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RESEARCH PAPER

Breeding Strategies for Climate Resilient Traits in Potato (Solanum Tuberosum L.)

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Abstract

Climate change factored rise in temperatures coupled with the climatic variation like temperature, rainfall pattern and humidity are going to be major limiting factors in sustainable vegetable production. Potato (Solanum tuberosum L.) is an important global food source, after wheat, rice and maize. CPRI has projected that against the current production of 45.1 mt India will have to produce 56.15 and 124.88 million tonnes of potato during the years 2025 and 2050, respectively to meet the future demands. At the same time the crop is sensitive to heat, drought and moderately sensitive to cold and salinity stress which results in reduction of size and number of tubers. However, large germplasm and wide range of species and genetic diversity in potato provide opportunity to develop climate resilient genotypes to minimize the impact of climate change.

Different breeding strategies for potato which could help in climate resilient breeding program includes 1) Screening of wild relative for resistant sources; 2) Utilization of the resistant species in hybridization and somatic hybridization; 3) Identification and mapping of stress tolerant QTLs; 4) Marker assisted selection of tolerant gene; and 5) Transfer of stress tolerant genes from other unrelated crop through transgenic approach. There is various report of successful transfer of genes in potato such as development of heat tolerant variety (Kufri Surya) through hybridization (Anonymous, 2006). Cardi et al., 1999, developed somatic hybrid between S. tuberosum and S. commersonii for frost tolerance. Anithakumar et al., 2012, identified 28 drought specific QTLs and 17 under recovery treatment in potato. A BADH gene from spinach under the control of the stress-induced promoter rd29A from Arabidopsis thaliana was introduced for salinity and drought tolerant in potato cv. Gannongshu 2 by Agrobacterium tumefaciens methods. Therefore, location specific suitable new breeding approaches need to be formulated for developing climate resilient varieties of vegetable crops for sustaining the self-sufficiency in this sector.

KEYWORDS:
Climate Change, Potato Climate Resilient Breeding, QTL Mapping, Abiotic Stress Tolerance

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Introduction

Climate change in IPCC usage refers to any change in climate over time, whether due to natural variability or as a result of human activity that alters the composition of the global atmosphere and that is in addition to natural climate variability observed over comparable time periods (IPCC, 2007).Climate change is a long-term continuous change (increase or decrease) to average weather conditions and the climate variation are the way climate fluctuates day/ season/yearly above or below a average value. Every year in a specific time period, the climate of a location is different. The changing patterns of climatic parameters like rise in atmospheric temperature, changes in precipitation patterns, excess UV radiation leads to higher incidence of extreme weather events like droughts, floods and salinity which are emerging major threats for vegetable production in the tropical zone (Tirado *et al.*, 2010). Globally the averaged surface temperature is expected to rise by between 1.1°C up to 6.4°C by the last decade of the 21st century (Minaxi *et al.,* 2011*),* likewise *t*he Indian climate has undergone significant changes showing increasing trends in annual temperature with an average of 0.56°C rise over last 100 years (Rao *et al.* 2009). This temperature increase will alter the timing and amount of rainfall, availability of water, wind patterns and causes incidence of weather extremes, such as droughts, heat waves, floods or storms. Under this changing climatic situation crop failure, reduction in yield, decrease in quality and higher incidence of pest and disease are common and which render vegetable cultivation unprofitable and thread to future productivity is loaming large on developing countries including India. At high altitudes, global warming will probably lead to changes in the time of planting, the planting of late-maturing cultivars, and a shift of the location of potato production. In many of these regions in India, changes in potato yield are likely to be relatively small in initial stage but expected to trigger in coming era of global warming. Shifting planting time or location is less feasible at lower altitudes, and in these regions global warming could have a strong negative effect on potato production. It is likely that the currently observed trend of global warming, which has been 0.6 ºC + 0.2 since 1900, will continue and that the average global temperature will increase by between 1.4 and 5.8 ºC over the period 1990 to 2100 (IPCC,2001). It is shown that heat-tolerant potato cultivars could be used to mitigate effects of global warming in (sub) tropical regions. Climate change is now an acknowledged fact and reality. Potato is an important global food source after wheat &rice. Potato is well known for its exact temperature and day length requirement for tuber formation as well as flowering, so it becomes the most vulnerable crop for climate change. Potato productivity is expected to decline in all potato growing states of India. Luck *et al.,* (2010) expected 16% decline in tuber yield of potato by 2050 for West Bengal if any special strategies are not adapted. However, they suggested planting of potato crop at a new optimal date of mid-November in order to minimize the yield losses up to 8%. Increase in temperature favours the potato cultivation by prolonging the crop growing season in high altitudes and temperate regions of the world like Europe, Russia and in India. It is estimated that by 2020 more than two billion people worldwide will depend on potato for food, feed, or income and the climate change is projected to have a large impact on future yields in many potato growing regions and its production in India is estimated to decline by 10 and 16% by 2020 and 2050, respectively, if no adaptation strategy is implemented. This review will have summarized the different effect of climate change on potato growth and development and the strategies to combat the effect.

1. Different breeding strategies for climate resilience traits

World crop production is increasingly impacted by global climate change and for the reliable food production during the period of climate change will require substantial changes in crop breeding, farming practices and infrastructure. The establishment of integrated agronomic and management approaches, along with strategies to improve crop adaptation to abiotic stress and yield stability under these variable environmental conditions is urgently required.

Resilience is the capacity to deal with change and recover after it. In many regions, farmers benefit from cropping systems that have evolved to provide stability of production over time, rather than maximising production in a year. In effect, climate change is forcing scientists to rethink priorities and focus on stress tolerant rather than high yielding varieties

The development and identification of climate resilient crop varieties, with enhanced tolerance to heat, drought, flooding, chilling and salinity stresses are essential in order to sustain and improve crop yields to cope with the challenges of climate change.

The different strategies are as follow

The management of abiotic stress depends upon the nature of stress and affected crop, the stage of the crop, intensity of the stress and duration of the stress. The nature of stress makes us understand the kind of interaction between the environment and crop plants.

1. Screening and selection for tolerance genotypes under stress condition/genomics strategies for germplasm characterization
2. Hybridization & wide hybridization
3. Marker Assisted Selection
4. Development of QTL associated with stress tolerant
5. Generation of stress tolerant transgenic Potato

2. Screening and selection of wild species for tolerance to different stresses

Potato has an extremely large secondary gene pool consisting of related wild species. Therefore, its taxonomy has been a subject of study for many years. Crop wild relatives and landraces constitute reservoirs of genetic diversity and are key resources for adaptation to climate change and provide genes and traits for developing stress resistant variety (Lane and Jarvis, 2007). According to (FOA, 1997) the major crops (potato, tomato, sugarcane) could not be grown without the contribution of CWRs to disease resistant. Efforts to protect wild plant genetic resources have focused on major cereal crops and legumes, only 5% of the accessions in global gene banks correspond to wild relatives of vegetable crops (FAO, 2010) .The potato has one of the richest genetic resources of any cultivated plant. Many wild species can be crossed directly with the common potato and moreover, possess a wide range of resistances to pests and diseases reported by different scientist and listed in Table 2.

Wild potato species, such as *S. commersonii* Dun. and *S. acaule* Bitt. (Chen and Li 1980a) and S. *spegazzinii* S. *demissum* and S. *tuberosum ssp. Andigena* (Luthra et al.,2008) and S. *Juzepczukii* (Tapia and Saravia,1997) were found promising for frost tolerance. these wild species have an ability to improve their freezing tolerance at low temperature by cold acclimation . S. *demissum*, S. *acaule*, and S. *juzepczukii* were not affected by frost of −6°C (Bukasov (1933)). So there is need of effective evaluation and exploitation of existing genetic variability in various species and genotypes of potato under different stress condition. 98 lines/cultivars for were evaluated for frost tolerance under natural conditions and showed that CP 1619, CP 2318, A.98-166, A.98-54,: J.95-229 and JX 576 suffered less than 10% foliage damage due to frost and among the cultivars evaluated for frost tolerance Kufri Pushkar was the best with foliage damage of about 30% as reported by Kang et al.,2008. The breeding line such SS 2040 and SS 1725-22 are the frost tolerant clone of *Solanum tuberosum ssp. Andigena* and diploid clone of *Solanum spegazzinii*, respectively which were registered at CPRI Shimla (Kumar *et al.* 2014) and can be used to developed frost tolerant varieties.

Screening for drought tolerance in potato landraces has been performed by Cabello *et al.* (2012, 2013) and a high proportion of accessions combining drought tolerance with high irrigated yield were found in Andean landraces, particularly in the species *S. curtilobum* (Juz. & Bukasov) in the *S. tuberosum* L. cultivar groups *Stenotomum, Andigenum*, and Chaucha. Watanabe *et al.* (2011) identified *S. chillonanum*, *S. jamesii*, and *S. okadae* as potential drought-tolerant species by screening 44 accessions of wild species selected based on their drought habitats derived from GIS information. *Solanum juzepczuckii* and *S. curtilobum* were identified as salt tolerant by their ability to form microtuber in medium with added salt (Silva *et al.*,2001)

Diverse late blight resistance genes are found in wild and cultivated relatives of potato e.g. *S. bulbocastanum, S. demissum and S. stoloniferum*. And other wild species possessing resistance are S. *tuberosum ssp. andigena, S. pinnatisectum, S. polyadenium, S. verrucosum, S. chacoense, S. berthaulti, S. vernei, S. polytrichon, S. simplicifolium and S. microdontum* (Bhardwaj.) were found to be most promising having high late blight resistance under laboratory and field testing as reported by Bhardwaj et al.2018 under Indian condition. CP 1722, CP 2000, CP 2011, CP 2163 and CP 2379, along with potato variety Kufri Girdhari showed resistance against late blight under both laboratory and field conditions in India (Srivastava *et al.*,2015).

A wide range of pest resistance has been identified in wild species. Various studies indicate that resistances to insects are due to glycoalkaloids, glandular trichomes, and other undetermined mechanisms (Flanders *et al.* 1992, Pelletier et al. 2013). Flanders et al. (1992) evaluated 100 species of wild potato for resistance to various insect and reported that resistance was associated with glycoalkaloid tomatine, dense hairs, and glandular trichomes. Jansky et al. (2009) reported resistance to Colorado potato beetle was confirmed in species characterized by high levels of glycoalkaloids (*S. chacoense*) or dense glandular trichomes (*S. polyadenium and S. tarijense*).The wild Solanum species mostly exploited in PCN resistance breeding are S. *tuberosum ssp. andigena*, S. *vernei* and S.*spegazzini*. PCN resistance has been reported in other wild sources viz., S. *gourlayi*, S. *sparsipilum*, S. *chacoense*, S. *phureja*, S. *demissum*, S. *gourlayi*, S. *microdontum*, S. *sucrense*, S. *tarijense*, S. *acaule*, S. *multidissectum*, S. *oplocense* (Phillips, 1994). Other sources of resistance genes to PVY are detected in wild species of S. *chacoense*, S. *hougasii*, S. *demissum* by Cockerham (1970) and Valkonen *et al.* (1994).

Table 1:Sources of resistance to various biotic stress in wild potato species (Dalamu, 2014, CPRI

Diseases/Pest	**Sources**
Potato virus X	*S. acaule, S. berthaultii, S. tuberosum* subsp. *andigena*
Potato virus Y	*S. phureja, S. demissum, S. stoloniferum*
Potato leaf curl virus	*S. acaule, S. demissum, S. tuberosum* subsp. *andigena*
Late blight - Vertical	*S. demissum, S. verrucosum, S. stoloniferum , S. berthaultii, S. chacoense, S. microdontum, S. vernei*
Wart	*S. acaule, S. berthaultii.*
Common scab	*S. chacoense, S. tuberosum* ssp. *andigena*
Bacterial wilt	*S. chacoense, S. microdontum,*
Cyst nematodes	*S. tuberosum* subsp. *andigena, S. berthaultii. S. vernei,*
Root knot nematode	*S. spegazzinii*
Aphids	*S. berthaultii. S. brachistotrichum*

Table 2: Wild species of potato tolerant to abiotic stress

Traits	Species	Reference
Drought	*S. acaule* and *S. demissum*	Arvin and Donnelly,2008
Salt	*S. acaule and S. demissum*	Arvin and Donnelly,2008
Heat	*S. chacoense* (2n), *S. commersonii* (2n), *S. demissum*, and *S. hjertingii* (2n)	Bilski *et al.* (1988) ; Arvin and Donnelly,2008
Frost	*S. spegazzinii* (2n) *S. demissum* (6n) and *S. tuberosum* ssp. *Andigena* (4n)	Luthra *et al.*, 2007
	S. acaule, S. commersonii, and S. demissum	Bamberg (1995)
	(*S. acaule* and *S. albicans*) *S. commersonii*, and *S. calvescens*	Hijmans *et al.*, 2002
	S. acaule and S. commersonii	Li,1977;Palta, 2014;Hijmans,2003
	S. Juzepczukii and ajanhuiri	Bruno Conduri,2013

3. Hybridization and somatic hybridization

Gene transfer is the basis of potato improvement, as wild potato species harbour numerous genes conferring resistance to biotic and abiotic stresses. However, many useful genes from wild species cannot be transferred through conventional breeding due to sexual incompatibility arising from differences in ploidy and endosperm balance number (EBN) (Spooner et al., 2001). Crossing 1 EBN wild species with cultivated potato (4 EBN) is particularly difficult (Jackson & Hanneman, 1999). Somatic hybridization through protoplast isolation, fusion and regeneration has emerged as an effective tool to overcome these barriers by enabling the transfer of both nuclear and cytoplasmic genes and broadening the genetic base in a single step (Zhou et al., 2001; Eeckhaut et al., 2013).

Several somatic hybrids have been developed for transferring stress tolerance genes from wild species to cultivated potato. Protoplast fusion has been widely used to introgress late blight resistance from *S. bulbocastanum*, *S. pinnatisectum*, *S. michoacanum*, *S. villosum* and *S. cardiophyllum*. Somatic hybrids between *S. tuberosum* and *S. bulbocastanum* facilitated mapping and cloning of the RB gene, a major late blight resistance gene (Song et al., 2003). Hybrids involving *S. berthaultii* enabled transfer of insect resistance with high yield potential (Serref et al., 1991).

At CPRI, interspecific somatic hybrids were developed between dihaploid *S. tuberosum* and *S. etuberosum* (resistant to PVY) and *S. pinnatisectum* (resistant to late blight), both tetraploid and male fertile (Kumar et al., 2014). Somatic hybrids of *S. tuberosum* and *S. commersonii* exhibited enhanced frost tolerance by 2.6 °C (Cardi et al., 2000). Chen et al. (2008) also reported somatic hybrids involving *S. pinnatisectum*, *S. cardiophyllum* and *S. chacoense*, with hybrids involving *S. pinnatisectum* showing high resistance to both late blight and Colorado potato beetle.

Table 3: List of stress tolerant gene transferred to cultivated potato using somatic hybridization

Recipient (Common potato)	Donor (Wild spp.)	Resistance trait transferred	References
S. tuberosum spp. *Tuberosum*	*S. bulbocastanum*, *S. cardiophyllum*, *S. chacoense*,	Resistance to late blight, Colorado potato beetle	Chen *et al.* (2008
	S. pinnatisectum	Resistance to late blight	Polzerova *et al.* (2011); Sarkar *et al.* (2011)
	S. bulbocastanum	Resistance to late blight	Song et al. 2003.
	S. tarnii	Resistance to PVY and late blight	Thieme *et al.* (2008)

	S. michoacanum	Resistance to late blight	Smyda *et al.* (2013)
	S. etuberosum	Resistance to PVY	Tiwari *et al.* (2010)
	S. chacoense	Resistance to bacterial wilt	Chen *et al.* (2013)
	S. cardiophyllum	Resistance to Colorado potato beetle, PVY and late blight	Thieme *et al.* (2010)
	S. berthaultii	Tolerance to salinity	Bidani *et al.* (2007)
	S. brevidens	Resistance to soft rot, early blight and PLRV	Tek *et al.* (2004)
	S. bulbocastanum *S. pinnatisectum*	Resistance to late blight, soft rot, nematode, heat and drought	Greplova et al. (2008)
	S. berthaultii	insect	Serraf *et al.*1991
	S.commersonni	Frost	Cardi *et al.*,1998

4. Marker Assisted Selection

The traditional approach to transferring genes from wild to cultivated species is based on interspecific hybridization followed by selection of hybrids that combine the "new wild" trait with the cultivated genetic background with series of back cross generation to the cultivated genotype with the aim of reducing the wild genome which was expensive and time consuming. In the last 10 years, the use of molecular markers has allowed this breeding approach to be greatly improved as the MAS allows for the selection of desirable genes using marker which are linked to the trait of interest and can apply at seedling stage without waiting for particular stage to express the trait. Using marker assisted back cross breeding 99% of the cultivated genome can be recovered with only three backcross generations instead of the six to seven generations required to recover the same percentage of genome without the use of molecular markers. DNA-based markers have also been used to study the relationships of different potato species with different marker system such as SSR (Spooner et al.,2007; Gavrilenko *et al.*,2010), RFLP (Gebhardt et al.,1991) RAPD (Hosaka *et al.*,1994), AFLP (Kim et al.,1998).The genome sequence of potato has recently been completed. The sequence information of the 844 Mb genome revealed 39,031 protein-coding genes in potato and suggested a paleohexaploid duplication event during the genome evolution (The Potato Genome Sequencing *Consortium* 2011). Genome sequence information will be a platform for genetic improvement of potato as well as for phylogenetic research on the genus *Solanum*. The use of molecular markers in potato breeding is reported for many purposes, such as cultivar identification (Gebhardt *et al.* 1989), phylogenetic studies (Kardolns *et al.* 1998), analysis of recombination between genomes (Williams *et al.* 1993), identification of genes controlling traits (Gebhardt 1994), and assisted selection (Hamalainen *et al.* 1997). In breeding programs ahned to transfer useful genes between different species with the aid of molecular markers, the first step is the identification of one or more markers linked to the gene(s) to be introgressed and their localization on the molecular map.

Barone *et al.* (2001) did obtain 48 chromosomes and evidence of recombination between *S. commersonii* (2x 1EBN) and *S. tuberosum* chromosomes in their molecular marker-assisted introgression of tuber soft rot resistance. SCAR marker tightly linked to the potato virus Y (PVY) resistant gene (*Ryadg*) and its further use to develop a triplex parental line using marker assisted selection (MAS) was done by Kaushik et al.,2013. The triplex clone, YY-6/3 C11 was identified as carrying the extreme resistance gene to PVY. Use of this elite parental line in potato breeding programmes would ensure that 96% of the progeny carried at least one copy of the *Ryadg* gene, thus having extreme resistance to PVY. Flis *et al.*, 2005 identified a novel locus for extreme resistance to Potato virus Y (PVY), Ry-fsto, on potato chromosome XII.The gene Ry-fsto has been introgressed from the wild potato species *Solanum stoloniferum*. Bulked segregant analysis identified an ISSR (inter-simple sequence repeat) marker UBC 857980 linked to Ry-fsto. This marker mapped to linkage group XII of a reference potato RFLP (restriction fragment length polymorphism) map.

An example of the successful development of marker-assisted breeding in tetraploid potato is described by Moloney et al. (2010) who selected for resistance to the potato cyst nematode *Globodera pallida*. Gebhardt et al. (2006) developed potato clones with multiple pathogen resistance traits by applying PCR-based markers to combine Ryadg (resistance to PVY), Gro1 (resistance to the nematode *Globodera rostochiensis*) and Rx1 (resistance to potato virus X), or Sen1 (resistance to potato wart, *Synchytrium endobioticum*)

5. QTL (Quantitative Trait Loci) mapping

Linkage maps are primarily used to identify chromosomal regions containing genes and quantitative trait loci (QTLs) associated with traits of interest, commonly referred to as genetic or QTL maps. QTL mapping is based on the segregation of genes and molecular markers through chromosome recombination during meiosis, allowing their detection in progeny populations (Paterson, 1996a). Closely linked genes and markers are inherited together more frequently than those located further apart.

The first potato genetic maps were developed using RFLP markers in different genetic backgrounds (Bonierbale et al., 1988) and were later aligned with the tomato RFLP map (Gebhardt et al., 1991). Subsequent development of molecular markers enriched the potato map with over 350 markers (Gebhardt et al., 2001). QTLs controlling plant height, maturity and yield components have been identified (Bradshaw et al., 2008). Early QTLs for biotic stress resistance included insect resistance (Bonierbale et al., 1994; Yencho et al., 1996), followed by resistance to *Phytophthora infestans*, *Erwinia carotovora*, *Globodera* spp. and potato leafroll virus (Gebhardt & Valkonen, 2001; Marczewski et al., 2001). Three major QTLs for late blight resistance were detected on linkage groups III, V and XI, explaining 23, 17 and 10% of phenotypic variation, respectively (Costanzo et al., 2005). Resistance to *G. rostochiensis* was mapped to chromosomes X, XI and III (Gro1.2, Gro1.3 and Gro1.4) using *S. spegazzinii* as the resistance source. Late blight resistance genes Rber (*S. berthaultii*) and Rblc (*S. bulbocastanum*) were mapped to chromosomes X and VIII, respectively (Ewing et al., 2000).

Potato virus Y (PVY) can cause up to 80% yield loss (Hane & Hamm, 1999). The Ryadg gene from *S. andigena*, conferring extreme resistance to all PVY strains, was mapped and cloned, and SCAR markers were developed for its detection (Hamalainen et al., 1997; Kasai et al., 2000). Ry genes have also been reported in *S. stoloniferum*, *S. phureja*, *S. brevidens* and *S. chacoense*. The hypersensitive response gene Ny and the Rysto gene were mapped to chromosome XII (Song et al., 2005; Szajko et al., 2008, 2014). For potato cyst nematode, the dominant Gro1 gene from *S. spegazzinii*, conferring resistance to all pathotypes of *G. rostochiensis*, was mapped to chromosome VII, while Gro1-4 provides resistance to pathotype Ro1 (Barone et al., 1990; Paal et al., 2004). Resistance to bacterial wilt has been identified in *S. phureja*, *S. stenotomum*, *S. commersonii* and *S. chacoense*, and transferred to cultivated potato through protoplast fusion and somatic hybridization.

Late blight remains the most destructive potato disease worldwide (CIP, 2013). Several broad-spectrum and durable R genes have been identified and cloned from wild species, including RB/Rpi-blb1, Rpi-blb2 and Rpi-blb3 from *S. bulbocastanum*, Rpi-sto1 from *S. stoloniferum*, Rpi-pta1 from *S. papita* and Rpi-vnt1.1 from *S. venturii*. Additional R genes have been reported from numerous wild *Solanum* species. Chakrabarti et al. (2014) identified two late blight resistance QTLs on linkage groups IX and X, explaining 14.7% and 3.4% variation, respectively. Anithakumar et al. (2007) identified 47 QTLs for drought tolerance, including 28 drought-specific QTLs, from populations involving *S. phureja*, *S. tuberosum* and *S. vernei*.

6. Development of stress tolerant transgenic

Gene technologies can offer alternative and complementary paths for adaptation of potato to changing environments. Resistance genes not present in the potato gene pool could be introduced by transgenic technologies into breeding populations. Recently, gene transfer approaches have been employed to improve the stress tolerance of plants. Enhanced tolerance to extreme environments through introduction of genes encoding antioxidant enzymes, those involved in modification of membrane lipids and in the biosynthesis of osmoprotectants. Major breakthrough in abiotic stress technology comes when the DREB/CBF genes from *Arabidopsis thaliana* and some other plants were identified. Transgenic potato plant over expressing potato St DREB1 or 2 genes accumulated higher levels of proline and showed reduced water loss under drought and salinity (Bouaziz et al., 2012, 2013) and more overexpression of Sc CBF1 gene from wild potato *solanum commersonii* enhanced drought stress tolerance in transgenic solanum tuberosum and S. commersonii planlet grown in vitro (Pino et al.,2013). The Arabidopsis CBF1gene has been shown to increase freezing tolerance in several species, including potato (Pino et al.,2008). Jeong *et al.*, 2001 introduced the glyceraldehydes-3-phosphate dehydrogenase gene into potato by genetic engeenering. The transgenic potato exhibited some degree of salinity tolerance. Celebi-Toprak *et al.* (2005) transformed *S. tuberosum* cv Desiree with the DREBIA (dehydration responsive element) gene under the control of a stress inducible promoter (rd29A) from *Arabidopsis* and selected nine of 78 transformants had exhibited salinity tolerance.

The Arabidopsis CBF1 gene (AtCBF1) increase drought tolerance was transformed into a cultivated potato line under the control of the stress inducible promoter COR15a (Nicho *et al.*, 2015).Transgenic potato plant with enhanced tolerance of oxidation, salt and drought stresses by synthesizing GB via the introduction of bacterial choline oxidase (codA) gene.

Glycine betaine is one of the most important osmolytes present in higher plants that enable them to cope with environmental stresses through osmotic adjustment. Potato is deficient of glycine betaine. To transfer betaine in cultivated potato Zang *et al.*, 2011, In his study a betaine aldehyde dehydrogenase (BADH) gene from spinach under the control of the stress-induced promoter rd29A from Arabidopsis thaliana was introduced into potato cultivar. For the transfer of BADH gene a plasmid pBIrB containing the BADH gene was constructed. The BADH activities of the transgenic plants were rather low when they were not stressed, but increased greatly 3 days after the treatment with NaCl and PEG had finished thus showed tolerance to heat and salt stress.introduction of the yeast TREHALOSE-6-PHOSPHATE SYNTHASE 1(TPS1) gene, which functions in the biosynthesis of osmolyte trehalose, into potato leads to drought tolerance by increasing the leave relative water content in source tissues (leaves) (Kondrak et al.,2012). Expression of gene associated with production of antioxidant, flavanoids, heat shock protein HSP) and late embryogenesis abundant (LEA) were found to be induced under water stress (Watkinson et al.,2006;Schafleitner et al.,2007) and these gene have been use to generate drought tolerant transgenic potato. In order to improve the drought tolerance in potato using antioxidant the Arabidopsis gene encoding for Dehydro Ascorbate Reductase (DHAR1) was overexpressed in potato, and therefore ascorbate levels increase in transgenic plants, causing better growth in drought condition (Eltayeb et al.,2011). Heat shock protein are synthesized in plant under high temperature stress (Sun et al.,2002). Transgenic approached utilizing HSPs in order to develop thermo tolerance were demonstrated in several plant species including rice (Katiyar Agarwal et al.,2003). Similar studies with HSPs can be carried out in potato as well since expression of HSP70 was found to be induced in potato plants exposed to high temperature (Dou et al.,2015). Potato transformation of Arabidopsis rd29 A:DREB1A have increased salinity tolerance (Behnam et al.,2006)

Two of the most damaging insect pests of potato are the Colorado potato beetle (CPB) and potato tuber moth

(PTM). CPB can completely destroy a plant by defoliating it and the insect has been observed to develop resistance rapidly to a wide variety of insecticides (Harris and Svec, 1981). PTM affects potato crops in temperate as well as tropical climates (Fenemore, 1988) and can cause damage in the field, as well as in storage. Potatoes transformed with a cry3A gene modified in this way were shown to be resistant to CPB (Perlak *et al.,* 1993). Potato plants expressing the Cry3A toxin were released by Monsanto under the name 'NewLeaf' (Hoy, 1999). They were commercially available in the USA from 1996 to 2000 and provided good CPB control, but were later discontinued following perceived concerns from consumers, marketing issues and the introduction of a novel insecticide that controls both beetles and aphids (Shelton et al., 2002). To engineer resistance to CPB in potato, Cry3B has also been shown to be effective (Arpaia et al., 2000). genes which encode cysteine proteinase inhibitors (cystatins) confer resistance to potato cyst nematodes (Globodera rostochiensis and G. pallida) (Urwin et al., 2003). Replicase and coat protein genes from Potato Leafroll Luteovirus and Potato Y Potyvirus, respectively, provide resistance to these viruses (Duncan et al., 2002)

Table 4: Commercial biotic and abiotic stress tolerant varieties

Stress	**Variety released**
Late Blight	Kufri Giriraj, K. Swarna and K. Girdhari , K. Megha Kufri Badshah, Kufri Bahar , Kufri Lalima , Kufri Anand, Kufri Pushkar, and Kufri Garima
Frost	Kufri Sheetman and Kufri Dewa
Wart disease	Kufri Sherpa , Kufri Jyoti ,Kufri Muthu , kufri Kanchan
Heat tolerant	Kufri Lauvkar, K. Surya
Nematode	Kufri swarna
Cracking and hollow heart	Kufri Garima
Late blight	Fortuna Transgenic
CPB	New leaf (Transgenic)

References

1. **Anithakumari, A. M., Karaba, N., Nataraja, N., Visser, R. G. F. & Van der Linden, C. G. (2012).** Genetic dissection of drought tolerance and recovery potential by quantitative trait locus mapping of a diploid potato population. *Molecular Breeding*, 30: 1413–1429.
2. **Bamberg, J. B., Palta, J. P. & Vega, S. E. (2005).** Solanum commersonii cytoplasm does not improve freezing tolerance in substitution backcross hybrids. *American Journal of Potato Research*, 82: 251–254.
3. **Barone, A., Salamini, F. & Gebhardt, C. (1990).** Genetic mapping of Gro1, a dominant gene conferring resistance to *Globodera rostochiensis*, on potato chromosome VII. *Theoretical and Applied Genetics*, 80: 577–583.
4. **Bhardwaj, V., Dalamu, Srivastava, A. & Chakrabarti, S. W. (2018).** Late blight resistance status in wild potato species against Indian population of *Phytophthora infestans*. *Indian Journal of Horticulture*, 75(1): 99.
5. **Bonierbale, M. W., Plaisted, R. L. & Tanksley, S. D. (1988).** RFLP maps based on a common set of clones reveal modes of chromosomal evolution in potato and tomato. *Genetics*, 120: 1095–1103.
6. **Bukasov, S. M. (1933).** The potatoes of South America and their breeding possibilities. Suppl. 58, *Bulletin of Applied Botany*, Leningrad, pp. 1–192.
7. **Bradshaw, J. E., Hackett, C. A., Pande, B., Waugh, R. & Bryan, G. J. (2008).** QTL mapping of yield, agronomic and quality traits in tetraploid potato (*Solanum tuberosum* subsp. *tuberosum*). *Theoretical and Applied Genetics*, 116: 193–211.
8. **Cabello, R., De Mendiburu, F., Bonierbale, M., Monneveux, P., Roca, W. & Chujoy, E. (2012).** Large-scale evaluation of potato varieties, genetic stocks and landraces for drought tolerance. *American Journal of Potato Research*, 89: 400–410.

9. **Chakrabarti, S., Sharma, S., Sahi, G., et al. (2014).** Identification of QTL for late blight resistance in a *Solanum spegazzinii* × *S. chacoense* diploid mapping population. *Journal of Plant Pathology*, 96: 331–339.
10. **Chandel, P., Tiwari, J. K., Ali, N., Devi, S., Sharma, S., Luthra, S. K. & Singh, B. P. (2015).** Interspecific potato somatic hybrids between *Solanum tuberosum* and *S. cardiophyllum*. *Plant Cell, Tissue and Organ Culture*, 123: 579–589.
11. **Chen, Q., Li, H. Y., Shi, Y. Z., Beasley, D., Bizimungu, B. & Goettel, M. S. (2008).** Development of an effective protoplast fusion system for production of new potatoes with disease and insect resistance using Mexican wild potato species as gene pools. *Canadian Journal of Plant Science*, 88: 611–619.
12. **Coakley, S. M., Scherm, H. & Chakraborty, S. (1999).** Climate change and plant disease management. *Annual Review of Phytopathology*, 37: 399–426.
13. **Cockerham, G. (1970).** Genetic studies in resistance to potato virus X and Y. *Heredity*, 25: 309–348.
14. **Costanzo, S., Simko, I., Christ, B. J. & Haynes, K. G. (2005).** QTL analysis of late blight resistance in a diploid potato family of *Solanum phureja* × *S. stenotomum*. *Theoretical and Applied Genetics*, 111: 609–617.
15. **Ewing, E. E., Strausbaugh, C. A. & Maddox, D. (2000).** A late blight resistance gene from *Solanum berthaultii*. *Theoretical and Applied Genetics*, 100: 335–344.
16. **Fahim, M. A., Hassanein, M. K., Abou Hadid, A. F. & Kadah, M. S. (2011).** Climate change and tomato diseases in Egypt. *Acta Horticulturae*, 914: 317–320.
17. **Fock, I., Collonnier, C., Purwito, A., Luisetti, J., Souvannavong, V., Vedel, F., Servaes, A., Ambroise, A., Kodja, H. & Ducreux, G. (2000).**Resistance to bacterial wilt in somatic hybrids between *Solanum tuberosum* L. and *Solanum phureja*. *Plant Science*, 160:165–176.
18. **Flanders, M. A., Metcalf, R. L. & Tingey, W. M. (1992).** Studies on insect resistance in wild *Solanum* species: relationships of glycoalkaloids and glandular trichomes to resistance against insect herbivores. *Journal of Economic Entomology*, 85: 1210–1219.
19. **Flynn, R., Phillips, R., Ulery, A., Kochevar, R., Liess, L. & Villa, M. (2002).** Chile seed germination as affected by temperature and salinity. *New Mexico Chile Task Force Report*, pp. 1–12.
20. **Fidalgo, F. A., Santos, I. & Salema, R. (2004).** Effects of long-term salt stress on potato plants. *Annals of Applied Biology*, 145: 185–192.
21. **Gebhardt, C., Blomendahl, U., Schachtschabel, T., Debener, F., Salamini, F. & Ritter, E. (1989).** Identification of 2n breeding lines using RFLP fingerprints. *Theoretical and Applied Genetics*, 78: 16–22.
22. **Gibson, R. W. (1971).** Glandular hairs providing resistance to aphids in potato species. *Annals of Applied Biology*, 68: 113–119.
23. **Hamalainen, J. H., Watanabe, K. N., Valkonen, J. P. T., Arihara, A., Plaisted, R. L., Pehu, E., Miller, L. & Slack, S. A. (1997).** Mapping and characterization of the extreme resistance gene Ry (Ryadg) to potato virus Y (PVY) in *Solanum tuberosum* subsp. *andigena*. *Genome*, 40: 645–653.
24. **Hijmans, R. J., Jacobs, M., Bamberg, J. B. & Spooner, D. M. (2003).** Frost tolerance in wild potato species. *Euphytica*, 130: 47–59.
25. **Hosaka, K., Hosaka, Y., Mori, M., Maida, T. & Matsunaga, H. (2001).** Detection of a RAPD marker linked to resistance to potato virus Y in tetraploid potato. *American Journal of Potato Research*, 78: 191–196.
26. **Jacobs, J. M., Zhang, N., Mastenbroek, C., et al. (2010).** Characterization of late blight resistance in *Solanum verrucosum*. *Theoretical and Applied Genetics*, 120: 1–12.
27. **Jansky, S. H., Simon, R. & Spooner, D. M. (2009).** A test of taxonomic predictivity: resistance to the Colorado potato beetle in wild relatives of cultivated potato. *Journal of Economic Entomology*, 102(1): 422–431.
28. **Kasai, K., Morikawa, Y., Sorri, V. A., Valkonen, J. P. T., Gebhardt, C. & Watanabe, K. N. (2000).** Development of SCAR markers to the PVY resistance gene Ryadg based on a common feature of plant disease resistance genes. *Genome*, 43: 1–8.
29. **Kardolus, H. J., Eck, V. & Van den Berg, R. G. (1998).** AFLPs in *Solanum* taxonomy. *Plant Systematics and Evolution*, 210: 87–103.
30. **King, B. A. & Stark, J. C. (1997).** Potato Irrigation Management. University of Idaho Extension Bulletin.
31. **Kim-Lee, H., Moon, J. S., Hong, Y. J., Kim, M. S. & Cho, H. M. (2005).** Bacterial wilt resistance in the progenies of the fusion hybrids between a potato haploid and *Solanum commersonii*. *American Journal of Potato Research*, 82:129–137
32. **Kuhl, J. C., Pahal, R., Yang, H., et al. (2005).** Characterization of late blight resistance in *Solanum pinnatisectum*. *Theoretical and Applied Genetics*, 110: 1004–1014.
33. **Li, P. H. (1977).** Frost killing temperatures of tuber-bearing *Solanum* species. *American Potato Journal*, 54: 452–456.
34. **Li, P. H. & Palta, J. P. (1978).** Frost hardening and freezing stress. In: *Plant Cold Hardiness and Freezing Stress*, Academic Press, pp. 49–71.
35. **Lokossou, A. A., Park, T. H., Pel, M. A., et al. (2009).** Sequence diversity and expression of late blight resistance genes Rpi-blb1, Rpi-blb2 and Rpi-blb3 in *Solanum bulbocastanum*. *Molecular Plant-Microbe Interactions*, 22: 930–941.
36. **Luthra, S. K., Gopal, J., Manivel, P., Kumar, V., Singh, B. P. & Pandey, S. K. (2007).** Screening of potato species for frost tolerance. *Potato Journal*, 34: 45–46.
37. **Luthra, S. K., Kumar, V., Singh, B. P. & Pandey, S. K. (2008).** Evaluation of potato germplasm for frost tolerance. *Indian Journal of Horticulture*, 65: 344–346.

38. **Marczewski, W., Flis, B., Syller, J., Schäfer Pregl, R. & Gebhardt, C. (2001).** A major quantitative trait locus for resistance to potato leafroll virus is located in a resistance hotspot on potato chromosome XI. *Molecular Plant-Microbe Interactions*, 14(12): 1420–1425.
39. **Martinez, C. A., Maestri, M. & Lani, E. G. (1996).** Salt tolerance and proline accumulation in Andean potato. *Plant Science*, 116: 177–184..
40. **Paal, J., Henselewski, H., Muth, J., Meksem, K., Menéndez, C. M., Salamini, F. & Gebhardt, C. (2004).** Molecular cloning of the potato Gro1-4 gene conferring resistance to pathotype Ro1 of the root cyst nematode *Globodera rostochiensis*. *The Plant Journal*, 38: 285–297.
41. **Sandbrink, J., Rodriguez, F., Forsyth, A., et al. (2000).** Mapping resistance traits in *Solanum microdontum* to *Phytophthora infestans*. *Plant Breeding*, 119: 123–128.
42. **Sarkar, D., Tiwari, J. K., Sharma, S., Sanjeev, P. S., Gopal, J., Singh, B. P., Luthra, S. K., Pandey, S. K. & Pattanayak, D. (2011).** Production and characterization of somatic hybrids between *Solanum tuberosum L.* and *S. pinnatisectum Dun*. *Plant Cell, Tissue and Organ Culture*, 107: 427–440.
43. **Shannon, M. C. & Grieve, C. M. (1999).** Tolerance of vegetable crops to salinity. *Scientia Horticulturae*, 78: 5–38.
44. **Song, J., Bradeen, J. M., Naess, S. K., Raasch, J. A., Wielgus, S. M., Haberlach, G. T., Liu, J., Kuang, H., Austin-Phillips, S., Buell, C. R., Helgeson, J. P. & Jiang, J. (2003).** Gene RB cloned from *Solanum bulbocastanum* confers broad spectrum resistance to potato late blight. *PNAS*, 100: 9128–9133.
45. **Song, Y., Koller, W., Wenzel, G., et al. (2005).** Mapping of extreme resistance to PVY (Ry-sto) on chromosome XII using anther culture derived primary dihaploid potato lines. *Theoretical and Applied Genetics*, 111: 879–887.
46. **Szajko, K., Strzelczyk Żyta, D., Czajkowski, R., et al. (2008).** Identification of the Ny-1 gene conferring hypersensitive resistance to PVY in potato. *Molecular Breeding*, 22: 439–450.
47. **Tan, M. L., Yang, X., Tai, H. H., et al. (2008).** Characterization of late blight resistance in *Solanum microdontum*. *Euphytica*, 164: 281–290.
48. **Thieme, R., Rakosy Tican, E., Nachtigall, M., Schubert, J., Hammann, T., Antonova, O., Gavrilenko, T., Heimbach, U., Thieme, T. (2010).** Characterization of the multiple resistance traits of somatic hybrids between *Solanum cardiophyllum Lindl.* and two commercial potato cultivars. *Plant Cell Reports*, 29: 1187–1201.
49. **Van der Vossen, E. A. G., Gros, J., Sikkema, A., Muskens, M., Wouters, D., Wolters, P., Pereira, A. & Allefs, S. (2005).** The Rpi-blb2 gene from *Solanum bulbocastanum* is a Mi-1 gene homolog conferring broad spectrum late blight resistance in potato. *The Plant Journal*, 44: 208–222.
50. **Valkonen, J. P. T., Slack, S. A., Plaisted, R. L. & Watanabe, K. N. (1994).** Extreme resistance is epistatic to hypersensitive resistance to Potato Virus Y in a *Solanum tuberosum* subsp. *andigena* derived potato genotype. *Plant Disease*, 78: 1177–1180.
51. **Wang, M., Gore, M., Zhang, Z., et al. (2008).** Late blight resistance loci from *Solanum stoloniferum*. *Molecular Genetics and Genomics*, 279: 347–356.
52. **Zhang, N., Si, H. J., Du, H. W., Liu, B. & Wang, D. (2011).** Enhanced drought and salinity tolerance in transgenic potato. *Plant Biotechnology Reports*, 5: 71–77.