PLANT SCIENCE TODAY
Vol 12(sp4): 01–13
https://doi.org/10.14719/pst.11154

eISSN 2348-1900

REVIEW ARTICLE

A systematic exploration of biotechnological breakthroughs in enhancing jasmine aroma and quality

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Received: 06 August 2025; Accepted: 11 September 2025; Available online: Version 1.0: 22 October 2025

Cite this article: Priyatharsini A, Ganga M, Thamaraiselvi SP, Manikanda BN, Manonmani S, Santhanakrishnan VP. A systematic exploration of biotechnological breakthroughs in enhancing jasmine aroma and quality. Plant Science Today. 2025;12(sp4):01–13. https:/doi.org/10.14719/pst.11154

Abstract

Jasminum sp. plays a crucial role in different industries such as food, pharmaceutical, ornamental and cosmetics, both in traditional as well as modern contexts. However, the dynamic shift in climatic conditions poses significant challenges to jasmine productivity by creating unfavourable biotic and abiotic environments. Though the conventional breeding strategies have made noteworthy contributions in the past, it often demands extended timeframes for the development of new varieties. Further, its success rate gets impeded by physiological, biotic and abiotic barriers. In recent years, a significant progress has been achieved in leveraging the biotechnology methods for jasmine molecular breeding, which has in turn promised better strategies to improve the fragrance and yield of jasmine. Particularly, molecular markers have offered new insights about the genetic foundations of yield and quality characteristics of jasmine besides shedding light on its evolution and potential for conservation efforts. Contemporary biotechnological tools such as the omics technologies, tissue culture and genome editing tools are now being actively employed and examined for its potential to overcome the limitations encountered in conventional breeding strategies, in terms of jasmine improvement. The current systematic review conducted based on the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA), synthesizes the status and trends of various biotechnological tools that are employed in improving the desirable traits of the *Jasminum* sp. The insights presented in this paper highlight the multifaceted biotechnological aspects of the *Jasminum* sp. and suggest future research directions to further improve their potential applications in food, pharmaceutical and cosmetic industries.

Keywords: genetic diversity; genome sequencing; *Jasminum*; molecular markers; systematic review; tissue culture

Introduction

The Oleaceae family, encompassing a diverse array of woody plant members such as trees, herbaceous shrubs and lianas, consists of five tribes namely, Myxopyreae, Jasmineae, Forsythieae, Fontanesieae and Oleeae (1). With ~200 species, *Jasminum* is the largest genus of lianas that belongs to the tribe Jasmineae which also comprises the genera *Menodora* with a recent addition, *Chrysojasminum* (2-4). The *Jasminum* shrubs are distributed across the tropical regions while a majority of the species are found notably in Asian countries (5). India, in particular, hosts 40 out of the 89 validated *Jasminum* sp. (6). Some of the popularly cultivated jasmine species include *J. auriculatum, J. sambac, J. grandiflorum, J. multiflorum* and *J. nitidum*. These plants are utilised for its fresh flowers, concrete and essential oil extraction, beverage production and in landscaping industry (7). Several ecotypes of these cultivated species are also popular, owing to their unique characteristics, for instance the single, double and multi-petal types of *J. sambac* and white and pink budded types of *J. grandiflorum* (6).

The enduring popularity of *Jasminum* sp. that spans from classical to contemporary times gets reflected in its comprehensive utilization across the industries such as the food, pharmaceutical, ornamental and cosmetics. However, in recent years, the drastic change in climatic conditions has created unsuitable biotic and abiotic environments, which in turn has become serious challenges for growth and development of the jasmine. In terms of breeding and cultivation, continuous research on improving the qualitative and quantitative traits of jasmine plants is required. It is essential to meet the ever-increasing market demand for novel floral and plant architectural attributes and the demand for huge quantities of bolder and long-lasting flowers across the global markets. Further, there is a growing need for the fabrication of suitable production and post-harvest techniques for value addition and waste reduction from the jasmine flowers (8).

The constant efforts taken to develop new breeds of jasmine varieties with increased tolerance to biotic and abiotic

stresses and improved economical traits led to the development of ten jasmine varieties from the Tamil Nadu Agricultural University (TNAU) and the Indian Institute of Horticultural Research (IIHR), India. These varieties belongs to the species *J. grandiflorum*, *J. auriculatum*, *J. nitidum* and *J. multiflorum* (6). These varieties were obtained with the help of the selection and mutation breeding approaches whereas the efforts made using the hybridization technique failed to create a positive impact. This failure might be attributed to several fertilization barriers such as the nocturnal flowering habit, early and rapid senescence of pistil, inter-specific incompatibility, low pollen fertility and viability, poor stigma receptivity, hybrid unviability, endosperm antagonism and embryo abortion, which altogether pose serious complications to fruit and seed setting (9).

In spite of its significant contributions, the conventional breeding strategies encounter a lot of hindrances, for instance prolonged timelines and impediments related to physiological, biotic and abiotic factors. Recently, a paradigm shift has occurred in the application of biotechnology for plant breeding and improvement requirements. The field of biotechnology offers potential tools like molecular markers, that aid in understanding the genetic basis of the characteristics of a plant, which in turn can serve as an important factor for plant improvement (10). Further, it also contributes to the advancement in improvement of plant characteristics through techniques such as tissue culture, genetic engineering and marker-assisted selection approach (11). Initially, the commercial jasmine plants were propagated using vegetative cuttings and layering method, since seed set is poor in most of the jasmine species (12). Hence, the need for rapid mass multiplication was addressed by tissue culture method (5). In the recent times, the application of this technology has become feasible for studying a wide range of crops, including jasmine, thanks to the studies that focused on curtailing the expenses of these technologies. The utilization of biotechnological tools such as molecular markers and omics technologies shows great potential for overcoming the challenges of conventional breeding in jasmine (13). The current review article systematically explores and provides insights about the evolving trends of various biotechnological and bioinformatics tools, employed for enhancing the desirable traits of *Jasminum* sp.

Methodology

A comprehensive examination of the scientific literature pertaining to biotechnological approaches applied to *Jasminum* sp. was done based on the PRISMA statement that guides the planning and execution of the review methodology (14). The methodology adopted for this systematic review is outlined below.

Literature search

In this systematic exploration of pertinent literature, an advanced search methodology was employed across several reputable databases such as Science Direct, Scopus, J-gate and MDPI. This approach aimed at ensuring a comprehensive retrieval of a substantial number of scholarly works. The literature search was performed on 7th January 2024 using the inclusion terms *viz.*, Jasmine' and '*Jasminum*'. Advanced search was also conducted including the terms, 'tissue culture', 'micropropagation', 'molecular markers', genetic engineering', 'genome sequencing', 'transgenic breeding', 'omics', 'genomics', 'proteomics', 'transcriptomics', 'molecular approaches' and 'metabolomics. Boolean operators were also used for advanced search to refine and optimize the search queries. The operators AND and OR were used for combining the inclusion terms whereas the operator AND NOT were used to exclude the records on 'jasmine rice' and 'jasmine tea'. The current review included only those original research articles, conference papers and short communications published in English language and no constraints were placed for the review with regards to date of publication. Some of the subjects irrelevant to the scope of the review (social sciences, arts and humanities, public health & healthcare, psychology, veterinary, nursing, medicine, pharmacology, dentistry, business & economics, physics and astronomy, computer science, chemical engineering and earth and planetary sciences) were deliberately excluded from the search parameters.

Selection of suitable records

The citations extracted from the literature search were meticulously curated using the EndNote, the citation management tool (http://www.endnote.com/). Each record was appropriately tagged against its respective database of origin. To ensure data integrity, the imported references were thoroughly screened for duplicates during when the entries with identical content were merged. As a precaution, any duplicates that eluded the initial screening were diligently identified through manual scrutiny and subsequently consolidated.

The initial corpus comprised 1534 literature records, inclusive of duplicates. After the consolidation process, 1293 distinct and unique records were filtered, as illustrated in Fig. 1. Subsequently, the title, objectives and abstract of the selected studies were scrutinized for their relevance to the focal subject area i.e., biotechnological approaches for jasmine improvement. A stringent manual screening process was performed upon the title and abstract of the individual records, which resulted in the identification of 56 articles that were deemed pertinent to the research focus of the current study. Upon full-text screening, irrelevant full-text records and records without full-texts were excluded. Further screening was conducted for the back references based on a few predefined criteria. The citations of 13 such relevant back references were subsequently imported into EndNote tool for comprehensive record maintenance. Following an in-depth examination of the back references, a carefully refined set of seven full-text articles was found to be suitable for inclusion in this scholarly review (Fig. 1).

Results and Discussion

Identification of the suitable records

A compilation of the individual records, predominantly emanated from Scopus, followed by ScienceDirect, J-gate and the MDPI database, is delineated in Fig. 2. This comprehensive search yielded a total of 56 distinct and pertinent records. However, due to irrelevance and unavailability, 12 records were excluded, leaving 44 records for in-depth review. The scrutiny of 13 back references identified additional literature for consideration. Subsequently, a thorough examination was conducted, which further narrowed down this subset to seven records after factoring in constraints such as the unavailability of full-text articles and the manuscript's language being non-English. This condition was primarily followed to avoid misunderstanding of the content and context. This stringent literature screening process culminated in a meticulously curated library of 51 records (Fig. 1) for inclusion

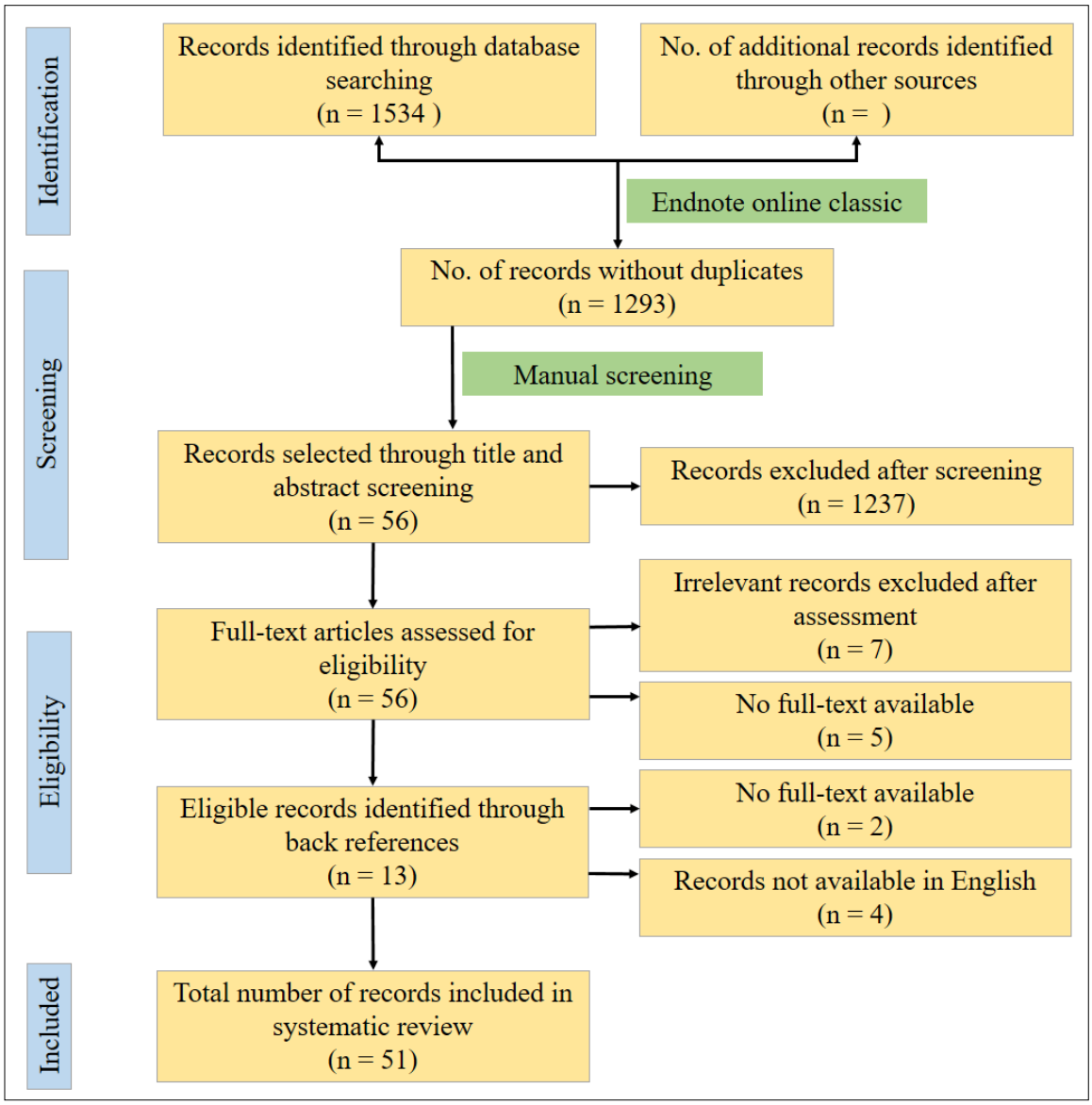

Fig. 1. PRISMA flow chart delineating the screening process involved in selection of records included in the review.

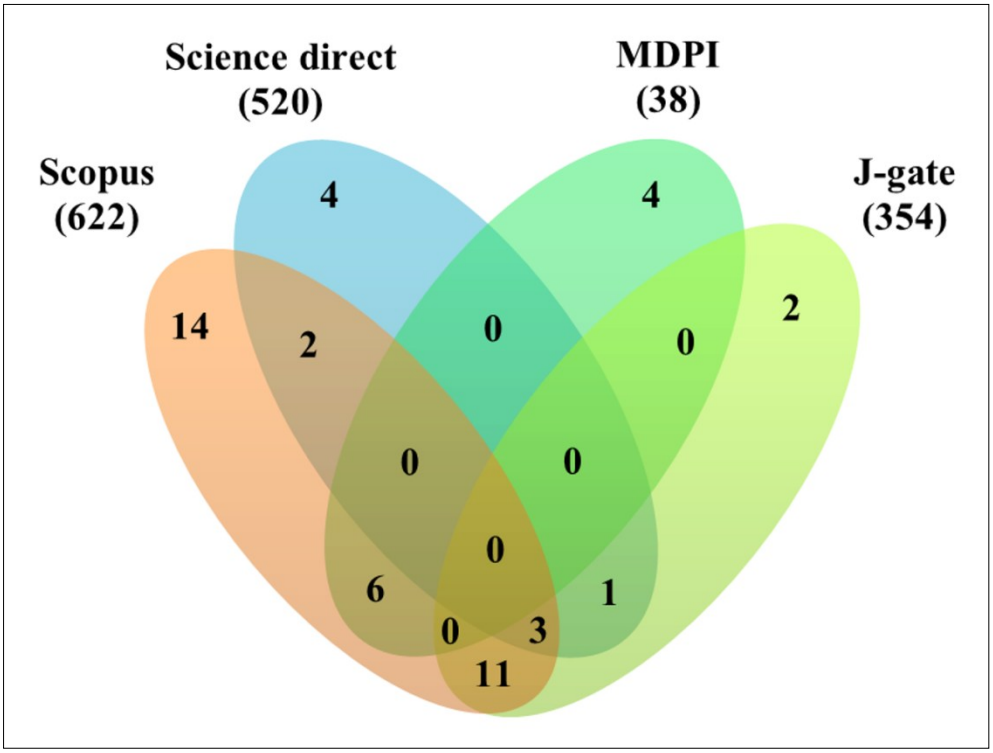

Fig. 2. Venn diagram of number of selected records retrieved from Scopus, Science direct, MDPI and J-gate.

in the current review. The numbers of research articles selected from the different databases and considered for the final review are represented in Fig. 2.

The historical evidence reveals that jasmine, despite its status as an ornamental crop, garnered comparatively lesser attention in scientific exploration than the rest of the food and medicinal crops in the previous century. The inception of journal articles regarding the application of biotechnology in jasmine can be traced back to the 1980s, as depicted in Fig. 3. Notably, until the last decade, the biotechnological efforts in jasmine production predominantly centered upon refining the micropropagation techniques to prevent from relying only upon the seed propagation technique. As the 21st century unfolded, the utilization of the molecular markers gained prominence which in turn facilitated an in-depth understanding of the evolutionary processes and genetic diversity within the *Jasminum* spp. This progress eventually catalysed the advancements in breeding programs. Simultaneously, the scientific substantiation of the pharmaceutical and therapeutic attributes of jasmine expanded significantly, underscoring the impetus for advancements in jasmine improvement. The revolution of genomics in the past decade (2011-2020) ushered in a discernible surge in the number of studies that leveraged biotechnological and bioinformatics tools, encompassing genomics, proteomics and transcriptomics. This period witnessed a concerted effort to enhance the quality and productivity of jasmine. The subsequent years (2021-2023) marked a paradigm shift, with the advent of cutting-edge biotechnological tools that are made feasible by the modern technologies. This transition further paved the way for significant molecular explorations of the *Jasminum* spp. and the development of methodologies to augment the production through molecular tools, thus delineating a noteworthy trajectory in the field (Fig. 3).

Biotechnological tools and approaches for jasmine improvement

In terms of enhancing the quality and production of jasmine, the prevalent biotechnological strategies to date involve the utilization of plant tissue culture, identification of molecular markers, protoplast fusion technique and genome-wide identification markers through genome sequencing methodologies (Table 1).

Plant tissue culture

Plant tissue culture stands out as a dependable tool to accomplish the mass multiplication of virus-free, genetically-identical progenies (15). This technique facilitates a rapid propagation under controlled *in vitro* conditions, thus mitigating the climatic influences and biotic stresses during the growth and development of the plantlets. Successful micropropagation protocols have been established previously reported for some of the key jasmine species such as *J. sambac, J. grandiflorum, J. officinale, J. polyanthum* and *J. nudiflorum* (13).

In literature, a micropropagation protocol was developed for *J. officinale* using the nodal explants and this protocol established the following compositions to stimulate shoot proliferation, stem elongation, root induction, root growth and elongation to achieve rapid multiplication (5, 16). Murashige and Skoog (MS) basal media with sucrose (45 g L^{-1}), 6-benzyladenine (BA) (4.0 mg L^{-1}) and 1-naphthalene acetic acid (NAA) (0.1 mg L^{-1}) remained the best for shoot proliferation. MS basal media containing sucrose (45 g L^{-1}), BA (4.0 mg L^{-1}), kinetin (2.0 mg L^{-1}) and NAA (0.1 mg L^{-1}) was an optimal media composition for stem elongation. Liquid rooting media containing Indole-3-Butyric Acid (IBA) (10 mg L^{-1}) and sucrose (20 mg L^{-1}) was best for root induction and solid rooting media containing sucrose (20 mg L^{-1}) was best for root growth and elongation. In case of *J. sambac*, shoot tip explants were used for rapid multiplication in media containing modified MS medium supplemented with kinetin (1.0 mg L^{-1}) and NAA (0.1 mg L^{-1}) for shoot proliferation. On the other hand, leaf explants were used with successful outcomes in terms of callus induction upon the modified MS medium with kinetin (1.0 mg/L) and 2, 4-dichlorophenoxy acetic acid (2, 4-D) (0.1 mg/L) (17).

For mass multiplication of *J. grandiflorum* using the nodal explants, the MS basal medium fortified with 6-benzylamino purine (BAP) (1.0 mg L^{-1}) and coconut water (60 mg L^{-1}) and MS medium with BAP (1.0 mg L^{-1}) and coconut water (45 mg L^{-1}) were found to be the successful compositions for shoot regeneration and shoot proliferation respectively (18). Hormonal treatment of *J. grandiflorum* leaf explants using 2, 4-D (1.5 mg L^{-1}) separately and in combination with Indole-3-acetic acid (IAA) (1.5 mg L^{-1}) yielded good callus performance. These results suggest that

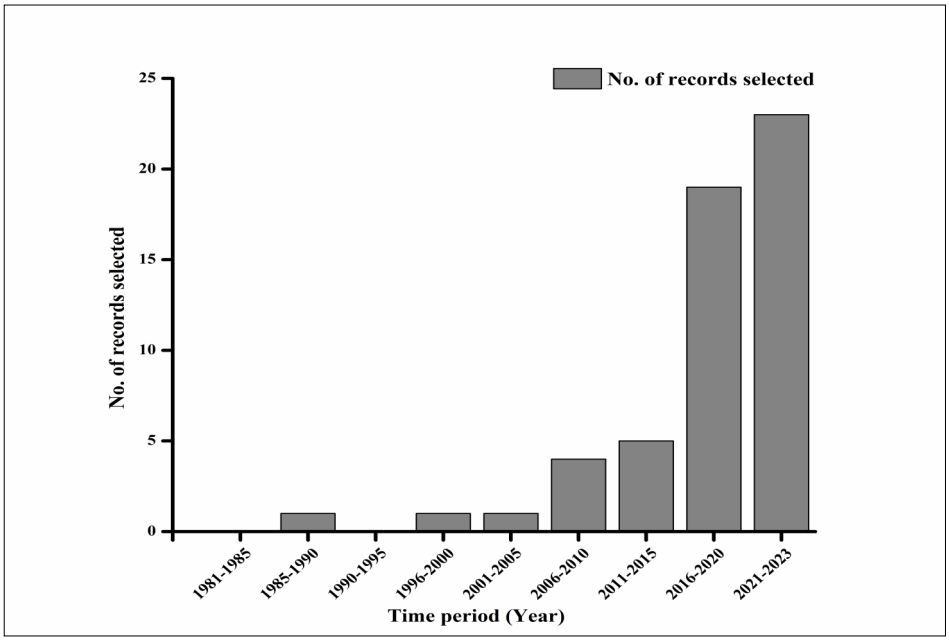

Fig. 3. Publication trend in application of biotechnological approaches for jasmine improvement.

Table 1. Biotechnological approaches implemented for *Jasminum* improvement

S.No.	Biotechnological tool	Function/Application	Reference
1.	Plant tissue culture	Callus culture for analyzing the enzymes involved in terpenoid biosynthesis	(23)
		Clonal propagation of nodal explants	(5, 16, 22)
		Callus induction (from leaf and shoot tip explants)	(17, 19-21)
		Callus culture to manipulate jasmine essential oil production	(24)
		Direct organogenesis (from stem node and shoot tip explants)	(18)
		Involvement of *WOX* genes in *de novo* organogenesis	(25)
		Phylogenetic relationship between *Jasminum* sp.	(3, 37, 46, 48)
2.	Molecular markers	Genetic diversity assessment based on random amplified polymorphic DNA (RAPD)	(38, 39, 49)
		Development of microsatellite (SSR) markers for *J. sambac*	(43)
		Evaluation of genetic diversity using amplified fragment length polymorphism (AFLP)	(45)
		Characterization of *Jasminum* accessions based on random amplified polymorphic DNA (RAPD)	(40)
3.	Protoplast fusion	Protoplast fusion of *J. sambac* and *J. mesnyi* through PEG-mediated DNA transfomation	(26)
4.	Genome wide Identification (GWI) strategy	Identification of *JsWRKY* genes in single-petal *J. sambac*, involved in heat stress tolerance and aroma compound production	(62)
		Identification and characterization of *TPS* genes involved in aroma compound and Jasmonate biosynthesis	(61)
		Expression analysis of *Auxin Response Factor (ARF)* genes in *J. sambac* growth and development	(65)
		Identification, comparison and expression analysis of *JsWRKY* genes between single and double-petal phenotypes of *J. sambac*	(66)
		Identification of floral-scent-formation-related lncRNAs in *J. sambac*	(67)
		Identification and expression analysis of basic leucine zipper (*bZIP*) genes involved in abiotic stress management in three jasmine genotypes	(68)
5.	Genome sequencing	Chloroplast genome sequencing of *J. nudiflorum* and *J. sambac*	(69, 70)
		Transcriptome sequencing and analysis of *J. sambac* and *J. grandiflorum*	(51-60, 63, 64)
		Nuclear genome sequencing of single and double petal types of *J. sambac*	(61, 71, 72)

both 2,4-D and IAA have the potential to promote callus formation and proliferation (19). Similarly, Biswal *et al* reported that the leaf explants of *J. sambac* exhibited the highest percentage of callus proliferation, when cultured in a medium enriched with MS basal salts and was supplemented with BAP (3.0 mg L^{-1}) and IAA (2.0 mg L^{-1}) (20).

J. polyanthum was micropropagated from both leaf and shoot explants using the modified MS media containing BA (1.0 mg L^{-1}) and NAA (0.5 mg L^{-1}) for shoot proliferation and IBA (2.0 mg L^{-1}) for rooting (21). On the other hand, *J. nudiflorum* was propagated using the nodal explants in MS media fortified with BAP (3 mg L^{-1}) and kinetin (0.5 mg L^{-1}) for culture establishment and callus proliferation. Further, it was propagated in MS media with IBA (2.0 mg L^{-1}) for rooting of the microshoots, obtained from the callus culture (22).

The tissue culture method has evolved beyond propagation, thus proving to be an instrumental technique in enzymatic studies on secondary metabolites and essential oil production (23, 24). The callus cultures of *J. officinale* and *J. sambac* exhibited the accumulation of valuable compounds, which in turn illustrated their potential as the source for enzymatic studies and essential oil production. The callus culture of *J. officinale*, obtained from the stem and leaf explants and cultured using the MS medium, showed the accumulation of nerol, linalool, citronellal, citronellol and citrals. This phenomenon remains a source for enzymatic studies on the biosynthesis of monoterpenes (23). The 12-week-old callus, propagated from the leaf explants of *J. sambac* in MS medium added with 20 % sucrose, produced the highest concentration of benzyl acetate (1.27 %) and jasmone (1.15 %). This outcome represents that the callus cultures may be a good source of essential oil (24).

Moreover, the recent insights about the genetic basis for organogenesis in *J. sambac* callus culture revealed the association of two specific genes (*JsWOX4* and *JsWOX1*) with callus proliferation and root primordium initiation (25). The overexpression of the gene *JsWOX4* resulted in the up-regulation of *JsWOX13*, which in turn got highly expressed during the later stages of callus formation. This scenario further elucidated the molecular mechanisms that govern the callus formation process.

In summary, the studies quoted above have established a list of efficient micropropagation protocols for *J. grandiflorum, J. nudiflorum, J. officinale, J. polyanthum* and *J. sambac*. The future research studies can focus on refining and optimizing the protocols for increased efficiency and reproducibility. The micropropagation protocols can be leveraged for conservation and mass multiplication of the endangered, rare and unique *Jasminum* sp. and varieties. Hormonal treatments, such as the use of kinetin, NAA, BAP and IAA, have been tailored for specific stages of tissue culture to promote shoot proliferation, stem elongation, callus induction and root induction. So, it is important to understand that species-specific responses to hormonal treatments would contribute to the development of highly-efficient protocols. Tissue culture has been instrumental in the enzymatic studies of secondary metabolites in *J. officinale,* essential oil production in *J. sambac* and the genetic studies on organogenesis in *J. sambac* callus cultures. Future research can also be focused upon the integration of the biotechnological approaches like metabolic engineering to enhance the production of valuable compounds in jasmine plants through tissue culture.

Protoplast fusion

The totipotent nature of the protoplasts aids in callus formation and organogenesis through which the plants can be regenerated. Protoplast fusion has emerged as a technique with substantial potential for the development of novel jasmine varieties/hybrids by transferring genetic material among different cultivars and species. This is especially commendable for those plants with pre- and post-fertilisation barriers during sexual hybridization.

In the pioneering research work, protoplast culture and transformation in jasmine species were explored using the protoplasts of *J. sambac* and *J. mesnyi* (26). The study demonstrated successful callus induction as well as protoplast isolation and it achieved 5 % protoplast fusion rate following a PEG (Polyethylene Glycol) mediated DNA transformation approach. Callus induction from young shoot explants of both the species, *J. sambac* and *J. mesnyi* was obtained from the media containing mineral salts of woody plant medium (WPM)-fortified with sucrose (30 g L^{-1}), agar (8 g L^{-1}), BA (2 mg L^{-1}) and NAA (0.2 mg L^{-1}) within 14 days under 23 to 27 °C temperature, 1200 to 2000 lux light and 12 hrs photoperiod per day. By leveraging the callus protoplasts of *J. sambac* and *J. mesnyi,* the research obtained 5 % protoplast fusion rate by treating with a fusion solution containing 40 % PEG-MW 6000 (*w/v*) supplemented with calcium chloride (0.1 M), sorbitol (0.1 M) and Tris buffer (1 M) for 20 min. However, the low (5 %) fusion rate posed challenges in microcolony formation and plantlet regeneration. Further, the genetic alterations that occur in individual cultivars, during the callus stage, contributed to diminished regeneration potential of the callus. The resultant colonies of the individual callus protoplasts exhibited weak growth. Despite these challenges, a foundational protocol for refining protoplast culture and fusion for the production of transgenic jasmine (26).

Protoplast fusion has been a successful venture in the development of somatic hybrids of other ornamental crops through electrofusion and PEG-mediated fusion (27). Electrofusion has been employed in the development of somatic hybrids (cybrids) from two species such as *Dendranthema grandiflorum* and *Artemisia sieversiana* for rust-resistance, *Gentiana cruciata* and *G. tibetica*, *Iris ensata* and *I. germanica* for albino and variegated shoots, *Rudbeckia hirta* and *R. laciniata* and *Gentiana kurroo* and *G. cruciate* for variations in morphological characteristics (28-32). Interestingly, electrofusion in *Lilium formolongi* cv. Hakucho and oriental hybrid lily cv. Acapulco; *L. formolongi* cv. Hakucho and oriental hybrid lily cv. Shirotae produced change in petal and anther colour and petal shape (33), PEG-mediated fusion has been utilised for performing the protoplast fusion of *Dianthus chinensis* and *D. barbatus* for dwarfness and continuous flowering, *Rosa damascena* and *R. bourboniana* and *Hydrangea macrophylla* 'Schneeball' and *H. macrophylla* 'Nachtigall' (34-36). Although PEG -mediated fusion in *Jasminum* sp. failed in plantlet regeneration, the future studies can focus on altering the composition of the fusion solution in PEG-mediated fusion and electrofusion to achieve efficient protoplast fusion and production of the *Jasminum* cybrids.

Application of molecular markers

Molecular markers constitute indispensable tools for the characterization of different plant species, genetic diversity estimation and elucidating the phylogenetic relationships among them. Further, it also helps in germplasm conservation and management. The development of molecular markers like Simple Sequence Repeats (SSR), Single Nucleotide Polymorphisms (SNP) and InDels helps in marker-assisted breeding to accomplish desirable economic traits in flowering plants such as petal colour, petal number and flower fragrance. Some of the commonly employed molecular markers for studying jasmine encompass Random Amplified Polymorphic DNA (RAPD), Inter-Simple Sequence Repeats (ISSR), Amplified Fragment Length Polymorphism (AFLP), chloroplast markers and microsatellite markers.

Random Amplified Polymorphic DNA (RAPD): The application of RAPD markers for the analysis of genetic variability of *Jasminum* sp. that encompass 32 varieties of *J. grandiflorum*, *J. auriculatum, J. sambac* and *J. multiflorum* (37). The study identified 158 polymorphic fragments and genetic dissimilarity analysis revealed significant variations. The genetic dissimilarity, calculated using Squared Euclidian Distance, inferred the highest species level dissimilarity i.e., 56 % between 'Bale Japani' of *J. sambac* and 'Manaamadhurai Mullai' of *J. auriculatum*. The least dissimilarity (8 %) between 'Rameshwaram mallige' and 'Nilakottai mallige', both belonging to *J. sambac*, infers that vegetative propagation might be a cause for low genetic variation. The cluster analysis, conducted based on Ward's minimum variance method, segregated the accessions into two major groups with group A containing *J. multiflorum* accessions and group B containing other three species. This was further subdivided with the accessions of *J. auriculatum* under sub-cluster B_1 and *J. sambac* (B_{2a}) and *J. auriculatum* (B_{2b}) accessions under sub-cluster B_2. This study suggested that the RAPD markers can be a valid tool for analysing the genetic diversity among *Jasminum* sp. Early works carried a similar kind of study focusing eight *J. sambac* varieties and two *J. grandiflorum* varieties (38). The study identified 120 polymorphic fragments whereas the principal component analysis grouped the varieties into clusters A and B, thus yielding results alike the previous study.

Previous findings also employed RAPD markers for the characterization of 8 *Jasminum* sp. and based on the outcomes, the authors suggested the application of morphological markers along with molecular markers for efficient characterization, conservation of genetic population and to understand the phylogenetic relationship among the *Jasminum* cultivars (39). Microscopic characteristics were employed as morphological markers, alongside RAPD markers, to assess genetic variability in 30 accessions from 22 *Jasminum* sp. *Pandorea jasminoides* was used as an outgroup (40). A wide inter-specific variation was observed among the *Jasminum* accessions with a genetic similarity index in the range of 0.022 to 0.477. The Unweighted Pair Group Method with Arithmetic mean (UPGMA) analysis produced three clusters grouping *J. coarctatum*, six *J. sambac* accessions and *J. grandiflorum* under cluster 1, *J. auriculatum, J. elongatum, J. nobile,* four *J. multiflorum* accessions, *J. laurifolium* f. *nitidum, J. adenophyllum* and two other *Jasminum* sp. under cluster 2 and *J. scandens, J. funale* ssp. *sootapense*, *J. fluminense* ssp. *gratissisimum, J. mesnyi, J. siamense, J. cordatum, J. humile, J. lanceolaria* and *J. nervosum* under cluster 3. The study also found that the phylogenetic relationships and botanical characteristics are not associated with each other. The genetic diversity of Bhatkal mallige, Udupi mallige and Mangalur mallige, belonging to *J. sambac* was analysed using both morphological

as well as RAPD markers (41). A high genetic diversity was reported between Mangalur mallige and Bhatkal mallige whereas the genotypes Bhatkal mallige and Udupi mallige were reported to have a close relationship.

These studies establish the validity of RAPD markers in the evaluation of genetic diversity among the *Jasminum* sp. Despite the significance of RAPD markers in genetic diversity analysis, the RAPDs were reported to have lower correlation than the rest of the methods in terms of distinguishing two subspecies (42). Thus, the RAPD markers can be inferred to have high sensitivity towards intraspecific variations and is better suited for examining the intraspecific diversity.

Simple Sequence Repeats (SSR): The only published study on the development of SSR markers for *Jasminum* sp. was conducted which focused on *J. sambac* using Illumina shortgun sequencing technology (43). The study resulted in the isolation of 1322 microsatellites and the identification of six polymorphic alleles, thus highlighting the potential of SSR markers in marker-assisted breeding for the development of jasmine varieties with economically-desirable traits. However, the demand for *de novo* isolation of these markers from each species, need for species-specific primers, homoplasy, high sequence repeats and the need for huge sample size for isolation are some of the disadvantages associated with SSR markers (44). These drawbacks might have resulted in limited application of the SSR markers for *Jasminum* sp.

Amplified Fragment Length Polymorphism (AFLP): AFLP markers used in the analysis of the phylogenetic relationship among 26 jasmine species which yielded 90.5 % polymorphism (45). This study revealed that both *J. grandiflorum* and *J. sambac* are closely related whereas *J. officinale* and *J. sp* Lalbagh are distantly related. The outcomes from the UPGMA analysis, conducted using Jaccard's similarity coefficient, showed that *J. auriculatum* formed a separate node whereas the remaining 47 accessions of 26 species were grouped under two major clusters namely, cluster I and cluster II.

Cluster I includes two sub-clusters in which the first sub-cluster included *J. mesnyi, J. sambac*11 and*J. primulinum* whereas the second sub-cluster included *J. multiflorum, J. officinale, J. flexile,* eight variants of *J. sambac,* two variants of *J. grandiflorum* and five other wild species. On the other hand, Cluster II included *J. auriculatum* and *J. sambac,* one variant in each species under sub-cluster 1 while four variants of *J. multiflorum,* one variant of *J. sambac, J. rottlerianum* and *J. ritchlei* were grouped under sub -cluster 2. These results contradicted with the outcomes of the previous study as the latter utilized RAPD markers to identify the genetic variability only among the cultivated species (37).

Inter Simple Sequence Repeats (ISSR): The ISSR analysis upon Iranian jasmine genotypes and the outcomes demonstrated the efficacy of ISSR markers in discerning the genetic diversity and elucidating the phylogenetic relationships within the *Jasminum* genus (46). The study involved 53 accessions of *J. sambac, J. grandliflorum, J. officinale, J. azoricum, J. humile, J. fruticans, J. nudiflorum* and *J. primulinum.* The UPGMA analysis outcomes revealed that the jasmine accessions can be grouped into two major clusters. The first major cluster has two sub-clusters containing three species namely, *J. grandiflorum, J. officinale, J. azoricum* in sub-cluster A and *J. sambac* in sub-cluster B. The second major cluster has two sub-clusters in which *J. nudiflorum*, *J. primulinum* and *J. humile,* have been reported in sub-cluster C and *J. fruticans* in sub-cluster D. The study highlighted the presence of high similarity between *J. officinale* and *J. azoricum* much contrarily to the substantial dissimilarity observed between the two species, *J. grandiflorum* and *J. primulinum*. Within *J. officinale,* a significant polymorphism rate (34.05 %) was reported, which suggests the potential bud sport occurrence based on Nei's unbiased genetic identity assessment. Additionally, ISSR markers used to assess the genetic diversity of Indian jasmine genotypes (47). The outcomes revealed 100 % polymorphism among 40 *Jasminum* accessions, which was inclusive of six endemic species as well. *J. bignoniaceum* was reported to have high genetic diversity. The neighbour-joining analysis helped in grouping the accessions into three clusters. The outcomes reported that the morphological traits are closely related with molecular characters. This finding contradicted results obtained from RAPD-based studies (40). This study also revealed that all the *Jasminum* sp. of the sections *Primulina, Unifoliata, Trifoliata* and *Jasminum* are descendants from the members of the section *Alternifolia* supporting the findings of the study that the white-flowered jasmine species (*Unifoliata, Trifoliata* and *Jasminum*) evolved from the yellow-flowered jasmine types (*Alternifolia*) (3).

The intra-specific and inter-specific diversity was investigated among 28 *Jasminum* accessions from Pakistan, encompassing *J. grandiflorum, J. sambac, J. eongatum, J. flexile, J. multiflorum, J. mesnyi, J. nitidum, J. polyanthum* and *J. azoricum* (48). The outcomes from the population analysis revealed the presence of high intra-specific variations among the accessions of *J. humile* and *J. sambac* with over 90 % genetic similarity. Further, a notable inter-specific variation was also observed in *J. nitidum* and *J. azoricum*, whereas the maximum genetic identity was reported in *J. elongatum* and *J. multiflorum*. Though placed under the same section i.e., *Unifoliata*, the accessions of *J. sambac* and *J. grandiflorum* were found to be distantly related to each other. This phenomenon challenged the genetic support for morphological classification since it affirmed the dissociation between morphological traits and genetic relationships, in line with the previous study (40). Based on the outcomes from the UPGMA analysis, it has been proposed that the sections such as *Unifoliata* and *Jasminum* got independently evolved multiple times and this phenomenon contributed to the observed genetic disparities.

On the other hand, both RAPD as well as ISSR markers used for the characterization of 18 *Jasminum* genotypes (49). The study outcomes revealed substantial polymorphism rates i.e., 94.35 % and 94.45 % from RAPD and ISSR markers, respectively. This study identified 94.35 % polymorphism from RAPD markers and 94.45 % polymorphism from ISSR markers. Notably, the outcomes from the UPGMA analysis isolated *J. primulinum* from the remaining genotypes, emphasizing its distinct genetic profile within the studied *Jasminum* population.

Chloroplast markers: In the literature, chloroplast markers such as *mat*K, *trn*L-F and *trn*H-*psb*A used to analyse the evolutionary relationship among the *Jasminum* sp. (3). This was the first of its kind investigation utilized for understanding the evolutionary relationship using molecular markers. The study utilized 27 accessions of 22 *Jasminum* sp. along with one cultivated variety. For this study, the authors utilised both nuclear Internal-Transcribed Spacer (ITS) region of nrDNA as well as the chloroplast

markers for the assessment. Phylogenetic analysis using the Bayesian method revealed that the genus *Jasminum* may form a monophyletic group. Further, the study also established that the yellow-flowered *Jasminum* sp. had evolved from the white-flowered ancestors. The study also suggested that *Menodora* can be placed under the genus *Jasminum* based on morphological and molecular markers. It also confirmed that the morphological markers have no association with molecular markers.

The application of different types of molecular markers has proven to be instrumental in understanding the genetic diversity, phylogenetic relationships and evolutionary aspects within the *Jasminum* genus. These findings contribute to a broader understanding and expand knowledge base for genetic improvement and conservation of the *Jasminum* sp. Most documented studies used hierarchical clustering distance-based methods for analysis. However, model-based methods have been proposed to overcome certain constraints, such as systemic errors in distance-based methods (50). Ward's minimum variance method, average linkage method, neighbour-joining method and UPGMA are the distance-based methods that are usually employed in genetic diversity analysis. Among these methods, UPGMA remains the most used method. On the other hand, one of the research was the only study that utilized model-based method (Bayesian method) (3). Other distance-based methods like Unweighted Paired Group Method using Centroids (UPGMC), single linkage, complete linkage and model-based methods can be tested for their reliability and efficiency in genetic diversity assessment of the *Jasminum* sp.

Genome sequencing

In the realm of genome sequencing, a plethora of technologies has emerged including sequencing the short reads and long reads, chromosome-level assembly, haplotype-resolved genome sequencing, pan-genome sequencing, transcriptomics sequencing and organelle genome sequencing. Transcriptomic analysis is a powerful tool for unravelling the molecular intricacies that govern the growth and developmental processes in plants. This tool has been particularly instrumental in deciphering the molecular changes that accompany flower blooming in *J. sambac*. The Illumina RNA-seq platform harnessed in order to scrutinize the temporal dynamics of gene expression during flower budding and full-bloom stages of *J. sambac* (51). This investigation unearthed a total of 4577 differentially expressed genes (DEGs) between the flower budding and full-bloom stages and were found to have implicated in steroid biosynthesis, plant hormone signal transduction and pentose and glucuronate interconversions. Notably, the study identified 92 floral scent-related unigenes among which only 19 unigenes were found to be related with major aromatic compounds of *J. sambac viz.,* linalool, alpha-farnesene, alpha-caryophyllene, 3-hexen-1-ol, benzoate, acetic acid, phenylmenthyl ester, methyl salicylate, benzyl benzoate, indole and benzyl alcohol. These notable findings play a major role in shedding light upon the genetic underpinnings of key aromatic compounds in *J. sambac.*

The expression patterns of alpha-farnasene biosynthesis genes across different developmental stages of *J. sambac* 'Biofoliatum' flowers were studied (52). The analysis elucidated the pivotal role of alpha-farnasene in the floral scent of *J. sambac*. The expression analysis was conducted at different flowering stages and the outcomes reported that a high concentration of alpha-farnasene in full-blooms coincided with high expression levels of *JsHMGS, JsHMGR, JsFPPS and JsTPS* genes that regulate the mevalonate (MVP) pathway. *JsHMGS* suggested to help in the activation of MVP pathway based on the high expression of *JsHMGS* during the initial stages of flowering. The genes such as *JsHMGR, JsFPPS* and *JsTPS* were opined to be involved in emission alpha-farnasene through MVP pathway, based on the high expression of these genes, during the final stage of flowering. Concurrently, Ghissing *et al* corroborated these findings and highlighted the presence of a correlation between the expression of certain genes and the heightened concentration of floral scent volatiles during the full-bloom stage (53). The high expression levels of *JsHMGS*, *JsGLS*, *JsFPPS* and *JsBEAT*, at the time of flower blooming stage, were found to eventually result in a high concentration of floral scent volatiles during the full-bloom stage. Jasmintides are a group of Cysteine - rich peptides (CRPs) that exhibit a wide range of bioactivities along with phenomenal pharmacological potential. Jasmintides extracted from *J. sambac* using Illumina Hiseq 2000 and other such peptidomic pipelines (54). The RNAseq analysis outcomes helped in the identification on 14 unique jasmintide precursor sequences, which get converted to jasmintides. Further, the peptidomic analysis results helped in the identification of 84 novel jasmintides. The identified jasmintides were reported to contain nine hydrophic amino acids including tryptophan, trypsin, leucine and isoleucine that possess excellent biological profile. Further, this study also validated the anti-feedant activity against *Tenebrio molitor* larvae.

The research works pertaining to transcriptomics too provided valuable insights about the sugar transporters. The Sugar Will Eventually Be Exported Transporter (*SWEET*) genes, sucrose Transporters/carriers (SUT/SUC) and Monosaccharide/ polyols transporters (MST) are the primary classes of sugar transporters that play a vital role in physiological growth, development, reproduction and pathophysiological stress response of the plants. With the help of transcriptomics data and the results from the expression analysis, a total of seven SWEET transporter-like unigenes was identified (55). Among these seven unigenes, five were found to be heavily expressed only in the flowers of *J. sambac* during the hours of darkness. Both *JsSWEET2* and *JsSWEET9* genes that have been identified to be localised close to the plasma membrane got highly expressed in fully opened flowers. This phenomenon depicts their role in mediating anthesis. *JsSWEET5*, localised in the plasma membrane, was identified to be a hexose transporter gene. Similarly, the high expression levels of *JscwINV* and *SWEET-11* like unigenes during flower maturation stage was also reported (53).

The regulatory role played by Benzylalcohol O-acetylt ransferase/ anthocyanin O-hydroxycinnamoyl transferases/ anthranilate N hydroxycinnamoyl/ benzoyl transferase/ deacetylvindoline 4-O-acetyl transferase (BAHD) superfamily in the production of several benzenoid esters (56). The transcriptome analyses helped in the identification of seven *JsBEAT* genes. The expression analysis outcomes inferred the high expression of the genes such as *JsBEAT1, JsBEAT4, JsBEAT6* and *JsBEAT7* at early night (23:00 hrs) while the genes *JsBEAT2, JsBEAT3* and *JsBEAT5* got expressed at late night (at ~ 3 to 6 hrs). The genes *JsBEAT1* and *JsBEAT2* were reported to be heavily expressed in all the tissues, especially the *JsBEAT1* gene got heavily expressed in stem and leaves while the genes *JsBEAT1, JsBEAT2, JsBEAT4* and *JsBEAT5* were heavily expressed in flower petals. Further, previous studies cloned *JsBEAT1* and *JsBEAT2* and created a transgenic *Petunia hybrida* to

analyse the function of both the genes by determining the floral volatiles. The outcomes revealed that these genes are ectopically expressed and it can increase the production of benzyl benzoate, benzyl acetate and other volatile organic compounds.

Transcriptomics has also been instrumental in deciphering the genetic basis of a few traits such as environmental adaptation, flower development and aroma formation in single-petal (SP) and double-petal (DP) *J. sambac* utilising *J. sambac* cv *Fuzhou Unifoliatum* and *J. sambac* cv. *Bifoliatum,* respectively (57). The results from the time-series transcriptome analysis revealed that the DEGs in single-petal jasmine, during F1 stage, possess anti-viral activity (*CAMTA1* motifs) (57). Further, it also corresponds to floral organogenesis, transition and flowering during F2-F4 stages. In terms of double-petal jasmine, wide environmental adaptability was found to be the consequence of significant up-regulation of DEGs during the F1 stage of flower development which are responsible for regulating and improving the photosynthetic activity in response to light. During F2 stage, it regulates the biosynthesis of cutin, suberine and wax. The DEGs that got up-regulated during F3 and F4 stages of the double-petal jasmine were found to regulate the production of terpenoids, phenylpropanes and fatty acid derivatives. Further, the *BMST* (benzoic acid/salicylic acid carboxyl methyl transferase) genes were found to be highly expressed only in DP jasmines. The differential expression of these genes, at various developmental stages, highlighted the underlying molecular mechanisms that tend to shape the distinctive floral scents in these cultivars. The *AGL63* and *PLT3* motifs were found to regulate the flower formation process in single and double-petal cultivars, respectively. With regards to terpenoid biosynthesis, the study identified a total of 58 and 38 *TPS* genes in SP and DP jasmines respectively. In agreement with the previous study, identified two *BEAT* genes in SP and one *BEAT* gene in DP jasmines (56, 57).

During the jasmine crossing period, the interplay between the pollen and pistil was probed and the results unravelled the congenital reasons and pre-fertilization barriers that make the sexual crossing, a difficult process (58). The results of the study speculated that the down-regulation of expansion and the up-regulation of peroxidases involving actively in biogenesis, reduction of APRTase and increase in pectinesterase contents biosynthesis of the flavonoids during crossing may be the reasons behind low pollen-pistil interactions. The up-regulation of peroxigenase 4 and the down-regulation of the genes involved in the biosynthesis of terpenoid backbone, monoterpenoids and carotenoids were found to promote male sterility, which in turn can help in successful crossing outcomes. Similarly, the nexus between the gibberellin-mediated stem elongation and flowering was analysed (59). The study revealed *JsGA2ox1, JsGA2ox3* and *JsGAS1* genes responsible for stem elongation through the regulation of GA accumulation. On the contrary, the results of GA inhibitors application were found to stimulate the terminal flowering process yet inhibit the stem elongation. Thus, the study validated the fact that GA mediates the stem elongation process in plants at a molecular level.

80 Differentially Expressed Transcriptomes (DETs) involved in terpenoid and phenylpropanoid/benzenoid metabolic pathways of *J. sambac* cv.'double-petal' during the post-harvest stage of flowers and published the first ever reference full-length transcriptome of *J. sambac* flowers after harvest (60). The results also correlated the emission of volatile organic compounds with the expression of 42 heat shock protein transcripts.

The above reviewed transcriptomics studies provide insights on the molecular grounds in terms of growth, development, reproduction, biotic and abiotic stress tolerance and post-harvest physiological process of *J. sambac* cultivars. This finding can help in genetic engineering and optimization of the cultivation practices followed for *J. sambac* cultivars. The accrued insights have profound implications upon genetic engineering and the optimization of cultivation practices that focus on enhancing the economic traits of this horticulturally significant species. Notably, the progress achieved so far in chloroplast sequencing and nuclear genome sequencing in *Jasminum* sp., outlined in Table 1, signifies a promising trajectory in understanding its genetic makeup. As of now, the chloroplast sequencing process has taken precedence and the complete chloroplast genome of *J. sambac* remains the only organelle that got its genome fully sequenced. The first whole-genome sequence of *J. sambac* was published in 2022 (61).

Genome Wide Identification (GWI) studies serve as a pivotal tool in elucidating the intricacies of phenotypic diversity, genome evolution, gene structures, functions, expression patterns and their roles in plant responses to diverse biotic and abiotic stresses. In this background, significant strides have been achieved in understanding the genomic landscape of *J. sambac* (Table 1). A notable contribution was made by sequencing the draft genome of *J. sambac* cv. 'Danbanmoli' (JSDB), a cultivar with single-petal (62). The meticulous computational analyses revealed 206 heat stress response genes in JSDB. Notably, aroma compound biosynthetic genes and transcription factors that are involved in shikimate pathway, phenylpyruvate and arogenate pathways at various flowering stages of JSDB were also discerned. This outcome provided insights about the genetic foundation of fragrance production. Similarly, the expression of linalool synthase genes was correlated with (R)-(-)-linalool emission and transformation to (S)-(+)-linalool during various flower developmental stages of *J. grandiflorum* (63).

Significant contributions was made by identifying the genes that are involved in fragrant compound biosynthesis pathways by following the *de novo* sequencing process of the genome of double-petal cultivars of *J. sambac* (61). The study identified a total of 47 *TPS* genes. Additionally, a comprehensive understanding of the Mevalonic Acid Pathway (MAP) and 2-C-methylerythritol 4-phosphate (MEP) pathways was elucidated through the identification of *HMGR* (3-hydroxy-3-methylglutarylcoenzyme A reductase), *HDS* (1-hydroxy-2-methyl-2-(E)-butenyl-4-diphosphate synthase) and *TPS* genes involved in the regulation of those pathways. (61). The high concentration of linalool found in full-bloom is proportionate with a higher expression of *JsTPS* genes in the flowers, which was also reported (64).

In parallel, the research endeavours made in *J. sambac* and delved into the genome-wide identification of *Auxin Response Factors* (*ARF*), *WRKY* genes and basic-leucine zipper (*bZIP)* transcription factors, respectively (65-67). A total of 24 *JsARF* genes, thus shedding insights on their localization and potential responses to auxin. Most of these 24 *JsARF* genes were anticipated to be confined to the nucleus, except *JsARF4* and *JsARF10* genes, which were confined to the cytoplasm (65). These 24 *JsARF* genes

were identified to be distributed in 11 out of 13 *J. sambac* chromosomes based on the phylogenetic analysis. The study outcomes further suggested that *JsARF4, JsARF19* and *JsARF21* genes may respond to auxin. The expression analysis results revealed the high expression levels of *JsARF5, JsARF12* and *JsARF17* genes in flowers, leaves, root and stem, which were anticipated to be involved only in the growth and development of *J. sambac*.

A total of 72 *JsWRKY* genes were identified and also elucidated their role in the production of aromatic terpenoids in *J. sambac* 'double petal cultivar'(66). The results revealed a positive correlation of *JsWRKY* genes with *JsTPS* genes suggesting that the *JsWRKY* genes might be involved in the regulation of *JsTPS* genes. Apart from these floral-scent regulatory genes, some of the long non-coding RNAs (lncRNA) also play a major role in the biosynthesis of volatile fragrant compounds (67). Genome-wide identification of the lncRNAs using the strand-specific RNA-Seq (ssRNA-seq) data and computational pipelines reported a total of 31079 novel lncRNAs and 2937 novel mRNAs. The pathway analysis outcomes confirmed the involvement of 24 lncRNAs in the regulation of MEP pathway, 25 lncRNAs in the regulation of MVA pathway, 65 DE_lncRNAs in the regulation of 34 *TPS* genes, 61 lncRNAs in the regulation of 35 genes involved in the phenylpropanoid/ benzenoid biosynthesis pathway and mostly the *cis*-regulated lncRNAs. In addition to these, 5 lncRNAs were involved in the regulation of two genes that play a key role in the synthesis of 3-ketoacyl-CoA-thiolase (KAT) while 7 lncRNAs were found to be regulating the genes that encode salicylic acid carboxyl methyltransferase. Some of the lncRNAs were found to be differentially expressed *i.e.* up-regulated or down-regulated across different flowering stages.

The *bZIP* transcription factors play a major role in conferring abiotic stress tolerance for the plants. 64 *bZIP* factors were scrutinized in single-petal jasmine and 63 each in double-petal and multi-petal jasmines (68). *HTbZIP27* was found to be highly expressed in all the tissues while *HTbZIP05, HTbZIP10, HTbZIP22, HTbZIP32* and *HTbZIP36* were highly expressed in roots, leaves and stems and *HTbZIP56* in all the three stages of flower development. On the contrary, the study reported that none of the *bZIP* genes got highly expressed in the leaves of single and double-petal jasmines. *HTbZIP36, SJbZIP53* and *DJbZIP36* were found to be highly expressed in the roots of multi-petal, single-petal and double-petal jasmines respectively. These genes were anticipated for their role in down-regulating the root growth. *HTbZIP27* was predicted to be a part of the endoplasmic reticulum stress pathway. The genes *SJbZIP37, SJbZIP57* and *SJbZIP62* were speculated to be responsible for the regulation of abscisic acid-mediated plant response in single-petal jasmine. Based on these evidence, the *bZIP* genes were anticipated to help the jasmine species in both survival and adaptation to unfavourable conditions.

The collective insights gained from these GWI studies significantly contribute to our understanding about the genomic intricacies, aroma compound biosynthesis and the responses of *J. sambac* to various environmental stresses. The knowledge from these studies can be utilised in breeding programs and in framing highly targeted and precision management practices for various climatic conditions, with optimum resource utilization and reduced environmental impact.

Future thrust

In spite of the significant advancements made in *Jasminum* biotechnological research, several areas warrant further in-depth exploration. As of now, most of the biotechnological tools have been employed in both exploration and improvement of the *J. sambac*, while the application of these tools in other economically important *Jasminum* sp. is awaited. The comparative genomic analyses revealed the presence of unique genomic features that help in the identification of genetic variations, associated with desirable traits. Future studies should focus on genome-wide studies to elucidate the role played by regulatory genes involved in biosynthetic and signalling pathways of key bioactive compounds like jasmonates, benzyl acetate, linalool, quercetin, kaempferol, oleuropein, coumaric acid in *Jasminum* sp. This way, the potentials of these regulatory genes in biosynthetic regulation and metabolic engineering can be explored. Further investigation on stress-responsive pathways such as the endoplasmic reticulum stress pathway, identified in *HTbZIP27*, should be conducted to elucidate their molecular mechanisms. This knowledge can help in devising strategies for enhancing stress tolerance trait in *Jasminum* cultivars. It is crucial to understand the genetic determinants of environmental adaptability to ensure the resilience of these plants during dynamic environmental conditions. The development of holistic breeding strategies that consider an intricate interplay between different genes and pathways can ensure the preservation of desirable traits while it also helps in introducing novel characteristics.

To summarize, the future thrust in jasmine research should be guided by a multidimensional approach that embraces functional genomics, advanced breeding technologies and other such collaborative efforts. By delving deeper into molecular intricacies of fragrance biosynthesis and stress responses, the researchers can contribute to sustainable cultivation and enhanced economic traits of this culturally significant and economically valuable plant. Additionally, the development of integrative approaches combining phytochemical, pharmacological and genomic analyses would provide comprehensive insights about the medicinal and ecological roles of *Jasminum* sp. Furthermore, collaborative efforts are needed to address the conservation challenges and ensure the long-term sustainability of *Jasminum* resources.

Conclusion

The integration of genomics, transcriptomics and metabolomics data offers a holistic perspective about the molecular basis of phenotypic traits and lists the implications for horticultural practices and potential applications in genetic engineering. As we navigate the complex interplay among the genes, pathways and environmental cues, the current review findings provide a foundation for future research endeavours that are aimed at enhancing the traits of economic significance in *J. sambac* cultivars. The development of feasible genomics, proteomics and transcriptomics pipelines pave the way for exploring the genomes of several cultivars of *J. sambac*. At present, the research on *J. sambac* has approached the pan-genome concept. Though molecular breeding approaches have established their prowess in other crops in terms of fast-tracking the breeding process, their application in jasmine improvement is still at infancy stage. So, the future studies on genome sequencing of the *Jasminum* cultivars other than *J. sambac* can aid in evolving novel varieties with desirable traits. The

advancements reported in this review underscore the multifaceted significance of improving the *Jasminum* sp. in ecological and conservational aspects. By integrating the interdisciplinary approaches and fostering international collaborations, the future research endeavours can unlock the full potentials of *Jasminum* sp. for the benefit of humanity and the environment.

Acknowledgements

We acknowledge the funding provided by Protection of Plant Varieties and Farmer's Rights Act (PPV&FRA) Scheme on DUS testing of jasmine provided by Government of India (GOI) for the systematic review.

Authors' contributions

Conceptualization was done by PA, GM and MBN. Methodology, data collection and analysis, writing-original draft were performed by PA. Writing the review and editing was done by TSP, MS and SVP. All the authors approved the final draft of the manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

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Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

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