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Next-generation onion (*Allium cepa*) breeding using molecular markers: progress and prospects--a review

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ABSTRACT

Onion (*Allium cepa* L.) is an indispensable vegetable crop throughout the globe. It is a member of family Amaryllidaceae (formerly Alliaceae family) and is characterized by 16 somatic chromosomes and a massive 16.4 Gbp genome. Despite its economic significance, the pace of genetic improvement has historically been hindered by the complex and biennial life cycle, photosensitivity, high inbreeding depression and a lack of sufficient genomic resources. The shift from low-throughput markers like RAPD and RFLP to high-resolution and reliable marker systems like SSRs and SNPs has facilitated the construction of saturated linkage maps, leading to identification of QTLs for various traits like resistance to downy mildew, purple blotch, anthracnose and thrips, apart from tolerance to drought stress. Development of specialized mapping populations like doubled haploids has also enabled rapid fixation of heterozygosity and led to identification of responsible loci for different nutritional and bulb-quality traits. Deployment of molecular markers like *PsaO*, *AcPMS1* for rapid identification of Cytoplasmic-Genetic Male Sterility (CGMS) systems, is paving the way for hybrid seed production in a cost-effective manner. Thus, this review synthesizes the evolution of onion breeding, transitioning from conventional phenotypic selection to modern genomic-assisted improvement to overcome the genome complexities for accelerated development of high-yielding, multi-stress-resistant onion cultivars.

Key words: Abiotic stress, *Allium*, Biotic stress, Diseases, Marker-Assisted Selection, Pests, Quality

Onion (*Allium cepa* L.), a member of family Amaryllidaceae (formerly Alliaceae), is characterized by a diploid chromosome complement of 2n = 2x = 16 (Tripathi *et al.*, 2017; Mahala *et al.*, 2024). The primary center of origin is localized to Central Asia-encompassing modern-day Uzbekistan, Turkmenistan, Tajikistan, Afghanistan, Iran and Pakistan (Tripathi and Lawande, 2019). Found growing wild in these regions, *Allium vavilovii* has been identified as the closest wild progenitor to cultivated onion, while Mediterranean basin is recognized as the secondary center of origin.

Globally, onion cultivation is spanned in 5.719 million ha area, yielding a total output of 108.260 million tonnes. Production is heavily concentrated in Asia, which accounts for 64.70% of global volume, followed by Africa (15.70%), Europe (9.70%), and the USA (9.70%). India has emerged as the largest producer of onion followed by China, the USA, Egypt and Bangladesh (FAO STAT, 2024). India produces about 24.266 million tonnes of fresh bulbs from 1.54 million ha area (Anonymous, 2024). It is regarded as the most important export vegetable, contributing to 1.3 million tonnes worth ₹ 2,107.14 crore from India (NHRDF, 2021).

Since the early era of domestication of onion, human being invariably conducted selection leading to the development of different types with respect to bulb shape, size, colour, pungency, photoperiodic response etc. However, despite presence of appreciable variability, speed of onion improvement is not at the pace of other monocot taxa (McCallum, 2007, Varshney *et al.*, 2012). Systematic onion breeding stated with mass selection during the 19th century, followed by discovery of cytoplasmic male sterility (CMS), paving the way for development of F_1 hybrids (Brewster, 2008; McCallum *et al.*, 2008). Presently, F_1 hybrids predominate in long-day season, whereas in short-day conditions, open-pollinated varieties predominate (Brewster, 2008).

The onion breeders following conventional breeding methods often face difficulties because of its high levels of cross-pollination and inbreeding depression, biennial life-cycle, photosensitivity and short seed viability. Genome sequencing poses challenge because of its large 16.4 giga base pairs (Gbp) genome size. Thus, there is an urgent need for deployment of genomic tools to facilitate rapid genetic improvement for yield, quality traits and multi-stress resistance in different genetic backgrounds.

Phenotypic selection of onion often leads to biased results due to the substantial influence of environment on trait expression. Moreover, it is also difficult to improve the traits which have low heritability. Marker-Assisted Selection (MAS) using tightly-linked markers, proves efficient in such cases. The MAS provide additional advantages like high accuracy, rapidity, early trait detection etc. Thus, this review collects the available

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information on progress made by identification and deployment of genomic resources for onion improvement and its prospects.

Genetic Resources

Availability of diverse germplasm is the most crucial factor for a successful breeding programme (Glaszmann *et al.*, 2010). Growing of onion in different agro-ecological zones over centuries led to development of a wide range of landraces, harbouring tremendous genetic variation (Brewster, 2008). However in the late 1980s, development of F_1 hybrids resulted in genetic erosion of those landraces in different countries. However, presently, a huge number of onion accessions are being maintained in different gene banks in the world (Table 1).

Table 1: Major onion gene banks in the world along with their germplasm holdings.

Institute	Location	Number of *Allium* accessions
European Cooperative Programme for Plant Genetic Resources	Germany	14400
Directorate of Onion and Garlic Research	India	2050
N.I. Vavilov Research Institute	Russia	1888
Warwick Crop Center	United Kingdom	1755
National Institute of Agro-biological Sciences	Japan	1352
US Department of Agriculture	USA	1304
Royal Botanic Gardens	United Kingdom	1100
AVRDC – The World Vegetable Center	Taiwan	1082

Despite the wide distribution, the knowledge of genome, population structure and genetic architecture are limited in onion (McCallum, 2007), necessitating genetic resource mining and accelerated genetic analysis (Baldwin *et al.*, 2012a). The genome of onion is very large (~16.4 Gbp) and very few ESTs are available in public domain (McCallum *et al.*, 2001; Kuhl *et al.*, 2004). Forming a partial onion BAC library, Jakše *et al.* (2008) reported genome composition, gene structure and very low gene density of one gene per 168 kb genome. The genomic data and genetic maps of onion and other economically important *Allium* species are available from an online genomic database named as *Allium Map* (https://allium.scinet.org.nz/) (McCallum *et al.*, 2012).

Mapping populations

Predominantly, early generation inbreds are used for development of the mapping populations in onion. The residual heterozygosity in such parental inbreds complicates both marker development and sequence analysis (Baldwin *et al.*, 2012b). In general, F_2 population is most used for molecular mapping owing to difficulties to maintain fertility and plant vigour, while developing Recombinant Inbred Lines (RILs). To overcome this, doubled haploid (DH) onion lines have been developed in both short- and long-day onions (Bohanec, 2009; Baldwin *et al.*, 2012b; Duangjit *et al.*, 2013) for mapping of quantitative and qualitative traits. However, major drawback of doubled haploid accessions is poor seed setting (Bohanec, 2002). In this context, Alan *et al.* (2003 and 2004) developed highly fertile doubled haploid lines from long-day US onion varieties, paving the foundation for better insights into onion genetics and genomics.

Genetic maps/ linkage maps

Linkage Map is a schematic representation of the relative locations of genetic markers present on chromosome of an organism as determined from the frequency of recombination between the marker pairs. The first genetic map of onion consisting of 12 linkage groups was developed by Bradeen and Havey (1995) by using 116 RFLP and RAPD markers in a population developed from BYG15-23 × AC43. To date, this map is regarded as a key reference genetic map of onion. Furthermore, Martin *et al.* (2005) placed 100 additional markers to the same intra-specific map for a better saturation with 14 linkage groups. This map predominantly contained dominant RFLP markers which implies that the large genome size of onion is mainly because of high levels of gene duplication.

Marker systems

RAPD

The RAPD (Randomly Amplified Polymorphic DNA) markers use 10 base long arbitrary primers (decamers) which amplify random segments of genomic DNA in a Polymerase Chain Reaction (PCR). Being random, this marker does not require any sequence information. RAPD had been deployed for characterization of onion germplasm comprising of both wild and cultivated genotypes by Maniruzzaman *et al.* (2010) and Sudha *et al.* (2019).

ISSR

The Inter Simple Sequence Repeat (ISSR) technique amplifies the genomic region falling between two Simple Sequence Repeats (SSRs) by using both anchored and non-anchored primers (Ziętkiewicz *et al.*, 1994). Smolik *et al.* (2007) analyzed genetic diversity of onion genotypes belonging to six different species using 16 ISSR markers. Mukherjee *et al.* (2013) used both RAPD and ISSR for diversity analysis of five *Allium* species and found ISSR to

Table 2: Linkage maps developed in onion along with the marker system utilized

Population type	Population derived from	Marker system employed	Reference(s)
F_2	NW-001 × NW-002	SNP	Jo *et al.* (2017)
F_2	BYG15-23 × AC43	InDel, SNP, SSR, RFLP	Martin *et al.* (2005)
F_2	BYG15-23 × AC43	RFLP, SSR and SNP	King *et al.* (1998); Duangjit *et al.* (2013)
F_2	*Allium cepa* × *Alliumroylei*	AFLP and SSR	Van Heusden *et al.* (2000), McCallum *et al.* (2012)
F_2	W202A × Texas Grano	SSR	McCallum *et al.* (2006, 2007)
F_2	Nasik Red × CUDH2150	SSR and SNP	Baldwin *et al.* (2012b)
F_2	OH1 × 5225	SSR and SNP	Duangjit *et al.* (2013)
F_2	DehyA × B5351C	SNP	Damon and Havey (2014)
F_2	*Allium cepa* × *A. fistulosum*	SSR, InDel, STS and RAPD	Tsukazaki *et al.* (2012)

be more polymorphic between *Allium cepa* and *A. sativum,* while RAPD markers showed better polymorphism within *A. porrum.* In overall, RAPD markers revealed more intraspecific diversity than ISSRs, whereas ISSRs showed more interspecific diversity than RAPD, proving its potential for diversity analysis.

SRAP

The Sequence Related Amplification Polymorphism (SRAP) is a simple marker designed for the amplification of Open Reading Frame (ORF). SRAP primers are generally 17-18 nucleotides long and consist of core sequences (13-14 base pairs) and nucleotides 'CCGG' in the forward primer and 'AATT' in the reverse primer.

RFLP

The Restriction Fragment Length Polymorphism (RFLP) involves a single restriction enzyme which generates fragments of different lengths from the same genomic region of different individuals/strains/lines or species, depending upon the presence or absence of recognition sites. Bark and Havey (1995) deployed this marker system to characterize onion inbred lines.

AFLP

The Amplified Fragment Length Polymorphism (AFLP) was developed by Zabeau and Vos (1993). This technique is a combination of restriction digestion and PCR. Ohara *et al.* (2005) constructed the first genetic linkage map of Japanese bunching onion (*Alliums fistulosum*) using 149 AFLP markers.

SSR

The term *Simple Sequence Repeat* (SSRs) was originally coined by Lilt and Luty (1989) to describe simple sequence fragments generated in PCR. This is also known as Short Tandem Repeat (STR) and Simple Sequence Length Polymorphism (SSLP). The multi-allelic nature and PCR-based detection of the SSR markers makes them more breeder friendly than the SNPs (Pal *et al.,* 2020). More than a hundred SSR markers were developed by Tsukazaki *et al.* (2008) from size-fractionated genomic DNA libraries. SSR makers have provided the greatest insights into onion diversity analysis (Khosa *et al.,* 2014). Mitrová *et al.* (2015) established a panel of 15 easy to score SSR markers which easily differentiated 16 commercial onion cultivars of Czech Republic, making them potential for future diversity analysis studies. Anwar *et al.* (2017) employed 16 SSR and three ISSR markers for diversity analysis in *Allium cepa* L., *A. sativum* L. and *A. kurrat* L. accessions. Ivchenko *et al.* (2017) used six SSRs for identification of onion varieties. While studying the genetic diversity of 16 onion genotypes, using RAPD, SSR and ISSR markers Kesraliker *et al.* (2017), concluded ISSR and SSR to be more reliable over RAPD. Singh *et al.* (2021) and Gupta *et al.* (2022) also deployed microsatellite markers for germplasm characterization and emphasized on these markers over the others for better reproducibility and preciseness.

Single Nucleotide Polymorphism (SNP)

Single Nucleotide Polymorphism (SNPs) are one of the most reliable marker systems owing to its preciseness and reproducibility. In recent times, the marker system is gaining importance with the reduction in the sequencing costs. This marker had been deployed for characterization of commercial cultivars by Labate *et al.* (2020), Lee *et al.* (2021) and Jeon *et al.* (2022).

QTL Mapping and Marker Assisted Breeding

Quantitative traits show continuous variation due to their polygenic inheritance and environmental influences. Polygenes produce small individual and cumulative effects on the phenotype. A quantitative trait locus (QTL) is a section of DNA which correlates with the variation of quantitative traits. Thus, QTL mapping employs an algorithm for detection of an association between a phenotypic trait and genetic marker(s).

Disease resistance

Downy mildew, caused by *Peronospora destructor*, is a major yield limiting factor, especially during the *rabi* season. The resistance is conditioned by two dominant genes. Introgression of the resistant genes have been made from *Allium royeli* with the help of tightly-linked AFLP markers are available (Scholten *et al.,* 2007; Khosa *et al.,* 2016). Eidlin *et. al.* (2021) carried out marker-assisted selection using DMR1 marker, linked to the resistant gene '*Pd*', to develop a maintainer line with downy mildew resistance.

Genetics of resistance to *Fusarium* basal rot varies from monogenic to polygenic, depending upon the resistant sources employed (Cramer, 2000, Galvan *et al.*, 2008, Taylor *et al.,* 2013). The resistance can also be precisely introduced in susceptible genotypes through CRISPR/Cas mediated genome editing (Pal *et al.*, 2025). Incomplete resistance (tolerance) to white rot (Hovius *et al.*, 2004) and resistance to pink root (Esfahani and Pour, 2008), *Stemphyllum* blight (Anitha *et al.,* 2011), black mold (Kamal *et al.,* 2012) and Iris Yellow Spot Virus (Bag *et al.,* 2014) has also been identified in onion or other alliums, which are to be deployed in future breeding programmes.

Among biotic stresses, purple blotch causes havoc crop loss ranging from 2.5 to 97% both in bulb and seed crops throughout the globe (Schwartz *et al.,* 2005; Kareem *et al.,* 2012; Tripathi *et al.,* 2013; Nanda *et al.,* 2016; Priya *et al.*, 2016). Chand *et al.* (2018) identified *ApR1* governing resistance to this disease in a population derived from Arka Kalyan (resistant parent) and Agrifound Rose (susceptible parent). They further identified one SSR, *i.e.*, AcSSR7 and one STS marker, *i.e.*, ApR-450 linked to the *ApR1* gene at 1.3 and 1.1 centi Morgan genetic distance, respectively. Recently, KASP based SNP (ApRsnip14, ApRsnip23), SSR (AcSSR7) and SRAP marker (ApR-450) have also been developed for marker-assisted introgression (Sahoo *et al.*, 2023) of purple blotch resistance.

Anthracnose disease, caused by *Colletotrichum gloeosporoides*, also poses serious threat to onion cultivation worldwide. Jayaswall *et al.* (2025) shortlisted a total of 131 differentially expressed genes, belonging to gene classes like Mitogen-activated protein kinases, *WRKY* and *MYB* transcription factors, R genes and transcriptional activators, putatively associated with resistance to anthracnose in wild species of onion. Scholten et al. (2016) identified a QTL (*Bs1*) on chromosome 6 for resistance to leaf blight disease caused by *Botrytis squamosa*. Kim *et al.* (2021) identified SCAR-OPAN-1 and SNP-3 HRM markers linked to gray mold disease resistance.

Epicuticular wax for insect resistance

Insects with piercing and sucking type mouth parts recognize their host plants by sensing the organic constituents of epicuticular waxes (Diaz-Montano *et al.,* 2011). Wide natural variation for the amount and types of epicuticular wax has been reported and reduced amount of epicuticular wax (glossy foliage) have been associated with thrips resistance (non-preference) in onion (Bag *et al.,* 2014; Damon and Havey, 2014). Recessive inheritance of reduced epicuticular waxes and found two QTLs each on chromosome 2 and chromosome 5, governing the production of hentriacontanone-16 (primary wax on leaves) and for production of several primary alcohols, respectively (Damon and Havey, 2014). SNP markers are being identified for marker-assisted selection for this trait (Bag *et al.,* 2014; Damon and Havey, 2014).

Drought tolerance

Caldwell *et al.* (2003) investigated soil moisture potential, leaf water potential, growth, photosynthesis, stomatal conductance, leaf transpiration, water use efficiency, membrane function, nature and accumulation of quaternary ammonium compounds in 21 days old onion seedlings which were subjected to various drought regimes by withholding irrigation. They concluded that the onion seedlings were able to tolerate drought by increasing water use efficiency. Though QTL mapping has not been followed in onion for drought tolerance, the related species, *viz. Allium fistulosum* and *A. munzii* and genotypes *viz.*, Arka Kalyan, MST 42 and MST 46 have been reported to be drought-tolerant (Singh, 2010), necessitating their deployment in QTL mapping.

Bulb pigmentation

A total of 54 types of flavanoids determine the bulb colour by their relative proportion (Slimestad *et al.,* 2007). However, the major colour compounds are anthocyanin (red), flavonols (pale yellow) and chalcones (bright yellow) (Schwinn *et al.,* 2016). Clarke *et al.* (1944) reported three pairs of genes, *viz.* C, R and I, being involved in the development of pigment in the onion bulbs. *C-c* is a basic color factor and dominant C is necessary to produce any pigment. Consequently, all *cc* plants produce white bulbs. Dominant *R* gene in the presence of *C* produces red pigment and recessive *r* allele is responsible for the production of yellow pigment. The gene, *I* is inhibitory to the coloured bulbs and presence of dominant allele of *I* results in white bulbs. El-Shafie and Davis (1967) reported five genes *viz., I, C, G, L, R* (all with two alleles each) responsible for onion bulb colour. Khar *et al.* (2008) developed three different families segregating for bulb colours and identified a SSR marker on chromosome 6 linked to C locus. In cross B2246×B11159, they further reported that red bulbs versus yellow bulbs were controlled by DFR and a locus (*L2*) linked at 6.3 cM to ANS (anthocyanidin synthase). Hence, authors proposed that onions with yellow bulbs were independently selected for numerous times and thus yellow genotypes carry independent mutations in structural or regulatory genes controlling the production of red bulb colour. Earlier, Kim *et al.* (2004) identified a critical mutation within the chalcone isomerase (CHI) gene that reduces the amount of quercetin, giving rise to gold-coloured bulbs. Further, Kim *et al.* (2005) reported that the inactivation of *DFR* was responsible for colour difference between yellow and red onions and two recessive alleles of *ANS* gene were responsible for the development of pink bulb colour. Later, Park *et al.* (2013) designed functional CAPS marker for differentiating two *DFR-A* alleles *viz.*, DFR-A^{PS} (present in yellow onion) and DFR-A^{DEL} (present in red onion). Tsukazaki *et al.* (2012) developed a linkage map from a population derived from *Allium cepa* and *Allium fistulosum* consisting of 11 linkage groups and total marker coverage of 1040 cM. A QTL for bulb pigmentation was reported on chromosome 7.

Pungency

Bulb pungency is an important determinant of end use of onion bulbs and consumer acceptance. McCallum *et al.* (2007) identified a major QTL for pungency on chromosome 3 by using a $F_{2:3}$ mapping population derived from W202A (pungent type) × Texas Grano 438 (sweet type). Marker assisted transfer of the QTL could be followed for improving pungency into non-pungent genotypes.

Tearless onion

Lachrymatory factor synthase (*LFS*) gene catalyzes the production of the lachrymatory factor in onion bulbs. Masamura *et al.* (2012) mapped a candidate *LFS* gene on chromosome 5 of onion using a complete set of *A. fistulosum*–shallot (*A. cepa* L. *aggregatum* group) monosomic alien addition lines. Eady *et al.* (2008) produced tearless onion by RNAi mediated suppression of *LFS* gene which prevented the conversion of isoalliin into thiosulfinates.

Kato *et al.* (2016) developed non-pungent onions by irradiating seeds with neon-ion at 20 Gy. The level of lachrymatory factor production of the selected bulbs in M_4 generation had 7.5 times lower than those of normal onion, confirmed by the lower mRNA production for the gene coding for Allinase enzyme.

Bulb quality and nutritional traits

Substantial genetic variation for fructo-oligosaccharides, quercetin, epigallocatechin gallate and epicatechin gallate, total and essential amino acids, carbohydrates, total soluble solids, trisulphinates and total antioxidant activity occurs among onion cultivars (Insani *et al.* 2016). The parameters *viz.*, bulb colour, firmness, number of scales, number of growing points, neck thickness, total soluble solids (TSS), pungency and antioxidants are the most important quality determinants in onion among the consumer (Brewster 2008; Goldman 2011. Dry matter, TSS and pungency are positively correlated and show moderate to high heritability, indicating the possibility of simultaneous improvement through selection. However, development of less pungent onion with high dry matter becomes critical (Galamarini *et al.*, 2001; Mallor *et al.,* 2011).

Galmarini *et al.* (2001) used the genetic map of BYG15-23 × AC43 to carry out mapping of loci for pungency, dry matter and TSS. One gene (acid invertase-API89) on chromosome 3 and another gene (phloem unloading sucrose transporter- API66) on chromosome 5, both being responsible for high TSS and dry matter accumulation was reported. Furthermore, the acid invertase gene also elevated pungency, which suggests a possible pleiotropic effect of the gene on bulb composition. Havey *et al.* (2004) conducted further QTL analysis in the same genetic map with extensive analysis of bulb carbohydrates and again reported significant effects of the acid invertase region of chromosome 3 on bulb sucrose content. Three loci each on chromosomes 3,5 and 8 have been identified in a population of *A. cepa* × *A. royeli,* regulating accumulation of non-structural carbohydrates like fructose, fructan, glucose and sucrose (McCallum *et al.,* 2006; Raines *et al.,* 2009), of which *Frc* locus on chromosome 8 is the major determinant for fructan content. This result was later confirmed by Yaguchi *et al.* (2008) by using *Allium fistulosum* and *A. cepa* var. *aggregatum* monosomic alien addition lines. Although two markers *viz.*, ACM033 and ACABE58 have been reported to be linked with the *Frc* locus on chromosome 8, but more tightly linked markers are urgently needed for marker-assisted selection.

Male sterility

Male sterility is the most important genetically controlled pollination control mechanism economizing the hybrid seed production in onion. Cytoplasmic-genetic male sterility (CGMS) system, owing to its ease of maintenance and restoration through the *Ms* locus, is preferred in onion over the CMS. The *Ms* locus codes for penta-trico-peptide repeat (PPR) proteins, leading to restoration of fertility.

The CGMS system has been reported in different cytoplasmic backgrounds of onion like CMS-S (Jones and Emsweller 1936), CMS-T (Berninger 1965) and CMS-T like or CMS-Y cytoplasm (Kim 2014). The fertility restoration of CMS-S cytoplasm gets restored by the fertility restorer, *Ms* locus (Jones and Clarke 1943). However, restoration of fertility in CMS-T cytoplasm is governed by three genes i.e., two complementary genes and an independent gene (Schweisguth 1973) while in CMS-T like cytoplasm, it is governed by a single nuclear gene (Kim and Kim 2019). Go¨kce *et al.* (2002) and Martin *et al.* (2005), carried out marker-assisted selection using a codominant and PCR-based marker. Manjunathgowda and Selvakumar (2021) validated PsaO marker for its co-dominance and tight linkage to restorer of fertility, *Ms* locus. Thus, the PsaO is suitable rapid identification of desirable recombinants with respect to male fertility while handling segregating generations. Saini et al. (2015) utilized 5'cob and *orfA50*1 markers, originally reported by Sato et al. (1998) and Engeleke et al. (2003), to distinguish between the male sterile and male fertile cytoplasm of accessions in three different populations. Further, upon testing of two markers *viz.*, OPT and PsaO-linked to *Ms* locus, *OPT* was proven better over the PsaO. Khar et al. (2022) used accD and MKFR markers for *cytotype* identification and AcPMS1 and AcSKP1 markers (Huo *et al.* 1015; Kim *et al.* 2015) to identify *Ms* locus in a diverse germplasm panel. While both accD and MKFR were equally potent for identification of cytoplasm, AcPMS1 was found more reliable to identify the *Ms* locus compared to AcSKP1. Manjunathagowda (2025) utilized two sets of PCR-based molecular markers linked to orf725, originally identified by Kim *et al.* (2009) and reported two short day and Indian accession *viz.* DOGR-MG-2 and DOGR-MG-70 carrying CMS-S cytoplasm.

CONCLUSION AND FUTURE PROSPECTS

Onion is an important vegetable cum spice crop with great impact on the economy across the globe. Though several attempts and significant progress have been made for the genetic improvement, the yield potential is many-a-times affected adversely due to the frequent occurrence of several biotic and abiotic stresses. Moreover, there is differences in the consumer appealing traits for specific end use. Thus, there is an urgent need to develop trait-specific varieties with multiple disease resistance, wider adaptability for varied agro-climatic conditions and suitability for various end use including processing into different products.

Keeping in view the large genome size of onion, there is an urgent need to develop more polymorphic and codominant markers to study genetic variation among the accessions. To meet the increasing demand, development of high-yielding varieties and hybrids in a short span can be achieved by through marker-assisted selection. For this, identification of tightly linked molecular markers and/or identification of candidate genes and functional markers within the gene(s) is urgently needed. Candidate gene association mapping for fructan content and bulb pungency is also required. Mainkar et al. (2023) standardized the genome editing protocol in onion and edited the *AcPDS* gene, paving the way for precise modification of other desirable genes. Keeping in view the dynamic and diverse market segments, less pungent and tearless onion need to be developed through genome editing, apart from development of multi-stress resistant varieties.

DECLARATION

The authors declare that they do not have any conflict of interest.

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