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Breeding Approaches against Climate Change and Quality Enhancement in Vegetables

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The climate plays a significant role either directly or indirectly in crop production. Changing climate poses serious challenges to food safety and food security worldwide. Plant physiology is affected by this factor in vegetable production, and quality of the produce is changed by the various a biotic factor. Biotechnological interventions are the need of the day to produce enough quality food to feed the world's ever-increasing population. Conventional breeding is no doubt a significant sphere of agriculture for improving vegetable production; however, advanced approaches, like genetic engineering and molecular techniques for genetic improvement, can play a considerable role in mitigating the food shortage. Breeders may make great efforts to create varieties that can withstand great stress. The challenge is to produce varieties that can withstand high temperatures and low inputs, high rusticity, and biotic and abiotic stresses of climate change.
Keywords: Climate change, abiotic and biotic stress, genetics improvement, conventional breeding, quality enhancement.

INTRODUCTION

The world's population is growing rapidly, and food demand is increasing. (Noya *et al.*, 2018). Demand for crops worldwide is predicted to grow in the coming years due to rapid population growth and high purchasing power per capita being translated into high consumption. (Ebert, 2020). Climate change has devastating results on all spheres of life. Agricultural production is directly related to climate change, adversely affecting climate change (Raza *et al.*, 2019).
Change in every day means utmost and least temperature is the main result of climate variation that harmfully influences vegetable production, as numerous plant biochemical, physiological, and metabolic processes depend on temperature (Pramanik *et al.*, 2019). Water ease of access is likely to be extremely responsive to changes in climate, and an adverse water scarcity environment will influence the production of vegetables. Water stress is a chief crisis in arid and semi-arid areas, and it is the most significant reason for crop failure globally, dropping the average yield for most crops up to 50% or more (Ayyogari *et al.*, 2014). Salinity is the severe difficulty that decreases the growth and production of vegetables in many salt-affected regions. Extreme soil salinity decreases the output of numerous cash and most vegetables, which is mainly sensitive all over
Climate change also affects pests' biology and ecology (Jat and Tetarwal, 2012). As a result of an increase in temperature, various insect groups with short life spans, such as aphids and diamondback moths, have elevated fecundity and earlier conclusion of the life cycle. Therefore, these can generate more generations yearly than the normal level. Opposing it, several insects might take years to finish their life cycle. Different species of insects that live in the soil throughout or at certain stages of the life cycle often suffer more than the insects that live above the ground because soil provides protective mechanisms by insulating that will have a tendency buffer to fluctuate in temperature beyond air. Due to climate change might change the stage of growth, level of development and pathogenicity of infectious means, physiology, and resistance to the host plants (Mboup *et al.*, 2012). The large plant pathogens population and the short period of regeneration may have made them the first living organisms to explain the effects of climate change.
In the past, breeders always had a great goal of harvesting and improving productivity, but now they focus on breeding for climate change. The genetic development of crops is essential in enhancing agriculture to tackle climate change challenges.

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(Henry, 2020). To increase crop yields under changing climatic conditions, effective field strategies can guide farmers. In addition, numerous approaches are accessible to reduce the damaging consequence of climate change. Efforts have been made to review mitigation methods against the results of climate change on vegetable crops using traditional and advanced methods. Considering this situation, new information suggests that the greater impact of intelligent climate change systems directly impacts vegetable production in increasing human capacity (Brar *et al.*, 2020). The adaptations of agriculture to climate change need the application of one or more of a choice of complementary plans.Like other crops, the vegetable crop is susceptible to climate change. The main difficulty in vegetable production is the serious occurrence of biotic and abiotic stresses. Due to the high susceptibility of vegetable crops to diseases and insect pests, it becomes tough to attain the highest yield potential. The uncontrolled use of pesticides for controlling diseases, insect pests, and nematodes is dangerous to human health and the environment.

Adaptation to withstand abiotic challenges**:** Abiotic pressures, such as high salt drought, heat, and cold, greatly affect crop growth and agricultural production and cause 50% of global crop losses annually. Researchers have tried to reduce these pressures and increase crop production under adverse conditions. The traditional measure is straightforward and indicates a high risk of climax conditions due to various rigidity of edaphic material. It is important to recognize how plants respond to drought, the genes that respond to drought.

Drought**:** Uneven rainfall is due to climate change, a significant pressure such as drought. Soil moisture in plants is increasing due to harsh drought and causing premature plant disease. Plants decrease shoot growth in drought conditions and reduce their metabolic requirements. When drought has been applied to the plants, plant growth cease is the first reaction of plants. The protective computers are then incorporated into the plants under drought by combining the metabolites needed to prepare the osmotic (Rejeb *et al.*, 2014). Plants in their natural habitat adapt to the pressure of drought in the environment through various methods, from short-term reactions to low soil moisture to large survival routes by flowering without annual rainfall. However, planting selected crops to produce products such as grain, vegetables, or fruit in favorable areas with high water inputs and fertilizers is estimated to produce economic produce in answer to inputs. Crops selected for their cost-effective harvest need to cope with the pressure of drought through methods that maintain crop yields. Therefore, experimental plant studies for survival under pressure are often interpreted to produce plants under pressure, and the various aspects of coping with drought need to be emphasized (Basu *et al.*, 2016).

Heat**:** Global warming has become a main difficulty, disturbing crop development, and productivity, particularly in farming crops. During reproductive growth under heat stress, the activity of the petal cells is lost, and the anther becomes dysplastic. (Fahad *et al.*, 2017). Florais are resistant to high temperatures using avoidance measures, such as air cooling, exposure to sunlight by increasing the hair follicles, and wax formation, enabling plants to maintain their temperature below ambient level. Heating stress causes the release of certain heat shock H.S. genes, leading to the formation of a new set of HSPs. This protein is produced from newly transcribed mRNAs within 5 minutes of exposure to heat stress. HSPs may prevent the accumulation of distorted proteins due to high-temperature stress.

Salinity**:** Salt tolerance involves the complexity of cellular, metabolic, physiological, and plant responses. Extensive research on molecular analysis, metabolism, and physiology has revealed that amid the various salt responses, ion channels or techniques to regulate ion absorption, transport and balance, osmotic control, hormone metabolism, antioxidant metabolism, and signature stress play a fundamental role in converting plants to salt stress. Using recent advances in the field of genomic, transcriptomic, proteomic, and metabolomic processes, biologists are focusing on developing a full profile of genes, metabolites, and proteins that address the various salt-tolerant ways of plant diversity (Gupta and Huang, 2014).

Adaptation Against Biotic Stress**:** Plant epidemics have led to severe financial failure and starvation. It is also revealed that various human actions cause many plant diseases. Plant disease is any alteration that disrupts normal plant growth and reduces profitability (Lucas *et al.*, 1992). The disease disrupts the normal functioning of parts of several plants and results in reduced yields or reduced quality. A significant reaction to plants is called "symptoms," which include wrinkles, stiffness, yellowing, death, and abnormal growth in whole or in part.

Climate changes will affect insects and germs in three different ways, all of which have a profound effect on plant reproduction:

Change in value of the pests and bacteria that affect the plant and the environment and the degree of damage if the plant is under stress due to inappropriate soil type and topography. Enlarged plant canopy from the effect of CO_2 fertilization enhances the number of infection cycles to improve the number of pathogens, which may increase the rate of new species emerging (Chakraborty and Datta, 2003). Although the chances of transitioning from avirulence to virulence increase with increasing human size, the mutation rate depends on the structure of avirulence and its relevance between the number of pathogens, predicting the emergence of new species did not occur.

Genetic improvement approaches for biotic stresses resistance in vegetable crops**:** Vegetable production is mainly affected by pests and diseases. Applying pesticide and fungicides is a way to control insect/pest, but the uncontrolled application of chemicals cause a hazard to the environment, residue in vegetables higher than threshold levels, and the emergence of new biotypes. Consequently, vegetable breeders' main breeding aim is to develop biotic-resistant cultivars. To develop resistant varieties, a source of resistance with genetic information is a requirement and the main strength of the breeding program. Efforts will be made to depict the resistance sources of various vegetable crops that are not in favor of major diseases and insect pests, inheritance of resistance, genetic manipulations, and biotechnological interventions and grafting, which will be useful to vegetable breeders for future breeding strategies.

***Conventional approaches*:** The conventional breeding methods utilize existing genetic variation and use the sexual cycle to reassemble DNA through independent chromosomes and interbreeding. A genetic mutation is also now part of the ancient reproductive system. In either case, the choice of individual plants and their offspring is emphasized. Therefore, knowing the appropriate options for each type and stress is important.

***Development of suitable criteria for selection*:** Choosing to withstand abiotic stress is difficult due to unpredictable weather conditions. Affected salt regions tend to have more salt marshes, salt marshes, and salt marshes in the same area. The patches can appear less than a meter horizontally or at a greater distance. It is caused by dissimilarity in perched water tables and through undulations in landscape (Cessna *et al.*, 2000).

As a result of this patchiness and because the plants can be easily grown in a solution of salty nutrients, many options have been made in the nutrient solution. The selection of nutrient mixtures may not work well in saline soils because the area with the patched scars differs greatly from that of salty mixtures.

***Selection*:** Natural selection for various plant species should increase genetic frequency by extremes in temperature. Usual selection would be useful for temperature and other pressures if the population increased in areas with high chances of pressure near the critical level (De Vos *et al.*, 2005). The choice includes selecting and distributing plants/genes from mixed/divisive individuals. For selection to work, there must be genetic diversity that can be identified and differentiated into biological variants

***Interspecific hybridization*:** If a stress-tolerant gene is not found in cultivated species, these can be passed on to wild species/species that are loaded sources of stress-tolerant genes. Marketable plants can be developed by carrying abiotic pressure genes to their wild relatives and their specific species, e.g., salt tolerance from Lycopersicon cheesmani to L. esculentum (Zheng *et al.*, 2002). Tepary bean is a frequently recommended source of drought tolerance, although some species of Phaseolus are worth considering. (Desikan *et al.*, 2001, Gong *et al.*, 2001). From interspecific hybridization between Pisum sativum and P. fulvum, two promising lines with heat and drought tolerance have been developed. If the tolerance level for improved crops is insufficient, collections of crop varieties may be tested to determine the sources of the desired variety. This variation may be used in the integration of a continuous system.

***Backcross method*:** The parent to whom the genetic material is passed is the donor parent. The affected parent to whom the resistance gene is transferred is called the recurring parent. The backcross method often helps restore the recurring parent phenotype and the transmission of resistant genes. Hybrids of late-potato hybrids; potato hybrids developed in combination with conventional potato varieties; promise species have been identified for the development of late rot. Powdery mildew is a severe disease of peas found in strong new resistant donors, a common method of breeding backcross as it works on a single gene-controlled character described by Gritton (Uzogara, 2000).

***Pedigree method*:** This method is ideal when resistance is horizontal or polygenic. In developing disease-resistant pathogens, a synthetic epidemic is often produced to assist in selecting disease-resistant strains. Reproduction is widely used when resistance is dominated by large genes and is highly genetic. If low genetic traits are used, then the selection method will take time as it takes some generations, generally, F5 or F6, to detect homozygosity (Stuthman *et al.*, 2007).

Non-conventional approaches

***Agrobacterium tumefaciens mediated transformation*:** Due to sexual sterility in garlic, genetic transformation is of utmost importance. Agrobacterium-mediated transformation was made the first move by (Kondo *et al.*, 2000), who could establish an alteration technique of garlic using extremely regenerative calli. A method of transformation was developed to create garlic plants with Bt-resistant genes for beet armyworm. A method was developed by (Kenel *et al.*, 2010) of garlic alteration from young leaves that have the hpt selectable gene and an mgfp-ER reporter gene. Transgenic garlic plants were synthesized and genetically engineered phosphinothricin acetyltransferase (PAT), showing that transgenic plants resist herbicides, whereas non-transgenic plants die. The quality and yield of garlic are reducing due to white rot disease (Sclerotium cepivorum Berk). A transformation method developed by (Lagunes-Fortiz *et al.*, 2013) transferred tobacco chitinase and glucanase genes into the embryogenic calli of A. tumefaciens and were able to develop genetically modified plants that were not fully resistant but could capture fungal infections.

***Biolistic Method*:** Biolistic transformation of tomato to introduce the β-glucuronidase (gusA) gene, various explants were used such as shoot tips, hypocotyls, and cotyledons of genotype IPA-3. I. The respective percentages of plant regeneration in different explants were 95.16, 79.30 and 90.14% on M.S. medium supplemented with BAP (2.0 mg L^{-1}) and Kinetin (1.0 mg L^{-1}) (Ruma *et al.*, 2009). The effects of physical parameters of the particle gun on the transient GUS expression rate, namely the amount of DNA, and the distance between the initial microcarrier array and the target tissue, were examined and biological factors associated with the target tissue, d. H. Effect of infiltration incubation time before bombardment and incubation time after bombardment.

***Somaclonal Variations*:** Somatic mutants generated through long-term tissue culture may be a possible alternative for garlic to generate genetic mutants and new plant species (Al-Zahim *et al.*, 1999). Such mutations were observed phenotypically and cytologically regenerated shoots in a salt-tolerant eggplant line (Solanum melongena) using an efficient regeneration protocol. Their high salinity tolerance was reflected in relatively higher fresh and dry weights, higher moisture content, and higher fruit values and weights than wild parental controls.

Molecular breeding

***Molecular Markers*:** Molecular markers are widely used in determining genetic diversity due to their neutral status, repetitive effects across all laboratories, and no natural influence on their expression. In first reported garlic diversity by microsatellite markers, where they upgraded the SSR library and finally reported eight SSRs for diversity estimation. (Khar, 2012) used 99 SSRs and reported 18 polymorphic SSR for genetic variation in garlic. A study performed RAPD to verify the genetic association among gray mold disease-resistant and susceptible genotypes through a dendrogram. (SCAR)-OPAN1 marker to select resistant genotype was developed using a polymorphic RAPD fragment. RNA- sequencing of the gray mold resistant and susceptible onion genotype by Next generation sequencing. Using the RNA-sequencing results and DEG and G.O. analyses were performed, and the variation, such as SNPs, was examined to establish a selectable marker for the resistant genotype. A total of 11,633 differentially expressed genes (DEGs) were recognized in pepper genotypes via RNA sequencing, and the differential expression of 14 randomly chosen DEGs was confirmed by using reverse-transcription PCR.

***Genetic linkage maps*:** Genetic linkage maps are the predominant technique for gene localization, marker breeding, consideration of the nature of multifaceted genetic traits, and mapping-based cloning of important genes. Advances in genetic linkage mapping will support garlic improvement by enabling marker-assisted selection and the recognition of genes controlling economically vital traits. The very first garlic genetic map was (Zewdie *et al.*, 2005) developed using the male fertility locus, 37 markers forming nine linkage groups were placed on the map.

***Genome Aided Breeding*:** Omics approaches offer potential resources for studying the biological functions of some genetic information for crop breeding (Stinchcombe and Hoekstra, 2008); almost all major breeding programs for crop modernization include genomic approaches coupled with conventional breeding to reduce time and evaluate elite germplasm. These recent biotechnological tools significantly aid the development of climate-smart crops with privileged yield potential in climate change.

***Conclusions*:** Numerous environmental, biological and ecological factors have the direct and indirect impact on food security. Feeding the population with enough quality food by producing more food through conventional and advance approaches is a big challenge for the plant breeders. They are focusing on the development of crops which can withstand adverse condition and full the requirements of the population. Breeders have to exploit the genetic potential of the vegetable crops for maximum output.

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REFERENCES

Al-Zahim, M., B. Ford-Lloyd and H. Newbury. 1999. Detection of somaclonal variation in garlic (Allium sativum L.) using RAPD and cytological analysis. Plant cell reports 18:473-477.

Ayyogari, K., P. Sidhya and M. Pandit. 2014. Impact of climate change on vegetable cultivation-a review. International Journal of Agriculture, Environment and Biotechnology 7:145.

Bale, J. and S. Hayward. 2010. Insect overwintering in a changing climate. Journal of Experimental Biology 213:980-994.

Basu, S., V. Ramegowda, A. Kumar and A. Pereira. 2016. Plant adaptation to drought stress. F1000Research. 5:F1000 Faculty Rev-1554.

Brar, N.S., T. Kumar and P. Kaushik. 2020. Integration of technologies under climate change for profitability in vegetable cultivation: an outlook.

Cessna, S.G., V.E. Sears, M.B. Dickman and P.S. Low. 2000. Oxalic acid, a pathogenicity factor for Sclerotinia sclerotiorum, suppresses the oxidative burst of the host plant. The Plant Cell 12:2191-2199.

Chakraborty, S. and S. Datta. 2003. How will plant pathogens adapt to host plant resistance at elevated CO2 under a changing climate New Phytologist 159:733-742.

De Vos, M., V.R. Van Oosten, R.M. Van Poecke, J.A. Van Pelt, M.J. Pozo, M.J. Mueller, A.J. Buchala, J.-P. Métraux, L. Van Loon and M. Dicke. 2005. Signal signature and transcriptome changes of Arabidopsis during pathogen and insect attack. Molecular plant-microbe interactions 18:923-937.

Desikan, R., J.T. Hancock, K. Ichimura, K. Shinozaki and S.J. Neill. 2001. Harpin induces activation of the Arabidopsis mitogen-activated protein kinases AtMPK4 and AtMPK6. Plant Physiology 126:1579-1587.

Ebert, A.W. 2020. The role of vegetable genetic resources in nutrition security and vegetable breeding. Plants 9:736.

Fahad, S., A.A. Bajwa, U. Nazir, S.A. Anjum, A. Farooq, A. Zohaib, S. Sadia, W. Nasim, S. Adkins, S. Saud, M.Z. Ihsan, H. Alharby, C. Wu, D. Wang and J. Huang. 2017. Crop Production under Drought and Heat Stress: Plant Responses and Management Options. Frontiers in Plant Science 8: 1147.

Gong, J., X. Zheng, B. Du, Q. Qian, S. Chen, L. Zhu and P. He. 2001. Comparative study of QTLs for agronomic traits of rice Oriza sativa L.) between salt stress and nonstress environment. Science in China Series C: Life Sciences 44:73-82.

Gupta, B. and B. Huang. 2014. Mechanism of salinity tolerance in plants: physiological, biochemical, and molecular characterization. International journal of genomics 2014:

Henry, R.J. 2020. Innovations in plant genetics adapting agriculture to climate change. Current Opinion in Plant Biology 56:168-173.

Jat, M.K. and A.S. Tetarwal. 2012. Important Pests of sugarcane & their Management.

Kenel, F., C. Eady and S. Brinch. 2010. Efficient Agrobacterium tumefaciens-mediated transformation and regeneration of garlic (Allium sativum) immature leaf tissue. Plant cell reports 29:223-230.

Khar, A. Cross amplification of onion derived microsatellites and mining of garlic EST database for assessment of genetic diversity in garlic. p. 289-295. VI International Symposium on Edible Alliaceae 969

Kondo, T., H. Hasegawa and M. Suzuki. 2000. Transformation and regeneration of garlic (Allium sativum L.) by Agrobacterium-mediated gene transfer. Plant cell reports 19:989-993.

Lagunes-Fortiz, E., A. Robledo-Paz, M.A. Gutiérrez-Espinosa, J.O. Mascorro-Gallardo and E. Espitia-Rangel. 2013. Genetic transformation of garlic (Allium sativum L.) with tobacco chitinase and glucanase genes for tolerance to the fungus Sclerotium cepivorum. African Journal of Biotechnology 12:

Lucas, G.B., C.L. Campbell and L.T. Lucas. 1992. Causes of Plant Diseases. p. 9-14. *In* Lucas, G. B., C. L. Campbell and L. T. Lucas (ed^.) Introduction to Plant Diseases: Identification and Management. Springer US, Boston, MA.

Mboup, M., B. Bahri, M. Leconte, C. De Vallavieille-Pope, O. Kaltz and J. Enjalbert. 2012. Genetic structure and local adaptation of European wheat yellow rust populations: the role of temperature-specific adaptation. Evolutionary Applications 5:341-352.

Noya, I., S. González-García, J. Bacenetti, M. Fiala and M.T. Moreira. 2018. Environmental impacts of the cultivation-phase associated with agricultural crops for feed production. Journal of Cleaner Production 172:3721-3733.

Pramanik, K., J. Pradhan, P.P. Mohapatra and C.J.a.L.K. Acharya. 2019. Impact of Temperature: An Important Climate Changing Factor on Vegetable Crops.

Raza, A., A. Razzaq, S.S. Mehmood, X. Zou, X. Zhang, Y. Lv and J. Xu. 2019. Impact of Climate Change on Crops Adaptation and Strategies to Tackle Its Outcome: A Review. Plants (Basel, Switzerland) 8:34.

Rejeb, I.B., V. Pastor and B. Mauch-Mani. 2014. Plant Responses to Simultaneous Biotic and Abiotic Stress: Molecular Mechanisms. Plants (Basel, Switzerland) 3:458-475.

Ruma, D., M. Dhaliwal, A. Kaur and S. Gosal. 2009. Transformation of tomato using biolistic gun for transient expression of the β-glucuronidase gene. Indian J Biotechnol 8:363-369.

Stinchcombe, J.R. and H.E. Hoekstra. 2008. Combining population genomics and quantitative genetics: finding the genes underlying ecologically important traits. Heredity 100:158-170.

Stuthman, D., K. Leonard and J. Miller-Garvin. 2007. Breeding crops for durable resistance to disease. Advances in agronomy 95:319-367.

Uzogara, S.G. 2000. The impact of genetic modification of human foods in the 21st century: A review. Biotechnology advances 18:179-206.

Wang, F., Y. Yin, C. Yu, N. Li, S. Shen, Y. Liu, S. Gao, C. Jiao and M. Yao. 2021. Transcriptomics Analysis of Heat Stress-Induced Genes in Pepper (Capsicum annuum L.) Seedlings. Horticulturae 7:339.

Wang, W., B. Vinocur and A. Altman. 2003. Plant responses to drought, salinity and extreme temperatures: towards genetic engineering for stress tolerance. Planta 218:1-14.

Zewdie, Y., M.J. Havey, J.P. Prince and M.M. Jenderek. 2005. The first genetic linkages among expressed regions of the garlic genome. Journal of the American society for Horticultural Science 130:569-574.

Zheng, X.-Y., Y. Wang and S.-H. Song. 2002. Identification of heat tolerance linked molecular markers of Chinese cabbage Brassica campestris ssp. pekinensis.