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EMERGING TALENTS IN HORTICULTURE BREEDING AND GENETICS

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Horticulture is a vital sector of agricultural output that gives farmers essential financial assistance. A varied and healthy diet depends on horticultural plants, such as fruit, vegetable and ornamental plants. They also improve the comfort of our homes and preserve the environment. horticulture products are now regularly available as a result of the significant advancements achieved in horticulture plant development, cultivation, and postharvest treatment in the past few years. This has led to a year-round availability of a wide variety of high-quality fruits and vegetables. Despite this, the horticulture sector continues to encounter difficulties, such as biotic and abiotic stress, the time-consuming breeding of superior cultivars with favourable features, elevated labour and cultivation costs, low productivity and waste and loss associated with postharvest interventions (Liu *et al.* 2023). Due to a continuous rise in global population and the associated demand for more food, sustainable and rising fruit and vegetable farming is a significant issue for ensuring future food security. Although conventional breeding methods have significantly contributed to the development of important cultivars, new approaches are required to further increase horticulture production of crops.

Crop variety improvement techniques are developing quite at pace. A group of biotechnology-based techniques called "New Breeding Technologies" aim to swiftly yet accurately modify plant characteristics (Anon., 2018). These developments have given horticulture breeding programmes a way to decrease the number of cycles and improve the accuracy and efficacy of new cultivar development (Xiong *et al.* 2015). Genome-wide selection (GWS) is one of the techniques that is evolving at an unprecedented rate. Instead of the estimated breeding values (EBVs) that fruit breeders have always used, GWS uses genomic estimated breeding values (GEBVs) as selection criteria. GEBVs are developed

employing dense genome-wide single-nucleotide polymorphism (SNP) markers for individuals in a phenotyped training population in order to demonstrate marker effects on complex phenotypes governed by a multitude of genetic loci. Then, in order to find those with outstanding qualities that may be considered "elite," individuals in breeders' selection populations are screened and their GEBVs are determined using genetic marker details. In order to outbreed woody perennial fruit crops, marker-assisted selection (MAS) for qualities governed by key genes or quantitative trait loci is now often used (Kumar *et al*. 2012; Van Nocker and Gardiner, 2014)

Genome Editing

This technique allows to make precise changes to the DNA of a plant. This can be used to improve traits such as yield, nutritional quality, and resistance to pests and diseases. It includes methods, based on recognising specific DNA sequences to direct where an enzyme will cut or modify a gene (Anon., 2018). These methods depend on engineered endonucleases (EENs), which break DNA according to a certain sequence owing to the presence of a specific DNA-binding domain or RNA sequence. These nucleases can efficiently yet accurately knock the targeted genes by identifying the relevant DNA sequence (Xiongand Ding. 2015). Due to cellular DNA repair processes including homology-directed repair (HDR) and error-prone non-homologous end joining breaks (NHEJ), the double-strand breaks (DSBs) of DNA ultimately lead to gene alteration at the targeted locations (Wyman and Kanaar, 2006).

- **Oligonucleotide-directed mutagenesis** adds a few additional bases into a gene resulting in a precise, specific mutation.

- **TALENs** (transcriptional activator-like effector nucleases) and **ZNF** (Zinc Finger Nucleases) use specially design proteins to identify the DNA sequence for the enzyme to cut. Until now, there have been no reports on ZFN applications in horticultural crops. TALENs, has rapidly emerged as an alternative to ZFNs for genome editing(Anon., 2018).

- **CRISPR:** Clustered regularly interspaced short palindromic repeats (CRISPR)- uses a short RNA guide sequence to identify the target. CRISPRs recognise and trim foreign DNA via a process similar to RNA interference. A novel breeding technique called CRISPR-associated protein-9 (Cas9) offers the ability to correctly and quickly

enhance a number of attributes in crops, including yield, quality, disease resistance, abiotic stress tolerance, and nutritional qualities. Due to its simple operation and high mutation effectiveness, this technology has been employed to get new germplasm resources through gene-directed mutation (Gaj*et el.* 2013; Mounika *et al.* 2022).

- **Ribonucleoprotein genome editing** is a novel technique to produce genome-edited plants without introducing foreign DNA at any stage (DNA is typically inserted at one stage and then removed). In this method, the DNA-cutting enzyme and the CRISPR guide RNA are combined before being delivered to plant cells.

- **Site-directed nucleases**: SDN1, SDN2, or SDN3 alterations are produced using TALENS, ZNF, and CRISPR. The DNA in the target gene is cut in SDN-1 and automatically repaired. A certain percentage of the restored cells will include a mistake, leading to a mutation. At the location of the break, one or more extra DNA nucleotides are specially inserted in SDN-2. The DNA that is inserted in SDN-3 is longer and can reach the size of a whole gene.

RNA Interference

The expression of particular genes may be turned down or off via RNA interference, also known as gene silencing. The target gene produces messenger RNA, which is bound by little RNA fragments that the cell is stimulated to generate. This prevents the gene from carrying out the function it was designed to perform. RNAi has been used to produce non-browning apples, as well as to lessen potato bruising and cold-sweetening.

- **Host-Induced Gene Silencing:** The interfering RNA used in HIGS is embedded into the plant and is intended to silence a critical gene in insect or pathogen. The interfering RNA causes the gene to be silenced when the pest or pathogen affects the plant. The host plant has therefore developed more resistance (Govindarajulu*et al.* 2015).

Marker Assisted Selection

With the fast development of molecular genetics and sequencing technology, scientists devised "marker-assisted selection" (MAS), a more efficient and accurate strategy, by incorporating DNA markers into phenotypic selection. Through marker-assisted selection (MAS), DNA markers offer a tremendous potential to increase the effectiveness and

precision of conventional plant breeding. An abundance of DNA marker-trait connections has been produced by the numerous quantitative trait loci (QTLs) mapping studies conducted for several crop species (Hasan *et al.* 2021). Environmental factors and agricultural plant growth circumstances have no influence on the regulation of molecular or DNA markers, which are not visible during the plant's developmental phases. As more molecular markers and genetic maps have been available, MAS has become possible for traits controlled by substantial quality as well as for quantitative trait loci (QTLs) (Collard and Mackill, 2018). The usefulness of a particular molecular marker depends on its capacity to identify nucleotide polymorphisms that allow segregation between different molecular marker alleles. Molecular methods such as restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), microsatellite or simple sequence length polymorphism (SSR), random amplified polymorphic sequences (RAPD), cleavable amplified polymorphic sequences (CAPS), single-strand conformation polymorphisms (SSCP), and single nucleotide polymorphisms (SNPs) are used to identify these polymorphisms.

Phenotyping

Plant phenotyping is the most important work of any plant breeding programme, and reliable assessment of plant attributes is required to choose genotypes with higher quality, higher yield, and greater climatic resistance. The bulk of phenotyping methods in use today are labor-intensive and harmful. The major method used in plant phenotyping investigations has recently been the development of numerous sensors and imaging systems for quick and accurate quantitative evaluation of plant features.

- **Image-Based High-Throughput Phenotyping**

In order to quantify morphological, physiological, biochemical, and performance parameters in a non-destructive manner, high-throughput phenotyping devices can photograph hundreds of plants every day utilising many different kinds of optical sensors (Chawade*et al.* 2019). The concept underlying image-based phenotyping is based on how electromagnetic radiation interacts with the surface of plants, causing changes in absorption, reflection, emission, transmission, and fluorescence between healthy and stressed plants as well as across genotypes (Abebe, 2023).

These are just a few of the emerging techniques in horticulture breeding and genetics. These techniques offer the potential to develop new crops that are more nutritious, resilient, and sustainable.

Here are some of the benefits of using these emerging techniques:

- They can be used to improve traits that are difficult to breed for using traditional methods.
- They can accelerate the breeding process, which can help to meet the growing demand for food.
- They can be used to develop crops that are more resistant to pests, diseases, and climate change.
- They can be used to develop crops that are more nutritious and have a better taste.

However, there are also some challenges associated with using these emerging techniques, such as:

- They can be expensive to develop and use.
- There are concerns about the safety of some of these techniques.
- There is a need for more research to understand the long-term effects of these techniques.

Conclusion

Despite these challenges, the potential benefits of using these emerging techniques are significant. As the field of horticulture breeding and genetics continues to evolve, these techniques are likely to play an increasingly important role in developing new crops that can help to feed a growing population and protect the environment.

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