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# Review on Genetics and Breeding of Potato *(Solanum tuberosum L.)*

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*ABSTRACT*

*Among root and tuber crops in Ethiopia, potato ranks first in volume produced and consumed followed by Cassava, Sweet potato and Yam and little is known concerning the genetic behavior of some of the most important characters of the potato. Weak progress in potato breeding is illustrated by many potato cultivars still lacking adequate levels of disease resistances and quality improvement, although these traits are needed and available in the potato germplasm. Traditional potato breeding for quantitative traits is mainly executed using phenotypic selection because the identification and mapping of genes involved in these quantitative traits have not yet resulted in validated genetic markers. Genetic resources of potato conserved through storage of tubers, in vitro plants and in cryopreservation. Since nature of potato (tetraploid) breeding on is challenging one.*

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***Keywords*:** Allel, Genetics, Germplasm, Potato, Reproduction

## 1. INTRODUCTION

Potato (*Solanum tuberosum* L.) is the fourth most important food crop after rice, wheat, and maize, and has historically contributed to food and nutrition security in the world and the primary non-grain food commodity in the world (FAOSTAT, 2015; FAO, 2015). It belongs to the botanical family Solanaceae and within it to the genus Solanum, which consists of more than 2,000 species. Apart from the cultivated potato Solanum tuberosum L. ssp.

tuberosum, seven other cultivated and 228 wild potato species have been identified (Veli-Matti Rokka, 2011). Leading hypotheses suggest that potato originated in the Andean highlands of Peru in northern South America and it was introduced to Ethiopia in 1858 by the German botanist Shimper (Berga et al., 1992). Potatoes are a high yielding short duration crop that produces high dry matter and protein per unit area and unit time among the major food crops (Mohammed Beriso, 2016).

Potato (*Solanum tuberosum* L.) is one of the important vegetable crops in Ethiopia with the potential to improve the national food supply and economic benefits to smallholder producers. It has been cultivated in Ethiopia for over 150 years; currently it is grown in many parts of the country. In Ethiopia, its production area has reached 59,504 ha cultivated by over one million households in the main cropping season of 2011(Waga Mazengia , 2012). Among root and tuber crops in Ethiopia, potato ranks first in volume produced and consumed followed by Cassava, Sweet potato and Yam (CSA, 2013). Potato is mainly produced as food and income security crop to overcome seasonal food shortage due to food crops depletion from stores. Its high yield per unit area and best maturity period are double advantages to be a food security crop.

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Genetics, breeding and genomics has emerged as three overlapping and complimentary disciplines for comprehensive and fine-scale analysis of plant genomes and their precise and rapid improvement. While genetics and plant breeding have contributed enormously towards several new concepts and strategies for elucidation of plant genes and genomes as well as development of a huge number of crop varieties with desirable traits (The Potato Genome Sequencing Consortium, 2011). Compared to other major food crops, progress in potato yield as the result of breeding efforts is very slow. Genetic gains cannot be fixed in potato due to obligatory out-breeding. Overcoming inbreeding depression using diploid self-compatible clones should enable to replace the current method of out-breeding and clonal propagation into an F1 hybrid system with true seeds (Pim Lindhout, 2011).

In today’s world, teaching, research, funding, regulation and utilization of plant genetics, genomics and breeding essentially require thorough understanding of their components including classical, biochemical, cytological and molecular genetics; and traditional, molecular, transgenic and genomics-assisted breeding. Slow progress in potato breeding is illustrated by the many potato cultivars still lacking adequate levels of disease resistances, although these traits are needed and available in the potato germplasm. Traditional potato breeding for quantitative traits is mainly executed using phenotypic selection because the identification and mapping of genes involved in these quantitative traits have not yet resulted in validated genetic markers (Li et al. 2010).

As a result of the traditional way of potato breeding, unfavorable alleles easily remain hidden in the tetraploid genome and become manifest at each breeding cycle. It takes large selection programmes on progeny plants derived from crosses between tetraploid potato cultivars to select a clone that has the right balance between unfavorable alleles and compensating alleles at the same or at other loci (Mohammed Beriso, 2016). Objective of this paper is reviewing on genetics and breeding of potato (*Solanum tuberosum* L.

## 2. GENETICS AND BREEDING OF POTATO

Potato geneticists and breeders have generated a great deal of information about the location of genes and QTLs coding for important potato traits, including pest and disease resistance and tuber traits. Developments in genetics and structural genomics are beginning to be matched by concomitant development of functional genomics tools. Potato has a strong need for a high density gene map or a genome sequence, to place gene sequences in their genetic/genomic context. Relatively high-throughput methods are also needed for testing and assessing gene function (Kimberly J. et al 2012)

### 2.1. Genetics of Potato

From the material available it is seen that little is known concerning the genetic behavior of some of the most important characters of the potato, such as yield, cooking quality, and resistance to various diseases, but the breeding work is being centered around such characters at present, and it is believed that, while they may be rather complex in their genetic behavior, they will all follow the general rule that a genetic character is the end result of the interaction of genes and environment(Getachew, A. 2015).

A cultivated diploid that is used in South American production is *S. phureja*. It is used in bridge crossing and other genetic studies. Triploid potato is sterile, and only a few are cultivated. Producing triploid potato by crossing $2n$ x $4n$ is seldom successful because of the so-called “triploid block”. Hexaploids are self-fertile. A widely used hexaploid is *S. demissum*. It is the source of the major *R* gene that confers resistance to late blight.

### 2.1.1. Genetic diversity of potato

Potato diversity is maintained in a number of germplasm banks in various parts of the world. The major repositories include the International Potato Center (CIP) in Peru (with the best collection of cultivated potatoes, especially Andigena, Phureja, and “bitter potatoes”). The genus *Solanum* contains about 2,000 species, of which only about 150 are tuber-bearing. The cultivated potato, *S. tuberosum*, is a tetraploid ($2n = 4x = 48$). Five cytological groups of potato have been identified, with somatic numbers of 24, 36, 48, 60, and 72. About 70% of tuber-bearing potatoes are diploids, while 5% and 8% are tetraploids and hexaploids, respectively. Most of the diploids are self-incompatible, producing seed only when fertilized by pollen containing a different *S* allele (Getachew, A. 2015).

Today, there are more than 4,500 varieties of S. tuberosum ssp. tuberosum (Hils and Pieterse 2009). Potato is known to have the richest genetic diversity of any cultivated plant because of its high number of varieties and related species (FAO 2007; Messer 2000).

### 2.1.2. Potato species and chromosome number

While it is necessary for the breeder to obtain a thorough knowledge of the cultivated varieties and their important economic characters, it is also important to know the related wild forms and species of potatoes. It is true that new genes and gene combinations are being brought to light in the cultivated varieties, but it is quite improbable that all the problems can be solved by the recombination of genes available in this group. Much work has already been done with the species of *Solanum* related to the potato, and a fund of valuable information is available concerning them. Crosses between species with different chromosome numbers are as a rule difficult to obtain. For example, crosses between species of the 24 group and the 48 group are very rare, although many attempts have been made to produce them. Certain species crosses have been reported, however, and as knowledge increases concerning the causes of incompatibility and sterility, it may be possible in the future to get hybrid combinations that at present seem quite impossible (Pim Lindhout, 2011).

Characters that would be especially valuable if they could be combined with those of the best commercial varieties have been found in a number of species. Among these are resistance to drought, frost, potato wart, viruses, and late blight. The characters for short-day development and short rest period are found in some of the species also. The character for short-day development might be valuable in potato districts where the crop is grown during the winter months under conditions of short-day length (Philippa J. Barrell, 2013)

### 2.1.3. Genetic conservation of potato

Genetic resources of potato (Solanum tuberosum L. ssp. tuberosum) and related cultivated species are conserved through storage of tubers, in vitro plants and in cryopreservation. To prevent the loss of potato genetic resources, long-term conservation of plant material is accomplished in genebanks, genetic resource centres and private collections worldwide. Conservation of potato genetic resources in genebanks is important, because of their high value as breeding material and for research, industry and private needs.

Potato is highly heterozygous, and the sexually produced seeds are, therefore, not true to type. Thus, maintenance of cultivated potato accessions is not possible by true potato seeds (Dodds et al. 1991). Gene bank stocks are therefore derived from vegetative material. To preserve the genetic resources of potato for the long term, cryopreservation is the best current option (Veli-Matti Rokka, 2011)

## 2.2. Breeding of Potato

The reproductive biology of potato is ideal for creating and maintaining variation. Potato breeders aim to produce new cultivars better adapted than existing ones to the conditions in which they are going to be grown and stored and the ways in which they are going to be used. This is also not an easy task in potato due to its polyploidy ($2n = 4x = 48$), tetrasomic inheritance and chromatid segregation. Breeding efforts are very much dependent on some reproductive features that are typical of the cultivated potato as well as its tuber and non-tuber related species (Shelley Jansky, 2011).

The high yields of potatoes grown on the research station (30-40 metric tons $ha^{-1}$) are not realized at the producer’s level (11-13 metric tons $ha^{-1}$). This might be partly attributed to lack of better yielding modern cultivars. The farmers need varieties that show high performance for yield and other essential agronomic traits. Their superiority should be reliable over a wide range of environmental conditions and also over years (MulugetaGedif and DessalegnYigzaw, 2014). Efforts have been done with different researchers to overcome the low productivity of potato.

### 2.2.1. Potato Breeding Methods

#### 2.2.1.1. Conventional breeding method

Potato breeding worldwide has traditionally involved making crosses between pairs of parents with complementary features and this is still the main route to new cultivars. Conventional breeding methods for potato involve the hybridization of parental clones followed by selection among large seedling populations for superior individuals with the desired combination of traits. Conventional breeding methods are of primary importance but are too slow (10–15 years) because they are essentially based on several generations of back crossing, field evaluation and phenotypic selection. Particularly, breeding efforts are very much dependent on typical reproductive features of potato (Gopal 2006).

Several hypotheses have been presented earlier for larger utilization of wild *Solanum* gene pools at tetraploid (4EBN) (endosperm balance number) and diploid (2EBN/1EBN) levels by designing specific crossing schemes. For several traits the genetic variance is almost entirely non-additive, so that breeders must maximize allelic diversity at any given locus to optimize heterozigosity and, consequently, heterosis. Conventional breeding methods based on sexual hybridization (ShelleyJansky, 2011)

#### a. The tetraploid 4EBN level

Tetraploid breeding is essentially based on phenotypic recurrent selection, involving crosses between 4*x*(4EBN) genotypes (often varieties) and then field evaluation and selection of descendants for several years. Parental selection is based on phenotypic character which is mostly in effective rather the use of test-crosses to identify desirable combination of parents has been reported by various authors (see Tarn et al. 1992; Bradshaw and Mackay 1994; Mackay 2005, and references therein). Test-crosses evaluate both general combining ability (GCA) and specific combining ability (SCA). Due to the high levels of heterozygosity of tetraploid potatoes, segregation of traits is expected in the F1 generation derived from 4*x* x 4*x* crosses. Thus, successful interspecific hybridization occurs only when parents produce gametes with the same EBN. The EBN is an arbitrary value experimentally assigned to each *Solanum* species based on its behavior in crosses with EBN standards, and assuming the 2:1 ratio as a prerequisite for normal endosperm development (ShelleyJansky, 2011).

### b. The diploid 2EBN level

In modern potato breeding, several programs operate at least in part at the diploid (2EBN) level. This not only takes advantage of disomic inheritance, which is less complicated than the typical tetrasomic patterns of the 4*x* (4EBN) level, but also requires a smaller population size at the start. In addition, this approach allows the most efficient exploitation of diploid potato germplasm. The first essential ingredient for potato breeding at the diploid 2EBN level is haploids. It is believed that haploids originate via parthenogenesis, and that both sperm nuclei fuse with the polar nuclei of the central cell of the female gametophyte. Potato haploids may also be obtained through in vitro microspore/anther culture, but this method is more complicated and strongly genotype-dependent compared to the *S. tuberosum* x *S. phureja* approach. From the breeding standpoint, *S. tuberosum* haploids are widely used in sexual interspecific hybridization programs (ShelleyJansky, 2011).

Haploid-wild species hybrids producing 2*n* gametes and with the desired traits are selected for the production of tetraploid hybrids through bilateral and unilateral sexual polyploidization (BSP and USP) respectively.

### 2.2.1.2. Biotechnological breeding method

Development of biotechnological tools for assaying potato gene function is likely to progress rapidly in the coming years (The Potato Genome Sequencing Consortium, 2011).

#### 2.2.1.2.1. Potato tissue culture

Potato is amenable to a number of tissue culture techniques, ranging from in vitro propagation via shoot cultures to regeneration of whole plants from protoplast. Micro propagation is a useful means of multiplying virus-free potato stocks and new or imported cultivars, for which few tubers may be initially available. In order to maintain genetic resources in potato, there is a need to store primitive potato cultivars and related wild species which cannot be stored as seeds.

#### 2.2.1.2.2. Molecular breeding method

Molecular breeding of potato is now a reality after several years of unfulfilled promise.

Biotechnologists and breeders are working together to elucidate the genome sequence, to identify genetic factors controlling important economic traits within breeding populations, and to develop transformation technology that is more acceptable to the public. Molecular studies have contributed to our understanding of the taxonomic relationships of wild and cultivated potato (James M. Bradeen, 2011).

The immense amount of diversity within cultivated potato and its relatives provides both opportunities and challenges. The demands of industry and the public for the rapid introduction of new and better varieties contrasts with the long-term efforts that are needed to incorporate beneficial diversity not present in the adapted germplasm. The greatest impact of molecular breeding in potato will be for pre-breeding and parental development activities. Molecular breeding provides the means to transfer this knowledge to the development of new cultivars for a variety of uses (Philippa J. Barrell, 2013)

### a. Germplasm and variety characterization

Random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP) and simple sequence repeat (SSR) markers have been used to generate phylogenetic data that have contributed to the revision of the relationships within cultivated and wild potato species germplasm. Various types of markers have contributed to the classification changes within section *Petota*, including AFLPs (Lara-Cabrera 44 *Genetics, Genomics and Breeding of Potato* and Spooner 2004; Jacobs et al. 2008; Jiménez et al. 2008), SSRs (Lara-Cabrera and Spooner 2005), or a combination of AFLPs, RAPDs, and SSRs (van den Berg et al. 2002). More recently, sequencing data from single-copy genes has been used to elucidate the relationships within *Solanum*. The issue of ploidy level is also very important in the study of cultivated potatoes and requires a critical assessment of the

The various studies examining molecular diversity in cultivated potato have not demonstrated that diversity is a limiting factor for breeding progress. However, the high levels of polymorphism at the sequence level are generally not captured by the commonly used marker systems. These markers are also not sensitive enough to quantify allele dosage on a routine basis. Rather than marker assessments of genetic relationships and diversity, it may be more useful to measure the diversity of genomic regions that have undergone selection within breeding programs. Comparison of AFLP, RAPD, and SSR markers for diversity analysis of tetraploid potato has not revealed a distinct advantage of one marker type over another (Milbourne et al. 1997; McGregor et al. 2000).

### b. Marker-assisted gene introgression

There is a growing collection of markers linked to important traits in potato. The genome location of pathogen resistance and tuber traits has been used to create potato function maps for pathogen resistance and tuber traits (Gebhardt 2005). The strategy of introgression depends on the extent the donor species is reproductively isolated from the cultivated potato gene pool. When fertile hybrids are produced, genome-wide marker genotyping may be employed to preferentially select clones with a higher level of *tuberosum*-type markers, as long as the selected clones maintain the desirable trait. Most published examples of this marker-assisted selection (MAS) scheme in potato involve the diploid wild donor species *S. commersonii* introgression into a tetraploid *S. tuberosum* background (Barone et al. 2001; Barone 2004; Carputo et al. 2002; Iovene et al. 2004).

PCR markers closely linked to genes or quantitative trait loci (QTL) of interest have been available to potato breeders for quite some time. Several PCR markers linked to virus resistance genes have been reported and Several PCR-based candidate gene markers are associated with the tuber quality traits chip color and starch content (Li et al. 2005, 2008a) and potato tuber skin and flesh color (De Jong et al. 2003a, 2003b; Brown et al. 2006; Zhang et al. 2009). For tuber quality characteristics, there are fewer applications of markers within breeding programs. Several marker-trait associations were detected with chip color and starch content in 243 clones using 36 microsatellite and candidate gene loci (Li et al. 2008a).

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In autotetraploid potato, a single genomic region may have up to four alleles or several possible combinations involving two or three alleles. Therefore, dosage-sensitivity and the ability to distinguish various haplotype combinations and their dosage should be considered when selecting a marker system for potato molecular breeding.

### c. Breeding strategies incorporating DNA markers

Marker-assisted germplasm characterization could occur on the genome wide or candidate gene level. Quantitative genetics theory predicts that cultivars with the best phenotypic performance will not necessarily be the best parents for subsequent generations in a heterozygous autotetraploid crop (Philippa J. Barrell, 2013).

Genomics technology may help clarify the distinction between parental line development and cultivar development by determining the molecular basis of heterosis and the relative roles of additive, dominant, and epistatic genetic controls. As gene action in autotetraploid potato is better understood, markers will likely play an even greater role in parental development in the future. The greatest impact of markers will be for traits predominantly under the control of additive genetic variation, since they will contribute the most to heritable differences upon which selection may act (James M. Bradeen, 2011).

### d. Parent development with DNA markers

Parental line breeding in hybrid potato cultivar development generally represents a smaller component of potato breeding programs relative to the selection of potential cultivars. For qualitatively inherited traits, such as the phenotype imparted by a dominant resistance allele, the benefits of developing parents with two or more copies of a favorable allele are evident by the predicted increase in proportion of progeny with the desired allele. Despite these advantages, the conventional development of parents with duplex genotypes is very difficult since it requires progeny testing before the parental genotype is known. Once a parent is identified with two or more copies of a resistance allele, there is a tendency among potato breeders to re-use these parents, even when these parents produce progeny which are discarded due to undesirable characteristics (ShelleyJansky, 2011).

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### Common breeding objectives

Some of the major breeding objectives in potato breeding

1. **Tuber yield**. Increased tuber yield is the primary objective of potato breeding. Tuber yield and shape are influenced by photoperiod. Responsiveness to photoperiod is quantitatively inherited (Kromann *et al.,* 2014).
2. **Adaptations**:

**a**. **Heat tolerance**. Temperature variation is critical in potato production. While germination and growth are favored by warm temperatures, tuberization is favored by cool temperatures. Tuberization is inhibited at temperatures above 29°C. Heat tolerance is desirable for tuberization when unseasonable weather occurs during the production season.

**b**. **Frost resistance**. This trait is desirable for areas where fall potatoes are grown.

**c**. **Drought resistance**. This trait is necessary for production under rain fed conditions (Kromann *et al.,* 2014).

### 3. Disease resistance.

Breeding for resistance is complicated by the fact that foliage resistance and tuber resistance may differ in the same plant. Resistance conditioned by major genes (designated *R1, R2, R3,* etc.) has been discovered. Several viral diseases occur in potato fields, the most economically important one being the virus X. Plant response to this virus is varied including resistance to infection, hypersensitivity, and immunity. Viral coat protein-based resistance to PLRV has been developed (Kromann *et al.,* 2014).

## 2.3. Reproduction in Potato

Potato can reproduce both sexually and asexual method. The reproductive biology of potato is ideal for creating and maintaining variation. Potatoes flower and set true seed in berries following natural pollination by insects, particularly bumble bees. Outcrossing is enforced in cultivated (and most wild) diploid species by a gametophytic self incompatibility system. Potato has a terminal inflorescence consisting of 1–30 (but usually 7–15) flowers, depending on the cultivar. The five petals give an open flower a star shape. Flowers stay open for only 2–4 days, and the receptivity of the stigma and duration of pollen production is about 2 days.

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### 2.3.1. Asexual reproduction

Vegetative propagation is one of asexual reproduction commonly used for potato production. Micro propagation is also important for potato production specially when there is limited planting material and for production of disease free materials. A number of mutations in the vegetative cells of potatoes have been studied and described, but they are too few and far between to be relied upon in a breeding program as the only source of variation. In many cases, too, the changes are of minor importance. There are several mutations that have occurred in the color of the skin and of the eyes. Mutations due to the loss of a character are by far the most common (George Acquaah, 2012).

### 2.3.2. Sexual Reproduction

Potato is predominantly self-pollinated. The peak time of pollination is early morning. True seed is a product of sexual reproduction and is found in the fruit or ball, which is quite similar to a small tomato. Under certain conditions these fruits are produced in abundance on some varieties but are rarely if ever seen on others. They are the result of the maturing of the flower, and each of them may contain 200 seeds or more.

The flower of the potato is what is known to botanists as a complete flower with calyx, corolla, stamens, and pistil. There are usually five stamens surrounding the pistil. The process of pollination is very simple because of the simple structure of the flower parts. Pollen may be brought to the stigma of the pistil in several ways (George Acquaah, 2012). The technique of cross-pollinating potatoes by hand is comparatively simple, but since relatively few varieties produce viable pollen, the setting of seed is often very small in amount. If a variety producing viable pollen is used as the female parent, the flower must be emasculated, that is, tube anthers must be removed. Generally speaking, the anthers should be removed before the pistil protrudes through the bud, or a day or two in advance the opening of the flower.

## 2.4. Progress of Potato Breeding and Achievements

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The wild and cultivated species of potato have been utilized in potato breeding to good effect, but only a very small sample of the available biodiversity has been exploited. New knowledge and technology will open possibilities for much greater use of these genetic resources in breeding. The strategy for utilizing the cultivars native to Latin America will either be the introgression of desirable genes or the direct use of parents from improved populations, depending on how far modern *S. tuberosum* cultivars have genetically diverged from them and the extent to which *S. tuberosum* cultivars have been improved in the process. Molecular marker-assisted selection will be used for faster introgression of desirable genes from wild species, and the possibility exists of moving genes directly from wild species to cultivated potato with transgenic methods (Getachew Asefa, 2015).

New cultivars will continue to come from crosses between pairs of parents with complementary features but adapted to local growing conditions. However, increasingly these parents will possess desirable genes which have been introgressed from wild species and may also be from complementary groups of cultivated germplasm to exploit hybrid vigour. Successful cultivars may be genetically modified, if consumers see benefits in the use of the technology, to introduce genes not present in cultivated potatoes and their wild relatives to achieve novel biochemistry and further desirable improvements (Mohammed Beriso, 2016).

**Table 1.** Varieties released in different research centers and university of Ethiopia.

| No | Variety Name | Breeder | Year of Release |
|---|---|---|---|
| 1 | Dagim | AdARC/ARARC | |
| 2 | Milki | SARC/OARC | |
| 3 | Moti | SARC/OARC | |
| 4 | Bubu | HU | 2011 |
| 5 | Belete | HARC | 2009 |
| 6 | Dancha | SARC/OARC | |
| 7 | KULUMSA (KP-90143.5) | KARC | 2007 |
| 8 | Hundee | SARC/OARC | 2006 |
| 9 | Araarsaa | SARC/OARC | 2006 |
| 10 | Gudanie | HARC | 2006 |
| 11 | Gabbisa | HU | 2005 |
| 12 | Shonkolla | AwARC/SRARC | 2005 |
| 13 | Bulle | AwARC/SRARC | 2005 |
| 14 | Mara Charre | AwARC/SRARC | 2005 |
| 15 | Chala | HU | 2005 |
| 16 | Gera | ShARC/ARARC | 2003 |
| 17 | Gorebela | ShARC/ARARC | 2003 |
| 18 | Guasa | AdARC/ARARC | 2002 |
| 19 | Jalenie | HARC | 2002 |
| 20 | Degemegn | HARC | 2002 |
| 21 | Zemen | HU | 2001 |
| 22 | Bedasa | HU | 2001 |
| 23 | Zengena | AwARC/SRARC | 2001 |
| 24 | Chirro | HU | 1997/98 |
| 25 | Wechecha | HARC | 1997 |
| 26 | Tolcha | HARC | 1993 |
| 27 | Menagesha | HARC | 1993 |
| 28 | Awash | HARC | 1991 |
| 29 | Alemaya 624 | HU | 1987 |

Source: Ministry of Agriculture, Animal and Plant health Regulatory Directorate, Crop variety register Issue No.15. June, 2012, Addis Ababa, Ethiopia.

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### 2.5. Challenges of Potato Breeding

Breeding new potato varieties is easy. What's not so easy is making careful plans and predictions for what you might get out of it, and that's because potatoes are tetraploid. In short, tetraploid are complex and contain a lot of genetic material which can be immensely variable. Scientists doing genetic research on potatoes often choose to work with diploid lines instead, because tetraploid make such a muddle of their data it's hard to interpret anything.

As a consequence of the high level of unfavourable alleles, techniques aimed at developing homozygote's in one step, although successful as a technology in various crops, certainly do not generate vigorous homozygous potatoes. For instance, if 20 of the 39,000 protein-encoding genes (PGSC 2011) on the potato genome harbor alleles causing severe fitness reduction, the chance to generate vigorous diploid selfed progenies without homozygous unfavourable loci from a parent genotype, that is heterozygous for these 20 loci, is only 0.3%.

For global potato production, the possible impacts of climate change have been assessed (Hijmans 2003). Assuming that the average global temperature will increase by between $1.4^{o}$C and $5.8^{o}$C over the period 1990 to 2100 (Houghton et al. 2001), global potato yield could decrease by 18% to 32% without adaptation and by 9% to 18% with adaptation (Hijmans 2003). Generally, climate change, genetic makeup of the crop, disease and insects and post-harvest handling (mostly in developing countries) are common challenges.

## 2.6. Future Prospects for Potato Research and Production

The potato is a nutritious food that can be grown in a wide variety of climates on scales both large and small, yielding more calories per hectare than any grain. The ability of the potato tuber to be stored for months with minimal technological inputs makes potato an ideal food for both developed and developing nations. Accordingly, recent decades have seen a marked increase in potato production in populous developing countries. This trend is likely to continue in coming years (*Lara-Cabrera SI, Spooner DM, 2005)*.

With shifting production and a changing global climate, there is a clear need for continued genetic improvement of the potato. Vast genetic resources for potato improvement, including gene bank collections of approximately 200 related wild species will undoubtedly be important for continued potato improvement. Researchers continue to study the genetic control of significant potato traits and to develop molecular and non-molecular strategies for the efficient utilization of genes derived from cultivated potato and wild potato relatives. The impending release of complete genome sequence for potato will undoubtedly speed these efforts in coming years (*FAO, 2015)*.

Potato has a long history of cultivation and utilization by humankind; ongoing research and recent potato production trends ensure potato will continue to play an important role in feeding the world.

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## 3. SUMMARY AND CONCLUSION

Potato (Solanum tuberosum L.) has been consumed by humankind for thousands of years. Molecular and historical evidence suggests that potato probably originated in the Andean highlands of southern Peru. From there, it spread to Europe and other parts of the world beginning in the 16th century. The potato tuber is composed primarily of carbohydrates, but is also a significant dietary source of potassium and other minerals, fiber, vitamins C and B6, and essential amino acids. Efforts are underway in numerous research programs to improve the nutritional value of potatoes by enhancing tuber concentrations of carotenoids, anthocyanins, and minerals. Cultivated potato is one of approximately 200 tuber-bearing Solanum species.

Plant breeding and genetics are powerful tools for increasing plant productivity through development of improved varieties. Many of these wild potato species have been used by breeders for crop improvement. Researchers use phylogenetic relationships, endosperm balance number, and the genepool concept to predict crossability amongst potato species. The cultivated potato is an autotetraploid (2n = 4x = 48 chromosomes) and, although it produces true botanical seed, is usually propagated asexually.

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Climate change, genetic makeup of the crop, disease and insects and postharvest handling (mostly in developing countries) are common challenges of potato breeding. With shifting production and a changing global climate, there is a clear need for continued genetic improvement of the potato. Vast genetic resources for potato improvement, including gene bank collections of approximately 200 related wild species will undoubtedly be important for continued potato improvement.

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