Vegetables are the group of plants, which constitute major part of human diet. They can be consumed raw or cooked. Vegetable crops are highly susceptible to abiotic and biotic stresses which largely reduce the yield and crop productivity. Several traditional breeding approaches are available for the crop improvement but these are time consuming, labour intensive, cost ineffectve and less accurate processes. The recent technological innovations have made this possible to study and manipulate the genetic variability of crop plant. It is evident that development of molecular markers and their utilization in plant breeding programs facilitates reliable selection and hasten the crop improvement programme. Assessment of genetic variability, molecular mapping, QTL mapping, marker assisted selection, DNA fingerprinting, introgression of resistance genes, gene pyramiding, genomic selection, marker assisted backcrossing, marker assisted recurrent selection and gene tagging are the novel techniques for crop improvement.

**Key words**: Molecular markers, Introgression, Gene pyramiding, Genomic selection, Marker assisted selection.
characterized phenotypic traits like plant height, disease response, shape or color of flower, fruits or seeds, surface of plant part, growth habits or pigmentation and many other visual characters and those gene loci that have direct effect on the morphology of plant (Hearne et al., 1992). These markers enable the assessment and evaluation of genetic variability among the population and diversity based on single phenotypic difference (Reddy et al., 2007). Biochemical markers (also known as protein polymorphism) 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 (Kumar et al., 2012). Such markers are related to variations in protein and amino acid banding patterns. Isozymes and Protein based markers are successful Biochemical markers. They can also be used to estimate the gene frequency, genotypic frequency and successfully help in the detection of genetic diversity, gene flow and gene structure (Fukuoka et al., 1994). To investigate the genetic difference between cultivated lettuce and wild lettuce genotypes biochemical markers where used (Cole et al., 1991; Collard and Mackill, 2008; Dziechciarkova et al., 2004). Cytological markers are the variations associated with the chromosome’s morphology such as variations in chromosomal number, size, shape, order, position, sequence specificity, meiotic behavior of chromosome (Pashley et al., 2006). A cytological marker detects the differences in the euchromatin and heterochromatin, mutated chromosomes and normal and used in the identification of mapping and linkage groups (Feng et al., 2018). Morphological markers, biochemical markers and cytological markers are classical markers (Ashraf et al., 2012). A marker is a DNA sequence or gene with known location on a chromosome which serves as flag post or signpost or landmark which is directly or indirectly linked to the trait gene of interest and is generally co-inherited with the trait (Lyamichev et al., 1993). Molecular markers or genetic markers are the 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 (Ghareyazie et al., 1995).

Properties desirable for ideal DNA markers (Jiang, 2013; Joshi et al., 2011)

1. High level of polymorphism (Clear distinct allelic features)
2. Co-dominant inheritance (can distinguish between heterozygote and homozygote)
3. Frequent occurrence in genome
4. Easy and fast assay
5. High reproducibility
6. Insensitive to environment
7. Markers can be easily exchangeable between laboratories
8. Non-epistatic

Types of molecular markers

On the basis of various polymorphism-searching methods, DNA markers have been used in different systems (Collard et al. 2005) (Fig. 1).

Markers available as mentioned literature (Semagn et al., 2006; Kumar et al., 2009; Ismail et al., 2016) (Table 1).

Applications of Molecular markers
Assessment of Genetic Diversity

Assessment of genetic diversity plays a crucial role in ex-situ germplasm conservation, germplasm characterization, management, utilization and in hybrid development. Molecular markers are the efficient tool which shows the adaptation, performance and agronomic qualities of the germplasm (Demeke et al., 1997). Molecular markers have made the evaluation of genetic diversity and classification of genetic material easier (Ridout et al., 1999). Ruiz and Martinez (2005) used SSR and SRAP markers for the study of genetic variability in some traditional tomato cultivars of Spain. RAPD (Random amplified polymorphic DNA) and SSR (Simple sequence repeats) markers were effectively used in differentiating among the genotypes of Solanum aethiopicum and Solanum melongena by Ansari and Singh (2014). Several researchers in studies revealed that SSR markers are efficient markers in assessment of

Fig. 1: Types of molecular markers.
Genetic diversity, genetic relationships and population structure improvement, DNA fingerprinting and molecular variance, genetic variation, evolutionary relatedness in Capsicum (Lee et al., 2021; La Cruz et al., 2020; Singh et al., 2020). Sharmin et al. (2018) also used SSR markers for the assessment of Genetic variability and genetic diversity in Brinjal. EST-SSR have been successfully used for the evaluation of genetic diversity and genetic relationships within and among potatoes from different geographical regions (Salimi et al., 2016). Gonias et al. (2019) carried out SSR and SCAR analysis to determine genetic diversity and resistance against fungal diseases in tomato.

**DNA fingerprinting for varietal and hybrid identification**

DNA fingerprinting is one of the important techniques for the varietal identification and detection of any genotype of crop (Provan et al., 2001). It is the only practical technique for ensuring the presence of multiple beneficial genes/QTL in a single variety or genotype. Any type of marker can be used for DNA fingerprinting but RFLPs markers were preferred earlier (Dirlewanger et al., 1998). Nowadays large number of markers are used viz., RAPD and AFLP markers are used for the identification of varieties of Pepper (Prince et al., 1995; Paran et al., 1998), Beans (Stockton et al., 1994), Carrot (Gwanama et al., 2000), Sweet potato (Danin et al., 2001), Tomato (Bredemeijer et al., 1998; Noli et al., 1999) and Potato (McGregor et al., 2000; Ashkenazi et al., 2001).

### Gene tagging

Gene tagging is detection/identification of DNA sequences in genome that can perform as a tag for desired genes. Tagging of valuable resistant genes is a prerequisite for Marker Assisted Selection (MAS) and map based cloning (Provan et al., 2001). There are so many Molecular markers linked to major resistant genes in different vegetable crops. In tomato, Ty2 gene linked with RFLP, which is resistant against Yellow leaf curl virus (Hanson et al., 2000), Tm2 gene against Tomato mosaic virus (Sobir et al., 2000), Cmr gene against Cucumber mosaic virus (Stamova and Chetalat, 2000). In pea, Mo is a resistant gene against common mosaic virus linked with molecular marker RFLP, similarly Erlinked with RAPD, which is resistant to *Erysiphe polygonae* (Dirlewanger et al., 1994). In cucumber, Fo gene is linked with SSR which resistant against *Fusarium oxysporum* f. sp. *melonis* (Wechter et al., 1998). Huang et al. (2000) using RAPD and SCAR markers tagged powdery mildew resistance gene ol-1 on chromosome 6 of tomato. Wechter et al. (1995) using RAPD marker tagged Fo and m2 genes which are resistant to *Fusarium oxysporum* f. sp. *melonis*. According to Baghour et al. (2019), double...
transgenic tomato plants overexpressing both LeNHX2 and SlSOS2 show an increased fruit yield and a better performance under NaCl stress than WT and single transgenic plants over expressing only one of these genes. Hansona et al. (2016) developed fresh tomato lines resistant to begomo viruses (tomato yellow leaf curl), Phytophthora infestans (late blight), Ralstonia solanacearum (bacterial wilt), Stemphyllium spp. (gray leaf spot), Fusarium oxysporum f. sp. lycopersici race 2 and Tobacco mosaic virus through integrated application of pedigree method and molecular markers to confirm the presence of targeted gene. Zhang et al. (2022), investigated the potential regulatory factors viz., Solyc01g008390 and Solyc01g008410 genes of cold tolerance related to molecular marker TGS377 located on chromosome 1 of the tomato.

Development of saturated genetic maps

Unlike morphological and biochemical markers, molecular markers are not affected by the environmental factors and developmental stage of the plant. Molecular/DNA markers can be used in number of ways in breeding studies. In Lettuce, 41 RFLP markers were used for the construction of linkage map (Landry et al., 1987). Yayeh (2005) identified first genetic linkages in male fertile garlic accessions using SNPs, SSRs and RAPDs. Zhang et al. (2004) constructed linkage map for watermelon by using RAPD and SCAR markers. Montero-Pau et al. (2017) reported SNP-based saturated genetic map and QTL analysis of fruit-related traits i.e. fruit weight and fruit length in Zucchini using Genotyping-by-sequencing. A molecular genetic map of Cassava (Manihot esculenta Crantz) has been constructed using 132 RFLPs, 30 RAPDs, 3 microsatellites and 3 isozyme markers segregating from the heterozygous female parent of an intra-specific cross (Fregene et al., 1997). Grzebelus et al. (2014) analyzed set of 900 Diversity Arrays Technology (DArT) markers for comparing 65 wild and 94 cultivated carrot accessions, to develop saturated linkage genetic map and to detect the genetic diversity of Carrot.

Detection of QTLs

Gene mapping gives a clear picture about the physical location of genes in the chromosomes. The prime objective of plant breeders engaged in resistance breeding is to identify and detect linkage between makers and QTLs (Moreno et al., 1998). QTL mapping is a unique technique for identification and detection of loci associated with quantitative components of resistance to infections in crop plants (Provan et al., 2001). Different types of QTLs have been identified in vegetable crops using molecular markers, some of them are presented in Tables 2 and 3.

Marker Assisted Selection (MAS) for trait of interest

Marker Assisted Selection is a selection method which uses molecular markers to facilitate the phenotypic selection in crop improvement (Li et al., 2001). Marker assisted selection has several advantages over phenotypic selection. Plant breeders use this selection method for the identification and detection of suitable dominant and recessive alleles across the generation the population (Kalander et al., 1999). Basically, in MAS, QTLs related to important agronomical traits and valuable resistant genes and their highly related DNA markers that are tightly linked to the trait of interest are used (Jaccoud et al., 2001). Geographic region as well as Pathogen specific QTLs controlling resistance have been identified by Truong et al. (2012) using intra-specific recombinant inbred line population of pepper. MAS breeding involve

<table>
<thead>
<tr>
<th>Crop</th>
<th>Trait</th>
<th>Gene/QTL</th>
<th>Ch. No</th>
<th>Markers</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tomato</td>
<td>Salt tolerance</td>
<td>QTL</td>
<td>6</td>
<td>SSR</td>
<td>Liu et al. (2021)</td>
</tr>
<tr>
<td></td>
<td>Cold stress germination</td>
<td>-</td>
<td>1, 4 and 8</td>
<td>RFLP</td>
<td></td>
</tr>
<tr>
<td>Cucumber</td>
<td>Salt tolerance</td>
<td>-</td>
<td>3</td>
<td>SSR</td>
<td>Kere et al. (2017)</td>
</tr>
<tr>
<td></td>
<td>Low temperature</td>
<td>-</td>
<td>5 and 6</td>
<td>SSR</td>
<td>Dong et al. (2019)</td>
</tr>
<tr>
<td></td>
<td>Low temperature</td>
<td>qLTG1.2</td>
<td>1</td>
<td>SNP</td>
<td>Yagcioglu et al. (2019)</td>
</tr>
<tr>
<td>Pea</td>
<td>Salt index</td>
<td>LG3</td>
<td>3 and 7</td>
<td>SNPs</td>
<td>Leonforte et al. (2013)</td>
</tr>
<tr>
<td></td>
<td>Winter frost damage</td>
<td>LG3</td>
<td>3,5,6 &amp; 7</td>
<td>SNPs &amp; SSR</td>
<td>Klein et al. (2014)</td>
</tr>
<tr>
<td>Common bean</td>
<td>Drought</td>
<td>Pv01, Pv08, Pv03, Pv09, Pv04, Pv07</td>
<td>-</td>
<td>SNP</td>
<td>Mukeshimana et al. (2014)</td>
</tr>
<tr>
<td>Cowpea</td>
<td>Salinity</td>
<td>LG1</td>
<td>-</td>
<td>SSR</td>
<td>Chankaew et al. (2012)</td>
</tr>
</tbody>
</table>
Application of Molecular Markers in Vegetable Improvement

There are several traditional and modern strategies that can be utilized for the crop improvement. Out of which, molecular breeding or use of molecular/DNA markers is one of the best strategy for minimizing yield losses due to various abiotic and biotic stresses. MAS is an effective approach, where conventional plant breeding is supplemented with molecular markers which facilitates selection efficiency and reliability.

**Conclusion**

There are several traditional and modern strategies that can be utilized for the crop improvement. Out of which, molecular breeding or use of molecular/DNA markers is one of the best strategy for minimizing yield losses due to various abiotic and biotic stresses. Application of molecular markers in the field of plant breeding is a boon to plant breeders. Molecular mapping, QTL mapping, MAS, DNA fingerprinting, introgression of resistance genes, Gene pyramiding and Gene tagging etc has given a new direction to conventional breeding methods. Molecular tools are highly valuable to utilize diverse genomic resources for development of superior vegetable cultivars. The past years have witnessed tremendous development of molecular markers from first generation to third generation markers, but still available markers are not enough. Currently, there is unavailability of molecular markers for the several important traits controlled by many genes or polygenes. But upcoming years are likely to see continued innovations and improvements.
advancement in the molecular marker technology.

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