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BREEDING STRATEGIES FOR BIOTIC AND ABIOTIC STRESS RESISTANCE IN TURMERIC

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ABSTRACT

Turmeric (*Curcuma longa* L.) is a high-value, clonally propagated spice and medicinal crop whose productivity and quality are constrained by major biotic stresses such as rhizome rot, foliar diseases, bacterial wilt and nematodes, as well as abiotic stresses including drought, salinity and heat. Genetic improvement through conventional recombination breeding is limited because cultivated turmeric is predominantly triploid, shows poor sexual fertility and is propagated vegetatively. Recent advances in genome sequencing, transcriptomics, miRNA profiling and molecular marker development have created new opportunities for resistance breeding and stress tolerance improvement in turmeric. This review critically examines breeding constraints, stress biology, screening methodologies and integrated improvement strategies for developing biotic- and abiotic-stress-resilient turmeric cultivars.

Keywords : Turmeric, Biotic and Abiotic stress, Resistance.

Introduction

Turmeric (*Curcuma longa* L.) is a high-value, clonally propagated spice and medicinal crop whose productivity and quality are constrained by major biotic stresses such as rhizome rot, foliar diseases, bacterial wilt and nematodes, as well as abiotic stresses including drought, salinity and heat (Ravindran *et al.*, 2007; Nayak *et al.*, 2013). Genetic improvement through conventional recombination breeding is limited because cultivated turmeric is predominantly triploid, shows poor sexual fertility and is propagated vegetatively (Sasikumar, 2005; Swapna & Sabu, 2017). Recent advances in genome sequencing, transcriptomics, miRNA profiling and molecular marker development have created new opportunities for resistance breeding and stress tolerance improvement in turmeric (Prasath *et al.*, 2018; Das *et*

al., 2019; Kumar *et al.*, 2020). This review critically examines breeding constraints, stress biology, screening methodologies and integrated improvement strategies for developing biotic- and abiotic-stress-resilient turmeric cultivars.

Recent advances in genomics, molecular markers, tissue culture and stress physiology have opened new opportunities for turmeric improvement (Sasikumar, 2005; Chakraborty *et al.*, 2021). Genome sequencing, transcriptomic analyses and marker systems now support precise clonal selection, mutation breeding, somaclonal variation and emerging genomics-assisted approaches (Li *et al.*, 2021; Santhi *et al.*, 2016; Yin *et al.*, 2022; Sahoo *et al.*, 2011). These advanced breeding strategies, integrated with robust stress phenotyping and clean planting material systems, offer promising avenues for developing turmeric varieties

with improved resistance to biotic and abiotic stresses while maintaining high yield and quality (Varshney *et al.*, 2005; Heffner *et al.*, 2009; Bharti *et al.*, 2023).

Breeding Strategies

Marker-Assisted Selection (MAS) in Turmeric:

Marker-assisted selection has emerged as a powerful tool for turmeric improvement, particularly due to its clonal mode of propagation. In turmeric, MAS is often referred to as marker-assisted clonal selection (MACS), where elite clones are selected based on molecular markers linked to desirable traits. This approach enables early and accurate selection of stress-tolerant genotypes without relying solely on phenotypic screening, which is often influenced by environmental conditions (Collard and Mackill, 2008).

Molecular markers such as simple sequence repeats (SSR), single nucleotide polymorphisms (SNP), and expressed sequence tag-based SSRs (EST-SSR) have been widely used in turmeric for genetic diversity analysis and trait association studies (Sahoo *et al.*, 2011). SSR markers are highly polymorphic and useful for germplasm characterization, while SNP markers provide high-resolution mapping and are suitable for genome-wide studies. EST-SSR markers are derived from expressed genes and are directly associated with functional traits, particularly stress responses (Sahoo *et al.*, 2011).

Resistance to biotic stresses in turmeric is associated with genes such as nucleotide-binding site-leucine-rich repeat (NBS-LRR) genes, pathogenesis-related proteins, and enzymes like chitinases and glucanases. Similarly, abiotic stress tolerance involves genes such as DREB, heat shock proteins, and ion transporters that regulate osmotic balance and stress signaling (Chakraborty *et al.*, 2021). Association mapping has been effectively used in turmeric to identify marker-trait relationships, as it does not require segregating populations and utilizes natural genetic variation (Varshney *et al.*, 2005).

Genomic Sequencing and Functional Genomics

Genomic sequencing has played a crucial role in advancing turmeric research by providing insights into genome structure and gene function. The draft genome of turmeric has revealed genes involved in curcumin biosynthesis, stress tolerance, and secondary metabolism (Chakraborty *et al.*, 2021). The genome is complex due to its triploid nature, high heterozygosity, and repetitive sequences, which pose challenges for assembly and analysis.

Whole genome sequencing has enabled the identification of important gene families such as NBS-

LRR, receptor-like kinases, and transcription factors including WRKY, MYB, and NAC, which are involved in stress responses (Chakraborty *et al.*, 2021; Bolger *et al.*, 2014). Functional genomics approaches, including gene annotation and expression studies, have further enhanced our understanding of these genes and their roles in plant defense mechanisms (Michael and VanBuren, 2020; Wang *et al.*, 2009). High-throughput sequencing techniques such as genotyping-by-sequencing (GBS) and re-sequencing have facilitated the discovery of genome-wide SNPs, which serve as valuable markers for genetic analysis and breeding (Varshney *et al.*, 2005; Elshire *et al.*, 2011).

These genomic resources are essential for developing advanced breeding strategies in turmeric (Heffner *et al.*, 2009; Yin *et al.*, 2022). High-throughput sequencing techniques such as genotyping-by-sequencing (GBS) and re-sequencing have facilitated the discovery of genome-wide SNPs, which serve as valuable markers for genetic analysis and breeding (Varshney *et al.*, 2005). These genomic resources are essential for developing advanced breeding strategies in turmeric.

Transcriptomics in Stress Resistance

Transcriptomics, particularly RNA sequencing (RNA-seq), is a powerful tool for studying gene expression under stress conditions. In turmeric, transcriptome analysis under *Pythium aphanidermatum* infection has revealed the upregulation of defense-related genes, including those involved in the phenylpropanoid pathway, which contributes to lignin biosynthesis and strengthens plant cell walls (Shetty *et al.*, 2016). Additionally, genes encoding pathogenesis-related proteins, chitinases, and antioxidant enzymes are highly expressed in resistant genotypes.

Transcription factors such as WRKY, MYB, NAC, and bZIP play a crucial role in regulating these stress responses by controlling the expression of downstream genes (Shetty *et al.*, 2016). Under abiotic stress conditions such as drought and salinity, transcriptomic studies have identified genes involved in osmotic adjustment, ion transport, and stress signaling pathways, including those regulated by abscisic acid (ABA), jasmonic acid (JA), and salicylic acid (SA) (Singh *et al.*, 2021). These findings provide valuable candidate genes for improving stress tolerance through molecular breeding.

Genome-Assisted Breeding and Genomic Selection

Genome-assisted breeding integrates genomic information with breeding programs to enhance selection efficiency (Varshney *et al.*, 2005; Collard and Mackill, 2008). The identification of genes and

quantitative trait loci associated with stress tolerance allows the development of molecular markers for selection (Varshney *et al.*, 2005; Xu and Crouch, 2008). Genome-wide association studies (GWAS) have been used to identify genomic regions linked to important traits in turmeric (Korte and Farlow, 2013; Chakraborty *et al.*, 2021). Genomic selection is an advanced breeding approach that uses genome-wide marker data to predict the performance of genotypes (Heffner *et al.*, 2009; Crossa *et al.*, 2017). This method is particularly useful in turmeric, where phenotyping is time-consuming and influenced by environmental factors (Heffner *et al.*, 2009; Varshney *et al.*, 2021). By combining genomic and phenotypic data, genomic selection enables rapid identification of superior clones with improved stress tolerance (Crossa *et al.*, 2017; Heffner *et al.*, 2009).

Genome Editing in Turmeric

In turmeric, genome editing can be used to enhance resistance to biotic and abiotic stresses by targeting genes involved in stress responses (Jinek *et al.*, 2012). For example, editing susceptibility genes can improve resistance to pathogens, while modifying genes involved in stress signaling pathways can enhance tolerance to drought and salinity.

However, the application of genome editing in turmeric is still limited due to challenges such as inefficient transformation systems and difficulties in plant regeneration. Advances in tissue culture techniques and gene delivery methods are expected to facilitate the adoption of genome editing in turmeric breeding (Chakraborty *et al.*, 2021).

Microbiome-Assisted Breeding

Microbiome-assisted breeding is an emerging approach that focuses on the use of beneficial microorganisms to enhance plant stress tolerance. In turmeric, the rhizosphere microbiome plays a critical role in plant health by suppressing pathogens and improving nutrient uptake. Beneficial microbes such as *Pseudomonas* and *Bacillus* species can induce systemic resistance and produce antimicrobial compounds that protect plants from diseases (Bharti *et al.*, 2023).

These microorganisms also enhance abiotic stress tolerance by improving water use efficiency, reducing oxidative stress, and modulating plant hormone levels (Compant *et al.*, 2019; Yang *et al.*, 2009). Recent studies suggest that plant genotypes differ in their ability to recruit beneficial microbiomes, indicating that microbiome interactions can be incorporated into breeding strategies (Bharti *et al.*, 2023; Berendsen *et al.*, 2012). Integrating microbiome-assisted approaches with genomic and transcriptomic data can further

enhance stress resilience in turmeric (Trivedi *et al.*, 2020; Compant *et al.*, 2019).



Fig. 1 : Graphical abstract for Biotic and Abiotic stress resistance breeding strategies in turmeric

Biotic Stress Rhizome rot and root rot

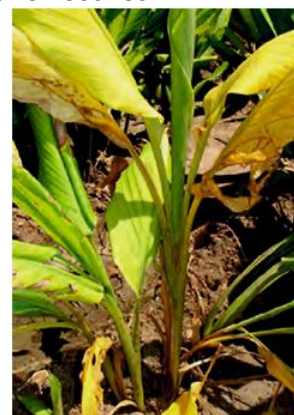


Fig. 2 : Rhizome rot

Pythium aphanidermatum, *P. graminicolum*, *P. myriotylum*, Association of *Pythium* sp. and *Fusarium* sp. This is an important disease prevalent in all turmeric growing area.

The disease was first reported from South India viz., Krishna district of Andhra Pradesh, Tiruchirappalli and Coimbatore of Tamil Nadu. The disease appears in patches in the field. In case of severe attack, yield is reduced considerably. Losses due to these of 50 percent and above have been reported in some parts of Telengana areas (Rao and Rao, 1988)

Symptoms: The infected plants initially show yellowing of leaves starting from the lower leaves, which gradually spreads to the upper regions of the plant (Rao, 1995; Ravindran *et al.*, 2007). The collar region of the pseudostem becomes soft and water-soaked, ultimately leading to collapse of the plant

clumps (Rao, 1995; Rathaiiah, 1982). The affected pseudostems can be easily pulled out, and the infected tillers topple over due to rotting at the basal region (Nair, 1994; Rao *et al.*, 1992). The infection spreads from the roots to the rhizomes, resulting in soft rot, where the affected rhizomes become soft to touch (Rathaiiah, 1982; Ravindran *et al.*, 2007). Infection is also evident at the tips of rhizomes, which exhibit varying shades of brown in contrast to the bright orange-yellow colour of healthy turmeric rhizomes (Rao, 1995; Dohroo, 1982).

Strategies:

- Developing easy, rapid and reliable molecular markers to identify new turmeric germplasm that could be used as a source of resistance to *Pythium aphanidermatum* is an important strategy for rhizome rot management (Kar *et al.*, 2014; Sahoo *et al.*, 2011).
- Bulk segregant analysis using pooled DNA from resistant and susceptible genotypes with 40 inter-simple sequence repeat (ISSR) markers resulted in the isolation of a putative resistance-specific marker, CIRSM (Kar *et al.*, 2014).
- The resistance-specific fragment was further converted into a sequence-tagged site (STS) marker, ClSTS, which successfully amplified a 720 bp fragment in resistant turmeric genotypes but not in susceptible plants (Kar *et al.*, 2014; Nayak *et al.*, 2005).
- Southern blot analysis confirmed that the marker represented a single-copy locus associated with resistant genotypes (Kar *et al.*, 2014).

Varieties:

- Elite turmeric cultivars, PCT-18 (Suvarna), PCT-13 (Suguna), and PCT-14 (Sudarsana) are found to be field tolerant to rhizome and root rot.
- Turmeric Cv. Shillong, a traditional cultivar from Assam, was reported to be resistant to *Pythium myriotylum* (Rathaiiah *et al.*, 1982)
- Dhindigam, Sonia and Kasturi (Short duration), Prathibha, Prasangali, KTS-9 (Medium)- Ranga, Salem, Salem-2, Wagon, PTS-12 are reported as resistant (Rao *et al.*, 1992 and Nandini *et al.* 2018)

Colletotrichum leaf spot:

Casual organism: *Colletotrichum capsici*, *Vermicularia curcume*, *V. capsici*, *C. curcuma*

The disease is more destructive and prevalent in majority of turmeric growing areas of Tamil Nadu viz., Coimbatore, Vellore, Thiruvannamalai, Salem and

Trichy districts. This was first recorded in Coimbatore district of erstwhile Madras State in 1917. (Mc rae, 1917)



Leaf spot disease

Leaf spots leading to blighting

Fig. 3 : *Colletotrichum* leaf spot

When the infection is severe resulting in drying up of the whole foliage, losses would exceed 50 percent. Reduction in the dry rhizome weight by 62.7 percent was also reported due to foliar infection.

Symptoms: Infection is usually confined to the leaf blades and occasionally extends to the leaf sheath (Nair, 1994; Ravindran *et al.*, 2007). The disease initially appears as elliptic to oblong spots of varying sizes, which enlarge up to 4–5 cm in length and about 3 cm in width, occupying a major portion of the leaf area (McRae, 1917; Nair, 1994). Mature lesions exhibit a grayish-white center surrounded by a brown margin and a characteristic yellow halo due to toxin production (Ravindran *et al.*, 2007; Singh *et al.*, 2003). The endotoxins produced by the pathogen play a significant role in symptom expression (Nair, 1994; Palarpawar and Ghurde, 1989). The whitish center containing dark acervuli often becomes papery and tears off under severe infection (Philip and Nair, 1981; Ravindran *et al.*, 2007). Rhizomes may also be affected, showing black stromatic structures on the scales covering them (Rao *et al.*, 1992; Nair, 1994). In severe cases, extensive foliar blighting results in drying and defoliation of leaves, leading to considerable yield reduction (Singh *et al.*, 2003; Ravindran *et al.*, 2007).

Strategies:

- Genome-wide association studies (GWAS) can be conducted to identify genes associated with resistance to leaf spot diseases in turmeric, enabling the discovery of resistance-linked loci and candidate defense genes (Korte and Farlow, 2013; Chakraborty *et al.*, 2021).
- CRISPR/Cas9 genome editing technology can be utilized to modify identified resistance-associated genes, thereby enhancing their expression or functional activity to confer improved resistance against leaf spot pathogens (Bortesi and Fischer, 2015; Chen *et al.*, 2019).

- Edited turmeric lines can be phenotypically evaluated for resistance to *Colletotrichum capsici* and *C. siamense* through controlled inoculation experiments under greenhouse and field conditions (Palarpawar and Ghurde, 1989; Singh *et al.*, 2003).

Varieties:

- The cvs. Nallakatla, Sugandham, Duvvur, and Gandikota are tolerant to leaf spots (Reddy *et al.*, 1963).
- Erode- Moderately resistant and Mannuthy Local-Tolerant (MY Palarpawar and VR Ghurde, 1989 and Philip and Nair, 1981)

Leaf blotch (*Taphrina* leaf spot):



Leaf blotch disease

Fig. 4 : Casual organism- *Taphrina maculans*

The disease is widely distributed in Southern States and the genetic plains in Uttar Pradesh and Bihar. This disease was first reported from Gujarat, Saharanpur (UP) and Rangpur (Bangladesh) in 1911. (Butler, 1911). The foliar destruction, it causes, would reduce the yields considerably especially when the disease starts in its early stages of crop growth.

Symptoms: The individual spots are small, about 1–2 mm in width, and are mostly rectangular in shape (Ravindran *et al.*, 2007; Butler, 1911). The disease is characterized by the appearance of several spots on both sides of the leaves, usually more numerous on the upper surface (Ravindran *et al.*, 2007; Nair, 1994). The spots are arranged in rows along the leaf veins (Ravindran *et al.*, 2007). These spots coalesce freely and form irregular lesions as the disease progresses (Ravindran *et al.*, 2007; Rao, 1995). The spots first appear as pale yellow discolorations and later become dirty yellow in colour (Ravindran *et al.*, 2007; Nair, 1994). Adjacent individual leaf spots of 1–2 mm diameter coalesce to form reddish-brown blotches, leading to varying degrees of leaf blight (Ravindran *et al.*, 2007; Panja and De, 2001).

Strategies:

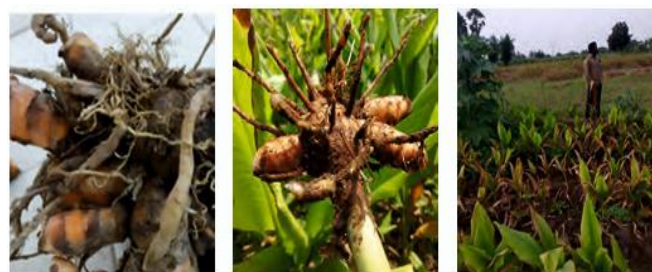
- Genetic diversity assessment through genome-wide association studies (GWAS) can be used to identify genetic markers associated with leaf blotch resistance in turmeric (Korte and Farlow, 2013; Chakraborty *et al.*, 2021).
- Marker-assisted selection (MAS) utilizing identified resistance-linked markers can accelerate the development of resistant turmeric varieties by enabling early and precise selection in breeding programs (Collard and Mackill, 2008; Xu and Crouch, 2008).
- Introgression of resistance genes from wild relatives or resistant cultivars into cultivated turmeric can be achieved through controlled hybridization and clonal selection approaches (Sasikumar, 2005; Ravindran *et al.*, 2007).
- CRISPR/Cas9-based genome editing technology can be employed to modify genes associated with disease susceptibility, thereby enhancing resistance against leaf blotch disease in turmeric cultivars (Bortesi and Fischer, 2015; Chen *et al.*, 2019).

Varieties:

- Mydukur, Amalapuram, CLL-324, Allepey, PTS 62, Roma, BSR1, Kasturi and Azad Haldi-1-Resistant (Philip and Nair;1981, Panja *et al.*, 2001, Singh *et al.*, 2003)

Nematode pests:

The important parasitic nematodes infecting turmeric are the Root-knot nematode (*Meloidogyne spp*), Lesion nematode (*Pratylenchus spp*), Burrowing nematode (*Radophulus similis*) and Reniform nematode (*Rotylenchulus reniformis*).



Root galls (A, B) and foliar symptom (C) caused by root knot nematodes

Fig. 5 : Root Galls and foliar symptoms caused by nematodes

Symptoms: Plant-parasitic nematodes usually cause damage by feeding on tender rhizomes, roots, and the basal region of the pseudostem, resulting in stunting, chlorosis, poor tillering, and necrosis of leaves (Sikora *et al.*, 2018; Ravindran *et al.*, 2007). *Meloidogyne spp.*

produce characteristic root galls and rhizomes with white creamy holes and a fissured appearance (Prasath *et al.*, 2014; Sikora *et al.*, 2018). Infection by *Pratylenchus* spp. leads to the development of lesions on the rhizome surface, varying from light brown to dark brown in colour (Sikora *et al.*, 2018; Mohanta *et al.*, 2015). These lesions are subsequently invaded by *Pythium* spp., resulting in rotting of the inner rhizome tissues (Rao, 1995; Sikora *et al.*, 2018). *Radopholus similis* and reniform nematodes mainly produce lesions on roots and, to a lesser extent, on rhizomes (Sikora *et al.*, 2018; Ravindran *et al.*, 2007). Infested rhizomes exhibit brown, water-soaked areas in the outer tissues, indicating severe nematode damage and secondary infection (Mohanta *et al.*, 2015; Sikora *et al.*, 2018).

Strategies:

Various approaches based on molecular markers such as cleaved amplified polymorphic sequence (CAPS), sequence characterized amplified region (SCAR), amplified fragment length polymorphisms (AFLPs), restriction amplified length polymorphisms (RALPs), random amplified polymorphic DNA (RAPD), SNPs, and reverse-transcription polymerase chain reaction (RT-PCR), have been used to identify cultivars with resistance to the RKN.

Varieties:

- IISR turmeric variety Pragati is moderately resistant to root knot nematodes.
- Kodur, Cheyapasupu, Armoor, Duggirala, Guntur 1, Guntur 9, Rajampet, Sugandham and Appalapadu -Resistant
- '361- Gorakhpur', 328- Sugandham' and 'PTS-21'- Moderately resistant- Dr. B. Verma *et al.* (2023) and Mohanta *et al.* (2015)

Shoot borer:

Symptoms:

- Larvae bore through the central shoots of the plants and feed on the growing buds resulting in withered and dried shoot referred to as "dead heart."



Fig. 6 : Causal organism: *Conognethes punctiferalis* (Fabricius, 1794)

- The presence of a bored hole on the pseudostem through which grass is extruded and withered and yellow central shoot is a characteristic symptom of this pest infestation. (Kumar and Singh, 2012)

Strategies:

- Molecular markers are increasingly used to identify and select resistant turmeric genotypes at the seedling stage, enabling rapid screening for nematode resistance (Sahoo *et al.*, 2011; Mohanta *et al.*, 2015).
- Resistant and moderately resistant genotypes such as Duggirala and Sugandham have been identified through molecular and phenotypic screening approaches (Prasath *et al.*, 2014; Mohanta *et al.*, 2015).

Varieties:

- NDH 79, NDH 1, CL 34, NDH 114, NDH 40, ACC 48, NDH 98, NDH 14, NDH 74, CL 54, CL 52- Moderately Resistant (Singh *Et Al.*, 2018)

Abiotic Stress

Drought:

Drought is one of the critical abiotic stresses that cause most crop losses (Santhi *et al.*, 2016)

Strategies:

- Genotyping approaches using molecular markers such as SSRs and SNPs can be employed to map important drought-related traits including relative water content, membrane stability, and osmotic adjustment in turmeric populations, thereby facilitating the identification of quantitative trait loci (QTLs) associated with drought tolerance (Sahoo *et al.*, 2011; Varshney *et al.*, 2005).
- Candidate gene and transcription factor studies can be used to investigate the role of drought-responsive homologs such as DREB, WRKY, and MYB genes in turmeric, and to determine whether their overexpression or suppression influences drought tolerance mechanisms (Shinozaki and Yamaguchi-Shinozaki, 2007; Santhi *et al.*, 2016).
- Genome editing technologies such as CRISPR/Cas9 can be applied to modify endogenous stress-responsive genes in turmeric, provided that efficient genome characterization and transformation systems are available (Bortesi and Fischer, 2015; Chen *et al.*, 2019).
- Omics-based approaches including transcriptomics (RNA-seq), proteomics, and metabolomics can identify genes, proteins, and metabolic pathways that are differentially regulated under drought stress, such as antioxidant systems and secondary metabolite biosynthesis pathways, which may serve as potential targets for stress-resilient

breeding (Wang *et al.*, 2009; Kumar *et al.*, 2020; Santhi *et al.*, 2016).

Varieties:

- IISR Pragati, SL 5, Suguna, and Suvarna- Tolerant (Banu *et al.* 2023)

Salinity:

Curcumin is the major component in turmeric plants with these unique properties. The levels of curcumin content, rhizome size, and total yield of the plants are greatly affected by the soil salinity, making the plants prone to stress, reducing yields, and ultimately inhibiting the death of the plants. Several breeding methods such as double haploid production, MAB, use of wild relatives and mutation breeding, transgenic approaches, and use of various candidate genes have been used to protect the plants against salinity stress conditions. The initial field contamination with salt is nullified by following careful irrigation practices and soil maintenance (Ravindran *et al.*, 2007).

Strategies:

- In addition, transgenic approaches such as gene transfer methods, recombinant DNA technology, hybridization techniques, tissue culture methods, and genome editing can enhance the growth and survival of turmeric plants under salt stress conditions (Bandi and Kaushik, 2022; Chen *et al.*, 2019).
- Growth-promoting genes may be introduced into plants to activate stress-responsive cellular functions, thereby minimizing yield losses under salinity stress (Zhu, 2001; Munns and Tester, 2008).
- Specific genes such as CDPK1, MAPK1, DCS, Polyketide III, and CURS are known to contribute to plant growth and stress adaptation through their upregulation under saline conditions (Bandi and Kaushik, 2022; Chakraborty *et al.*, 2021).
- The differential expression of these genes at various stages of turmeric crop growth enhances plant tolerance to salinity stress by regulating signaling pathways, osmotic balance, and secondary metabolite biosynthesis (Bandi and Kaushik, 2022; Santhi *et al.*, 2016).

Varieties:

- Vallabh Sharad, New Selection 1- Tolerant (Shankar *et al.*, 2022)

Conclusion

Breeding for biotic and abiotic stress resistance in turmeric is fundamentally constrained by sterility, polyploidy, and clonal propagation, making conventional hybridization ineffective. Consequently, genetic improvement relies on advanced strategies that generate and exploit non-recombinational variability, including clonal selection, mutation breeding, somaclonal variation, ploidy manipulation, and wild germplasm utilization. The integration of managed stress phenotyping with physiological, omics-based, and genomic prediction tools represents a critical shift toward mechanism-driven and accelerated selection. Future progress in turmeric breeding will depend on holistic, systems-based approaches that combine host genetics, stress physiology, and rhizosphere interactions to develop stable, climate-resilient cultivars with durable stress resistance.

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