



# The Impact of Pre-Breeding on Vegetable Crop Improvement: A Review

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## **Authors' contributions**

*This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.*

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## **ABSTRACT**

Pre-breeding begins with the finding of beneficial genes from wild relatives, native species, and various other unadapted materials. These advantageous qualities are subsequently transferred to a moderate pool of resources so that breeders can create new varieties for farmers. With the process of discovering useful characteristics, preserving their genetic diversity, and incorporating these genes into a form that can be used, crop improvement innovation is generated. Connecting genetic diversity from wild relatives along with other uncontrolled sources is the main goal. Pre-breeding strategies aim to introduce genes for tolerance to environmental difficulties and resistance to major diseases and pests from wild relatives into cultivated crops using the application of introgression and integration procedures. Pre-breeding provides the base for commercially

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important techniques for plant breeding by broadening the diversity of germplasm and providing breeders with easily accessible resources to breeding beneficial characteristics, while adhering to the basic concepts of the field. The comprehensive discussion of pre-breeding is a valuable resource for scientists and researchers alike, addressing all aspects of this crucial phase in improving vegetable crops.

*Keywords: Breeding; cultivated; diversity; Pre-breeding; tolerance.*

## 1. INTRODUCTION

India has made remarkable progress in vegetable production over the last thirty years, becoming the world's second-largest producer after China. However, to meet the demands of both local and global markets, there is a need for innovative methods in researching and breeding approved varieties and hybrids, as well as providing improved planting materials. Traditionally, crop development using plant genetic resources has relied on two techniques: introgression, which involves incorporating a few desirable genes into adapted stocks, and incorporation, which involves expanding locally adapted populations to enrich the genetic base of crops. While wild relatives offer genetic diversity for traits like tolerance to various stresses such as heat, drought, pests, and diseases, challenges like sexual incompatibility and hybridization barriers limit their use in crop improvement. The accumulation of 64,056 germplasm accessions comprising cultivated vegetable varieties and wild relatives from different regions in India between August 1976 and January 2019 showcases the nation's diverse vegetable genetic reservoir. 64,056 germplasm accessions of different vegetable genetic resources (VGR) have been collected from different locations across India during August 1976 and January 2019. Considerable numbers of cultivated vegetable germplasm (58,250) and wild relatives/wild vegetable resources (5,806) from different phytogeographical regions have been included in this collection. Cucurbitaceous vegetables (16,750), solanaceous vegetables (14,646), root/tuberous vegetables (8,298), bulbous vegetables (4,769), brassica/cole crops (1,776), leafy vegetables (2,084), leguminous vegetables (5,435), okra (4,235), and tree crops (257) had been the most common groups of cultivated crops collected [1].

### 1.1 Need for Pre-Breeding

The enhancement of agricultural yields relies heavily on the presence of adequate genetic diversity that can be economically. The

deficiency in reliability and diversity has hindered progress in breeding. The susceptibility to pests and diseases has increased due to the substitution of diverse native cultivars and landraces with genetically uniform modern types. Pre-breeding plays a pivotal role in initiatives focusing on germplasm diversity and plant breeding. Pre-breeding is instrumental in acclimating various germplasms to different genetic backgrounds and geographic regions. It serves to expand the genetic variability in crops to improve productivity, resistance to pests and diseases, and other desirable traits, thereby diminishing genetic homogeneity. Shimelis and Laing [2] emphasize that the choice of pre-breeding relies on the anticipated success in integrating desired traits into cultivars. Given the limited genetic foundations, diminished biodiversity resulting from contemporary varieties, and heightened susceptibility to pests and diseases, pre-breeding emerges as a critical solution. It also addresses the challenges arising from climate change and new pest occurrences. Hence, pre-breeding is indispensable for fortifying crop resilience and supporting sustainable agriculture in response to evolving environmental and agricultural demands. According to Kumar and Shukla [3] pre-breeding is needed when target genes are limited to gene bank accessions that are unsuitable for target ecosystems, closely associated wild species, and distant wild counterparts that are more sensitive to cross-breeding.

### 1.2 Pre-Breeding Work Aims to Achieve Four Goals

- 1) Using a broader collection of genetic material will help reduce genetic consistency in crops.
- 2) Identifying and transferring desirable characters and genes
- 2) Improving parental stocks for prompt usage in breeding applications; and
- 3) Finding potentially beneficial changes in a healthy-maintained and recognized gene bank.

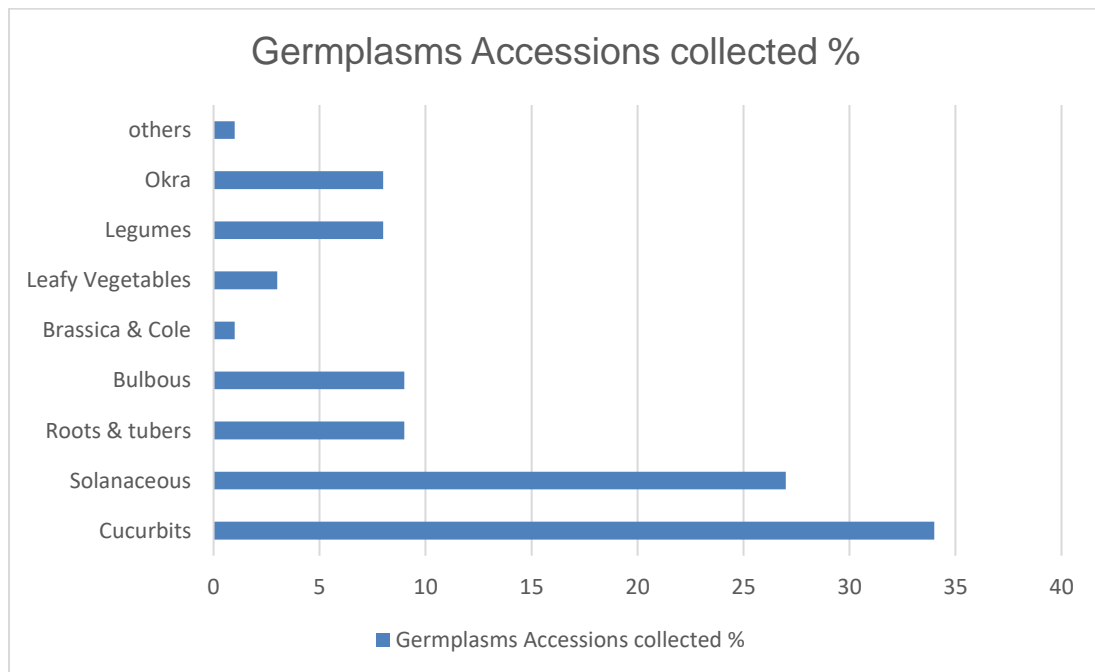
### 1.3 Objective of pre-Breeding

1. Improved gene information and germplasm that improve resistance appearance and variety.
2. Utilizing a bigger pool of genetic material to boost production, resistance to diseases and pests, and additional beneficial features would reduce genetic uniformity in crops.
3. Finding advantageous features or genes and then transferring them to a good pair of parents to proceed with the selection procedure.
4. Improved methods for selection and better parental stocks that are easily useful to breeding operations.
5. Locate genes that may be supportive in a well maintained and recognized gene bank.
6. creating plans that result in stronger germplasm that has been collected for use in cultivar development.

### 1.4 Concept of Pre-Breeding

To safeguard this unique genetic resource and fully utilize the abundant and easily accessible germplasm available in the country, thorough examination is essential. Pre-breeding

provides a mechanism for incorporating specific genes from wild germplasm into genetic backgrounds to achieve desired traits. It serves as the starting point in the breeding process. Pre-breeding, as defined by Singh et al. [4] constitutes a series of steps in plant breeding research that precede cultivar development, testing, and release. The connection between breeding efforts and genetic resources shows great potential. Materials developed through pre-breeding activities are considered valuable for integration into regular breeding procedures. The exotics used in pre-breeding encompass germplasm that has not been through adaptation selection and does not immediately display favourable characteristics [5]. Hence, races, populations, inbred lines, and similar groups may represent alien germplasms. Building on the work of Hausmann et al. [6] pre-breeding utilizes a wider range of genetic materials to establish a new foundational population for the breeding program. To achieve outstanding outcomes, exotics require several generations of breeding to enable genetic recombination and mild selection. A minimum of five generations involving random mating under moderate selection pressure is necessary before beneficial recombinants can be identified [7].



**Fig. 1. Percentage of germplasm accessions collected in different groups of cultivated vegetable crops**

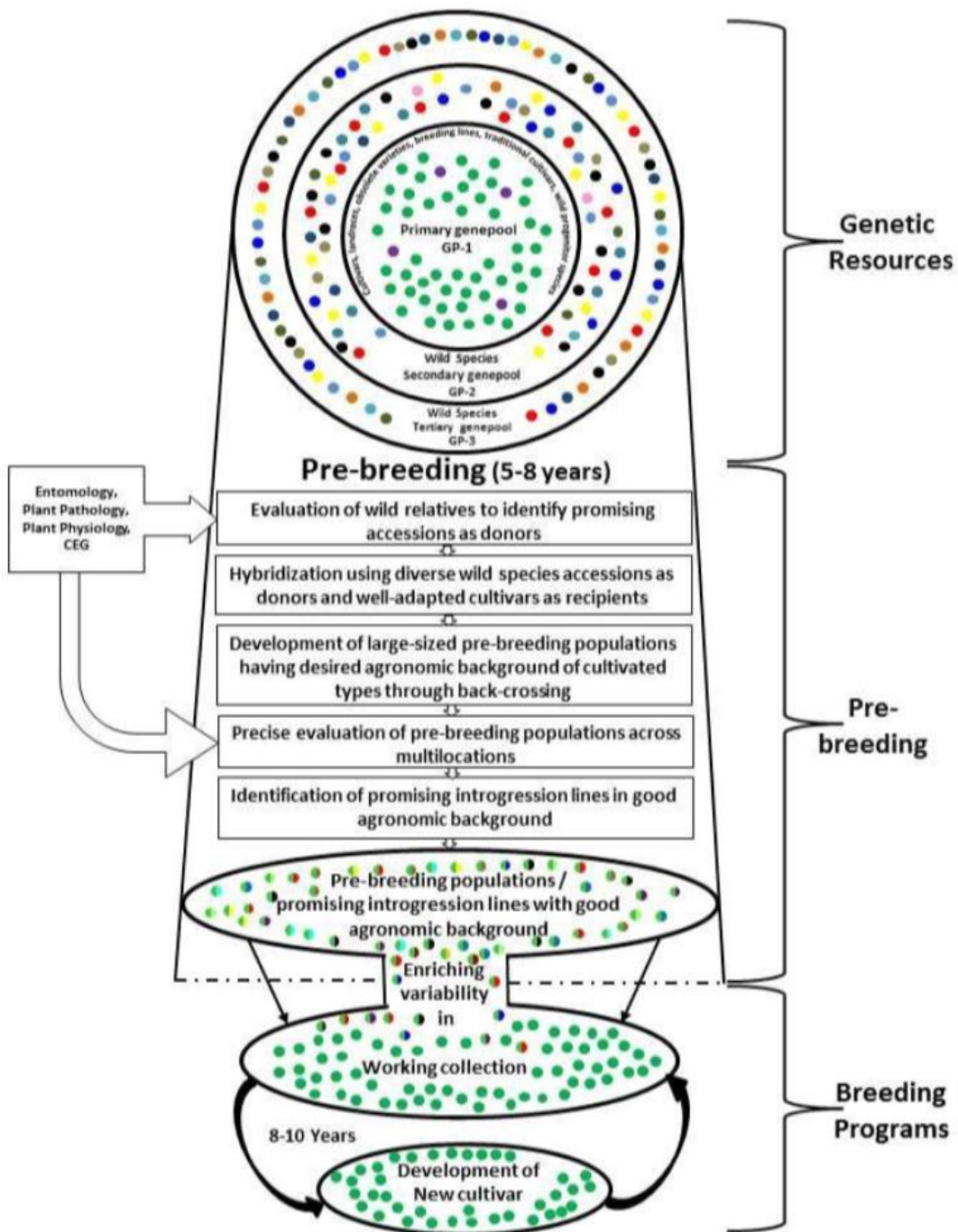


Fig. 2. Pre-breeding as an association between crop growth and genetic resources

### 1.5 The Gene Pool Concept

According to Haussmann et al. [6]. The term "gene pool" refers to the whole set of genes present in a species' reproductive population, including related species that are capable of

interbreeding. The gene pool for crops includes botanical varieties, landraces, inbred lines, historic and modern landraces, related wild species, subspecies, and weedy companion species.

**Primary gene pool:** The same species, both cultivated and wild.

**Secondary gene pool:** Species different from the cultivated one.

**Tertiary gene pool:** More distantly related species.

**Quaternary gene pool:** Unrelated plant species or other organisms.

## 2. METHODS OF PRE-BREEDING

Introgression involves transferring one or more genes from unadapted germplasm (the donor parent) to elite breeding material (the recurrent parent) through repeated backcrossing, using Dr. Edger Anderson's concept. Three backcross strategies can optimize the recombination frequency between the parents.

### 2.1 Repeated Backcross

This method involves performing repeated backcrosses, usually six times, between the recurrent parent and the donor parent, with or without selection.

### 2.2 Inbred Backcross

This approach, first proposed by Wehrhahn and Allard in 1965, involves a small number of backcrosses, usually three, followed by multiple generations of selfing.

### 2.3 Congruity Backcross

In this method, backcrossing is conducted using both the donor and recurrent parents in different generations.

## 3. APPROACHES TO PRE-BREEDING

Under the field of agricultural development, numerous strategies propel advancements in crop breeding. Dr. Edgar Anderson invented introgression, which refers to the process used to introduce genes from wild or foreign stocks into breeding populations through strictly controlled crossings, most notably through backcrossing methods. Simmonds suggested integration to increase crop resilience and diversity by

incorporating foreign genetic factors into populations that had already adapted locally. As demonstrated by the breeding of the potato wide crossings which break down species boundaries help to expand crop gene pools, especially for characteristics like disease resistance. In opposition to conventional procedures, Decentralized Participatory Plant Breeding is a cooperative effort between farmers and breeders that performs trials in farmers' fields, promoting more widespread use and local adaptation. Chromosome manipulation, such as the generation of Aneuploids and Polyploids, alters the gene pool to provide desired characteristics like disease resistance, improving the effectiveness of breeding. By mixing somatic cells, somatic hybridization avoids species boundaries and creates an avenue for hybridization across species that are taxonomically different. Advances in technology in plant breeding, including as biotechnology and molecular marker technologies, revolutionize trait selection and recognition by providing increased accuracy and efficiency. Pre-breeding efforts use wild species' genetic variety to improve agricultural varieties; multi-national programs like as LAMP serve as examples of this. Collectively, these methods encourage crop breeding innovation and sustainability, ensuring constant advances in agricultural resilience and manufacturing.

### 3.1 Characterization of Landrace Populations

Landraces, extinct cultivars, wild relatives, advanced breeding lines, popular varieties, synthetic aneuploid and polyploid lines, and more have been included in the germplasm. These genetic lines had genes necessary for useful characters such as resistance to diseases and insects, early maturity, yield-related characteristics, and local adaptability [17]. They are additionally useful to find new characters that are lacking in domesticated germplasm or to develop existing ones (Tables 1, 2 and 3). These lines may be defined using several markers (biochemical, physiological, morphological, and molecular) in the present-day context of genomics and proteomics to assist in breeding and assess genetic diversity [18,19]. Because of their farmer-preferred traits which have several applications—local varieties are usually grown in countries that are developing [20,21].

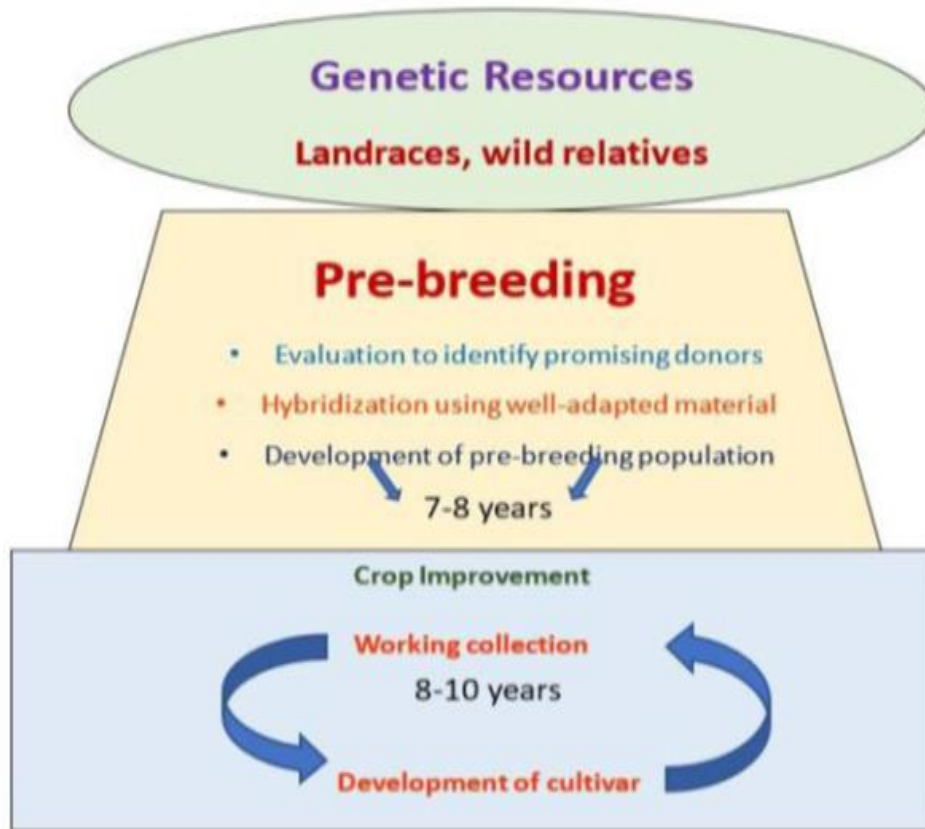


Fig. 3. Pre-breeding as a link between crop development and genetic resources

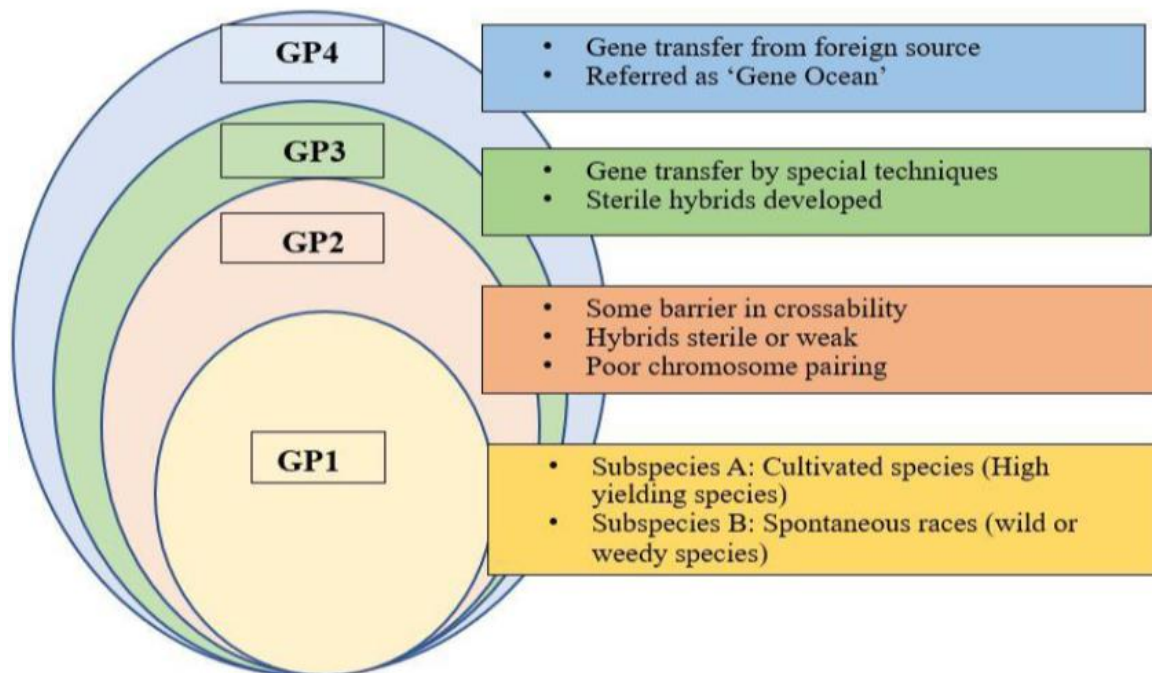


Fig. 4. Modified gene pool concept in plants based on the hybridization study

**Table 1. Important traits improved in vegetable crops through pre breeding approach**

S. no.	Crop	Findings	Reference
1	Tomato	Demonstrated that diploid plants from the offspring of monosomic alien addition lines (MAALs) of <i>S. lycopersicoides</i> may be identified for use as donors in tomato breeding to improve characteristics that are wanted. novel characteristics in the MDILs associated with drought tolerance that are not present in the fields of parents.	Mangat et al. [8]
		Divergent genes resistant to infections have been backcrossed and included in commercial hybrids produced with various natural resources. These genes are found on distinct tiny chromosomal regions that derive from various donor species. Fruit with an important gene introduced from a wild tomato species ( <i>Lycopersicon pennellii</i> B.) raised by a factor of fifteen in pro-vitamin A attention to detail.	Ronen et al. [9]
2	Brinjal	It has been tried to pre-breed for bacterial wilt resistance.	Neelambika et al. [10]
3	Potato	In the genetically incompatibility species <i>S. bulbocastanum</i> , four cloned wide-spectrum genes (Rpi) resistant to the infection of <i>Phytophthora infestans</i> were discovered. Plants having each of the four-leaf blight-resistant genes had been chosen in trials performed in both greenhouse and outside environments. Somatic hybridization combined with gene-specific markers along with associated Avr effectors offers a successful approach of discovering and delivering late blight genes for resistance through the potato gene pool.	Rakosy-Tican et al. [11]
		Induced mutagenesis has been carried out on the potato using ethyl methane sulfonate (EMS) with the goal to expand the genetic potential of diploid potatoes for use as pre-breeding resource in both polyploid and diploid potato breeding.	Somalraju et al. [12]
4	Cauliflower	Interspecific asymmetric somatic hybrids of <i>Brassica oleracea</i> var. <i>botrytis</i> (cauliflower) and <i>Brassica nigra</i> (black mustard) were created by protoplast fusion, and the backcrossed (BC <sub>3</sub> ) and selfed (S <sub>3</sub> ) offspring were seen at.	Wang et al. [13]
5	Asparagus	Using crop wild relatives (CWR) such as <i>A. maritimus</i> , <i>A. pseudoscaber</i> , <i>A. brachyphyllus</i> , and <i>A. macrorrhizus</i> to produce novel plant material has widened the genetic base. The results demonstrate an increase in genetic variability, presenting new opportunities for improving asparagus.	Wang et al. [13]
6	French Bean	Wild relatives are a valuable source of novel alleles that can be utilized to enhance yield and other quantitative traits.	Acosta-gallegos et al. [14]

**Table 2. List of landraces and their potential applications in various vegetable crops**

<b>Crops</b>	<b>Traits</b>	<b>Germplasm conserved</b>
Melon	Powdery mildew Downy mildew Fruitfly Nematode Whitefly	PMR 45, PMR 450, PMR 5, PMR 6, PI 124111 DMDR-1, DMDR-2 <i>Cucumis callosus</i> <i>Cucumis metuliferus</i> <i>Cucumis denteri, Cucumis dipsaceus, Cucumissagittatus</i>
Watermelon	Fusarium wilt Anthracnose	Summit, Conqueror, Charleston gray, Dixilee, Crimson sweet Charleston gray, Congo, PI 189225
Bottle gourd	CMV, SqMV, Fusarium Wilt	WMVPI 271353 Taiwan variety Renshi
Cucumber	Downy mildew, powdery mildew Anthracnose Powdery mildew CMV	Poinsette PI 175111, PI 175120, PI 179676, PI 182445 PI 200818, <i>Cucumis hardwickii</i> Wisc SMR-12, SMR-15, SMR-18
Pumpkin	Powdery Mildew and Viruses ZYMV, WMVC.	<i>Cucurbita lundelliana, Cucurbita martenezii</i> <i>Cucurbita ecuadorensis, Cucurbita faetidistima, Cucurbita martenezii</i>
Tomato	Bacterial wilt Fusarium wilt Root knot Nematode Heat tolerant lines	EC 467725-935, EC 438314-317, EC 182761-182874, EC 26511-13 Pan American, Florida, PI 79532 Nemared, VNF-8, Florida, Hawaii cross EC 198416, EC 501573-83, EC 479027, 31, 34, 36, 139, 140, 141 and 143
Brinjal	Bacterial wilt Phomopsis fruit rot Tolerance to frost Tolerance to drought	EC 104107, Florida Market EC 305069, 316274 Black torpedo, Long Tom '4' Supreme, Violette round
Chilli	Cucumber mosaic virus PBNV mosaic virus Aphids YVMV	EC 312342-312349 EC 121490 EC 28, 30 and 34 EC 133408, EC169333, EC 169334, Ghana red, <i>Abelmoschus manihot ssp tetraphyllus, Abelmoschusmanihot ssp manihot</i>
Okra	Jassids	EC 305656, 305694, 305695
Cabbage	Black rot	EC 24855, EC 28770, Cabbage Standby
Cauliflower	Black rot	Aemel, Olympus, Lawyana
Onion	Purple blotch	EC 328494, EC 328492, EC 328501, EC 321463
Pea	Powdery mildew	EC 342007
Muskmelon	Downey mildew, Powderymildew, Anthracnose	Crimson sweet, shipper

Source: Pandey et al., [15]



**Table 3. Germplasm of cucurbits with unique traits has been registered with the National Bureau of Plant Genetic Resources (NBPGR) in New Delhi Rai et al., [16]**

<b>Crop</b>	<b>Line</b>	<b>Registered name</b>	<b>Trait associated</b>
Pointed gourd	IIVR PG- 105	INGR-03035	Parthenocarpic fruits
Bitter gourd	GY-63	INGR-03037	Gynoecious sex with high yield
Watermelon	RW-187-2	INGR-01037	High yield and yellow coloured flesh
	RW-177-2	INGR-01038	Leaf mutant with simple unlobed leaves
Bottle gourd	Androman-6	INGR-99009	Andromonoecious sex
	PBOG-54	INGR-99022	Segmented leaves
Cucumber	AHC-2	INGR-98017	High yield and long fruit
	AHC-13	INGR-98018	Small fruit, drought and temperature tolerant
<i>Cucumis melo</i> var. <i>callosus</i>	AHK-119	INGR-98013	High yield and drought tolerance
Round melon	HT-10	INGR-99038	Tolerant to downy mildew and root rot wilt
Snap melon	AHS-10	INGR-98015	High yield and drought tolerance
	AHS-82	INGR-98016	High yield and drought tolerance
	B-159	INGR-07044	Downy mildew resistance

### 3.2 Marker Assisted Breeding

Breeding techniques which use DNA molecular marker patterns in addition to or instead of characteristic values have become more common. Plant breeders can select desirable and attractive crop includes more effectively due to this technique. When molecular markers that extremely co-segregate with candidate genes are available, marker-assisted selection (MAS) may enhance the effectiveness of selecting fundamental characteristics in conventional plant breeding programs [22, 18].

### 3.3 Tagging or Mapping of Gene/QTLs

The use of wild material as a source of resistance has expanded significantly as an outcome of molecular mapping and gene tagging for many disease resistance genes. These days, QTL mapping and gene cloning have become popular methods. Plant height, male sterility, yield-related characteristics, biotic and abiotic stress traits, and certain quality features belong to a number of characteristics that have been discovered and mapped in an array of crops [23,24,25].

### 3.4 Identification of Novel Allele

Significant variation for a single gene/QTL has been identified with the use of allele analysis methods. Several reverse techniques for breeding are currently employed to find new mutations that provide specific characteristics and can be utilized in plant breeding, including genome editing, site-directed mutagenesis, TILLING, Eco TILLING, and others. Materials derived from germplasm may help in understanding the nature of the causes of mutations that contributed to the evolutionary history of specific crops [26,27].

### 3.5 Creating New Parent Populations

The selection of the most suitable parents with enhancing and desirable attributes are crucial to crop breeding success. Therefore, possible parent populations are continuously selected through breeders from a wide range of sources, including landraces, modern cultivars, obsolete or ancient cultivars, and wild or semi-wild species. To find parents with a significant amount of general or specific combining ability, progeny testing is frequently used. Breeders can evaluate the genetic potential of parents while determining

the type of variation that is likely to be developed through progeny testing.

### 3.6 Somatic Hybridization

Most of crops contain barriers among species which restrict sexual hybridization, which restricts the ability to improve crops. This has been suggested somatic cell fusion, that generates viable cell hybrids, offers an approach around these barriers. Exciting possibilities for somatic cell genetics and agricultural enhancement are presented by plant protoplasts. Somatic hybridization is a method that generates hybrids by fusing isolated somatic protoplasts in vitro and then developing their progeny, also known as a heterokaryon, into a hybrid plant. Through the use of this method, the limitations of sexual crossability may be avoided as hybrids between taxonomically distinct plant species may be generated.

### 3.7 Creation of Aneuploids & Polyploids

By changing the basic chromosome set or by adding or removing certain chromosomes, a breeder may alter the number of chromosomes in a species or create different diversity. A species' genome may be doubled to generate euploid individuals, or unrelated species may be crossed and the resultant interspecific hybrid may have the chromosomes doubled. A number of methods can be utilized to artificially induce polyploids, such as submitting plant materials to environmental shocks (such as being exposed to high or low temperatures or x-ray radiation) or through chemicals (like colchicine) that interact with normal chromosome division [28,29,30]. Double haploids (DHs) develop whenever anther culture-derived haploid plants from F<sub>1</sub> undergo chromosome doubling. Lefebvre and colleagues in [31] investigated the significance of doubled haploid progenies for mapping studies in pepper. The simplest approach of generating pure breeding doubled haploids (DHs) is to develop haploid plants in vitro and then double their chromosomes. somatically [32,33]. Anther culture [34] or genome elimination following distant hybridization [35] are both techniques utilized for producing haploids. Because DHs fix genes in a homozygous background, they limit an important genetic variation and segregation, allowing selection easier for oligogenic or polygenic traits [32]. Therefore, in an entirely homozygous situation, double haploid relatives can be selected for improved traits such as yield, earliness, plant height, nutritional quality, and resistance to diseases and

pests. In the future, selected genotypes may be used as breeding parents in subsequent intersections and selection cycles, or as uniform varieties.

#### 4. USE OF GENOMIC APPROACHES TOOLS IN PRE-BREEDING

When considering to complex traits, genomics methods are particularly helpful as these characteristics tend to be multigenic and significantly affected by environment factors [36,37,38]. The use of genomic techniques make it easier to find QTL and favorable alleles with little impact which are already present but are often undetected or are not included in the gene pool used in breeding [39]. Innovative methods have a chance to provide new light on gene expression and regulation in cells and identify metabolic pathways associated with desirable characteristics in major and model crops in addition to in under-resourced crop species which have been referred as "indigenous" crops.

##### 4.1 DNA Based Molecular Markers and their Applications

Molecular markers discover variations in the individual's core DNA structure [40,41]. The significance of wild relatives and their relationship to cultivated improved cultivars can be determined through methods such as Marker-Assisted Selection (MAS), combined marker-assisted selection, marker-assisted backcrossing, marker-assisted recurrent selection, and marker-assisted pyramiding. It makes simpler to recognize and transfer desired characteristics or genes from genetic resources of unadapted crops to an intermediate output that breeder can change for selection and improvement. By identifying the allele of a DNA marker, MAS enhances phenotypic screening by enabling the recognition of plants with specific genes or quantitative trait loci (QTLs) based on genotype rather than phenotype. According to Eglinton et al. [42] MAS is especially useful in early-generation selections because it allows to eliminate undesired gene combinations and keep more effectively breeding lines, particularly those which lack essential genes underlying disease resistance. According to Hiremath et al. [43] the efficacy of MAS is greatest for factors with low heritability. In plant breeding, backcrossing transfers beneficial characteristics controlled by a small number few genes from a donor plant to an elite genotype (recurrent parent). Large donor

segments can remain associated with the target allele throughout many generations in traditional backcrossing; however, marker examines minimize this linkage drag [44]. Additionally, markers accelerate recurrent selection by allowing several selection cycles in a single year and allowing the breeding population to gather favorable QTL alleles Eglinton et al., [42]. Whenever matched races are unavailable or when one gene hides the presence of a different one, MAS is essential for pyramiding disease resistance genes with similar phenotypic effects [43,45]. According to Lande et al. [46] the use of 'combined MAS,' which integrates phenotypic screening with MAS, may maximize genetic gain. For an important QTL on chromosome 3BS for *Fusarium* head blight resistance in wheat, Zhou et al. found that combined MAS was more effective than phenotypic screening alone [47]. According to Ribaut et al. [48] genetic gain obtained through Marker-Assisted Recurrent Selection (MARS) may be higher than that gained by Marker-Assisted Backcrossing (MABC). Major genes associated with resistance are frequently approached by marker-based recurrent backcross programs [49]. Tomato TMV resistance (Tm-2 locus), nematode resistance (Mi gene), *Fusarium oxysporum* resistance, and powdery mildew resistance were examples of significant gene tagging in vegetable crops. Huang et al. utilized RAPD and SCAR markers to tag the tomato chromosome 6 powdery mildew resistance gene, *ol-1* [24]. The DNA fingerprinting of cultivars and breeding lines in a number of vegetable crops, including tomato, beans, pepper, and potatoes, is done nowadays utilizing a broad spectrum of molecular markers [50,51]. The establishment of nematode-resistant tomato hybrids gained benefit due to the genetic linkage in tomato between the *Aps-1* isozyme locus and the *Mi* locus, which controls resistance to the root knot nematode [52]. Storage protein polymorphism in French beans (*Phaseolus vulgaris* L.) has been used to select for resistance to bean seed weevils, which are common in tropical and subtropical areas.

##### 4.2 SNP Marker Arrays or SNP Chips Approach

Genome-Wide Association Studies (GWAS) and QTL analysis have made the procedure of finding and identifying new genes. The accessible nature of genome-wide association studies in natural populations has risen with the development of high-density SNP marker arrays.

For example, [49] conducted a meta-analysis utilizing 2,316,117 SNPs from three GWAS panels and 775 tomato accessions, including wild types. A total of 305 significant relationships pertaining to sugars, acids, amino acids, and flavor-related volatiles have been identified through their research.

#### **4.3 Genotyping by Sequencing (GBS) Approach**

Genotyping by sequencing (GBS) technique, combined with phenotyping, enables the discovery of QTLs influencing various traits. Genome-wide genotype-to-phenotype associations (GWAS) have gained popularity, thanks to SNP markers derived from whole-genome re-sequencing data and cost-effective automated genotyping systems.

#### **4.4 Mechanical and Precision Phenotyping (Phenomics Tools)**

The rapid advancement of mechanical and precision phenotyping technologies has resulted in rapid development in germplasm assessment and dependable outcomes. For improved assessment, several direct and indirect methodologies are being developed. Many methodologies exist, such as NDVI estimation [53] phenotyping by drones [54] GIS-based phenotyping, non-destructive root phenotyping, and other techniques have made it possible to characterise germplasm in large quantities in a variety of crops [55].

#### **4.5 Genome-Wide Selection**

Genome-wide selection (GWS) is a different method that can be used to integrate beneficial alleles for minor impact QTLs across the entire genome in addition to MARS. GWS analyzes the effect of markers throughout the entire genome, considering all phenotypic variation. Genomic estimated breeding values (GEBVs) are estimated utilizing the available genome-wide marker data on progeny lines. It's important to remember that GEBVs are generated from genotyping data using a model that had been developed on people whose genotyping and phenotyping data were provided. From then, these GEBVs are employed to select progeny lines for additional stages in the process of breeding. In result, GWS offers a method to select individuals without phenotypic data by evaluating their breeding value using a model [56].

## **5. CHALLENGES AND FUTURE PROSPECTS**

Inadequate character development, genetic diversity assessment, and funding pose hurdles to pre-breeding. Emphasizing the urgency of acquiring, characterizing, and documenting wild species, especially crop wild relatives, vital for conservation. Rising demand for specific genes in germplasm and genome banks aims to boost agriculture against biotic and abiotic challenges. Techniques such as genome mapping and genetic transformation offer avenues for crop improvement, enhancing stress resistance. To tackle complex traits, innovative breeding strategies and bioinformatics tools are essential, leveraging insights from genetic and genomics research [57-60].

## **6. CONCLUSION**

Pre-breeding finds a significant characteristic in inadequate materials, "captures" its genetic diversity, and uses numerous methods to combine those genes into a form that is useful: There is adequate genetic variability in the form of landraces and wild relatives to enhance field crops, as they carry numerous valuable genes for cultivar improvement. Nevertheless, it demands time and resources for using these resources in breeding projects. Pre-breeding efforts should be undertaken to overcome this, utilizing promising landraces and wild relatives to create new genetic diversity that breeders may exploit in crop development efforts. Pre-breeding should not be done with the intention of increasing yield; rather, it should be done with a regular input of valuable variances into the breeding pipeline to create new high-yielding cultivars with a broad genetic basis. Pre-breeding is a time-consuming and challenging process, even if it is useful for improving cultivars by increase the fundamental gene pool.

### **DISCLAIMER (ARTIFICIAL INTELLIGENCE)**

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

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## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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