Molecular markers: A novel vista in vegetable improvement.

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Abstract

Vegetables are the major source of nutrients in the daily diet in both developing and developed countries. But these groups of plants are most susceptible to a variety of pests. The growth and economic yield are severely reduced under a variety of biotic and abiotic stresses. A number of conventional breeding methods are available for genetic improvement of vegetable crops. But, selection of desirable plants in the breeding programme often becomes misleading due to inadequate biotic and abiotic stress conditions and other environmental factors. Recent advances in the development of molecular markers have made it possible for reliable selection and to speed up the breeding cycle in vegetable crops. Molecular markers directly reveal the polymorphism at the level of DNA. These are tags that can be used to identify specific genes and locate them in relation to other genes. Therefore, in the present article, the authors offered a detailed review of the role of molecular markers to assist breeding programme of important vegetable crops.

Keywords: Molecular markers, Gene tagging, QTL detection, Marker aided selection, Vegetable crops.

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Introduction

Conventional plant breeding (classical breeding or traditional breeding) is basically the development of new varieties of plants by using older tools and natural processes [1]. Breeding for improved varieties can no longer rely on ten years cycles and all the technologies to shorten the selection cycles must be mobilized, use of markers is one such technology [2]. Marker is basically a tag which is prominent or helps in the identification of the trait [3]. Markers are classified into four type's viz., morphological, biochemical, cytological and molecular markers [4]. Morphological markers are visually characterized phenotypic traits like flower colour, seed shape, growth habit and those gene loci that have direct effect on the morphology of plant [5]. These markers enable the assessment of genetic variability and diversity based on single phenotypic difference yet there are limitations associated with these markers and these limitations led to the development of molecular markers [6]. Biochemical markers or isozymes are molecular form of enzyme that is based on the protein staining but having different electrophoretic mobilities. Basically these biochemical markers are encoded by different genes and have same functions [7]. Biochemical markers are allelic variations of enzymes and can be used to estimate the gene frequency, genotypic frequency and successfully help in the detection of genetic diversity, gene flow, structure and subdivision of population [8]. Cytological markers are the variations associated with morphology of chromosomes such as chromosome number, size, sequence specificity, meiotic behavior of chromosome. These are the variations present in the number, size, shape, order, position and banding patterns of chromosomes are called as cytological markers [9]. A cytological marker reveals the differences in the euchromatin and heterochromatin, normal and mutated chromosomes and used in the identification of mapping and linkage groups [10].

A marker is a sequence of DNA which serves as flag post or signpost which is directly or indirectly linked to the trait gene of interest and is generally co-inherited with the trait [11]. Molecular markers are nucleotide sequences which are estimated by level of polymorphism present between the nucleotide sequences of different individuals. The level of polymorphism is based on insertion, deletion, duplication, translocation and point mutations whereas they did not affect the activity of genes [12]. These markers are basically the landmarks whose position in the genome is known and are directly exposed the polymorphism at DNA level [13]. The ideal molecular marker must have following properties *viz*., marker should be easily available, inexpensive, non-time consuming, abundant in number, polymorphic in nature, tightly linked to target loci, frequently distributed throughout the genome, preferably <5 centi Morgan (cM) from a gene of interest,

indiscriminating, easily reproducible, multiallelic, easy to operate, neutral phenotypically and co-dominant [14]. The occurrence of different molecular techniques and different principles and methodologies need cautious deliberation in choosing one or more of such marker types [15]. DNA markers are advantageous and beneficial to use as they are efficiently used in the detection of presence or absence of allelic variation in the genes associated with the trait of interest and tremendously increased the precision and accuracy [16]. The theoretical benefits of utilizing DNA markers, the potent value of genetic linkage construction maps and direct selection was first reported about eighty years ago in crop improvement [17]. Now-a-days more efficient molecular markers systems that are inexpensive and involves better detection systems are being developed [18]. Molecular marks were divided into many groups on the basis of mode of their gene action (dominant or co-dominant markers), method of detection (hybridization based molecular markers or PCR based markers) and method of transmission (maternal organelle inheritance, paternal organelle inheritance, biparental nuclear inheritance or maternal nuclear inheritance [19]. Molecular marker were proven to be the most effective and efficient tool in the genetic variation evaluation and in clarification of genetic relationships within and among species [20]. So, the use of molecular genetics or molecular/DNA markers in detecting the DNA differences of single plant has many applications in vegetable crops improvement [21]. Various types of molecular markers have been reported till date and discussed in Table 1.

Literature Review

Advantages and disadvantages of molecular markers

The first big size efforts to produce genetic maps were performed mainly by using RFLP markers, the best known genetic markers at the time [22,23]. Molecular markers are advantageous over morphological and biochemical markers as they have high reproducibility, detect coupling phase of DNA, show co dominant alleles and easily estimate the linked trait to the gene of interest in both homozygous and heterozygous individuals [24]. The major disadvantage of utilizing molecular marker is that they are highly expensive, labor intensive, time consuming and requires higher amount of maximum molecular weight DNA [25]. There are several advantages and disadvantages of different types of molecular marker that are discussed in detail (Table 2).

Applications of molecular markers in vegetable crops improvement

There are several applications of molecular markers that aid in improvement of vegetable crops viz., (i) assessment of genetic diversity (ii) gene tagging (iii) DNA fingerprinting for varietal identification (iv) Detection of Quantitative Trait Loci (QTLs) (v) Marker Assisted Selection (MAS) for traits of interest [26].

Assessment of genetic diversity: Recent advancements in the field of molecular markers and genome sequencing offer a great and potential opportunity to examine the genetic diversity in a large number of germplasm [27]. Molecular markers have been proven as an efficient tool for the assessment of genetic diversity in a very wide range of plant species. This tool is of direct use to plant breeders as it showed the adaption, performance and agronomic qualities of the germplasm [28]. This information gives an idea about the overall genetic range of germplasm of the crops and plant breeders can effectively utilize the germplasm particularly to the unique genes and search aspects [29]. Assessment of genetic diversity is very helpful in the study of evolution of plants, their comparative genomics and helps to understand the structure of different populations [30]. Molecular markers now days have been successfully used for the evaluation of genetic diversity and the classification of the genetic material [31]. Many researchers have reported to use molecular markers to assess genetic diversity in various vegetable crops (Table 3).

Table 1. *Various types of molecular markers.*

S.No.	Name of marker	Full form	
		PCR/Hybridization based molecular marker	
1	RFLP	Restriction fragment length polymorphism	Botstein et al., 1980
		PCR based molecular marker	
1.	RAPD	Random amplified polymorphic DNA	Williams et al., 1990
2.	AFLP	Amplified fragment length polymorphism	Vos et al., 1995 Kumar et al., 2003
3.	SSR	Simple sequence repeats	Hearne et al., 1992
4.	ISSR	Inter simple sequence repeat	Reddy et al., 2002
5.	SNP	Single nucleotide polymorphisms	Kumar et al., 2012
6.	STS	Sequence tagged site	Fukuoka et al., 1994
7.	EST	Expressed sequence tags	Pashley et al., 2006
8.	SCAR	Sequence characterized amplified region	Feng et al., 2018
9.	CAPS	Cleaved amplified polymorphism sequence	Lyamichev et al., 1993
10.	ALP	Amplicon length polymorphism	Ghareyazei et al., 1995

11.	SSCP	Single- strand conformation polymorphism	Orita et al., 1989
12.	SSLP	Minisatellite simple sequence length polymorphism	Jarmen and Wells, 1989
13.	SSLP	Microsatellite simple sequence length	Saghai et al., 1994
14.	AP-PCR	Arbitrarily-primed PCR	McClelland and Welsh, 1994
15.	AS-PCR	Allele specific PCR	Sarkar et al., 1990
16.	DAF	DNA amplification finger printing	Caetano-Anolles et al., 1991
17.	SRAP	Sequence-related amplified polymorphism	Robarts and Wolfe et al., 2014
18.	DarT	Diversity Array Technologies	Jing et al., 2009
19.	Transposon	Retrotransposons	Han, 2010
20.	ScoT	Start codon targeted	Zhang et al., 2015
21.	DAMD	Direct amplified minisatellite DNA	Somers and Demmon, 2002
22.	InDels	Insertion or deletion of bases in the genome	Guo et al., 2019

Table 2. *Advantages and disadvantages of different molecular markers.*

S. No.	Marker	Advantages	Disadvantages	Reference (s)
		Highly reproducible	Time consuming	Beckmann and Soller, 1986
		Robust and reliable	Expensive	Tanksley et al., 1989
1.	RFLP	Locus specific	High quality of pure DNA needed	Mishra et al., 2014
		Co-dominant	Limited polymorphism	
		Transferable across the population	Not amenable for automation	
		No need of prior sequence information		
		Easy to use	Not locus specific	Demeke et al., 1997
		Quick and simple	Dominant marker	Jiang, 2013
2.	RAPD	Inexpensive	Low reproducibility	
		Polymorphic	Generally not transferrable	
		Small quantity of DNA required	Highly purified DNA is required	
		Reliable	Dominant marker	Blears et al., 1998
		High reproducibility	Complicated methodology	Ridout and Donini, 1999
3.	AFLP	Highly polymorphic	High quality and quantity of DNA required	
		More informative		
		Provide good genome coverage		
		Co dominant marker	Developmental cost is high	Provan et al., 2001
		High reproducibility	Time consuming and laborious	Zane et al., 2002
		Robust and reliable	Polyacrylamide electrophoresis is required	Kalia et al., 2011
4.	SSR	Locus specific	Presence of more null alleles	
		Transferable across the population	Occurrence of homoplasy	
		Less quantity of DNA is required		
		Amenable for automation and technically simple		
		Highly polymorphic	Low reproducibility	Dirlewanger et al., 1998
		Simple and easy to use	Pure DNA is required	Moreno et al., 1998
5.	ISSR	No need of prior sequence information	Generally not transferable	Arcade et al., 2000
			Fragment are not same sized	Ng and Tan, 2015
		Cost effective		
		Co-dominant marker		
6.	SNP	High reproducibility	Developmental cost is high	Jiang, 2013
		Widely distributed throughout genome		
		No need of prior sequence information		
		Co-dominant marker		
		Highly reproducible, robust and reliable	Marker development is limited	
7.	EST	High degree of sequence conservation	to species for which sequencing	Cato et al., 2001
		Enable a transfer of linkage information between species	database already exist	
		Simple	Dominant marker	Li et al., 2001
		Easy to use	Moderate to high throughput ratio	Uzun et al., 2009
8.	SRAP	Reliable		
		Easy isolation of bands		

9.	DarT	Cost-effective High reproducibility Highly polymorphic High throughput Prior sequence information not needed	Dominant marker Developmental cost is high	Jaccoud et al., 2001 Wenzl et al., 2004
10.	Retrotransposons	Simple Easy to use High reproducibility No need of prior sequence information	Dominant marker	Kalender et al., 1999 Kalender et al., 2011 Roy et al., 2015

Table 3. *Molecular markers for genetic diversity in different vegetable crops.*

S.No.	Crop	Molecular marker	Traits improved	Reference (s)
1.	Tomato	RAPD and ISSR	Genetic divergence and high yield of genotypes under high temperature	El-Mansy et al., 2021
		ISSR	Genetic diversity and genetic variability	Vargas et al., 2020
		SSR and SCAR	Genetic diversity and resistance against fungal diseases	Gonias et al., 2019
		RAPD	Genetic diversity	Herison et al., 2018
		ISSR	Genetic diversity and genetic relationships among varieties	Kiani and Siahchehreh, 2018
		SRAP	Genetic variation and genetic diversity	Shaye et al., 2018
		SSR	Genetic diversity and morphological variation	Kaushal et al., 2017
		SSR	Genetic variation and genetic diversity studies	Benor et al., 2008
		RAPD	Genetic variation	Archak et al., 2002
		RAPD	Genetic diversity	Villand et al., 1998
		SSR	Genetic diversity and population structure	Liu et al., 2018
2	Brinjal	RAPD	Genetic diversity	Sultana et al., 2018
		RAPD	Genetic diversity, molecular characterization and genetic variation	Ansari and Singh, 2013
		RAPD and SSR	Genetic variation and genetic diversity	Verma et al., 2012
		EST-SSR	Genetic diversity and evolutionary relationships analysis	Tumbilen et al., 2011
		RAPD and SSR	Molecular characterization and genetic variation	Demir et al., 2010
		SSR	Genetic variability and genetic diversity	Sharmin et al., 2018
3	Chilli	ISSR	Genetic diversity, level of polymorphism and potential of digital fingerprinting	Thuy et el., 2016
		AFLP	Genetic diversity, genetic studies and identification of chilli genotypes	Krishnamurthy et al., 2015
		SSR	DNA fingerprinting and genetic diversity analysis	Hossain et al., 2014
		RAPD	Genetic diversity and level of polymorphism	Bahurupe et al., 2013
		SSR and SNP	Wide genetic variability and genetic diversity	Yumnam et al., 2012
4	Capsicum	RAPD	Genetic diversity	Makari et al., 2009
		SCoT and DAMD	Genetic diversity, genetic structure and estimate of gene flow	Igwe et al., 2019
		SSR	Pungency characterization, population structure, genetic diversity	Jesus et al., 2019
		Microsatellite and InDel	Genetic diversity and anthracnose resistance	Nugroho et al., 2019
		SSR	Genetic diversity, genetic relationships and population structure improvement	Xiao-min et al., 2016
		SSR	Genetic diversity and population structure	Lee et al., 2021
		SSR	Genetic diversity, DNA fingerprinting and molecular variance	La Cruz et al., 2020
		SSR	Genetic diversity and level of polymorphism	Singh et al., 2020
5	Potato	SSR and RAPD	Genetic diversity, genetic variation, evolutionary relatedness, genetic relationships and molecular characterization	Kapuria et al., 2019
		SSR	Genetic diversity, DNA fingerprinting and detect genetic differences	Tillault and Yevtushenko, 2019
		SSR	Evaluation of genetic diversity and population structure	Wang et al., 2019
		EST-SSR	Genetic diversity and genetic relationships within and among potatoes from different geographical regions	Salimi et al., 2016
		SSR	Genetic diversity, resistance to bacterial wilt, potato virus Y and low chilling temperature	Carputo et al., 2013
		SSR and RAPD	Genetic diversity and cultivar identification	Rocha et al., 2010

		AFLP	Genetic diversity, genetic variability and level of polymorphism	Massucato et al., 2020
		AFLP	Genetic and phenotypic diversity	Muhanad et al., 2018
		SSR and RAPD	Genetic diversity and yellow vein mosaic virus resistance	Patel et al., 2018
		SSR	Genetic diversity and genetic variation	Kumar et al., 2016
6	Okra	SSR	Genetic diversity and genetic relationships among cultivars	Fougat et al., 2015
		AFLP	Genetic diversity and genetic heterogeneity	Kyriakopoulou et al., 2014
		ISSR	Genetic diversity and differentiation	Yuan et al., 2014
		RAPD	Genetic diversity and genetic relatedness	Prakash et al., 2011
		RAPD	Genetic diversity and crop improvement	Sawadogo et al., 2009

Gene tagging: Gene tagging is a pre requisite for Marker Assisted Selection (MAS) and map based cloning in crop improvement programme [32]. Gene tagging refers to the gene mapping of economic value close to well-known markers. Molecular marker play important role in facilitating the method of traditional gene transfer. Molecular markers that are very closely related to the trait of interest and gene act as tag and these tags are effectively utilized for the indirect selection of genes in breeding programmes [26]. By constructing molecular maps, different genes of economic importance *viz*., stress tolerance, disease resistance, insect-pests resistance and yield contributing characters have been tagged [33]. Different genes have been tagged to impart resistance in various vegetable crops in resistance by several scientists (Table 4).

DNA fingerprinting for varietal identification: It is one of the most important aspects that identifies and detect any genotype of crops along with whole living organisms [32]. DNA fingerprinting can successfully utilize for varietal identification as well as for detecting variability in a wide variety of germplasm [34]. Although any type of marker can be used for DNA fingerprinting but RAPDs, microsatellite and RFLPs are the markers of preference for the purpose because all these markers are PCR based and did not require any pre information on nucleotide sequences [35]. Identification of different varieties of vegetable crops has been reported by several workers (Table 5).

Detection of QTLs: The identification and detection of linkage between QTLs and markers are the prime and foremost objective of the breeders that are engaged in the resistance breeding of plants though it can be performed using various statistical methods [36]. Disease resistance can be detect with ordinary scales whether data do not always show normal distribution, so researchers have been testing putative QTLs with non-parametric statistical tests and procedures [37]. The conclusion of genetic studies of complex interactions has been observed and first time reported the insect resistance in tomato [38]. In addition to this, QTL mapping could be useful for identify and detect the loci associated with quantitative components of resistance to infections in crop plants, its rate of multiplication as well as its movement and in the host and progression of the disease [32]. By this unique technique of detection of QTL new genes for partial resistance might be identified and utilized for resistance in crop plants [39]. Different types of QTLs have been detected by several researchers in vegetable crops (Table 6).

Table 4. *Molecular markers linked to major resistant genes in different vegetables.*

S. No.	Crop	Pathogen/Pest	Gene	Marker (s)	Reference (s)
		Yellow leaf curl virus	*Ty2*	RFLP	Hanson et al., 2000
		Tomato mosaic virus	*Tm2*	SCAR	Sobir et al., 2000
		Cucumber mosaic virus	*Cmr*	RFLP	Stamova and Chetalat, 2000
1	Tomato	*Verticillium dahliae*	*Ve*	RFLP	Diwan et al., 1999
		Fusarium oxysporum f. sp. Radicislycopersici	*Fr2*	RAPD	Fazio et al., 1999
		Cladosporium fulvum	*Cf2*	RFLP	Dixon et al., 1995
		Meloidogyne javanica	*Mi3*	RAPD	Yaghoobi et al., 1995
		Meloidogyne incognita	*Mi*	RAPD	Williamson et al., 1994
		Tomato spotted wilt virus	*Tsw*	RAPD	Jahn et al., 2000
2	Pepper	*Tomato spotted wilt virus*	*Tsw*	CAPS	Moury et al., 2000
		Xanthomonas vesicatoria	*Bs2*	AFLP	Tai et al., 1999
3	Pea	*Pea common mosaic virus*	*Mo*	RFLP	Dirlewanger et al., 1994
		Erysiphe polygone	*Er*	RAPD	Dirlewanger et al., 1994

4	Bean	*Common bean mosaic virus*	*I*	RAPD	Meiotto et al., 1996
5	Cucumber	*Fusarium oxysporum f. sp. Melonis*	*Fo m2*	SSP	Wechter et al., 1998
6	Melon	*Fusarium oxysporum f. sp. Melonis*	*Fo m2*	RAPD	Wechter et al., 1995

Table 5. *Identification of varieties of different vegetables by using molecular markers.*

	Vegetable crop (s)	Molecular marker (s)	Reference (s)
1	Tomato	Microsatellites, RAPD, RFLP	Kaemmer et al., 1995 Bredemeijer et al., 1998 Noli et al., 1999
2	Brinjal	RAPD	Karihaloo et al., 1995
3	Chilli	RAPD, ISSR	Mongkolporn et al., 2004
4	Pepper	RAPD, AFLP	Prince et al., 1995 Paran et el., 1998
5	Potato	RAPD, AFLP, ISSR, Microsatellites	McGregor et al., 2000 Ashkenazi et al., 2001
6	Pea	RAPD	Thakur et al., 2018
7	Beans	RAPD, RFLP	Stockton and Gepts, 1994
8	Onion, garlic and related species	AFLP, Microsatellites, ISSR, RAPD	Arifin et al., 2000 Fischer and Bachmann, 2000
9	Brassica	RAPD, Microsatellites	Margale et al., 1995 Cansian and Echeverrigaray, 2000
10	Cucurbits	RAPD, ISSR, Microsatellites	Gwanama et al., 2000 Danin et al., 2001
11	Carrot	RAPD, AFLP	Gwanama et al., 2000
12	Sweet potato	RAPD, AFLP	Danin et al., 2001
13	Lettuce	AFLP, Microsatellites	Margale et al., 1995
14	Asparagus	RAPD	Khandka et al., 1996 Roose and Stone, 1996
15	Spinach	Microsatellites	Groben and Wricke, 1998
16	Artichoke	RAPD	Tivang et al., 1996

Table 6. *Detection of QTLs in different vegetable crops.*

S.No.	Crops	Traits	QTL/ gene	Chromosome number	Marker	Population used	Source	Reference (s)
1	Tomato	Fruit morphology	QTL	10	SNP	RIL	NC30PXNC-22L-1	Adhikari et al., 2020
		Late blight and yield	QTL	11	SNP	F2	Koralik	Brekketet et al. 2019
		Glandular trichomes	QTL	1	SNP	BC	Solanum habrocha-ites	Bennewitz et al. 2018
		Late blight	QTL	2,3,10	SNP	F2	PI163245	Ohlson et al. 2018
		Early flowering	QTL	1	SNP	F2	BoneMM cultivar	Ruanggrak et al. 2018
		Fruit mineral content	QTL	-	SSR	RIL	Solanum pimpinellifolium	Capel et al., 2017
		Late blight	QTL	9 and 12	SNP	F2	L3707	Panthee et al., 2017

		Salt tolerance	QTL	6	SSR	RIL	CG104 and CG37	Liu et al., 2021
		Fruit size and fruit shape	QTL	1 and 6	SNP	F2 and BC1F1	Inbred line CNS21 and Inbred line RNS7	Gao et al., 2020
		Low temperature	qLTG1.2	1	-	RIL	Low germination tolerant variety	Yagcioglu et al. 2019
		Germination ability	qLTG2.1	2	-	RIL	Low germination tolerant variety	Yagcioglu et al. 2019
2	Cucumber	Cucumber mosaic virus	CMV6.1	6	SSR	RIL	Inbred line 02245	Shi et al., 2018
		Alternaria leaf spot	Ps15.1, ps15.2	5	SSR	RIL	GY14	Slomnicka et al. 2018
		Fruit peduncle length	Qfp16.1	6	SSR	F2	Inbred line 1101	Song et al. 2016
		Powdery mildew	Pm1.1, pm1.2	1	SSR	F2.3	WI 2757	He et al., 2013

Marker assisted selection: Marker assisted selection refers to the use of molecular (DNA) markers to assist phenotypic selection in crop improvement [40]. Basically, it is a technique in which phenotypic selection is made on the basis of genotype of a marker [41]. It is based on the concept that it is possible to infer presence of a gene from the presence of a marker which is tightly linked to the trait of interest [42]. MAS provided a tremendous potential for increasing the selection efficiency by allowing for earlier selection and reducing plant population size used during selection [43]. It is a molecular breeding technique which helps to avoid the difficulties related to traditional plant breeding and it has tremendously changed the standard of selection [44]. Plant breeders mostly use MAS for the identification and detection of suitable dominant or recessive allele across the generation and for the identification of most favourable individuals across the segregating progeny [45]. There are four important schemes in marker assisted selection namely marker-assisted backcrossing, gene pyramiding, marker-assisted recurrent selection, genome selection in crop plants [46]. Marker-assisted selection for the traits of interest has been reported in different vegetable crops by several scientists (Table 7).

Table 7. *Marker assisted selection in different vegetable crops.*

S.No.	Crop	Marker/gene	Lines used	Trait improved	Reference (s)
1	Cabbage	InDel markers A1 and M10	D21, D29, D70, D120 and D162	Head splitting and Fusarium wilt resistance	Li et al., 2020
		*TG10*1 (RFLP) and *Fr1* gene	Pusa Ruby	Fusarium wilt resistance	Devran et al., 2018
2	Tomato	*SNP* and *Bwr-6* and *Bwr-12*	Pusa Rohini, Pusa 120	Bacterial wilt resistance	Kim et al., 2018
		ACY (InDel) and *Ty-3* gene	Pusa Rohini, Pusa 120	Yellow leaf curl virus resistance	Nevame et al., 2018
3	Onion	*Orf*725	A and B lines of onion in Brazilian germplasm	Cytoplasmic male sterility	Ferreira and Santos, 2018
4	Cucumber	*SSR11*	Cmv6.1	Cucumber mosaic virus resistance	Shi et al., 2018
		pmsSR27 pmSSR17	Pm-s	Powdery mildew resistance	Liu et al., 2017
5	Watermelon	*MCPI11, CYSTSIN* and *Pm* gene	Arka Manik	Powdery mildew resistance	Gama et al., 2015
6	Pea	*SCAR* and *er*-2 gene	JI2480	Powdery mildew resistance	Katoch et al., 2010

Discussion and Conclusion

Genetic diversity means the variety of genes in all organisms from human beings to crops, fungi, bacteria and viruses. It determines the distinctiveness of each individual or population within the species. There are basically four methods of measuring genetic diversity namely ethino-botanical classification, morphological, biochemical and molecular characterization. Morphological markers allow the finding of genetic variation based on Individual phenotypic variations. However, there are limitations confined to these types of markers. Morphological markers limitations lead to the assessment of biodiversity from relying on morphological markers to using isozymes and DNA markers that is popularly known as molecular markers. There are various types of molecular markers which are classified based on variation type at the DNA level, mode of gene action and method of analysis. They are key tools in genome analysis which ranges from localization of a gene to improvement of plant varieties through marker aided selection. Even though there are various uses of DNA markers but among all Marker Assisted Selection (MAS) is the most promising technique for crops cultivar development. MAS can be employed as an effective tool to facilitate selection of progeny in an early generation who have desirable traits resulting speeding up of the selection procedure in the breeding programme. There are different conventional and modern breeding tools and techniques that can be utilized for crop improvement of vegetable crops despite the ban on genetically modified organisms. The controlled crosses between individuals produce desirable genetic variation to be recombined and transferred to next progeny through natural process.

The last thirty years have witnessed a continuous and tremendous development I the molecular markers technology from RFLP to SNPs and a diversity of array-technology-based markers. In spite of the presence of these highly advanced molecular genetic techniques, we are still not achieving our goals. Unfortunately, molecular markers are currently unavailable for several important traits controlled by many genes or polygenes. The main reason behind these lies in inaccurate phenotyping. High-throughput phenotyping techniques solve these problems by using light, cameras, sensors, computers and highly modified devices for the collection of very precise phenotypic data, which is a core requirement to achieving our breeding goals successfully. The coming years are likely to see continued innovations in molecular marker technology to make it more precise, productive and cost-effective in order to investigate the underlying biology of various traits of interest.

Disclosure Statement

No potential conflict of interest was reported by the authors.

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