Plant Archives Vol. 24, No. 1, 2024 pp. 929-937 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2024.v24.no.1.127

A COMPREHENSIVE REVIEW ON FAST TRACK BREEDING OF FRUIT CROPS: A NEW APPROACH

Aditya Gaurha[1]*, Ram Kumar Dewangan[2], Varsha Minz[1], Swati Shukla[1], Pragya Shrivastava[3] and Yamini[1]

[1]Department of Fruit Science, I.G.K.V., Raipur (C.G), India.

[2]Department of Fruit Science, K.D.C.H.R.S.- M.G.U.V.V., Jagdalpur (C.G), India.

[3]Department of Fruit Science, C.H.R.S.- M.G.U.V.V., Sankara, Durg (C.G), India.

*Corresponding author E-mail : adityagaurha460@gmail.com

(Date of Receiving-23-11-2023; Date of Acceptance-07-02-2024)

ABSTRACT

Given the rapid growth of the global population, it is crucial to accelerate food production to meet the ever-increasing demand for food and nutrition. Given the limited potential for expanding cultivation areas, it is crucial for plant breeders to prioritize the development of new varieties that not only have higher productivity but also possess the ability to withstand different types of pests, diseases and environmental challenges. Nevertheless, the development of new varieties requires a meticulous and time-consuming process. The duration of a breeding program is primarily determined by the number of years needed to develop homozygous lines from the segregating generations resulting from the crossbreeding of two parents. Woody perennial plants, such as fruit and nut trees, often have lengthy breeding cycles. Plant breeders may need to go through multiple cycles and wait for several years to develop and introduce improved cultivars. However, recent advancements in biotechnologies and genomics have the potential to greatly accelerate cultivar development in all crops. Through the utilization of various genetic engineering techniques, Fast-track breeding systems are able to induce early flowering, leading to generation cycles of one year or less. This method has been used on various crops to effectively generate homozygous lines after crossing carefully selected parents with contrasting traits. The technique is dependent on precise control of various factors including photoperiod, light intensity, temperature, soil moisture, soil nutrition, and high-density planting. This brief review provides an overview of strategies aimed at minimizing the frequency and length of breeding cycles for horticultural crops, while maximizing their yield.

Key words : Fast-track breeding, Fruits, Growth.

Introduction

The world's population is about 7.8 billion people now, and it's expected to hit 9.9 billion by 2050 (Samantara *et al.*, 2022). Climate fluctuations, such as increasing temperatures, more frequent floods, and drought, are anticipated to result in new diseases and more frequent pest outbreaks. This will necessitate a flexible approach to plant breeding. So, we have to emphasize on the pressing need to accelerate the current rate of genetic gain in crucial food crops in order to protect global food security. Enhancing the rate of genetic gain hinges on expediting crop breeding pipelines to enable swift delivery of enhanced crop varieties. As indicated by the breeder's equation (Moose and Mumm, 2008), the process of plant breeding can be expedited by enhancing the factors that impact the genetic gain over time (Sinha *et al.*, 2021; Varshney *et al.*, 2021), particularly the duration of the breeding cycle (Cobb *et al.*, 2019).

A conventional breeding method involves carefully choosing parental genotypes that possess the desired traits, followed by a series of crosses and selections to improve the quality of the offspring and ultimately produce cultivars that satisfy market requirements (Shimelis and Laing, 2012). When developing a crop cultivar, it is important to establish breeding goals that focus on increasing yield, improving nutritional quality, and enhancing tolerance to biotic and abiotic stresses (Samantara *et al.*, 2022). On the other hand, it typically

takes a significant amount of time, often up to ten years, to develop and release an enhanced variety (Ahmar *et al*., 2020). Fruit crops generally have a long breeding period which is because of its lengthy juvenile phase, which may vary from 3-15 years or more. In nature, the process of juvenility plays a crucial role in ensuring that plants do not start flowering until they have the necessary photosynthetic capacity to produce fruit and viable seeds (Hackett, 2011). This mechanism also prevents resources from being allocated to flowering before a plant has reached a competitive size in its environment. Nevertheless, this inherent protection can be manipulated by breeders, who possess the ability to cultivate plants in ideal growth conditions (van Nocker and Gardiner, 2014). Various methods have been employed to enhance the characteristics of fruit crop plants, such as yield, quality, and resistance to environmental and biological challenges. These techniques include genetic manipulation, mutational breeding, somaclonal variations, whole-genome sequencing, physical mapping, and functional genomics. Owing to recent scientific advancements, new plant breeding techniques have emerged that allow for more precise and efficient modifications to a plant's genome compared to traditional methods (Hussain *et al*., 2023). These innovative methods encompass a series of advancements, from genome editing techniques to fast-track breeding and the integration of omics technology. These approaches provide valuable, adaptable, cost-effective, and efficient ways to ensure accuracy in plant breeding and shortening of juvenile periods. Fast-track breeding systems have been the most efficient and useful for shortening the breeding cycles of horticultural crops as well as enhancing the horticultural crops for yield, biotic and abiotic stresses.

Fast-track breeding systems employ a range of genetic engineering techniques to trigger early flowering, resulting in generation cycles of one year or less. Fast-track breeding have been employed on a range of crops to efficiently produce homozygous lines following initial crosses of carefully chosen parents with contrasting traits. The technique relies on carefully controlling factors such as photoperiod, light intensity, temperature, soil moisture, soil nutrition and high-density planting (Hussain *et al*., 2023). This method enables a cycle of generally 3–9 breeding generations per year. Procedures for the development of Fast-track breeding are currently being explored for a variety of crops. This review will focus on the status of implementation of fast-track breeding technologies on fruit crops development.

Objectives of Fast-track breeding systems

The objectives of Fast-track breeding systems are same as that of conventional breeding systems. The primary goal of Fast-track breeding is to create high-yielding varieties that are resistant to pests and diseases, have a shorter maturity period, lack toxic substances, mature at the same time, are not affected by changes in light, can withstand environmental stress, and have improved quality (van Nocker and Gardiner, 2014). Ultimately, this breeding technique aims to contribute to the achievement of zero hunger goals. However, for fruit crops, reducing the length of breeding cycle is one of the most important objectives (Scorza *et al*., 2012) (Fig. 1).

Components of Fast-track breeding

Speed breeding involves creating ideal growth conditions and expediting the breeding process by cultivating crops in controlled environments (Fig. 2). Here are some important components of a speed breeding setup:

1. Growth chambers with controlled environments

Speed breeding involves cultivating crops in carefully controlled environments that replicate optimal growing conditions, including temperature, humidity, and lighting. By utilizing growth chambers equipped with adjustable light and temperature settings, researchers have the ability to create specific conditions that can accelerate the growth of plants (Watson *et al*., 2018).

2. Light

Speed breeding often requires the use of artificial lighting, such as LEDs, to provide crops with a steady light source that accelerates plant growth. Speed breeding can be achieved using any light source that emits a spectrum covering the PAR (Photosynthetically Active Radiation) region (400-700 nm), with a particular focus on the blue, red, and far-red wavelengths (Tiwari, 2021).

3. Photoperiod

Photoperiodism refers to the way plants respond to changes in day length, allowing them to adapt to the seasonal variations in their surroundings (Thomas, 2017). The photoperiod plays a vital role in speed breeding, as it allows for precise control over the flowering time of plants, thus expediting the breeding process. According to Meena *et al*. (2022), it is recommended to have a photoperiod of 22 hours with 2 hours of darkness in a 24-hour diurnal cycle. However, the photoperiod used for speed breeding can vary depending on the crop species and the goals of the breeding programme, as it is important to consider these factors for optimal results.

4. Temperature

According to Meena *et al*. (2022), one temperature cycle should consist of 22 hours of light and 2 hours of darkness with a temperature difference of 17^0C.

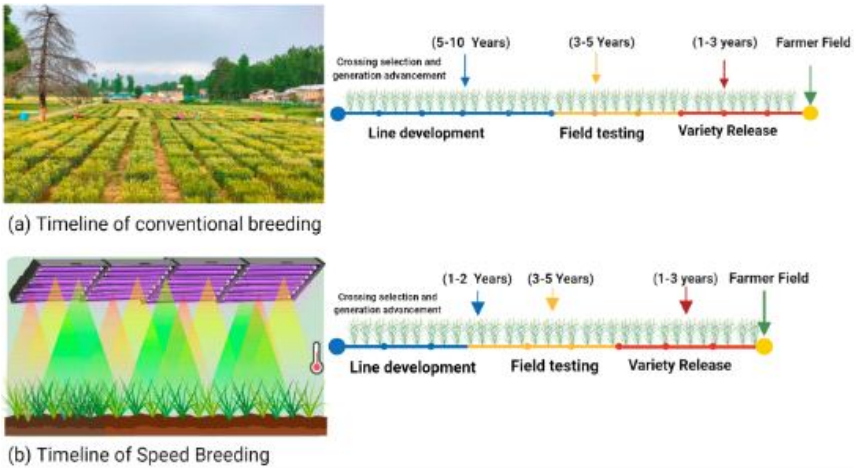

Fig. 1 : Timeline of development of varieties (Conventional Breeding vs. Fast-track/Speed Breeding) (Source: Samantara *et al*., 2022).

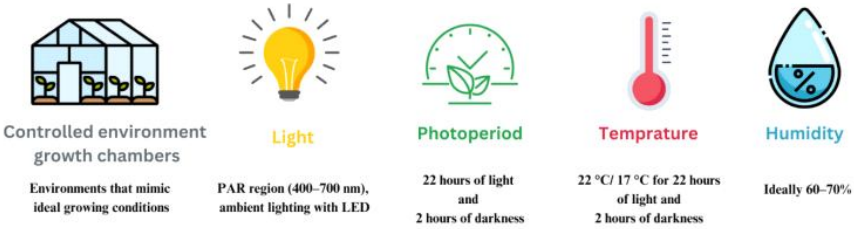

Fig. 2 : Components of Speed Breeding [Source: Tiwari (2021)].

5. Humidity

Humidity is typically recommended to be maintained within a range of 60-70% (Tiwari, 2021). Considering crops that are better suited to arid environments, it may be prudent to maintain a lower humidity level.

Types of speed breeding/Fast-track breeding system

Early speed Breeding activities involved the use of in vivo-in vitro cycling or complete in vitro lifecycle turnover (Croser *et al*., 2016; Varshney *et al*., 2021). However, fully in vivo systems have been extensively utilized in improvement programmes. In their study, Watson *et al*. (2018) introduced three distinct Speed Breeding facilities that can be tailored to match the available resources. Speed Breeding I systemutilized controlled environment plant growth chambers equipped with a 22-hour photoperiod generated by a combination of white LED bulbs, far-red bulbs, and ceramic metal hydrargyrum quartz iodide bulbs. The temperature was maintained at 22 °C during the day and 17°C at night. Under the specified conditions, wheat (*Triticum aestivum*, *T. durum*) and barley (*Hordeum vulgare*), exhibited a significantly early flowering time as compared to the control group grown in unregulated glasshouse conditions during the spring and early summer. A slightly altered configuration, known as Speed Breeding system II, utilized the identical temperature conditions as SB I, while a 22-hour photoperiod was maintained through the use of high-pressure sodium vapour lamps. Immature seeds were harvested and subjected to cold treatment in order to quicken the generation time. The growth stage results for wheat, barley, canola, and chickpea plants showed that under Speed Breeding conditions, plant development was accelerated and there was a consistent time to anthesis (Samantara *et al*., 2022). A more economical option is the Speed Breeding III system, which consists of a 3 m^3 well-insulated room, a total of seven LB-8 LED light crates, as well as a 1.5 HP inverter split system domestic air conditioner. The lighting was modified to a 12-hour photoperiod for a duration of four weeks, which was then followed by an 18-hour photoperiod. The temperatures were carefully controlled, with a lower temperature of 18°C during the dark period and a slightly higher temperature of 21°C during the light period. This system can be flexible as per the crop's requirements and breeding objectives (Samantara *et al*., 2022).

Effect of Fast-track breeding on fruit crops

Certain fruit crops have a lengthy period of immaturity before they are able to produce flowers, sometimes lasting over 20 years (van Nocker and Gardiner, 2014). Scientific techniques have resulted in significant advancements in apple and chestnut cultivation. These techniques have led to accelerated vegetative growth and early flowering in apple trees (in just ten months instead of the usual five years) and chestnut trees (in just two years instead of the usual seven years) (Baier *et al*., 2012). A new cultivar with desirable traits was successfully developed in apple using Speed Breeding technology. This technology relies on transgenic, early-flowering plants and MAS (Flachowsky *et al*., 2011). Some crops that are propagated through cloning, such as banana, roots, and tubers (not fruit crops) are now using Speed Breeding to shorten the time it takes for them to flower and increase the rate at which they flower. This also helps make the flowering process more predictable, which is useful for introducing disease-resistant traits, like bacterial wilt resistance in bananas (Vira *et al*., 2015; Souza *et al*., 2018).

Fast-track breeding through manipulations of environmental / Cultural conditions

Manipulation of environmental condition of growth of the fruit crops can tend to faster transition from juvenile to adult phase (Zimmerman, 1972). In apple (*Malus domestica*), the flowering process usually takes around 5 years for field-grown seedlings. However, with optimal growth conditions, plants can be induced to enter the adult reproductive phase in just 10 months. The mature apical part of the plant can be grafted onto a rootstock to facilitate continued growth and maintenance (Aldwinckle, 1975). One potential limitation of this method is that plants may reach significant heights, posing challenges for their maintenance in a controlled environment or greenhouse.

Plant growth regulators (PGRs) can be used to effectively manage growth, but it is important to first evaluate any potential negative impacts on the phase transition. Studying the impact of plant growth regulators (PGRs), such as phytohormones, on the flowering process in young woody perennials has been a fascinating area of scientific investigation (Zimmerman *et al.*, 1985). Numerous noteworthy findings have emerged from this research. Nevertheless, the efficacy and reliability of PGR treatments have demonstrated significant variation across different genotypes, species and experimental settings.

Optimal growth may not be enough for woody plants to transition to the adult phase. Even after reaching this stage, they may still require a period of chilling and/or defoliation lasting up to 10 weeks in order to ensure proper floral development (Aldwinckle, 1975). It is worth noting that transgenic plants that express the flowering gene *FT* in an abnormal manner are able to bypass the need for chilling in order to develop flowers. This indicates that chilling has an impact on the early stages of flowering pathways. The endogenous genetic mechanism of chill requirement is an intriguing subject for further investigation and could potentially be a valuable focus for shortening the breeding cycle.

Long stretches of low temperatures during the winter under high moisture conditions naturally overcome dormancy in most temperate-zone tree fruits and nuts. Extended periods of low-temperature stratification, lasting up to 12 weeks, may be necessary to disrupt dormancy *in vitro*. When conducting experiments in controlled environments, it is important to consider how certain factors can impact the length of the breeding cycle, especially when dealing with rapid-breeding protocols (Bridgen, 1994). As a result, methods to overcome seed dormancy are becoming more and more common. An alternative method involves carefully removing the embryo from the seed while it is still in the early stages of development, and then cultivating the embryo in an environment that encourages direct growth into a seedling. This technique is commonly employed in the rescue of embryos that result from wide crosses, as these embryos may not be able to develop into viable seedlings without intervention (Shen *et al*., 2011).

Enhancing Flowering with Biotechnological interventions

One of the most intriguing possibilities for shortening the breeding cycle involves the biotechnologically altering the genetic flowering pathways. Almost two decades ago, Weigel and Nilsson (1995) found that by introducing a specific gene from Arabidopsis called *LEAFY (LFY)* through genetic modification, they were able to induce the flowering process. Over the past two decades, there has been significant progress in refining this ground breaking technology. This includes incorporating more flowering genes, utilizing inducible promoters to control transgenic expression, and exploring new methods to transmit the transgenic stimulus through grafting. Early flowering mutants may also be used to enhance flowering. Early flowering Mutants has been observed in grapefruit (*Citrus paradisi*), pummelo (*Citrus grandis* L.), their hybrids, yamamikan (*Citrus intermedia* Hort ex Tanaka), and ponkan (*Citrus reticulata* cv. Blanko). These species can achieve early flowering through the use of specific treatments. However, in these instances, after flowering, the plants returned to the juvenile stage for a number of years (Holland *et al*. 1995). A study conducted by Hisada *et al*. (1997) introduced the citrus FT homolog (CiFT) and its successful application in promoting flowering in trifoliate orange (*P. trifoliata* L. Raf.) (Endo *et al*., 2005) and pear (*Pyrus communis* L.) (Matsuda *et al*., 2006). The over expression of *CiFT* in pear resulted in the occurrence of *in vitro* flowering from transgenic shoots. Suppressing the *MdTFL1* gene, similar to the findings of Kotoda *et al*. (2006), led to a notable decrease in the juvenile period. After 8 months of grafting on glasshouse plants, the researchers discovered the first solitary flowers (Kotoda *et al*., 2002). A vast amount of scientific literature indicates that, in general, these genes and mechanisms have been extensively preserved among flowering plants (Albani and Coupland, 2010; Amasino, 2010). Therefore, they function as a basic set of tools for genetically modifying the flowering of various economically significant tree fruit and nut crops. It is worth noting that due to the dominant nature of transgene effects, plants that are hemizygous for flowering transgenes are likely to exhibit early flowering.

The need for early flowering in just one parent enables breeding cycles in which progeny that flower early can be repeatedly bred with the desired genotype and utilized for the subsequent cycle (van Nocker and Gardiner, 2014). Once the transgene is deemed unnecessary or unwanted in the final modified cultivar, it can be removed through segregation in the population (Flachowsky *et al*., 2011; Hanke *et al*., 2014). This method is currently being utilized in conjunction with marker-assisted selection to introduce resistance to various fungal (Le Roux *et al*., 2012) and bacterial pathogens into commercially grown apples, as well as resistance to Plum Pox Virus into plums (Scorza *et al*., 2012). A notable advantage of the methods is that the resulting genotype does not have to be transgenic. Therefore, the produce could potentially bypass the usual regulatory obstacles faced by genetically modified organisms and be more readily embraced by the public.

The use of Genomic Technologies in the Fast-track Breeding of Horticultural crops

Over the past two decades, there has been a significant reduction in the cost and effort required to analyse a plant's DNA sequence. Additionally, there have been notable advancements in the infrastructure for storing and analysing this data. These advancements have allowed for a more streamlined approach in horticultural breeding programmes, resulting in fewer cycles and improved accuracy and effectiveness in developing new cultivars (van Nocker and Gardiner, 2014). One of the most rapidly advancing methods is genome-wide screening (GWS). GWS utilises genomic estimated breeding values (GEBVs) as selection parameters, as opposed to the estimated values (EBVs) traditionally employed by fruit breeders (Kumar *et al*., 2012). GEBVs are calculated for individuals in a training population by analyzing a vast number of single-nucleotide polymorphism (SNP) markers across the genome. This allows us to determine the effects of these markers on complex traits that are influenced by many different genetic factors. Individuals in breeders' selection populations are carefully evaluated and their GEBVs (Genomic Estimated Breeding Values) are calculated using genetic marker information. This process helps identify exceptional individuals with elite qualities. These can be utilized to further progress generations, or assessed in the field as possible cultivars (Kumar *et al*., 2012).

Marker-assisted selection (MAS) is a widely used technique in the field of Cross-breeding the woody perennial fruit crops. It allows for the selection of traits controlled by major genes or quantitative trait loci. Nevertheless, MAS is gaining recognition as a crucial tool in making Genome Wide Selection more affordable. It allows for the removal of undesirable genotypes from the initial breeding population (selection population) after relatively inexpensive MAS pre-screen using a small number of markers (less than 10) (Calus *et al*., 2010). Only the seedlings that meet these criteria undergo a more costly screening process involving thousands of genetic markers needed for Genome Wide Selection. A recent study emphasizes the practicality of using Genome Wide Selection (GWS) as an invaluable method for tree fruit breeders. These breeders often encounter lengthy time intervals, up to 7 years in the case of apples, before they can identify a tree as a potential paren (Kumar *et al*., 2012). GWS helps to address this challenge. This research used an ongoing scion breeding program to examine fruit quality parameters that apple breeders often choose for. It employed a training population of 1,120 seedlings, consisting of seven complete sib families in a factorial mating scheme, to guarantee relevance. It was discovered that when analyzing the 2500 SNPs individually in the training population, they only accounted for a small portion of trait variation. However, when all the markers were considered together, they were able to capture most of the trait heritability for various fruit characteristics. In the second stage of the study, seedlings with high GEBVs were selected as the pollen parents for a second generation called the "Selection Validation Population." This population consisted of 10 full-sib families. A total of two thousand seedlings underwent a series of scientific techniques, including MAS and GWS, in addition to an environmental regime specifically designed to stimulate early flowering (Kumar *et al*., 2012). It was observed that a portion of the seedlings began to flower after 27 months from seed. It is anticipated that all of the seedlings was in full bloom by the 36-month mark. It was observed that a portion of the seedlings began to flower after 27 months from seed. It is anticipated that all of the seedlings was in full bloom by the 36-month mark.

Transgenic approach: A Fast-track approach

The use of genetic engineering techniques that are based on genetic transformation techniques is now commonplace in the process of improving plants (Gambino and Gribaudo, 2012). Since fruit crop breeding is hampered by issues including extended life cycles, propagation techniques, high heterozygosity, and reproductive obstacles, transgenic breeding is crucial to the enhancement of fruit crops (Kramer and Redenbaugh, 1994). *Agrobacterium tumefaciens* mediation is a commonly employed transformation method due to its effectiveness. The genetic transformation of fruit crops

has yielded impressive results in terms of improving disease resistance, as well as enhancing tolerance to drought, frost, and salt. It has also led to modifications in plant growth patterns and improvements in fruit quality (Litz and Padilla, 2012). There have been numerous instances of inducing abiotic stress tolerance in fruit crops (Sun Waterhouse, 2011). Apple has been made more tolerant to cold temperatures by introducing the cold-inducible *Osmyb4* gene (Pasquali *et al*., 2008). Similarly, banana plants have been engineered to withstand multiple stresses by overexpressing the stress-responsive WRKY transcription factor gene (*MusaWRKY71*) (Shekhawat *et al*., 2011a). Drought and salt tolerance have been enhanced in bananas by introducing the *dehydrin* gene (Shekhawat *et al*., 2011b). Papaya has been made more cold-tolerant by expressing a Transcriptional activator gene called C-repeat binding factor (CBF) (Dhekney *et al*., 2007). Kiwi fruit, on the other hand, has been engineered to be more salt-tolerant by introducing AtNHX1 gene with a high K to Na ratio (Tian *et al*., 2011). A study was conducted to enhance the resistance of Grand Naine banana plants to fungal diseases. This was achieved by introducing three specific genes into the plants: an endochitinase gene from *Trichoderma harzianum*, a stilbene synthase gene from grape, and a superoxide dismutase gene from tomato (Vishnevetsky *et al*., 2011). An example of a successful transgenic event in banana involves the enhancement of pro-vitamin A through the utilization of *phytoene synthaseenzyme* (*PSY*) and iron (Ferritin gene from soybean) (Paul *et al*., 2017; Kumar *et al*., 2011).The European plum has undergone genetic modification by incorporating the *FLOWERING LOCUS T1 (FT1)* gene from *Populus trichocarpa*. As a result, transgenic plants with elevated levels of *FT1* exhibited accelerated flowering and fruit production in the greenhouse, with a time frame ranging from 1 to 10 months (Srinivasan *et al*., 2012). The plums demonstrated a remarkable ability to consistently produce flowers and fruit, unaffected by variations in daylight or chilling duration, and even withstood the harsh winter temperatures. Higher concentrations of terminal flowering protein (*TFL*) are commonly linked to this early phase flowering. *TFL* plays a major role in suppressing the process of flowering. It achieves this by repressing the production of various proteins that promote flowering, such as *FT* (*FLOWERING LOCUS T), LFY (LEAFY),* and (*APETALA1*) *AP1* **(**Martín-Valmaseda *et al*., 2023). In their study, Charrier *et al*. (2019) employed the CRISPR/Cas9 technology to make targeted modifications to the apple *TFL1* gene. Two distinct sgRNAs were utilized to specifically target the *TFL1* gene, while the same construct was employed to make edits to the pear *TFL1*. It was noted that there was an early flowering occurrence in transgenic pear lines (9%) and transgenic apple lines (93%) that specifically targeted the *PcTFL1.1* and *MdTFL1.1* genes, respectively.

Fast-track Breeding for Domestication

Domestication of plants refers to the practice of artificially changing wild plant species into agricultural plants. This process starts with early hybridization and ends with selective breeding. Plant breeding is closely linked to polyploidy crops. This technique can be quite time-consuming, but a solution has been found by integrating it with speed breeding. This innovative approach helps to minimize the time and number of generations required for the crops. Evidence of plant domestication can be observed in polyploid plants such as peanuts and bananas, which have undergone rapid breeding. O'Connora *et al*. (2013) conducted a study to assess the viability of employing the speed breeding technique in peanut breeding. Compared to the typical breeding phase, this study significantly shortened the time required to produce successive generations in a shorter time frame.

Combining Fast-track breeding techniques with advanced breeding technologies to enhance tolerance to abiotic stress.

Abiotic stresses pose significant challenges to crop production and are responsible for approximately 50% of yield losses in agricultural crops globally. According to research conducted by Ashraf *et al*. (2008), different types of stress can cause significant yield loss in crops. High-temperature stress is responsible for approximately 40% of the loss, while salinity accounts for 20%. Drought and low temperature contribute to 17% and 15% of the yield loss, respectively. Other abiotic stresses, such as low temperature, excess water, heavy metal exposure, mineral deficiency, and radiation, can also result in considerable yield loss. Gaining a comprehensive understanding of the mechanisms behind how plants tolerate abiotic stress, from sensing environmental signals to responding at the cellular level, is crucial for developing strategies to improve crop stress tolerance (Suprasanna *et al*., 2016). When it comes to abiotic-stress experiments, generation advancement, or phenotypic evaluation in abiotic-stress studies, speed breeding can be seamlessly incorporated by utilizing controlled growth conditions of a glasshouse. Utilizing a controlled environment can effectively minimize experimental error and simplify the analysis of genetic and environmental effects on phenotype (G 3 E interaction) (Berger *et al*., 2010; Roy

et al., 2011).

By creating a controlled environment, it becomes possible to closely observe the onset of various stresses, such as drought stress through water limitation, salinity stress through the addition of salts to hydroponics, and excessive watering. However, it is important to note that control conditions do not perfectly replicate the natural environment and the cost-effective reality. This is because plants are being grown in pots rather than in the field (Passioura, 2006). In controlled greenhouse environments, initial experiments are typically conducted to study abiotic stress factors such as water-deficit stress (drought), excessive water, extreme temperatures and salinity. Speed breeding is a highly dependable tool that can seamlessly integrate into standard breeding programs. Advanced breeding technologies, such as transgenics, marker-assisted breeding, genomic selection, and express genome editing, are being utilized to enhance tolerance to abiotic stresses. This can be utilized at different stages during the development of stress-tolerant cultivars. Speed breeding is a valuable tool in the scientific community. It helps researchers define target stress and environments, identify superior parents, standardize screens for stress tolerance, understand the mechanisms of stress tolerance, identify and characterize genes that contribute to tolerance, and combine different tolerance traits in elite lines through marker-assisted breeding (Ahmad *et al*., 2021). Additionally, it allows for the evaluation of breeding lines in specific stress environments. Nevertheless, the application of speed breeding in enhancing abiotic-stress tolerance is still in its early stages.

Conclusion

Most crop breeding projects are not producing crops at a pace that can keep up with the rising demand for food brought on by the world's constantly expanding population. The extended duration of crop growth poses a challenge in developing enhanced crop varieties through plant breeding. Developing improved plant varieties is a key approach to address food scarcity and enhance food security. Fast-track breeding is a scientific protocol that has the potential to significantly boost agricultural yield. By manipulating factors such as light duration, intensity, and temperature-controlled zones, as well as developing disease-resistant varieties and reducing salt sensitivity in crops, Fast-track breeding can help improve crop productivity. When compared to traditional breeding methods, this approach enables the release of multiple generations of the same crop in a more condensed timeframe. Fast-track breeding is an innovative method that allows for the rapid development of new long-day plant cultivars by significantly reducing the generation time. In addition, the integration of Fast-track breeding with traditional breeding techniques such as marker-assisted selection and gene editing can enhance the identification of superior genotypes and lines that possess novel traits such as increased yield, improved nutritional quality, and enhanced resistance to both biotic and abiotic stresses. Nevertheless, in numerous developing nations, especially within public plant breeding initiatives, the utilization of Fast-track breeding encounters constraints. These limitations arise from a scarcity of proficient plant breeders and technicians, as well as inadequate infrastructure and unreliable access to water and electricity. Currently, there is insufficient government support, both in terms of regulations and funding, to initiate and sustain Fast-track breeding in plant breeding initiatives. In order to expedite the production, testing, and commercial release of crop varieties, it is essential to integrate Fast-track breeding with other breeding techniques, along with cost-effective high-throughput genotyping and phenotyping.

References

Ahmad, S., Makhmale S., Bosamia T.C., Sangh C. and Nawade B. (2021). Fast-track breeding: a potential tool for mitigating abiotic stresses. In : *Stress Tolerance in Horticultural Crops* (pp. 51-61). Woodhead Publishing.

Ahmar, S., Gill R.A., Jung K., Faheem A., Qasim M., Mubeen M. and Zhou W. (2020). Conventional and Molecular Techniques from Simple Breeding to Fast-track Breeding in Crop Plants: Recent Advances and Future Outlook. *Int. J. Mol. Sci.*, **21(7)**, 2590.

Albani, M.C. and Coupland G. (2010). Comparative analysis of flowering in annual and perennial plants. *Curr. Topics Develop. Biol.*, **91**, 323-348.

Aldwinckle, H.S. (1975). Flowering of Apple Seedlings 16-20 Months after Germination1. *HortScience*, **10(2)**, 124-126.

Amasino, R. (2010). Seasonal and developmental timing of flowering. *The Plant J.*, **61(6)**, 1001-1013.

Ashraf, M., Athar H.R., Harris P.J.C. and Kwon T.R. (2008). Some prospective strategies for improving crop salt tolerance. *Adv. Agron.*, **97**, 45-110.

Baier, K.M., Maynard C., Powell W., Barakat A., Staton M. and Cheng C.H. (2012). Early flowering in chestnut species induced under high dose light in growth chambers. *J Am Chestnut Found*, **26**, 8-10.

Bridgen, M.P. (1994). A review of plant embryo culture. *HortScience*, **29(11)**, 1243-1246.

Calus, M.P. (2010). Genomic breeding value prediction: methods and procedures. *Animal*, **4(2)**, 157-164.

Charrier, A., Vergne E., Dousset N., Richer A., Petiteau A. and Chevreau E. (2019). Efficient targeted mutagenesis in apple and first time edition of pear using the CRISPR-

Cas9 system. *Front. Plant Sci.*, **10**, 40.

Cobb, J.N., Juma R.U., Biswas P.S., Arbelaez J.D., Rutkoski J., Atlin G., Hagen T., Quinn M. and Ng E.H. (2019). Enhancing the rate of genetic gain in public-sector plant breeding programs: lessons from the breeder's equation. *Theoretical and Applied Genetics*, **132**, 627-645.

Croser, J.S., Pazos-Navarro M., Bennett R.G., Tschirren S., Edwards K., Erskine W., Creasy R. and Ribalta F.M. (2016). Time to flowering of temperate pulses in vivo and generation turnover *in vivo–in vitro* of narrow-leaf lupin accelerated by low red to far-red ratio and high intensity in the far-red region. *Plant Cell, Tissue and Organ Culture (PCTOC)*, **127**, 591-599.

Dhekney, S.A., Litz R.E., Moraga Amador D.A. and Yadav A.K. (2007). Potential for introducing cold tolerance into papaya by transformation with C-repeat binding factor (CBF) genes. *In Vitro Cellular & Developmental Biology-Plant*, **43**, 195-202.

Endo, T., Shimada T., Fujii H., Kobayashi Y., Araki T. and Omura M. (2005). Ectopic expression of an FT homolog from Citrus confers an early flowering phenotype on trifoliate orange (*Poncirus trifoliata* L. Raf.). *Transgenic Research*, **14**, 703-712.

Flachowsky, H., Le Roux P.M., Peil A., Patocchi A., Richter K. and Hanke M.V. (2011). Application of a high Fast-track breeding technology to apple (*Malus× domestica*) based on transgenic early flowering plants and marker assisted selection. *New Phytologist*, **192(2)**, 364-377.

Gambino, G. and Gribaudo I. (2012). Genetic transformation of fruit trees: current status and remaining challenges. *Transgenic Research*, **21(6)**, 1163-1181.

Hackett, W.P. (2011). Juvenility, maturation, and rejuvenation in woody plants. *Horticult. Rev.*, **7**, 109-154.

Hanke, M.V., Flachowsky H., Wenzel S., Barthel K. and Peil A. (2014, January). The fast track breeding system in apple based on transgenic early flowering plants and marker assisted selection: an update. In : *Proceedings of the 1st International Rapid Cycle Crop Breeding Conference* (pp. 7-9).

Hisada, S., Akihama T., Endo T., Moriguchi T. and Omura M. (1997). Expressed sequence tags of Citrus fruit during rapid cell development phase. *J. Am. Soc. Horticult. Sci.*, **122(6)**, 808-812.

Holland, D., Abied M.A., Nachman S. and Saad S. (1995). Cotyledon detachment inhibits development but does not affect precocious flowering of 'Duncan' grapefruit. *Plant Cell, Tissue and Organ Culture*, **41**, 79-82.

Hussain, K., Mahrukh, Nisa R.T., Zaid A. and Mushtaq M. (2023). The utilization of Fast-track breeding and genome editing to achieve zero hunger. In : *Sustainable agriculture in the era of the OMICs revolution* (pp. 1-15). Cham: Springer International Publishing.

Kotoda, N., Iwanami H., Takahashi S. and Abe K. (2006). Antisense expression of MdTFL1, a TFL1-like gene, reduces the juvenile phase in apple. *J. Am. Soc. Horticult. Sci.*, **131(1)**, 74-81.

Kotoda, N., Wada M., Masuda T. and Soejima J. (2002, August). The break-through in the reduction of juvenile phase in apple using transgenic approaches. In : *XXVI International Horticultural Congress: Biotechnology in Horticultural Crop Improvement: Achievements, Opportunities*, **625** (pp. 337-343).

Kramer, M.G. and Redenbaugh K. (1994). Commercialization of a tomato with an antisense polygalacturonase gene: The FLAVR SAVR™ tomato story. *Euphytica*, **79**, 293-297.

Kumar, G.B.S., Srinivas L. and Ganapathi T.R. (2011). Iron fortification of banana by the expression of soybean ferritin. *Biol. Trace Elem. Res.*, **142**, 232-241.

Kumar, S., Chagné D., Bink M.C., Volz R.K., Whitworth C. and Carlisle C. (2012). Genomic selection for fruit quality traits in apple (*Malus× domestica* Borkh.). *PloS One*, **7(5)**, e36674.

Kumar, S., Garrick D.J., Bink M.C., Whitworth C., Chagné D. and Volz R.K. (2013). Novel genomic approaches unravel genetic architecture of complex traits in apple. *BMC Genomics*, **14**, 1-13.

Le Roux, P.M., Flachowsky H., Hanke M.V., Gessler C. and Patocchi A. (2012). Use of a transgenic early flowering approach in apple (*Malus× domestica* Borkh.) to introgress fire blight resistance from cultivar Evereste. *Molecular Breeding*, **30**, 857-874.

Litz, R.E. and Padilla G. (2012). Genetic transformation of fruit trees. *Genomics of Tree Crops*, 117-153.

Martín-Valmaseda, M., Devin S.R., Ortuño-Hernández G., Pérez-Caselles C., Mahdavi S.M.E., Bujdoso G., Salazar J.A., Martínez-Gómez P. and Alburquerque N. (2023). CRISPR/Cas as a Genome-Editing Technique in Fruit Tree Breeding. *Int. J. Mol. Sci.*, **24(23)**, 16656.

Matsuda, N., Ikeda K., Kurosaka M., Isuzugawa K., Endo T., Omura M. and Takashina T. (2006, March). *In vitro* flowering on transgenic pears (*Pyrus communis* L.) expressing CiFT, a Citrus ortholog of the Arabidopsis FT gene. In : *Abstract Book of the 3rd Intl. Rosaceae Genomics Conf* (pp. 19-20).

Meena, R.K., Koli D.K., Koli G.K., Meena R.K. and Annu (2022). Fast-track Breeding: A Powerful Tool to Accelerate Crop Research. *Biotica Res. Today*, **4(5)**, 382-384.

Moose, S.P. and Mumm R.H. (2008). Molecular plant breeding as the foundation for 21st century crop improvement. *Plant Physiology*, **147(3)**, 969-977.

O'Connor, D.J., Wright G.C., Dieters M.J., George D.L., Hunter M.N., Tatnell J.R. and Fleischfresser D.B. (2013). Development and application of Fast-track breeding technologies in a commercial peanut breeding program. *Peanut Science*, **40(2)**, 107-114.

Pasquali, G., Biricolti S., Locatelli F., Baldoni E. and Mattana M. (2008). Osmyb4 expression improves adaptive responses to drought and cold stress in transgenic apples. *Plant Cell Reports*, **27**, 1677-1686.

Paul, J.Y., Khanna H., Kleidon J., Hoang P., Geijskes J., Daniells

J., Zaplin E., Rosenberg Y., James A., Mlalazi B. and Deo P. (2017). Golden bananas in the field: elevated fruit pro vitamin A from the expression of a single banana transgene. *Plant Biotech. J.*, **15(4)**, 520-532.

Samantara, K., Bohra A., Mohapatra S.R., Prihatini R., Asibe F., Singh L., Reyes V.P., Tiwari A., Maurya A.K., Croser J.S. and Wani S.H. (2022). Breeding more crops in less time: A perspective on Fast-track breeding. *Biology*, **11(2)**, 275.

Scorza, R., Dardick C.D., Callahan A.M., Srinivasan C., Delong T., Harper J., Raines C.D. and Castro S. (2012) May. Fast-track'-a revolutionary approach to long-generation cycle specialty crop breeding. In : *Meeting Abstract* (Vol. **101**).

Shekhawat, U.K.S., Ganapathi T.R. and Srinivas L. (2011a). Cloning and characterization of a novel stress-responsive WRKY transcription factor gene (MusaWRKY71) from *Musa* spp. cv. Karibale Monthan (ABB group) using transformed banana cells. *Mol. Biol. Rep.*, **38**, 4023-4035.

Shekhawat, U.K.S., Srinivas L. and Ganapathi T.R. (2011b). MusaDHN-1, a novel multiple stress-inducible SK 3-type dehydrin gene, contributes affirmatively to drought-and salt-stress tolerance in banana. *Planta*, **234**, 915-932.

Shen, X., Gmitter F.G. and Grosser J.W. (2011). Immature embryo rescue and culture. *Plant Embryo Culture: Methods and Protocols*, 75-92.

Shimelis, H. and Laing M. (2012). Timelines in conventional crop improvement: pre-breeding and breeding procedures. *Aust. J. Crop Sci.*, **6(11)**, 1542-1549.

Sinha, P., Singh V.K., Bohra A., Kumar A., Reif J.C. and Varshney R.K. (2021). Genomics and breeding innovations for enhancing genetic gain for climate resilience and nutrition traits. *Theoret. Appl. Gen.*, **134(6)**, 1829-1843.

Souza, L.S., Diniz R.P., de Jesus Neves R., Alves A.A.C. and de Oliveira E.J. (2018). Grafting as a strategy to increase flowering of cassava. *Scientia Horticulturae*, **240**, 544-551.

Srinivasan, C., Dardick C., Callahan A. and Scorza R. (2012). Plum (*Prunus domestica*) trees transformed with poplar FT1 result in altered architecture, dormancy requirement, and continuous flowering.

Sun Waterhouse, D. (2011). The development of fruit based functional foods targeting the health and wellness market: a review. *Int. J. Food Sci. Tech.*, **46(5)**, 899-920.

Thomas, B. (2017). *Photoperiodism*. Elsevier EBooks, 448–454.

Tian, N., Wang J. and Xu Z.Q. (2011). Overexpression of Na+/H+ antiporter gene AtNHX1 from Arabidopsis thaliana improves the salt tolerance of kiwifruit (*Actinidia deliciosa*). *South Afr. J. Bot.*, **77(1)**, 160-169.

Tiwari, S. (2021). 021. Fast-track Breeding : An Advance Approach. *ResearchGate*, **II(2)**, 104–108.

van Nocker, S. and Gardiner S.E. (2014). Breeding better cultivars, faster: applications of new technologies for the rapid deployment of superior horticultural tree crops. *Horticulture Research*, **1**.

Varshney, R.K., Bohra A., Yu J., Graner A., Zhang Q. and Sorrells M.E. (2021). Designing future crops: genomics-assisted breeding comes of age. *Trends Plant Sci.*, **26(6)**, 631-649.

Vira, B., Wildburger C. and Mansourian S. (2015). Forests, trees and landscapes for food security and nutrition: A global assessment report. *IUFRO World Series*, 33.

Vishnevetsky, J., White T.L., Palmateer A.J., Flaishman M., Cohen Y., Elad Y., Velcheva M., Hanania U., Sahar N., Dgani O. and Perl A. (2011). Improved tolerance toward fungal diseases in transgenic Cavendish banana (*Musa* spp. AAA group) cv. Grand Nain. *Transgenic Research*, **20**, 61-72.

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. and Adamski N.M. (2018). Fast-track breeding is a powerful tool to accelerate crop research and breeding. *Nature Plants*, **4(1)**, 23-29.

Weigel, D. and Nilsson O. (1995). A developmental switch sufficient for flower initiation in diverse plants. *Nature*, **377(6549)**, 495-500.

Zimmerman, R.H. (1972). Juvenility and Flowering in Woody Plants: A Review. *HortScience*, **7(5)**, 447-455.

Zimmerman, R.H., Hackett W.P. and Pharis R.P. (1985). Hormonal aspects of phase change and precocious flowering. In *Hormonal regulation of development III: Role of environmental factors* (pp. 79-115). Berlin, Heidelberg: Springer Berlin Heidelberg.