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# Climate Change and Indian Agriculture: Challenges and Adaptation Strategies

Editors

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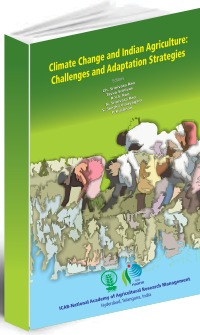
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### **Preferred Citation of Book**

Srinivasarao, Ch., Srinivas, T., Rao, R.V.S., Srinivasarao, N., Vinayagam, S.S., Krishnan, P. (2020). Climate Change and Indian Agriculture: Challenges and Adaptation Strategies, ICAR-National Academy of Agricultural Research Management, Hyderabad, Telangana, India. p-584.

### **Preferred Citation of Chapters**

Kumar, K., Bhattacharjee, S., Vaikuntapu, PR., Sharma, CL., Jayaswal, D., Sharma, R., Sundaram, R.M. 2020. Climate Change Mitigation and Adaptation Through Biotechnological Interventions. In: Ch. Srinivasarao *et al.*, (Eds). Climate Change and Indian Agriculture: Challenges and Adaptation Strategies, ICAR-National Academy of Agricultural Research Management, Hyderabad, Telangana, India. pp-1-22.

ISBN No. : 978-81-943090-7-9

### **Published by**

Director  
ICAR-NAARM  
Hyderabad - 500 030

July 2020

For Copies contact:

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# Accelerated Crop Breeding Towards Development of Climate Resilient Varieties

3

## Abstract

Climate change may pose a great risk to food security in near future. Developing climate resilient varieties will prepare the human community to face unprecedented climate change. The pace at which the current varietal development programs are marching may not help in ensuring self-sufficiency in food production. The recent advancements in molecular genetics needs to be favorably incorporated in conventional breeding strategies, in order to shorten the breeding cycle and to meet the expected outcomes with greater precision. In addition, more emphasis on breeding of orphan crops widens the scope for crop diversification. Climate change may have a multitude of effects on crop growth and development. So, to tackle the detrimental effects of climate change, comprehensive breeding strategies should be developed to accelerate the crop improvement programs for a hunger free world in future.

**Key words:** Accelerated Plant Breeding, Crop Breeding, Climate Changes, Climate Resilient Varieties, Stress Tolerance.



## I. Introduction

The major challenges in food production are ever growing population and unprecedented climate change. World population is increasing in a rapid phase which is expected to reach 9.8 billion by 2050 (United Nations, 2017). Broadly, climate change refers to increase in temperature, elevated CO<sub>2</sub> concentration, melting of ice, increased global sea level and increased frequency of natural calamities and droughts (Lenaerts *et al.*, 2019a). Each of above changes has adverse effects on crop productivity and thereby negatively influence food security. Plant breeders must address each of these issues to make food production sustainable in the climate change scenario. Plant breeding procedures have been constantly evolving to meet the increasing food demand. The art of plant breeding has been practiced in various forms since the start of human civilization. In conventional plant breeding, development of a cultivar may take around 10 years and may even exceed this period based on the plant habit, reproductive cycle and complexity of traits involved. The rapid climate change necessitates the development of varieties in a shorter span to tackle with the unpredictable weather parameters. Accelerated Plant Breeding is the concept of integrating conventional breeding strategies with advanced molecular tools to shorten the breeding cycle. This enables varietal development in a quick succession in order to respond to unpredictable changes in crop production environments and variable climatic conditions.

One among the 17 Sustainable Development Goals is to have zero hunger by 2030 (FAO, 2019). In order to achieve self-sufficiency in food production, there should be a transition in breeding work to develop crop varieties that can give sustainable yields under rapid climate change. Climate change will aggravate the occurrence of abiotic stress and biotic stresses in crop plants and hitherto, minor pests and diseases can become economically important. Drought alone is expected to reduce crop productivity in half of the global arable land by 50% in the next five decades (Dhankher and Foyer, 2018). Hence, development of climate resilient varieties ensures food security in adverse climatic conditions.

## II. Breeding Challenges in a Climate Change Scenario

Agriculture and climate change are interrelated processes. Climate change can adversely affect agriculture in different ways, through changes in average temperatures (heat and cold stress), distribution of rainfall (drought and floods) and increased occurrence of biotic stresses (pests and diseases). Production and quality of food is affected by climate change. In general, stabilizing yield is simple by creating an improved variety resistant to various biotic and abiotic stresses, rather than by improving management practices.

In traditional breeding methods, plant breeders develop new cultivars by selecting directly or indirectly for yield and its components in specific environments as most varieties will

not be able to have stable performance across the environments. Moreover, these methods require longer time for varietal development. Most common breeding methods used by breeders are pedigree and backcross. Pedigree is a proven breeding method, but it depends on growing all of the field's plant populations and takes a longer period to fix lines. Another commonly used method is backcrossing used for incorporating a target gene into a popular variety. Dependence on the crop stage for trait evaluation and need of repeated screening environment that increases the time required for development of variety is the main limitation of this method.

New breeding approaches such as Rapid Generation Advance (RGA), Doubled Haploid (DH), Shuttle Breeding, Marker Assisted Back Crossing (MABC), Marker Assisted Recurrent Selection (MARS), Genomic Selection (GS), Speed Breeding, etc. have been used to help shorten the breeding cycle along with efficient screening for specific biotic and abiotic stresses. Hence, accelerated breeding has gained popularity in the recent past and is an efficient tool for developing new varieties in a shorter period of time, tailored to the current environment to reduce the impact of climate change (Atlin *et al.*, 2017).

### III. Accelerated Breeding Approaches

#### III.1 Classical Approaches

Genetic improvement of crop plants is traditionally a slow process and it takes at least 12 years for release of new varieties as the

breeding process includes development of genetically fixed lines, evaluation and identification, hybridization and obtaining homozygous lines by selfing. Recent developments in crop breeding methodology have resulted in persistent increase in crop performance, but the major constraint is generation time of plants which is biologically fixed. Hence, the major challenge for current breeding is to speed up the generation time of breeding cycle in order to accelerate the genetic gain in any breeding program (Begheyn *et al.*, 2016).

#### a. Shuttle Breeding

The concept of this method was devised by the Noble Laureate Dr. Norman E. Borlaug at International Wheat and Maize Improvement Centre (CIMMYT), Mexico (Lenaerts *et al.*, 2019b). Shuttle breeding will allow an additional generation per year by raising the crop at a different location. Wheat breeding programme in Mexico utilized two different locations, which allowed use of the off season for breeding activities (Ortiz *et al.*, 2007). In India during winter season main crop is taken and in off season *i.e.* during summer wheat is grown in regional station of Directorate of Wheat Research, Karnal in Lahaul-Spiti, or regional station of IARI at Wellington. By utilizing these locations generations can be advanced by taking additional crop cycle. Along with shortening of breeding durations breeding materials can be tested against various biotic stresses (rusts, powdery mildew and loose smut) that are occurring naturally at these locations. By this way it will be helpful for making selection for biotic as well as

can shorten the period for cultivar development. In case of rice in 1983, shuttle breeding was started at China National Rice Research Institute and International Rice Research Institute (IRRI) initiated the shuttle breeding project to develop early maturing rice varieties with high yields, grain quality, wide adaptability and multiple resistance. The Eastern India RLSBN (Rainfed Lowland Shuttle Breeding Network) for rice was formed in the year 1991 (Collard and Ismail, 2013) and after that, several improved cultivars were developed and released, for various stresses including varieties for submergence-tolerance (Ismail *et al.*, 2013). Shuttle breeding approach has been utilized to improve breeding materials for low temperature tolerance and for rainfed lowland, upland, deep water and tidal wetland conditions in rice (Singh, 2015). The merits of this approach are development of varieties/breeding lines adopted across large geographical and agro ecological areas, except perhaps poorest of the environment. However, over the years this method is used to a limited extent due to logistical problems, particularly during the exchange of seeds across international territories, issues related to intellectual property and security of national germplasm (Lenaerts *et al.*, 2019b).

#### **b. Rapid Generation Advance (RGA)**

This is the most successful breeding technique in rice and in this method, extensive single plant selections are made and screening for desired characters is done in segregating generations and finally yield testing of identified

homozygous lines in target environment. RGA breeding method is used to develop homozygous lines. RGA or Single Seed Descent (SSD) uses only one seed from each plant from  $F_2$  to  $F_6$  generations to forward each generation by inbreeding and produce 'true lines'. Essentially, RGA facilitates the development of true breeding lines to be achieved rapidly by controlling plant growth conditions there by enforcing early dehiscence and rapid seed set than under normal growing conditions. In this method, plants are grown in a controlled condition from  $F_2$  to  $F_6$  generations within a shorter time period than under routine growing conditions.

It was learnt from theories of plant breeding that delaying selection after several cycles of inbreeding may have rewards. First report on use of RGA in rice was from Japan (Heu *et al.*, 1982). During the 1980s, RGA was widely employed at IRRI, especially for rainfed rice and deep-water rice development programs. Merits of RGA method in comparison to other breeding methods lie in its high flexibility with respect to number of generations of inbreeding, speed in terms of advancement of generations, technical simplicity, requiring less space, efforts and labour and makes best use of the off season green house facilities. Some of the drawbacks associated with this method are plant loss, and fails to allow any form of selection during early segregating generations. This method is broadly used for obtaining high transgressive variation for different characters (Moon *et al.*, 2003). The modified SSD method *i.e.*, *In IVASSD (in vitro-assisted single-seed*

descent) approach was used to speedup generations number in short time period in various crops such as faba bean, field pea, lentil, peanut and lupin (Ochatt *et al.*, 2002; Asawaphan *et al.*, 2005; Ochatt and Sangwan, 2010; Surma *et al.*, 2013; Mobini *et al.*, 2015; Bermejo *et al.*, 2016; Ribalta *et al.*, 2017). By IVASSD method, six generations of pea and lupin per year could be obtained (Croser *et al.*, 2016; Ribalta *et al.*, 2017). At present for Quantitative trait loci (QTL) mapping, SSD is widely used in development of mapping populations particularly RILs (recombinant inbred lines) (McCouch and Doerge, 1995).

To sum it up, it is estimated that increased demand for rice due to increased population growth, adverse effects of climate vagaries on food production, and biotic stress factors, it is a prerequisite for rice breeders to adopt speed breeding techniques to fast track the developments and to achieve more genetic gain (Atlin *et al.*, 2017).

### c. Doubled Haploids (DH)

DH systems were used to hasten the breeding cycle in many of crops. DH plants are homozygous at each loci which significantly reduces line fixation time since completely homozygous lines are produced instantly (Mishra and Rao, 2016). DH production includes both *in vivo* or *in vitro* methods. Haploid embryos are produced *in vivo* by pseudogamy, parthenogenesis, or wide crossing. Whereas *in vitro* techniques are androgenesis (anther and microspore culture) and gynogenesis (ovary, ovule and flower culture) (Barnabas *et al.*, 1999). Androgenesis is widely

used among all the methods.

Bulbosum technique is the most preferred method in barley haploid production, in which related species of barley *i.e.*, *Hordeum vulgare* was crossed with *H. bulbosum*. After crossing, fertilization may take place but, chromosomes of *H. bulbosum* are selectively eliminated at the early stages of seed development resulting in haploid embryo formation. Double haploid production at large scale depends on the embryogenesis rate and regeneration of plants, the amount of obtaining albinism among regenerants and the frequency of chromosome doubling required to obtain fertile DH plants (Castillo *et al.*, 2009). Colchicine is commonly used as chromosome doubling agent (Tefera, 2017) and may also affect the androgenetic process. Embryogenesis, regeneration rate and percentage of obtaining green plants are negatively affected by time of application as well as concentration of chromosome doubling agents (Castillo *et al.*, 2009).

In rice, by using DH method two varieties have been developed by Central Rice Research Institute (CRRI) now known as National Rice Research Institute (NRRI), Cuttack-Orissa having resistance towards gall midge, leaf blast namely CR Dhan 801 and Phalguni. These varieties also show moderate resistance against brown spot, sheath rot, yellow stem borer, tenui virus and sheath blight (Mishra and Rao, 2016). DH rice lines are more viable as reported earlier, and more than 100 rice breeding varieties or lines have been developed in China through use of anther culture, while few lines have been developed in India, Hungary, Japan, South Korea and the USA (Siddique, 2015). Various

rice varieties have been released in different countries with valuable features such as good grain quality, resistance to brown plant hopper, blast, bacterial blight, and tolerance to varying abiotic stress. In China, two new cultivars of wheat Jinhua No.1 and No. 764 were released which were produced through DH method (Hu *et al.*, 1983; Hu *et al.*, 1988). Series of DH wheat lines containing rust resistance genes have been developed (Wessels and Botes, 2014). In maize breeding programme, *in vivo* haploid induction-based DH are recognized worldwide. During the past 10-15 years, this method has been adapted for commercial corn breeding programs in countries like China (Chen *et al.*, 2009) and North America (Seitz, 2005). Recently for establishing DH facility in maize at the Agricultural Research Station in Kunigal, Karnataka, University of Agricultural Sciences-Bangalore (UAS-Bangalore) and CIMMYT have entered in to an agreement.

For Brassicas, there are many methods for DH production such as anther culture, microspore culture and ovule culture, but well-known method is microspore culture (Maluszynski *et al.*, 2003; Xu *et al.*, 2007). Despite the developments, DH is not popularized as much in brassica due to various problems associated with anther/microspore culture namely high frequency of callogenesis, genotype-specific response, low regeneration rate and recovery of DH plants (Pratap and Gupta, 2007).

To summarize, the DH technique has played a significant role in crop improvement. It has the potential to reduce the generation time of line development leading to production

of complete homozygous plants. DH technique is best suited for variety development, fixation of heterosis, back cross breeding, mapping, gene identification, discovery of gene and genetically modified plant development. DH provides an opportunity to hasten up conventional breeding methods, and also provides more opportunity in that it can be employed at any time.

### III.2 Advanced Approaches

#### a. Genomic Assisted Breeding Approaches

To develop climate resilient crops and for decoding the stress responsiveness of crop species, genomics tools appear to be most promising. The hitherto development of genomic breeding techniques serve as main tools in reducing generation time and breeding crop varieties for climate resilience.

#### b. Marker Assisted Breeding (MAB)

MAB is described as improving the effectiveness of various breeding activities, including the planning and execution of breeding programmes, and improving selection efficiency through the use of molecular markers. MAB involves multiple breeding techniques, including marker-assisted selection (MAS) and MARS. In MAS, molecular marker that is tightly linked with desirable allele of gene or Quantitative trait loci (QTL) is used for selection instead of phenotypic selection. In MABC, selections are performed at three different levels, target gene/QTL indirectly selected based on linked molecular marker called foreground selection (Tanksley, 1983) whereas,

selection of recurrent parent based on codominant markers that are distributed throughout the genome called background selection (Tanksley *et al.*, 1989; Young and Tanksley, 1989). Recombinant selection is a selection of rare recombinants with no donor parent genome beyond the codominant marker on either side of the targeted gene used for selection (Young and Tanksley, 1989). MARS is a recurrent selection method that uses molecular markers to identify various genomic regions involved in the expression of complex traits to gather best performers within the single population or throughout the associated population (Ribaut *et al.*, 2010). MARS deals with genotypic selection and intercrossing among the selected individuals in the same crop season for one cycle of selection (Jiang *et al.*, 2007). MARS has been suggested for native gene breeding and multiple QTLs pyramiding for complex characters such as grain yield, resistance to abiotic and biotic stresses (Ragot *et al.*, 2000; Ribaut, De Vincente and Delannay, 2010; Eathington, 2005; Crosbie *et al.*, 2006). With the emergence of molecular breeding, QTL detection and use of QTLs in breeding programmes facilitated in increased drought tolerance in maize, rice, wheat, *etc.* Identifying and using QTLs /gene in marker assisted breeding help to develop new varieties for stresses such as cold, heat, salinity and submergence. CIMMYT has made significant success in developing early generation yellow drought tolerant maize inbred lines using MARS technique in their AMDROUT (Asia Maize Drought Tolerance) project. Apart from maize

breeding programme, this technique has also been employed in other crops like sunflower, soybean, to bring desirable alleles at several target loci spread across several parents into single elite lines.

### **c. Genomic Selection (GS)**

GS is a specialized method of MAS in which genotype data on marker alleles covering the entire genome constitutes the basis of selection i.e. Genomic Estimated Breeding Values (GEBVs) determined from the effects of all marker loci (Singh, 2015).

For training population (TP) firstly, genotyping and phenotyping is done for the targeted trait. Then model training is carried out *i.e.*, the data of the phenotype and marker genotypes are used to compute the parameters of the GS model. The breeding population without phenotyping is evaluated for the same set of markers on which basis, model parameters were estimated in the training population. The marker genotype data and associated effects calculated from the training population are used for estimating the GEBVs of the breeding population's individuals / lines.

In wheat, GS models are developed for identifying genotypes that exhibits better adaptation to the negative effects of climate change (Taranto *et al.*, 2018) *i.e.* heading date as an important component of wheat adaptation (Huang *et al.*, 2018) and water deficit stress (Ly *et al.*, 2018).

Xu *et al.* (2014) utilized 278 randomly selected rice hybrids obtained from 210 recombinant inbred lines (RIL) as a training set and predicted 21,945

potential hybrids. Genotyping of landraces were carried out with 5,568 Single Nucleotide Polymorphisms (SNPs) using an Illumina 9 K chip, and the prediction accuracy ranged from 0.27 to 0.44 for three traits. The average yield of the top 100 showed an improvement of 16 per cent relative to the average performance of all potential hybrids. This method is even more effective when applied to heterosis breeding, because hybrid genotypes can be inferred from their inbred parents, that leads to lower genotyping cost (Kadam *et al.*, 2016; Beukert *et al.*, 2017). Recently, rice hybrid performance based on North Carolina mating design II (NC II) was predicted by Wang *et al.* (2017) and GS to study drought tolerance in maize by Shikha *et al.* (2017). For phenotypic prediction not only genomic, but also metabolomic and transcriptomic data could be utilized. Genomic and metabolic data were used to predict complex traits in hybrid corn (Riedelsheimer *et al.*, 2012).

#### **d. Genome Editing**

There are two categories of genome editing first one is Oligonucleotide-Directed Mutagenesis (ODM) in which chemically synthesized 20-100 nucleotides are delivered into plant cells where they induce mutations in the target site. Site-directed nucleases (SDNs) are enzymes that can bind specifically to targeted short DNA sequences that range from 9 to 40 nucleotides and leads to introduction of Double-Strand Breaks (DSBs), acetylation, methylation, demethylation, and deamination to alter a biological activity (e.g., base editing, gene silencing, gene

expression, etc.) (Puchta, 2017). For repairing of DSB, homologous recombination and non-homologous end joining are the two mechanisms in living cells. SDNs includes Zinc Finger Nucleases (ZFNs), meganucleases (or homing endonucleases, HE), Transcription Activator-Like Effector Nucleases (TALENs), and clustered regularly interspaced short palindromic repeats (CRISPR)-associated protein (CRISPR/Cas). Genome editing has been used recently in soybean for incorporating salt and drought tolerance by disrupting the *DREB2b* and *DREB2a* genes (Cardi *et al.*, 2017; Curtin *et al.*, 2018).

#### **e. Speed Breeding**

Speed breeding is the technique which uses supplemental lighting in enclosed and controlled-environment growth chambers that shortens generation time and speeds up the breeding and research programmes. The single seed descent method for rapid advancement of the generation and harvesting the immature seed and proceeding to next generation without losing their viability helps to shorten the generation time. By using light-emitting diode (LED) and harvesting immature seeds, six generations per year can be obtained in crops like spring wheat, durum wheat, barley, chickpea and pea, and four generations for canola, instead of 2–3 under normal glass house conditions (Watson *et al.*, 2018). With the help of speed breeding, climate resilient varieties can be developed in a short period of time. Variations of the speed breeding method have been shown as an effective method for rapid screening of wheat germplasm for disease resistance,

such as leaf rust, fusarium head blight (FHB), and wheat stripe rust (Alahmad *et al.*, 2018; Dinglasan *et al.*, 2016; Riaz *et al.*, 2016; Hickey *et al.*, 2012). This approach has also been employed for pyramiding of multiple disease resistance in barley (Hickey *et al.*, 2017). According to Dr. Lee Hickey (Senior Research Fellow), UQ Queensland Alliance for Agriculture and Food Innovation (QAAFI), speed breeding may be a better part of the solution to mitigate the devastating effects of drought and climate change on crops in future and would allow researchers and plant breeders to contribute more tolerant crop varieties (Ghosh *et al.*, 2018).

## IV. Climate Resilient Variety Development - Major Achievements

Designing breeding strategies targeting the adaptive traits for multiple stresses due to rapid change in climatic conditions is the need of the hour. Extensive efforts have been made to dissect the genetic make of abiotic stress adaptive traits in the past decade. Given the quantitative nature of inheritance of abiotic stress tolerance, detecting and introgressing the QTLs into elite cultivars through marker assisted breeding (MAB) is extensively deployed in food crops (Borrel *et al.*, 2014; Lynch *et al.*, 2014). A few successful attempts have been made to develop cultivars to mitigate the climatic vagaries. Sounding example in case of rice is identification and introgression of *Sub1* QTL to overcome waterlogging stress due to submergence during flooded conditions. *Sub1* QTL hosts three ethylene response factors and

accounts for major portion of submergence tolerance (Xu *et al.*, 2006). Following *Sub1* QTL identification, three cycles of MABC was employed to efficiently convert the submergence-susceptible Swarna rice variety into tolerant variety and released as Swarna-sub1 in India in 2009. Subsequently, *Sub1* QTL was introgressed into six popular cultivars across the globe to meet the needs of farmers in flood-prone regions (Bailey-Serres *et al.*, 2010). IRRI Philippines announced “climate change-ready rice” program, under which it has developed several rice cultivars for different adverse climate conditions (IRRI, 2016). Similar efforts in maize are also made at CIMMYT which led to the development of 18 pre-commercialized heat tolerant maize hybrids to suit the needs of farmers in Africa and Southeast Asia (CG Platform, 2019).

In wheat, two major QTLs explaining 27 and 17% of phenotypic variance due to tolerance to drought and heat, respectively were identified to be present on chromosome 4A (Pinto *et al.*, 2010). Two major QTLs controlling Na<sup>+</sup> accumulation under saline condition have been identified in durum wheat (James *et al.*, 2006). Active expression of tolerant allele at *TmHKT1;5-A* under saline conditions increases the yield up to 25% compared to durum wheat lacking this beneficial allele (Munns *et al.*, 2012). Pyramiding these genes using marker aided breeding into a single cultivar will enhance the wheat productivity. Three major QTLs for grain yield were identified in pearl millet, one among these three was associated with drought stress. Introgression of these QTLs into elite



lines increased the yield by 30% under drought condition (Yadav *et al.*, 2011).

Among pulses, chickpea and pigeonpea are highly affected by several abiotic stresses which pose serious threat to production. The draft genome sequences of chickpea (Varshney *et al.*, 2013) and pigeonpea (Varshney *et al.*, 2012) have been published. These sequence data help to genetically improve the pulse crops for enhanced productivity under climatic changing condition. In oilseed crops, the large-scale genomic resources have been developed in peanut to facilitate molecular breeding. Major QTLs have been identified and deployed in peanut for abiotic stress tolerance (Gautami *et al.*, 2012).

## **V. Crop Simulation Models in Plant Breeding**

The phenotype of an individual depends upon genotype (G), environment (E) and the G×E interaction (Falconer and Mackay, 1996). The main role of plant breeding in agriculture is to develop a genetically superior genotype or variety which is suitable for a specific as well as general desired population of particular environment to give higher production (Falconer and Mackay, 1996). In order to achieve this, a plant breeder employs various breeding procedures for designing crosses and makes selection of the best breeding method for combining desired traits into a single target genotype (Allard, 1999; Hallauer *et al.*, 1988). Basically, field experiments are conducted for comparison of the efficacies of different breeding strategies and conventional breeding

procedures mainly depend on phenotype of plant and experience owned by a breeder which often results in low breeding efficiency and an inaccurate prediction (Allard, 1999). However, the conventional plant breeding methods are time consuming and concerted efforts are required for conducting field experiments. Realizing the importance of genomic resources to expedite the breeding programs, huge amount of genetic data related to genes and QTLs are generated after the advent of molecular biology and biotechnology (Wang, 2007).

In this context, the concept of crop simulation modelling can be an effective way for identification of the best breeding methodology in terms of defining complicated crop simulation genetic models of various genes involved in mechanism(s) like multiple allelism, pleiotropy and gene interaction by macro and micro environmental factors, and delivers a suitable information to efficiently utilize the available genetic data regarding crops by a plant breeder (Wang, 2012). Simulation genetic models are computer-based tools that predict the growth and development of a crop under a particular environmental condition (Muller and Martre, 2019). As a whole, one can say that crop modeling helps in precise prediction of the effects of various factors on the response to selection and other variables like genetic gain, selection intensity and genetic variance like additive dominance and epistasis variances of breeding methods, which is advantageous to breeders for the selection of best plant breeding method for crop improvement in

shorter period of time (Wang, 2007; Li *et al.*, 2012; Liu *et al.*, 2019; Muller and Martre, 2019).

In general, softwares are available to design breeding procedures and methods which mainly emphasize on the characteristics, functions and elementary assumptions in simulation modelling (Sun *et al.*, 2011). GREGOR forecasts the outcome of mating designs like diallel or line  $\times$  tester and selection underneath of various genetic assumptions like normal diploid segregation, gene action, maternal effects, linkage and random mating population (Tinker and Mather, 1993); QU-GENE crop simulation models like QuLine, QuHybrid and QuMARs are able to run crop simulate modelling for simple to complex genetic models like line breeding programs, including conventional plant breeding procedure, molecular plant breeding like marker assisted selection and Genomic Selection (Wang *et al.*, 2003; Wang and Dieters, 2008; Li *et al.*, 2012; Wang, 2011).

QU-GENE is a crop simulation stage which performs genetic modeling for quantitative traits. This platform is mainly composed of two steps (Podlich and Cooper, 1998). The primary phase is the engine, which helps in defining the genotype and environmental (macro and micro environment) G+E+G $\times$ E interaction, (*i.e.*, the gene, environment and interaction between genotype and environment data of the simulation test), the subsequent phase of this platform is to develop the initial collection of base germplasm (Fig.1). The second phase includes parameters of modules, which takes participation in investigation, analysis, or handling

of the initial collection of germplasm due to Genotype $\times$ Environmental interaction which is identified by the engine in first phase.

QuLine (formerly termed QuCim) is a specific tool which helps in crop simulation modelling of genetics and plant breeding system, which integrates number of genes under multiple allelism phenomenon in epistatic gene interaction with different environments, and based on this predict, the cross combination followed by application of selection of best breeding method is made (Wang *et al.*, 2003; 2004). This platform can reduce gap between genetic information and the breeder's questions on selection of genetic gain and breeding effectiveness. QuLine helps in comparing breeding methods (Wang *et al.*, 2003), to know additive, dominance and epistasis gene action effects on selection (Wang *et al.*, 2004), to expect cross performance by utilizing known information regarding genetic factors and gene information (Wang *et al.*, 2005), furthermore to improve selection based on molecular marker for efficiently pyramiding the manifold genes (Kuchel *et al.*, 2005; Wang, 2007).

ADAM-plant, a computer-based simulation model helps in designing plant breeding procedures in autogamous as well as and allogamous crops by utilizing stochastic simulation (Liu *et al.*, 2019). This software simulates a plant population and considers the changes that takes place at genetic level in the population as a whole under various breeding procedures. ADAM-plant focus is mainly on sub-population of population structures, genetic

models, selection tactics and crossing block procedure which helps in selection of the best breeding method. It includes concepts of genomic selection, speed breeding, imitate G×E interactions which results into development of cultivars in future climatic conditions like elevated temperature, high concentration of CO<sub>2</sub>, disturbed rainfall, etc. This software is also used to simulate genetic datasets of QTLs linked loci produced from molecular biology and biotechnology in order to examine new statistical methods for analysis of huge data.

Simulation genetic modelling has played a key role in breeding by design mainly in case of cereals like wheat ideotypes for future climate situations, calibrated model for assessment of impacts of heat shocks/stress occurs during anthesis leads to reduction in fertile florets in barley and ideotype breeding in maize for DH production (Semenov *et al.*, 2014; Moriondo *et al.*, 2011; Nendel *et al.*, 2011; Wang, 2007). Moreover, it's difficult to design a genetic model based on the current knowledge of genotype to phenotype relationship and G×E interaction (Wang, 2007). However, in this

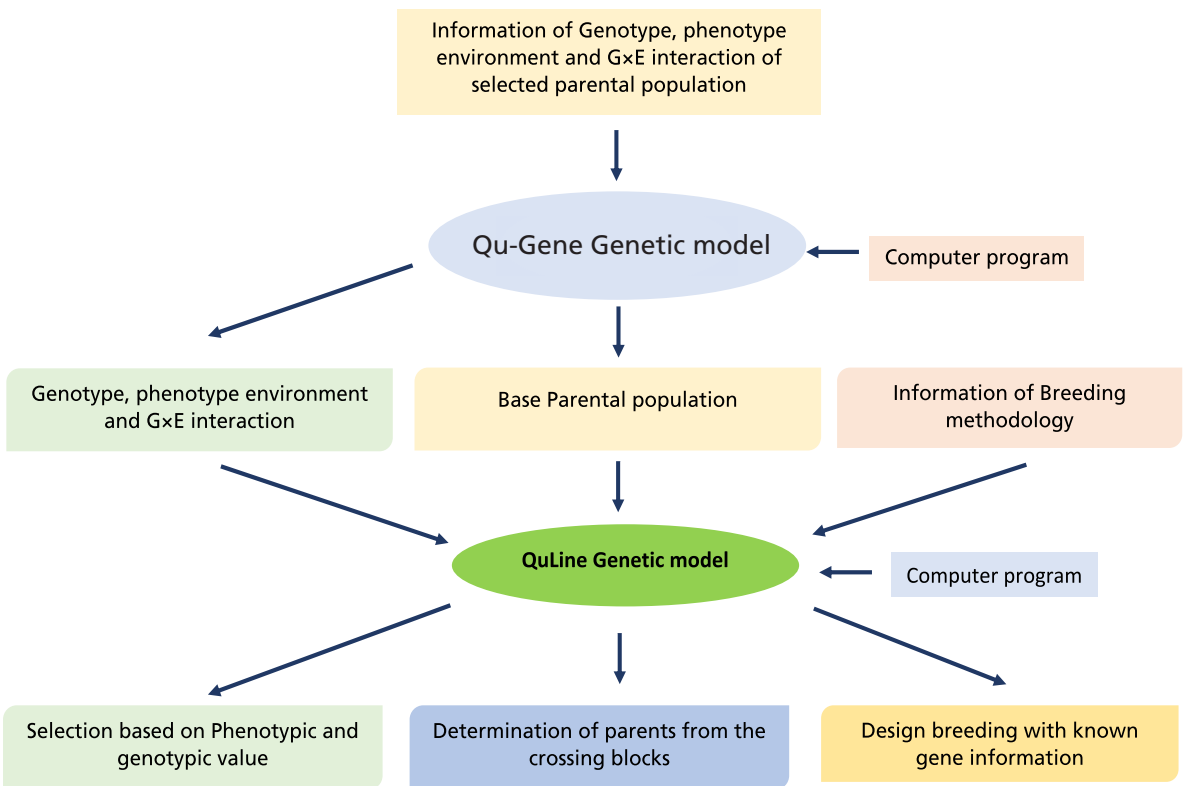


Fig. 1: Flow Chart of Crop Simulation Modelling using QU-GENE and QuLine in Plant Breeding

genomics era, crop simulation modelling helps in prediction of impact of climate change and design breeding based on the information available of gene frequency of almost all breeding traits, phenotypic value and G×E interaction.

## **VI. Future Needs and Way Forward**

1. Developing multiple stress tolerant crops to combat yield losses in climate change scenario.
2. To tackle the yield losses in C3 crops and harness the benefits of increasing CO<sub>2</sub> concentration due to climate change, on-going research on converting C3 to C4 crops should be given more emphasis.
3. To address the new races of pathogens and crop pests, more number of resistant genes should be identified for the major and minor pest and diseases.
4. More extensive study on root systems should be conducted to develop crop varieties that can thrive well under water stress conditions.
5. Climate change on the other hand increases the problematic soil area, and efforts should be made to develop crop varieties tolerant to grow under such soils.
6. Speed Breeding protocol must be developed and optimised for all crops to accelerate the breeding programs.
7. Genomic prediction tools must be utilised for effective and enhanced crop breeding program to tackle climate change.
8. The untapped plant genetic resources must be exploited favourably to look for genes and new traits that confer better adaptability under changing climate.
9. Genetic engineering and gene editing tools like CRISPR/Cas should be utilised to precisely induce gene mutations in key genes that have role in climate change adaptation, to improve their functionality.
10. The phenomics technology should be used for precise phenotyping of large number of lines to enhance the breeding efficiency.
11. The knowledge obtained for whole genome sequencing of major crops should be favourably integrated in breeding programs.
12. The crop ideotypes should be relooked to include traits that help crops to produce better under variable climatic conditions.
13. Extending breeding programs to minor crops to facilitate crop diversification.
14. Crop simulation genetic modelling can help in prediction and selection of best breeding methodology based on gene frequency, breeding value and genotype environment interaction under different climatic conditions in order to develop climate resilient cultivar or genotype.

## VII. Conclusion

The advancement in precise phenotyping and genotyping offers tremendous opportunities to develop crop varieties that suit better to changing climatic conditions. More emphasis towards gene function, molecular dissection of traits related to biotic and abiotic stresses, should be given priority in future plant breeding programs. Focus on orphan crops to develop new varieties with photo period-insensitivity and thermo-insensitivity widens the scope for crop diversification. Making use of participatory plant breeding in developing climate resilient varieties helps in boosting the plant breeding activities.

Simulation genetic modelling can play a key role in identification and investigation of crossing block performance of selected parents leading to selection of best breeding program, which can utilize even *in-silico* based techniques for further advancement. Vast scope exists for integration of speed breeding with high-throughput genotyping and phenotyping, genome editing, genomic selection, simulation modeling for accelerating the crop improvement process. Thus, accelerated plant breeding helps in alleviating hunger which is one of the objectives of sustainable development goals given by Food and Agriculture Organization.

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