International Journal of Psychosocial Rehabilitation, Vol. 23, Issue 05,
2019 ISSN: 1475-7192

Improved Potato Breeds using Recombinant Technology

1Ajoy K Pattnaik, 2P Mahapatra

Abstract--- *Potato is the third most significant global non-cereal crop, with nearly 400 million tons produced every year worldwide and which in general, represents a non-fattening, nutritious and wholesome food. It is a vigorously managed crop which requires irrigation, fertilization and many other applications for the highest yield possible. The potato tubers consist of variable amounts of carbohydrates, minerals, vitamin C, essential amino acids, etc. and are the major staple food in many developing countries. Significant characteristics are easily found in the members of wild potato, but conventional breeding can take 15-20 years to implement. This is due to the fact that certain wild species are sexually incompatible, which desires to exclude the unwanted species from adapted germplasms, and have difficulties in identifying widely applicable molecular markers. All these aspects have diverted the scientific attention to the nutritional value of the potato by keeping the yield unaffected. Several experimental studies have demonstrated the improved nutritional value of the potato tubers. Moreover, potato is one of the crops which are facing great losses due to many pests and diseases and some of them causing too much loss of the product. Since, most of the quality traits of the potato are genetically controlled, so the breeding technology can surely meet the requirements of the good quality of potato yield. The recombinant technology of breeding potato for the good quality traits requires a continuous flow of new genes and their diversity into the gene of Solanum tuberosum (potato).*

Index Terms--- *Non-fattening, irrigation, fertilization, conventional breeding, germplasms, breeding technology, recombinant technology, Solanum tuberosum.*

I. INTRODUCTION

The rising demand of food requires anexcellent quality of food source for the increasing number of population in the world. Since the introduction of first genetically modified (GM) crop plants in the mid 1990s, the agriculture industry has seen a great increase in the crops planted and harvested worldwide each year. In the year 2014, 18 million farmers have planted 447 million acres of area with different varieties of crops such as soybean, maize, cotton, papaya, sugar beet, tomato, etc. in 28 countries [1].

Potato (Solanum tuberosum)which is one of the most significant tuber crops is used worldwide for consumption of various living beings. It is the world's major staple crops, which produces more dry matter and proteins per hectare as compared to the major cereal crops [2][3]. Moreover, being a raw material, potato is widely used for the manufacturing and production of various food products, alcohol, starch and for biofuel production [4][5].

According to a research, over 300 million tonnes of potatoes are produced worldwide out of which, one-third of

Department of Agriculture, Siksha 'O' Anusandhan (Deemed to be University), Bhubaneswar,
ajoypattnaik@soa.ac.in, pmahapatra@soa.ac.in

Received: 10 Nov 2018 | Revised: 20 Dec 2018 | Accepted: 02 Jan 2019

potato production takes place in developing countries, and over 1 billion people requires potato as their staple food source[6]. Potato is a member of the family Solanaceae, with a wide family of plants having more than 3000 species. There are around 190 wild and primitive species in the Petota portion of the genus Solanum which has one of the richest genetic resources of all the crops. Short plant life and wide climatic adaptability made it easy for the crops of potatoes to spread from South American sources across the diverse geological regions. Now more than 3000 potato cultivars, mainly in temperate, subtropical and tropical regions with a major economic share in a global agriculture market, are widely distributed in more than 125 countries [7].

The tuber-bearing species of Solanum are grouped in the Petota section and this section is divided into two sub-sections – Potatoe and Estolonifera. The Potatoe subsection consists of all tuber-bearing species of potato, which includes the common potato (S. tuberosum which belongs to the Tuberosa series) [8]. The Estolonifera subsection consists of two non-tube bearing series namely, Etuberosa and Juglandifolia[9][10].

It is mandatory to utilize the most significant and valuable cultivars for achieving the enhanced production of crops. However, crops like tetrasomes and plant breeding lack genetic diversity and may be difficult to further improve by conventional breeding procedures. There is a limited utilization of genetic resources which have been used for improving the quality of commercial species due to the incompatibility of sex with several related wild species. In particular, potato has a large diversity of wild tuber Solanum species in South and North America, which represents a rich reservoir of potato-enhancing resistance genes[11]. The recent advancements in the new technologies, mainly biotechnological tools such as genomics, phenomics and metabolomics are based on the improvements for the breeding of resistance traits in potato crops and allow these tools to further research and make new methods for more improvement in the breeding procedure of potato crops by using recombinant technology.

The production value of potatoes in U.S. is $4.2 billion each year, and the crops are grown under one million acres of land (NASS 2015). The introduction of recombinant traits can be achieved by using the biotechnology on potato crop [12]. Moreover, potato was one of the first crops to be genetically modified, which was done by Monsanto in 1995, after the introduction of virus-resistant tobacco in China (1992) and FlavrSavr tomato in U.S. (1994). Conventional potato breeding procedure is an ancient process of breeding the potato but it is slow and an inefficient process. Potato crops requires appropriate nutrients, pesticides, other important things for maintaining its yield, quality and various other factors to protect itself from the pests and diseases. The potato breeding efforts have been focused on the production, fresh marketing, quality and storage as well as protection from diseases. The genetic variation for these recombinant traits in commercial cultivars is low whereas, the related wild species have high recombinant traits found in the commercial cultivars and especially demonstrate a rich source of disease and tuber quality genes [13][14].

Various experimental studies have been conducted for bringing the nutritional qualities, disease resistance and abiotic stresses from wild species in the cultivated potatoes, but popular cultivars have some traits which have been derived from the wild germplasm due to the complexity of the genes, their unpredictable manifestation and desire to limit the variability in processed quality by the industry [15]. Though, in terms of nutrition, potato is considered to be one of the richest sources of nutrients, which includes vitamins, carotenoids, proteins, magnesium, etc. and also some

Received: 10 Nov 2018 | Revised: 20 Dec 2018 | Accepted: 02 Jan 2019

of the anti-nutrients, primarily "glycoalkaloids". The potato tubers consists of about 77% water, 20% carbohydrates and less than 3% pminerals, vitamins, etc. [16]. In poor countries, which have low income source, potato is the main food source which could replace high-priced foods and can be used as a cheap food which have enough nutrients and calories for a person to survive [17].

The Solanum tuberosum is classified into two sub-species – tuberosum and andigena. The difference between the two is that, the sub-species tuberosum (table 1) is the cultivated potato which has been originated from Peru and is widely used as a crop plant in "Asia, North America and Europe". The sub-species andigena is derived from the "Andean mountains"and its cultivation is done in Central and South America [18][19][20].

Table 1. Taxonomic position of *S. tuberosum* subspecies *tuberosum*

Taxonomic Rank	**Latin Name**
Family	*Solanaceae*
Genus	*Solanum*
Section	*Petota*
Subsection	*Potatoe*
Series	*Tuberosa*
Species	*Solanum tuberosum*
Sub-species	*tuberosum*

The use of cell and tissue culture forimproving crops has traditionally been part of plant biotechnology. From the mid-1980s, transgenic plant development and application have been the major research activities linked to plant biotechnology. The research work has been expanded to include the utilization of genomics. Many developments in plant biotechnology, in particular due to their tendency of growth and development in cell culture, have been targeted at Solanaceae family, especially for "tobacco and petunia". In the same way, genotypes of many elite potatoes highly react to the cellular culture and provide several opportunities for biotechnology applications for improvement of potatoes. These new opportunities for potato biotechnology have been presented in the recent publication of the complete genome sequence of potato (The Potato genome Sequencing Consortium 2011) [21][22].

Various molecular and breeding techniques have been employed for improvement of breeds in potato plant. The conventional breeding techniques are directed towards the increase in the yield, processing and storing[23]. Potato

Received: 10 Nov 2018 | Revised: 20 Dec 2018 | Accepted: 02 Jan 2019

breeders have incorporated the resistance against many diseases such as “early and late blight disease” by crossing of hybrid lines with wild species, i.e. “S. brevidens and S. bulbocastanum” which inherits the resistance against fungal diseases [24][25][26]. However, the conventional breeding technology has been successfully used to improve the characteristics of leading individuals in successive generations and with a lower intra-specific variance, the progress is relatively slow and limited.

II. GENETICS AND CHROMOSOMAL VARIATIONS FOR IMPROVING THE POTATO BREEDS:

The process of increasing the number of genes in polyploid crops by using the conventional breeding technique is difficult, laborious and time consuming[27][28]. Several reproductive efforts have been made for the improvement of a specific trait by using the wild species germplasm, but it did not gained much success [29]. In the tetraploid (2n=4x=48) genome of cultivated potato (S. tuberosum), the existence of four copies (alleles) of the genes makes it difficult for researchers/breeders to accurately edit the genome by using conventional breeding tools [30][31]. Therefore, new breeding technologies such as “CRISPR/Cas9, TALENs, and ZFNs” have great potential for expediting the editing of genome in a more accurate and time-saving manner [32][33][34].

The process of breeding potatoes is an inefficient method due to the inherent genetic and biological characteristics. The chromosome number of potato is 12 that range from diploid to hexaploid species. Majority of the species are “diploids (about 73%), tetraploids (about 15%), hexaploids (around 6%), triploids (about 4%) and pentaploids (about 2%).” The diploid species include S. stenotomum, S. phurejaand S. ajanhuri, out of which two are more sexually fertile as compared to the one which is less fertile. The species of potato, i.e. S. tuberosum and S. demissum are autotetraploid species with chromosome number, 2n = 4x=48 are usually fertile in a good number. So, it has been seen that all the diploid species are self-incompatible while all the teraploid species and hexaploid species are self-compatible [35].

As compared to the conventional breeding technique, the Agrobacterium-mediated method of introducing the specific gene into the potato plant takes only 6 – 12 months. Moreover, the “targeted germplasm” consist of desirable agronomic traits which are suitable for the potato plant and produces tubers with superior postharvest processing qualities. According to a study, the introduction of stable tDNA into the host plant cell, i.e. the potato plant cells for improving their breedshas been reported[36], which in turn, allows for the introduction of multiple genes at the same time.

Transformation provides a very effective way to add single genes into the current elite potato clones with very small or no genetic disruption [37][38]. This is virtually impossible through conventional breeding technique, as the genetic integrity of potato clones is lost in the course of sexual reproduction due to a high heterozygosity in the tetraploid potato genome. The only effective means by which isogenic lines of specific genotypes/cultivars can be produced is thus, potato transformation [39].

“TALENs technology” is used for interrupting the activity of Vlnv to enhance the nutritional value of potato tubers and to decrease the accumulation of sugars during “cold-induced processing (CIS)” [40].

Other methods of introducing the nutrients in potato plants includes starch alterations using TALENs technology

Received: 10 Nov 2018 | Revised: 20 Dec 2018 | Accepted: 02 Jan 2019

[41] and CRISPR/Cas9 [42]. A system termed as "Emerald – Gateway TALEN System" designed by a scientist targets a host gene "Granule – bound starch synthase (GBSS)" in potato for site-specific mutation. During the starch granulation, GBSS is involved in the biosynthesis of amylase. The disruption of the GBSS could result in the reduction of amylase/amylopectin content and their ratio [43], which can affect the quality of starch in potato.

III. BIOTIC AND ABIOTIC STRESSES RESISTANCE FACTORS:

The utilization of pesticides reduces the introduction of pest resistance in cultivated species. In the same way, manipulation of the gene expression that regulates the water efficiency of water enables the increased performance under water deficit conditions. Fortunately, wild and cultivated germplasm collections are diverse and many wild species have economic resistance against various diseases. Resistance against diseases is comparatively easy to integrate because most of the traits are single genes and which are bound in a dominant fashion. Single genes can have a dramatic effect on the host plant when the pathogen is present, but the rapid growth and development of pathogen has led to the collapse of disease resistance after deployment [44][45].

IV. CONCLUSION

The population of world in the upcoming years is expected to increase to at least 9 billion by 2050, which represents an increase of about 2 billion population in next 40 years that requires a 70% increase in the production of food. The destruction of cultivated and wild species of potato crops has the ability to make whole set of chromosomes whih has a good ability to produce new and valuable genotypes having high quality. Availability of potato genome sequencing has facilitatedthe comparative genome analysis to classify the genes to enhance some agronomically significant characteristics, such as "tuberization, disease resistance", etc.

REFERENCES

[1] ISAAA, "Global status of Commercialized biotech / GM Crops : 2016," ISAAA Br. No. 52, 2016.
[2] D. Vreugdenhil et al., Potato Biology and Biotechnology: Advances and Perspectives. 2007.
[3] Potato Biology and Biotechnology. 2007.
[4] G. J. Scott and V. Suarez, "The rise of Asia as the centre of global potato production and some implications for industry," Potato J., 2012.
[5] S. Liang and A. G. McDonald, "Chemical and thermal characterization of potato peel waste and its fermentation residue as potential resources for biofuel and bioproducts production," J. Agric. Food Chem., 2014.
[6] B. Leff, N. Ramankutty, and J. A. Foley, "Geographic distribution of major crops across the world," Global Biogeochem. Cycles, 2004.
[7] P. R. J. Birch et al., "Crops that feed the world 8: Potato: Are the trends of increased global production sustainable?," Food Secur., 2012.
[8] K. Watanabe, "Potato genetics, genomics, and applications," Breeding Science. 2015.
[9] E. J. Tepe, F. T. Farruggia, and L. Bohs, "A 10-gene phylogeny of Solanum section Herpystichum (Solanaceae) and a comparison of phylogenetic methods," Am. J. Bot., 2011.
[10] F. M. Shapter, P. Eggler, L. S. Lee, and R. J. Henry, "Variation in Granule Bound Starch Synthase I (GBSSI) loci amongst Australian wild cereal relatives (Poaceae)," J. Cereal Sci., 2009.

Received: 10 Nov 2018 | Revised: 20 Dec 2018 | Accepted: 02 Jan 2019

[11] Margaret Chiipanthenga, "Potential of aeroponics system in the production of quality potato (Solanum tuberosum l.) seed in developing countries," AFRICAN J. Biotechnol., 2012.
[12] "National Agricultural Statistics Service," Choice Rev. Online, 2006.
[13] Y. S. Chung, C. Kim, and S. Jansky, "New source of bacterial soft rot resistance in wild potato (Solanum chacoense) tubers," Genet. Resour. Crop Evol., 2017.
[14] D. D. Stuthman, K. J. Leonard, and J. Miller-Garvin, "Breeding Crops for Durable Resistance to Disease," Advances in Agronomy. 2007.
[15] C. N. Hirsch et al., "Retrospective view of North American potato (Solanum tuberosum L.) breeding in the 20th and 21st centuries," G3 Genes, Genomes, Genet., 2013.
[16] K. Zaheer and M. H. Akhtar, "Potato Production, Usage, and Nutrition—A Review," Crit. Rev. Food Sci. Nutr., 2016.
[17] B. Burlingame, B. Mouillé, and R. Charrondière, "Nutrients, bioactive non-nutrients and anti-nutrients in potatoes," Journal of Food Composition and Analysis. 2009.
[18] R. Henry, "Plant Genetic Resources," in Routledge Handbook of Agricultural Biodiversity, 2018.
[19] P. Ahmad et al., "Role of transgenic plants in agriculture and biopharming," Biotechnology Advances. 2012.
[20] K. N. Singh, D. Kumar, M. Shamim, and M. Kumar, "Biosafety for sustainable agriculture," in Biotechnology for Sustainable Agriculture: Emerging Approaches and Strategies, 2017.
[21] S. Gómez-Galera, A. M. Pelacho, A. Gené, T. Capell, and P. Christou, "The genetic manipulation of medicinal and aromatic plants," Plant Cell Reports. 2007.
[22] A. J. Conner, N. W. Albert, and S. C. Deroles, "Transformation and regeneration of Petunia," in Petunia: Evolutionary, Developmental and Physiological Genetics (Second Edition), 2009.
[23] D. Halterman, J. Guenthner, S. Collinge, N. Butler, and D. Douches, "Biotech Potatoes in the 21st Century: 20 Years Since the First Biotech Potato," American Journal of Potato Research. 2016.
[24] T. H. Park et al., "The late blight resistance locus Rpi-blb3 from Solanum bulbocastanum belongs to a major late blight R gene cluster on chromosome 4 of potato," Mol. Plant-Microbe Interact., 2005.
[25] A. L. Tek, W. R. Stevenson, J. P. Helgeson, and J. Jiang, "Transfer of tuber soft rot and early blight resistances from Solanum brevidens into cultivated potato," Theor. Appl. Genet., 2004.
[26] A. J. Conner and P. J. Barrell, "Towards transfer of soft rot resistance to potato via somatic hybrids with Solanum brevidens," in 17th Biennial Meeting of the New Zealand Branch of the IAPTC&B. Conference Proceedings, 2007.
[27] D. P. Weeks, "Gene Editing in Polyploid Crops: Wheat, Camelina, Canola, Potato, Cotton, Peanut, Sugar Cane, and Citrus," in Progress in Molecular Biology and Translational Science, 2017.
[28] D. P. Weeks, Gene Editing in Polyploid Crops : Cotton , Peanut , Sugar Cane , and Citrus. 2017.
[29] D. Carputo and A. Barone, "Ploidy level manipulations in potato through sexual hybridisation," Ann. Appl. Biol., 2005.
[30] X. Xu et al., "Genome sequence and analysis of the tuber crop potato," Nature, 2011.
[31] R. G. F. Visser et al., "Sequencing the Potato genome: Outline and first results to come from the Elucidation of the sequence of the world's third most important food crop," American Journal of Potato Research. 2009.
[32] M. M. Mahfouz, T. Cardi, and C. Neal Stewart, "Next-generation precision genome engineering and plant biotechnology," Plant Cell Reports. 2016.
[33] J. F. Petolino, V. Srivastava, and H. Daniell, "Editing Plant Genomes: A new era of crop improvement," Plant Biotechnology Journal. 2016.
[34] S. Schiml and H. Puchta, "Revolutionizing plant biology: Multiple ways of genome engineering by CRISPR/Cas," Plant Methods. 2016.
[35] B. D. Singh and A. K. Singh, Marker-assisted plant breeding: Principles and practices. 2015.
[36] S. B. Gelvin, " Integration of Agrobacterium T-DNA into the Plant Genome ," Annu. Rev. Genet., 2017.
[37] A. J. Conner, "Field-testing of transgenic potatoes," in Potato Biology and Biotechnology: Advances and Perspectives, 2007.
[38] J. Muthoni and D. O. Nyamongo, "Traditional food crops and their role in food and nutritional security in kenya," J. Agric. Food Inf., 2010.
[39] V. Balasubramanian and N. Sakthivel, "Genetically engineered crops and their implications," in Genetically Engineered Crops: Biotechnology, Biosafety and Benefits, 2011.
[40] B. M. Clasen et al., "Improving cold storage and processing traits in potato through targeted gene knockout," Plant Biotechnol. J., 2016.
[41] H. Kusano, H. Onodera, M. Kihira, H. Aoki, H. Matsuzaki, and H. Shimada, "A simple Gateway-assisted construction system of TALEN genes for plant genome editing," Sci. Rep., 2016.

[42] M. Andersson, H. Turesson, A. Nicolia, A. S. Fält, M. Samuelsson, and P. Hofvander, “Efficient targeted multiallelic mutagenesis in tetraploid potato (Solanum tuberosum) by transient CRISPR-Cas9 expression in protoplasts,” Plant Cell Rep., 2017.
[43] S. C. Zeeman, J. Kossmann, and A. M. Smith, “Starch: Its Metabolism, Evolution, and Biotechnological Modification in Plants,” Annu. Rev. Plant Biol., 2010.
[44] I. Ben Rejeb, V. Pastor, and B. Mauch-Mani, “Plant responses to simultaneous biotic and abiotic stress: Molecular mechanisms,” Plants. 2014.
[45] N. Suzuki, R. M. Rivero, V. Shulaev, E. Blumwald, and R. Mittler, “Abiotic and biotic stress combinations,” New Phytol., 2014.

Received: 10 Nov 2018 | Revised: 20 Dec 2018 | Accepted: 02 Jan 2019