % CI[3]
SP				
Retained	57	6.32	0.52	0.03-1.02
Discarded	418	6.84		
4x-4x				
Retained	26	6.54	0.38	-0.34-1.09
Discarded	262	6.92		

[1] Selection group based on the 2002 3-month cold chipping evaluations: chip colors ≤ 4.0 were retained and >4.0 were discarded.

[2] Response = 2003 Discarded selection group mean chip color score – 2003 Retained selection group mean chip color score mean.

[3] Confidence intervals for response to selection calculated from two sample t-test.

Chapter 2: Comparison of genetic gain for the cold chipping ability of diploid, tetraploid, and sexual polyploid potato (*Solanum tuberosum* L.) genotypes.

Introduction

Color in processed potato products, such as potato chips, is an important market limiting trait because a cultivar may be superior for every trait but may still be rejected by the processor if it does not produce acceptable light-colored products (Smith 1987; Thill and Peloquin 1995). Dark colors develop due to a non-enzymatic reaction between reducing sugars and the amino acids of the tubers during heat processing (Marque and Anon 1986). Dark color is also correlated with off-flavor and accumulation of acrylamide, a neurotoxin and potential carcinogen, which further reduces product marketability (Coffin et al. 1987; Mottram et al. 2002).

Cold storage temperatures have been shown to reduce overall potato losses, but without careful management can result in increased reducing sugar levels, leading to darker processed colors and increased acrylamide levels (Sowokinos and Preston 1988; Amrein et al. 2003). The conversion of starch to reducing sugars in the tuber under cold storage conditions is known as cold-induced sweetening (CIS) (Sowokinos 2001b). Cultivars such as 'White Pearl' and 'Dakota Diamond' that resist CIS at temperatures near 4C and produce light colored chips directly from cold storage are considered to have the cold chipping (CC) trait (Groza et al. 2006; Thompson et al. 2008). Cultivars with CC have the benefits of reduced shrinkage and tuber degradation in storage, as well as reduced dependence on sprout inhibitors and other agro-chemicals (Sowokinos 2001b). Recent research has shown that the suppression of the vacuolar invertase gene (*VInv*)

prevents CIS (Bhaskar et al. 2010). They also found that the wild tuber-bearing species *S. raphanifolium* has *VInv* gene expression levels as low as the transgenic suppression lines.

In a potato breeding program selection efficiency is critical because population sizes following sexual hybridizations are reduced by 99 percent in the first three years (Tai and Young 1984). The earliest opportunity for selection occurs in the first year after botanical seeds are produced. Seedlings can either be transplanted to the field or kept in the greenhouse to produce greenhouse mini-tubers (Tarn et al. 1992; Bradshaw and MacKay 1994). The effectiveness of early generation selection (EGS) in the first year depends on the trait selected (Anderson and Howard 1981). Improvements in yield, morphological, and most agronomic traits have not been as successful using EGS as improving maturity, vigor, stolon length, and defects (Brown et al. 1987; Tai and Young 1984). Breeders typically wait to evaluates chipping ability in year two through four of the breeding process, but selection for chip color in early generations, including the first clonal generation, has been shown to be effective (Neele and Louwes 1989; Thill and Peloquin 1995; Hayes and Thill 2003; Hayes and Thill 2002b).

The feasibility of CC selection in early generations was demonstrated by Thill and Peloquin (1995), who successfully selected for CC in the first field year by retaining genotypes that produced light colored potato chips. The benefits of this breeding method were to objectively measure CC in the first year, allowing good clones to be identified and utilized as parents or replanted the next season for further evaluation (Thill and Peloquin 1995). Hayes and Thill (2003) found significant genetic gains for CC from a population developed using 4x-4x matings and suggested that future research should use favorable alleles for CC from wild *Solanum* species to increase the genetic variation and

therefore potential genetic gain in a population. Many wild potato species are diploid (2x), and can be utilized by breeders working at the tetraploid level (4x) through sexual polyploidization (SP) using 2n gametes (Peloquin et al. 1989b). Previous research has shown that SP, especially 4x-2x matings, tend to result in superior breeding success compared to 4x-4x matings for many important breeding objectives such as tuber yield and percent solids (Buso et al. 2000a).

This research examined the potential genetic gains of sexual polyploidization using early generation selection for CC. The objectives were 1) to determine the variation for CC from progeny of 2x-2x, 2x-4x, 4x-2x, and 4x-4x matings and 2) to compare the genetic gain for CC of those progeny as measured by responses to selection in the earliest generation.

Materials and Methods

A population of 119 families was developed by mating 26 diploid and 37 tetraploid parents. The parents included commercial cultivars and advanced breeding lines with good, intermediate, and poor CC ability. Field transplant (FTR) group seeds were sown in the greenhouse on May 25, 2002. Greenhouse grown tuber (GGT) group seed was sown September 2, 2002 to be transplanted to pots in the greenhouse (Figure 1).

The FTR group was transplanted to an irrigated field at Morris, MN, on July 2, 2002. Genotypes of each family were planted in a family plot with 0.91 meters between plants and 5.5 meters between family plots in a row, with rows 0.91 meters apart. At harvest on October 25 an average of 25 selections were made per family. The selections consisted of the first 20 genotypes of a family plot with tubers plus any other genotypes of the family plot with visual merit. All 2,127 harvested genotypes were placed into 4C

storage at the United States Department of Agriculture Potato Research Worksite (USDA-PRW), East Grand Forks, MN. Potato chips were made after three months of storage at 4C and chip color scores were immediately assessed by taking a 1mm thick, longitudinal slice from the center of one tuber per genotype and frying it in vegetable oil at 185C until bubbling ceased (Chavez 2005). The colors of the resulting chips were visually assessed on a scale from 1 (light) to 10 (dark) where a score of 4 or less was considered market acceptable.

The GGT group was transplanted in the University of Minnesota greenhouses at St. Paul, MN on September 23, 2002 into 9 cm x 6.5 cm pots. On January 18, 2003, greenhouse grown tubers (GGT) of up to 24 genotypes per family were harvested and placed into cold (4C) storage with clonal and family identity retained. Potato chips were made from the second largest tuber of each genotype after 3 months storage at 4C and evaluated for chip color score as previously described (Figure 1).

In 2003, all genotypes were planted in the field at Morris, MN with their family and clonal identity maintained. Each family was planted in a single plot on May 22, 2003 with row, plant, and family spacing as described in the 2002 field planting. After more than 120 days of growth, all genotypes were harvested on October 14th and 15th and placed in 4C storage. Chips were made and evaluated for color after 3 and 6 months of storage following the same protocol used in 2002. The FTR progeny had enough tubers to allow a second trial field to be planted on May 28th at the Northern Plains Potato Growers Association Research Farm at Grand Forks, ND. Family and clonal identity were maintained in the field plots and plant, family, and row spacing were as previously described. Tubers were harvested from October 1st – 4th after more than 120 days of

growth and chip tests were conducted after 3 and 6 months cold storage as previously described.

Retained and discarded selection groups were established using the 2002 chip color scores. Genotypes having a score ≤4 were placed into the retained selection group, while those with a score > 4 were placed in the discarded selection group. Selection differential (**S**), selection intensity (**I**), expected response (**E**) and selection response (**R**) were calculated following Hayes (2002) and using the following equations from Falconer and MacKay (1996):

S = (2002 discarded group mean) – (2002 retained group mean)

I = **S** / (progeny phenotypic variance)

E = **I** * heritability * (Progeny phenotypic standard deviation)

R = 2003 discarded group mean – 2003 retained group mean

The heritability estimates used to calculate the expected responses (**E**) were 0.45 (Oltmans and Novy 2002b), 0.77 (Accatino 1973) and 0.88 (Jakuczun and Zimnoch-Guzowska 2004). A nested analysis of variance (ANOVA) was generated with families nested within mating type. The percentages of acceptably chipping genotypes were compared using a 99% confidence interval based on exact binomial distributions. Statistical analysis was conducted using SAS Statistical Software Version 9.1.1 (SAS Institute Inc., Cary, NC, USA).

Results

In 2002, 3,575 progeny from 119 families grown as transplants in Morris MN produced an overall mean chip color score of 7.0 and a variance of 2.7 (Table 1). Nine percent of all the genotypes (319) produced acceptable potato chip color and formed the

"retained" selection group. In 2003, the genotypes with unacceptable chip colors were kept as the "discarded" selection group and grown in field plots at Morris, MN and Grand Forks, ND adjacent to the plots where the retained selection group was grown.

The 2x-2x mating type produced a mean chip score of 6.6 and 12.5 percent of the genotypes were of acceptable chip color, which was significantly better than the mean color and percentage of acceptability compared with the other mating types (Table 1). Significant differences in mean chip color were also measured among the other three mating types, with the 2x-4x mean score of 7.4 significantly darker than the others. There were no significant differences in the percentage of acceptable genotypes between the 2x-4x (5.1%), 4x-2x (7.3%), and 4x-4x (7.6%) matings. The variance of the 2x-2x mating type was slightly larger than the variances of the other mating types. Selection differential, selection intensity and expected responses were lowest for the 2x-2x and highest for the 2x-4x matings.

In 2003, the means of the retained groups were better than the discarded groups when grown in the field and tested after both 3 and 6 months (Table 2). However, no significant differences were found between the retained and the discarded group means of the 2x-4x mating type in Grand Forks and the 4x-4x groups in both locations after 3 months of storage. Chip scores at the Grand Forks location were lower than the scores from the Morris location, and mean scores increased between the 3- and 6-month storage intervals at both locations. Variances were similar for both selection groups within each mating type after both storage durations and between locations (Table 2).

Retained selection groups had a higher percentage of good chippers compared to the discarded selection groups in both Morris and Grand Forks (Table 2) after both

storage durations. When there was a significant difference between the selection groups, the retained group was always superior. At Morris, only the 4x-4x retained group did not have significantly more good chippers than the discarded selection group after either 3 or 6 months of storage. No significant difference in the percent of acceptable chippers was found between selection groups in the 2x-2x after 6 months storage. At Grand Forks, the 4x-4x selection groups were not significantly different in percent acceptable chippers after either storage duration (Table 2). The 2x-4x selection groups were not different after 3 months and the 2x-2x were not different after 6 months. The percentage of acceptably chipping genotypes in both retained and discarded groups of every mating type observed at the Grand Forks location were higher than those in the Morris location, but the frequency of good chippers typically decreased from the 3-month test to the 6-month test in both locations. Within each location the frequency of acceptably chipping genotypes was similar within each selection group of each mating type as indicated by overlapping confidence intervals (Table 2).

Response to selection was positive and significantly different from zero in both locations except for the 4x-4x mating type from the Morris location (Table 3). At Morris, the highest genetic gain was 1.5 after 3 months and 1.4 after 6 months from the 2x-4x mating type. The lowest responses were 0.2 for the 4x-4x after 3 months and 0.5 for the 2x-2x after 6 months. The 4x-2x responses were stable with a 0.9 and 0.8 genetic gain after the 3- and 6-month test, respectively. At Grand Forks, the highest responses were from the 4x-4x mating type with 1.2 and 1.9 after the 3- and 6-month test, respectively. The 2x-2x responses were 0.5 after 3 months and 0.4 after 6 months, which was the lowest response, but not significantly different from the responses of the other mating

types. The 2x-4x and 4x-2x responses were 0.6 and 0.7 after 3 months and 0.9 and 0.8 after 6 months, respectively.

Discussion

The high frequencies of CC genotypes observed in this study coupled with the low chip color scores and large variances (Table 1) indicated good potential for genetic gain for CC (Hayes and Thill 2003). The percentage of acceptably chipping genotypes found in this study (9%) was similar to the frequency observed by Hayes and Thill (2002c) in a population developed by 2x-4x, 4x-2x, and 4x-4x matings, and greater than the one percent in a population developed exclusively from 4x-4x matings (Hayes and Thill 2003). The results show that genetic gain for CC was positive and typically significantly different than zero for nearly all mating types in both locations and storage durations (Table 3). These results are in agreement with the results of Hayes and Thill (2003), which demonstrated that selection for CC based on an early objective test is effective and sufficient to lead to significant genetic gains. One reason for the success of selection for cold chipping may be the high heritability of the trait that has been estimated at 0.77 (Accatino 1973) and 0.88 (Jakuczun and Zimnoch-Guzowska 2004), although Oltmans and Novy (2002b) calculated a heritability estimate of 0.45.

Many correct selection decisions for CC were made from both the field and the greenhouse groups. This was demonstrated by the genotypes that were retained in 2002 and then produced market acceptable chip color in 2003, and by the significant differences between the chip color scores and percentage of acceptably chipping genotypes in the retained selection groups versus the discarded selection groups (Table 2). Correct selection decisions typically led to positive genetic gains despite only a few

statistically significant differences that were found between responses due to mating type (Table 3). This may have been due to excellent chip color scores and variances in the 4x-4x group that were nearly equal to those in the other mating types (Table 1). If the variances of the other mating types had been higher than the 4x-4x group, greater genetic gains may have occurred. Higher than expected means and variances in the 4x-4x group may have occurred because eight of the thirteen parents used were non-commercial experimental lines. Three of the eight experimental lines were specifically bred for improved CC only two to three years prior to being used as parents in this research. These excellent performing CC parents led to 44 percent (15 of the 34) good chipping 4x-4x clones found in 2002 in this study. The overall frequency of acceptable 4x-4x progeny in this study was 7.6 percent in contrast to the one percent found in 4x-4x progeny using more conventional 4x parents (Hayes and Thill 2003). Previous research has shown 4x-4x crosses to be inferior to 4x-2x crosses for traits such as yield (Ortiz 1998; Buso et al. 2000b) but 4x-4x progeny from experimental parent lines improved for CC had chip color variances that were not different than those of 4x-2x crosses (Hayes and Thill 2002b). These results are also a demonstration of the effectiveness of identifying good chipping clones earlier in the breeding cycle to be used as parents more quickly as suggested by Thill and Peloquin (1995).

The differences in mean chip color scores and genetic gains between the Grand Forks and Morris locations illustrate the genotype-by-environment interactions that have been shown to be common in CC research (Pereira et al. 1994; Tai and Coleman 1999) and typically contribute to reduce genetic gains for CC (Hayes and Thill 2003). Within each location, mean chip colors generally changed due to storage duration, with the

harsher 6-month score typically darker than the 3-month score. Similar genotype-by-storage-duration results have been reported previously in the literature (Ewing et al. 1981; Loiselle et al. 1989). These results illustrate the need for breeders to test breeding lines over multiple locations and storage durations as an important part of developing CC varieties (Thill 1994; Hayes and Thill 2003).

The 2x-2x progeny performed very well in this research with both the best mean chip color score and the highest percentage of acceptable genotypes in 2002. The 2x-2x progeny represented only 38 percent of the total population, but account for 53 percent (168 clones) of the good chippers. The good performance of the 2x-2x continued in 2003 with 69 percent of the 2x-2x retained selection group at Grand Forks and 37 percent of the retained selection group at Morris producing acceptable chip color after 3 months (Table 2). At the Morris location, the 2x-2x retained selection group had significantly more acceptable chippers than any other mating type after 3 months and more than the 2x-4x and 4x-2x after 6 months (Table 2). Despite this excellent performance, the genetic gain was typically lower than the other mating types. Several explanations for this result include the relatively good performance in 2002, the stringent selection truncation point (color score $\leq$ 4.0), and the good performance of both the retained and the discarded groups at both locations (Table 2). Relaxing the truncation point may be useful for selection in some cases (Chavez 2005). Excellent overall performance in the 2x-2x progeny resulted in the lowest selection differential, selection intensity, and expected responses compared to the other mating types in 2002.

The lower means and higher proportion of acceptably chipping genotypes in the 2x-2x progeny of this study is reasonable, especially considering the excellent CC

germplasm that is available from diploid cultivated and wild species (Hanneman 1993; Hamernik 1998; Bhaskar et al. 2010). The use of 2n gametes, SP, and EGS has allowed some of this superior 2x germplasm to be efficiently transferred to the 4x level (Thill and Peloquin 1995; Hayes and Thill 2002c; Hayes and Thill 2002b). Most of the research using SP has focused on unilateral SP (USP) but the genetic benefits of bilateral SP (BSP) have been demonstrated (Werner and Peloquin 1991; Ortiz 1998).

The excellent performance of the 2x-2x progeny in this study suggests that further research should be done that can capitalize on that performance. Combining early generation selection with bilateral sexual polyploidization for CC may increase the probability of selecting a tetraploid CC genotype with cultivar potential.

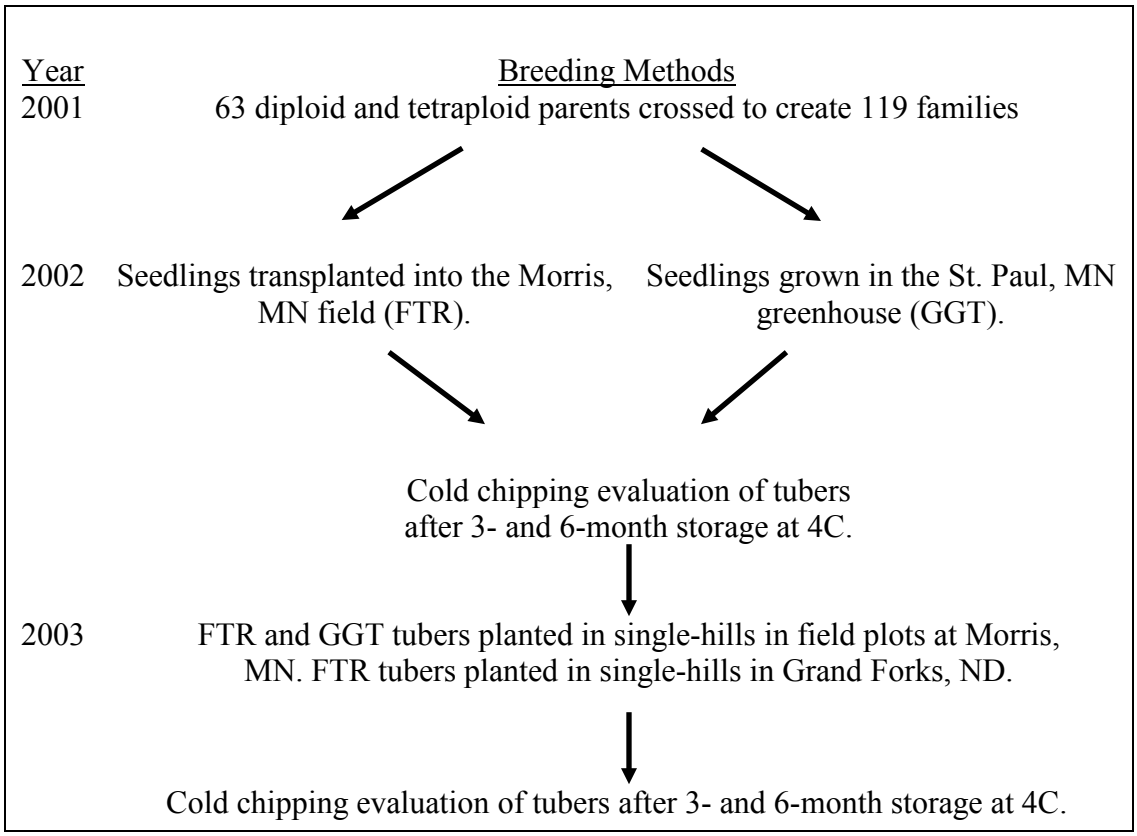

Figure 1. Summary of breeding activities conducted from 2001 to 2003.

Table 1. Potato chip color means, variances, percent acceptable chipping genotypes, selection differentials, selection intensities, and expected responses of the retained and discarded selection groups of the 2x-2x, 2x-4x, 4x-2x, and 4x-4x matings when grown at Morris, MN and St. Paul, MN in 2002 and stored at 4C for 3 months.

		2002 Chip Color[1]									
Mating	Selection	No.			Acceptable chipping[5]		Selection	Selection	Expected Responses[8]		
Type	group[2]	Progeny	Mean[3]	Variance[4]	Percent	95% CI	Differential[6]	Intensity[7]	0.45	0.77	0.88
2x-2x	Retain	168	3.5	0.5							
	Discarded	1177	7.0	1.7							
	Total	*1345*	*6.6[a]*	*2.9*	*12.5*	*11-14*	*3.5*	*2.1*	*1.6*	*2.7*	*3.5*
2x-4x	Retain	30	3.4	0.6							
	Discarded	563	7.7	1.7							
	Total	*593*	*7.4[d]*	*2.5*	*5.1*	*4-7*	*4.2*	*2.7*	*1.9*	*3.3*	*4.2*
4x-2x	Retain	87	3.7	0.3							
	Discarded	1100	7.4	1.6							
	Total	*1187*	*7.2[c]*	*2.5*	*7.3*	*6-9*	*3.7*	*2.4*	*1.7*	*2.9*	*3.3*
4x-4x	Retain	34	3.6	0.4							
	Discarded	416	7.2	1.6							
	Total	*450*	*7.0[b]*	*2.4*	*7.6*	*5-10*	*3.6*	*2.4*	*1.6*	*2.8*	*3.2*
Total		3575	7.0	2.7	*8.9*	*8-10*					

[1] Chip color was scored on a 1-10 scale, chip colors $\leq$ 4 are industry acceptable.
[2] Selection groups within each mating type, genotypes with chip colors $\leq$ 4 were put in the retained and $\geq$5 were put in the discarded group.
[3] Mean chip color scores with different letters indicate a significant difference between means.
[4] Variances significantly greater than zero at $p<0.01$.
[5] Percentage of genotypes with a chip color score $\leq$ 4 and a 95 percent confidence interval of that percentage shown in the table as lower limit – upper limit.
[6] Selection differential = discarded group mean – retained group mean.
[7] Selection intensity = selection differential/phenotypic standard deviation.
[8] Expected responses = selection intensity*heritability*phenotypic standard deviation. Heritability estimates at 0.45 (Oltman and Novy 2002), 0.77 (Accatino, 1973) and 0.88 (Jakuczun and Zimnoch-Guzowska 2004).

Table 2. Potato chip color means, variances, and percentage of acceptably chipping genotypes of the retained and discarded selection groups within each mating type after 3- and 6-month storage at 4C when grown at Morris, MN and Grand Forks, ND in 2003.

		3-month					6-month				
Mating Type	Selection Group	No. Progeny	Mean[1]	Variance	Percent Acceptable[2]	95% CI[3]	No. Progeny	Mean	Variance	Percent Acceptable	95% CI
Morris, MN											
2x-2x	Retain	103	5.2[a]	1.8	37	28-47	105	5.8[a]	2.0	19	13-28
	Discarded	693	6.0[b]	2.3	17	15-20	653	6.3[b]	2.0	11	9-14
2x-4x	Retain	23	5.3[a]	1.9	30	16-51	23	5.7[a]	2.8	26	13-47
	Discarded	368	6.8[b]	1.6	4	2-6	349	7.1[b]	1.9	4	2-6
4x-2x	Retain	73	5.6[a]	2.3	23	15-34	68	5.9[a]	1.7	16	9-27
	Discarded	670	6.5[b]	1.2	4	3-6	603	6.7[b]	1.6	5	4-7
4x-4x	Retain	27	6.6[a]	2.4	15	6-33	25	5.6[a]	2.1	20	9-39
	Discarded	339	6.8[a]	1.7	7	5-11	333	6.7[b]	2.0	7	5-10
Grand Forks, ND											
2x-2x	Retain	52	4.6[a]	1.7	69	55-80	55	5.3[a]	2.0	33	22-46
	Discarded	251	5.1[b]	1.9	41	35-47	260	5.7[b]	1.9	19	15-24
2x-4x	Retain	14	4.6[a]	1.9	57	32-79	16	4.8[a]	2.7	56	33-77
	Discarded	258	5.3[a]	2.3	38	33-44	188	5.7[b]	1.9	24	18-31
4x-2x	Retain	32	4.8[a]	2.3	50	34-66	32	5.2[a]	2.8	47	31-64
	Discarded	422	5.5[b]	1.7	23	20-28	430	6.0[b]	1.8	15	12-19
4x-4x	Retain	2	4.5[a]	4.5	50	9-91	2	4.0[a]	2.0	50	9-91
	Discarded	77	5.7[a]	1.8	19	12-30	75	5.9[b]	2.4	20	13-30

[1] Mean chip color scores with different letters following the mean indicating a significant difference between means within each mating type.
[2] Percentage of acceptably chipping clones based on a 1-10 scale where chip colors ≤ 4 are industry acceptable.
[3] CI= confidence interval, shown in the table as lower limit – upper limit.

Table 3. Response to selection of acceptable chipping genotypes when grown in 2003 at Morris, MN and Grand Forks, ND.

	3-month		6-month	
Mating Type	Response[1]	99% CI[2]	Response	99% CI
Morris, MN				
2x-2x	0.8	0.6-1.0	0.5	0.2-0.8
2x-4x	1.5	1.1-1.9	1.4	0.2-1.1
4x-2x	0.9	0.6-1.1	0.8	0.3-1.0
4x-4x	0.2	(-0.1)-0.5	1.0	(-0.6)-3.0
Grand Forks, ND				
2x-2x	0.5	0.3-0.7	0.4	0.1-0.7
2x-4x	0.6	0.9-1.9	0.9	0.4-1.4
4x-2x	0.7	0.6-1.0	0.8	0.4-1.2
4x-4x	1.2	0.6-1.4	1.9	0.6-3.3

[1] Response = 2003 Discarded selection group mean chip color score – 2003 Retained selection group mean chip color score mean.

[2] CI= confidence interval, shown in the table as lower limit – upper limit.

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Appendices

Summary

I generated a significant amount of data between 2002 and 2004 that is not represented in the previous two chapters. The information presented in this section may be useful to researchers working to develop cold chipping genotypes using sexual polyploidization. Twelve data tables are presented that give raw information about the parents and the progeny used in this dissertation including potato chip color scores, horticultural and agronomic information, dedicated yield trials, and ploidy assessments.

The first table includes ploidy, 2n gamete production, cold chipping classification, parents, and wild species background of the parents used in this dissertation (Table 1). The total yield, marketable yield, chip color scores from two storage durations, specific gravity, eye depth, flesh color, tuber shape, and skin color of many of the parents used in this dissertation are presented in Table 2. The rating scales for each of those traits are discussed below. Table 3 is an attempt to assign a practical breeding value for cold chipping to each of the parents used in this dissertation regardless of the mating type or the direction of the cross. Table 3 includes the number of crosses, the total number of chip color score evaluations performed, the mean chip color score of the progeny, the standard deviation of the mean, and the rank based on the overall mean score. The data in table 3 are not intended to be a definitive breeding value of a parental genotype for cold chipping based on a perfectly designed statistical experiment, rather it is meant as a practical guide to indicate broad trends of cold chipping value based on progeny performance. For example, it is clear that ADX-1523-1 would be a parent that would likely produce good chipping progeny based on the

mean progeny score of 5.6 and rank of 2 from 10 crosses and more than 1700 data-points. On the other hand, MSG274-3 would likely produce poor chipping progeny based on its mean progeny score of 7.9 and rank of 71 from 5 crosses and 274 data-points.

The cold-chipping scores in Table 4 represent the heart of the research in this dissertation and subsets of this data are used in chapter 1 and 2 of this dissertation. Table 4 is the summary data of chip color score information of all the families created for this dissertation. Acceptably chipping genotypes selected in the field in 2002 were retained and retested in 2003 and 2004 for cold chipping (Table 5) but also for agronomic and horticultural traits such as yield and specific gravity if enough seed tubers remaining for a multiple hill plot to be planted (Table 6). In 2002, superior individual genotypes were selected based on appearance in the field. The chip color scores were evaluated in 2002 and revaluated in 2003 and 2004 (Table 7). Those with sufficient seed tubers were evaluated for horticultural and agronomic traits from a multiple hill plot grown in 2003 and 2004 (Table 8).

Two specialized yield trials were planted in 2004 at two locations with 2 replications per location. The breeding efficiency trial was planted in a randomized complete block design at Grand Forks, ND and Becker, MN with 4 hills per replicated field plot. There were 252 clones from 41 families. Chip color scores were evaluated as well as horticultural and agronomic evaluations (Table 9). The breeding efficiency trial was intended to be set up following the experimental design known as North Carolina mating design I, as recommended by Ortiz and Golmirzaie (Ortiz and Golmirzaie 2002).

Design I requires that the families in the trial be inter-related such that each male parent was mated to the same 4 or 5 female parents. At some point during the planting preparations, I made an error in selecting the families to use in the trial choosing common male parents regardless of the female. The data obtained could not be analyzed as had been planned for publication.

The second specialized yield trial of the 2004 season was the 2x-2x trial that was also planted at Grand Forks, ND and Becker, MN with 4 hills per replicated plot. The trial had 172 clones from 25 families that were developed via 2x-2x matings. Chip color scores were evaluated as well as horticultural and agronomic evaluations (Table 10).

One of the benefits of using 2x-2x matings is the possibility of tetraploid progeny that can occur via bilateral sexual polyploidization (BSP) if both parents have 2n gametes. Tetraploid plants are often larger and have stronger vigor than diploid plants, but visual observation of vigor alone is not definitive. The last two tables of this section demonstrate the attempts that were made to estimate the ploidy of clones from 2x-2x families (Table 11) and from 2x-2x clones that were visually selected in the field as potentially tetraploid (Table 12). The data collected included a leaf ratio collected by subjective visual evaluation, measured whole leaf ratio, measured leaflet ratio, and chloroplast counts of guard cell pairs. The need to test a large number of clones resulted in a sieve type of approach where the simplest methods were used first on the largest number of genotypes. Estimation methods that were more difficult to perform were performed on fewer and fewer genotypes as the ploidy estimation became clear. In retrospect, this approach resulted in data analysis challenges because the most definitive

method (i.e. chloroplast counts) was not used on a wide enough sample of genotypes to confirm the results of the more subjective methods. The chloroplast counts were further challenged by an undiagnosed problem resulting in a much higher than expected number of chloroplasts and therefore a higher frequency of plants considered tetraploid.

I believe that the most valuable data in these appendices is the parent information presented in Tables 1-3. The development of high performing cultivars with cold chipping or other traits of interest requires the use of excellent parents. In retrospect, I should have spent far more time trying to understand the traits of the parents, especially their potential contribution to cold chipping and all of the traits of interest, before I started making crosses. Further, I should have been more diligent in sourcing additional seed pieces of all of the parents used in the 2003 planting so that every parent was tested for yield and the other agronomic and horticultural traits side-by-side with their progeny. Had I done those two things, I would have been able to design a compact experiment that focused more closely on solving some of the problems of developing a cold chipping cultivar using ploidy manipulations.

Many research questions could be answered in full or partially using the data tables presented in this section. From the first three tables clues about the contributions of specific wild species to the genetic background of parents and their progeny may be determined. It is possible that specific wild species should be excluded or included based on the information that can be analyzed in this section. From a practical breeding perspective, this data may be enough to retain or discard particular parents from being used for cold chipping breeding. The information in the first table could be revised

based on the information from the other tables. For example, the column indicating 2n gamete production could be updated to reflect information from successful 2x-4x or 4x-2x crosses that require 2n gametes in order to be successful. A comparison of the yield potential of the parents and the progeny could be built from this data to determine which parents of those tested would lead to progeny with higher yield. Additional information about the ability of the parents to transmit cold chipping, specific gravity general tuber appearance and any of the other important traits that were measured in the progeny. The information in this section would also be useful for a breeder to narrow the number of potential parents to use before starting a new round of crossing for cold chipping.

The variation in the acceptable group for traits other than cold chipping such as specific gravity could be explored in Tables 5 and 6. It is important that there is enough variation left in the population after selecting for cold chipping to have high performance for all the essential traits of a cultivar. The information of this progeny group could also be related back to the parents to understand which parents contributed the most to chip color improvement without the negatively correlated traits such as deep eyes, rough tubers, or purple skin. Also, an understanding of the correlation of the total yield to the marketable yield could be analyzed.

The selection group data in Table 7 and 8 could help a potato breeder understand which parents simultaneously contributed to visual merit and cold chipping. Those parents could then be reused in new crosses. The fact that no 2x-2x clones were selected for visual merit could be explored in terms of what was lacking in the 2x parents

utilized in this research and what traits in a 2x parent should be sought after in future research. Analyzing the data for the other traits measured could address whether there is enough variation for cold chipping, specific gravity, smoothness, and other vital traits for cultivar development. The relationship of total yield and marketable yield could be analyzed for this group and related back to the parents used in the crosses.

The data in Table 9 has the greatest potential for further analysis to answer some very important potato breeding questions if a method to analyze it can be determined considering the structure of the population. The results may shed light on the efficiency of breeding using ploidy manipulations versus the typical 4x-4x methods. The effects of mating type on all measured traits including chip color may be more fully evaluated.

The 2x-2x group data in Table 10 also represents a treasure trove of data that could be analyzed to answer questions about 2x parent breeding values for cold chipping and all of the other measured traits. It could suggest what parents should be reused and which should be abandoned. The effect of location and replication on each of the traits could be determined as well as a better understanding of the relationship between total yield and marketable yield in diploid crosses. If the ploidy values determined in Tables 11 and 12 can be trusted for the 2x-2x crosses the data in Table 10 becomes even more valuable. Confirmed progeny ploidy would help a researcher confirm 2n gamete production and potentially and estimate of the frequency of 2n gametes. Genotypes in the same family with different ploidy would be very interesting research tools to understand the effect of the transmission of heterozygosity and epistasis from parent to

offspring. The results could help advance the understanding of potato breeding with ploidy manipulations.

Rating Scales

The horticultural and agronomic data generated in the tables below include some or all of the following ratings:

- Score or Chip Color was the chip color score rating evaluated visually on a scale from 1 (excellent color) to 10 (poor color) using a color photograph of potato chips with standard colors. Ratings of 4 or less are considered acceptable for processing. Potato chips were made directly after storage at 4C and chip color scores were assessed by taking a 1mm thick, longitudinal slice from the center of one tuber per genotype and frying it in vegetable oil at 185C until bubbling ceased.
- Total Tuber Yield (TTY) was the total grams of potatoes per field plot as measured by a commercial scale grading machine that washed and weighed each potato individually. Yields were determined prior to cold storage at the USDA/ARS Potato Research Worksite, East Grand Forks, MN.
- A-sized Tuber Yield (ATY) was the total grams of potatoes per plot minus those that weighed 50 grams or less.
- Gravity was the specific gravity of a sample of potatoes from each plot measured as weight in air/ (weight in air - weight in water). Specific gravity was measured using a scale with a hook on the bottom that was hung over a tub of water. Specific gravity measurements were performed prior to cold storage in either St. Paul, MN or East Grand Forks, MN.
- Sprout was the amount of sprouting observed on a sample of potatoes rated on a scale from 0 to 3. Tubers with no sprouts were rated as 0, those with sprouts starting to emerge or “peeping” were rated as a 1, those with sprouts less than 1.5 cm in length were rated as a 2, and those with sprouts greater than 1.6 were rated as a 3. Sprouting was rated at the same time as chipping was performed.

- Eye depth was a rating of the growth node depth of the potato. The ratings were visually determined on a sample of tubers and ranged from shallow (1) to medium (2) to deep (3). Eye depth was rated at the same time as chipping was performed.
- Tuber shape was a rating of the overall shape of a sample of tubers ranging from round (1), to oval-ovate (2), to long (3). Tuber shape was visually determined at the same time as chipping was performed.
- Skin color was a rating of the overall skin color of a sample of tubers ranging from buff (1), to brown (2), to other (3) which included purple, red, or mixed. Skin color was visually determined at the same time as chipping was performed.
- General Tuber Appearance (GTA) was a visual rating of the general tuber appearance of a sample of tubers ranging from excellent (1) to average (3) to poor (5). GTA was rated at the same time as chipping was performed.
- Flesh color was a visual rating of the color of the flesh of a sample of tubers ranging from white (1), to cream (2), to yellow (3), and other (4) which included purple and variable colors. Flesh color was rated at the same time as chipping was performed.
- Maturity was a subjective visual rating of the estimated maturity of the plants in the field plots based on plant senescence. The ratings ranged from early (5) to medium (3) to late (1) and were typically performed one to two times during the growing season.

Table 1. Parents used in this dissertation with known information including ploidy, reported 2n gamete production, original 2001 cold-chipping classification, parents, and wild species background if known. Species abbreviations are: ber = S. berthaultii, buk = S. bukasovii, chc = S. chacoense, grl = S. gourlayi, phu = S. phureja, stn = S. stenotomum, spl = S. sparsipilum, tar = S. tarijense.

Parent	Ploidy (2x)	2n gametes	CC Class 2001	Female	Male	Wild Species
ADX-1523-1	2	no	Good	.	.	.
C159	2	no	int.	H551 x ber	W973 x ber	ber
C189	2	no	unk.	H551 x ber	H482 x ber	ber
C190	2	both	Poor	H551 x ber	H482 x ber	ber
C213	2	pollen	Good	H551 x ber	H322 x ber	ber
C215	2	pollen	Good	H551 x ber	H322 x ber	ber
C231	2	eggs	Good	W730 x ber	H322 x ber	ber
C254	2	unk.	Poor	H551 x ber	H322 x ber	ber
C27	2	unk.	unk.	W730 x spl	W973 x ber	spl & ber
C301	2	unk.	int.	W973 x spl	H482 x ber	spl & ber
C307	2	both	Good	W973 x spl	H322 x ber	spl & ber
C320	2	unk.	unk.	W973 x spl	W1887 x grl	spl & grl
C33	2	unk.	unk.	H551 x spl	H482 x ber	spl & ber
C336	2	eggs	Good	W1887 x grl	H482 x ber	grl & ber
C36	2	unk.	unk.	H551 x spl	H482 x ber	spl & ber
C367	2	unk.	Poor	W1887 x grl	W973 x spl	grl & spl
C372	2	unk.	Poor	H551 x chc36	W730 x ber	chc & ber
C374	2	pollen	Poor	H551 x chc36	W730 x ber	chc & ber
C380	2	unk.	Poor	H551 x chc36	W730 x ber	chc & ber
C392	2	eggs	Poor	W730 x buk	W730 x ber	buk & ber
C396	2	eggs	Good	W973 x buk	H551 x ber	buk & ber
C411	2	eggs	Good	H551 x buk	W730 x ber	buk & ber
C43	2	unk.	int.	H551 x spl	H482 x ber	spl & ber
C435	2	unk.	Poor	A121a x chc26	W730 x ber	chc & ber
E-29-1	2	eggs	Good	.	.	stn
E-51-2	2	eggs	int.	.	.	.
E-51-4	2	eggs	int.	.	.	.
IVP-101	2	unk.	unk.	.	.	.
MN-85393	2	pollen	int.	phu	phu	phu
MN-85430	2	pollen	int.	phu	phu	phu
MN-85432	2	pollen	int.	phu	phu	phu
Parent	**Ploidy (4x)**	**2n gametes**	**CC Class 2001**	**Female**	**Male**	**Wild Species**
Andover	4	no	int.	Allegany	Atlantic	.
Atlantic	4	no	Poor	Wauseon	Lenape	chc
Atzimba	4	unk.	Poor	US 133.3	52-AT-1	.
C181	4	no	Good	H551 x ber	H551 x ber	ber

Parent (cont.)	Ploidy (4x)	2n gametes	CC Class 2001	Female	Male	Wild Species
C182	4	no	Good	H551 x ber	H551 x ber	ber
C20	4	pollen	Good	OP unk.	OP unk.	.
C208	4	unk.	Poor	H551 x ber	H322 x ber	ber
C332	4	unk.	unk.	W1887 x grl	H551 x spl	grl & spl
C341	4	no	Poor	W1887 x grl	H482 x ber	grl & ber
C342	4	unk.	unk.	W1887 x grl	H482 x ber	grl & ber
C385	4	no	Good	W730 x buk	H322 x ber	buk & ber
C41	4	unk.	Poor	241a x tar	H373 x ber	tar & ber
C444	4	unk.	Good	[(W730xmlt) x (W730xverr)]	H373 x ber	mlt & verr & ber
C71	4	unk.	Good	H551 x spl	W973 x ber	spl & ber
Cal-White	4	no	Poor	Pioneer	BC8370-4	.
E-13	4	unk.	unk.	.	.	.
E-20	4	unk.	unk.	.	.	.
E-58	4	unk.	unk.	.	.	.
LBR-8	4	unk.	unk.	.	.	.
MN-16404	4	no	int.	.	.	.
MN-85554	4	pollen	unk.	phu	phu	phu
MSA-091-1	4	unk.	Poor	MS702-80	Norchip	.
MSB-073-2	4	unk.	Poor	.	.	.
MSE-250-1	4	unk.	int.	.	.	.
MSG-274-3	4	no	Poor	Tollocan	Chaleur	.
ND-3828-15	4	no	Good	.	.	.
ND-860-2	4	no	Poor	.	.	.
NDO-1496-1	4	unk.	unk.	ND 292-1	A77268-4	.
NY112	4	no	int.	Atlantic	Q155-3	.
RH-071-20	4	no	Good	MN 86125	ND 2676-10	.
RH-076-3	4	no	Good	MN 86128	Yukon Gold	.
RH-120-4	4	no	Good	ND 2417-6	ND 3929-6	
RH-122-3	4	no	Good	ND 2470-27	ND 2676-10	.
RH-135-1	4	no	Good	NY 112	NY 115	.
RH-138-2	4	no	Good	NY 119	NY 120	.
RH-176-11	4	no	Good	NDA2031-2	C127-3	.
S438	4	no	Poor	MN 86125	ND 2676-10	tar
S440	4	no	int.	P100-4	W231	tar
Snowden	4	no	int.	Lenape	Wischip	chc
W-1355-1	4	no	int.	Snowden	S440	chc & tar
Yukon Gold	4	no	Poor	Norgleam	USW 5279-4	phu
Zarevo	4	unk.	int.	76920C/68	Bekra	.

Table 2. Average values for total tuber yield (TTY), general tuber appearance (GTA), chip color score at 3- and 6-months, specific gravity, eye depth, flesh color, tuber shape, and skin color for the parents used in this dissertation as evaluated in 2003 and 2004. See table footnote for rating scales.

Parent (2x)	TTY	GTA	Chip Color (3-Mon.)	Chip Color (6-Mon.)	Specific Gravity	Eye Depth	Maturity	Flesh Color	Tuber Shape	Skin Color
ADX-1523-1	1753	2	4.8	4.5	1.078	2	5	2	3	2
C159	3105	3	5.5	7.0	1.061	2	3	1	2	2
C189	2809	3	6.0	8.0	1.192	2	.	2	2	2
C190	1137	4	7.3	9.0	1.070	2	3	2	3	1
C213	871	2	7.5	10.0	1.030	1	.	3	1	1
C215	790	3	6.0	8.0	1.069	1	5	1	2	2
C231	1364	2	4.8	6.5	1.054	1	4	2	1	2
C254	2944	4	7.3	7.5	1.059	2	.	2	1	2
C27	933	3	6.3	6.5	1.068	1	4	2	2	1
C301	.	.	.	.	.	.	.	.	.	.
C307	718	4	5.7	5.0	1.090	2	4	1	3	2
C320	3830	4	6.8	10.0	1.054	1	.	1	2	1
C33	779	.	6.0	9.0	1.008	.	.	.	.	.
C336	576	.	6.5	8.0	1.088	.	5	.	.	.
C36	1037	2	7.3	7.0	1.057	1	4	2	1	1
C367	.	.	.	.	.	.	.	.	.	.
C372	365	.	7.5	7.0	1.081	.	4	.	.	.
C374	658	.	6.0	10.0	1.075	.	4	.	.	.
C380	1090	4	5.5	8.0	1.084	2	4	2	2	3
C392	2652	3	7.0	9.0	1.067	1	4	2	1	2
C396	890	3	5.5	6.0	1.047	2	.	2	3	2
C411	47	.	7.0	7.0	1.118	.	5	.	.	.
C43	1863	3	7.0	7.5	1.061	1	3	1	1	2
C435	421	4	6.7	9.0	1.075	2	4	2	1	1
E-29-1	3090	4	4.5	4.0	1.077	2	4	1	2	1
E-51-2	4522	5	7.0	6.5	1.085	3	3	1	2	1
E-51-4	3929	4	5.3	4.5	1.091	2	4	1	2	1
IVP-101	.	.	.	.	.	.	.	.	.	.
MN-85393	.	.	.	.	.	.	.	.	.	.
MN-85430	3501	4	6.3	6.0	1.075	2	3	3	2	2.75
MN-85432	2627	4	5.8	4.0	1.083	3	3	3	3	2.25

Parent (4x)	TTY	GTA	Chip Color (3-Mon.)	Chip Color (6-Mon.)	Specific Gravity	Eye Depth	Maturity	Flesh Color	Tuber Shape	Skin Color
Andover	4177	2	6.2	7.5	1.080	1	4	2	2	1
Atlantic	5375	2	7.3	7.5	1.089	2	4	2	2	1.75
Atzimba	8375	.	6.0	7.5	1.093	.	4	.	.	.
C181	4794	4	6.3	7.0	1.103	1	4	1	2	1
C182	2501	4	5.7	7.0	1.105	1	3	2	3	2
C20	1398	4	6.0	6.5	1.073	1	4	1	2	2

Parent (4x) – cont.	TTY	GTA	Chip Color (3-Mon.)	Chip Color (6-Mon.)	Specific Gravity	Eye Depth	Maturity	Flesh Color	Tuber Shape	Skin Color
C208	1644	3	6.7	7.5	1.064	1	4	1	2	1
C332	2170	1	6.3	9.0	1.039	1	3	2	2	2
C341	1128	3	5.0	7.0	1.058	2	.	2	3	2
C342	2685	2	7.0	8.5	1.081	2	4	1	2	1
C385	2477	3	6.3	7.0	1.146	2	4	2	3	2
C41	7411	2	7.5	10.0	1.077	2	.	1	2	1
C444	873	3	5.7	6.5	1.053	1	4	1	1	1
C71	1315	4	6.3	8.5	1.085	1	4	1	3	2
Cal-White	6937	.	10.0	8.0	1.073	.	3	.	.	.
E-13	2770	.	8.0	8.0	1.076	.	3	.	.	.
E-20	.	.	.	.	.	.	.	.	.	.
E-58	2261	.	9.0	10.0	1.066	.	3	.	.	.
LBR-8	.	.	.	.	.	.	4	.	.	.
MN-16404	6347	3	6.5	7.5	1.079	2	4	2	2	1.75
MN-85554	3043	4	8.3	9.0	1.070	2	4	2	2	1
MSA-091-1	9785	.	8.0	7.0	1.086	.	4	.	.	.
MSB-073-2	.	.	.	.	.	.	.	.	.	.
MSE-250-1	.	.	.	.	.	.	.	.	.	.
MSG-274-3	3032	2	7.5	8.5	1.071	1	4	2	3	1.25
ND-3828-15	4115	2	4.8	7.0	1.082	1	4	1	2	1.3
ND-860-2	5828	.	5.5	6.0	1.085	.	5	.	.	.
NDO-1496-1	4948	1	6.5	7.0	1.082	2	4	2	2	1
Norchip	4289	3	7.0	6.5	1.080	2	4	1	2	1
NY112	3810	1	6.8	6.5	1.083	1	4	2	2	2
RHST99-071-20	3068	2	6.0	7.0	1.077	1	5	2	2	1.25
RHST99-135-1	4167	.	7.0	7.0	1.091	.	5	.	.	.
RHST99-176-11	5381	.	5.0	5.0	1.095	.	5	.	.	.
RHTR99-076-3	.	.	.	.	.	.	.	.	.	.
RHTR99-122-3	4623	2	7.8	9.5	1.089	1	4	1	2	1.75
RHTR99-138-2	5848	2	6.4	7.0	1.074	2	4	1	2	1.25
S438	1791	2	6.8	8.5	1.073	1	4	2	1	1
S440	4470	3	6.2	7.0	1.091	2	4	2	2	1.75
Snowden	6225	3	6.8	6.0	1.085	2	4	2	2	1.75
W-1355-1	4759	2	6.0	5.5	1.087	2	4	1	2	1
Yukon Gold	4863	3	7.5	9.5	1.079	2	4	3	2	1.75
Zarevo	5119	2	6.3	6.0	1.102	1	4	1	2	2.75

TTY: grams per plot
GTA rating: 1(excellent) to 5 (poor)
Chip color rating: 1 (excellent) to 10 (poor). 4 or less is market acceptable
Specific gravity calculation: weight in air/(weight in air-weight in water)
Eye depth rating: 1= shallow, 2=medium, 3=deep
Maturity rating: 1=late to 5=early
Flesh color rating: 1=white, 2=cream, 3=yellow, 4=other (purple, variable, etc)
Tuber shape rating: 1=round, 2=oval-ovate, 3=long
Skin color rating: 1=buff, 2=brown, 3=other (purple, red, etc)

Table 3. Number of crosses, number of color score evaluations of the progeny, Mean chip color score of the progeny, standard deviation of the progeny chip color score, and mean chip color score rank for the parents used in this research.

Parent (2x)	No. Crosses	No. color score data points	Mean progeny color score	Stand. Dev. progeny color score	Chip color Rank
ADX-1523-1	10	1787	5.6	1.44	2
C159	3	369	6.0	1.55	7
C189	4	166	6.1	1.56	13
C190	16	401	6.7	1.33	35
C213	10	568	6.3	1.56	21
C215	9	441	6.7	1.54	36
C231	6	276	5.7	1.82	3
C254	2	388	6.4	1.47	26
C27	1	9	7.2	1.86	56
C301	1	140	6.8	1.11	41
C307	19	850	6.2	1.67	17
C320	1	2	8.5	0.71	73
C33	13	394	6.8	1.63	46
C336	5	211	7.2	1.61	55
C36	2	21	6.3	1.06	24
C367	15	1130	7.5	1.40	63
C372	4	365	7.4	1.47	60
C374	3	367	6.3	1.68	23
C380	1	205	6.0	1.82	10
C392	2	95	7.1	1.21	53
C396	23	2754	6.7	1.48	39
C411	1	6	6.8	0.75	47
C43	1	41	6.4	1.47	29
C435	4	156	6.7	1.66	38
E-29-1	12	1118	6.2	1.61	19
E-51-2	12	430	6.5	1.78	30
E-51-4	17	1724	6.5	1.65	32
IVP-101	1	4	5.3	0.50	1
MN-85393	12	626	6.5	1.57	31
MN-85430	20	482	6.1	1.53	12
MN-85432	1	192	5.7	1.33	4

Parent (4x)	No. Crosses	No. color score data points	Mean progeny color score	Stand. Dev. progeny color score	Chip color Rank
Andover	8	556	6.5	1.46	33
Atlantic	8	692	6.8	1.36	45
Atzimba	2	33	7.6	1.12	65
C181	15	737	6.3	1.53	20
C182	11	690	6.3	1.54	22
C20	6	233	6.4	1.35	27
C208	1	163	6.8	1.49	43
C332	1	24	7.8	0.68	67
C341	6	105	6.7	1.40	37
C342	1	70	7.5	1.21	61
C385	13	1088	6.4	1.58	28

Parent (4x) – cont.	No. Crosses	No. color score data points	Mean progeny color score	Stand. Dev. progeny color score	Chip color Rank
C41	1	112	7.8	1.10	69
C444	1	208	7.1	1.60	54
C71	1	70	7.5	1.21	62
Cal-White	7	186	7.3	1.38	59
E-13	1	72	7.3	0.87	58
E-20	1	1	7.0	0.00	52
E-58	1	20	8.2	1.18	72
LBR-8	2	16	5.9	1.31	5
MN-16404	2	9	6.0	1.58	8
MN-85554	1	31	7.3	0.86	57
MSA-091-1	1	112	7.8	1.10	70
MSB-073-2	1	150	7.7	1.50	66
MSE-250-1	2	320	7.0	1.54	50
MSG-274-3	5	274	7.9	1.35	71
ND-3828-15	2	288	6.1	1.44	14
ND-860-2	1	14	6.2	1.12	18
NDO-1496-1	5	132	7.8	1.74	68
NY-112	5	214	6.8	1.30	44
RH-071-20	2	16	6.0	1.59	9
RH-076-3	8	307	5.9	1.59	6
RH-120-4	3	244	7.0	1.37	49
RH-122-3	8	568	6.8	1.51	42
RH-135-1	6	176	6.1	1.40	16
RH-138-2	2	78	6.7	1.45	40
RH-176-11	7	100	6.1	1.47	15
S438	11	534	7.0	1.51	51
S440	11	616	6.9	1.37	48
Snowden	5	324	6.7	1.35	34
W-1355-1	7	254	6.1	1.35	11
Yukon Gold	8	213	7.5	1.37	64
Zarevo	3	130	6.4	1.44	25

Table 4. The progeny number, average color score, and number of acceptably chipping progeny from 3-month and 6-month chipping tests conducted in 2002 and 2003 from the 213 families utilized in this dissertation. Table sorted by mating type then by family number.

2x-2x matings				2002		2003		
Family	Female	Male	Values	3-mon	6-mon	3-mon	6-mon	Avg.
001	ADX-1523-1	C159	Count	20	15	21	21	77
			Color Avg.	6.0	6.5	5.4	6.2	6.0
			No. Accept.	3	0	7	3	13
002	ADX-1523-1	C213	Count	60	32	51	47	190
			Color Avg.	5.8	6.4	5.0	5.4	5.6
			No. Accept.	12	3	22	13	50
017	C159	ADX-1523-1	Count	57	32	56	58	203
			Color Avg	6.2	5.9	5.1	5.5	5.6
			No. Accept.	7	8	19	16	50
039	C189	ADX-1523-1	Count	32	8	38	37	115
			Color Avg.	5.9	6.0	5.4	6.3	5.9
			No. Accept.	4	0	9	4	17
040	C190	C33	Count	24	0	24	22	70
			Color Avg.	7.4	.	6.6	7.5	7.1
			No. Accept.	2	0	3	0	5
051	C213	C189	Count	2	0	2	2	6
			Color Avg.	7.0	.	6.0	7.5	6.8
			No. Accept.	0	0	0	0	0
052	C231	ADX-1523-1	Count	56	31	47	48	182
			Color Avg.	4.9	5.4	5.0	5.5	5.2
			No. Accept.	25	9	21	14	69
054	C231	C189	Count	9	9	8	10	36
			Color Avg.	7.4	8.0	4.8	5.9	6.6
			No. Accept.	1	0	3	3	7
055	C231	C33	Count	23	0	0	0	23
			Color Avg.	6.0	.	.	.	6.0
			No. Accept.	3	0	0	0	3
059	C254	ADX-1523-1	Count	64	35	60	60	219
			Color Avg.	6.3	6.2	5.4	6.0	5.9
			No. Accept.	7	2	13	8	30
061	C301	C190	Count	47	20	35	38	140
			Color Avg.	6.7	7.5	6.6	6.6	6.8
			No. Accept.	2	0	1	2	5
062	C307	ADX-1523-1	Count	50	23	62	64	199
			Color Avg.	5.8	6.3	4.8	5.4	5.4
			No. Accept.	12	4	27	18	61
063	C307	C372	Count	24	0	15	14	53
			Color Avg.	6.2	.	6.8	7.8	6.8
			No. Accept.	5	0	2	0	7
064	C307	C43	Count	8	8	12	13	41
			Color Avg.	6.0	7.0	5.8	7.0	6.4
			No. Accept.	1	0	2	1	4
065	C307	C435	Count	51	22	37	37	147
			Color Avg.	6.8	7.8	5.6	6.8	6.7
			No. Accept.	7	0	11	2	20

2x-2x matings (cont.)				2002		2003		
Family	**Female**	**Male**	**Values**	**3-mon**	**6-mon**	**3-mon**	**6-mon**	**Avg.**
074	C336	C33	Count	22	0	17	15	54
			Color Avg.	7.1	.	7.4	7.9	7.4
			No. Accept.	1	0	0	0	1
075	C336	C372	Count	51	27	21	13	112
			Color Avg.	6.8	8.7	6.2	6.5	7.1
			No. Accept.	6	0	4	0	10
089	C367	C33	Count	21	21	26	14	82
			Color Avg.	8.1	8.0	6.8	6.2	7.3
			No. Accept.	0	0	1	1	2
090	C367	C372	Count	55	30	27	16	128
			Color Avg.	8.1	7.9	7.6	7.4	7.9
			No. Accept.	0	1	0	0	1
100	C374	ADX-1523-1	Count	59	35	55	56	205
			Color Avg.	6.2	5.9	5.2	5.3	5.6
			No. Accept.	7	5	19	21	52
109	C392	C190	Count	12	0	10	10	32
			Color Avg.	5.4	.	6.9	7.5	6.5
			No. Accept.	4	0	1	0	5
112	C396	MN-85430	Count	17	15	18	19	69
			Color Avg.	5.9	6.3	5.3	5.1	5.6
			No. Accept.	2	3	7	7	19
140	E-51-2	C215	Count	53	28	48	47	176
			Color Avg.	7.3	8.0	6.2	6.6	6.9
			No. Accept.	3	3	13	4	23
141	E-51-2	C307	Count	8	6	13	14	41
			Color Avg.	6.0	6.3	4.5	5.2	5.3
			No. Accept.	1	1	6	3	11
142	E-51-2	C33	Count	24	0	22	22	68
			Color Avg.	6.8	.	6.1	6.2	6.4
			No. Accept.	3	0	5	5	13
152	E-51-4	ADX-1523-1	Count	60	33	58	54	205
			Color Avg.	6.3	6.0	5.2	5.6	5.7
			No. Accept.	15	8	21	9	53
153	E-51-4	C159	Count	37	18	12	22	89
			Color Avg.	7.0	7.1	6.2	6.3	6.7
			No. Accept.	4	1	2	4	11
155	E-51-4	C189	Count	3	0	3	3	9
			Color Avg.	6.3	.	5.7	6.3	6.1
			No. Accept.	0	0	0	0	0
156	E-51-4	C213	Count	60	32	43	42	177
			Color Avg.	7.1	7.6	5.7	6.6	6.7
			No. Accept.	3	1	7	0	11
157	E-51-4	C215	Count	53	28	29	30	140
			Color Avg.	7.1	7.3	6.1	6.6	6.8
			No. Accept.	3	0	1	1	5
158	E-51-4	C254	Count	58	36	39	36	169
			Color Avg.	7.4	8.1	5.7	6.4	7.0
			No. Accept.	0	0	4	2	6

2x-2x matings (cont.)				2002		2003		
Family	**Female**	**Male**	**Values**	**3-mon**	**6-mon**	**3-mon**	**6-mon**	**Avg.**
159	E-51-4	C307	Count	54	37	47	54	192
			Color Avg.	6.7	6.9	5.6	5.7	6.2
			No. Accept.	7	5	16	11	39
160	E-51-4	C33	Count	24	0	20	20	64
			Color Avg.	6.7	.	5.4	6.2	6.1
			No. Accept.	2	0	8	2	12
162	E-51-4	C367	Count	57	29	37	36	159
			Color Avg.	7.3	7.3	6.7	6.3	6.9
			No. Accept.	2	0	4	3	9
163	E-51-4	C380	Count	63	35	53	54	205
			Color Avg.	6.5	7.2	4.7	6.1	6.0
			No. Accept.	14	4	27	4	49
175	MN-85432	ADX-1523-1	Count	64	38	47	43	192
			Color Avg.	6.1	6.0	5.2	5.3	5.7
			No. Accept.	4	3	14	4	25
2x-2x Total			**Count**	**1382**	**683**	**1113**	**1091**	**4269**
			Color Avg.	**6.6**	**6.9**	**5.6**	**6.1**	**6.3**
			No. Accept	**172**	**61**	**300**	**165**	**698**

2x-4x matings				2002		2003		
Family	**Female**	**Male**	**Values**	**3-mon**	**6-mon**	**3-mon**	**6-mon**	**Avg.**
053	C231	C181	Count	6	0	4	4	14
			Color Avg.	8.0	.	8.0	8.0	8.0
			No. Accept.	0	0	0	0	0
058	C231	S438	Count	8	0	5	5	18
			Color Avg.	6.6	.	6.8	7.8	7.0
			No. Accept.	2	0	0	0	2
060	C27	Atzimba	Count	3	0	3	3	9
			Color Avg.	5.3	.	8.0	8.3	7.2
			No. Accept.	1	0	0	0	1
071	C320	LBR-8	Count	2	0	0	0	2
			Color Avg.	8.5	.	.	.	8.5
			No. Accept.	0	0	0	0	0
073	C336	C182	Count	1	1	2	2	6
			Color Avg.	9.0	8.0	8.5	7.5	8.2
			No. Accept.	0	0	0	0	0
076	C336	S438	Count	12	9	9	8	38
			Color Avg.	7.0	7.8	6.3	6.9	7.0
			No. Accept.	0	0	2	0	2
077	C336	W-1355-1	Count	1	0	0	0	1
			Color Avg.	8.0	.	.	.	8.0
			No. Accept.	0	0	0	0	0
085	C367	Atlantic	Count	23	0	23	23	69
			Color Avg.	8.0	.	8.1	8.1	8.1
			No. Accept.	0	0	0	0	0
087	C367	C182	Count	10	7	5	6	28
			Color Avg.	8.4	8.3	7.0	7.5	7.9
			No. Accept.	0	0	0	0	0

2x-4x matings (cont.)				2002		2003		
Family	**Female**	**Male**	**Values**	**3-mon**	**6-mon**	**3-mon**	**6-mon**	**Avg.**
091	C367	C385	Count	40	36	29	27	132
			Color Avg.	8.2	8.5	7.1	7.3	7.8
			No. Accept.	0	0	0	1	1
092	C367	E-58	Count	10	10	0	0	20
			Color Avg.	8.5	7.8	.	.	8.2
			No. Accept.	0	0	0	0	0
093	C367	ND-860-2	Count	5	0	5	4	14
			Color Avg.	6.2	.	6.0	6.5	6.2
			No. Accept.	0	0	0	0	0
094	C367	NDO-1496-1	Count	22	0	19	19	60
			Color Avg.	9.0	.	8.9	9.1	9.0
			No. Accept.	0	0	0	1	1
095	C367	RH-076-3	Count	2	0	2	2	6
			Color Avg.	7.5	.	6.5	7.5	7.2
			No. Accept.	0	0	0	0	0
096	C367	RH-135-1	Count	7	0	5	5	17
			Color Avg.	6.6	.	6.6	7.0	6.7
			No. Accept.	2	0	1	0	3
097	C367	S438	Count	29	6	28	29	92
			Color Avg.	8.2	8.3	7.0	7.2	7.5
			No. Accept.	0	0	2	1	3
098	C367	S440	Count	65	35	58	46	204
			Color Avg.	8.0	8.0	7.1	6.5	7.4
			No. Accept.	0	0	3	3	6
099	C367	Yukon Gold	Count	24	0	0	0	24
			Color Avg.	8.7	.	.	.	8.7
			No. Accept.	0	0	0	0	0
110	C392	S440	Count	12	12	23	16	63
			Color Avg.	7.3	7.9	7.0	7.6	7.4
			No. Accept.	0	0	0	0	0
113	C396	S438	Count	2	0	2	2	6
			Color Avg.	7.0	.	5.5	7.0	6.5
			No. Accept.	0	0	1	0	1
114	C396	S440	Count	1	1	2	1	5
			Color Avg.	6.0	7.0	6.0	5.0	6.0
			No. Accept.	0	0	0	0	0
115	C411	C182	Count	1	1	2	2	6
			Color Avg.	7.0	8.0	6.0	7.0	6.8
			No. Accept.	0	0	0	0	0
126	E-29-1	C181	Count	27	25	27	24	103
			Color Avg.	6.8	7.5	4.9	5.8	6.3
			No. Accept.	0	0	12	7	19
127	E-29-1	C20	Count	25	19	33	31	108
			Color Avg.	6.2	6.8	5.4	6.0	6.0
			No. Accept.	5	1	10	4	20
128	E-29-1	C385	Count	24	17	37	38	116
			Color Avg.	5.8	6.4	4.9	4.8	5.3
			No. Accept.	6	2	16	19	43

2x-4x matings (cont.)				2002		2003		
Family	**Female**	**Male**	**Values**	**3-mon**	**6-mon**	**3-mon**	**6-mon**	**Avg.**
129	E-29-1	MSG-274-3	Count	33	32	35	21	121
			Color Avg.	8.8	8.6	5.8	7.6	7.7
			No. Accept.	0	0	4	0	4
130	E-29-1	NDO-1496-1	Count	6	6	10	6	28
			Color Avg.	8.2	6.7	5.9	5.5	6.5
			No. Accept.	0	0	2	2	4
131	E-29-1	RH-120-4	Count	22	19	34	17	92
			Color Avg.	8.0	7.8	5.9	7.2	7.0
			No. Accept.	1	0	9	0	10
132	E-29-1	RH-122-3	Count	40	35	43	40	158
			Color Avg.	6.6	6.8	5.1	5.7	6.0
			No. Accept.	5	0	17	6	28
133	E-29-1	RH-135-1	Count	32	29	31	27	119
			Color Avg.	7.0	6.6	4.8	5.3	5.9
			No. Accept.	1	0	14	9	24
135	E-29-1	S438	Count	18	13	25	25	81
			Color Avg.	6.4	7.6	5.2	6.4	6.2
			No. Accept.	2	0	9	1	12
136	E-29-1	S440	Count	22	20	33	31	106
			Color Avg.	6.4	7.3	5.8	6.3	6.3
			No. Accept.	2	0	5	1	8
137	E-29-1	W-1355-1	Count	14	14	27	25	80
			Color Avg.	6.9	5.7	5.5	5.5	5.8
			No. Accept.	1	4	6	4	15
138	E-29-1	Yukon Gold	Count	3	0	2	1	6
			Color Avg.	4.7	.	6.5	5.0	5.3
			No. Accept.	1	0	0	0	1
139	E-51-2	C181	Count	1	0	1	1	3
			Color Avg.	7.0	.	5.0	6.0	6.0
			No. Accept.	0	0	0	0	0
143	E-51-2	C341	Count	2	2	5	5	14
			Color Avg.	7.5	7.0	4.8	5.4	5.7
			No. Accept.	0	0	3	2	5
144	E-51-2	C385	Count	3	3	6	6	18
			Color Avg.	6.7	6.7	4.5	4.8	5.3
			No. Accept.	0	0	4	3	7
145	E-51-2	LBR-8	Count	5	0	5	4	14
			Color Avg.	6.0	.	5.0	5.5	5.5
			No. Accept.	0	0	1	0	1
146	E-51-2	MN-16404	Count	2	0	0	0	2
			Color Avg.	5.5	.	.	.	5.5
			No. Accept.	1	0	0	0	1
147	E-51-2	RH-122-3	Count	9	9	17	9	44
			Color Avg.	8.4	8.0	5.9	6.8	7.0
			No. Accept.	0	0	1	0	1
148	E-51-2	RH-176-11	Count	1	1	2	2	6
			Color Avg.	8.0	7.0	4.5	4.5	5.5
			No. Accept.	0	0	1	1	2

2x-4x matings (cont.)				2002		2003		
Family	**Female**	**Male**	**Values**	**3-mon**	**6-mon**	**3-mon**	**6-mon**	**Avg.**
149	E-51-2	S438	Count	10	7	12	14	43
			Color Avg.	8.5	7.3	6.6	6.3	7.0
			No. Accept.	0	0	3	2	5
150	E-51-2	S440	Count	0	0	1	0	1
			Color Avg.	.	.	5.0	.	5.0
			No. Accept.	0	0	0	0	0
154	E-51-4	C182	Count	1	0	1	0	2
			Color Avg.	7.0	.	8.0	.	7.5
			No. Accept.	0	0	0	0	0
164	E-51-4	C385	Count	13	12	26	25	76
			Color Avg.	8.0	8.1	6.0	6.6	6.9
			No. Accept.	0	0	5	4	9
165	E-51-4	C444	Count	64	31	60	53	208
			Color Avg.	7.3	8.0	6.7	6.9	7.1
			No. Accept.	3	1	5	7	16
167	E-51-4	NDO-1496-1	Count	3	3	5	6	17
			Color Avg.	7.0	7.3	6.4	5.7	6.4
			No. Accept.	0	0	0	2	2
168	E-51-4	RH-176-11	Count	1	1	2	2	6
			Color Avg.	7.0	7.0	6.0	7.5	6.8
			No. Accept.	0	0	0	0	0
170	E-51-4	W-1355-1	Count	2	0	1	1	4
			Color Avg.	6.0	.	4.0	8.0	6.0
			No. Accept.	1	0	1	0	2
171	E-51-4	Zarevo	Count	0	0	1	1	2
			Color Avg.	.	.	8.0	8.0	8.0
			No. Accept.	0	0	0	0	0
174	MN-85430	C385	Count	5	4	4	3	16
			Color Avg.	6.2	7.3	4.3	5.0	5.8
			No. Accept.	0	0	2	0	2
2x-4x Total			**Count**	**674**	**420**	**712**	**622**	**2428**
			Color Avg.	**7.5**	**7.5**	**6.1**	**6.5**	**6.8**
			No. Accept	**34**	**8**	**139**	**80**	**261**

4x-2x matings				2002		2003		
Family	**Female**	**Male**	**Values**	**3-mon**	**6-mon**	**3-mon**	**6-mon**	**Avg.**
003	Andover	C190	Count	1	1	2	2	6
			Color Avg.	9.0	7.0	6.0	7.0	7.0
			No. Accept.	0	0	0	0	0
004	Andover	C213	Count	3	3	6	5	17
			Color Avg.	7.7	7.3	6.8	6.8	7.1
			No. Accept.	0	0	0	1	1
005	Andover	C215	Count	1	1	2	2	6
			Color Avg.	8.0	8.0	6.5	6.5	7.0
			No. Accept.	0	0	0	0	0
006	Andover	C307	Count	5	4	8	8	25
			Color Avg.	8.0	6.5	5.1	4.8	5.8
			No. Accept.	0	0	2	3	5

4x-2x matings (cont.)				2002		2003		
Family	**Female**	**Male**	**Values**	**3-mon**	**6-mon**	**3-mon**	**6-mon**	**Avg.**
007	Andover	C396	Count	65	38	51	54	208
			Color Avg.	7.7	7.2	6.1	6.5	6.9
			No. Accept.	0	2	6	3	11
008	Andover	MN-85393	Count	23	0	23	0	46
			Color Avg.	6.1	.	5.8	.	6.0
			No. Accept.	2	0	3	0	5
009	Andover	MN-85430	Count	12	12	21	22	67
			Color Avg.	6.8	6.3	5.4	5.6	5.9
			No. Accept.	0	3	5	4	12
011	Atlantic	C190	Count	2	2	2	2	8
			Color Avg.	7.5	6.0	6.5	6.5	6.6
			No. Accept.	0	0	0	0	0
012	Atlantic	C213	Count	1	0	1	1	3
			Color Avg.	7.0	.	7.0	7.0	7.0
			No. Accept.	0	0	0	0	0
013	Atlantic	C307	Count	19	18	28	28	93
			Color Avg.	7.4	7.3	5.8	6.1	6.5
			No. Accept.	0	1	3	5	9
014	Atlantic	C374	Count	1	1	1	2	5
			Color Avg.	10.0	8.0	5.0	8.5	8.0
			No. Accept.	0	0	0	0	0
015	Atlantic	C396	Count	65	41	65	43	214
			Color Avg.	7.6	7.5	6.5	6.5	7.0
			No. Accept.	0	1	1	2	4
018	C181	C190	Count	3	3	4	4	14
			Color Avg.	6.3	8.0	6.8	6.5	6.9
			No. Accept.	0	0	0	0	0
019	C181	C213	Count	6	6	12	12	36
			Color Avg.	5.3	6.7	5.3	5.8	5.7
			No. Accept.	2	0	2	2	6
020	C181	C215	Count	5	5	6	5	21
			Color Avg.	6.2	7.6	6.0	7.2	6.7
			No. Accept.	1	0	2	0	3
021	C181	C231	Count	1	0	1	1	3
			Color Avg.	7.0	.	4.0	5.0	5.3
			No. Accept.	0	0	1	0	1
022	C181	C307	Count	1	0	1	1	3
			Color Avg.	5.0	.	4.0	4.0	4.3
			No. Accept.	0	0	1	1	2
023	C181	C36	Count	2	2	4	4	12
			Color Avg.	6.0	7.0	7.0	6.5	6.7
			No. Accept.	0	0	0	0	0
024	C181	C396	Count	64	39	61	64	228
			Color Avg.	6.2	7.1	5.9	6.3	6.3
			No. Accept.	15	2	8	10	35
025	C181	MN-85393	Count	36	36	32	26	130
			Color Avg.	7.2	6.9	5.1	4.9	6.2
			No. Accept.	1	0	8	6	15

4x-2x matings (cont.)				2002		2003		
Family	Female	Male	Values	3-mon	6-mon	3-mon	6-mon	Avg.
026	C181	MN-85430	Count	3	0	2	2	7
			Color Avg.	5.0	.	4.5	5.5	5.0
			No. Accept.	2	0	1	0	3
029	C182	C213	Count	5	5	10	8	28
			Color Avg.	6.4	6.4	5.3	5.3	5.7
			No. Accept.	0	0	3	3	6
032	C182	C307	Count	3	2	4	4	13
			Color Avg.	6.3	5.5	6.8	6.3	6.3
			No. Accept.	1	1	0	0	2
033	C182	C33	Count	4	0	3	3	10
			Color Avg.	6.3	.	5.0	6.7	6.0
			No. Accept.	1	0	1	0	2
034	C182	C367	Count	18	18	27	32	95
			Color Avg.	7.4	7.6	5.3	6.3	6.5
			No. Accept.	1	0	3	2	6
036	C182	C396	Count	65	40	66	66	237
			Color Avg.	6.8	7.2	5.4	5.7	6.2
			No. Accept.	5	1	25	12	43
037	C182	MN-85393	Count	64	38	66	57	225
			Color Avg.	6.4	7.0	5.5	6.0	6.2
			No. Accept.	9	2	14	4	29
038	C182	MN-85430	Count	9	7	12	12	40
			Color Avg.	6.8	7.0	6.4	6.4	6.6
			No. Accept.	2	0	0	1	3
043	C20	C190	Count	4	0	4	2	10
			Color Avg.	7.5	.	7.3	6.5	7.2
			No. Accept.	0	0	0	0	0
048	C20	C435	Count	1	0	1	1	3
			Color Avg.	7.0	.	8.0	8.0	7.7
			No. Accept.	0	0	0	0	0
049	C20	MN-85393	Count	5	4	7	7	23
			Color Avg.	7.2	6.3	5.7	5.3	6.0
			No. Accept.	0	0	2	0	2
050	C20	MN-85430	Count	4	4	5	6	19
			Color Avg.	7.5	6.3	6.2	5.7	6.3
			No. Accept.	0	0	0	1	1
078	C341	C307	Count	1	0	1	1	3
			Color Avg.	8.0	.	8.0	10.0	8.7
			No. Accept.	0	0	0	0	0
079	C341	C33	Count	2	0	1	1	4
			Color Avg.	6.0	.	7.0	6.0	6.3
			No. Accept.	0	0	0	0	0
081	C341	MN-85393	Count	2	0	2	2	6
			Color Avg.	5.0	.	7.0	7.5	6.5
			No. Accept.	1	0	0	0	1
082	C341	MN-85430	Count	2	0	3	3	8
			Color Avg.	7.0	.	5.3	5.7	5.9
			No. Accept.	0	0	1	0	1

4x-2x matings (cont.)				2002		2003		
Family	Female	Male	Values	3-mon	6-mon	3-mon	6-mon	Avg.
102	C385	C190	Count	12	10	16	16	54
			Color Avg.	6.8	6.7	5.4	5.8	6.0
			No. Accept.	1	0	2	2	5
103	C385	C213	Count	17	17	13	13	60
			Color Avg.	6.9	7.5	5.1	5.6	6.4
			No. Accept.	1	0	4	0	5
104	C385	C215	Count	20	6	17	17	60
			Color Avg.	5.1	6.7	6.1	6.6	6.0
			No. Accept.	9	0	1	1	11
105	C385	C307	Count	1	1	1	2	5
			Color Avg.	4.0	4.0	4.0	4.5	4.2
			No. Accept.	1	1	1	1	4
106	C385	C33	Count	1	0	0	0	1
			Color Avg.	7.0	.	.	.	7.0
			No. Accept.	0	0	0	0	0
107	C385	C396	Count	64	39	62	56	221
			Color Avg.	6.8	7.1	6.2	6.1	6.5
			No. Accept.	5	2	10	13	30
108	C385	MN-85430	Count	44	23	41	40	148
			Color Avg.	6.2	7.1	5.1	6.2	6.0
			No. Accept.	4	2	13	0	19
116	Cal-White	C190	Count	1	1	2	2	6
			Color Avg.	10.0	10.0	8.0	7.5	8.5
			No. Accept.	0	0	0	0	0
117	Cal-White	C215	Count	4	3	8	8	23
			Color Avg.	6.5	5.3	6.9	6.1	6.3
			No. Accept.	1	1	0	1	3
118	Cal-White	C307	Count	4	3	2	1	10
			Color Avg.	7.8	8.3	7.5	8.0	7.9
			No. Accept.	0	0	0	0	0
119	Cal-White	C33	Count	1	0	1	1	3
			Color Avg.	6.0	.	7.0	7.0	6.7
			No. Accept.	0	0	0	0	0
120	Cal-White	C396	Count	28	28	38	40	134
			Color Avg.	8.2	7.7	6.5	7.5	7.4
			No. Accept.	0	0	1	0	1
121	Cal-White	C435	Count	1	0	1	1	3
			Color Avg.	8.0	.	6.0	7.0	7.0
			No. Accept.	0	0	0	0	0
122	Cal-White	MN-85430	Count	3	1	2	1	7
			Color Avg.	8.3	8.0	6.5	8.0	7.7
			No. Accept.	0	0	0	0	0
123	E-13	C372	Count	24	0	24	24	72
			Color Avg.	7.7	.	7.1	7.2	7.3
			No. Accept.	0	0	0	0	0
124	E-20	C307	Count	0	0	0	1	1
			Color Avg.	.	.	.	7.0	7.0
			No. Accept.	0	0	0	0	0

4x-2x matings (cont.)				2002		2003		
Family	Female	Male	Values	3-mon	6-mon	3-mon	6-mon	Avg.
172	MN-16404	MN-85430	Count	2	2	1	2	7
			Color Avg.	5.5	7.5	4.0	6.5	6.1
			No. Accept.	1	0	1	0	2
178	MSB-073-2	MN-85393	Count	40	37	35	38	150
			Color Avg.	8.8	8.2	6.7	7.1	7.7
			No. Accept.	2	0	1	1	4
180	MSE-250-1	C374	Count	61	36	28	32	157
			Color Avg.	7.8	7.6	6.1	6.5	7.2
			No. Accept.	2	2	3	6	13
181	MSG-274-3	C190	Count	1	1	2	2	6
			Color Avg.	9.0	9.0	7.0	7.5	7.8
			No. Accept.	0	0	0	0	0
182	MSG-274-3	C307	Count	1	0	0	0	1
			Color Avg.	9.0	.	.	.	9.0
			No. Accept.	0	0	0	0	0
183	MSG-274-3	C396	Count	33	33	37	37	140
			Color Avg.	9.0	8.4	7.5	7.9	8.2
			No. Accept.	0	0	0	0	0
184	MSG-274-3	MN-85430	Count	1	1	2	2	6
			Color Avg.	10.0	6.0	7.5	8.0	7.8
			No. Accept.	0	0	0	0	0
188	NDO-1496-1	C307	Count	2	1	4	4	11
			Color Avg.	8.0	9.0	8.0	7.8	8.0
			No. Accept.	0	0	0	0	0
189	NDO-1496-1	C396	Count	3	3	6	3	15
			Color Avg.	7.3	7.7	6.7	4.7	6.6
			No. Accept.	0	0	1	1	2
190	NDO-1496-1	MN-85393	Count	1	0	0	0	1
			Color Avg.	6.0	.	.	.	6.0
			No. Accept.	0	0	0	0	0
192	NY-112	C190	Count	5	5	7	6	23
			Color Avg.	7.2	7.4	6.1	5.2	6.4
			No. Accept.	0	0	1	1	2
195	NY-112	C33	Count	3	0	3	0	6
			Color Avg.	7.0	.	6.3	.	6.7
			No. Accept.	0	0	0	0	0
196	NY-112	C396	Count	36	34	45	41	156
			Color Avg.	7.7	6.9	6.6	6.5	6.9
			No. Accept.	0	1	2	3	6
197	NY-112	MN-85393	Count	5	0	3	3	11
			Color Avg.	5.4	.	7.7	8.0	6.7
			No. Accept.	2	0	0	0	2
198	NY-112	MN-85430	Count	8	2	3	5	18
			Color Avg.	5.9	7.0	6.7	6.8	6.4
			No. Accept.	2	0	0	0	2
199	RH-071-20	C190	Count	4	0	4	3	11
			Color Avg.	5.8	.	5.8	6.0	5.8
			No. Accept.	2	0	1	0	3

4x-2x matings (cont.)				2002		2003		
Family	Female	Male	Values	3-mon	6-mon	3-mon	6-mon	Avg.
200	RH-071-20	C396	Count	1	1	1	2	5
			Color Avg.	6.0	8.0	6.0	6.0	6.4
			No. Accept.	0	0	0	1	1
203	RH-076-3	C307	Count	1	0	1	1	3
			Color Avg.	9.0	.	6.0	8.0	7.7
			No. Accept.	0	0	0	0	0
204	RH-076-3	C33	Count	1	0	1	1	3
			Color Avg.	7.0	.	8.0	9.0	8.0
			No. Accept.	0	0	0	0	0
205	RH-076-3	C396	Count	43	38	42	42	165
			Color Avg.	6.3	5.9	5.5	5.2	5.7
			No. Accept.	7	7	12	13	39
206	RH-076-3	C435	Count	1	0	1	1	3
			Color Avg.	8.0	.	7.0	8.0	7.7
			No. Accept.	0	0	0	0	0
207	RH-076-3	MN-85430	Count	1	0	1	1	3
			Color Avg.	4.0	.	4.0	6.0	4.7
			No. Accept.	1	0	1	0	2
211	RH-120-4	C215	Count	1	1	2	2	6
			Color Avg.	7.0	8.0	5.0	5.5	6.0
			No. Accept.	0	0	1	1	2
213	RH-120-4	C396	Count	34	33	41	38	146
			Color Avg.	7.4	7.4	6.5	6.7	6.9
			No. Accept.	1	0	2	0	3
214	RH-122-3	C190	Count	1	0	1	1	3
			Color Avg.	5.0	.	8.0	8.0	7.0
			No. Accept.	0	0	0	0	0
215	RH-122-3	C213	Count	11	8	15	15	49
			Color Avg.	8.6	7.8	7.0	7.5	7.7
			No. Accept.	0	0	0	0	0
216	RH-122-3	C396	Count	66	41	67	49	223
			Color Avg.	7.6	8.0	6.1	6.6	7.0
			No. Accept.	2	0	7	5	14
217	RH-122-3	MN-85393	Count	4	0	4	4	12
			Color Avg.	5.8	.	6.8	6.8	6.4
			No. Accept.	0	0	0	0	0
218	RH-122-3	MN-85430	Count	4	1	6	6	17
			Color Avg.	5.8	7.0	6.8	7.3	6.8
			No. Accept.	1	0	0	0	1
220	RH-135-1	C190	Count	4	0	4	4	12
			Color Avg.	7.3	.	5.8	4.5	5.8
			No. Accept.	0	0	0	2	2
221	RH-135-1	C396	Count	8	8	1	2	19
			Color Avg.	7.3	6.0	7.0	8.0	6.8
			No. Accept.	0	0	0	0	0
222	RH-135-1	MN-85393	Count	2	0	0	0	2
			Color Avg.	6.5	.	.	.	6.5
			No. Accept.	0	0	0	0	0

4x-2x matings (cont.)				2002		2003		
Family	**Female**	**Male**	**Values**	**3-mon**	**6-mon**	**3-mon**	**6-mon**	**Avg.**
223	RH-135-1	MN-85430	Count	2	1	2	2	7
			Color Avg.	7.5	6.0	5.5	7.0	6.6
			No. Accept.	0	0	1	0	1
224	RH-138-2	C190	Count	0	0	1	1	2
			Color Avg.	.	.	5.0	5.0	5.0
			No. Accept.	0	0	0	0	0
225	RH-138-2	MN-85393	Count	6	0	4	4	14
			Color Avg.	5.3	.	6.5	6.5	6.0
			No. Accept.	2	0	0	0	2
227	RH-176-11	C33	Count	2	0	2	2	6
			Color Avg.	6.5	.	4.5	5.0	5.3
			No. Accept.	0	0	1	1	2
228	RH-176-11	C396	Count	14	10	19	21	64
			Color Avg.	7.1	5.7	5.7	6.1	6.1
			No. Accept.	1	2	4	2	9
229	RH-176-11	IVP-101	Count	2	0	2	0	4
			Color Avg.	5.0	.	5.5	.	5.3
			No. Accept.	0	0	0	0	0
230	RH-176-11	MN-85393	Count	2	0	2	2	6
			Color Avg.	4.0	.	7.5	7.0	6.2
			No. Accept.	2	0	0	0	2
231	RH-176-11	MN-85430	Count	2	2	2	2	8
			Color Avg.	5.5	6.5	6.0	7.5	6.4
			No. Accept.	1	0	0	0	1
233	S438	C307	Count	2	0	1	1	4
			Color Avg.	9.0	.	5.0	6.0	7.3
			No. Accept.	0	0	0	0	0
234	S438	C396	Count	17	0	17	17	51
			Color Avg.	6.6	.	7.2	7.8	7.2
			No. Accept.	2	0	0	0	2
236	S440	C215	Count	1	1	2	2	6
			Color Avg.	7.0	7.0	5.0	5.0	5.7
			No. Accept.	0	0	0	0	0
237	S440	C307	Count	1	1	1	2	5
			Color Avg.	7.0	7.0	7.0	8.0	7.4
			No. Accept.	0	0	0	0	0
238	S440	C396	Count	34	29	30	31	124
			Color Avg.	7.4	7.5	5.8	6.3	6.8
			No. Accept.	0	0	4	4	8
239	S440	MN-85430	Count	1	1	2	2	6
			Color Avg.	8.0	7.0	6.0	6.0	6.5
			No. Accept.	0	0	0	0	0
240	Snowden	C190	Count	1	1	1	1	4
			Color Avg.	7.0	6.0	5.0	5.0	5.8
			No. Accept.	0	0	0	0	0
241	Snowden	C396	Count	62	37	36	38	173
			Color Avg.	7.3	7.1	6.5	6.0	6.8
			No. Accept.	6	1	2	4	13

4x-2x matings (cont.)				2002		2003		
Family	**Female**	**Male**	**Values**	**3-mon**	**6-mon**	**3-mon**	**6-mon**	**Avg.**
242	Snowden	MN-85430	Count	1	1	2	0	4
			Color Avg.	7.0	8.0	8.0	.	7.8
			No. Accept.	0	0	0	0	0
249	W-1355-1	C36	Count	3	0	3	3	9
			Color Avg.	7.3	.	5.3	5.0	5.9
			No. Accept.	0	0	0	1	1
250	W-1355-1	C396	Count	14	12	22	24	72
			Color Avg.	7.1	6.2	6.3	6.1	6.4
			No. Accept.	0	1	2	4	7
251	W-1355-1	MN-85430	Count	7	1	7	7	22
			Color Avg.	5.9	4.0	5.3	4.6	5.2
			No. Accept.	1	1	3	4	9
252	Yukon Gold	C213	Count	1	0	1	0	2
			Color Avg.	9.0	.	8.0	.	8.5
			No. Accept.	0	0	0	0	0
253	Yukon Gold	C215	Count	1	0	1	1	3
			Color Avg.	8.0	.	7.0	6.0	7.0
			No. Accept.	0	0	0	0	0
254	Yukon Gold	C396	Count	15	14	23	27	79
			Color Avg.	8.6	7.7	6.6	6.7	7.2
			No. Accept.	0	0	2	1	3
255	Yukon Gold	MN-85430	Count	1	0	1	1	3
			Color Avg.	9.0	.	4.0	8.0	7.0
			No. Accept.	0	0	1	0	1
	4x-2x Total		**Count**	**1314**	**859**	**1325**	**1254**	**4752**
			Color Avg.	**7.1**	**7.2**	**6.1**	**6.3**	**6.6**
			No. Accept	**103**	**34**	**177**	**133**	**447**

4x-4x matings				2002		2003		
Family	**Female**	**Male**	**Values**	**3-mon**	**6-mon**	**3-mon**	**6-mon**	**Avg.**
016	Atlantic	ND-3828-15	Count	66	39	63	62	230
			Color Avg.	6.9	6.5	5.6	5.9	6.2
			No. Accept.	2	5	10	6	23
027	C181	RH-076-3	Count	24	0	24	18	66
			Color Avg.	4.5	.	7.3	5.5	5.8
			No. Accept.	12	0	1	4	17
042	C20	Atlantic	Count	24	0	23	23	70
			Color Avg.	6.9	.	6.7	7.4	7.0
			No. Accept.	0	0	0	0	0
072	C332	Atzimba	Count	24	0	0	0	24
			Color Avg.	7.8	.	.	.	7.8
			No. Accept.	0	0	0	0	0
083	C341	Zarevo	Count	24	0	24	22	70
			Color Avg.	6.8	.	7.3	6.8	7.0
			No. Accept.	2	0	0	1	3
084	C342	C71	Count	24	0	23	23	70
			Color Avg.	7.8	.	7.1	7.6	7.5
			No. Accept.	0	0	1	0	1

4x-4x matings (cont.)				2002		2003		
Family	**Female**	**Male**	**Values**	**3-mon**	**6-mon**	**3-mon**	**6-mon**	**Avg.**
101	C385	Andover	Count	42	40	52	47	181
			Color Avg.	7.8	7.5	5.7	5.6	6.6
			No. Accept.	0	0	8	10	18
176	MN-85554	C181	Count	17	0	7	7	31
			Color Avg.	7.1	.	7.4	7.4	7.3
			No. Accept.	0	0	0	0	0
177	MSA-091-1	C41	Count	20	20	36	36	112
			Color Avg.	9.1	7.7	7.2	7.8	7.8
			No. Accept.	0	0	0	1	1
179	MSE-250-1	C208	Count	45	21	46	51	163
			Color Avg.	7.4	6.9	6.6	6.3	6.8
			No. Accept.	1	1	7	4	13
187	ND-3828-15	Zarevo	Count	24	0	17	17	58
			Color Avg.	5.4	.	5.6	5.8	5.6
			No. Accept.	8	0	5	4	17
208	RH-076-3	S438	Count	20	0	19	19	58
			Color Avg.	7.5	.	5.4	5.4	6.1
			No. Accept.	0	0	7	4	11
219	RH-122-3	RH-138-2	Count	24	0	19	19	62
			Color Avg.	6.1	.	7.7	7.3	7.0
			No. Accept.	3	0	0	0	3
243	Snowden	S438	Count	24	0	24	23	71
			Color Avg.	7.3	.	6.5	6.1	6.7
			No. Accept.	0	0	2	3	5
244	Snowden	S440	Count	24	0	24	24	72
			Color Avg.	6.8	.	6.6	5.7	6.4
			No. Accept.	1	0	2	6	9
245	W-1355-1	C181	Count	24	0	21	21	66
			Color Avg.	6.0	.	6.9	6.1	6.3
			No. Accept.	5	0	2	1	8
256	Yukon Gold	S438	Count	24	0	24	24	72
			Color Avg.	7.5	.	8.1	8.3	8.0
			No. Accept.	0	0	0	0	0
257	Yukon Gold	S440	Count	24	0	0	0	24
			Color Avg.	6.8	.	.	.	6.8
			No. Accept.	1	0	0	0	1
4x-4x Total			**Count**	**498**	**120**	**446**	**436**	**1500**
			Color Avg.	**7.0**	**7.1**	**6.6**	**6.5**	**6.7**
			No. Accept	**35**	**6**	**45**	**44**	**130**
Combined Total			**Count**	**3868**	**2082**	**3596**	**3403**	**12949**
			Color Avg.	**7.0**	**7.2**	**6.0**	**6.3**	**6.6**
			No. Accept	**344**	**109**	**661**	**422**	**1536**

Table 5. Chip color scores of the acceptably chipping clones retained in 2002 after 3-months storage and re-evaluated in 2003 and 2004.

				2002	2003	2004		
Mating	Clone	Female	Male	Morris	Morris	Becker	GF	Avg.
2x-2x	DE02-001-08	ADX-1523-1	C159	3.0	4.0	4.5	4.0	4.0
2x-2x	DE02-001-12	ADX-1523-1	C159	3.0	3.0	5.5	3.5	4.0
2x-2x	DE02-002-03	ADX-1523-1	C213	4.0	4.0	3.5	4.0	3.8
2x-2x	DE02-002-09	ADX-1523-1	C213	4.0	4.0	6.5	2.0	4.2
2x-2x	DE02-002-16	ADX-1523-1	C213	3.0	4.0	5.0	4.0	4.2
2x-2x	DE02-017-31	C159	ADX-1523-1	3.0	4.0	6.5	4.5	4.8
2x-2x	DE02-052-05	C231	ADX-1523-1	4.0	4.0	5.5	3.0	4.2
2x-2x	DE02-052-12	C231	ADX-1523-1	4.0	3.0	5.0	4.0	4.2
2x-2x	DE02-052-17	C231	ADX-1523-1	4.0	4.0	6.0	5.0	5.0
2x-2x	DE02-052-29	C231	ADX-1523-1	2.0	4.0	5.5	4.0	4.2
2x-2x	DE02-052-30	C231	ADX-1523-1	4.0	4.0	6.5	3.0	4.5
2x-2x	DE02-052-31	C231	ADX-1523-1	3.0	4.0	4.5	4.5	4.2
2x-2x	DE02-062-12	C307	ADX-1523-1	3.0	4.0	.	6.0	4.3
2x-2x	DE02-100-04	C374	ADX-1523-1	4.0	4.0	6.0	3.5	4.5
2x-2x	DE02-100-15	C374	ADX-1523-1	2.0	4.0	5.0	4.5	4.2
2x-2x	DE02-141-01	E-51-2	C307	3.0	2.0	5.5	5.0	4.3
2x-2x	DE02-152-22	E-51-4	ADX-1523-1	4.0	4.0	6.5	5.0	5.2
2x-2x	DE02-153-02	E-51-4	C159	4.0	4.0	6.0	4.0	4.7
2x-2x	DE02-153-10	E-51-4	C159	4.0	4.0	5.0	4.0	4.3
2x-2x	DE02-163-32	E-51-4	C380	3.0	4.0	7.0	6.0	5.5
2x-4x	DE02-127-11	E-29-1	C20	4.0	4.0	6.0	5.5	5.2
2x-4x	DE02-128-02	E-29-1	C385	3.0	4.0	5.5	4.5	4.5
2x-4x	DE02-128-20	E-29-1	C385	4.0	4.0	4.0	4.5	4.2
2x-4x	DE02-137-05	E-29-1	W-1355-1	4.0	4.0	5.0	5.0	4.6
2x-4x	DE02-140-06	E-51-2	C215	3.0	2.0	7.0	4.5	4.7
2x-4x	DE02-156-15	E-51-4	C213	4.0	4.0	6.0	5.0	4.8
2x-4x	DE02-159-03	E-51-4	C307	3.0	4.0	5.5	3.5	4.2
2x-4x	DE02-159-05	E-51-4	C307	3.0	4.0	5.5	4.5	4.5
2x-4x	DE02-159-11	E-51-4	C307	4.0	4.0	6.0	2.5	4.2
2x-4x	DE02-159-30	E-51-4	C307	3.0	3.0	7.0	5.0	5.0
2x-4x	DE02-175-01	MN-85432	ADX-1523-1	3.0	4.0	6.0	4.0	4.5
4x-2x	DE02-020-04	C181	C215	4.0	4.0	8.0	6.5	6.2
4x-2x	DE02-024-13	C181	C396	3.0	4.0	7.0	5.0	5.2
4x-2x	DE02-025-08	C181	MN-85393	4.0	3.0	7.0	5.5	5.3
4x-2x	DE02-037-28	C182	MN-85393	4.0	4.0	5.5	5.0	4.8
4x-2x	DE02-037-29	C182	MN-85393	4.0	4.0	7.0	5.5	5.5
4x-2x	DE02-105-01	C385	C307	4.0	2.0	7.0	4.5	4.4
4x-2x	DE02-107-01	C385	C396	4.0	4.0	4.0	4.5	4.2
4x-2x	DE02-107-26	C385	C396	4.0	4.0	6.5	6.0	5.5
4x-2x	DE02-108-01	C385	MN-85430	4.0	3.0	6.5	6.0	5.3
4x-2x	DE02-108-03	C385	MN-85430	3.0	4.0	6.5	5.5	5.2
4x-2x	DE02-205-10	RH-076-3	C396	3.0	3.0	5.0	6.5	4.8
4x-2x	DE02-205-12	RH-076-3	C396	3.0	4.0	5.0	6.5	5.0
4x-2x	DE02-205-13	RH-076-3	C396	3.0	3.0	4.0	4.5	3.8
4x-2x	DE02-205-16	RH-076-3	C396	3.0	4.0	5.5	4.5	4.5
4x-4x	DE02-016-07	Atlantic	ND-3828-15	3.0	4.0	4.5	3.5	3.8
	Grand Total			**3.46**	**3.72**	**5.72**	**4.57**	**4.61**

Table 6. Average horticultural and agronomic traits of acceptably chipping clones retained in 2002 and re-evaluated in 2003 and 2004. Average values for total tuber yield (TTY), general tuber appearance (GTA), chip color score at 3- and 6-months, specific gravity, eye depth, flesh color, tuber shape, and skin color for the parents used in this dissertation as evaluated in 2003 and 2004. Table sorted by mating type then by clone. Rating scales and definitions located in table footnote.

Mating	Clone	Female	Male	GTA	Specific Gravity	TTY	ATY	Sprout	Eye Depth	Shape	Maturity
2x-2x	DE02-001-08	ADX-1523-1	C159	3.4	1.107	5370	4682	0.2	1.8	2.0	4.0
2x-2x	DE02-001-12	ADX-1523-1	C159	2.8	1.078	5503	5263	0.4	1.8	1.4	4.4
2x-2x	DE02-002-03	ADX-1523-1	C213	3.0	1.069	1522	1378	0.6	1.2	1.2	4.2
2x-2x	DE02-002-09	ADX-1523-1	C213	2.8	1.083	2281	2474	0.4	1.6	1.4	4.0
2x-2x	DE02-002-16	ADX-1523-1	C213	3.2	1.079	4004	2565	0.8	2.2	1.6	4.0
2x-2x	DE02-017-31	C159	ADX-1523-1	2.6	1.099	4712	3698	0.4	1.6	1.6	4.0
2x-2x	DE02-052-05	C231	ADX-1523-1	3.0	1.088	2555	1893	0.2	1.4	1.2	3.6
2x-2x	DE02-052-12	C231	ADX-1523-1	3.2	1.082	3246	2679	0.6	1.8	1.0	3.8
2x-2x	DE02-052-17	C231	ADX-1523-1	3.2	1.061	1277	1187	0.2	1.8	1.0	3.4
2x-2x	DE02-052-29	C231	ADX-1523-1	3.4	1.083	4322	3563	0.4	2.0	1.6	4.4
2x-2x	DE02-052-30	C231	ADX-1523-1	2.8	1.085	2787	1654	0.2	1.6	1.6	4.2
2x-2x	DE02-052-31	C231	ADX-1523-1	3.4	1.096	1792	1789	0.2	1.8	1.8	3.6
2x-2x	DE02-062-12	C307	ADX-1523-1	2.0	1.109	1793	1712	0.5	1.0	2.0	5.0
2x-2x	DE02-100-04	C374	ADX-1523-1	3.4	1.090	8440	6287	0.8	2.4	1.4	4.4
2x-2x	DE02-100-15	C374	ADX-1523-1	3.2	1.082	5321	5202	0.2	2.4	2.0	4.8
2x-2x	DE02-141-01	E-51-2	C307	4.4	1.077	4934	2743	0.2	2.8	1.8	4.2
2x-2x	DE02-152-22	E-51-4	ADX-1523-1	3.0	1.080	7065	4740	1.0	2.3	1.5	3.2
2x-2x	DE02-153-02	E-51-4	C159	4.2	1.104	5330	4404	0.4	2.4	2.2	4.0
2x-2x	DE02-153-10	E-51-4	C159	3.2	1.086	5887	5548	0.4	1.6	2.4	4.0
2x-2x	DE02-163-32	E-51-4	C380	4.0	1.088	2901	2584	0.2	2.2	2.4	4.0
2x-4x	DE02-127-11	E-29-1	C20	3.6	1.105	4910	3006	0.6	1.6	1.8	2.4
2x-4x	DE02-128-02	E-29-1	C385	3.2	1.092	4598	4003	0.2	1.2	1.4	4.8
2x-4x	DE02-128-20	E-29-1	C385	2.4	1.096	4448	3762	0.2	1.4	1.6	4.6
2x-4x	DE02-137-05	E-29-1	W-1355-1	2.3	1.084	5395	5192	0.5	1.3	1.3	4.4
2x-4x	DE02-140-06	E-51-2	C215	4.2	1.252	5337	3006	0.4	3.0	1.4	3.2
2x-4x	DE02-156-15	E-51-4	C213	4.0	1.085	3755	3195	0.2	2.2	2.0	3.6
2x-4x	DE02-159-03	E-51-4	C307	3.0	1.095	3346	2673	0.4	1.8	1.0	3.8
2x-4x	DE02-159-05	E-51-4	C307	3.0	1.093	3630	2781	0.4	2.0	1.4	3.8
2x-4x	DE02-159-11	E-51-4	C307	3.8	1.088	2852	2474	0.2	2.0	2.2	4.2
2x-4x	DE02-159-30	E-51-4	C307	3.3	1.092	6575	6560	0.5	2.3	1.0	4.3
2x-4x	DE02-175-01	MN-85432	ADX-1523-1	3.2	1.083	1948	1374	0.8	1.6	1.6	4.0
4x-2x	DE02-020-04	C181	C215	3.8	1.098	3153	2390	0.2	1.6	2.4	3.6
4x-2x	DE02-024-13	C181	C396	2.4	1.098	2943	2053	0.4	1.2	1.0	2.0
4x-2x	DE02-025-08	C181	MN-85393	3.8	1.093	4890	2625	1.4	2.4	1.8	3.6
4x-2x	DE02-037-28	C182	MN-85393	3.0	1.104	2669	2380	0.2	1.6	1.2	4.0
4x-2x	DE02-037-29	C182	MN-85393	3.4	1.096	2109	2019	0.6	2.0	1.8	3.0
4x-2x	DE02-105-01	C385	C307	4.5	1.106	2098	473	0.3	1.8	2.3	3.0
4x-2x	DE02-107-01	C385	C396	2.8	1.096	5871	5419	0.2	2.0	1.8	4.0
4x-2x	DE02-107-26	C385	C396	3.6	1.098	4514	4147	4.6	1.6	1.6	4.2
4x-2x	DE02-108-01	C385	MN-85430	3.0	1.081	8034	7190	0.6	2.0	2.0	4.0

Mating (cont.)	Clone	Female	Male	GTA	Specific Gravity	TTY	ATY	Sprout	Eye Depth	Shape	Maturity
4x-2x	DE02-108-03	C385	MN-85430	3.2	1.095	4150	3481	0.4	2.2	1.6	3.4
4x-2x	DE02-205-10	RH-076-3	C396	3.4	1.095	8079	7275	0.8	1.8	1.2	4.2
4x-2x	DE02-205-12	RH-076-3	C396	4.0	1.076	6127	5252	0.6	1.8	1.8	4.2
4x-2x	DE02-205-13	RH-076-3	C396	3.4	1.091	7914	7445	0.4	1.6	2.0	3.8
4x-2x	DE02-205-16	RH-076-3	C396	3.0	1.088	7567	7232	0.8	1.6	1.4	3.6
4x-4x	DE02-016-07	Atlantic	ND-3828-15	2.2	1.073	2770	2009	0.4	1.0	1.6	4.2
Grand Total				**3.27**	**1.093**	**4364**	**3597**	**0.53**	**1.84**	**1.63**	**3.88**

GTA rating: 1(excellent) to 5 (poor)
Specific gravity calculation: weight in air/(weight in air-weight in water)
TTY: grams per plot of all tubers
ATY: gram per plot of tubers > 50 grams
Sprout: 0= none, 1=peeping, 2<=1.5cm, 3>=1.6
Eye depth rating: 1= shallow, 2=medium, 3=deep
Tuber shape rating: 1=round, 2=oval-ovate, 3=long
Maturity rating: 1=late to 5=early

Table 7. Average chip color scores of the clones selected in 2002 in the field for visual merit and re-evaluated in 2003 and 2004. Table sorted by mating type then by clone.

				2002	2003	2004		
Mating	**Clone**	**Female**	**Male**	**Morris**	**Morris**	**Becker**	**GF**	**Avg.**
2x-4x	DE02-110-07	C392	S440	7.0	7.0	7.0	7.0	7.00
2x-4x	DE02-128-08	E-29-1	C385	4.0	6.0	5.5	3.5	4.67
2x-4x	DE02-129-08	E-29-1	MSG-274-3	9.0	8.0	7.0	6.0	7.20
2x-4x	DE02-132-27	E-29-1	RH-122-3	7.0	6.0	6.5	6.5	6.50
2x-4x	DE02-132-32	E-29-1	RH-122-3	7.0	6.0	6.5	4.5	5.83
2x-4x	DE02-159-25	E-51-4	C307	6.0	6.0	6.5	6.0	6.17
2x-4x Average				**6.7**	**6.5**	**6.5**	**5.6**	**6.20**
4x-2x	DE02-006-05	Andover	C307	8.0	8.0	6.5	4.5	6.33
4x-2x	DE02-015-31	Atlantic	C396	9.0	8.0	7.0	4.5	6.67
4x-2x	DE02-015-41	Atlantic	C397	8.0	8.0	7.0	5.0	6.67
4x-2x	DE02-036-06	C182	C396	5.0	6.0	7.5	6.5	6.50
4x-2x	DE02-037-02	C182	MN-85393	7.0	7.0	5.5	6.0	6.20
4x-2x	DE02-037-36	C182	MN-85393	8.0	6.0	5.0	3.5	5.17
4x-2x	DE02-120-06	Cal-White	C396	8.0	7.0	7.5	5.0	6.67
4x-2x	DE02-120-18	Cal-White	C396	7.0	4.0	5.0	5.0	5.17
4x-2x	DE02-178-27	MSB-073-2	MN-85393	9.0	6.0	7.5	6.0	7.00
4x-2x	DE02-192-01	NY112	C190	6.0	5.0	7.5	5.5	6.17
4x-2x	DE02-196-09	NY112	C396	7.0	7.0	6.0	6.0	6.33
4x-2x	DE02-196-10	NY112	C396	8.0	7.0	7.0	6.5	7.00
4x-2x	DE02-196-33	NY112	C396	8.0	7.0	5.5	4.0	5.67
4x-2x	DE02-196-34	NY112	C396	7.0	7.0	5.5	6.0	6.17
4x-2x	DE02-205-41	RH-076-3	C396	5.0	5.0	6.0	5.5	5.50
4x-2x	DE02-213-01	RH-120-4	C396	7.0	7.0	5.5	5.0	5.83
4x-2x	DE02-213-34	RH-120-4	C396	7.0	7.0	6.0	6.0	6.33
4x-2x	DE02-216-16	RH-122-3	C396	8.0	7.0	7.0	5.0	6.50
4x-2x	DE02-216-21	RH-122-3	C396	8.0	7.0	7.0	7.0	7.17
4x-2x	DE02-216-24	RH-122-3	C396	8.0	7.0	6.5	5.5	6.50
4x-2x	DE02-216-43	RH-122-3	C396	6.0	7.0	7.5	6.5	6.83
4x-2x	DE02-254-01	Yukon Gold	C396	9.0	9.0	7.5	6.0	7.50
4x-2x	DE02-254-13	Yukon Gold	C396	8.0	.	6.0	4.5	5.80
4x-2x Average				**7.4**	**6.8**	**6.5**	**5.4**	**6.34**
4x-4x	DE02-016-20	Atlantic	ND-3828-15	5.0	4.0	5.5	4.0	4.67
4x-4x	DE02-016-21	Atlantic	ND-3828-15	5.0	5.0	6.0	3.5	4.83
4x-4x	DE02-016-26	Atlantic	ND-3828-15	5.0	4.0	4.0	3.0	3.83
4x-4x	DE02-101-21	C385	Andover	7.0	6.0	7.0	6.5	6.67
4x-4x	DE02-177-01	MSA-091-1	C41	8.0	7.0	6.0	4.0	5.83
4x-4x	DE02-177-03	MSA-091-1	C41	9.0	7.0	7.5	5.5	7.00
4x-4x	DE02-177-07	MSA-091-1	C41	10.0	.	7.5	5.5	7.20
4x-4x	DE02-179-21	MSE-250-1	C208	4.0	4.0	5.5	5.0	4.83
4x-4x Average				**6.6**	**5.3**	**6.1**	**4.6**	**5.57**
Grand Average				**7.1**	**6.4**	**6.4**	**5.3**	**6.15**

Table 8. Average horticultural and agronomic traits of clones selected for visual merit in 2002 in the field and re-evaluated in 2003 and 2004.

Mating	Clone	Female	Male	GTA	Gravity	TTY	ATY	Sprout	Eye Depth	Shape	Maturity
2x-4x	DE02-110-07	C392	S440	3.0	1.090	5081	4983	0.2	1.8	1.6	4.2
2x-4x	DE02-128-08	E-29-1	C385	2.6	1.090	4625	4245	0.2	1.4	2.0	4.2
2x-4x	DE02-129-08	E-29-1	MSG-274-3	2.3	1.094	4777	4288	0.3	1.5	2.0	3.8
2x-4x	DE02-132-27	E-29-1	RH-122-3	3.0	1.075	6124	4667	0.4	2.0	1.6	4.2
2x-4x	DE02-132-32	E-29-1	RH-122-3	2.6	1.088	9494	8345	0.4	1.8	1.8	4.0
2x-4x	DE02-159-25	E-51-4	C307	3.2	1.084	4138	3811	0.2	2.2	1.6	4.0
2x-4x Average				**2.8**	**1.087**	**5707**	**5057**	**0.3**	**1.8**	**1.8**	**4.1**
4x-2x	DE02-006-05	Andover	C307	2.6	1.085	5464	4443	0.2	1.6	1.8	4.2
4x-2x	DE02-015-31	Atlantic	C396	3.6	1.084	10321	9488	0.2	2.2	2.4	4.0
4x-2x	DE02-015-41	Atlantic	C397	2.0	1.088	5653	4169	0.4	1.8	1.8	3.8
4x-2x	DE02-036-06	C182	C396	3.0	1.087	6365	5000	0.4	2.0	2.2	4.2
4x-2x	DE02-037-02	C182	MN-85393	2.3	1.088	9993	8385	0.5	1.3	2.0	4.0
4x-2x	DE02-037-36	C182	MN-85393	2.2	1.086	5894	5109	0.2	1.6	2.4	4.0
4x-2x	DE02-120-06	Cal-White	C396	2.6	1.083	5782	3536	0.8	1.4	2.2	5.0
4x-2x	DE02-120-18	Cal-White	C396	3.6	1.081	6231	5476	0.6	2.2	1.8	4.4
4x-2x	DE02-178-27	MSB-073-2	MN-85393	1.6	1.085	7623	7622	0.4	1.8	2.0	4.2
4x-2x	DE02-192-01	NY112	C190	3.2	1.078	5906	4537	0.2	1.6	2.0	4.2
4x-2x	DE02-196-09	NY112	C396	3.0	1.090	6967	5888	0.4	1.6	1.8	4.2
4x-2x	DE02-196-10	NY112	C396	2.2	1.084	7768	7284	0.2	2.0	1.8	4.0
4x-2x	DE02-196-33	NY112	C396	2.6	1.076	8262	3320	0.2	2.4	2.2	4.0
4x-2x	DE02-196-34	NY112	C396	3.0	1.087	5277	5113	0.2	2.2	2.2	3.8
4x-2x	DE02-205-41	RH-076-3	C396	3.6	1.073	6232	5327	0.6	2.0	2.2	4.0
4x-2x	DE02-213-01	RH-120-4	C396	3.2	1.087	6134	5631	0.4	2.4	2.0	4.2
4x-2x	DE02-213-34	RH-120-4	C396	2.6	1.080	6830	6306	0.6	2.0	2.4	4.2
4x-2x	DE02-216-16	RH-122-3	C396	2.4	1.085	5335	3988	0.6	1.6	1.6	4.4
4x-2x	DE02-216-21	RH-122-3	C396	2.6	1.090	8284	5916	0.4	1.8	2.0	4.2
4x-2x	DE02-216-24	RH-122-3	C396	2.6	1.092	4360	3072	0.6	2.0	2.2	4.0
4x-2x	DE02-216-43	RH-122-3	C396	2.0	1.089	6256	5916	0.2	1.4	2.6	4.2
4x-2x	DE02-254-01	Yukon Gold	C396	3.2	1.214	7065	6304	0.2	1.8	2.2	4.2
4x-2x	DE02-254-13	Yukon Gold	C396	2.6	1.070	4299	2652	0.2	1.6	1.4	4.5
4x-2x Total				**2.7**	**1.090**	**6622**	**5413**	**0.4**	**1.8**	**2.1**	**4.2**
4x-4x	DE02-016-20	Atlantic	ND-3828-15	1.4	1.081	6176	6035	0.4	1.0	1.8	4.6
4x-4x	DE02-016-21	Atlantic	ND-3828-15	3.2	1.090	5838	4443	0.4	1.8	1.8	4.4
4x-4x	DE02-016-26	Atlantic	ND-3828-15	1.6	1.080	7277	7192	0.4	2.0	2.0	4.0
4x-4x	DE02-101-21	C385	Andover	2.0	1.087	3800	3559	0.2	1.6	1.8	4.0
4x-4x	DE02-177-01	MSA-091-1	C41	2.8	1.081	6738	5786	0.2	1.8	1.6	3.8
4x-4x	DE02-177-03	MSA-091-1	C41	3.0	1.082	7934	6610	0.2	2.0	2.0	3.6
4x-4x	DE02-177-07	MSA-091-1	C41	2.2	1.086	6647	6003	0.2	1.6	2.0	4.2
4x-4x	DE02-179-21	MSE-250-1	C208	2.6	1.096	5889	5800	0.6	1.8	1.6	4.0
4x-4x Total				**2.4**	**1.085**	**6287**	**5679**	**0.3**	**1.7**	**1.8**	**4.1**

Table 9. Average horticultural and agronomic trait values from the breeding efficiency trial planted in 2 replicated field plots grown and harvested in Grand Forks, ND and Becker, MN and the chip color score from the Morris, MN field plot grown in 2003. The table is sorted by mating type then by family.

2x-2x Matings				2003	2004		
Family	Female	Male	Data	Morris	Becker	GF	Avg.
17	C159	ADX-1523-1	Score Avg	6.1	5.6	5.5	5.7
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	51	16	34
			TTY Avg	.	4913	1867	3390
			ATY Avg	.	4525	1801	3163
			Gravity Avg	.	1.079	1.082	1.081
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	2.4	2.0	2.2
			Tuber Shape Avg	.	1.7	1.8	1.8
			Skin Color Avg	.	1.2	1.3	1.3
			GTA Avg	.	3.6	3.5	3.5
			Flesh Color Avg	.	1.8	1.4	1.6
			Maturity Avg	.	3.9	4.0	4.0
40	C190	C33	Score Avg	6.4	7.3	6.4	6.7
14 clones			Plant Count Avg	.	3	2	3
			Tuber Count Avg	.	31	13	21
			TTY Avg	.	2166	1566	1836
			ATY Avg	.	1611	1525	1564
			Gravity Avg	.	1.064	1.085	1.076
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.4	1.8	1.7
			Tuber Shape Avg	.	1.4	1.6	1.6
			Skin Color Avg	.	1.8	1.5	1.6
			GTA Avg	.	3.3	2.8	3.1
			Flesh Color Avg	.	2.1	1.7	1.9
			Maturity Avg	.	4.0	3.2	3.5
63	C307	C372	Score Avg	7.0	7.5	6.1	6.8
14 clones			Plant Count Avg	.	3	3	3
			Tuber Count Avg	.	28	13	21
			TTY Avg	.	1616	1300	1465
			ATY Avg	.	1140	1260	1197
			Gravity Avg	.	1.070	1.076	1.073
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.9	1.7	1.8
			Tuber Shape Avg	.	1.5	1.7	1.6
			Skin Color Avg	.	2.2	1.8	2.0
			GTA Avg	.	3.7	2.7	3.2
			Flesh Color Avg	.	2.2	1.7	2.0
			Maturity Avg	.	3.3	3.8	3.6

74	C336	C33	Score Avg	6.7	7.7	6.3	7.1
14 clones			Plant Count Avg	.	2	3	3
			Tuber Count Avg	.	15	8	13
			TTY Avg	.	1274	966	1172
			ATY Avg	.	1129	966	1075
			Gravity Avg	.	1.065	1.058	1.063
			Sprout Avg	.	0.0	0.5	0.1
			Eye Depth Avg	.	1.4	1.5	1.4
			Tuber Shape Avg	.	1.7	1.8	1.7
			Skin Color Avg	.	1.3	1.8	1.4
			GTA Avg	.	3.5	3.0	3.4
			Flesh Color Avg	.	1.7	1.8	1.7
			Maturity Avg	.	4.5	3.7	4.0
75	C336	C372	Score Avg	5.0	7.1	7.1	6.5
12 clones			Plant Count Avg	.	2	3	2
			Tuber Count Avg	.	12	6	9
			TTY Avg	.	799	663	735
			ATY Avg	.	577	629	601
			Gravity Avg	.	1.064	1.065	1.064
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.7	2.1	1.9
			Tuber Shape Avg	.	1.6	1.8	1.6
			Skin Color Avg	.	2.4	2.3	2.4
			GTA Avg	.	3.2	3.8	3.5
			Flesh Color Avg	.	2.3	3.1	2.7
			Maturity Avg	.	4.3	3.8	4.0
90	C367	C372	Score Avg	7.5	7.8	7.4	7.6
14 clones			Plant Count Avg	.	3	3	3
			Tuber Count Avg	.	13	8	11
			TTY Avg	.	640	556	602
			ATY Avg	.	391	508	444
			Gravity Avg	.	1.057	1.072	1.064
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.3	1.4	1.3
			Tuber Shape Avg	.	1.8	1.9	1.8
			Skin Color Avg	.	2.3	2.4	2.4
			GTA Avg	.	3.6	3.2	3.4
			Flesh Color Avg	.	2.3	2.3	2.3
			Maturity Avg	.	3.7	3.8	3.8

142	E-51-2	C33	Score Avg	6.3	6.7	6.4	6.5
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	41	12	26
			TTY Avg	.	4757	1384	3008
			ATY Avg	.	4537	1359	2889
			Gravity Avg	.	1.072	1.083	1.077
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	2.6	2.3	2.5
			Tuber Shape Avg	.	2.1	1.9	2.0
			Skin Color Avg	.	1.3	1.4	1.3
			GTA Avg	.	4.4	3.6	4.0
			Flesh Color Avg	.	1.9	1.7	1.8
			Maturity Avg	.	4.0	3.4	3.6
152	E-51-4	ADX-1523-1	Score Avg	6.1	7.0	6.3	6.6
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	35	15	25
			TTY Avg	.	4552	1601	3131
			ATY Avg	.	4324	1697	3111
			Gravity Avg	.	1.081	1.084	1.082
			Sprout Avg	.	0.4	0.0	0.2
			Eye Depth Avg	.	2.6	2.4	2.5
			Tuber Shape Avg	.	2.9	2.4	2.6
			Skin Color Avg	.	2.4	2.2	2.3
			GTA Avg	.	4.6	3.9	4.3
			Flesh Color Avg	.	1.5	1.6	1.6
			Maturity Avg	.	3.1	3.2	3.2
160	E-51-4	C33	Score Avg	5.4	6.6	6.5	6.3
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	38	16	28
			TTY Avg	.	3444	1824	2696
			ATY Avg	.	3094	1921	2578
			Gravity Avg	.	1.078	1.080	1.079
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	2.7	2.3	2.5
			Tuber Shape Avg	.	2.1	2.0	2.0
			Skin Color Avg	.	1.9	1.6	1.7
			GTA Avg	.	4.0	3.8	3.9
			Flesh Color Avg	.	1.7	1.6	1.7
			Maturity Avg	.	3.7	3.6	3.6

	MN-	ADX-					
175	85432	1523-1	Score Avg	5.4	7.1	5.6	6.2
14 clones			Plant Count Avg	.	4	3	4
			Tuber Count Avg	.	43	20	32
			TTY Avg	.	5191	2081	3694
			ATY Avg	.	4922	1982	3506
			Gravity Avg	.	1.078	1.084	1.081
			Sprout Avg	.	0.6	0.0	0.3
			Eye Depth Avg	.	2.6	2.2	2.4
			Tuber Shape Avg	.	2.6	2.1	2.4
			Skin Color Avg	.	2.1	1.3	1.7
			GTA Avg	.	4.7	3.8	4.3
			Flesh Color Avg	.	2.2	1.8	2.0
			Maturity Avg	.	3.9	3.4	3.6

2x-4x Matings				**2003**	**2004**		
Family	**Female**	**Male**	**Data**	**Morris**	**Becker**	**GF**	**Avg.**
58	C231	S438	Score Avg	6.8	6.7	6.3	6.6
10 clones			Plant Count Avg	.	3	4	3
			Tuber Count Avg	.	30	17	24
			TTY Avg	.	4601	1738	3170
			ATY Avg	.	4470	1704	3087
			Gravity Avg	.	1.078	1.081	1.079
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	2.0	1.9	1.9
			Tuber Shape Avg	.	2.0	1.8	1.9
			Skin Color Avg	.	1.4	1.6	1.5
			GTA Avg	.	3.2	3.2	3.2
			Flesh Color Avg	.	1.8	1.8	1.8
			Maturity Avg	.	4.0	3.4	3.6
98	C367	S440	Score Avg	7.7	6.6	5.9	6.5
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	34	20	27
			TTY Avg	.	2921	2243	2582
			ATY Avg	.	2671	2181	2417
			Gravity Avg	.	1.084	1.081	1.082
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.4	1.8	1.6
			Tuber Shape Avg	.	2.0	1.9	1.9
			Skin Color Avg	.	1.1	1.1	1.1
			GTA Avg	.	3.1	3.4	3.3
			Flesh Color Avg	.	1.4	1.1	1.3
			Maturity Avg	.	4.1	4.0	4.0

110	C392	S440	Score Avg	6.8	6.9	6.7	6.8
10 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	49	21	35
			TTY Avg	.	5597	2797	4197
			ATY Avg	.	5334	2744	4039
			Gravity Avg	.	1.073	1.080	1.076
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.2	2.2	1.7
			Tuber Shape Avg	.	2.0	2.1	2.1
			Skin Color Avg	.	1.2	1.3	1.3
			GTA Avg	.	2.5	3.0	2.8
			Flesh Color Avg	.	1.6	1.5	1.6
			Maturity Avg	.	4.2	4.0	4.1
113	C396	S438	Score Avg	5.5	6.3	5.8	5.9
4 clones			Plant Count Avg	.	4	3	4
			Tuber Count Avg	.	34	13	23
			TTY Avg	.	4516	1659	3087
			ATY Avg	.	4387	1633	3010
			Gravity Avg	.	1.087	1.082	1.084
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.5	1.8	1.6
			Tuber Shape Avg	.	2.3	2.0	2.1
			Skin Color Avg	.	2.0	1.5	1.8
			GTA Avg	.	4.0	3.5	3.8
			Flesh Color Avg	.	1.5	1.0	1.3
			Maturity Avg	.	4.0	4.0	4.0
128	E-29-1	C385	Score Avg	5.3	5.7	5.6	5.6
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	46	21	34
			TTY Avg	.	4584	2145	3413
			ATY Avg	.	4294	2087	3235
			Gravity Avg	.	1.095	1.089	1.092
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.9	1.6	1.8
			Tuber Shape Avg	.	2.0	1.8	1.9
			Skin Color Avg	.	1.2	1.2	1.2
			GTA Avg	.	3.3	3.3	3.3
			Flesh Color Avg	.	1.8	1.7	1.8
			Maturity Avg	.	4.3	3.7	3.9

135	E-29-1	S438	Score Avg	6.0	5.4	6.3	5.9
6 clones			Plant Count Avg	.	3	4	4
			Tuber Count Avg	.	33	19	25
			TTY Avg	.	4651	3011	3756
			ATY Avg	.	4525	3005	3696
			Gravity Avg	.	1.084	1.087	1.086
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.4	1.7	1.5
			Tuber Shape Avg	.	2.8	2.2	2.5
			Skin Color Avg	.	1.4	1.2	1.3
			GTA Avg	.	2.6	2.3	2.5
			Flesh Color Avg	.	1.2	2.2	1.7
			Maturity Avg	.	4.3	4.0	4.1
150	E-51-2	S440	Score Avg	5.0	6.5	6.5	6.2
2 clones			Plant Count Avg	.	4	3	4
			Tuber Count Avg	.	39	19	29
			TTY Avg	.	3613	2757	3185
			ATY Avg	.	3361	2715	3038
			Gravity Avg	.	1.072	1.084	1.078
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	3.0	1.5	2.3
			Tuber Shape Avg	.	2.0	1.5	1.8
			Skin Color Avg	.	1.0	1.5	1.3
			GTA Avg	.	4.5	2.5	3.5
			Flesh Color Avg	.	2.5	1.0	1.8
			Maturity Avg	.	4.0	4.0	4.0
4x-2x Matings				**2003**	**2004**		
Family	**Female**	**Male**	**Data**	**Morris**	**Becker**	**GF**	**Avg.**
7	Andover	C396	Score Avg	7.3	6.6	5.6	6.3
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	34	16	25
			TTY Avg	.	7492	2325	4908
			ATY Avg	.	7416	2234	4825
			Gravity Avg	.	1.062	1.078	1.070
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	2.1	1.9	2.0
			Tuber Shape Avg	.	2.0	1.8	1.9
			Skin Color Avg	.	1.2	1.1	1.2
			GTA Avg	.	2.9	3.1	3.0
			Flesh Color Avg	.	1.4	1.6	1.5
			Maturity Avg	.	3.7	3.8	3.8

15	Atlantic	C396	Score Avg	6.5	7.1	6.3	6.7
14 clones			Plant Count Avg	.	3	3	3
			Tuber Count Avg	.	25	16	20
			TTY Avg	.	5302	2528	3915
			ATY Avg	.	5285	2484	3885
			Gravity Avg	.	1.070	1.089	1.080
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.8	2.8	2.3
			Tuber Shape Avg	.	2.0	2.3	2.1
			Skin Color Avg	.	1.8	1.0	1.4
			GTA Avg	.	3.0	3.5	3.3
			Flesh Color Avg	.	1.8	2.0	1.9
			Maturity Avg	.	3.0	3.8	3.5
24	C181	C396	Score Avg	6.7	7.3	6.8	7.0
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	31	19	25
			TTY Avg	.	2418	1853	2135
			ATY Avg	.	2096	1767	1932
			Gravity Avg	.	1.086	1.086	1.086
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	2.2	1.9	2.0
			Tuber Shape Avg	.	2.3	1.8	2.0
			Skin Color Avg	.	1.4	1.0	1.2
			GTA Avg	.	3.6	3.3	3.5
			Flesh Color Avg	.	1.7	1.8	1.7
			Maturity Avg	.	3.6	3.7	3.7
25	C181	MN-85393	Score Avg	5.0	7.6	6.5	6.8
4 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	57	33	45
			TTY Avg	.	4550	2010	3280
			ATY Avg	.	3959	1704	2832
			Gravity Avg	.	1.102	1.093	1.098
			Sprout Avg	.	0.8	0.0	0.4
			Eye Depth Avg	.	2.0	2.5	2.3
			Tuber Shape Avg	.	1.8	2.3	2.0
			Skin Color Avg	.	1.0	1.0	1.0
			GTA Avg	.	3.8	3.8	3.8
			Flesh Color Avg	.	3.0	2.5	2.8
			Maturity Avg	.	3.0	3.5	3.3

37	C182	MN-85393	Score Avg	5.6	7.3	6.7	6.7
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	75	26	51
			TTY Avg	.	6858	2310	4584
			ATY Avg	.	6264	2185	4225
			Gravity Avg	.	1.093	1.086	1.090
			Sprout Avg	.	0.3	0.1	0.2
			Eye Depth Avg	.	2.5	2.4	2.4
			Tuber Shape Avg	.	1.6	1.8	1.7
			Skin Color Avg	.	1.1	1.3	1.2
			GTA Avg	.	2.9	3.1	3.0
			Flesh Color Avg	.	3.0	2.4	2.7
			Maturity Avg	.	3.7	3.8	3.8
38	C182	MN-85430	Score Avg	7.0	8.2	6.0	7.5
4 clones			Plant Count Avg	.	2	4	3
			Tuber Count Avg	.	13	14	13
			TTY Avg	.	997	2081	1268
			ATY Avg	.	851	2081	1158
			Gravity Avg	.	1.081	1.084	1.082
			Sprout Avg	.	0.3	0.0	0.3
			Eye Depth Avg	.	2.3	1.0	2.0
			Tuber Shape Avg	.	2.3	2.0	2.3
			Skin Color Avg	.	2.3	1.0	2.0
			GTA Avg	.	3.7	3.0	3.5
			Flesh Color Avg	.	3.0	1.0	2.5
			Maturity Avg	.	4.0	3.5	3.7
43	C20	C190	Score Avg	7.3	7.4	6.7	7.0
8 clones			Plant Count Avg	.	2	4	3
			Tuber Count Avg	.	15	16	15
			TTY Avg	.	2221	2479	2361
			ATY Avg	.	2145	2450	2311
			Gravity Avg	.	1.088	1.084	1.086
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	2.8	1.8	2.2
			Tuber Shape Avg	.	2.0	1.8	1.9
			Skin Color Avg	.	1.3	1.0	1.1
			GTA Avg	.	4.8	2.8	3.6
			Flesh Color Avg	.	1.5	1.5	1.5
			Maturity Avg	.	3.3	4.0	3.8

108	C385	MN-85430	Score Avg	5.9	7.6	6.8	6.9
14 clones			Plant Count Avg	.	4	3	4
			Tuber Count Avg	.	33	14	24
			TTY Avg	.	2475	1619	2047
			ATY Avg	.	2140	1593	1867
			Gravity Avg	.	1.086	1.084	1.085
			Sprout Avg	.	0.1	0.0	0.0
			Eye Depth Avg	.	1.7	2.2	1.9
			Tuber Shape Avg	.	1.8	2.0	1.9
			Skin Color Avg	.	2.0	1.5	1.8
			GTA Avg	.	3.6	3.2	3.4
			Flesh Color Avg	.	2.5	1.9	2.2
			Maturity Avg	.	4.0	3.6	3.7
178	MSB-073-2	MN-85393	Score Avg	7.0	6.4	6.8	6.7
6 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	74	25	50
			TTY Avg	.	7764	2439	5102
			ATY Avg	.	7256	2303	4779
			Gravity Avg	.	1.085	1.069	1.077
			Sprout Avg	.	0.2	0.0	0.1
			Eye Depth Avg	.	1.8	2.2	2.0
			Tuber Shape Avg	.	1.8	1.8	1.8
			Skin Color Avg	.	1.5	1.0	1.3
			GTA Avg	.	2.3	3.0	2.7
			Flesh Color Avg	.	3.0	2.2	2.6
			Maturity Avg	.	3.3	3.0	3.1
183	MSG-274-3	C396	Score Avg	8.0	7.6	6.4	7.3
10 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	51	17	35
			TTY Avg	.	7452	2488	5101
			ATY Avg	.	7217	2429	4949
			Gravity Avg	.	1.075	1.084	1.079
			Sprout Avg	.	0.1	0.0	0.1
			Eye Depth Avg	.	2.0	1.9	1.9
			Tuber Shape Avg	.	2.1	1.8	1.9
			Skin Color Avg	.	1.3	1.2	1.3
			GTA Avg	.	3.7	3.2	3.5
			Flesh Color Avg	.	1.7	1.9	1.8
			Maturity Avg	.	3.8	3.8	3.8

197	NY112	MN-85393	Score Avg	7.7	6.8	6.2	6.6
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	52	20	37
			TTY Avg	.	8238	2731	5586
			ATY Avg	.	8039	2851	5541
			Gravity Avg	.	1.074	1.079	1.076
			Sprout Avg	.	0.3	0.0	0.1
			Eye Depth Avg	.	2.1	2.2	2.1
			Tuber Shape Avg	.	2.1	2.0	2.1
			Skin Color Avg	.	1.4	1.4	1.4
			GTA Avg	.	3.0	2.8	2.9
			Flesh Color Avg	.	2.7	2.0	2.4
			Maturity Avg	.	3.7	3.3	3.4
199	RHST99-071-20	C190	Score Avg	7.0	6.8	6.2	6.6
6 clones			Plant Count Avg	.	4	3	4
			Tuber Count Avg	.	43	11	27
			TTY Avg	.	5395	1017	3206
			ATY Avg	.	5229	889	3059
			Gravity Avg	.	1.908	1.068	1.488
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.8	1.2	1.5
			Tuber Shape Avg	.	2.2	1.8	2.0
			Skin Color Avg	.	1.8	1.3	1.6
			GTA Avg	.	3.3	2.7	3.0
			Flesh Color Avg	.	1.8	1.7	1.8
			Maturity Avg	.	4.3	3.8	4.0
205	RHTR99-076-3	C396	Score Avg	6.3	6.8	6.5	6.6
6 clones			Plant Count Avg	.	4	3	4
			Tuber Count Avg	.	32	13	23
			TTY Avg	.	4513	1685	3099
			ATY Avg	.	4383	1661	3022
			Gravity Avg	.	1.077	1.083	1.080
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	2.2	1.8	2.0
			Tuber Shape Avg	.	1.8	1.8	1.8
			Skin Color Avg	.	1.0	1.0	1.0
			GTA Avg	.	3.2	3.2	3.2
			Flesh Color Avg	.	2.0	2.0	2.0
			Maturity Avg	.	4.3	3.8	4.0

220	RHST99-135-1	C190	Score Avg	5.8	6.9	6.1	6.4
12 clones			Plant Count Avg	.	4	3	3
			Tuber Count Avg	.	29	19	25
			TTY Avg	.	3126	2401	2815
			ATY Avg	.	2930	2235	2632
			Gravity Avg	.	1.087	1.081	1.084
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.3	2.0	1.6
			Tuber Shape Avg	.	2.3	1.7	2.0
			Skin Color Avg	.	1.3	1.1	1.2
			GTA Avg	.	2.8	2.9	2.9
			Flesh Color Avg	.	1.9	1.4	1.7
			Maturity Avg	.	4.0	3.8	3.9
225	RHTR99-138-2	MN-85393	Score Avg	6.5	6.4	6.3	6.4
12 clones			Plant Count Avg	.	4	3	4
			Tuber Count Avg	.	62	16	39
			TTY Avg	.	7743	2299	5021
			ATY Avg	.	7413	2686	5049
			Gravity Avg	.	1.080	1.074	1.077
			Sprout Avg	.	0.2	0.0	0.1
			Eye Depth Avg	.	1.7	1.7	1.7
			Tuber Shape Avg	.	1.9	1.8	1.9
			Skin Color Avg	.	1.5	1.2	1.3
			GTA Avg	.	2.3	2.4	2.4
			Flesh Color Avg	.	3.0	2.6	2.8
			Maturity Avg	.	3.5	3.8	3.7
234	S438	C396	Score Avg	7.2	5.5	5.6	5.8
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	50	17	33
			TTY Avg	.	6831	2536	4683
			ATY Avg	.	6653	2509	4581
			Gravity Avg	.	1.086	1.087	1.086
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.6	1.5	1.6
			Tuber Shape Avg	.	2.1	1.9	2.0
			Skin Color Avg	.	1.6	1.4	1.5
			GTA Avg	.	3.1	2.7	2.9
			Flesh Color Avg	.	2.4	1.4	1.9
			Maturity Avg	.	4.3	4.0	4.1

4x-4x Matings				2003	2004		
Family	Female	Male	Data	Morris	Becker	GF	Avg.
83	C341	Zarewo	Score Avg	7.6	7.4	6.9	7.2
14 clones			Plant Count Avg	.	4	3	3
			Tuber Count Avg	.	38	14	26
			TTY Avg	.	5218	2070	3644
			ATY Avg	.	5074	2019	3547
			Gravity Avg	.	1.095	1.087	1.091
			Sprout Avg	.	0.2	0.0	0.1
			Eye Depth Avg	.	1.3	1.7	1.5
			Tuber Shape Avg	.	2.0	2.3	2.2
			Skin Color Avg	.	2.1	1.6	1.8
			GTA Avg	.	2.8	3.5	3.2
			Flesh Color Avg	.	1.8	1.8	1.8
			Maturity Avg	.	3.7	3.5	3.6
176	MN-85554	C181	Score Avg	7.4	8.3	6.8	7.5
14 clones			Plant Count Avg	.	4	3	4
			Tuber Count Avg	.	24	12	18
			TTY Avg	.	3393	1163	2237
			ATY Avg	.	3337	1184	2260
			Gravity Avg	.	1.089	1.003	1.043
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	2.6	2.2	2.4
			Tuber Shape Avg	.	2.3	1.9	2.1
			Skin Color Avg	.	1.3	1.0	1.1
			GTA Avg	.	4.1	3.3	3.7
			Flesh Color Avg	.	1.8	1.6	1.7
			Maturity Avg	.	3.6	3.9	3.8
187	ND-3828-15	Zarewo	Score Avg	6.4	5.6	6.4	6.1
14 clones			Plant Count Avg	.	4	3	4
			Tuber Count Avg	.	37	14	26
			TTY Avg	.	6189	2650	4420
			ATY Avg	.	6096	2633	4365
			Gravity Avg	.	1.091	1.079	1.085
			Sprout Avg	.	0.1	0.0	0.1
			Eye Depth Avg	.	1.2	1.6	1.4
			Tuber Shape Avg	.	2.0	1.9	2.0
			Skin Color Avg	.	2.3	1.7	2.0
			GTA Avg	.	1.9	2.2	2.1
			Flesh Color Avg	.	1.9	1.6	1.8
			Maturity Avg	.	4.0	3.8	3.9

208	RHTR99-076-3	S438	Score Avg	5.4	5.7	5.2	5.5
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	50	16	33
			TTY Avg	.	7768	2669	5218
			ATY Avg	.	7591	2626	5108
			Gravity Avg	.	1.093	1.085	1.089
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.2	1.6	1.4
			Tuber Shape Avg	.	1.9	1.8	1.8
			Skin Color Avg	.	1.1	1.2	1.1
			GTA Avg	.	2.2	2.5	2.3
			Flesh Color Avg	.	1.7	1.4	1.5
			Maturity Avg	.	3.7	3.6	3.7
243	Snowden	S438	Score Avg	6.7	7.0	6.6	6.8
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	38	13	26
			TTY Avg	.	7840	1900	5099
			ATY Avg	.	7798	1865	5059
			Gravity Avg	.	1.080	1.085	1.083
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.4	1.6	1.5
			Tuber Shape Avg	.	2.1	1.7	1.9
			Skin Color Avg	.	1.5	1.3	1.4
			GTA Avg	.	1.7	2.5	2.1
			Flesh Color Avg	.	1.9	1.3	1.6
			Maturity Avg	.	3.9	4.1	4.0
244	Snowden	S440	Score Avg	7.0	6.5	5.9	6.4
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	46	18	32
			TTY Avg	.	8187	2989	5684
			ATY Avg	.	8087	2933	5606
			Gravity Avg	.	1.076	1.082	1.079
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.5	1.4	1.4
			Tuber Shape Avg	.	2.1	1.9	2.0
			Skin Color Avg	.	1.3	1.2	1.3
			GTA Avg	.	2.5	2.5	2.5
			Flesh Color Avg	.	1.9	1.6	1.7
			Maturity Avg	.	4.1	3.7	3.9

245	W-1355-1	C181	Score Avg	7.0	7.6	6.9	7.2
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	47	20	34
			TTY Avg	.	6274	2841	4558
			ATY Avg	.	6034	2805	4419
			Gravity Avg	.	1.089	1.088	1.088
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.7	1.8	1.8
			Tuber Shape Avg	.	1.8	1.9	1.8
			Skin Color Avg	.	1.2	1.3	1.3
			GTA Avg	.	3.0	3.2	3.1
			Flesh Color Avg	.	1.9	1.5	1.7
			Maturity Avg	.	3.4	3.7	3.6
256	Yukon Gold	S438	Score Avg	7.9	7.2	6.7	7.1
14 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	47	15	32
			TTY Avg	.	8554	2196	5619
			ATY Avg	.	8397	2023	5328
			Gravity Avg	.	1.085	1.086	1.085
			Sprout Avg	.	0.0	0.0	0.0
			Eye Depth Avg	.	1.2	1.6	1.4
			Tuber Shape Avg	.	2.2	1.9	2.1
			Skin Color Avg	.	1.3	1.0	1.2
			GTA Avg	.	1.9	2.8	2.3
			Flesh Color Avg	.	1.8	1.4	1.6
			Maturity Avg	.	3.9	3.8	3.8
00221DP	Unknown	Unknown	Score Avg	.	7.8	7.5	7.6
10 clones			Plant Count Avg	.	4	3	4
			Tuber Count Avg	.	25	12	19
			TTY Avg	.	4212	1617	3059
			ATY Avg	.	4156	1569	3006
			Gravity Avg	.	1.083	1.077	1.080
			Sprout Avg	.	0.5	0.0	0.3
			Eye Depth Avg	.	1.8	2.1	1.9
			Tuber Shape Avg	.	2.1	1.8	1.9
			Skin Color Avg	.	3.0	2.3	2.7
			GTA Avg	.	2.3	3.0	2.6
			Flesh Color Avg	.	2.5	1.3	1.9
			Maturity Avg	.	3.2	3.3	3.3

00236DP	Unknown	Unknown	Score Avg	.	7.3	6.6	7.0
8 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	37	15	27
			TTY Avg	.	3942	2498	3268
			ATY Avg	.	3720	2475	3139
			Gravity Avg	.	1.081	1.084	1.082
			Sprout Avg	.	0.1	0.0	0.1
			Eye Depth Avg	.	1.1	1.6	1.3
			Tuber Shape Avg	.	1.8	2.0	1.9
			Skin Color Avg	.	2.8	2.1	2.5
			GTA Avg	.	2.1	2.6	2.3
			Flesh Color Avg	.	1.6	1.9	1.7
			Maturity Avg	.	4.5	3.8	4.0
22N	S438	C181	Score Avg	.	7.1	6.2	6.6
20 clones			Plant Count Avg	.	4	4	4
			Tuber Count Avg	.	48	18	33
			TTY Avg	.	5300	2296	3757
			ATY Avg	.	5019	2243	3594
			Gravity Avg	.	1.089	1.086	1.088
			Sprout Avg	.	0.2	0.0	0.1
			Eye Depth Avg	.	1.6	1.5	1.6
			Tuber Shape Avg	.	2.4	1.8	2.1
			Skin Color Avg	.	1.3	1.0	1.1
			GTA Avg	.	3.4	2.4	2.9
			Flesh Color Avg	.	1.5	1.3	1.4
			Maturity Avg	.	3.7	3.7	3.7
Chip color score Grand Average					6.5	6.9	6.3
Plant Count Grand Average						.	4
Tuber Count Grand Average						.	40
TTY Grand Average					.	5008	2060
ATY Grand Average					.	4778	2030
Specific Gravity Grand Average						.	1.091
Sprout Grand Average					.	0.1	0.0
Eye Depth Grand Average						.	1.8
Tuber Shape Grand Average						.	2.0
Skin Color Grand Average				.	1.6	1.4	1.5
GTA Grand Average				.	3.2	3.1	3.1
Flesh Color Grand Average				.	2.0	1.7	1.8
Maturity Grand Average				.	3.8	3.7	3.7

Score = Chip color score rating: 1 (excellent) to 10 (poor) with 4 or less “acceptable”
TTY: grams per plot of all tubers
ATY: gram per plot of tubers > 50 grams
Gravity = Specific gravity: calculation: weight in air/(weight in air-weight in water)
Sprout: 0= none, 1=peeping, 2<=1.5cm, 3>=1.6
Eye depth rating: 1= shallow, 2=medium, 3=deep
Tuber shape rating: 1=round, 2=oval-ovate, 3=long
Tuber shape rating: 1=round, 2=oval-ovate, 3=long
Skin color rating: 1=buff, 2=brown, 3=other (purple, red, etc)
GTA rating: 1(excellent) to 5 (poor)
Flesh color rating: 1=white, 2=cream, 3=yellow, 4=other (purple, variable, etc)
Maturity rating: 1=late to 5=early

Table 10. Average horticultural and agronomic trait values from the first year of the 2x-2x trial planted in 2 replicated field plots grown at Grand Forks, ND and Becker, MN in 2004.

				Becker		GF		
Family	**Female**	**Male**	**Values**	**1**	**2**	**1**	**2**	**Avg.**
1	ADX-1523-1	C159	Chip color Avg	5.8	5.6	5.0	5.0	5.4
5 clones			TTY Avg	6131	4768	1417	1671	3497
			GTA Avg	3.6	2.8	2.8	2.2	2.9
			Plant Count Avg	3.6	3.6	3.6	3.4	3.6
			Tuber Count Avg	53.0	42.4	15.6	18.4	32.4
			Yield per plant Avg	1648	1366	.	.	1507
			Maturity Avg	4.4	4.4	3.6	4.2	4.2
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	2.0	2.0	1.6	1.4	1.8
			Tuber Shape Avg	1.8	1.2	1.6	1.4	1.5
			Eye Depth Avg	2.4	2.4	1.4	1.8	2.0
			Skin Color Avg	1.6	1.8	2.2	1.4	1.8
2	ADX-1523-1	C213	Chip color Avg	6.8	6.0	4.4	4.8	5.5
8 clones			TTY Avg	3128	4405	1239	1565	2584
			GTA Avg	2.9	3.3	2.9	2.6	2.9
			Plant Count Avg	3.9	3.6	3.6	3.1	3.6
			Tuber Count Avg	34.6	52.1	13.9	17.9	29.6
			Yield per plant Avg	807	1210	.	.	1008
			Maturity Avg	4.4	4.1	4.3	4.1	4.2
			Sprouting Avg	0	0.25	0	0	0.0625
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	2.0	1.9	1.4	1.4	1.7
			Tuber Shape Avg	1.5	1.4	1.4	1.5	1.4
			Eye Depth Avg	2.0	2.0	1.8	1.8	1.9
			Skin Color Avg	2.3	2.1	2.3	2.3	2.2
39	C189	ADX-1523-1	Chip color Avg	6.4	6.8	6.6	6.7	6.7
10 clones			TTY Avg	3195	3982	1421	989	2385
			GTA Avg	3.3	3.1	3.0	3.3	3.2
			Plant Count Avg	3.4	3.3	3.8	3.4	3.5
			Tuber Count Avg	34.2	37.6	13.8	12.5	24.5
			Yield per plant Avg	959	1166	.	.	1062
			Maturity Avg	3.9	3.9	3.4	3.5	3.7
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	2.0	1.8	1.4	1.7	1.7
			Tuber Shape Avg	1.8	1.6	1.8	1.4	1.6
			Eye Depth Avg	2.4	2.0	2.1	1.9	2.1
			Skin Color Avg	1.4	2.2	1.4	1.7	1.7

51	C213	C189	Chip color Avg	6.5	7.3	7.5	7.5	7.2
2 clones			TTY Avg	2014	1706	409	458	1146
			GTA Avg	3.0	3.0	3.5	3.5	3.3
			Plant Count Avg	3.5	4.0	4.0	4.0	3.9
			Tuber Count Avg	20.5	16.5	6.0	6.5	12.4
			Yield per plant Avg	637	426	.	.	532
			Maturity Avg	4.5	4.5	4.0	4.0	4.3
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	2.0	2.5	1.5	2.0	2.0
			Tuber Shape Avg	2.5	2.5	1.5	2.0	2.1
			Eye Depth Avg	2.0	1.5	1.5	1.0	1.5
			Skin Color Avg	1.5	1.0	1.0	1.5	1.3
		ADX-1523-						
52	C231	1	Chip color Avg	6.1	6.1	5.2	5.0	5.6
10 clones			TTY Avg	3463	3516	1524	1382	2444
			GTA Avg	3.0	2.9	2.4	2.8	2.8
			Plant Count Avg	3.7	3.8	3.7	3.6	3.7
			Tuber Count Avg	34.5	33.1	17.1	15.3	24.8
			Yield per plant Avg	969	916	.	.	944
			Maturity Avg	4.1	3.5	3.8	3.7	3.8
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	1.5	1.9	1.3	1.2	1.5
			Tuber Shape Avg	1.9	1.8	1.5	1.5	1.7
			Eye Depth Avg	2.0	2.2	1.5	1.3	1.8
			Skin Color Avg	1.5	1.9	1.8	1.6	1.7
		ADX-1523-						
59	C254	1	Chip color Avg	5.9	6.8	5.6	5.3	5.9
10 clones			TTY Avg	3505	3515	2199	1632	2713
			GTA Avg	3.2	3.1	3.1	2.4	3.0
			Plant Count Avg	3.3	3.3	3.8	3.7	3.5
			Tuber Count Avg	43.1	43.4	21.4	18.7	31.7
			Yield per plant Avg	1135	1148	.	.	1141
			Maturity Avg	4.2	4.1	4.0	4.0	4.1
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	1.8	1.7	1.4	1.1	1.5
			Tuber Shape Avg	1.7	1.6	1.9	1.6	1.7
			Eye Depth Avg	2.0	1.8	1.9	1.8	1.9
			Skin Color Avg	2.3	2.4	2.4	2.1	2.3

61	C301	C190	Chip color Avg	7.1	6.6	6.6	6.7	6.8
9 clones			TTY Avg	2050	1767	825	1044	1434
			GTA Avg	3.4	3.0	2.6	2.3	2.8
			Plant Count Avg	3.2	3.2	2.7	3.1	3.1
			Tuber Count Avg	27.5	24.1	13.1	15.0	20.1
			Yield per plant Avg	631	.	.	.	.
			Maturity Avg	4.3	3.7	3.8	3.6	3.9
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	1.9	1.8	1.3	1.3	1.5
			Tuber Shape Avg	1.8	1.5	1.1	1.3	1.4
			Eye Depth Avg	1.3	1.5	1.3	1.3	1.3
			Skin Color Avg	1.9	1.8	1.0	1.1	1.5
62	C307	ADX-1523-1	Chip color Avg	6.9	6.4	6.2	5.8	6.3
10 clones			TTY Avg	5027	4170	2233	1836	3295
			GTA Avg	3.4	3.6	3.4	3.5	3.5
			Plant Count Avg	3.7	3.9	4.0	3.5	3.8
			Tuber Count Avg	51.1	42.4	21.3	15.8	32.4
			Yield per plant Avg	1385	1067	.	.	1235
			Maturity Avg	3.1	3.5	3.0	3.2	3.2
			Sprouting Avg	0.1	0	0	0	0.03
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	1.5	1.7	1.5	1.2	1.5
			Tuber Shape Avg	1.8	1.8	1.7	1.8	1.8
			Eye Depth Avg	2.0	1.9	2.3	2.4	2.2
			Skin Color Avg	2.3	2.4	2.0	2.3	2.3
64	C307	C43	Chip color Avg	7.0	7.5	6.0	7.0	6.8
2 clones			TTY Avg	1922	2933	572	640	1595
			GTA Avg	3.0	3.0	3.5	3.0	3.2
			Plant Count Avg	3.0	3.5	2.0	3.0	2.9
			Tuber Count Avg	31.0	36.5	7.0	13.0	21.8
			Yield per plant Avg	641	765	.	.	724
			Maturity Avg	4.0	4.0	4.0	4.0	4.0
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	2.0	2.0	2.0	2.0	2.0
			Tuber Shape Avg	1.0	2.0	2.0	2.0	1.8
			Eye Depth Avg	2.0	2.5	1.5	3.0	2.2
			Skin Color Avg	1.0	1.5	1.0	3.0	1.5

65	C307	C435	Chip color Avg	6.3	6.8	6.7	6.9	6.7
10 clones			TTY Avg	2128	3403	1087	1143	1897
			GTA Avg	3.3	3.2	2.9	3.0	3.1
			Plant Count Avg	3.6	3.7	3.3	3.5	3.5
			Tuber Count Avg	25.2	36.9	12.1	16.1	22.1
			Yield per plant Avg	600	941	.	.	770
			Maturity Avg	4.1	4.0	4.0	4.0	4.0
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	1.8	1.9	1.6	1.4	1.7
			Tuber Shape Avg	2.1	1.8	1.7	1.6	1.8
			Eye Depth Avg	1.9	1.8	1.4	1.8	1.7
			Skin Color Avg	1.0	1.1	1.0	1.0	1.0
89	C367	C33	Chip color Avg	7.0	7.0	6.0	7.0	6.8
1 clone			TTY Avg	2526	3075	498	716	1704
			GTA Avg	2.0	2.0	2.0	3.0	2.3
			Plant Count Avg	4.0	4.0	3.0	3.0	3.5
			Tuber Count Avg	41.0	37.0	8.0	13.0	24.8
			Yield per plant Avg	632	769	.	.	700
			Maturity Avg	2.0	5.0	4.0	4.0	3.8
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	2.0	2.0	2.0	2.0	2.0
			Tuber Shape Avg	2.0	2.0	2.0	2.0	2.0
			Eye Depth Avg	1.0	1.0	1.0	1.0	1.0
			Skin Color Avg	1.0	1.0	1.0	1.0	1.0
100	C374	ADX-1523-1	Chip color Avg	6.7	6.4	4.8	4.8	5.7
10 clones			TTY Avg	5225	5157	1248	2211	3417
			GTA Avg	3.4	3.1	2.6	3.2	3.1
			Plant Count Avg	3.8	3.6	3.4	3.5	3.6
			Tuber Count Avg	41.6	39.0	11.7	15.3	26.6
			Yield per plant Avg	1351	1370	.	.	1360
			Maturity Avg	3.9	3.5	3.4	3.4	3.6
			Sprouting Avg	0	0.3	0	0	0.075
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	1.4	1.7	1.1	1.2	1.4
			Tuber Shape Avg	2.0	2.0	1.9	1.8	1.9
			Eye Depth Avg	1.7	1.6	1.5	1.5	1.6
			Skin Color Avg	2.0	2.1	2.0	2.1	2.1

109	C392	C190	Chip color Avg	7.0	7.1	7.0	7.8	7.2
4 clones			TTY Avg	2609	3127	1106	1175	1964
			GTA Avg	2.3	2.5	3.5	3.0	2.9
			Plant Count Avg	3.8	3.8	3.3	3.3	3.5
			Tuber Count Avg	30.3	37.5	15.8	15.8	24.5
			Yield per plant Avg	704	804	.	.	761
			Maturity Avg	3.3	3.8	3.8	3.8	3.6
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	1.0	1.5	1.5	1.5	1.4
			Tuber Shape Avg	2.0	1.8	2.0	1.8	1.9
			Eye Depth Avg	1.3	1.3	3.5	1.3	1.9
			Skin Color Avg	1.0	1.0	1.0	1.0	1.0
112	C396	MN-85430	Chip color Avg	7.2	8.0	6.7	6.3	7.0
3 clones			TTY Avg	4000	4370	917	1203	2623
			GTA Avg	3.7	4.0	3.3	3.7	3.7
			Plant Count Avg	4.0	4.0	4.0	3.3	3.8
			Tuber Count Avg	43.3	40.7	13.7	13.3	27.8
			Yield per plant Avg	1000	1092	.	.	1046
			Maturity Avg	3.7	2.7	3.3	3.3	3.3
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.0	1.1	1.1	1.1
			Flesh Color Avg	3.0	3.0	2.7	3.0	2.9
			Tuber Shape Avg	2.0	2.0	1.7	2.3	2.0
			Eye Depth Avg	2.7	2.7	2.7	2.3	2.6
			Skin Color Avg	1.7	2.0	1.7	1.7	1.8
140	E-51-2	C215	Chip color Avg	7.4	7.2	7.7	7.6	7.5
10 clones			TTY Avg	2024	2549	896	847	1527
			GTA Avg	3.8	3.8	2.9	3.5	3.5
			Plant Count Avg	3.0	3.4	3.3	3.4	3.3
			Tuber Count Avg	23.4	27.0	10.4	11.5	17.6
			Yield per plant Avg	673	675	.	.	674
			Maturity Avg	2.9	3.6	3.2	2.8	3.1
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	2.0	2.0	1.6	1.5	1.8
			Tuber Shape Avg	1.5	1.9	1.4	1.5	1.6
			Eye Depth Avg	2.4	2.1	1.8	1.8	2.0
			Skin Color Avg	1.1	1.4	1.0	1.3	1.2

141	E-51-2	C307	Chip color Avg	6.0	4.5	7.0	3.0	5.1
1 clone			TTY Avg	2953	4783	1149	2751	2909
			GTA Avg	4.0	4.0	4.0	3.0	3.8
			Plant Count Avg	4.0	4.0	4.0	4.0	4.0
			Tuber Count Avg	39.0	47.0	18.0	30.0	33.5
			Yield per plant Avg	738	1196	.	.	967
			Maturity Avg	2.0	4.0	4.0	4.0	3.5
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	2.0	2.0	1.0	1.0	1.5
			Tuber Shape Avg	2.0	2.0	2.0	2.0	2.0
			Eye Depth Avg	2.0	2.0	3.0	3.0	2.5
			Skin Color Avg	1.0	1.0	1.0	1.0	1.0
153	E-51-4	C159	Chip color Avg	5.5	5.3	5.0	4.5	5.1
2 clones			TTY Avg	2584	2827	701	960	1768
			GTA Avg	3.0	3.0	3.5	3.5	3.3
			Plant Count Avg	3.5	3.0	4.0	3.5	3.5
			Tuber Count Avg	31.5	32.0	12.0	12.5	22.0
			Yield per plant Avg	679	815	.	.	747
			Maturity Avg	4.0	3.5	4.0	4.0	3.9
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	2.5	2.5	2.0	2.5	2.4
			Tuber Shape Avg	3.0	2.0	2.0	2.0	2.3
			Eye Depth Avg	2.0	2.0	2.0	2.0	2.0
			Skin Color Avg	2.0	1.0	1.0	1.0	1.3
155	E-51-4	C189	Chip color Avg	7.0	7.0	5.5	6.5	6.6
3 clones			TTY Avg	3006	1227	837	1285	1746
			GTA Avg	3.3	3.0	4.0	3.0	3.3
			Plant Count Avg	3.7	4.0	3.3	3.3	3.6
			Tuber Count Avg	34.7	19.5	12.0	17.0	22.3
			Yield per plant Avg	912	307	.	.	670
			Maturity Avg	3.3	4.3	3.7	3.3	3.7
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	2.3	2.0	3.0	2.0	2.3
			Tuber Shape Avg	2.0	1.7	2.5	1.5	1.9
			Eye Depth Avg	2.3	1.7	2.0	1.5	1.9
			Skin Color Avg	1.3	1.3	1.0	1.0	1.2

156	E-51-4	C213	Chip color Avg	6.3	7.1	6.8	6.6	6.7
8 clones			TTY Avg	4214	4575	1418	1739	2986
			GTA Avg	3.5	2.8	3.6	3.9	3.4
			Plant Count Avg	3.9	4.0	3.5	3.8	3.8
			Tuber Count Avg	43.0	49.3	15.0	15.3	30.6
			Yield per plant Avg	1101	1144	.	.	1122
			Maturity Avg	3.9	3.4	3.4	3.8	3.6
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	2.0	2.0	1.4	1.5	1.7
			Tuber Shape Avg	2.3	1.9	2.5	2.1	2.2
			Eye Depth Avg	2.0	2.1	1.9	2.1	2.0
			Skin Color Avg	1.5	1.9	1.5	1.1	1.5
157	E-51-4	C215	Chip color Avg	7.5	7.3	7.7	7.2	7.4
6 clones			TTY Avg	1933	3117	523	925	1624
			GTA Avg	3.8	3.2	3.8	3.8	3.7
			Plant Count Avg	3.0	3.7	3.7	3.8	3.5
			Tuber Count Avg	26.2	35.0	8.0	11.3	20.1
			Yield per plant Avg	743	800	.	.	771
			Maturity Avg	4.2	3.8	3.2	3.3	3.6
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	2.2	1.8	1.5	1.3	1.7
			Tuber Shape Avg	1.6	2.2	2.0	2.2	2.0
			Eye Depth Avg	1.8	1.5	1.2	2.0	1.6
			Skin Color Avg	1.6	1.5	1.0	1.0	1.3
158	E-51-4	C254	Chip color Avg	6.9	6.8	6.7	6.5	6.7
10 clones			TTY Avg	2775	3095	1320	1806	2227
			GTA Avg	2.7	3.4	2.8	2.8	2.9
			Plant Count Avg	2.9	3.1	3.6	3.2	3.2
			Tuber Count Avg	32.1	46.1	17.0	17.9	27.8
			Yield per plant Avg	1112	984	.	.	1051
			Maturity Avg	3.1	3.4	3.1	3.1	3.2
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	2.2	1.9	1.4	1.4	1.7
			Tuber Shape Avg	1.4	1.9	1.7	2.0	1.7
			Eye Depth Avg	1.7	2.1	1.5	1.6	1.7
			Skin Color Avg	1.0	1.3	1.0	1.2	1.1

159	E-51-4	C307	Chip color Avg	7.5	7.5	7.3	7.2	7.4
10 clones			TTY Avg	3189	3274	1848	2030	2585
			GTA Avg	4.1	3.5	4.1	3.9	3.9
			Plant Count Avg	3.9	3.8	3.4	3.8	3.7
			Tuber Count Avg	29.0	34.2	16.1	19.2	24.6
			Yield per plant Avg	832	871	.	.	852
			Maturity Avg	3.8	3.4	3.5	3.6	3.6
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	2.0	2.0	2.0	1.8	2.0
			Tuber Shape Avg	2.4	2.3	2.4	2.4	2.4
			Eye Depth Avg	2.7	2.1	2.8	2.4	2.5
			Skin Color Avg	1.8	1.2	1.8	1.2	1.5
160	E-51-4	C33	Chip color Avg	6.8	6.7	6.7	6.6	6.7
10 clones			TTY Avg	4817	4879	1686	1298	3170
			GTA Avg	4.1	3.6	4.1	3.4	3.8
			Plant Count Avg	4.0	3.9	3.9	3.9	3.9
			Tuber Count Avg	47.1	44.3	20.5	16.8	32.2
			Yield per plant Avg	1204	1115	.	.	1160
			Maturity Avg	4.1	4.1	3.2	3.0	3.6
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	1.8	1.9	1.7	1.6	1.8
			Tuber Shape Avg	1.8	1.7	1.7	1.6	1.7
			Eye Depth Avg	2.6	2.6	2.3	2.0	2.4
			Skin Color Avg	1.8	2.1	1.8	1.4	1.8
162	E-51-4	C367	Chip color Avg	6.5	7.1	6.7	6.3	6.6
7 clones			TTY Avg	1747	1710	496	698	1166
			GTA Avg	3.3	3.1	2.8	3.1	3.1
			Plant Count Avg	3.3	3.7	3.9	3.3	3.5
			Tuber Count Avg	26.0	27.3	7.8	9.7	17.8
			Yield per plant Avg	473	498	.	.	487
			Maturity Avg	3.6	3.7	3.4	3.7	3.6
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	2.0	1.9	1.2	1.4	1.6
			Tuber Shape Avg	1.5	1.6	1.5	1.4	1.5
			Eye Depth Avg	1.7	1.6	1.8	1.4	1.6
			Skin Color Avg	1.2	1.4	1.0	1.1	1.2

163	E-51-4	C380	Chip color Avg	6.9	6.8	6.0	5.8	6.4
10 clones			TTY Avg	3555	3868	1210	1133	2475
			GTA Avg	3.8	3.6	3.6	3.8	3.7
			Plant Count Avg	3.6	3.8	3.9	3.5	3.7
			Tuber Count Avg	37.4	40.5	16.3	17.0	28.1
			Yield per plant Avg	979	973	.	.	976
			Maturity Avg	3.4	3.3	3.4	3.2	3.3
			Sprouting Avg	0	0	0	0	0
			Sp. Gravity Avg	1.1	1.1	1.1	1.1	1.1
			Flesh Color Avg	1.7	1.9	1.3	1.6	1.6
			Tuber Shape Avg	2.3	1.9	2.1	1.9	2.1
			Eye Depth Avg	2.6	2.1	2.1	2.3	2.3
			Skin Color Avg	1.4	1.9	1.4	1.3	1.5
Grand Average Chip color				6.7	6.7	6.3	6.2	6.5
Grand Average TTY				3392	3590	1321	1406	2417
Grand Average GTA				3.4	3.2	3.2	3.2	3.2
Grand Average Plant Count				3.5	3.6	3.6	3.5	3.6
Grand Average Tuber Count				35.8	38.2	14.9	15.5	26.0
Grand Average Yield per plant				966	.	.	.	.
Grand Average Maturity				3.8	3.7	3.5	3.5	3.6
Grand Average Sprouting				0.01	0.03	0	0	0.01
Grand Average Sp. Gravity				1.1	1.1	1.1	1.1	1.1
Grand Average Flesh Color				1.9	1.9	1.5	1.5	1.7
Grand Average Tuber Shape				1.9	1.8	1.8	1.7	1.8
Grand Average Eye Depth				2.1	2.0	1.9	1.8	1.9
Grand Average Skin Color				1.6	1.8	1.5	1.5	1.6

Score = Chip color score rating: 1 (excellent) to 10 (poor) with 4 or less “acceptable”
TTY: grams per plot of all tubers
ATY: gram per plot of tubers > 50 grams
Gravity = Specific gravity: calculation: weight in air/(weight in air-weight in water)
Sprout: 0= none, 1=peeping, 2<=1.5cm, 3>=1.6
Eye depth rating: 1= shallow, 2=medium, 3=deep
Tuber shape rating: 1=round, 2=oval-ovate, 3=long
Tuber shape rating: 1=round, 2=oval-ovate, 3=long
Skin color rating: 1=buff, 2=brown, 3=other (purple, red, etc)
GTA rating: 1(excellent) to 5 (poor)
Flesh color rating: 1=white, 2=cream, 3=yellow, 4=other (purple, variable, etc)
Maturity rating: 1=late to 5=early

Table 11. Ploidy assessment of clone from various 2x-2x families estimated by subjective visual leaf ratio (no data column in the table, ploidy estimate is in the Ploidy(Visual) column), measured leaf ratio, measured leaflet ratio, and stomatal guard cell chloroplast number.

Family	Clone	Ploidy (Visual)	Ratio (Leaf)	Ploidy (Leaf)	Ratio Leaflet	Ploidy (Leaflet)	Number Chloroplasts	Ploidy (Chlor.)
2	1	2	2.2	2	2.2	2	.	.
	2	2	1.8	2	2.2	2	.	.
	3	3	1.8	2	1.6	3	20.7	4
	4	2	2.8	2	1.6	2	.	.
	5	2	2.2	2	2.0	2	.	.
	6	2	2.1	2	2.2	2	.	.
	7	2	2.0	2	2.0	2	.	.
	8	2	2.2	2	2.1	2	.	.
	9	2	1.9	2	1.4	4	19.5	4
	10	4	2.0	2	1.6	2	18.0	4
	25	2	2.2	2	2.1	2	.	.
	26	2	2.1	2	2.3	2	.	.
12	5	2	1.9	2	1.9	2	.	.
15	3	2	2.2	2	2.8	2	.	.
	4	2	2.5	2	1.6	2	.	.
	5	2	1.5	4	1.6	2	.	.
16	1	2	2.1	2	1.9	2	.	.
	2	2	1.8	2	2.0	2	.	.
	3	2	2.5	2	1.5	4	19.6	4
	4	2	1.5	4	2.4	2	23.0	4
	5	2	2.1	2	2.5	2	.	.
	6	2	1.8	2	2.2	2	.	.
17	1	3	1.8	2	2.0	3	15.8	2
	2	3	1.9	2	2.3	2	20.3	4
	3	4	1.8	2	1.9	2	19.5	4
	4	2	2.1	2	2.2	2	.	.
	5	3	2.0	2	2.0	2	18.5	4
	6	3	1.9	2	2.2	2	18.9	4
	7	2	2.0	2	1.7	3	19.8	4
	8	2	2.0	2	2.1	2	.	.
	9	2	1.8	2	2.0	2	.	.
	10	4	1.8	2	2.1	2	18.0	4
	11	2	2.1	2	2.6	2	.	.
27	1	2	2.0	2	2.2	2	.	.
	2	2	2.4	2	2.1	2	.	.
	3	4	2.4	2	1.8	2	19.6	4
	4	2	2.4	2	2.4	2	.	.
39	1	2	1.9	2	2.1	2	.	.
	2	2	1.9	2	2.3	2	.	.
	3	2	1.8	2	2.1	2	.	.
	4	3	2.0	2	2.2	2	22.4	4
	5	2	2.0	2	2.1	2	.	.
	6	2	1.5	4	1.7	2	20.7	4
	7	2	1.9	2	1.8	2	.	.

40	1	2	1.8	2	1.6	2	.	.
	2	2	1.8	2	1.7	2	.	.
	3	2	1.8	2	1.7	2	.	.
	4	4	1.6	2	1.9	2	25.0	4
	5	4	1.9	2	1.7	2	19.0	4
52	1	4	1.9	2	1.9	2	19.4	4
	2	2	2.1	2	1.6	2	.	.
	3	4	1.7	2	1.7	2	22.1	4
	4	4	2.1	2	2.1	2	18.6	4
	5	4	2.2	2	2.0	2	20.5	4
	7	2	1.8	2	1.8	2	.	.
	8	4	1.7	2	2.1	2	20.4	4
	9	2	1.7	2	2.2	2	.	.
59	1	2	2.2	2	2.0	2	.	.
	2	3	2.1	2	1.7	2	19.1	4
	3	2	2.2	2	2.0	2	.	.
	4	4	1.9	2	1.9	2	17.5	2
	5	3	1.9	2	2.0	2	21.4	4
	6	4	2.1	2	2.0	2	20.4	4
	7	2	2.0	2	1.8	2	13.2	2
	8	2	2.0	2	2.3	2	.	.
	9	2	2.1	2	1.9	2	.	.
	10	2	1.9	2	2.0	2	.	.
	11	2	2.3	2	2.2	2	.	.
	4G	2	1.9	2	1.6	4	19.4	4
61	1	2	1.6	2	1.6	2	.	.
	2	2	1.8	2	1.4	4	.	.
	3	4	1.7	2	1.4	4	20.4	4
	4	2	1.5	4	1.8	2	23.1	4
	5	2	1.5	4	1.8	2	21.6	4
	6	4	1.8	2	1.9	2	16.0	2
	7	2	1.2	4	1.5	4	.	.
62	1	2	2.1	2	1.7	2	.	.
	2	2	2.0	3	2.0	2	20.6	4
	3	2	1.8	2	1.6	3	17.9	4
	4	2	2.1	2	2.2	2	.	.
	5	2	2.6	2	1.9	2	.	.
	6	2	2.1	2	2.0	2	.	.
	7	2	2.4	2	2.0	2	.	.
	8	3	2.3	2	1.9	3	19.6	4
	9	2	2.6	2	2.0	2	.	.
	10	3	2.1	2	1.8	2	18.4	4
	11	2	2.4	2	1.9	2	.	.
63	1	2	3.5	2	2.0	2	.	.
	2	2	2.3	2	2.0	2	.	.
	3	2	1.8	2	2.6	2	.	.
	4	2	2.3	2	2.0	2	.	.

64	1	2	1.5	4	2.1	2	23.0	4
	2	4	1.6	4	2.4	2	19.2	4
	3	4	2.2	2	2.2	2	20.5	4
	7	2	1.7	2	2.2	2	.	.
65	1	2	2.3	2	2.1	2	.	.
	2	2	1.7	2	2.1	2	.	.
	3	2	1.9	2	2.1	2	.	.
	4	2	1.8	2	2.0	2	14.3	2
	5	2	1.9	2	2.4	2	.	.
	6	2	1.6	2	1.8	2	.	.
	7	2	2.0	2	1.8	2	.	.
	8	2	2.2	2	2.0	2	.	.
	9	2	1.9	2	2.1	2	.	.
	10	2	1.8	2	2.1	2	.	.
	11	2	2.2	2	1.8	2	.	.
	12	2	2.1	2	1.9	2	.	.
89	2	4	2.1	2	1.2	4	25.3	4
	3	4	2.0	2	1.4	4	21.7	4
90	1	2	1.6	2	2.3	2	14.6	2
100	1	3	2.2	2	2.1	2	18.9	4
	2	2	2.0	2	2.1	2	.	.
	3	2	2.4	2	2.0	2	19.1	4
	4	3	2.4	2	2.0	2	17.3	2
	5	2	2.5	2	2.2	2	.	.
	6	3	2.3	2	2.5	2	13.8	2
	7	2	2.3	2	1.8	2	14.3	2
	8	4	1.9	2	1.9	2	19.3	4
	9	2	2.2	2	1.7	2	.	.
	10	2	2.0	2	2.2	2	.	.
	11	2	2.8	2	2.3	2	.	.
	13	2	2.6	2	2.2	2	.	.
	14	2	2.0	2	2.0	2	.	.
	15	2	2.7	2	2.2	2	.	.
112	1	2	1.9	2	1.5	4	21.1	4
	2	2	2.2	2	1.3	4	.	.
	3	2	1.9	2	1.9	2	.	.
	4	2	2.0	2	1.8	2	.	.
	5	2	1.8	2	1.6	2	.	.
	6	2	2.0	2	1.7	2	.	.
	7	2	3.0	2	1.6	2	.	.
	8	2	1.9	2	1.7	2	.	.
	9	2	2.4	2	1.1	4	19.3	4
	10	2	2.3	2	1.9	2	.	.
	11	2	1.7	2	1.9	2	.	.
127	7	4	1.6	2	2.2	2	.	.

132	2	2	2.3	2	1.6	2	.	.
	5	2	1.8	2	1.9	2	.	.
	7	4	1.8	2	2.1	2	.	.
	8	2	1.9	2	2.0	2	.	.
	11	2	1.9	2	2.0	2	.	.
	12	4	1.7	2	2.2	2	.	.
	13	2	2.4	2	1.3	4	18.4	4
	14	2	2.2	2	2.2	2	.	.
	15	2	2.0	2	1.7	2	.	.
142	1	2	1.9	2	1.7	2	.	.
	2	4	1.9	2	1.8	2	12.9	2
	3	4	1.8	2	2.0	2	18.4	4
	4	4	3.5	2	2.2	2	18.4	4
	5	4	2.0	2	1.5	4	18.1	4
	6	2	2.0	2	1.8	2	.	.
	7	4	2.0	2	1.7	2	18.0	4
	8	2	1.9	2	2.2	2	16.1	2
152	1	3	2.0	2	1.7	2	24.1	4
	2	2	2.4	2	1.9	2	.	.
	3	2	2.0	2	1.9	2	.	.
	4	2	2.3	2	2.1	2	.	.
	5	2	2.0	2	1.6	3	18.0	4
	6	2	2.1	2	1.8	3	20.2	4
	8	2	2.1	2	1.7	2	.	.
	9	4	1.9	2	2.1	2	15.0	2
153	1	2	1.9	2	2.8	2	.	.
	2	2	2.2	2	2.0	2	.	.
	3	4	1.9	2	1.9	2	14.0	2
	4	2	1.9	2	1.7	2	.	.
155	1	2	2.0	2	1.8	2	.	.
	2	2	2.2	2	1.8	2	.	.
158	1	3	1.8	2	2.0	2	17.3	2
	2	3	1.9	2	2.0	2	19.9	4
	3	3	2.1	2	1.9	2	19.9	4
	4	3	2.0	2	2.1	2	15.8	2
	5	2	2.2	2	2.2	2	.	.
	6	4	1.8	2	2.2	2	14.4	2
	7	3	2.0	2	2.3	2	19.8	4
	8	2	2.0	2	2.3	2	.	.
	10	2	1.8	2	1.9	2	.	.
	11	4	1.9	2	1.6	2	21.2	4
	12	2	1.9	2	1.9	2	.	.
	13	2	2.2	2	2.5	2	.	.
	14	2	1.6	4	2.3	2	16.1	2
	15	2	1.9	2	1.9	2	.	.
159	1	2	2.5	2	1.7	2	.	.
	2	4	2.7	2	1.6	4	15.7	2
	3	4	2.8	2	2.0	2	18.2	4
	4	2	2.2	2	1.6	2	.	.
	5	4	2.0	2	1.7	2	19.6	4
160	1	4	2.1	2	1.4	4	20.5	4
	2	4	1.8	2	1.5	4	18.3	4
	3	4	3.0	2	1.6	2	19.0	4

160	4	4	2.3	2	1.6	2	17.0	2
(cont.)	5	2	2.7	2	2.6	2	.	.
	6	4	2.1	2	1.8	2	17.2	2
	7	4	1.6	2	2.2	2	23.4	4
	8	4	2.0	2	2.4	2	20.2	4
	9	2	1.7	2	1.9	2	.	.
	10	4	1.9	2	1.6	2	19.8	4
	11	4	1.6	4	1.8	2	18.4	4
	12	2	1.8	2	1.9	2	.	.
	13	4	2.0	2	1.6	2	21.6	4
	14	4	1.8	2	1.4	4	16.3	2
162	1	4	2.1	2	1.5	4	14.8	2
	2	2	2.0	2	1.5	4	18.8	4
163	1	2	1.6	3	2.2	2	19.1	4
	2	2	2.1	2	2.1	2	.	.
	3	2	1.7	2	2.1	2	13.3	2
	4	2	2.2	2	2.3	2	.	.
	5	3	2.0	2	1.9	3	.	.
	6	2	2.1	2	2.0	2	.	.
	7	2	2.2	2	2.0	2	.	.
	8	2	1.8	3	2.1	2	19.2	4
	9	2	1.7	2	1.8	2	.	.
	10	2	1.9	2	2.0	2	.	.
	11	2	1.8	2	2.3	2	.	.
	12	2	1.8	2	2.1	2	.	.
	13	2	1.9	2	2.5	2	.	.
	14	2	2.0	2	2.7	2	.	.
	15	2	2.1	2	2.1	2	.	.
165	1	4	1.7	2	2.0	2	.	.
	2	2	1.4	4	2.2	2	22.4	4
	3	4	1.5	4	1.5	4	19.6	4
	4	2	1.6	2	2.0	2	.	.
	5	4	1.9	2	1.6	4	21.0	4
	6	4	2.4	2	1.6	2	23.9	4
	7	4	1.7	2	1.5	4	15.1	2
	8	2	1.6	2	2.1	2	.	.
	9	2	1.9	2	2.1	2	.	.
	10	2	1.7	2	1.8	2	.	.
	11	4	2.0	2	1.2	4	24.9	4
	12	2	1.7	2	1.9	2	.	.
	13	2	1.7	2	1.7	2	.	.
	14	2	1.8	2	2.5	2	.	.
	15	2	1.9	2	2.0	2	.	.
	16	2	2.4	2	2.2	2	.	.

175	1	2	1.8	2	1.7	2	.	.
	2	2	1.8	2	1.8	2	.	.
	3	2	2.7	2	1.9	2	.	.
	4	2	2.5	2	1.9	2	.	.
	5	2	3.1	2	2.5	2	.	.
	6	2	2.7	2	2.0	2	.	.
	7	2	2.6	2	1.6	2	.	.
	8	2	2.0	2	2.2	2	.	.
177	1	4	2.0	2	1.4	4	24.4	4
Check	E-51-4	2	2.0	2	1.8	2	12.5	2
Check	Norchip	4	1.4	4	1.3	4	19.8	4
Check	Snowden	4	1.5	4	1.4	4	19.5	4

Table 12. Potential ploidy assessment of clones selected in the field as potentially tetraploid (pBSP) from 2x-2x families. Ploidy was estimated by subjective visual leaf ratio (no data column in the table, ploidy estimate is in the Ploidy(Visual) column), measured leaf ratio, measured leaflet ratio, and stomatal guard cell chloroplast number.

Family	Clone	Ploidy (Visual)	Ratio (Leaf)	Ploidy (Leaf)	Ratio (Leaflet)	Ploidy (Leaflet)	Chloroplast Number	Ploidy (Chlor.)
7	2	4	2.1	2	1.5	2	22.2	4
16	1	4	1.6	4	1.1	2	20.7	4
	2	4	2.1	2	1.2	2	20.5	4
	3	2	2.0	2	1.4	2	.	.
37	1	4	2.1	2	1.5	2	31.5	4
39	3	4	2.7	2	1.4	2	20.4	4
	.	.	.	.	.	.	24.0	4
76	1	4	2.1	2	1.3	2	28.9	4
82	1	4	2.5	2	1.3	2	23.2	4
89	1	4	1.9	2	1.3	2	23.7	4
	2	4	1.9	2	1.4	2	25.8	4
	3	4	1.7	2	1.6	4	24.6	4
100	5	2	2.2	2	1.8	4	.	.
101	1	4	2.1	2	1.6	4	22.8	4
	2	4	1.8	2	1.3	2	21.7	4
	3	4	2.5	2	1.7	4	19.4	4
	4	4	2.3	2	1.4	2	22.8	4
116	1	4	1.8	2	1.2	2	19.5	4
120	1	4	1.9	2	1.4	2	22.0	4
132	2	4	2.8	2	1.2	2	24.5	4
159	1	4	2.5	2	1.5	2	22.0	4
162	1	4	2.4	2	1.3	2	20.0	4
172	1	4	1.9	2	1.7	4	22.8	4
178	1	4	2.2	2	1.0	2	23.5	4
179	1	4	2.3	2	1.5	2	22.3	4
	2	4	2.1	2	1.4	2	19.1	4
183	1	.	.	.	.	.	22.5	4
207	1	4	2.2	2	1.8	4	21.0	4
215	1	4	1.7	2	1.5	2	23.2	4
216	1	4	2.1	2	1.5	2	22.5	4
	2	4	2.0	2	1.4	2	22.2	4
	3	4	1.9	2	1.6	4	22.0	4
	4	4	1.8	2	1.4	2	21.0	4
	5	4	2.1	2	1.4	2	19.8	4
	6	4	2.0	2	1.5	2	24.2	4
218	1	4	1.8	2	1.4	2	20.0	4
238	1	3	1.8	3	1.3	2	22.3	4
240	1	4	1.9	2	1.3	2	.	.
254	1	4	2.3	2	1.6	4	20.4	4
	2	4	3.0	2	1.5	2	23.2	4
Check	E-51-2	2	2.0	2	1.8	4	12.5	2
Check	Norchip	4	1.4	4	1.3	2	19.8	4
Check	Snowden	4	1.5	4	1.4	2	19.5	4
Check	Sn x Nor	4	1.5	4	1.3	2	.	.