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Resource characteristics and genomic advances in *Melastoma* species: progress and perspectives

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Abstract

Melastoma species, widely distributed across tropical and subtropical areas, exhibit remarkable morphological diversity and environmental adaptability, with significant horticultural, ecological, and medicinal value in China. Recent genomic and multi-omics advances have made an initial contribution to the molecular bases of key traits, including hetero-morphic stamen regulation, aluminum hyper-accumulation, stress tolerance, and growth habit determination. The application of chromosome-level reference genomes, integrated with metabolomic and transcriptomic, have provided candidate genes and regulatory networks underpinning these traits. However, challenges remain, including limited sequenced species, insufficient functional validation, and the absence of robust breeding systems. Future efforts can focus on pan-genome construction, multi-omics integration, and functional studies to enable targeted molecular breeding, elite germplasm improvement, and sustainable utilization. These advances will facilitate the rational exploitation of *Melastoma* species for horticultural, medicinal, and ecological applications.

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Introduction

With the accelerated global push for ecological civilization and the rapid growth of the green economy, wild flowers, which have both ecological and economic value, are increasingly deemed as a key link between biodiversity conservation and sustainable development[1]. Among them, *Melastoma* species attract attention due to their wide distribution in tropical and subtropical regions, distinctive traits such as heteromorphic stamens, and diverse uses in ornamental horticulture, traditional medicine, and ecological restoration[2−4].

Recent advances in high-throughput sequencing, multi-omics integration, and gene-editing technologies have shifted research on *Melastoma* from basic taxonomy and resource surveys to molecular studies of evolution and functional genes. Analyses of nuclear, mitochondrial, and chloroplast genomes clarified how genetic diversity forms and evolves in the genus[5−8]. They have also revealed molecular networks controlling key traits, including heteromorphic stamen differentiation and aluminum hyper-accumulation[9,10].

This review summarizes the distribution, phenotypic and functional diversity, medicinal and edible potential, and genomic research progress of *Melastoma*. It also examines how morphological traits co-evolve with ecological adaptation and highlights current research challenges. Finally, future directions for breeding and applications are proposed. These efforts aim to support targeted improvement, sustainable utilization, and practical use of *Melastoma* in ecological restoration, horticulture, and medicine. They will also contribute to ecological civilization and the green economy.

World-wide distribution of the genus *Melastoma*

The Melastomataceae family, comprising approximately 5,857 species across 176 genera, is divided into three subfamilies: Kibessioideae (15 species), Olisbeoideae (556 species), and Melastomatoideae (5,287 species). These species are primarily found in tropical and subtropical regions worldwide[11−13]. Approximately 100 species are distributed from southern Asia to northern Oceania and the Pacific islands. In China, around nine native species are distributed in regions south of the Yangtze River[14]. Among them, *Melastoma dodecandrum* is widely distributed in regions south of the Yangtze River, excluding Hainan and Taiwan. *Melastoma dendrisetosum* and *Melastoma penicillatum* are found only in Hainan, while *Melastoma imbricatum* is restricted to Yunnan in China. In terms of vertical distribution, the distribution of *Melastoma* species varies with altitude, geographical location, and terrain. *M. imbricatum*, *M. candidum*, *M. dendrisetosum*, *M. sanguineum*, and *M. sanguineum* var. *latisepalum* grow at lower altitudes, while the other five species are found at altitudes above 1,000 m[7,15,16] (Figs. 1, 2).

For a long time, there have been significant disagreements in the classification of the *Melastoma* genus in China. To clarify the relationships among species, Chinese researchers conducted scanning electron microscopy (SEM) observations of the leaf surface morphology of six *Melastoma* species and performed cluster analysis on these characteristics. The results showed that, except for the upper surface of the leaves of *M. dodecandrum*, the upper and lower surfaces of the leaves of the other five species were covered with epidermal hairs. Both *M. candidum* and *M. malabathricum* had conical and scale-shaped surface hairs on the mid-vein of the lower surface, with *M. candidum* having long conical hairs and *M. malabathricum* having short conical hairs. The surface hairs on the mid-vein of both *M.*

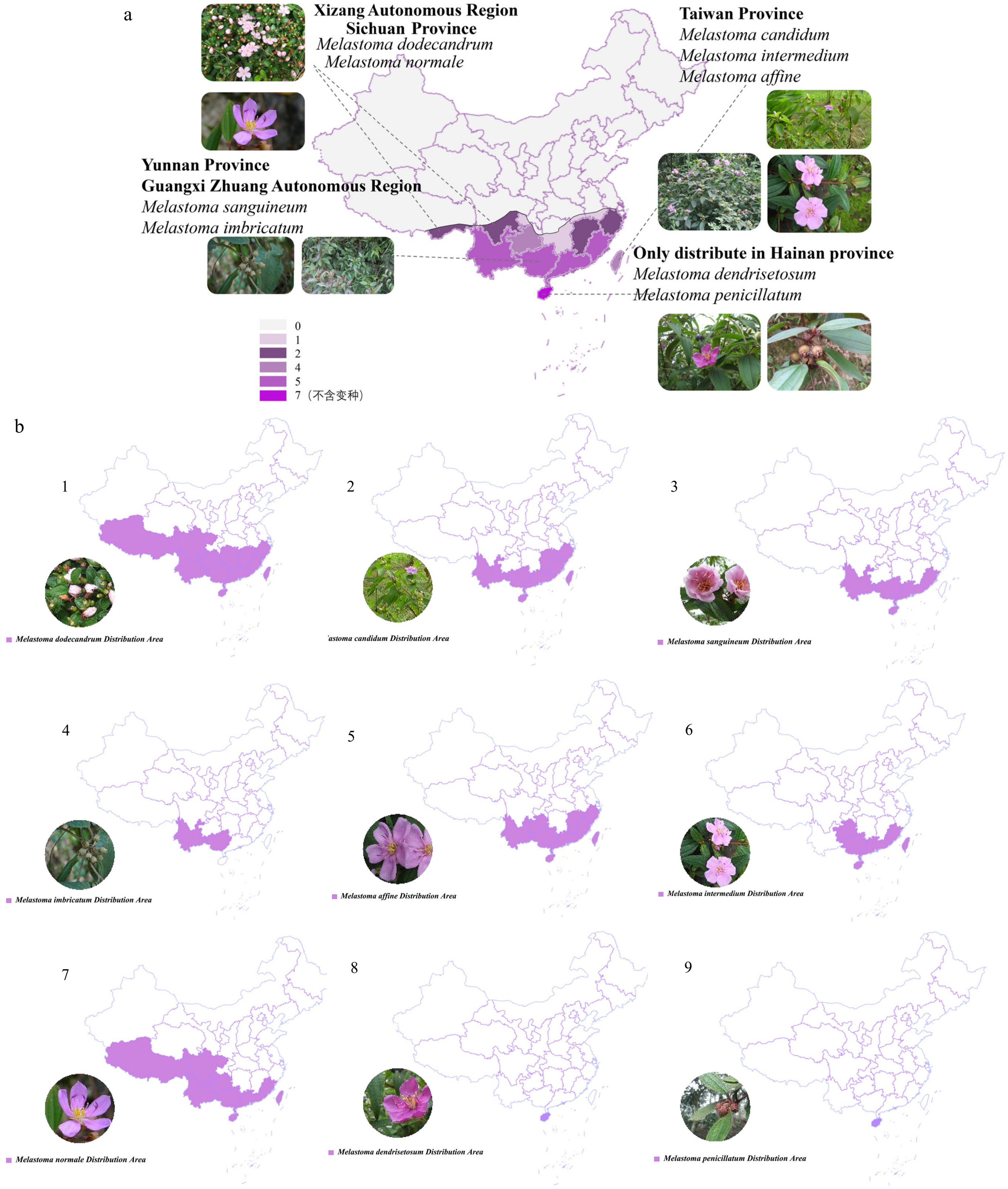


Fig. 1 Quantity distribution maps. (a) Species of *Melastoma* in various provinces of China. (b) The specific distribution of nine species of *Melastoma* plants. 1: *Melastoma dodecandrum*, 2: *Melastoma candidum*, 3: *Melastoma sanguineum*, 4: *Melastoma imbricatum*, 5: *Melastoma affine*, 6: *Melastoma intermedium*, 7: *Melastoma normale*, 8: *Melastoma dendrisetosum*, 9: *Melastoma penicillatum*.

intermedium and *M. dodecandrum* were conical, but the base of the hairs in *M. intermedium* extended backward, while in *M. sanguineum*, it did not. The epidermal hairs on the mid-vein of *M. normale* were long and scale-like. Cluster analysis revealed that *M. intermedium*, *M. normale*, and *M. malabathricum* were closely related and grouped together, while *M. candidum*, *M. sanguineum*, and *M. dodecandrum*

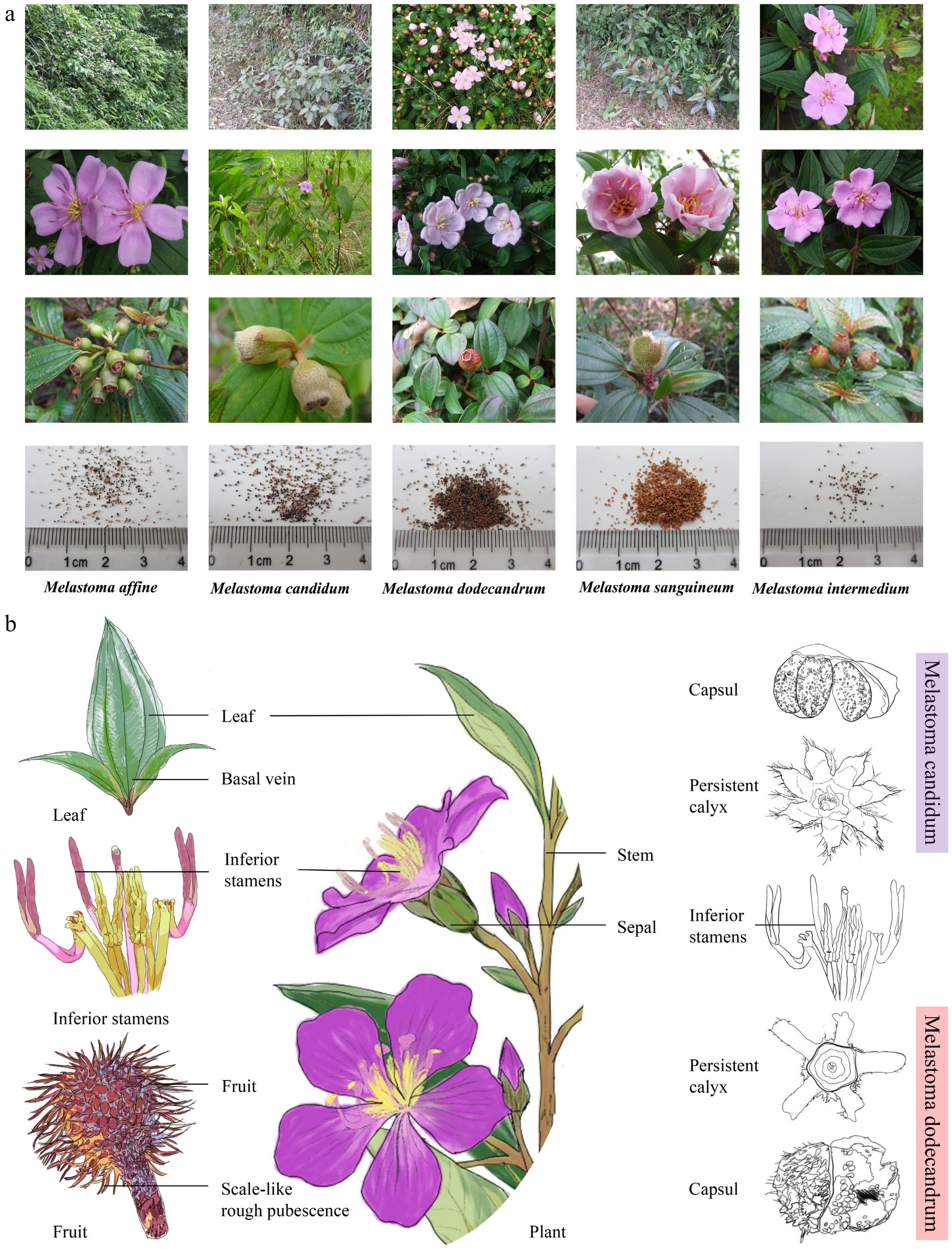


Fig. 2 (a) Characteristic images of five Melastoma species; the seed images were published in the monograph[19]. (b) Schematic diagram of plant structure of *Melastoma* represented by *Melastoma dodecandrum* and *Melastoma candidum*, including leaves, flowers, and fruits.

formed another, more distantly related group. Based on flowering period observations, it was inferred that *M. candidum* and *M. malabathricum* are two distinct species. These findings suggest that leaf surface characteristics can serve as a reliable basis for the classification and identification of *Melastoma* species[16−18].

Morphological variations and functions in *Melastoma* plants

The genus *Melastoma* exhibits remarkable morphological diversity, with most species being shrubs or sub-shrubs that vary greatly in stature, from the low, creeping *M. dodecandrum* to the tall, upright *M. sanguineum*. Their leaves are highly variable in shape, ranging from ovate to lanceolate or elliptical. Leaf margins may be smooth and satin-like or serrated with ciliate edges, while some surfaces are densely covered with strigose hairs, imparting a distinctive texture. Leaf coloration also ranges widely, from vivid emerald green to purplish red, and even within the same individual, color can shift with light intensity and developmental stage[18,19]. Morphological variation is especially pronounced in the flowers of *Melastoma*, reflecting close associations with pollination strategies, reproductive functions, and ecological adaptations. Research on floral traits largely focused on the interplay between phenotype and function, including the co-evolution of floral morphology with pollinators[20], and the ecological significance of floral symmetry in tropical environments[21]. Here, the evolutionary importance and adaptive functions of stamen heteromorphism are the focus.

Stamen diversity and functional differentiation are characteristic features of Melastomataceae. They exhibit extensive variation in size, shape, color, dehiscence mode, and accessory structures[22]. Among these traits, heteranthery provides a solution to the 'pollen dilemma' through a division of labor: pollen must function both as a nutritional reward for pollinators and as the plant's gametes to ensure reproduction[23−25]. In *Melastoma*, stamens are typically dimorphic, consisting of long and short stamens. Pollens from long stamens primarily serve a reproductive role, adhering to 'safe sites on pollinators' bodies where it is less likely to be groomed off. In contrast, pollen from short stamens primarily serves as a food reward, and flowers of *Melastoma* are frequently visited by carpenter bees (Xylocopa)[26]. Similarly, in *Macairea radula*, heteromorphic stamens are preferentially visited by *Centris aenea*[27]. This division of labor is achieved through the alignment of stamen length with pollinator body size and the adjustment of style length to match pollinator morphology. The long stamens extend beyond the bee's abdomen, depositing pollens on their dorsum, a region that is difficult for the bee to groom, whereas the short stamens contact the ventral abdomen, where pollen can be easily collected and utilized (Fig. 3). In some species, stamen coloration further reinforces this division of function. Short stamens are often bright yellow, which attracts pollinators to forage on them first, while long stamens typically resemble the petal color or background, thereby reducing disturbance and ensuring effective transfer of reproductive pollen[19,25,28,29]. Pollen release in *Melastoma* is closely linked to pollination strategy. Most species possess poricidal anthers, which release pollen only through apical pores when vibrated by pollinators. This dehiscence mode regulates pollen dispensing, prevents wastage, and excludes non-vibrating visitors, ensuring efficient transfer. For example, the anthers of *Rhynchanthera grandiflora* possess rostrate appendages that guide directional pollen release during vibration, thereby enhancing pollen deposition on pollinators[24]. In a few species, the anthers are polythecous, with septa dividing them into multiple thecae. This condition may alter the timing of pollen release and allow adaptation to a wider diversity of pollinators[21,30,31]. Stamen appendages, including connective extensions, glands, and trichomes, also play important roles in functional adaptation. In some species, extended connectives or dorsal appendages serve as 'mechanical grips' for pollinators, stabilizing anther vibrations and enhancing pollen release efficiency. The reproductive system has co-evolved with floral morphology. Most species rely on pollinators to achieve out-crossing, but some exhibit partial self-compatibility. This mechanism ensures reproductive assurance under pollinator scarcity while balancing reproductive efficiency and genetic diversity[32]. For example, *M. candidum* possesses typical heteromorphic stamens and is strictly entomophilous. Its breeding system is predominantly out-crossing with partial self-compatibility. However, reproduction still depends on pollinators, and its relative reproductive success is very low, indicating significant limitations in the process of sexual reproduction[24,33].

Morphological variation in *Melastoma*, particularly in floral traits, represents fine-scale adaptations to the pollination environment. Through strategies such as functional division of labor, visual signaling, and mechanical matching, these plants optimize pollen utilization and reproductive success. This makes them a typical example of co-evolution between plants and their pollinators.

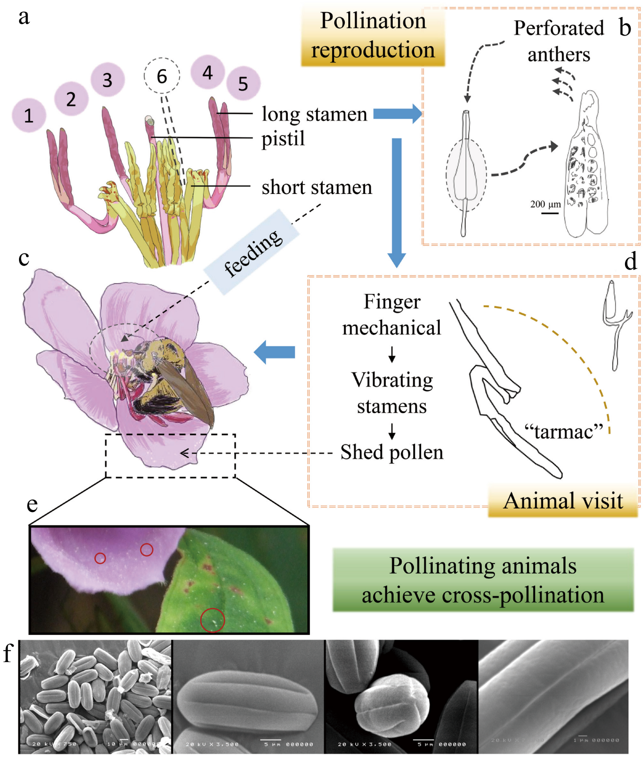


Fig. 3 Characteristics of heteromorphic stamens of *Melastoma candidum* and their co-evolution with pollinating animals. (a) Characteristics of heterosexual stamens. (b) The process of pollen release from long stamens. (c) The synergy between the heteromorphic stamen structure and the feeding behavior of *Xylocopa aeratus*. (d) The structure of long stamens. (e) After the *Xylocopa aeratus* feed, their pollen scatters on the flowers and leaves. (f) Electron microscope scanning image of *M. candidum* pollen[19].

Breeding and cultivar development

Advances in horticultural techniques have enabled the introduction and domestication of wild *Melastoma* species, leading to the development of artificial cultivars[34−36]. Selective breeding and hybridization are the main strategies for resource utilization and cultivar innovation. Several ornamental cultivars have been successfully developed, including *Melastoma* 'Tianjiao', 'Xinyuan', 'Zishan', and 'Hongfei'[37,38]. *Melastoma* 'Tianjiao' was bred by crossing female *M. candidum* with male *M. sanguineum*. It has a compact form with dense branches and bears abundant light purple flowers, blooming from June to October and fruiting from June to November. *Melastoma* 'Xinyuan', developed from a cross between female *M. sanguineum*, and male *M. intermedium*, bears fuchsia flowers with petaloid stamens coiled into inner petal rings, flowering from June to August and fruiting from July to October. Both cultivars thrive in warm, humid climates with full sun and prefer acidic loam or sandy loam[37]. *Melastoma* 'Zishan' was bred by crossing female *M. ultramaficum* from Malaysia with male *M. penicillatum* from China. It has a compact habit with glossy dark green leaves and flowers nearly year-round, peaking from April to September. The cultivar is vigorous, low-maintenance, and slightly tolerant of weakly alkaline soils. *Melastoma* 'Hongfei', obtained from a cross between female *M. penicillatum* and male *M. normale*, shows an open crown, bright red flowers, and red-glossed young leaves, flowering from April to May under warm, humid, sunny conditions[38]. All four cultivars are suitable for tropical and subtropical regions and are commonly propagated through tissue culture or stem cuttings. Pruning after flowering and fruiting improves branching and canopy shaping, while careful water management enhances growth performance.

Native Chinese *Melastoma* species such as *M. candidum*, *M. normale*, *M. affine*, and *M. sanguineum* are predominantly propagated by seeds. In contrast, artificial cultivars are mainly propagated by stem cuttings or tissue culture[16,39,40]. For cutting propagation, healthy, pest-free semi-lignified or tender shoots about four to six centimeters long are preferred. Half of the two upper leaflets are retained, with the upper cut made flat and the lower cut oblique. Cutting should be completed on the same day. After planting, maintain 65%–70% shading, 70%–85% relative humidity, and a temperature of 24–35 °C. Water twice daily (morning and evening) to sustain moisture, and disinfect with 0.1% carbendazim every 7–10 d while removing diseased branches and fallen leaves[34]. Peat soil is considered an ideal substrate, or alternatively, a 1:1 mixture of peat and perlite disinfected with carbendazim. Exogenous rooting treatments significantly improve success rates. Soaking cuttings in 500 mg/L IBA, NAA, or ABT rooting regulators for 15 min enhances rooting efficiency. Optimal conditions for *M. sanguineum* cuttings include a substrate of yellow soil : sand (1:2), pretreatment with 5 mg/L NAA, and exposure to a blue : red light ratio of 2:1 during rooting[41].

Ecological adaptability

Aluminum (Al^{3+}) hyper-accumulation has been reported in approximately 45 plant families, most of which are tropical or subtropical woody taxa, including Melastomataceae and Symplocaceae. Within Melastomataceae, species of the genus *Melastoma* represent an important group of Al hyper-accumulators[42,43]. Among them, *M. malabathricum* is a representative Al^{3+} hyper-accumulating species that thrives in tropical acidic soils, where root mucilage plays a specific role in Al uptake[44]. Under Al-deficient conditions, the concentrations of water-soluble calcium, magnesium, and oxalate in the plant decline significantly, indicating that Al^{3+} acquisition mechanisms are essential for sustaining normal growth[45]. Moreover, hydroponic experiments have shown that the application of Al^{3+} promotes the growth of *M. malabathricum*, possibly by alleviating Fe toxicity or maintaining organic acid metabolic balance[45]. These findings highlight the unique dependence of *Melastoma* species on Al in strongly acidic environments and reveal their specialized physiological mechanisms for Al^{3+} hyper-accumulation.

In addition to adaptation to acidic soils, *Melastoma* species exhibit ecological potential for remediation under polluted or stressful environments. Experiments on six *Melastoma* species under cadmium (Cd) and lead (Pb) stress demonstrated that with increasing metal concentrations, seed germination rates and root growth were progressively inhibited. However, *M. malabathricum*, *M. candidum*, and the cultivar *Melastoma* 'Tianjiao' exhibited stronger Cd and Pb tolerance, suggesting their potential as pioneer species for the remediation of heavy metal-contaminated soils[46−48]. Similarly, salt stress experiments on six *Melastoma* species revealed significant interspecific differences in morphological and physiological responses, with *M. malabathricum* displaying the strongest salt tolerance, thereby demonstrating its suitability for cultivation in coastal regions or saline–alkali soils[47]. Collectively, these studies indicate that *Melastoma* species not only rely on Al^{3+} to promote growth in acidic soils but also possess resilience to heavy metal and salt stress, underscoring their potential applications in soil improvement and ecological restoration of degraded environments.

Potential edible and medicinal functions

Plants of the genus Melastoma (Melastomataceae) possess diverse pharmacological activities attributable to their rich repertoire of bio-active compounds, including flavonoids, tannins, phenolic acids, and triterpenoids. *M. malabathricum* is particularly notable for its anti-inflammatory, antibacterial, and anti-tumor properties, which are primarily mediated by quercetin, ursolic acid, and related constituents. Traditionally, it has been employed in Southeast Asia to treat diarrhea, wound infections, and postpartum inflammation[4, 49,50]. *Melastoma dodecandrum*, widely used in Traditional Chinese Medicine (TCM) and ethnic medicine, exhibits a broad spectrum of therapeutic effects. Its flavonoids and polysaccharides confer anti-inflammatory activity by suppressing mediators such as nitric oxide (NO) and tumor necrosis factor-α (TNF-α), and anti-diabetic effects through modulation of the PI3K/Akt and AMPK signaling pathways, improving insulin sensitivity. Additionally, *M. dodecandrum* demonstrates lipid-lowering, hepatoprotective, hemostatic, and wound-healing activities, partly mediated by luteolin and xanthylium pyran derivative, which also contribute to its anticoagulant and antioxidant effects[51,52]. These multi-component, multi-target properties underpin its clinical relevance in treating postpartum hemorrhage, gastric ulcers, and snakebites[53]. Other species, including *M. affine*, *M. normale*, and *M. sanguineum*, display complementary pharmacological profiles. *M. affine*, rich in gallic acid, primarily exerts antibacterial and hemostatic effects, supporting its use in wound repair[54,55]. The roots and whole plant of *M. normale* are rich in polyphenols and tannins (including ellagitannins) and have shown notable anti-inflammatory activity *in vitro*. These compounds, together with the general antioxidant effects of flavonoids and tannins, theoretically support cardiovascular protective effects. Traditionally, plants of the genus *Melastoma* have been used to treat dysentery, diarrhea, bleeding, and traumatic hemorrhage, which may be related to their hemostatic and anti-inflammatory actions; however, specific *in vivo* evidence for the hemostatic or cardiovascular protective mechanisms of *M. normale* is still lacking[56,57]. Seeds of *M. saigonense*, which are rich in phenolic acids (e.g., gallic and caffeic acids) and flavonoids, exhibit pronounced *in vitro* α-glucosidase inhibitory activity, underscoring their potential hypoglycemic properties. Nevertheless, direct evidence for the inhibition of advanced glycation end-product formation or the stimulation of bile secretion by *M. saigonense*, as well as for analogous effects of *M. sanguineum* attributed to afzeloside, has yet to be substantiated[58] (Fig. 4, Table 1) .

Collectively, these findings indicate that *Melastoma* species represent a rich source of bioactive compounds, including flavonoids, phenolic acids, and tannins, which exhibit antioxidant, anti-inflammatory, and antibacterial activities. Some species have also demonstrated hepatoprotective and hypoglycemic effects in limited *in vivo* or *in vitro* studies, suggesting their potential for the development of natural therapeutics.

Genome resources and genetic diversity

Nuclear genome

The nuclear genome of *Melastoma* underpins its morphogenesis, physiological adaptation, and ecological traits, providing essential information for functional studies and resource utilization[76].

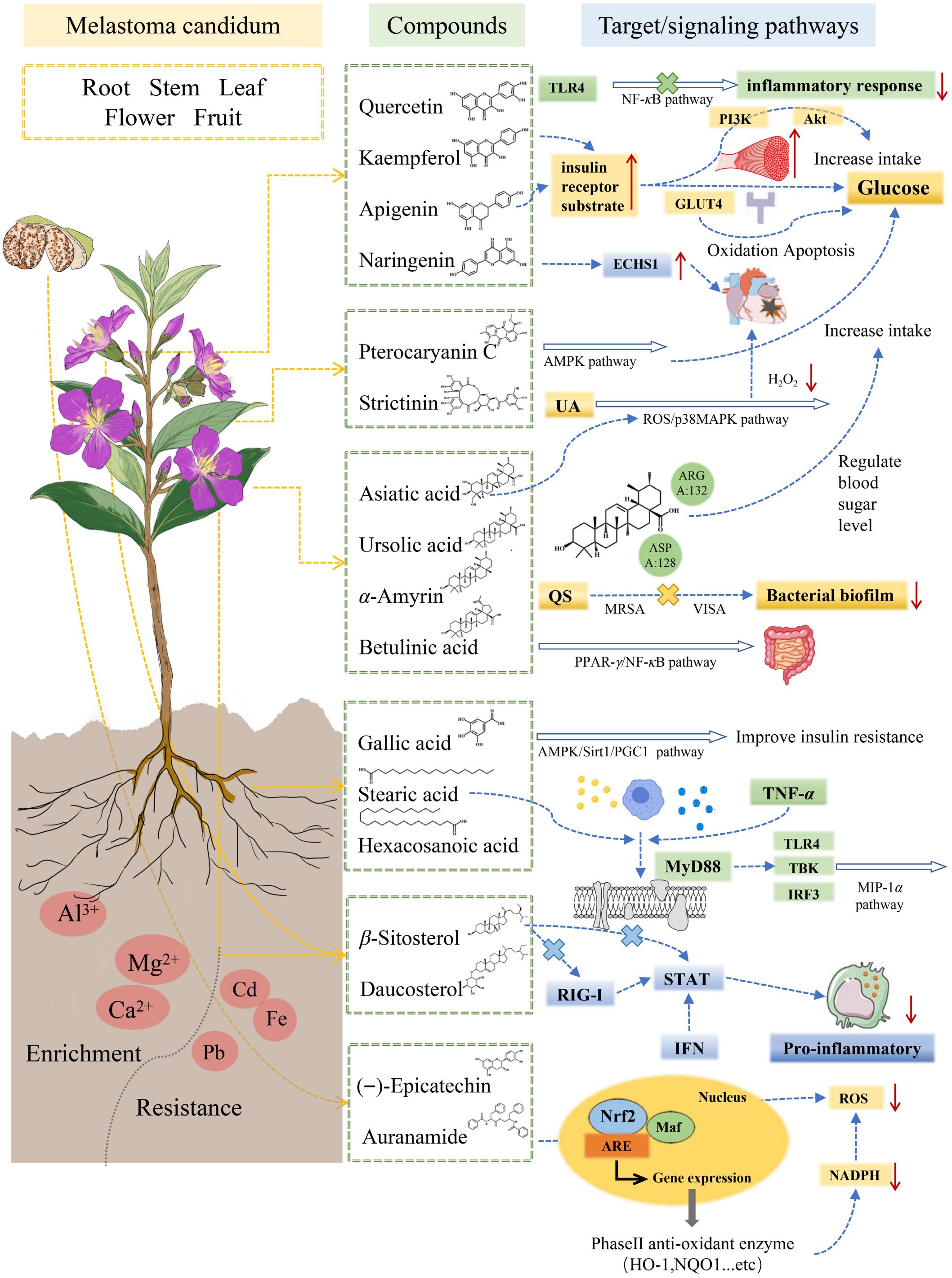


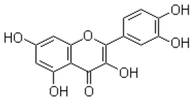
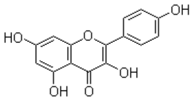
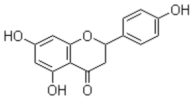
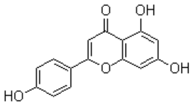
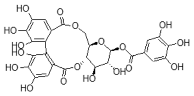
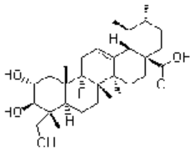
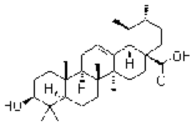
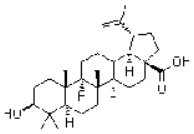
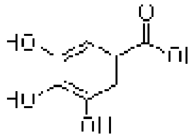
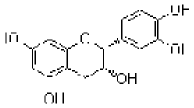
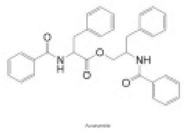
Fig. 4 Medicinal components of the tissues and organs of plants of *Melastoma* and their functional signaling pathways.

Chromosome-level reference genomes for *M. dodecandrum* and *M. candidum* have been generated using PacBio long-read sequencing combined with Hi-C technology, enabling investigations into evolutionary mechanisms and functional associations within the genus (Table 2).

The *M. candidum* genome is 256.2 Mb, with 98.0% of sequences anchored to 12 pseudo-chromosomes, a scaffold N50 of 20.5 Mb, and an LTR Assembly Index (LAI) of 25.5. BUSCO analysis recovered 96.9% of core eukaryotic genes, indicating high assembly completeness. Repetitive sequences constitute 31.5% of the genome, predominantly long terminal repeat retrotransposons (LTR-RTs), including Ty3/Gypsy (11.7%) and Ty1/Copia (7.8%). A total of 40,938 protein-coding genes were predicted, 91.3% of which are functionally annotated, with an average length of 2,387.2 bp and 5.2 exons per gene. Additionally, 1,818 non-coding RNAs (ncRNAs) were identified[77].

M. dodecandrum genome spans 299.81 Mb, with a contig N50 of 3.00 Mb, and 90.8% of sequences anchored to 12 pseudo-chromosomes. Repetitive sequences account for 40.9%, with LTR transposons contributing 33.5%, substantially higher than in related species such as *Eucalyptus grandis* (21.9%) and *Punica granatum* (18.9%). Gene annotation identified 35,681 protein-coding genes

Table 1. Types, representative compounds, and mechanisms of action of bioactive compounds in the genus Melastoma.

Types	Representative compounds	Chemical structural formula	Target/signaling pathway	Mechanism of action	Species	Ref.
Flavonoids	Quercetin		The nf-kappa B	Inhibition of the NF-κB pathway reduces TNF-α expression in LPS-induced RAW264.7 cells	*M. candidum* *M. dodecandrum* *M. malabathricum* *M. normale* *M. villosum*	[53, 59–62]
	Kaempferol		PI3K/Akt/GLUT4	Up-regulate the gene and protein expression of PI3K, Akt, and GLUT4 in skeletal muscle, promote glucose transport and utilization, and reduce blood glucose	*M. candidum* *M. dodecandrum* *M. malabathricum* *M. normale* *M. villosum*	[55, 62,63]
	Naringenin		ECHS1–PPARα/AMPK	Reduces doxorubicin-induced myocardial oxidative stress and apoptosis by upregulating ECHS1 protein	*M. malabathricum*	[64,65]
	Apigenin		PI3K/Akt/GLUT4	Up-regulated the expression of GLUT4 and improved glucose consumption and glycogen synthesis in IR-HepG2 cells. Slightly increased expression of PI3K and p-Akt	*M. candidum* *M. dodecandrum* *M. candidum*	[63, 66]
Tannins	Strictinin		ROS/p38MAPK	Provide hydrogen atoms to remove ROS and reduce oxidative stress; UA regulates the p38MAPK pathway and inhibits H_2O_2-induced apoptosis	*M. malabathricum* *M. dodecandrum* *M. normale*	[67–69]
Terpenoids	Asiatic acid		MAPK/STAT3	Activation of ERK and p38 MAPK pathways induces apoptosis and cell cycle arrest in breast cancer cells; Inhibition of STAT3 and Claudin-1	*M. dodecandrum*	[65, 70]
	Ursolic acid		AMPK /PPARα	Hypoglycemic mechanisms	*M. malabathricum* *M. dodecandrum* *M. intermedium*	[61, 71]
	Betulinic acid		PPAR-γ/NF-κB	Improvement of intestinal inflammation through the PPAR-γ/NF-κB pathway	*M. malabathricum* *M. dodecandrum* *M. intermedium*	[68, 72]
Organic acids	Gallic acid		AMPK/Sirt1/PGC1	Promotes mitochondrial function and improves insulin resistance	*M. candidum* *M. intermedium* *M. malabathricum* *M. polyanthum* *M. normale* *M. affine*	[73,74]
	Stearic acid		TLR4/TBK/IRF3	Enhance MIP-1α expression and promote inflammatory response; Activates the lactate-HIF1α pathway at high concentrations, upregulating VEGF and pro-inflammatory cytokines	*M. dodecandrum*	[62, 75]
Others	(-)-Epicatechin		Nrf2	Promote the expression of antioxidant enzymes (HO-1, NQO1), inhibit NADPH oxidase activity, and reduce ROS production	*M. dodecandrum*	[65, 73]
	Auranamide		NF-κB/Nrf2	Provide hydrogen atoms to remove ROS and reduce oxidative stress; UA regulates the p38MAPK pathway and inhibits H_2O_2-induced apoptosis	*M. malabathricum*	[75]

(functional annotation rate: 98.98%) and 1,818 ncRNAs, including 105 microRNAs and 633 tRNAs[76].

Mitochondrial genome

The mitochondrial genomes of *Melastoma* species exhibit a circular structure, ranging in size from 391,595 bp in *M. candidum* to 411,944 bp in *M. dodecandrum*, with GC contents of approximately 44.2%–44.4%. They contain a relatively low proportion of repetitive sequences (3.52%–3.81%), which are predominantly short repeats of 30–34 bp, while long repeats (more than 100 bp) rarely undergo recombination. This feature is similar to that observed in Nymphaeaceae but markedly lower than in parasitic plants[5, 78]. Notably,

Table 2. The nuclear genome of *Melastoma candidum* and *Melastoma dodecandrum*.

Species	Genome size (Mb)	Anchored pseudo-chromosomes	Scaffold/contig N50 (Mb)	Repetitive sequence	Protein-coding genes	Functional annotation (%)	ncRNAs
M. candidum	256.2	12	20.5 (scaffold)	31.5%	40,938	91.3	1,818
M. dodecandrum	299.81	12	3.00 (contig)	40.9%	35,681	98.98	1,818 (miRNA 105, tRNA 633)

Table 3. The mitochondrial genome of *M. dodecandrum*, *M. candidum*, and *M. sanguineum*.

Species	Genome size (bp)	GC content	Structure	Repetitive sequence
M. dodecandrum	411,944	44.18%	Circular	3.52%
M. candidum	391,595	44.36%	Circular	3.52%–3.81%
M. sanguineum	395,542	44.37%	Circular	3.52%–3.81%

IDT events exist in the mitochondrial genomes of eight species, reflecting a common ancestral origin.

chloroplast-derived DNA insertions, also referred to as intra-cellular DNA transfer (IDT) events, have been detected in several *Melastoma* species, including *M. candidum*, *M. sanguineum*, and *M. malabathricum*. A shared region of approximately 5.1 kilobases contains pseudogenes such as *ψrbcL*, *ψatpB*, *ψatpE*, and *ψtrnM-CAU*. This region is conserved across species but exhibits nucleotide substitutions and insertions/deletions, suggesting an origin from a common ancestor. Furthermore, in species such as *M. penicillatum*, nearly intact rbcL and partial atpB sequences were identified, indicating the occurrence of recent IDT duplication events[79] (Table 3).

Chloroplast genome

The chloroplast genomes of *Melastoma* species encode a broad spectrum of genes, including protein-coding genes, transfer RNA (tRNA) genes, and ribosomal RNA (rRNA) genes. Among protein-coding genes, those directly associated with photosynthesis are conserved, such as psbA (encoding the D1 protein of photosystem II), psaA (photosystem I reaction center), and rbcL (the Rubisco large subunit). Genes essential for chloroplast gene expression are also well represented, including ribosomal protein genes (rpl, rps) and RNA polymerase subunit genes (rpo). In addition, functional genes related to pigment synthesis and lipid metabolism, such as chlB, involved in chlorophyll biosynthesis, are consistently present[80]. Comparative analyses of complete chloroplast genomes across 20 species of the family Melastomataceae revealed a typical quadripartite structure, comprising large single-copy (LSC), small single-copy (SSC), and two inverted repeat (IR) regions. Genome sizes ranged from 153,311 to 157,216 base pairs (bp), with an average of 155,806 bp. Most species harbored 84 protein-coding genes, 37 tRNA genes, and 8 rRNA genes (129 in total, including duplicates). Gene content and arrangement were highly conserved across species in the order Myrtales, although rps16 and rpl2 were identified as pseudogenes in some lineages. The overall GC content averaged 37%, with the highest GC content in the IR regions and the lowest in the SSC regions. Seventeen genes were found to contain introns, and some intergenic spacers and introns have been identified as highly informative phylogenetic markers. Phylogenetic analyses based on complete chloroplast genomes provided strong resolution of relationships within Melastomataceae, underscoring both the evolutionary conservation of chloroplast genomes and their utility for taxonomic and phylogenetic studies[6,81−83] (Table 4). Comparative analyses underscore the structural and functional conservation of Melastomataceae plastomes, while complete chloroplast genome data significantly improve phylogenetic resolution and support, providing a robust genomic resource for evolutionary, taxonomic, and phylogenetic studies[6, 81].

Evolutionary relationships

The remarkable morphological plasticity and ecological adaptability of *Melastoma* species arise from the interplay of multi-level genomic variations. A central driver of this diversification is the combination of gene functional differentiation and whole-genome duplication (WGD). In *M. dodecandrum*, transferase genes and plant

Table 4. The chloroplast genome of melastomataceae.

Species	GenBank accession number	Plastome length (bp)	LSC (bp)	SSC (bp)	IR (bp)	GC content (%)
Allomaieta villosa	KX826819	156,452	85,914	16,975	26,781	36.9
Bertolonia acuminata	KX826820	156,045	85,571	17,011	26,733	37.0
Blakea schlimii	KX826821	155,862	85,370	16,998	26,747	37.1
Eriocnema fulva	KX826822	155,994	85,431	16,953	26,805	37.0
Graffenrieda moritziana	KX826823	155,733	85,341	16,924	26,734	37.0
Henriettea barkeri	KX826824	156,527	85,991	17,036	26,750	36.9
Merianthera pulchra	KX826825	156,168	85,621	17,001	26,773	37.0
Miconia dodecandra	KX826826	157,216	86,609	16,999	26,804	37.0
Nepsera aquatica	KX826827	155,110	84,644	17,066	26,700	37.1
Opisthocentra clidemioide	KX826828	156,352	85,866	16,942	26,772	37.0
Pterogastra divaricata	KX826829	154,948	84,718	17,156	26,537	37.2
Rhexia virginica	KX826830	154,635	84,459	16,924	26,626	37.2
Rhynchanthera bracteata	KX826831	155,108	85,093	16,729	26,643	37.0
Salpinga maranoniensi	KX826832	153,311	85,128	16,653	25,765	37.4
Tibouchina longifolia	KX826833	156,789	86,297	17,124	26,684	37.1
Triolena amazonica	KX826834	156,652	86,200	16,970	26,741	36.9
Melastoma candidum	KY745894	156,682	86,084	17,094	26,752	37.17
Tigridiopalma magnifica	MF663760	155,663	85,161	16,932	26,785	37.11
Melastoma dodecandrum	MH748092	156,611	86,014	17,097	26,750	37.1
Scorpiothyrsus erythrotrichus	MZ434958	160,731	85,482	17,007	26,780	36.9

hormone signaling pathways collectively modulate environmental adaptability, facilitating survival across heterogeneous habitats. Members of the MADS-box gene family exemplify functional diversification: the expansion of AP1-like genes (eight members) underpins floral meristem regulation and floral organ development, while four LAZY1-like genes contribute to the prostrate growth habit through negative regulation of branch angles. At the genomic level, *Melastoma* shares two ancient WGD events with its sister genus Osbeckia: the relatively recent σ event (Ks: 0.256–0.280) and the older ρ event (Ks: 0.927–1.022). Both events occurred after the γ whole-genome triplication common to core eudicots, providing the substrate for lineage-specific gene family expansion and functional innovation[76].

Transcription factor families further illuminate the links between genomic changes and morphological outcomes. The WOX (WUSCHEL-related homeobox) family in *M. dodecandrum* comprises 22 members, grouped into three evolutionary clades (ancient, intermediate, and WUS) and nine structural types, all harboring a conserved Homeodomain (Helix-Loop-Helix-Turn-Helix motif). These genes are distributed across ten chromosomes and shaped by 15 pairs of segmental duplications, with no tandem duplications observed. Promoter analyses revealed enrichment of cis-elements responsive to light (e.g., G-box), stress (LTR), and growth (CAT-box). Expression profiles show strong tissue specificity: *MedWOX4* is stem-specific expressed, whereas *MedWOX13* is broadly expressed across roots, stems, leaves, and flowers. Such diversification, reinforced by WGD-driven duplications, indicates that WOX genes play a pivotal role in regulating stem development and the evolution of prostrate growth forms[84].

Organelle genomes also contribute to evolutionary insights by revealing patterns of functional adaptation and phylogenetic placement. In *M. dodecandrum* and *M. candidum*, substantial intracellular DNA transfer (IDT) from chloroplast to mitochondria has been detected, including an ~8 kb chloroplast-derived region containing both intact and pseudogenized genes[5,6].

Molecular mechanisms for the formation of core characteristics

The core characteristics of *Melastoma* species arise from the coordinated action of multiple regulatory layers, encompassing growth and developmental control, secondary metabolite production, trait optimization, and hormone-mediated signaling. Within this framework, transcription factor families such as ARF and WOX form the regulatory backbone of trait specification. In *M. dodecandrum*, 27 ARF genes orchestrate auxin signaling, with *MedARF6C* and *MedARF7A* responding to exogenous auxin to drive organogenesis. More than half of the ARF family shows elevated expression in stems, thereby contributing to the formation of species-specific stem architectures[85]. Complementarily, the 22 WOX family members predominantly regulate meristem activity and stem development: stem-specific *MedWOX4* and broadly expressed *MedWOX13* collectively maintain meristem function, supporting the prostrate growth habit characteristic of *M. dodecandrum*[84]. These core regulators operate within hierarchical networks, modulated by upstream factors such as AP2/ERF and bHLH, and their functional capacity is amplified through gene duplication events driven by whole-genome duplications (WGDs). For instance, expansion of *MedWOX4* enhances stem developmental regulation, distinguishing prostrate growth from erect forms.

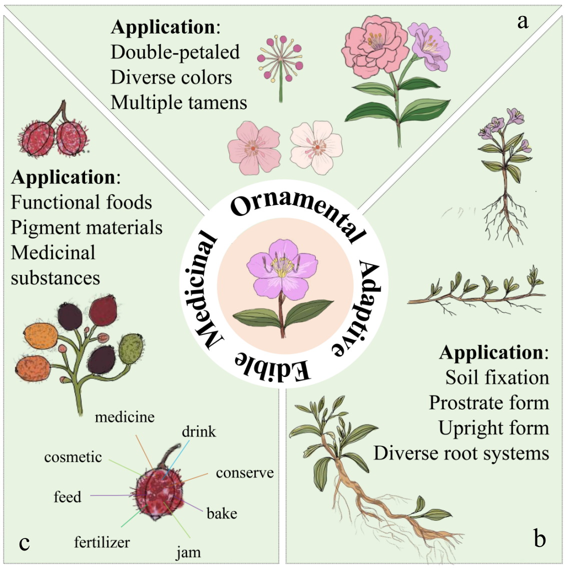


Fig. 5 Breeding directions of *Melastoma*. (a) In terms of ornamental applications, it includes the double-petal morphology of flowers, the diversity of flower colors, and the multiple stamens of heteromorphic stamens. (b) The aspects of adaptive application include the diversity of root systems and the upright/creeping forms of plants. (c) In terms of food and medicinal applications, it includes functional foods, fruit color, and medicinal substances such as alkaloids rich in fruits.

Prospects

Future research on *Melastoma* is expected to advance through integrated genomic, transcriptomic, proteomic, and metabolomic analyses, enabling systematic elucidation of the molecular networks governing stem architecture, flower pigmentation, stamen heteromorphism, and secondary metabolite biosynthesis[86]. High-quality, chromosome-level genome assemblies will facilitate identification of key transcription factors (e.g., *ARF*, *WOX*, *MYB*) and hormone signaling components, providing targets for precise molecular breeding and genome editing, including CRISPR/Cas9-mediated modulation of anthocyanin synthesis and other trait-specific pathways. Concurrently, the ecological resilience of *Melastoma* manifested in aluminum hyper-accumulation, heavy metal tolerance, and salt stress adaptation (Fig. 5). This supports its potential applications in soil remediation, ecological restoration, and sustainable landscaping[87]. Further phytochemical and pharmacological investigations are needed to characterize bio-active compounds and their multi-target mechanisms, informing the development of medicinally and nutritionally valuable cultivars[88]. Integrating germplasm evaluation, optimized propagation techniques, and standardized cultivation systems will enhance both conservation and commercial utilization. Collectively, these approaches will bridge fundamental research and applied innovation, promoting the rational exploitation of *Melastoma* species for ecological, ornamental, and therapeutic purposes.

Author contributions

The authors confirm their contributions to the paper as follows: conceptualization, methodology, supervision, writing, review and editing: Zhao K, Peng D, Zhou Y; data curation, writing−original draft preparation: Tang F, Zhao Y, Zhan S, Huang R; resources: Li X, Peng Y, Su Q. All authors reviewed the results and approved the final version of the manuscript.

Data availability

The relevant data can be obtained by contacting the corresponding author.

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Conflict of interest

The authors declare that they have no conflict of interest.

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