



REVIEW ARTICLE

Onion: Breeding and Genomics

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Abstract

Onion is a long-cultivated vegetable crop that originated in Central Asia. Almost everywhere in the world, onions are cultivated because of their culinary, nutritional, medicinal and health benefits. Using traditional breeding methods, breeders and farmers have been working to enhance onion yield for years. While it is currently difficult to meet growing customer demand and deal with unfavorable climate conditions. Due to its biennial life cycle, cross-pollination and inbreeding depression, it has been challenging to characterize significant traits. Consequently, the recently available onion genome sequence and the use of contemporary molecular breeding techniques will help researchers to overcome those challenges and speed up the development of the onion crop.

Keywords: Onion, *Allium cepa*, Genetic resources, Quality traits, Genomics and Molecular breeding.

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Introduction

Onion (*Allium cepa* L. $2n = 16$) is one of most important spice vegetables grown around the world in tropical, temperate and boreal regions. The economic value of onion is derived from its culinary importance around the world, therapeutic benefits with potentially good health impacts, such as anti-cancer, antibacterial actions and nutritional benefits (Griffith *et al.*, 2002; Galavi *et al.*, 2020; Gupta and Lawande, 2018). It is a highly appealing crop for exporting and earning foreign currency. In India, onions are grown under varied agro-climatic conditions and occupy an area of 1.62 million ha with the production of 26.64 million tonnes during 2020-21. Although India ranks first in area and production and contributes 20% world's production, its productivity is low (16.4 t/ha) as compared to world's productivity (18.4 t/ha) (FAOSTAT, 2023).

Onion is a biennial monocotyledonous crop belonging to the family *Alliaceae*. Several forms of *Alliums* with their wild relatives have been cultivated worldwide. Phylogenetically, *Allium vavilov* is the closest wild relative of onion whereas, *Allium asarense*, *Allium galanthum*, *Allium oschaninii* and *Allium pskemense* more distant (Araki *et al.*, 2010). While, based on meiotic data, *Allium roylei* is concluded to be a closer relative of *Allium cepa* than *Allium fistulosum* (Vries *et al.*, 1992). The cultivation of onions extended from Central Asia to the West through the Mediterranean region and into Northern Europe, then from Europe and North America to the Southern Hemisphere from Europe and Africa and into Asia. In India onion is grouped under short day and being cultivated throughout the year during *rabi*, *kharif*

and late *kharif* seasons in the north and eastern parts of the country which has revolutionized the onion production and marketing in the country. Being cultivated for the last 5000 years, this crop has adapted to varied climatic conditions. This has resulted in a wide range of cultivars and landraces that suit the diverse climatic conditions and consumer preferences (Brewster, 2008).

Several conventional breeding approaches had been used to improve yield, quality and resistance to grown in wide geographical range. Traditional assessment of genetic diversity based on morphological traits is influenced by the environment, leading to biased diversity estimation. However, the demand of onion is increasing day-by-day; therefore, there is a need to enhance onion breeding programme through the integrated use of advanced breeding techniques, genomics tools and available genome data (McCallum, 2007; Singh *et al.*, 2021a; Finkers *et al.*, 2021). Despite of high level of diversity in onion, the onion breeding progress has lag behind than other vegetable crops, this is primarily due to its biennial life cycle, severe inbreeding depression, out breeding, high level of heterozygosity, cross-pollinating nature, large genome size (16.3Gb), and infrequency of selection markers (Lee *et al.*, 2021; Sudha *et al.*, 2019). In order to improve onion breeding programs for both farmers and consumers and to strive ahead of these challenges, breeders need to focus to speed up onion breeding programme using available genetic variations for the improvement of genotypes for quality and yield traits, stress tolerance, and adaptability to adverse climatic conditions through the use of new insights and modern molecular tools (Khosa *et al.*, 2016). Need to focus on the preservation of onion landraces to use as a source of valuable traits for climate-resilient breeding (Enciso *et al.*, 2015; Walters *et al.*, 2018).

The main objective of onion breeding is the improvement of crop yield and productivity over a long period of time. Given the importance of onion and its genetic diversity, the main goals of the present study include breeding and genomics in onion study. In this review, we outline traditional breeding methods, modern genomic approaches, and progress in onion genomics and molecular genetics to improve onion production and addresses negative environmental influences on onion crop, as well as future prospects for improving onion yield and quality.

Genetic Resources and Diversity

The variation in the genetic resources from the wild germplasm, landraces, ecotypes and cultivated crops are important for breeding new varieties with desired traits. Onion genetic resources are conserved in gene banks namely, the ICAR-NBPGR in India and the National Plant Germplasm System (NPGS) in the United States. ICAR-DOGR, Pune has been recognized as active germplasm site for onion, a total of 1429 germplasm (Table 1) are maintained

Table 1: Status of onion germplasm collection and maintenance at ICAR-DOGR, Pune

S. No.	Onion types	Number of accessions
1	Onion (Dark Red)	325
2	Onion (Light Red)	518
3	Onion (White)	309
4	Onion (Yellow)	35
5	Onion (Rose Type)	9
6	Multiplier Onion	62
7	Exotic Onion	82
8	Wild species	89
	Total	1429

and characterized for desirable traits under field conditions. The genetic resources of *Allium* in India are potential sources of genes for widening the crop genetic base. There are several genomic resources available in onion, including Next-Generation Sequencing (NGS), which is a successful method to generate the genetic resources required for molecular study in onion.

Transcriptome sequencing and recently available genome sequences serve candidate genes and molecular markers for marker-assisted selection and molecular breeding approaches (Baldwin *et al.*, 2012b; Duangjit *et al.*, 2013; Lee *et al.* 2013; Kim *et al.*, 2014; Finkers *et al.*, 2021). These innovative sources and advanced tools have the potential to greatly accelerate the scope and pace of novel onion cultivar development when used in conjunction with current methods.

Despite the economic and medicinal value of wild *Alliums*, a limited number of germplasm accessions of wild species have been collected and conserved mainly due to difficult access to areas of occurrence. Information on species diversity distribution and utilization of wild *Allium* species to assess the value of Indian germplasm and prioritization for future collection and conservation programme (Gupta *et al.*, 2018; Gopal *et al.*, 2016). An increase in onion productivity can be attributed to the adoption of wild relatives in crop modification to boost crop tolerance to biotic and abiotic stress. Interspecific hybridization in the genus *Allium* has created new opportunities for advancement due to the introgression of candidate genes from *Allium roylei*, *Allium galanthum* and *Allium fistulosum* (Scholten *et al.* 2007; Vu *et al.*, 2012; Kunchge *et al.*, 2012; Gupta *et al.*, 2015).

Genetic diversity assessment of gene bank collections aids breeders, and farmers in selecting genotypes for breeding programme, avoiding deceptions in genotypes, and help them to grow new varieties with improved traits. However, in the present scenario of the genomic revolution, onion seems to be lagging far behind other crops, could be due to the biennial breeding cycle, cross-pollinated nature,

inbreeding depression and rarity of molecular markers which hampers the genetic improvement and diversity studies in commercially important onion. Previous studies reported variety of molecular markers for diversity analysis in onion as mentioned in Table 2 (Khosha *et al.*, 2014).

Numerous studies showed that Indian short-day germplasm is more diverse than other foreign germplasm; it may be a source of novel genes for onion breeding (McCallum *et al.* 2008, Khar *et al.* 2011, Baldwin *et al.* 2012a, Mallor *et al.* 2014, Gupta *et al.*, 2018). It would also be worthwhile to screen this material for resistance to different infections that may be used in breeding programs given the genetic variety of the short-day germplasm from Central Asia and India. The characterization of the genetic diversity of Indian onion accessions with the accessions sourced from exotic sources towards understanding the diversity pattern and determination of heterotic groups for heterosis breeding in future studies.

Breeding Objective

The improvement of onion crop has not attracted much attention of the breeders in India. Perhaps, because of biennial habit of the crop requiring a longer time for breeding and difficulties in attaining and maintaining genetic uniformity due to high degree of natural cross pollination and rapid inbreeding depression and biennial life cycle. Though a number of varieties have been developed in India, still there is enough scope to develop varieties to

tackle climate change. The following breeding objectives were necessary for further research in onion because of the issues and demand for onions throughout the world.

- Breeding for seasonal adaptability for year-round availability.
- Development of onion varieties free from doubles and bolters.
- Breeding for bulb quality traits like shape, size, color and firmness.
- Breeding for development of F₁ hybrids for uniformity, earliness and high yield.
- Breeding for enhance bulb storability.
- Breeding for processing qualities.
- Development of varieties suitable for export.
- Breeding for resistance to biotic and abiotic stresses.
- Improving onion through biotechnological approaches.
- Development of disease-resistant F₁ hybrids with superior quality bulbs.
- Development of haploids through conventional and advanced methods.
- Induction of double haploids for inbred development.
- Exploitation of heterosis for enhancing productivity and wider adaptability.

Varietal development

Till date eighty varieties and hybrids were developed using the traditional breeding method. Varietal development is presented in the Tables 3 and 4.

Genetic improvement through traditional breeding

Quality traits

The category of onion cultivars is mainly determined based on the bulb quality traits, DUS characteristics; bulb color, size and shape, TSS and pungency, dormancy and storage ability, firmness, quantity of scales, centerness (Goldman 2011, Gupta *et al.*, 2022). A number of traits comprise important genetic components and respond to selection. The chromosome assignment of different quality traits in onion have been presented in Table 5.

Bulb colour

One of the significant characteristics being addressed in breeding programs is the onion bulb color. Commercial onion bulbs come in a variety of colors, including red, white, yellow, golden, pink, and chartreuse. Six loci (*I, C, G, L, L2* and *R*) and their interaction regulate flavonoid levels resulting in a wide range of variations in onion bulb color. The studies demonstrated that *L* locus encodes anthocyanidin synthase and *R* locus encodes Dihydroflavonol 4-reductase in an anthocyanin biosynthesis pathway. Dominant alleles at the *R, L, or L2* loci produce red-colored bulbs, while the dominant allele at the *I* locus produces white-colored bulbs. Golden colored bulbs appeared when the dominant allele at the *G* loci (Kim *et al.*, 2005a, b; Khar *et al.*, 2008; Duangjit

Table 2: List of onion germplasm characterized using different molecular marker

S. No.	Type of germplasm	Type of marker	References
1	Cultivated and wild onion germplasm	RAPD	Ennequin <i>et al.</i> (1997), Tanikawa <i>et al.</i> (2002), Mousavizadeh <i>et al.</i> (2006), Sangeeta <i>et al.</i> (2006), Leite and Anthonisen (2009), Maniruzzaman <i>et al.</i> (2010), Sudha <i>et al.</i> (2019)
2	Onion inbreds	RFLP	Bark and Havey (1995)
3	Cultivated and wild onion germplasm	SSR	Jakse <i>et al.</i> (2005), McCallum <i>et al.</i> (2008), Mahajan <i>et al.</i> (2009), Nikhil and Jadhav (2017), Khar <i>et al.</i> (2011), Baldwin <i>et al.</i> (2012a), Mallor <i>et al.</i> (2014), Gupta <i>et al.</i> (2022), Singh <i>et al.</i> (2021a), Sudha <i>et al.</i> (2019)
4	Commercial cultivars	SNP	Jakse <i>et al.</i> (2005), Villano <i>et al.</i> (2019), Jo <i>et al.</i> (2017) Lee <i>et al.</i> (2021), Labate <i>et al.</i> (2020), Jeon <i>et al.</i> (2022)
5	Cultivated onion germplasm	ILP	Khade <i>et al.</i> (2022), Singh <i>et al.</i> (2021a)

Table 3: Onion varieties released through AICRP & AINRPOG and recommended for cultivation

S. No.	Name of Varieties	Special Feature	Institutes	Recommended zones and seasons	Year of Release
1	Punjab Selection	Red	PAU, Ludhiana	IV, VII & VIII	1975
2	Pusa Red	Red	IARI, New Delhi	IV, VII & VIII	1975
3	Pusa Ratnar	Red	IARI, New Delhi	IV & VI	1975
4	S-131	-	IARI, New Delhi	-	1977
5	N-257-9-1	White	Agril. Dept., MS	-	1985
6	N-2-4-1	Red	Agril. Dept., MS	-	1985
7	Line-102	-	IARI, New Delhi	I, IV, VI, VII	1987
8	Arka Kalyan	Red	IIHR, Bangalore	IV, VI, VII, VIII	1987
9	Arka Niketan	Red	IIHR, Bangalore	IV, VII, VIII	1987
10	Agrifound Dark Red	Dark Red	NHRDF, Nashik	IV	1987
11	VL-3	Red	VPKAS, Almora	I	1990
12	Agrifound Light Red	Light Red	NHRDF, Nashik	VI, VIII	1993
13	Punjab Red Round	Red	PAU, Ludhiana	IV	1993
14	PBR-5	Red	PAU, Ludhiana	VI	1997
15	L-28	Red	NHRDF, Nashik	IV & VII	2006
16	HOS-1	Red	HAU, Hissar	VI	2006
17	Bhima Raj	Red	ICAR-DOGR, Pune	VI	2008
18	Bhima Red	Red	ICAR-DOGR, Pune	VII for <i>rabi</i> & II, V & VI** for <i>kharif</i>	2009 & 2013
19	PKV White	White	PDKV, Akola	VI	2009
20	Phule Samartha (RHOR-S1)	Red	MPKV, Rahuri	VI, VIII	2009
21	Bhima Kiran	Red	ICAR-DOGR, Pune	III & VI*	2010
22	Line-355	Red	NHRDF, Nashik	III, IV & VI*	2010
23	Bhima Shakti	Medium Red	ICAR-DOGR, Pune	III, IV, V, VI*	2011
24	Bhima Shweta	White	ICAR-DOGR, Pune	III, V, VI* for <i>rabi</i> & IV, V, VI** for <i>kharif</i>	2011 & 2013
25	Sel-126	Brown	IARI, N. Delhi	III, IV, V*	2011
26	Bhima Super	Pinkish	ICAR-DOGR, Pune	II, IV, V & VI** for <i>kharif</i>	2013
27	Bhima Dark Red	Dark Red	ICAR-DOGR, Pune	II, IV, V & VI**	2013
28	Bhima Shubra	White	ICAR-DOGR, Pune	IV, V & VI** for <i>kharif</i>	2013
29	Bhima Safed	White	ICAR-DOGR, Pune	IV, V & VI** for <i>kharif</i>	2015
30	Bhima Light Red	Light Red	ICAR-DOGR, Pune	VI	2016
31	Sel. 153-1	-	IARI, New Delhi	II	2016
32	Col. 819	Red	NHRDF, Nashik	II	2016

Note: Zone I = Himachal Pradesh & U.P. Hills, (**Srinagar, Almora, Mukteshwar, Palampur, Ooty); Zone II = West Bengal & Assam, (**Jammu, Ludhiana, Delhi, Karnal, Hissar, Durgapura); Zone III = Sikkim, Meghalaya, Manipur, Nagaland, Mizoram, Tripura, Arunachal Pradesh and Andaman & Nicobar Islands, (*Delhi, UP, Haryana, Bihar and Punjab); Zone IV = Punjab, Tarai region of U.P. & Bihar, (*Rajasthan & Gujarat), (**Jabalpur, Raipur, Chiplima, Akola, Jhalawar); Zone V = Chhattisgarh, Orissa & Andhra Pradesh, (*MP, Chhattisgarh & Orissa), (**Junagadh, Nashik, Rahuri, Pune); Zone VI = Rajasthan, Gujarat, Haryana & Delhi, (*Maharashtra, Karnataka and Andhra Pradesh), (**Bagalkot, Bangalore, Coimbatore, Dharwad); Zone VII = Madhya Pradesh & Maharashtra, Zone VIII = Karnataka, Tamil Nadu & Kerala.

et al., 2014; Khandagale and Gawande, 2019; Jeon *et al.*, 2022). Bulb color phenotypes in segregating populations and several breeding lines were completely matched with *AcLAC12* genetic marker genotypes. The *DFR-A* gene, which determines the color of red bulbs, is inactive in all breeding lines of chartreuse plants, suggesting that chartreuse color results from the combined inactivation of the *AcLAC12* and *DFR-A* genes. According to linkage

maps, *AcLAC12* was located near the end of chromosome 7. Comparing chartreuse bulk to yellow bulk, transcription levels of structural genes that encode the enzymes involved in the anthocyanin pathway were generally lower (Seo *et al.* 2020; Jeon *et al.* 2022). This variation in bulb colors is caused by mutations in the structural and regulatory genes (transcription factor) in the anthocyanin and flavonoid pathways. Development of functional markers from these

Table 4: Onion varieties released by different research institutes in India

S. No.	Variety	Special feature	Recommended season	Organization	Year of release	
1	N-53	Red	<i>kharif</i>	Agriculture Department, Maharashtra	1975	
2	N-2-4-1	Red	<i>rabi</i> and late <i>kharif</i>		1985	
3	N-257-9-1	White	<i>rabi</i>		1985	
4	Baswant-780	Red	<i>kharif</i>	MPKV, Rahuri	1989	
5	Phule Safed	White	late <i>kharif</i> and <i>rabi</i>		1994	
6	Phule Suvarna	Yellow	<i>rabi</i> and late <i>kharif</i>		2001	
7	Phule Samarth	Red	late <i>kharif</i>		2006	
8	Pusa White Flat	White	<i>rabi</i>	IARI, New Delhi	1975	
9	Pusa White Round	White	<i>rabi</i>		1975	
10	Early Grano (Long Day)	Yellow	<i>rabi</i>		1975	
11	Brown Spanish (Long Day)	Brown	Hills		1975	
12	Pusa Red	Red	<i>rabi</i>		1975	
13	Pusa Ratnar	Red	<i>rabi</i>		1975	
14	Pusa Madhavi (Line-120)	Red	<i>rabi</i>		1987	
15	Selection 126	Brown	<i>rabi</i>		2012	
16	Arka Pragati	Red	<i>kharif</i> and <i>rabi</i>		IIHR, Bangalore	1984
17	Arka Niketan	Red	<i>rabi</i> and late <i>kharif</i>			1987
18	Arka Kalyan	Red	<i>kharif</i>	1987		
19	Arka Pitamber	Yellow	<i>rabi</i>	2006		
20	Arka Bindu	Red	<i>kharif</i> , late <i>kharif</i> and <i>rabi</i>	2006		
21	Arka Ujjwal (multiplier onion)	Red	<i>rabi</i>	2010		
22	Arka Swadista	White	<i>rabi</i>	2010		
23	Arka Vishwas (Rose onion)	Dark red	<i>kharif</i> and <i>rabi</i>	2011		
24	Arka Sona	Yellow	<i>rabi</i>	2011		
25	Arka Bhim (tri parental synthetic)	Red	<i>rabi</i>	2011		
26	Arka Akshay (tri-parental synthetic)	DarkRed	<i>rabi</i>	2011		
27	Arka Lalima (F ₁ hybrid)	Red	<i>kharif</i> and <i>rabi</i>		1998	
28	Arka Kirthiman (F ₁ hybrid)	Red	<i>kharif</i> and <i>rabi</i>		1998	
29	Arka Yojith	White	<i>rabi</i>		-	
30	Hissar-2	Red	<i>rabi</i>	HAU, Hissar	1976	
31	HOS-1	Red	<i>rabi</i>		2006	
32	Hissar Onion-3	Bronze	<i>rabi</i>		2010	
33	Hissar Onion-4	Rose Red	<i>rabi</i>		2016	
34	Agrifound Light Red	Red	<i>rabi</i> and late <i>kharif</i>	NHRDF, Nashik	1988	
35	Agrifound Dark Red	Red	<i>kharif</i>		1996	
36	NHRDF Red (L-28)	Red	<i>rabi</i>		2006	
37	NHRDF Red-2 (L-355)	Red	<i>rabi</i>		2012	
38	NHRDF Red -3 (L-625)	Light bronze	<i>rabi</i>		-	
39	NHRDF-Red-4 (L-744)	Dark red	<i>rabi</i>		-	
40	NHRDF Fursungi (L-819)	Red	<i>rabi</i>		-	
41	Agrifound Rose	Red	<i>Rabi</i>		1987	
42	Agrifound Red (Multiplier)	Red	<i>kharif</i> and <i>rabi</i>		1987	
43	Agrifound White	White	<i>rabi</i>		1994	

44	VL-67 (Long Day)	Red	Hills	VPKAS, Almora	1973
45	VL-3 (Long Day)	Red	Hills		1990
46	Udaipur 101	Red	<i>rabi</i>	RAU, Rajasthan	-
47	Udaipur 102	White	<i>rabi</i>		-
48	Udaipur 103	Red	<i>rabi</i>		-
49	PKV White	White	<i>rabi</i>	PDKV, Akola	2009
50	Gujarat White Onion (GWO)-1	White	<i>rabi</i>	GAU, Junagarh	2000
51	GJRO-11	Red	<i>rabi</i>		2016
52	GJWO-3	White	<i>rabi</i>		2016
53	Kalyanpur Red Round	Red	<i>rabi</i>	CSAUAT, Kanpur	1983
54	Punjab Selection	Red	<i>rabi</i>	PAU, Ludhiana	1973
55	Punjab Red Round	Red	<i>rabi</i>		1993
56	Punjab-48 (S-48)	White	<i>rabi</i>		1978
57	Punjab White	White	<i>rabi</i>		1998
58	Punjab Naroya (PBR-5)	Red	<i>rabi</i>		1997
59	CO-1 (Multiplier)	Red	<i>kharif and rabi</i>	TNAU, Coimbatore	1965
60	CO-2	Red	<i>kharif and rabi</i>		1978
61	CO-3	Red	<i>kharif and rabi</i>		1982
62	CO-4	Red	<i>kharif and rabi</i>		1984
63	CO-5	Pink	<i>kharif and rabi</i>		2001
64	MDU-1	Red	<i>rabi</i>		1982
65	CO-6	Pink	<i>kharif and rabi</i>		2020
66	Rajasthan Onion-1 (RO-1)	Red	<i>rabi</i>	RARS, Durgapura	2004
67	Arpita (RO-59)	Red	<i>rabi</i>		2005
68	RO-252	Red	<i>rabi</i>		2011
69	Bhima Super	Pink	<i>kharif, late kharif and rabi</i>	ICAR-DOGR, Pune	2013
70	Bhima Raj	Dark Red	<i>kharif and rabi</i>		2008
71	Bhima Red	Medium Red	<i>kharif and late kharif</i>		2009 & 2013
72	Bhima Shakti	Medium Red	Late <i>kharif and rabi</i>		2011
73	Bhima Kiran	Light Red	<i>rabi</i>		2010
74	Bhima Shweta	White	<i>kharif and rabi</i>		2011 & 2023
75	Bhima Shubhra	White	<i>kharif and late kharif</i>		2013
76	Bhima Dark Red	Dark Red	<i>kharif</i>		2013
77	Bhima Safed	White	<i>kharif</i>		2015
78	Bhima Light Red	Light Red	<i>rabi</i>		2016

candidate genes could be used in marker-aided selection and marker-assisted back cross-breeding for bulb color variations in onion (Masuzaki *et al.*, 2006; Khar *et al.*, 2008; Kim *et al.*, 2009; Park *et al.*, 2013; Duangjit *et al.*, 2014)

Size and shape

A wide range of variations are found in size from small to large, while bulb shapes vary from round to piriform, elongated and flat. Previous studies reported low level of heritability in shape and size in diameter and weight whereas, high heritability in height and shape and showed that bulb shape responds to selection but not size (Nakamura 1959; McCollum 1976; Dowker *et al.*, 1984; Dowker, 2018). High

genetic progress was reported for bulb weight (Lee *et al.*, 2020). The shape of the bulb is determined by several genes and heritability values that range from moderate to high (Jones and Mann, 1963; McCollum, 1976).

TSS and pungency

Being a tropical country, India has a distinct advantage because onions grown there have a high protein content, pungency and flavor that enhance processed goods as well. Today's processing business struggles with a lack of high TSS white onion types, irregular year-round supply, low seed supply, significant post-harvest losses, and greening of bulbs (Kulkarni, 2011; Mahajan *et al.*, 2019). The

Table 5: Different quality traits of onion and their chromosome assignments

S. No.	Traits	Chromosomes	Locus	References
1	Red bulb colour	4, 7	L L2 R	Kim <i>et al.</i> , 2004a, Kim <i>et al.</i> , 2005a, Khar <i>et al.</i> , 2008, Khandagale <i>et al.</i> , 2019, Khar <i>et al.</i> , 2008, Duangjit <i>et al.</i> , 2014, Havey <i>et al.</i> , 2004
2	White bulb colour	6	C	Khar <i>et al.</i> , 2008
3	Golden bulb colour	9	G	Kim <i>et al.</i> , 2005a and b, Khar <i>et al.</i> , 2008, Duangjit <i>et al.</i> , 2014
4	Bolting resistance	1	<i>AcBl1</i>	Baldwin <i>et al.</i> , 2014
5	Male-fertility restoration for S cytoplasm	2	<i>Ms</i>	Gokce <i>et al.</i> , 2002, Martin <i>et al.</i> , 2005, Khrustaleva <i>et al.</i> , 2016, Damon and Havey, 2014
6	Downy mildew resistance	3	<i>Dmr1</i>	Galmarini <i>et al.</i> , 2001, Havey <i>et al.</i> , 2004, McCallum <i>et al.</i> , 2007, Scholten <i>et al.</i> , 2007
7	Cuticular and epicuticular wax	2, 5		Damon and Havey (2014), Galmarini <i>et al.</i> , 2001, Raines <i>et al.</i> , 2009
8	Soluble carbohydrates	3, 4, 5, 6, 8	<i>Frc</i> , fructans 6-fructosyl transferase, 1-sucrose-sucrose fructosyltransferase and Sucrose transporter, and Acid invertase	McCallum <i>et al.</i> , 2006, Raines <i>et al.</i> , 2009, Fujishima <i>et al.</i> , 2005
9	Pungency, Tearness	3, 5, 6	Serine acetyl transferase, ATP sulfurylase (ATPS), Ferredoxin-Sulphite reductase), Lacrymatory factor synthase	McCallum <i>et al.</i> , 2006, Raines <i>et al.</i> , 2009, Masamura <i>et al.</i> , 2012

dehydration phenotype is characterized by pure white, globe-shaped bulbs with a narrow neck, a strong flavor and a high TSS. Within two to three years, short-day, high TSS open-pollinated cultivars that are suitable for *rabi* and late *kharif* seasons could be created (Mahajan and Gupta, 2015). It has been found that TSS and pungency are correlated and display excessive heritability, which permits simultaneous development through choice. However, the improvement of less pungency onions with longer storage life is challenging (Mallor *et al.*, 2011; Rao *et al.*, 2015). Onion bulbs accumulate non-structural carbohydrates, such as fructans, fructose, glucose and sucrose governed by three loci on chromosome 3, 5, and 8 (McCallum *et al.*, 2006; Raines *et al.*, 2009). *Frc* is a major locus on chromosome 8 responsible for differences in fructan content. Two enzymes 1-sucrose-sucrose fructosyltransferase and fructans 6-fructosyl transferase are involved in fructans biosynthesis mapped to chromosome 6 (Fujishima *et al.*, 2005). Sucrose transporter and acid invertase candidate genes involved in carbohydrate metabolism mapped to chromosomes 3 and 5. Pungency in onion is controlled by number of candidate genes (Serine acetyl transferase), *ATP sulfurylase* (ATPS), and Ferredoxin-Sulphite reductase. *ATP sulfurylase* (ATPS) and Ferredoxin-Sulphite reductase are closely linked on chromosome 3 and associated with pungency QTL, therefore mutation in either of them led to variations in the pungency (McCallum *et al.*, 2007). A lacrymatory factor synthase (LFS) is responsible for teariness in onion mapped to chromosome 5 and linked with

dry matter QTL (Masamura *et al.*, 2012). For both, fructans and pungency high dominance was recorded so use of MAS is ideal for onion breeding. The candidate gene association mapping for these traits might be productive in future.

Dormancy and storage ability

Dormancy is crucial for onions that are kept and sold for a long time. The storage ability is affected by curing conditions, storage temperature and incidence of pathogens (Ko *et al.*, 2002). The ratio of monosaccharides to disaccharide sucrose and the concentration of zeatin riboside were distinguishing characteristics between dormant and sprouting onion.

Firmness

It is an essential characteristic of dried bulb onions that are kept in storage for a long time. Dry onions' solid texture determines whether or not consumers will like them. Onions' dry matter content and texture both decline during storage, which decreases their market value (Islam *et al.*, 2018).

Quantity of scales

The onion bulb scales (both outer and inner) are organized corresponding to their chronological ages because, when an onion bulb reaches maturity, it has one to three dry skins made of scales that serve as a protective layer, prevents water loss and pathogen contamination, and preserve the quality of the bulb throughout storage (Maude *et al.*, 1984; Chope *et al.*, 2012; Galsurker *et al.*, 2017). Due to their functional and physiological differences, the outer and

Table 6: Different Biotic stresses and sources of resistance (Lawande and Gupta, 2015)

S. No.	Biotic stresses and causal organism	Source of resistance	Genes/QTLs	References
1	Purple blotch (<i>Alternaria porri</i> (Ellis) Ciferri)	Arka Kalyan is source for ApR1 gene Other resistant cultivars: IIHR 56-1 VL-67, Pusa Red, IIHR 25, N-2-4-1, Punjab Selection-3, and Pusa Ratnar	A single dominant gene, <i>ApR1</i> , determine resistant to purple blotch, Seven putatively linked ISSR and SSR markers flank the ApR1 gene, which may be useful in MAS.	Chand <i>et al.</i> , 2018, Dar <i>et al.</i> , 2020
2	<i>Stemphyllium</i> blight (<i>Stemphyllium vesicarium</i>)	Five lines of welsh onion (<i>A. fistulosum</i>) showed resistance to <i>Stemphyllium</i> blight and was reported to be under dominant gene control (Pathak <i>et al.</i> , 2001) Other resistant cultivars: IIHR IC-32176, 42900, 47954, 48001, 48575, 49121 and 48503, RO-1, Pusa Soumya, Red Creole 2	-	Pathak <i>et al.</i> , 2001, Sharma and Sain 2003, Behera <i>et al.</i> 2013, Dangi <i>et al.</i> 2019
3	Leaf blight (<i>Botrytis squamosa</i>)	<i>A. roylei</i>	A single dominant gene, <i>Bs₁</i> , resistant to leaf blight QTL for resistance identified on the chromosome 6	Vries <i>et al.</i> , 1992; Scholten <i>et al.</i> , 2016
4	Downey mildew (<i>Peronospora destructor</i> [Berk.] Casp.)	<i>A. roylei</i> Resistant inbred line No. 136	Two genes <i>Pd₁</i> and <i>Pd₂</i> determine Downey mildew resistance	Vries <i>et al.</i> , 1992
5	Fusarium basal rot	<i>A. fistulosum</i> another resistant cultivar (Poona Red, Patna Red, N-257-9-1. IIHR-141, Telagi Red, White Large, Bellari Red, IIHR-506 and Udaipur 1037	Steroidial saponins compound, alliospiroside A showed antagonistic report	Abdelrahman <i>et al.</i> , 2017
6	Anthracnose (Twister disease caused by <i>Colletotrichum</i> spp)	Moderate resistance: red onion DOGR-1666 and DOGR Hy-50		ICAR-DOGR 2015, 2017
7	Thrips (<i>Thrips tabaci</i>) transmit Iris yellow spot virus	N-2-4-1, Sel-104, Pusa Ratnar, Kalyanpur Red Round, Udaipur-103, White Persian and BDR	Cuticular and epicuticular wax depositions on onion leaves, Two loci on Chro 2 and 5 for thrips resistance	Silva <i>et al.</i> , 2015, Bag <i>et al.</i> 2014, Damon and Havey, 2014, Gupta <i>et al.</i> , 2020

inner scales make a good system to study how each reacts to abiotic stress.

Centerness

Single-centered bulbs have grown in importance for the fresh market and onion ring industries since multiple centres impair the efficiency of onion ring production. Previous studies showed that, it is a heritable onion feature that allows for the development of cultivars with a high percentage of single centres (Gamie *et al.*, 1995; Wall *et al.*, 1996; Cramer, 2006).

Biotic Stress Resistance

Onion bulbs and seed crops are susceptible to a number of bacterial, fungal, and viral diseases; among all fungal diseases, Anthracnose (Twister disease) is the one that causes the most issues for onions and affect the yield productions (Brewster, 2008; Dutta *et al.*, 2022). Some reports are available on partial tolerance to these diseases (Galvan *et al.* 2008; Anitha *et al.*, 2011; Kamal *et al.*, 2012; Taylor *et al.*,

2013; Bag *et al.* 2014; Kale and Ajjappalavara 2014; Kalman *et al.*, 2020). Insufficient disease resistance in onions prompted researchers to seek out wild-related species. In accordance with a study, (Scholten *et al.*, 2007), downy mildew resistance originating from *A. roylei* introgression into *A. cepa* through marker-assisted breeding demonstrated total resistance based on a single dominant gene. Kim *et al.*, (2021) developed the SCAR-OPAN1 and SNP-3 HRM markers that could be utilized in a breeding programme in order to reduce the ecological damage caused by the grey mold disease. The identification of prospective sources emanating from wild *Alliums*, or landraces for resistance, R-genes, as well as the application of revolutionary molecular breeding techniques are necessary to establish comprehensive resistance to these diseases. Onion thrips (*Thrips tabaci* L.), is a worldwide pest of onion, more serious when transmits the Iris yellow spot virus (Bag *et al.*, 2014). The most prevalent epicuticular wax is hentriacontanone-16, usually high in waxy leaves, followed by semi-glossy and glossy varieties which play an important

role in resistant to sucking insect pests (Diaz-Montano *et al.*, 2011; Bag *et al.*, 2014; Damon and Havey, 2014). Two loci on chromosomes 2 and 5 regulate the quantity of wax, and in order to change the types and amounts of epicuticular waxes, SNP markers associated with these loci are being found for marker-assisted breeding (Bag *et al.*, 2014; Damon and Havey, 2014). Genetic studies showed that thrips resistance is not heritable, so it would be gainful in family-based selection to boost genetic improvement (Hamilton *et al.* 1999). Previous studies also reported, Bhima Dark Red variety had the lowest thrips (15.89%) and purple leaf blotch (28.95%) infestation rates compared to the Agrifound Dark Red and N-53 variety (Gupta *et al.*, 2020; Hiremath and Mantur, 2018). Sources of resistance to disease and insect pests in onion as presented in Table 6.

Abiotic Stress Resistance

Abiotic stresses including cold, drought, heat, salt, heavy metal, UV-B stress, water logging and flooding etc. potentially restricts crop production and quality which becomes an international concern due to climate change (Ingram, 2011). The growth and production of the onion crop are negatively impacted by a number of cellular alterations brought on by the different abiotic stresses such as, drought, waterlogging, heat, flooding, salinity, cold and oxidative stress (Pelter *et al.*, 2004; Yiu *et al.*, 2009; Sta-Baba *et al.*, 2010). Drought stress has serious impact on onion production, in order to develop varieties resilient to drought, onion breeders focus on selecting effective germplasm (Gedam *et al.*, 2021). Central Asia is the hub of diversification for the *Allium* species and breeders' top priority is to create climate-smart cultivars and superclass onion that can withstand abiotic stresses (Khar *et al.*, 2022). Sources of resistance for different abiotic stresses have been presented in Table 7.

Molecular Breeding Approaches

Despite of high level of diversity available in onion, crop improvement is not at the pace of other crops (McCallum *et al.*, 2007; Varshney *et al.*, 2014). Presently, F₁ hybrids are predominate in regions where long-day onions are grown and open-pollinated varieties (OP) predominate in the short-day growing regions of Asia and Africa, both were contributed for a doubling of production in onion (Brewster, 2008). However, climate change, population pressure, biennial life cycle, inbreeding depression, high cost of seed production and time taking conventional breeding all these are posing serious threats to increasing onion production. To tackle these challenges onion improvement programme should be strengthened by strategic use of molecular tools to aid germplasm conservation, combining genome-assisted breeding along with conventional breeding tools, to enhance productivity, quality, adaptability, storage and resistance to biotic and abiotic stresses.

Marker Assisted Selection (MAS)

The use of molecular markers has been demonstrated in a variety of crop plants for accelerating genetic gains and shortening the breeding cycle (Varshney *et al.*, 2014), onion being one of them (McCallum, 2007). Marker-assisted selection of male sterile and maintainer lines in onion can accelerate the breeding process (Havey, 2013). Several molecular markers have been developed for differentiating male sterile (S and T) and male fertile (N) cytoplasm (Cho *et al.*, 2006; Kim *et al.*, 2008; Kohn *et al.*, 2013). Many studies have identified markers tightly linked with fertility restoration locus *Ms*, to assist in marker assisted selection and developing new maintainer lines in onion (Bang *et al.*, 2013; Yang *et al.*, 2013; Havey, 2013; Park *et al.*, 2013; Kim *et al.*, 2014; Huo *et al.*, 2015; Kim *et al.*, 2015a). *AcPMS1* gene found to be most probable candidate for regulating fertility restoration in onion exhibiting high linkage disequilibrium with *Ms* loci in different populations which could prove useful for marker aided selection of maintainer lines (Kim *et al.*, 2015a). High dominance was observed for pungency and fructans content in onion, so making the use of MAS ideal for onion breeding to avoid selfing (McCallum *et al.*, 2007). Functional markers have been developed for *DFR* and *ANS* candidate genes, which could be used in MAS for bulb colour (Park et 2013, Duangjit *et al.*, 2014). Introgression of Downey mildew resistance from a wild *Allium*, *A. roylei* into *A. cepa* has an important example of MAS in onion allowing more rapid development of resistant cultivars (Scholten *et al.*, 2007). Although different traits have been mapped on onion genetic maps, identification of more tightly linked markers are needed for MAS. Different trait loci and associated markers for marker-assisted selection have been displayed in Table 8.

Marker-Assisted Back Cross Breeding (MABC)

It is a straightforward type of MAS to develop varieties rapidly that are impossible to produce through traditional breeding methods. It entails the discovery and selection of key candidate genes in the inferior source and introgression into an elite cultivar with retaining the essential characteristics of recurrent parent, i.e., well suited to the environment (Collard and Mackill, 2008). MABC can also be employed to produce near-isogenic lines by reducing linkage drag and offering precision introgression of specific genes for in-depth characterization of the QTLs. Through MABC, high-yield, superior-quality, and stress-tolerant onion varieties can be developed within a short period of time.

Genome-wide association studies (GWAS)

It is the robust method than QTL mapping to detect quantitative trait loci (QTLs) associated with target traits by looking at marker-trait interactions (Sukumaran *et al.*, 2015). Genome-wide association studies have been shown to be

Table 7: Different Abiotic stresses and sources of resistance

S. No.	Abiotic stresses	Source of tolerance	References
1	Drought	Acc. 1656, Acc. 1658, W-009, and W-085, Breeding lines U12, U47, U49 and commercial cultivar K52	Gedam <i>et al.</i> , 2021
2	Salinity	Ac Bog 409, Ac Bog 414, Ac Bog 424, Ac Bog 430, Ac Bog 417, Ac Bog 419, Ac Bog 420, Ac Bog 422, and Ac Bog 425), POS35, NHRDF Red (L-28), GWO 1, POS36, NHRDF Red-4 (L-744), POS37, and POS38, Breeding lines U12, U47, U49 and commercial cultivar K52	Gokce, 2021, Alam <i>et al.</i> , 2023, Sanwal <i>et al.</i> , 2022
3	Water logging	Acc. 1666, Acc. 1622, W-355, W-208, KH-M-2 and RGP-5 DOGR-1666 and DOGR Hy-50	Gedam <i>et al.</i> , 2022, ICAR-DOGR 2015, 2017
4	Heat	Genes in the outer scales, POD and CYP450, PLA2 and LOX1, XTH, PME1, and AO upregulated on Heat stress	Wang <i>et al.</i> , 2013, Galsurker <i>et al.</i> , 2018

an effective method for identifying various traits namely, stress tolerance, virulence factors and antibiotic resistance (Farhat *et al.*, 2013; Sheppard *et al.*, 2013; Chewapreecha *et al.*, 2014; Hall, 2014; Laabei *et al.*, 2014; Holt *et al.*, 2015; Desjardins *et al.*, 2016; Earle *et al.*, 2016; Agarwal *et al.*, 2021). Understanding the tolerance mechanism or genetics behind quality traits and identifying loci mediating these characteristics is important for any breeding research for the enhancement of crop improvement. GWAS is crucial for *Allium* genetics research or in future breeding programmes to dissect and identify the function of genes responsible for the targeted traits in shaping genetic diversity for yield and bulb quality in onions.

Allele mining

Three methods of allele mining, TILLING (Targeted Induced Local Lesions in Genomes)/Eco-tilling, next-generation sequencing, and association mapping, help to find relevant

alleles influencing important phenotypes among the large genetic diversity reservoirs (Reddy *et al.*, 2022; Kumar *et al.*, 2016; Kumari *et al.*, 2018). Finkers *et al.*, (2021) reported the recently sequenced onion genome, which brings new opportunities to enhance onion production and quality improvement in *Alliums*. In order to effectively exploit this genomic information for the development of new cultivars, novel and superior alleles of agronomically important traits, must be isolated from wild and landrace gene pools. It aids in the tracking of allele evolution, the discovery of novel haplotypes, and the creation of allele-specific markers for use in marker-aided selection.

Genetic Transformation/Genetic Engineering

Controlling climate change, enhancing quality traits and yield production, regulating metabolic pathways, and developing resilience to biotic and abiotic stresses have all been made possible by genetic engineering. Despite the fact

Table 8: Details of various traits and linked marker in onion for MAS

S. No.	Traits	Gene(s)/Locus	Marker name	References
1	Fructan content	Frc	ACM033 and ACABE58	Galamarini <i>et al.</i> 2001, Havey <i>et al.</i> 2004, McCallum <i>et al.</i> 2006, Raines <i>et al.</i> 2009
2	Male sterility related	Ms (male sterility restoration locus)	PsaO, jnurf20, AcPMS1 and AcSKP1, jnurf13, 5`cob: orfA501 for N, S and T cytoplasm, cytotype: accD, and MKFR	Manjunathagowda and Selvakumar, 2021, Khar <i>et al.</i> , 2022, Eidlin <i>et al.</i> , 2021
3	Bolting, Vernalization	AcBl1, AcVRN1 gene		Baldwin <i>et al.</i> , 2014, Khosa, 2018
4	Downy mildew resistance	<i>Pd gene</i>	DMR1 marker	Eidlin <i>et al.</i> , 2021, Kim <i>et al.</i> , 2015
5	Botrytis leaf blight	<i>Bs1</i>	RF-SNP markers, onion-SNP markers	Scholten <i>et al.</i> , 2016
6	Purple blotch	<i>ApR1</i>	KASP SNP marker ApRsnip14, ApRsnip23, SSR marker, AcSSR7, STS marker ApR-450	Sahoo <i>et al.</i> , 2023
7	Pungency	lachrymatory factor, alliinase gene	Plastidic ferredoxin-sulfite reductase (SiR) and plastidic ATP sulfurylase (ATPS) closely linked on chromosome 3, AFLP marker	McCallum <i>et al.</i> , 2007, Heusden <i>et al.</i> , 2000
8	Bulb Colour	Pink-P, Red- L, L2, R, White-C, Gold-G	Anthocyanidin synthase, Chalcone isomerase, Dihydroflavonol 4-reductase	Kim <i>et al.</i> , 2005a and b, Khar <i>et al.</i> , 2008, Duangjit <i>et al.</i> , 2014, Kim <i>et al.</i> , 2004a, Khandagale <i>et al.</i> , 2019, Havey <i>et al.</i> , 2004

that onion is a monocot crop, many studies have shown that genetic transformation using an *Agrobacterium*-mediated methodology is successful (Eady *et al.*, 2003; Zheng *et al.*, 2001; Aswath *et al.*, 2006; Manape *et al.*, 2022). A variety of biotechnology methods can be used to improve onion crops with the aid of this method, including the establishment of resistance against the damaging insect pest thrips, the fungus anthracnose, and the enhancement of qualitative and quantitative traits. Successful genetic transformation in onions opens new and alternative avenues for conventional breeding.

Gene Pyramiding

The pyramiding of candidate genes from multiple parents into a single genotype to provides better and durable expression in crops. This approach is broadly used for combining multiple biotic stress resistance genes for specific races of a pathogen or insect to develop durable resistance. It aids in crop improvement programmes and shortens breeding duration. MAS-based gene pyramiding could facilitate in pyramiding of genes effectively into a single genetic background (Joshi and Nayak, 2010).

RNAi technology

The most popular genetic engineering method, RNAi, is employed to silence particular genes for crop improvement (Saurabh *et al.*, 2014). By disrupting the lachrymatory factor synthase gene, which is responsible for generating tears with their distinct flavor and high nutritional content, tearless onions may be developed. A previous work (Eady *et al.*, 2008) showed that RNAi-mediated inhibition of *LFS* inhibited the *Lacrymatory factor synthase* gene and produced tearless onion. The development of male sterile lines in various crops is produced through RNAi-mediated suppression of a number of genes, including MutS homolog 1 (*MSH1*), S-adenosylmethionine decarboxylase (*SAMDC*), and sucrose transporter (*CsSUT1*); a similar study may be possible to develop male sterile lines in onion for hybridization. RNA silencing has become critical in inducing resistance against viruses in plants and provides a technical platform for creating novel antiviral strategies in the resilience breeding of onions. This approach will help in combating viruses in plants for future breeding programs.

Genome Editing

CRISPR/cas9 is a method of choice for precise gene editing which results in knockouts of gene expression in a variety of crop plants (Voytas and Gao, 2014). It permits precise modifications to the endogenous gene by allowing DNA sequence insertions, deletions, and substitutions at predetermined locations (Barrangou and Doudna, 2016). With the help of this technology, it may be possible to introduce value-added features into inbred lines or cultivars already in use and to shorten the time required to select and market novel onion phenotypes (Schiml *et al.*, 2016). This

approach could be applied to onions to develop tearless onions, induce haploidy, generate male sterile lines, and modify quality features. Recently, two innovative rapid-breeding approaches, IMGE (haploid-inducer mediated genome editing) and Hi-edit (haploid induction-edit), which combine haploid induction with CRISPR/Cas9-mediated genome editing was used to introduce desirable traits into elite inbred lines within two generations, avoiding the time-consuming crossing and back-crossing processes (Kelliher *et al.*, 2019). To have a successful impact on agricultural production under environmental stresses, more efforts are required to enhance and improve the CRISPR/Cas9 technology to produce easy, approachable, and accessible methods for researchers. In a recent breakthrough, Mainkar *et al.* (2023) achieved a milestone by successfully establishing a CRISPR/Cas9-mediated genome editing protocol in onions, showcasing the editing of the *AcPDS* gene. This pioneering study is poised to catalyze both basic and applied research on onions, providing crucial momentum for future investigations in the field.

Future prospects

Identification of polymorphic co-dominant markers

In the future, onion breeders will need to concentrate heavily on finding new polymorphic co-dominant molecular markers (SSR, SNPs) for genetic variation.

Development of day-length insensitive onion

The genetic control of day-length responses could be modified in onion for the development of day-length insensitive onion by employing knowledge of similar genetic control system in *Arabidopsis* (Lee *et al.*, 2013; Manoharan *et al.*, 2016; Mahajan and Gupta, 2016). This would allow for easier crossing among diverse germplasm, providing unique genetic variation and enabling the production of the same cultivars across latitudes.

Induction of haploid/double haploids

Through conventional breeding and in vitro development of gametophytic embryos, attempts to develop homozygous lines of onion in a short amount of time have failed (Jakse and Bohanec, 2003; Fayos *et al.*, 2015; Britt and Kuppu, 2016; Khan *et al.*, 2020). Contrarily, the haploid induction method using *CENH3* (centromere histone 3 variant) has been demonstrated in a number of plant species, including *Arabidopsis*, maize, wheat, and cotton (Ravi and Chan, 2010; Kuppu *et al.*, 2015; Karimi-Ashtiyani *et al.*, 2015; Kelliher *et al.*, 2016; Gao *et al.*, 2020; Lv *et al.*, 2020). Therefore, by employing innovative molecular methods like RNAi or genome editing, it may be possible to generate *CENH3*-mediated haploidy in onions, hastening the generation of novel types. Further, from haploid lines, double haploid could be developed and used as a cultivar which reduces the time for varietal development.

Development of CMS line

Cross-pollinating nature and huge inbreeding depression harden inbred lines development in onion, whereas, development of CMS lines through genome editing or RNAi mediated could be possible. Previous, research demonstrated that male sterility was triggered by downregulating some potential genes in various crops, including *SAMDC* (Cheng *et al.*, 2022), *CsSUT1* (Sun *et al.*, 2019), *MSH1* (Zhao *et al.*, 2016), *AcMSH1* (Mainkar *et al.*, 2023), and *CsHT1* (Cheng *et al.*, 2015). In order to develop male sterile lines in *Alliums*, this gene would either be knocked down or eliminated in onions.

Research on adaptability and stability of genotypes

In India onion crop is grown round the year, during *rabi*, *kharif* and late *kharif* seasons, most of the genotypes are available for *rabi* season, however limited genotypes are available for *kharif* and late *kharif* season. Therefore, in the future need to focus on developing varieties suitable for *kharif* and late *kharif* season, this will help to produce onion throughout the year and reduce the scarcity of onion.

Development of low pungency and tearless onion

The development of the tearless onion with higher sulfur compounds that have health advantages, could be facilitated by genetic manipulation of genes related to pungency and the lachrymatory factor by genome editing or RNAi techniques.

Need to focus on the development of stress resistance genotypes

Increased incidence of adverse environmental conditions i.e drought, flooding, salinity and highly damaging insects i.e, thrips and serious diseases i.e Anthracnose, damping off, *Stemphylium* blight leads to significant decrease in growth and productivity of onion crop. Genetic manipulation of genes associated with resistance could be used for crop improvement.

Research on herbicide tolerant crop

Onion is a poor competitor of weed basically at the seedling stage of crop, which affect the crop yield, so the development of herbicide tolerant crop will help to reduce the crop losses.

Bolting resistance onion

Bolting is essential for seed production while it is an undesirable trait for bulb production which directly affect the yield (Gupta *et al.*, 2018), so the development of resistant for bolting through manipulation of genes involved in bolting conditions.

Developments of F₁ Hybrids of Onion

Gupta *et al.* (2019) highlight the critical importance of onion crop hybrid development, emphasizing advancements in uniformity, disease resistance, and adaptability. The focus

extends to efficient seed production and catering to market preferences, including unique colours and shapes, in the ongoing development of onion hybrids.

Focus on reduction of generation time

Every onion breeding programme wants to reduce the biennial generation time to an annual cycle. In long day onions, research on breaking bulb dormancy and ensuring proper vernalization has resulted in an annual generation time while still making selection progress. However, there is need to focus for the reduction of generation time in Indian short onions.

Development of waxy/glossy onion

The onion leaf compositions of cuticular and epicuticular wax have been associated with lower onion thrips and lower onion thrips associated with less Iris yellow spot disease symptoms. Waxy/glossy onion have been developed that exhibit less disease symptoms when challenged with onion thrips and IYSV.

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सारांश

प्याज, एक लंबे समय से खेती की जाने वाली सब्जी की फसल है जिसकी उत्पत्ति मध्य एशिया में हुई। दुनिया में लगभग हर जगह, प्याज की खेती उनके पाक, पोषण, औषधीय और स्वास्थ्य लाभों के कारण की जाती है। पारंपरिक प्रजनन विधियों का उपयोग करते हुए प्रजनक और किसान वर्षों से प्याज की उपज बढ़ाने के लिए प्रयास कर रहे हैं। हालांकि मौजूदा समय में ग्राहकों की बढ़ती मांग को पूरा करना और प्रतिकूल जलवायु परिस्थितियों से निपटना मुश्किल है। अपने द्विवार्षिक जीवन चक्र, पर-परागण और अंतः प्रजनन ह्रास के कारण, महत्वपूर्ण लक्षणों को चिह्नित करना चुनौतीपूर्ण रहा है। नतीजतन, हाल ही में उपलब्ध प्याज जीनोम अनुक्रम और समकालीन आणविक प्रजनन तकनीकों के उपयोग से शोधकर्ताओं को उन चुनौतियों से उबरने और प्याज की फसल के विकास को गति देने में मदद मिलेगी।