Journal of Advances and Scholarly Researches in Allied Education
Vol. 18, Issue No. 6, October-2021, ISSN 2230-7540

Study on Plant Breeding and Crop Improvement

Dr. Sushil Kumar*

Assistant Professor, Department of Botany, K. K. P. G. College Etawah (U.P.) 206001 India

Abstract – When it comes to crop breeding, the rate at which yields improve is not fast enough to keep up with the growing world population. In plant breeding, the extremely extended harvest period limits the creation of superior crop types. Because of the several processes of cross-breeding, selection, and testing, it can take up to two decades for a new cultivar to be established. New plant varieties can help relieve food shortages and food instability. Traditional agricultural techniques have resulted in a decrease in crop genetic diversity. To increase agronomic qualities like as yield quality and resilience to biotic and abiotic stressors in agricultural plants by genetic selection and mutagenesis breeding, somaclonal variants, physical mapping, and functional genomics methods have been applied. Clustered palindromic repeats and programmable nucleases are used in gene editing (CRISPR). Plant breeders and the rest of the world are taking use of cutting-edge techniques like speed breeding, genome editing, and high-throughput phenotyping to increase crop breeding efficiency.

Keywords – Plant Breeding, Crop Improvement, Food Security, Food Scarcity, Molecular Markers, etc.

----------X----------

INTRODUCTION

Plant breeding has had a considerable impact on food supply globally [1]. However, as the world's population continues to grow at an alarming rate, there have been growing concerns about food quality and quantity. Farmers all across the world are dealing with major production losses as a result of climate change-induced drastic shifts in weather conditions. The Irish potato blight of the 1840s, for example, was a catastrophic catastrophe that led to millions of fatalities owing to food shortages [2]. There has been a significant drop in the ratio of food production to consumption in recent years, while the pace of urbanization and population expansion has grown worldwide. Nowadays, individuals are more inclined to eat processed meals, which have been stripped of their nutritious value. Ten billion people are anticipated to populate this planet by the year 2050, yet there are no adequate plans in place to feed them. Food production in developed nations has seen a rise in stress as agricultural productivity has improved to fulfil some of the country's food needs. Using plant breeding, it is possible to create plants with desired characteristics.. Humans have been using artificial selection to select and develop plants with improved nutritional values for the past 10,000 years. Many traditional farming practises were designed to enhance the nutritional value of various food crops. Plant breeding can benefit from a wide variety of recent scientific advances. Plant-based goods are becoming more and more popular, which necessitates the need to double yearly productivity increases in important crop species [2–3].

Figure 1: Plant breeding accomplishments throughout the years. Farmers and breeders have been inventing and upgrading crops for more than 10,000 years.

Mutagens for Molecular Breeding

Human, animal, and plant disease genes are among the primary goals of molecular biology. Research in this area uses genomic tools such as restriction enzymes (biomarkers), molecular glue (ligases), transcription machinery, and post-translational modification machinery [3]. With molecular biology, the production of crops and plant kinds that have high yields, unique traits as well as pest and disease resistance may be achieved. Approximately 40 million hectares of land have been planted with transgenic cultivars after passing bio-safety studies. As time passed, scientists began to combine conventional approaches with molecular ones in

order to study phenotypic shifts caused by changes in the genotype of plant characteristics. Scientists may utilize NGS to read genomes and construct huge gene libraries for bioinformatics studies before the use of molecular tools, which is critical. It is now possible to find gene regulatory sequences and molecular markers using NGS, which opens a new route for evolutionary and phylogenetic study. Additionally, molecular biology is being used to detect several cytoplasmic male infertility origins during hybrid breeding. Withdrawal of undesired mutations is among the downsides of using traditional methods. An extensive screening process is required as well as significant time investment. Because of its simplicity, MAS is an ideal tool for studying mutations that increase backcrossing efficiency (also known as "breeding by design") (or "breeding by design").

Speed Breeding for Accelerating Plant Breeding

Research and breeding projects are sometimes stymied due to a lack of technology that can speed up plant development and generation turnover. All plant scientists were inspired by NASA's efforts in the early 1980s. An innovative set of techniques used to speed up wheat breeding was coined the phrase "speed breeding" by University of Queensland researchers in 2003. [5] A number of crops are now working on speed-breeding techniques. Like double haploid (DH) technique, speed breeding may be used with varied germplasm and doesn't necessitate the use of particular equipment for in vitro cultivation. By manipulating light intensity and temperature as well as daytime length to induce early blooming and yearly seed harvesting, speed breeding is able to reduce the generation time. Flowering is regulated by light intensity and wavelength. Peas, Chickpeas, Beans, and Lupins were able to be bred with early and late blooming genotypes by light spectrum management (blue and far red-improved LED lights and metal halide). These species' decreasing red:far red-red molar ratio was shown to be positively associated (R:FR). As a result, the FR region's brightest light is also its most inductive. Incandescent lights, for example, have low R:FR, which leads to more stem elongation. Whereas high R:FR lowers stem enlargement and increases lateral branching and blooming. Regulated by phytochrome FR, this activity is mediated by blue light (Pfr).

Plant breeding and genetics have made significant contributions to the production of better cultivars in recent years. In addition to the normal techniques, innovative agronomic strategies have yielded outstanding agricultural results. Although private enterprises, extension workers, and public sector investments are all necessary for sustainable crop production to maintain global food security, they are not sufficient alone.

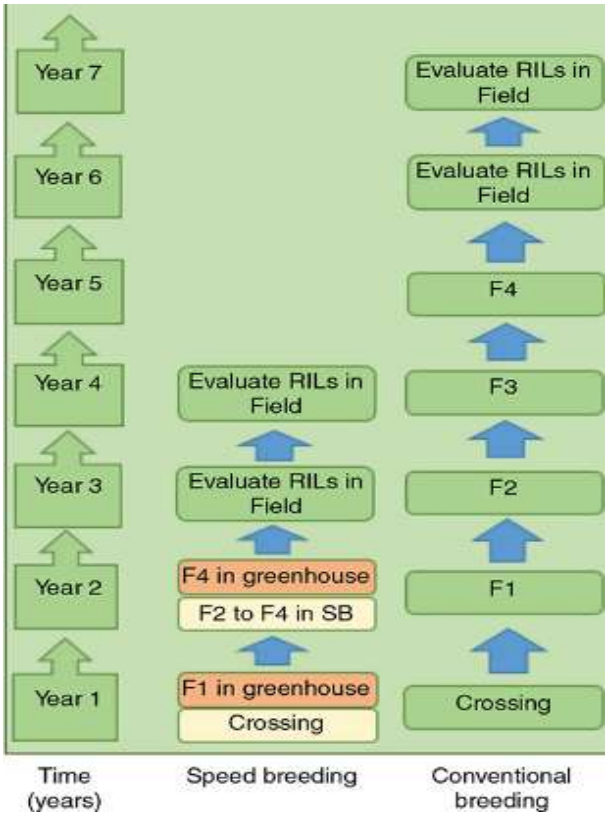

Figure 2: Speed breeding in pulses to improve breeding

CLASSICAL BREEDING

1. Release/production of variation

Mendel's theory dictates that this is done by crossing cultivated lines with each other. By crossing two parents with the appropriate character expression between them, we can look for new combinations of plants with the desired character later on in the evolutionary process. As a result, the segregation of all needed genetic loci during proper meiosis is critical to this process. The embryo, which eventually becomes the seed, is formed by the chance union of gametes during fertilization [7].

2. Select amongst the variation

The decision of which characters to use is the first hurdle to overcome. On the surface, this seems simple, but in reality, it involves attempting to rank the traits needed in the new cultivar in proportion to both the traits that need to be improved and those whose expression is already adequate in the parents. If this wasn't enough, the breeder is also confronted with a number of practical issues. For starters, there are just too many characters to attempt to account for in any meaningful way. The time and effort it takes to measure some characteristics [8] means they may require more resources than are available. Breeding programmes have the challenge of dealing with a huge number of

diverse genotypes, yet only a limited supply of planting material for each of these genotypes exists.

3. Stabilizing and multiplying the desired types

When it comes to the specifics of this aspect of plant breeding, the natural breeding system plays a significant role. In breeders, out crossers, and clonally reproduced organisms are the three basic types of natural breeding systems (i.e. clonal or vegetative propagation). Classical breeding may be divided into three broad groups as a result of these three key variations in the natural breeding system.

CROSS-POLLINATED CROPS

Allium sativum, ryegrass, forage legumes such as red clover, forage legumes such as clover and alfalfa are examples of cross-pollinated crops. In the selection of new cultivars of cross-pollinated crop species, In order to maintain a high level of heterozygosity in the general population, it is necessary to raise the frequency of advantageous alleles in mixed genotype populations. Individual genes are not as significant as population traits (as in self-pollinating crops). To reach the desired outcome, the population must have an intricate mix of genotypes that all act in concert [9]. They are split into open-pollinating and synthetic cultivars depending on the methods used to maintain and reproduce them.

CONTRIBUTION OF PLANT BREEDING TO CROP IMPROVEMENT

With the advent of modern molecular plant breeding, crop development has undergone a sea change, which has resulted from genomics and molecular marker selection as well as traditional breeding methods. Only 5–6 years were needed to develop a new wheat cultivar instead of 10–12 years. Time-consuming work is involved in the development of homozygous and comparable lines in hybrid and pure line crop breeding. With DHs, it is now possible to produce homogenous and homozygous lines in many crops in just two generations, cutting the cycle time from five to two. Maize DH employs the R1-NJ color marker, which is one of the most prevalent. The DH system, on the other hand, has a number of genotypic and biological drawbacks. Different crop species show genotype dependence for haploid induction, changing tissue culture (e.g., in the event of a different culture), and chromosomal doubling by colchicine. Unintentionally, breeders employing the DH method make a large number of selections for loci, which increases the likelihood of a successful breeding programme, but this may reduce genetic variety in the breeding populations. Multiple plant species can benefit from RNAi inhibition of genes, which alters plant defence, phytohormone and abiotic stress response pathways, as well as a wide spectrum of developmental modifications [10].

Figure 3: Molecular markers and marker-assisted breeding in plants

MOLECULAR BREEDING (MB)

Plant and animal qualities of interest can be improved by molecular breeding, which includes genetic engineering/gene manipulation, molecular marker assisted selection, genomic selection, and other techniques. "Molecular breeding," on the other hand, refers to the technique of employing molecular biotechnologies, such as molecular markers, in conjunction with linkage maps and genomics, to change and improve plant or animal traits based on genotypic testing. [11] Marker assisted backcrossing (MABC), MARC, and genomic selection (GWS) are all examples of current breeding techniques that use this term. The most widely used terms are MAS, MABC, MARC, and GWS. A variety of strategies, such as marker-assisted selection, marker-assisted backcrossing, marker-based pyramiding of multiple genes, and so on, will be covered in this article.

Types of Molecular breeding:-

1. Classical markers

Morphological markers: Many years ago, marker-aided selection of plants with desirable features was used in breeding. To begin with, plant breeders focused on qualities that could be seen, such as the form of the plant's leaves or the flower's pubescence or the pod's color or the seed's shape or the awn's color or length. It's possible to identify and alter genetic polymorphisms using morphological markers. It is because of this that two- and three-point tests [12] are commonly employed in the creation of linkage maps.

Cytological markers: The chromosomal karyotype and bands in cytology can demonstrate the structural characteristics of chromosomes. Eukaryotic and non-eukaryotic chromosomes are seen in different colour, breadth, order and location banding patterns.

As an example, Giemsa stain creates G bands, whereas quinacrine hydrochloride produces Q bands.

Biochemical/protein markers: Molecular markers can also include protein markers; however DNA markers are more commonly used. Despite their differing molecular weights and electrophoretic mobility, all isozymes serve the same biological function. Isozymes. A change in electrophoretic mobility due to amino acid substitution causes the difference in electrophoretic mobility of isozymes, not the products of separate genes.

2. DNA markers

It is possible to detect a gene pool's distinct genotypes and alleles through the use of DNA markers that are specific to the population or gene pool they belong to. Molecular approaches can be used to find genetic fragments that are connected to a certain genomic location. The existence of polymorphism (base deletions, insertions, and substitutions) in a population can be demonstrated by a DNA marker. Southern blotting and polymerase chain reaction (PCR) techniques can be used to identify polymorphism in a sample. PAGE (polyacrylamide gel electrophoresis) and/or molecular hybridization, followed by electrophoresis, such as AGE (agarose gel electrophoresis) or CE (capillary electrophoresis) can be used to identify polymorphic regions of DNA. Sothern blotting and PCR, for example, have been created as novel detection technologies. In order to use DNA markers for marker-assisted breeding, they must meet the following criteria:

- Polymorphism is at a high level.
- Uniform distribution over the genome-wide array.
- Codominance of words and phrases
- Allelic characteristics that are easily distinguished
- There is no pleiotropic impact from a single copy.
- Affordability
- Nature is genome-specific
- There is no negative impact on phenotypic.

RFLP markers: In the early days of plant genome mapping, one of the most useful tools was RFLP markers, a first-generation DNA marker. In the South, they're known as "Southern Bolting." At restriction sites or between nearby restriction sites, mutations (deletions and insertions) can occur in the DNA of living organisms (deletion and insertion). As a result of base pair mutations and insertions or deletions at restriction sites inside the restriction fragments, the size of restriction fragments may be changed. Some restriction enzyme recognition sites may be changed or removed as a result of this.

RAPD markers: It is a DNA-based marker known as the RAPD system. This PCR technique uses a single, short, and random primer to amplify an individual's whole genomic DNA. It is necessary for the primer to bind to many unique loci in order to amplify random DNA sequences that are complementary to the template. Amplification may occur during the PCR if two hybridization sites are at least 3000 bp apart and in separate directions.

AFLP markers: These markers are simple RFLPs that may be detected by selectively amplifying DNA restriction segments in the presence of certain primers. Selective amplification of genomic DNA utilizing high-stringency PCR under conditions that combine polymorphism at restriction sites with arbitrary primer hybridization can be achieved with this method. To distinguish it from other amplification techniques, it's called selective restriction fragment amplification (SRFA). [14] An AFLP primer is composed of an endonuclease recognition sequence, synthetic adapter sequence, and non-degenerate "chosen" (1-3 nucleotides) sequence. The primers used in this method, which can anneal to the adaptor and restriction sites, can only anneal a small number of nucleotides close to the restriction sites precisely.

SSR markers: A PCR-based marker that is also known as microsatellites, STRs, or sequence tagged microsatellite sites are used in the study of human genetic variation (STMS). Nucleotide sequences that are between 2 and 6 bases in length are found throughout the genome. In the genomes of both plants and mammals, there are a number of repetitions of the nucleotides (GT), (AATN)n, and (GATAN). Polymorphism in plants is caused by the variation in the number of copies of these repetitions. Primers for PCR usage in microsatellite area amplification have been developed due to the conservation of the DNA sequences bordering these regions. Due to their high amount of allelic diversity, microsatellite loci are extremely useful genetic markers.

SNP markers: Individuals or DNA sequences can be distinguished by a single nucleotide base variation (SNP). As a result of the nucleotide substitution, SNPs can be categorized as either transitions or transversions. There are two types of SNPs: cDNA (mRNA) variants and genome-wide deletions and insertions (indels). As the smallest unit of heredity, SNPs are the most effective approach to generate molecular markers. Animals and plants both have a high frequency of SNPs.

APPLICATIONS OF GENETIC ENGINEERING TO PLANT BREEDING

Alfalfa, apple, carrot, cauliflower, celery and cotton are just a few of the many crops that have been successfully transformed. An initial focus on conventional farming-related features has led to the production of new cultivars utilizing recombinant DNA technology. Insects, weeds, and plant diseases have all been dealt with. Genetically engineered crops have been deployed for the first time into large-scale farming (such as maize and tomato; canola; squash; potato; soybean; and cotton). When it comes to final use (including oil composition, starch, vitamin content, and even vaccinations), focus has recently switched [15].

CONCLUSION

The cross breeding, mutation breeding, and transgenic breeding are the principal strategies of crop enhancement in modern agriculture. Untargeted breeding efforts that take months or years to complete will not be able to keep up with the rising worldwide demand for food. Crop selection efficiency has been improved by using marker-assisted breeding and transgenic techniques, which introduce desirable characteristics into elite varieties via exogenous transformation. It is possible to uncover the exact plant molecular pathways responsible for crop improvement using these genome editing methods, which allow quick, focused mutagenesis. The introduction of next-generation breeding methods has changed crop breeding. Traditional agricultural approaches are far outclassed by genome editing technologies because of the former's ease of use, efficiency, high degree of specificity, and potential for multiplexing. Increased agricultural improvement can be achieved by genetic tools and resources combined with speed breeding.

REFERENCES

1. Araus, J.L.; Kefauver, S.C.; Zaman-Allah, M.; Olsen, M.S.; Cairns, J.E. (2018). Translating High-Throughput Phenotyping into Genetic Gain. Trends Plant Sci., 23, pp. 451–466.

2. Basey, A.C.; Fant, J.B.; Kramer, A.T. (2015). Producing native plant materials for restoration: 10 rules to collect and maintain genetic diversity. Nativ. Plants J., 16, pp. 37–53.

3. Cheema, K.S. K. (2018). Plant Breeding its Applications and Future Prospects. Int. J. Eng. Technol. Sci. Res., 5, pp. 88–94.

4. Ghosh, S.; Watson, A.; Gonzalez-Navarro, O.E.; Ramirez-Gonzalez, R.H.; Yanes, L.; Mendoza-Suárez, M.; Simmonds, J.; Wells, R.; Rayner, T.; Green, P.; et. al. (2018). Speed breeding in growth chambers and glasshouses for crop breeding and model plant research. Nat. Protoc., 13, pp. 2944–2963.

5. Godwin, I.D.; Rutkoski, J.; Varshney, R.K.; Hickey, L.T. (2019). Technological perspectives for plant breeding. Theor. Appl. Genet., 132, pp. 555–557.

6. Hajjar, R.; Hodgkin, T. (2007). The use of wild relatives in crop improvement: A survey of developments over the last 20 years. Euphytica., 156, pp. 1–13.

7. Kandemir, N.; Saygili, ˙I. (2015). Apomixis: New horizons in plant breeding. Turkish J. Agric. For., 39, pp. 549–556.

8. Li, H.; Rasheed, A.; Hickey, L.T.; He, Z. (2018). Fast-forwarding genetic gain. Trends Plant Sci., 23, pp. 184–186.

9. Majid, A.; Parray, G.A.; Wani, S.H.; Kordostami, M.; Sofi, N.R.; Waza, S.A.; Shikari, A.B.; Gulzar, S. (2017). Genome Editing and its Necessity in Agriculture. Int. J. Curr. Microbiol. Appl. Sci., 6, pp. 5435–5443.

10. Samineni, S.; Sen, M.; Sajja, S.B.; Gaur, P.M. (2019). Rapid generation advance (RGA) in chickpea to produce up to seven generations per year and enable speed breeding. Crop J.

11. Shiferaw, B.; Smale, M.; Braun, H.-J.; Duveiller, E.; Reynolds, M.; Muricho, G. (2013). Crops that feed the world 10. Past successes and future challenges to the role played by wheat in global food security. Food Secur., 5, pp. 291–317.

12. Tester, M.; Langridge, P. (2010). Breeding technologies to increase crop production in a changing world. Science (80-), 327, pp. 818–822.

13. Voss-Fels, K.P.; Stahl, A.; Hickey, L.T. (2019). Q & A: Modern crop breeding for future food security. BMC Biol., 17, pp. 18.

14. Watson, A.; Ghosh, S.; Williams, M.J.; Cuddy, W.S.; Simmonds, J.; Rey, M.D.; Asyraf Md Hatta, M.; Hinchliffe, A.; Steed, A.; Reynolds, D.; et. al. (2018). Speed breeding is a powerful tool to accelerate crop research and breeding. Nat. Plants, 4, pp. 23–29.

15. Zhang, F.; Wen, Y.; Guo, X. (2014). CRISPR/Cas9 for genome editing: Progress,

implications and challenges. Hum. Mol. Genet., 23, pp. R40–R46.

Corresponding Author

Dr. Sushil Kumar*

Assistant Professor, Department of Botany, K. K. P. G. College Etawah (U.P.) 206001 India

sushilsiretw@gmail.com