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ROLE OF MOLECULAR MARKERS IN AUTHENTICATION GENETIC DIVERSITY AND CONSERVATION OF ENDANGERED MEDICINAL PLANTS

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ABSTRACT

The escalating global demand for herbal therapeutics, combined with relentless habitat fragmentation and overexploitation, has pushed a substantial proportion of medicinal flora toward extinction. Conventional morphological identification and broad-spectrum conservation strategies often prove inadequate for these taxa, particularly when processed plant parts enter international supply chains or when cryptic species inhabit remote ecosystems. Molecular markers provide a robust, reproducible, and increasingly cost-effective alternative for authenticating species identity, quantifying intraspecific genetic diversity, and implementing precision conservation. This review synthesizes current knowledge on the deployment of DNA barcoding, microsatellites, inter-simple sequence repeats, and next-generation sequencing-derived single nucleotide polymorphisms in endangered medicinal plant systems. We examine how the core barcode loci rbcL and matK, augmented by the nuclear internal transcribed spacer 2 (ITS2), resolve taxonomic uncertainty and expose commercial adulteration. Population-level analyses using codominant SSRs and genome-wide SNPs reveal patterns of gene flow, genetic bottlenecks, and demographic decline that are invisible to census-based assessments. Furthermore, we present an integrated framework demonstrating how molecular data inform in situ reserve design, ex situ germplasm banking, and sustainable harvest protocols. Drawing on literature published primarily between 2020 and 2025, we highlight persistent gaps in reference library coverage, bioinformatics accessibility, and policy integration. We conclude that the future of medicinal plant conservation depends on embedding molecular authentication and genomic monitoring into national pharmacopoeias, international trade regulations, and community-based management plans.

KEYWORDS: DNA barcoding, ITS2, conservation genomics, medicinal flora, microsatellites, next-generation sequencing, population structure, sustainable harvest.

1. INTRODUCTION

Medicinal plants underpin healthcare systems across every inhabited continent. The World Health Organization estimates that traditional medicine remains the primary source of health care for roughly 80% of the population in developing countries, and global trade in herbal raw materials exceeds several billion dollars annually (Chen et al., 2014). Paradoxically, the commercial success of botanical medicine has become a primary driver of biological decline. Overharvesting for roots, bark, bulbs, and whole herbs-often exacerbated by poverty-driven wild collection-has decimated wild populations of high-value species such as Panax ginseng C.A. Meyer, Taxus chinensis (Pilger) Rehder, and Saussurea obvallata (DC.) Edgew. (Ghorbani et al., 2021). Simultaneously, land conversion for agriculture, logging, and urban expansion has fragmented the habitats that sustain these species, restricting gene flow and accelerating genetic erosion (Liu et al., 2021; Pimm et al., 2014). The result is a conservation crisis in which the very plants required for human health are vanishing before they can be scientifically inventoried.

Accurate identification represents the foundation upon

which sustainable use and conservation rest. Species names link organisms to their pharmacological profiles, toxicological risks, and legal protections. Yet morphological identification is fraught with difficulty. Many endangered medicinal species belong to taxonomically complex genera characterized by cryptic diversity, convergent leaf architecture, or reduced floral displays (Raja et al., 2023). The problem intensifies once plants enter trade: roots are peeled, bark is shredded, leaves are powdered, and rhizomes are decocted, obliterating diagnostic morphological characters. Microscopic examination of anatomical features can assist in some cases, but it requires specialist expertise, is labor-intensive, and often cannot distinguish between closely allied congeners (Mishra et al., 2021). Consequently, markets worldwide are rife with substitution, adulteration, and mislabeling, with documented cases of toxic species replacing sought-after medicinals with fatal consequences (Parveen et al., 2020).

Molecular markers circumvent these obstacles by relying on heritable DNA sequence variation rather than phenotypic expression. Beginning with isozymes and hybridization-based methods in the late twentieth century, the field has evolved through PCR-based fingerprinting techniques to the current era of high-throughput sequencing and genome-wide SNP discovery (Zhang et al., 2022). The introduction of DNA barcoding in the early 2000s offered a standardized approach to species identification by amplifying universally accepted short genetic regions, thereby enabling non-specialists to compare unknown samples against curated reference libraries (Hebert et al., 2003). For land plants, the Consortium for the Barcode of Life (CBOL) Plant Working Group proposed the two-locus combination of the chloroplast genes rbcL and matK as the core barcode, while subsequent empirical studies across Chinese, Indian, and South American medicinal floras demonstrated that the nuclear ribosomal ITS2 region provides superior resolution in many angiosperm families (Hollingsworth et al., 2009; Hollingsworth, 2011; China Plant BOL Group et al., 2011).

While barcoding addresses the authentication challenge, conservation genetics employs a complementary suite of markers to probe population structure, mating systems, and historical demography. Microsatellites, or simple sequence repeats (SSRs), have been the workhorse of population-level studies owing to their high polymorphism and codominant inheritance (Yu et al., 2023). More recently, reduced-representation sequencing methods such as double-digest restriction-site-associated DNA sequencing (ddRAD-seq) and genotyping-by-sequencing (GBS) have unlocked thousands of single nucleotide polymorphisms (SNPs) in non-model organisms, facilitating genomic diversity monitoring with unprecedented resolution (Zhang et al., 2022). These data empower managers to define evolutionarily significant units, detect genetic bottlenecks, and design breeding and reintroduction programs that preserve adaptive potential.

In this review, we examine the tripartite contribution of molecular markers to endangered medicinal plant science. We first outline the principal categories of markers and their methodological underpinnings. We then discuss authentication applications, from forensic identification of raw drugs to the resolution of cryptic species complexes. The third section addresses genetic diversity assessment, emphasizing how marker data reveal spatial structure, gene flow, and demographic decline. Fourth, we demonstrate how molecular insights feed directly into conservation planning—guiding the selection of reserves, the composition of seed banks, and the regulation of harvest quotas. Finally, we identify remaining hurdles, including incomplete barcode libraries, bioinformatics bottlenecks, and the need for stronger policy integration, while charting a course toward genomic-informed conservation in the coming decade.

2. Molecular Markers: Taxonomy, Methodology, and Comparative Utility

The selection of a molecular marker is dictated by the biological scale of inquiry. Species discrimination demands conserved regions with reliable primer binding and moderate interspecific divergence, whereas population genetics requires hypervariable loci capable of resolving fine-scale allele frequency differences. This section reviews the dominant marker classes applied to endangered medicinal plants, from organelle barcodes to genome-wide SNPs.

2.1 DNA Barcoding and Mini-Barcoding

DNA barcoding seeks a standardized, short genomic region that can be recovered across broad taxonomic groups while providing sufficient variation to separate species (Hebert et al., 2003). Following extensive testing across the plant tree of life, the CBOL Plant Working Group endorsed rbcL and matK as the core two-locus barcode (Hollingsworth et al., 2009). The rbcL gene is easily amplified and aligned, offering strong discriminatory power at higher taxonomic levels, but its slow evolutionary rate renders it incomplete within recently radiated genera. The matK gene evolves more rapidly and contributes greater species-level resolution, yet its primer universality is compromised in certain families such as Orchidaceae and Asteraceae. To fill these gaps, supplementary chloroplast regions—trnH-psbA, atpF-atpH, and psbK-psbI—have been recommended on a taxon-specific basis (Ghorbani et al., 2021), and the plastid gene ycf1 has shown considerable promise as a third-tier marker in several angiosperm lineages (Dong et al., 2014).

The nuclear ribosomal internal transcribed spacer 2 (ITS2) has emerged as a particularly powerful supplementary barcode for medicinal plants. ITS2 evolves rapidly due to relaxed functional constraints,

enabling discrimination of sibling species that share identical plastid haplotypes. Meta-analyses of Chinese pharmacopoeial species indicate that the combination of rbcL + matK + ITS2 resolves approximately 85–95% of taxa, compared to roughly 70% for the plastid pair alone (Chen et al., 2014). Secondary structure modeling of ITS2 transcripts further enhances identification accuracy by incorporating conserved stem-loop constraints into phylogenetic analyses. For highly processed herbal products in which DNA is fragmented, mini-barcodes—short amplicons of 100–200 bp derived from ITS2 or trnH-psbA—provide the only viable amplification strategy (Mishra et al., 2021).

2.2 PCR-Based Fingerprinting and Microsatellites

Before the sequencing revolution, PCR-based fingerprinting techniques dominated conservation genetics. Random amplified polymorphic DNA (RAPD) uses short, arbitrary primers to generate dominant banding profiles. While RAPD requires no prior sequence knowledge, its poor reproducibility has relegated it to preliminary screening studies. Inter-simple sequence repeat (ISSR) and sequence-related amplified polymorphism (SRAP) markers offer improved reliability by anchoring primers within known repetitive motifs or coding regions, respectively. These dominant markers are cost-effective for assessing clonal diversity, as demonstrated in vegetatively propagated species such as Dioscorea opposite Thunb. and Gastrodia elata Blume (Liu et al., 2021).

Microsatellites (SSRs) remain the benchmark for population genetic analyses of endangered medicinal plants. These 1–6 bp tandem repeats exhibit high mutation rates via slipped-strand mispairing, yielding dozens of alleles per locus. Because they are codominant, SSRs provide direct estimates of heterozygosity, inbreeding coefficients, and allelic richness—parameters critical to IUCN Red List assessments. Species-specific SSR libraries have been developed for Panax ginseng, Paeonia suffruticosa Andrews, and Cypripedium calceolus L., among others, revealing severe genetic erosion in wild populations relative to cultivated or reintroduced stands (Yu et al., 2023).

2.3 Next-Generation Sequencing and Single Nucleotide Polymorphisms

The declining cost of sequencing has shifted the field toward SNP discovery via reduced-representation genomic approaches. Double-digest RAD sequencing (ddRAD-seq) and GBS generate thousands of SNPs by sequencing restriction-site-associated fragments, circumventing the need for a fully assembled reference genome (Zhang et al., 2022). For many endangered medicinal plants—characteristically large, repetitive, and heterozygous genomes—ddRAD-seq offers a pragmatic route to population genomic data. Studies on Panax japonicus C.A. Meyer and Lilium species have employed SNP data to detect loci under selection, infer historic effective population size trajectories, and identify genetically distinct lineages warranting separate management (Wu et al., 2024). Whole-genome skimming and transcriptome sequencing further yield expressed sequence tag (EST)-SSRs and functional SNPs tied to secondary metabolite pathways, linking conservation genetics to the biochemical quality control of germplasm collections.

Table 1: Comparison of Molecular Marker Systems used in Authentication and Conservation of Endangered Medicinal Plants.

Marker class	Target / method	Information content	Dominance	Strengths	Principal limitations
DNA barcoding	Chloroplast (rbcL, matK) and nuclear (ITS2) loci	Sequence-based	Haploid / diploid	Standardized; universal primers; database-backed	Incomplete resolution in some genera; plastid capture
Mini-barcoding	Short ITS2 / trnH-psbA amplicons	Sequence-based	Haploid / diploid	Works on degraded DNA in processed products	Reduced phylogenetic signal
ISSR / SRAP	Anchored repetitive or open-reading-frame primers	Multilocus profile	Dominant	Rapid; no sequence prerequisite	Reproducibility issues; homoplasy
SSR (microsatellite)	Di- to tetra-nucleotide tandem repeats	Single-locus genotype	Codominant	High polymorphism; inbreeding estimates	Development cost; null alleles in polyploids
SNP (ddRAD-seq)	Genome-wide restriction-site variants	Thousands of loci	Codominant	Genome-wide coverage; demographic inference	Bioinformatic demands; ascertainment bias
DNA metabarcoding	Multiplex amplicon sequencing (ITS2 / rbcL)	Community composition	Haploid / diploid	Detects admixtures in polyherbal preparations	PCR bias; incomplete reference libraries

3. Authentication of Endangered Medicinal Plants

Molecular authentication serves two convergent goals: protecting consumer health by ensuring product integrity and protecting wild populations by verifying that traded material is correctly identified and legally sourced.

3.1 Forensic Identification and Species Assignment

The primary application of DNA barcoding in medicinal

plant science is the assignment of unknown specimens to known taxa. Standard barcoding workflows (Figure 1) involve DNA extraction, PCR amplification using universal primers, bi-directional Sanger sequencing, and comparison against reference databases such as GenBank, the Barcode of Life Data System (BOLD), and the Medicinal Plant DNA Barcode Database (Liu et al., 2021). Correct identification is not merely academic: the roots of Stephania tetrandra S. Moore are used in traditional Chinese medicine for arthritis and hypertension, whereas the morphologically similar roots of Aristolochia fangchi Y.C. Wu ex L.D. Chow & S.M. Hwang contain aristolochic acids that induce irreversible renal failure and urothelial carcinoma (Chen et al., 2014). Barcoding studies have repeatedly detected Aristolochia species fraudulently or accidentally substituted for Stephania, prompting regulatory bans and highlighting the necessity of molecular screening at points of import and retail.

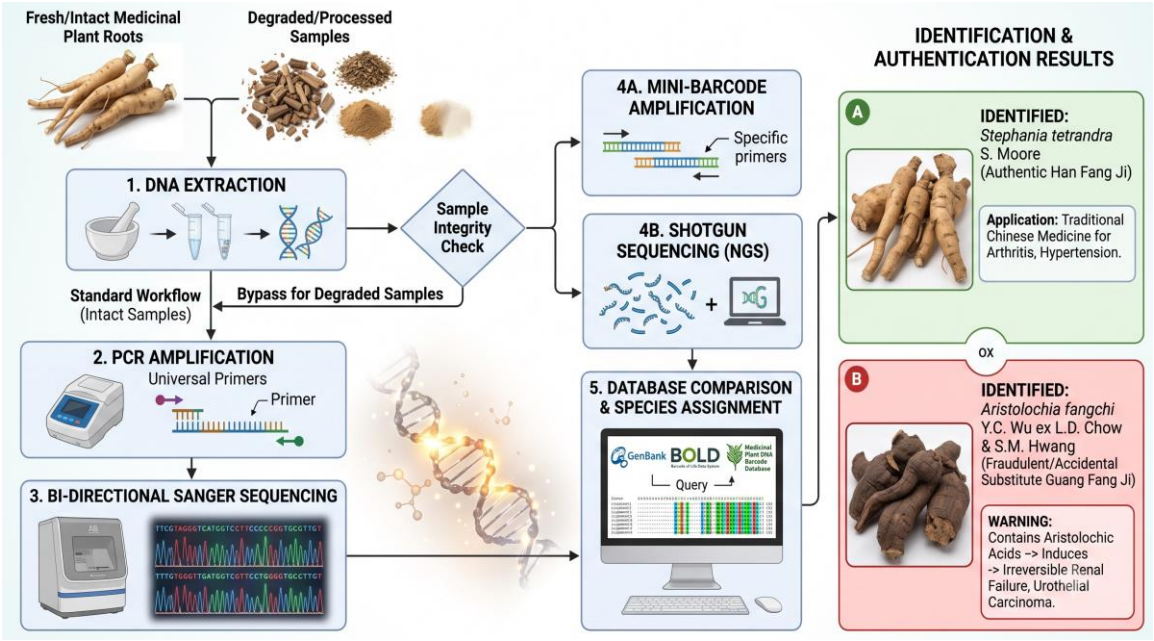

Figure 1. DNA barcoding workflow for authentication of endangered medicinal plant materials.

3.2 Detection of Adulteration in Commercial Products

Global herbal supply chains are complex and opaque. Raw materials harvested in Himalayan, Andean, or Southeast Asian forests pass through multiple intermediaries before reaching pharmaceutical manufacturers. At each node, profit incentives encourage substitution with cheaper, more abundant species. DNA metabarcoding, which utilizes next-generation sequencing to read millions of amplicon molecules simultaneously, has proven effective in revealing the composition of polyherbal preparations, capsules, and teas (Raja et al., 2023). In a recent survey of anti-rheumatic herbal formulations, metabarcoding identified the presence of undeclared Rauwolfia species and authenticated trace quantities of endangered Taxus derivatives that were invisible to chromatographic methods (Gao et al., 2021). Such molecular audits are indispensable for enforcing CITES appendices and national red lists that prohibit or restrict trade in threatened taxa.

3.3 Resolving Cryptic Diversity and Species Delimitation

Conservation legislation operates on species lists; if a single named species actually comprises multiple cryptic lineages with restricted ranges, standard management may unwittingly permit the extinction of evolutionarily distinct units. Molecular markers have repeatedly uncovered such hidden diversity within medicinal plant clades. In the alpine genus Saussurea, which includes the endemic and threatened S. obvallata (Brahma Kamal), combined analyses of ITS2 and matK revealed two divergent lineages separated by deep valleys in the Himalayan range, each exhibiting distinct elevational niches and flowering phenologies (Ghorbani et al., 2021). Recognition of these lineages as separate conservation units triggered the designation of an additional protected area in the eastern Himalaya. Similarly, in the orchid genus Dendrobium, barcoding and genotyping studies exposed numerous species masquerading under the trade name shi hu, leading to revised pharmacopoeial monographs that now require molecular confirmation for certified supplies (Yu et al., 2023).

4. Genetic Diversity and Population Structure

Conservation genetics operates on the principle that genetic diversity underlies adaptive capacity. Small, isolated populations of endangered medicinal plants lose alleles through drift and suffer inbreeding depression, undermining their ability to respond to pathogens,

climate shifts, and altered disturbance regimes (Frankham et al., 2010).

4.1 Assessing Genetic Variation and Allelic Richness

Population-level molecular surveys quantify the raw material of evolution: heterozygosity, allelic diversity, and effective population size (Ne). Microsatellite analyses of wild Panax ginseng populations across Russia, China, and Korea have documented drastically reduced allelic richness compared to historical herbarium collections, evidence that centuries of wild harvest have eroded genetic diversity (Zhang et al., 2022). In contrast, some outcrossing forest herbs such as Asarum species retain unexpectedly high within-population diversity despite small census sizes, suggesting effective long-distance pollen dispersal by specialist flies (Liu et al., 2021). Chloroplast DNA haplotype networks further illuminate range-wide phylogeography. In the endangered alpine medicinal Rhodiola crenulata (Hook.f. & Thomson) H. Ohba, cpDNA sequencing identified two major glacial refugia in the Hengduan Mountains and the Qinghai–Tibetan Plateau, with post-glacial colonization routes traversing modern political borders that complicate transboundary conservation planning (Parveen et al., 2020).

4.2 Spatial Structure, Gene Flow, and Landscape Genetics

Understanding how genetic variation is partitioned across landscapes enables managers to identify corridors and barriers to dispersal. Bayesian clustering algorithms such as STRUCTURE and ADMIXTURE, applied to SSR and SNP datasets, routinely detect cryptic population subdivision invisible to field observation. Research on Cypripedium calceolus, a slipper orchid harvested for traditional European and Chinese medicine, revealed that populations separated by as little as five kilometers exhibited significant genetic differentiation (FST = 0.18–0.31), attributed to extreme site fidelity of pollinating bees and limited seed dispersal (Yu et al., 2023). Such findings mandate that conservation plans protect every extant population rather than assuming regional connectivity (Mimi NS et al., 2026).

Landscape genetic approaches, which correlate genetic distance with ecological or geographic distance, have identified roads, agricultural fields, and elevational gradients as gene flow barriers for species such as Aconitum heterophyllum Wall. ex Royle and Picrorhiza kurroa Royle ex Benth. (Mishra et al., 2021). Mitigating these barriers through habitat bridges or stepping-stone reserves may be as important as increasing local population sizes.

4.3 Demographic Bottlenecks and Effective Population Size

Endangered medicinal plants frequently show genetic signatures of recent demographic contraction. Under the infinite allele model (IAM), stepwise mutation model (SMM), and two-phase model (TPM), heterozygosity excess relative to allele number, or a mode-shift in allele frequency distributions, indicates a population bottleneck. SSR-based studies on Fritillaria cirrhosa D. Don and Gentiana crassicaulis D. Don ex G. Don confirmed such signatures, correlating genetic data with local harvesting history: populations subjected to intensive bulb or root collection since the 1980s exhibited stronger bottleneck signals than those in remote or sacred groves protected by community taboos (Wu et al., 2024). Estimates of contemporary effective population size (Ne) using the linkage disequilibrium or sibship assignment methods frequently fall below Ne = 50, the threshold below which inbreeding depression and loss of adaptive potential become severe over the long term (Zhang et al., 2022; Frankham et al., 2010).

Table 2: Representative case studies applying molecular markers to endangered medicinal plant authentication and conservation genetics.

Species / taxon	Family	Markers employed	Findings	Conservation application
Panax ginseng	Araliaceae	SSR, SNP (ddRAD-seq)	Wild populations exhibit severe allelic erosion vs. historical baseline; low Ne	Genetically informed reintroduction; breeding program design
Cypripedium calceolus	Orchidaceae	SSR, ISSR	High genetic structure over short distances; clonal reproduction dominant	Protect all populations as distinct MUs; mycorrhizal co-conservation
Taxus wallichiana	Taxaceae	cpDNA haplotypes, SSR	Weak differentiation across Himalayan range; historically high gene flow	Prioritize in situ habitat protection over translocation
Saussurea obvallata	Asteraceae	ITS2, matK	Cryptic lineage divergence across eastern and western Himalaya	Recognition of separate ESUs; expanded protected area
Fritillaria cirrhosa	Liliaceae	SSR, cpDNA	Bottleneck signatures in heavily harvested populations	Community quotas; establishment of no-take sacred groves
Dendrobium nobile Lindl.	Orchidaceae	rbcL + ITS2, AFLP	Widespread adulteration in commercial shi hu products	Mandatory molecular certification in

				pharmacopoeias
Coptis chinensis Franch.	Ranunculaceae	cpDNA, SSR	Distinct western and eastern phylogeographic lineages	Provenance-specific restoration plantings

5. From Genetic Data to Conservation Action

Molecular markers are of little conservation value unless they influence management decisions. In recent years, a paradigm shift has occurred from descriptive genetic surveys to prescriptive conservation frameworks that integrate molecular, ecological, and sociopolitical data.

5.1 Delineating Evolutionarily Significant and Management Units

One of the most direct applications of population genetic data is the definition of units for conservation below the species level. Evolutionarily significant units (ESUs) are populations with unique evolutionary histories, often identified through reciprocal monophyly of organelle haplotypes or significant divergence in nuclear markers. Management units (MUs), conversely, are demographically independent populations identified through significant allele frequency differences at nuclear loci, regardless of phylogenetic distinctiveness (Allendorf et al., 2013). In the endangered tree peony Paeonia rockii (S.G. Haw & L.A. Lauener) T. Hong & J.J. Li ex D.Y. Hong, combined cpDNA and SSR analyses identified three ESUs across the Qinling Mountains and five finer-scale MUs, indicating that a single large reserve would be insufficient to capture the species' genetic diversity (Yu et al., 2023). Instead, a network of community-managed micro-reserves was established, each designed to protect a distinct MU.

5.2 Informing Ex Situ Collections and Germplasm Banking

Botanical gardens and seed banks serve as insurance policies against extinction. However, without genetic guidance, ex situ collections often underrepresent rare alleles or overrepresent genotypes that thrive in cultivation. Molecular pre-screening of wild provenances ensures that seed collections capture the full spectrum of genetic diversity. In Gastrodia elata, an achlorophyllous orchid used for neurological disorders, genotyping of living collections revealed that 60% of accessions belonged to a single fungal-symbiosis genotype favored by cultivators. This clonal bias prompted a recollection campaign targeting genetically underrepresented wild populations to broaden the germplasm base (Liu et al., 2021). Cryopreservation of embryonic axes and shoot tips similarly relies on molecular fingerprinting to confirm accession identity after years of storage.

5.3 Sustainable Harvest Quotas and Certification

For species that cannot be fully protected from harvest, molecular data can set sustainable offtake limits. If genetic surveys reveal that a population is a single genetic individual spread clonally—common in species that reproduce vegetatively—harvesting every visible ramet could extirpate the genotype. SSR studies of the medicinal sedge Cyperus and the lily Lilium have distinguished clonal from genotypic diversity, allowing managers to base harvest permits on genet rather than ramet counts (Wu et al., 2024). Moreover, DNA-based certification labels already piloted for Panax and Mahonia products empower consumers to verify that purchased material originates from sustainably managed populations rather than illegal wild harvest (Gao et al., 2021). Figure 2 give Integrated conservation framework illustrating how molecular marker data flow through bioinformatic pipelines into specific conservation actions. Feedback loops from monitoring outcomes to adjusted genetic thresholds are indicated implicitly through iterative surveys.

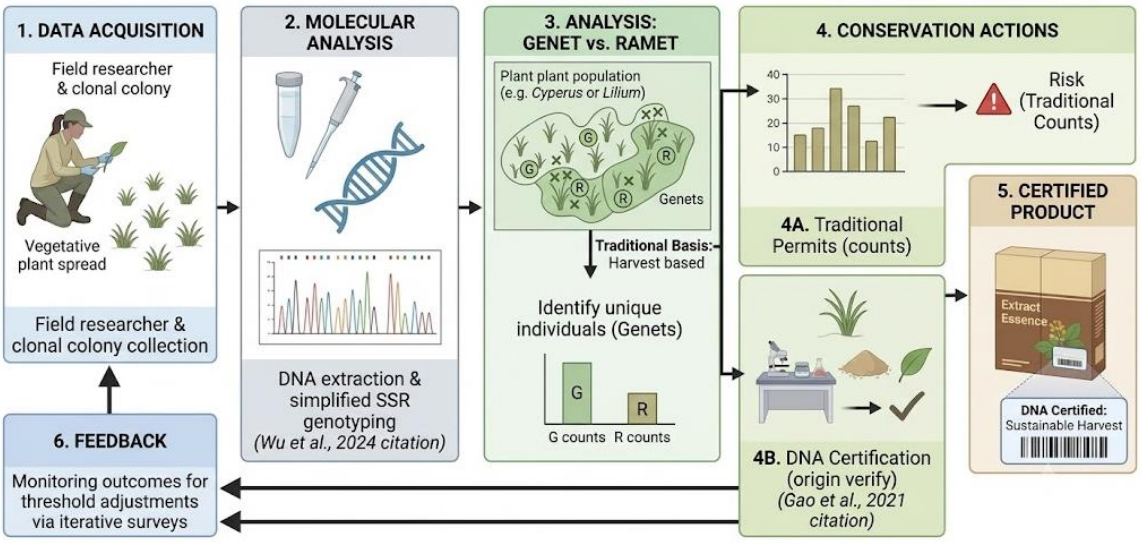

Figure 2: Integrated conservation framework Sustainable Harvest and Certification.

6. Challenges, Limitations, and Future Directions

The integration of molecular markers into medicinal plant conservation is neither complete nor without obstacles. Recognizing these limitations is essential for responsible application.

6.1 Gaps in Barcode Reference Libraries

The utility of any DNA-based identification system depends on the breadth and quality of its reference database. While BOLD and GenBank contain millions of plant sequences, coverage of tropical Asian, African, and Neotropical medicinal floras remains patchy. Many entries lack voucher specimens, precise locality data, or herbarium cross-references, leading to misidentifications that propagate through the literature (Mishra et al., 2021; Hollingsworth, 2011). The Medicinal Plant DNA Barcode Database and similar regional initiatives have made progress, but taxonomic and geographic gaps persist. Closing these gaps requires coordinated, voucher-linked sequencing campaigns involving taxonomists, ethnobotanists, and molecular biologists.

6.2 Biological Complexity: Hybrids, Polyploids, and Incomplete Lineage Sorting

Medicinal plant lineages are replete with polyploid complexes—such as Achillea, Arnica, and Panax—in which multiple ploidy levels coexist within nominal species. SSR loci in polyploids require specialized allele-calling software, and barcoding loci may be complicated by multiple-copy ITS variants (paralogs) or concerted evolution. Hybridization further muddles species boundaries; in sympatric populations of Epimedium and Paeonia, interspecific gene flow produces spurious barcode matches and admixed genotypic clusters that confound assignment tests (Raja et al., 2023). Resolving such complexity increasingly demands phylogenomic approaches that sample hundreds of unlinked loci rather than one or two barcode regions.

6.3 Accessibility and Equity in Genomic Technologies

High-throughput sequencing and the computational pipelines required for SNP calling remain economically and technically out of reach for many research institutions in biodiversity-rich developing countries. This inequity risks creating a genomics divide in which the genetic resources of the Global South are analyzed and published by Northern laboratories without local capacity building. Simplified, field-based DNA extraction protocols, low-cost nanopore sequencing, and cloud-based bioinformatics platforms are beginning to lower barriers (Zhang et al., 2022). International funding agencies should prioritize kits and training that empower local scientists and communities to lead conservation genetic monitoring.

6.4 From Science to Policy: Implementation Gaps

Perhaps the most formidable challenge is translating genetic findings into enforceable policy. While barcoding can identify illegal timber or medicinal bark at customs checkpoints, law enforcement agencies rarely possess the capacity or mandate to perform molecular testing. Similarly, IUCN Red List assessments have begun incorporating genetic data, but many medicinal plant evaluations still rely on geographic range estimates alone. The integration of molecular authentication into pharmacopoeias—such as the European Pharmacopoeia and the Chinese Pharmacopoeia—represents a critical step forward, yet harmonized international standards are lacking (Gao et al., 2021). Future progress depends on multi-stakeholder platforms that link academic researchers with customs officials, conservation NGOs, and the herbal industry.

6.5 Emerging Frontiers

The next decade promises several transformative developments. Environmental DNA (eDNA) metabarcoding of soil and water samples may non-invasively monitor the presence of endangered medicinal plants across landscapes, reducing the need for destructive sampling. Third-generation sequencing platforms (PacBio HiFi, Oxford Nanopore) now generate full-length ITS and chloroplast genome reads from herbarium specimens over a century old, opening historical baselines for diversity studies. Artificial intelligence and deep learning algorithms trained on barcode sequences are accelerating species assignment with greater than 98% accuracy in some plant families (Wu et al., 2024). Finally, genome editing tools such as CRISPR-Cas9, while primarily applied to crop improvement, may eventually assist in introgressing adaptive traits during genetic rescue of extremely small populations.

7. CONCLUSION

Molecular markers have transitioned from experimental curiosities to essential instruments in the conservation toolkit for endangered medicinal plants. DNA barcoding delivers the taxonomic precision required to police herbal markets and protect consumers from toxic adulterants, while population genetic markers illuminate the hidden demographic trajectories of wild populations. Together, these technologies enable a shift from reactive, morphology-based conservation to proactive, genomically informed stewardship. The evidence reviewed here demonstrates that authentication, diversity assessment, and conservation planning are most effective when integrated within a unified framework powered by molecular data.

Realizing the full potential of these tools demands more than technical innovation. It requires the expansion of openly accessible reference libraries, the democratization of sequencing and bioinformatics capacity across biodiverse regions, and the harmonization of molecular standards with international trade regulations. Conservation success also hinges on respecting indigenous knowledge and involving local communities in sampling, monitoring, and decision-making. As climate change and habitat loss accelerate, the window for safeguarding medicinal plant diversity narrows.

Embedding molecular markers into the fabric of pharmacopoeial regulation, protected area management, and sustainable trade certification is not merely a scientific opportunity—it is an ethical imperative. Only through such integrated, interdisciplinary action can we ensure that the pharmacopeia of the future retains the biological richness upon which it was founded.

REFERENCES

1. Allendorf, F.W., Luikart, G., & Aitken, S.N. (2013). Conservation and the Genetics of Populations (2nd ed.). Wiley-Blackwell.
2. Chen, S., Yao, H., Han, J., Liu, C., Song, J., Shi, L., Zhu, Y., Ma, X., Gao, T., Pang, X., Luo, K., Li, Y., Li, X., Jia, X., Lin, Y., & Leon, C. Validation of the ITS2 region as a novel DNA barcode for identifying medicinal plant species. PLoS ONE, 2014; 9(1): e86182.
3. China Plant BOL Group, Li, D.Z., Gao, L.M., Li, H.T., Wang, H., Ge, X.J., Liu, J.Q., Chen, Z.D., Zhou, S.L., Chen, S.L., Yang, J.B., Fu, C.X., Zeng, C.X., Yan, H.F., Zhu, Y.J., Sun, Y.S., Chen, S.Y., Zhao, L., Wang, K., Yang, T., & Duan, G.W. Comparative analysis of a large dataset indicates that internal transcribed spacer (ITS) should be incorporated into the core barcode for seed plants. Proceedings of the National Academy of Sciences, 2011; 108(49): 19641–19646.
4. Dong, W., Liu, J., Yu, J., Wang, L., & Zhou, S. Highly variable chloroplast markers for evaluating plant phylogeny at low taxonomic levels and for DNA barcoding. PLoS ONE, 2014; 9(4): e94371.
5. Frankham, R., Ballou, J.D., & Briscoe, D.A. (2010). Introduction to Conservation Genetics (2nd ed.). Cambridge University Press.
6. Gao, T., Yao, H., Song, J., Zhu, Y., Liu, C., & Chen, S. Evaluating the practicability of using DNA barcoding to identify medicinal plants: current progress and future prospects. Frontiers in Plant Science, 2021; 12: 789184.
7. Ghorbani, A., Gravendeel, B., Naghibi, F., & de Boer, H. DNA barcoding of traded medicinal plants and phytopharmaceuticals: strengths, limitations, and challenges. Journal of Ethnopharmacology, 2021; 264: 113411.
8. Hebert, P.D.N., Cywinska, A., Ball, S.L., & deWaard, J.R. Biological identifications through DNA barcodes. Proceedings of the Royal Society of London. Series B: Biological Sciences, 2003; 270(1512): 313–321.
9. Hollingsworth, P.M. Refining the DNA barcode for land plants. Proceedings of the National Academy of Sciences, 2011; 108(49): 19451–19452.
10. Hollingsworth, P.M., Forrest, L.L., Spouge, J.L., Hajibabaei, M., Ratnasingham, S., van der Bank, M., Chase, M.W., Cowan, R.S., Erickson, D.L., Fazekas, A.J., Graham, S.W., James, K.E., Kim, K.J., Kress, W.J., Schneider, H., van AlphenStahl, J., Barrett, S.C.H., van den Berg, C., Bogarin, D., Burgess, K.S., Cameron, K.M., Carine, M., Chacon, J., Clark, A., Clarkson, J.J., Conrad, F., Devey, D.S., Ford, C.S., Hedderson, T.A.J., Hollingsworth, M.L., Johnson, M.G., Kellogg, E.A., Kerr, K.A., Kim, J.S., Le Roux, J.J., Lee, S., Lidgard, S., Madrinan, S., Maurin, O., Meierhoff, K., Muller, K.F., Neyland, R., Perez-Espona, S., Petersen, G., Richardson, J.E., Salazar, G.A., Savolainen, V., Seberg, O., Simmons, M.P., Smith, J.F., Smith, S.A., Soreng, R.J., Stevenson, D.W., Tank, D.C., Wurdack, K.J., Yang, J., Yu, W.B., & Xiang, J.G. A DNA barcode for land plants. Proceedings of the National Academy of Sciences, 2009; 106(31): 12794–12797.
11. Liu, J., Wang, X., Xu, Q., Liu, Z., Li, X., Wang, Y., Li, J., Shi, Y., Zhang, Z., & Sun, X. Application of DNA barcoding in the identification of traditional Chinese medicine. Chinese Medicine, 2021; 16(1): 102.
12. Mishra, P., Kumar, A., Nagireddy, A., Mani, D.N., Shukla, A.K., Tiwari, R., & Sundaresan, V. DNA barcoding: an efficient tool to overcome authentication challenges in the herbal market. 3 Biotech, 2021; 11(5): 234.
13. Mimi NS, Noman AA, Parvez MJ, Nath B, Roshnee TA, Talukder MAA, Shaku IA, Singh S, Rajput DS, Subramaniyan V. Clinical Efficacy, Safety, and Pharmacologic Determinants of Antimicrobial Peptides: A Systematic Review and Meta-analysis. Eurasian Journal of Medical Oncology, 2026; 10(3): 026110120. https://doi.org/10.36922/EJMO026110120
14. Parveen, I., Gafner, S., Techen, N., Murch, S.J., & Khan, I.A. DNA barcoding for the identification of botanicals in herbal medicine and food: strengths and limitations. Planta Medica, 2020; 86(1): 36–52.
15. Pimm, S.L., Jenkins, C.N., Abell, R., Brooks, T.M., Gittleman, J.L., Joppa, L.N., Raven, P.H., Roberts, C.M., & Sexton, J.O. The biodiversity of species and their rates of extinction, distribution, and protection. Science, 2014; 344(6187): 1246752.
16. Raja, S., Arif, I.A., Bakir, M.A., Khan, H.A., Al Farhan, A.H., Al Homaidan, A.A., & Al Sadoon, M. DNA barcoding for species identification in the Orchidaceae family: implications for conservation of medicinal orchids. Saudi Journal of Biological Sciences, 2023; 30(2): 103568.
17. Wu, Z., Chen, S., Pan, Y., Zhang, D., & Zhou, Y. ddRAD-seq reveals genetic erosion and local adaptation in an endangered Lilium species: implications for conservation genomics. BMC Plant Biology, 2024; 24(1): 112.
18. Yu, K., Zhang, X., Wang, Y., Li, M., Chen, J., Wang, S., Zhang, W., & Li, L. Genetic diversity and structure of an endangered medicinal orchid (Cypripedium calceolus) based on SSR markers: implications for conservation. Plant Diversity, 2023; 45(3): 312–323.
19. Zhang, X., Chen, S., Shi, L., Li, M., Zhang, J., Han, J., Zhang, L., Li, Y., & Gao, T. Conservation genomics of endangered medicinal plants: progress, challenges, and prospects. Journal of Genetics and

Genomics, 2022; 49(8): 789–801.