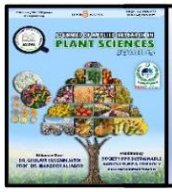
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Population Diversity of *Tecomella undulata* across South Asia: Diversity identification Markers, Possible Causes, and Potential for Conservation

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ABSTRACT

Tecomella undulata (Sm.) Seem., the sole species of its genus in the family Bignoniaceae, is a keystone tree of the arid and semi-arid tracts of South Asia, valued equally for its ecological role in desert stabilization and its long history of use in traditional medicine. Habitat fragmentation, unsustainable timber and herbal extraction, weak natural regeneration, grazing pressure and a warming/drying climate has together pushed the species toward endangered status in the Thar Desert of Sindh, Pakistan. Since there is a lack of such study which integrate anatomical, phytochemical, and molecular analysis as diversity identification markers, this review explores and summarizes the available information on population diversity identification using molecular (chiefly ISSR and RAPD), anatomical structure and the phytochemical profile as markers to understand variations in *T. undulata* populations. Published marker-based work shows substantial genetic diversity retained within populations despite geographic isolation, while anatomical and phytochemical surveys, though comparatively sparse, point to xeromorphic adaptations and stress induced shifts in secondary metabolism that likely track local aridity and soil conditions. We argue that combining molecular, anatomical and phytochemical data is not simply additive but necessary though other approaches like common garden experiment may also be needed to fully distinguish genetically fixed divergence from environmentally plastic response, and thereby to identify populations that are both genetically distinct and ecologically or medicinally valuable. This information would give conservation planners, across South Asian range, an evidence based strategy for prioritizing germplasm collection, in situ protection, and restoration efforts before further population decline erodes the genetic resources.

KEYWORDS: *Tecomella undulata,* Population Diversity, Genetic Diversity, Molecular Markers, Phytochemical Profiling, Conservation Strategies

INTRODUCTION

What are the genetic, anatomical, and phytochemical markers that determine the distinctiveness of *Tecomella undulata* populations, and how can this understanding aid in its conservation? The genetic, anatomical, and phytochemical diversity of plants is essential for understanding species adaptation, evolutionary relationships, and conservation strategies, especially in species with conservation problems, such as medicinal plants. *Tecomella undulata* (Sm.) Seem. is an important member of the family Bignoniaceae and is naturally present in arid and semi-arid areas of South Asia such as Pakistan (Sindh and Balochistan), India, Afghanistan and Oman. It is now listed as 'Endangered' in IUCN red list of species owing to its ecological sensitivity and over-exploitation for medicinal and timber uses, and so it is imperative that scientific studies are conducted for the purposes of conservation (Vats *et al*., 2025).

The recent studies reveal that *T. undulata* has a diverse array of secondary metabolites like flavonoids, phenolic compounds, terpenoids, alkaloids, quinones, steroids, and many more, making it an interesting medicinal plant. The antimicrobial, hepatoprotective, antioxidant, anti-inflammatory and anticancer activities have been reported for these compounds which explain its traditional medicinal applications in indigenous healthcare systems (Riaz *et al*., 2022; Bhardwaj et al., 2014; Thanawala & Jolly, 1993). This biochemical variation suggests a potential variation in phytochemical profile which can be the impact of environmental stress on metabolite expression.

Anatomical characterization of plant species offers valuable taxonomic and adaptive information, particularly in xerophytes like *T. undulata* where structural adaptations are present to cope with water-limited environments. Environmental adaptation is often reflected by the differences of leaf, stem and vascular tissues and can be used as reliable diagnostic features for species differentiation (Kalia *et al*., 2014). As a result, anatomical analysis plays an important role in the comprehension of intraspecific diversity.

Apart from morphological and phytochemical parameters, molecular markers are an essential tool to investigate the genetic variation and population structure. While RAPD and ISSR markers effectively reveal genetic polymorphism, the dominant nature of these markers limits their ability to distinguish heterozygotes from homozygotes, which limits precision in estimating population level genetic parameters. The tools are especially important in the context of endangered species, where they can be used to distinguish genetically distinct populations and develop conservation plans to address those (Riaz *et al*., 2022).

Moreover, using a combination of anatomical, phytochemical, and molecular methods offers a comprehensive tool for the diversity analysis. This multidisciplinary approach will not only help to improve the knowledge about genetic and biochemical diversity but also serve in the identification of elite genotypes for conservation and restoration, as well as for possible medicinal use. *T. undulata* is ecologically important and its natural population in Sindh is under serious threat; such integrated studies are therefore essential for sustainable management and preservation of genetic resources.

Taxonomy, Distribution, and Ecological Importance of *Tecomella undulata*

Taxonomy of *Tecomella undulata:* *Tecomella undulata* (Sm.) Seem. (desert teak or Rohida) is a member of the family Bignoniaceae, a family that is well known for its woody trees and climbers of great ecological and medicinal importance. The species is classified as follows:

- Kingdom: Plantae
- Clade: Angiosperms
- Clade: Eudicots
- Order: Lamiales
- Family: Bignoniaceae
- Genus: *Tecomella*
- Species: *Tecomella undulata* (Sm.) Seem.

The genus *Tecomella* is monotypic, meaning it contains only a single species, *T. undulata*, which makes it taxonomically unique and evolutionarily significant. The lack of congeneric species underscores the importance of investigating genetic diversity within (Shankarnarayan and Nanda., 1963).

Molecular phylogenetic investigations of the Bignoniaceae have supported the independent evolutionary status of *T. undulata* among arid adapted species of the family (Olmstead *et al*., 2009).

Geographical Distribution of *Tecomella undulata:* *Tecomella undulata* is naturally found in arid and semi-arid areas of South Asia (Figure. 1) and the Arabian Peninsula and is able to withstand extreme conditions, including drought, heat, and low rainfall. It is found throughout Pakistan (Sindh, Balochistan and southern Punjab), India (Rajasthan and Gujarat), Afghanistan and Oman (Khan *et al*., 2019).

The species occurs primarily in the Thar Desert of the province of Sindh in Pakistan, growing in the sandy soils, as natural xerophytic vegetation. Despite this, the populations in the wild have been reduced due to habitat loss, overgrazing, deforestation, and climate change. Consequently, its regional assessments indicate that *T. undulata* is now considered endangered (Vats *et al*., 2025).

This species is found in different parts of desert ecosystems, suggesting that populations may be often isolated from one another, which could lead to an increase in genetic differentiation among populations and a reduction in gene flow. This makes it an appropriate species to do diversity studies from anatomical, phytochemical, and molecular markers.

Ecological Importance of *Tecomella undulata:* Figure. 1 summarizes the key ecological roles of *Tecomella undulata* in arid ecosystem stability and desertification control, which highlights the conservation importance of its genetic diversity (Chaudhary *et al*., 2018).

Additionally, the species offers habitats and shelter for wildlife, including birds and insects, which contributes a great benefit to the local biodiversity. It flowers and produces nectar for pollinators, including bees, which play an important role in these sensitive desert ecosystems.

Moreover, the plant has been used for traditional medicine by the local people using its bark, leaves and flowers, which make it ethanobotanically important. This has resulted in higher harvest pressure and continuing to put the natural populations at risk.

Beyond its ecological role, *T. undulata* is culturally and medicinally important, though it faces severe threats, underscoring the critical need of genetic and conservation focused research.

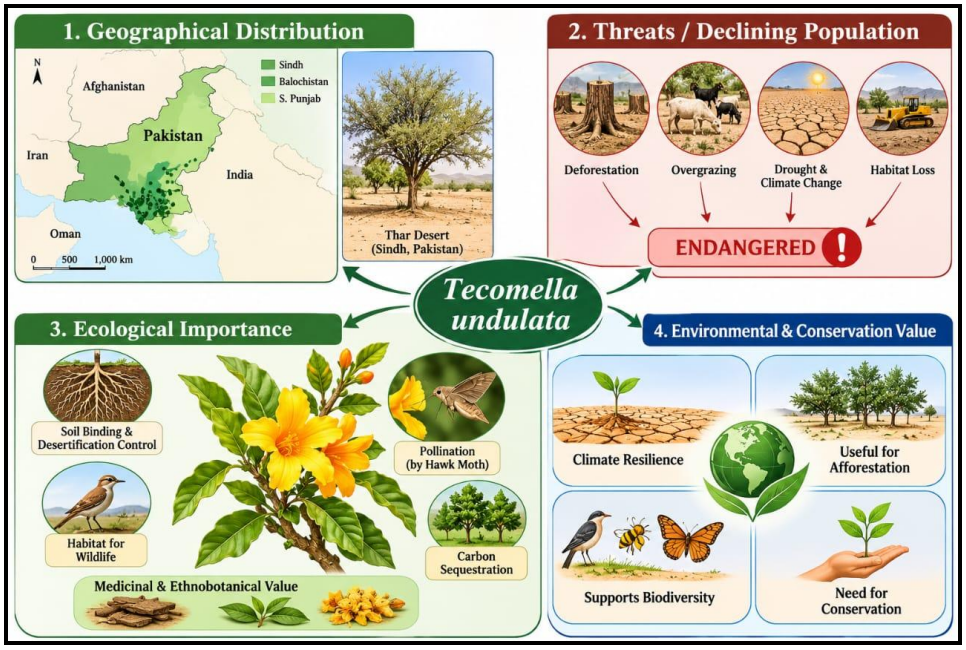


Figure 1. Diagramtic presentation that shows Geographical Distribution and Ecological Importance of *Tecomella undulata*.

Conservation Status and Threats: *Tecomella undulata* (Sm.) Seem. is one of the most ecologically and economically important trees of the arid and semi-arid areas of South Asia. Natural populations have been drastically reduced in the past few decades due to growing anthropogenic pressures and environmental degradation, yet the species is highly adapted to desert conditions. It is now considered to be endangered or locally threatened in some areas of its range, especially in Pakistan and India, where it has been suffering from continuous habitat degradation and unsustainable utilization, impacting on its regenerative potential (Vats *et al*., 2025). Due to the progressive decrease in size of its populations, it has become a matter of concern that it needs to be conserved in the long-term in terms of its genetic resources and ecological functions. Some common factors of threat are summarized in Figure. 2 and Table 1 and explained in following sections.

Habitat destruction: One of the major causes of the disappearance of *T. undulata* is habitat destruction. There has been a lot of fragmentation of its natural habitats, due to rapid land-use change in the agricultural sector, urbanization, infrastructure development and the replacement of natural vegetation from deserts by cultivated landscapes. Populations may become fragmented, or geographically isolated, leading to limited pollen and seed movement between populations and limited gene flow. This isolation can lead to genetic drift and risk of local extinction, especially for species whose populations are already small (Frankham, 2018; Arshad *et al*., 2022). In addition, fragmentation of the habitat changes the ecological conditions that are necessary for successful germination of the seed and establishment of seedlings, thus lowering the natural regenerative ability of the species.

Over-harvesting for timber. One of the major threats to the existence of *T. undulata* includes un-sustainable harvesting for timber wood by the local populations. It is a highly valued species for its strong and termite-resistant durable wood that is used in furniture industry, in agricultural production, as building materials and in handicrafts. Besides, various parts of the plant such as bark, leaves, flowers and roots have been widely used in traditional medicine for treating inflammatory disorders, liver ailments, diabetes, wounds and microbial infections (Mathur & Mathur., 2024). An increasing commercial value of timber and herbal products has resulted in significant harvesting pressure on the natural population, frequently without any management or replanting plan. Regular removal of mature reproductive trees leads to a decrease in population density and seed production which results in a decreased recruitment of trees in the future (Thanawala & Jolly, 1993; Vats *et al*., 2025).

Poor natural regeneration: This species is further declining due to poor natural regeneration. Successful recruitment under natural conditions is generally low because of low seed viability, low soil moisture, and erratic and irregular rainfall patterns, as well as competition from grasses and invasive plant species. Seedlings are especially susceptible when they are young, and when drought and high temperatures prevail, the survival of seedlings is greatly reduced. Regeneration failure has been reported as one of the major factors contributing to the ageing population structure of many of the desert tree species, such as *T. undulata*, wherein mature trees are more abundant and

young trees are less (Rajawat *et al*., 2014; Mathur & Mathur, 2024).

Grazing pressure: Domestic livestock, especially goats, sheep and camels, are also problematic for the conservation of *T. undulata*, due to overgrazing of the species. Recruitment success is greatly reduced and stand regeneration is delayed by browsing at very young ages. Soil compaction, reduced water penetration and increased soil erosion are also caused by continuous grazing, which make it difficult for the seeds to germinate and for the roots to grow. Intense grazing pressure can have long term ecological effects, in arid ecosystems where natural regeneration can be slow, resulting in further degradation of already fragile habitats (Chaudhary *et al*., 2018; Mathur & Mathur, 2024).

Climate change stress: Climate change has become a more important threat to the survival of *T. undulata*. Desert habitats are likely to change due to higher temperatures, longer droughts, inconsistent patterns of precipitation, and more extreme weather events. Reproductive success can be affected by such environmental changes that can influence flowering phenology, seed production, pollinator activity and seedling establishment (Arshad *et al*., 2022). Furthermore, the influence of climate change on geographical distribution of suitable habitats may lead to change in the geographical extent of populations, which consequently will be forced to occupy more and more restricted ecological niche. *T. undulata* is highly drought tolerant but may suffer from adaptive stress under sustained climatic stress, especially in the context of degradation of its habitat, coupled with anthropogenic disturbances (Rajawat *et al*. 2014; Vats *et al*. 2025).

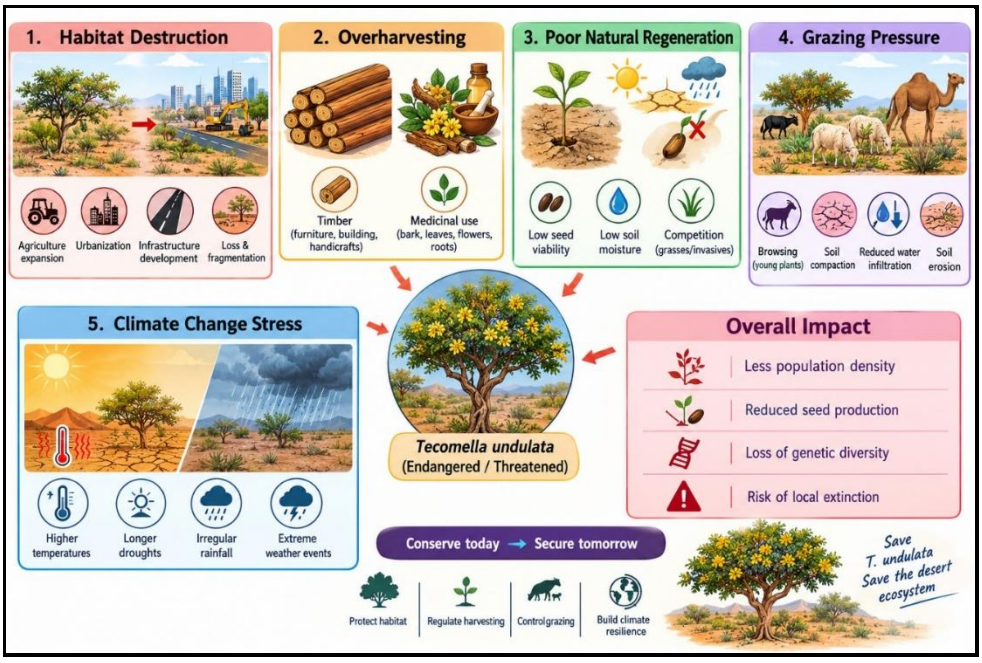


Figure 2. Major threats to *Tecomella undulata* conservation, including habitat destruction, overharvesting, poor natural regeneration, grazing pressure, and climate change, leading to population decline and reduced regeneration.

Table 1. Major threats driving population decline in *Tecomella undulata*

Threat	Mechanism of impact	Reference
Habitat destruction/fragmentation	Land-use change isolates populations, reduces pollen/seed flow, increases genetic drift risk	Frankham *et al*. 2018; Arshad *et al*., 2022)
Overharvesting (timber & medicinal use)	Removal of mature reproductive trees lowers population density and future recruitment	Thanawala & Jolly (1993); Vats *et al*. (2025)
Poor natural regeneration	Low seed viability, erratic rainfall, and competition from invasive species reduce seedling survival	Rajawat *et al*. 2014; Mathur & Mathur, P. 2024)
Grazing pressure	Livestock browsing delays recruitment; soil compaction reduces germination and root growth	Chaudhary *et al*. (2018)
Climate change stress	Rising temperature and drought alter flowering phenology, seed production, and habitat suitability	Rajawat *et al*. (2014); Vats *et al*. (2025)

T. undulata is in critical condition, as an endangered species, requiring integrated in situ and ex situ approaches to preserve its ecological and medicinal value. Integrating molecular tools will help identify genetically diverse populations, allowing for targeted prioritization in future breeding and conservation initiatives. Conservation actions needed to secure the long-term survival of this endangered desert tree include protecting natural habitats, implementing measures for timber extraction, restoring degraded

habitats, creating seed orchards and germplasm banks, implementing community-based conservation programs' and introducing molecular tools for population identification of genetically diverse trees. The conservation efforts by these multidisciplinary efforts are expected to not only conserve the species, but also the valuable genetic diversity needed for future breeding, restoration, and sustainable utilization efforts.

Genetic Diversity and Population Structure: *Tecomella undulata* maintains high genetic diversity due to its naturally fragmented desert ecosystems across Pakistan and India's arid region **(**Figure 3**).** Hamrick and Godt (1996) showed that all of the within-population genetic variation remained high in long-lived, woody perennials compared to annual and self-pollinated species, and that this within-population genetic diversity was a reflection of the life-history traits of the species. These benefits, however, quickly become negligible if populations are divided or separated by human activities.

The species is genetically diverse because naturally fragmented desert ecosystems result in a high degree of environmental heterogeneity in *Tecomella undulata*. The arid areas in Pakistan and India have a wide range of seasonal rainfall, temperature, soil type and water availability. These ecological differences lead to local adaptation and could lead to genetic differentiation between geographically distant populations. Because of this variation, it is necessary to understand this variation in order to identify potentially valuable populations for genetic purposes and to implement sound conservation and restoration strategies.

Population structure is the distribution of genetic variation within and among populations and is due to a combination of evolutionary processes including mutation, natural selection, migration, gene flow, and genetic drift. The degree of genetic differentiation is usually low in healthy populations with continuous interpopulation gene exchange because pollen and seeds are free to flow between populations. But if fragmentation occurs, the opportunities for gene flow are greatly reduced and the isolated populations may begin to diverge genetically over time. This can lead to lower genetic connectivity and greater population subdivision, which can detract from long term population viability (Frankham, 2018).

There has been a significant increase in the importance of habitat fragmentation as a cause of genetic erosion in endangered tree species. Previously continuous populations are now fragmented by human activities such as agriculture, urban development, roads, over-exploitation of forests, and land-use change. Fragmentation of the population also has another significant effect, namely a decrease in heterozygosity and a rise in inbreeding. Because opportunities for outcrossing become limited in small populations, these populations may be prone to inbreeding. Inbreeding would lead to increased homozygosity and could cause the exposure of deleterious recessive alleles which would lead to decreased seed viability, reduced reproductive success, decreased seedling vigor, and reduced adaptive capacity.

However, the loss of genetic populations does not necessarily mean an immediate loss of adaptive capability. Further studies integrating genomic and phenotypic data are essential to confirm specific adaptive traits related to drought and heat tolerance in *Tecomella undulata.* Understanding population genetic structure is of significant importance for conservation planning. Data on gene flow, genetic differentiation and genetic diversity help to locate genetically distinct populations, set conservation units and prioritize in situ and ex situ conservation. Moreover, a high genetic diversity population is a good source of germplasm for afforestation and ecological restoration and can be used as good material for future breeding program. Combination of molecular marker analysis with ecological, anatomical and phytochemical studies, therefore, gives a complete picture of the species diversity and helps towards the conservation management based on evidences.

Molecular Markers in Diversity Analysis: Molecular markers technologies have been a revolution in the analysis of genetic diversity, population structure, and phylogenetic relationships in plant species. Molecular markers detect DNA polymorphisms directly and thus the level of genetic variation measured from them is more accurate and reliable than the one measured by morphological or biochemical markers, which are often affected by environmental conditions and developmental stages. Such markers have been essential in plant genetics, plant conservation biology, germplasm characterization and breeding for their usefulness in identifying genetic variation that is not related to environmental effects (Kalia *et al*., 2011). In the case of threatened species like *Tecomella undulata*, molecular markers can give valuable insights into the level of genetic variation found in natural populations and aid in the formulation of conservation plans.

The main purpose of molecular marker analysis is to measure the genetic diversity within and between populations.

RAPD and ISSR are utilized for assessing genetic diversity in non model species due to their procedural simplicity and cost effectiveness. However, their application is limited by lower reproducibility and challenge is directly comparing diversity estimates across different studies (Kalia *et al*., 2011).

ISSR Markers: The ISSRs are highly reproducible and are very polymorphic, making them very useful. Rajawat *et al*. (2014) investigated the *T. undulata* populations with ISSR markers and found:

- High genetic diversity (H = 0.1646)
- Many more within-population variations than between-population variations (58:42%).

Nei's gene diversity (h) was found to be 0.1646. Analysis of molecular variance (AMOVA) revealed that 58% of the genetic variation resides within populations and 42% among populations, confirming high intraspecific variation.

RAPD Markers: Kaur *et al*. 2018 used RAPD analysis to evaluate the sampled population, identifying 87 total amplified fragments with 75 being polymorphic. The Nei's genetic diversity value (h) of 0.266 confrims substantial intraspecific variation within the collected material.

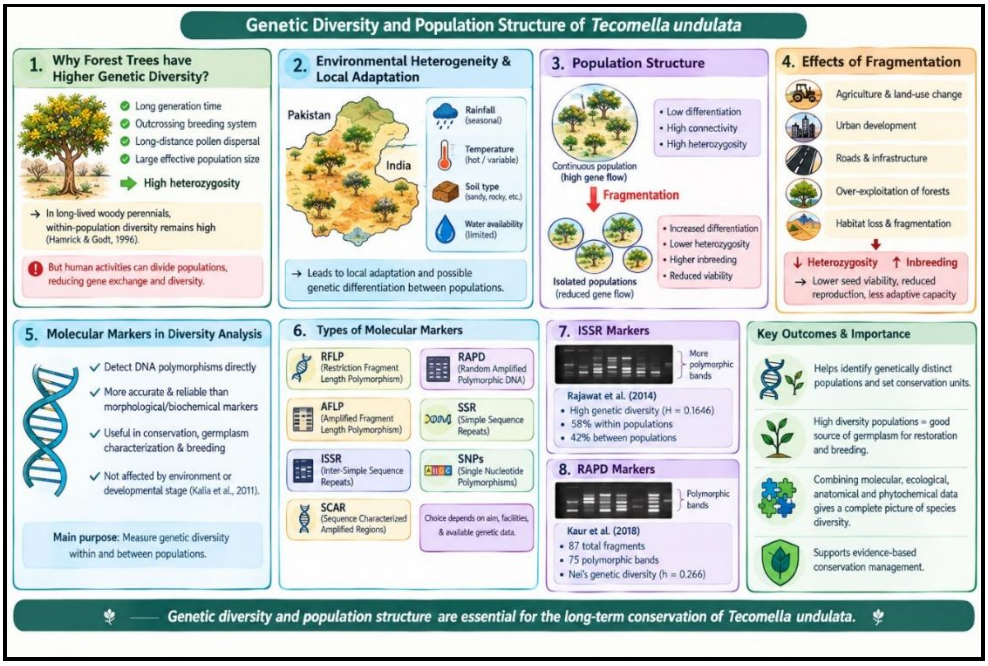


Figure 3: Genetic diversity and population structure of *Tecomella undulata*, showing gene flow, fragmentation, molecular markers, and conservation significance.

Table 2. Molecular marker studies on genetic diversity in *Tecomella undulata* (redesigned)

Marker system	Key genetic parameter	Main finding	Reference
ISSR	Shannon diversity index H = 0.1646	High within-population diversity; 58% of variation within populations vs. 42% among populations	Rajawat *et al*. (2014)
RAPD	Nei's gene diversity h = 0.266	87 total fragments amplified, 75 polymorphic (highly polymorphic profile)	Kaur *et al*. (2018)
ISSR	% polymorphic loci = 62.36%	Confirms substantial molecular variation even in declining populations	Daneva *et al*. (2023)

Molecular Diversity in *Tecomella undulata:* Figure 4: Molecular diversity is the amount of genetic variation at the DNA level within and between individuals and populations. While morphological or physiological trait variation can be significant due to environmental conditions, the variation in molecular traits will be smaller and will be due to genetic variation which can be passed down from one generation to the next. In that respect, molecular diversity is one of the most reliable tools to assess evolutionary relationship, population structure, adaptive potential and long-term survival of endangered plant species. In conservation biology, molecular diversity is of great significance as it allows the quantification of genetic resources which are not detectable by traditional morphological measurements (Frankham *et al*., 2018).

The first extensive molecular study of T. undulata was done by Rajawat *et al*. (2014) using Inter-Simple Sequence Repeat (ISSR) markers. Their analysis indicated there was relatively high amount of genetic diversity (H = 0.1646) within the natural populations and that almost 58% of the total variation was within populations, while approximately 42% was among populations. This is a typical feature of many long-lived outcrossing tree species and suggests that genetic variability remains large even with geographical isolation of the individual populations. The authors recommended the conservation of several populations at the same time throughout the species' geographic range, in order to ensure the greatest gene pool conservation.

Important biological implications of the predominance of within-population genetic variation. `the high within population genetic variation shows significant local diversity, but this does not directly imply adaptive potential, The results of such studies highlight the need to not rely on only a few

populations for conservation efforts since alleles that are genetically different might be found all over the species' range. Thus, genetic resources should be conserved by integrating populations from different ecological regions so that genetic resources can be conserved in a comprehensive manner.

Subsequent molecular studies have also confirmed that there is significant DNA level variation within *T. undulata*. Kaur *et al*. (2018) amplified 87 DNA fragments using RAPD markers out of which 75 were found to be polymorphic, indicating a high level of genetic polymorphism among the genotypes sampled. There was also a high intraspecific variation, as indicated by the Nei's genetic diversity index (h = 0.266) reported. These findings suggest that RAPD markers are good for discriminating the genotypes and can be used along with ISSR to assess variation in the population. Despite the greater degree of irreproducibility of RAPD markers compared with ISSRs, when handled with great caution and standardization, RAPD markers can provide a very informative data set for genetic diversity study, especially in species with less extensive genomic resources (Chhajer *et al*., 2017).

Recently, Daneva *et al*. (2023) used ISSR markers to assess the molecular diversity between various *T. undulata* genotypes and found about 62.36% polymorphic. The proportion of polymorphic loci proved that there is still a lot of molecular variation within the species even in the case of declining population numbers. Their study also validated that ISSRs markers have excellent discriminatory power for genetically distinct individuals and for evaluating genetic relationships between geographically separated populations. The results further illustrate the value of DNA based marker systems for determining the state of conservation of rare forest tree species.

However, it is interesting to note that molecular diversity studies have revealed that low cytological stability does not always reflect low genetic variation. Zahedi *et al*. (2025) found that *T. undulata* is a species with a stable chromosome number (2n = 36; n = 18), which showed great stability there (Chhajer *et al*., 2017).

Conservation-wise, molecular diversity studies offer a scientific basis for the identification of priority populations that need to be conserved. Highly allelic-rich and genetically variable populations are more likely to be resilient to adverse environmental events and thus are important sources of adaptive genetic resources.

Anatomical Variation in Plants: Plant anatomical features are significant both for taxonomic, ecological and evolutionary information, as they are the result of both genetic inheritance and environmental influences. In contrast to many external morphological characters, internal anatomical structures offer relatively stable diagnostic characters which can be used to identify species, assess intraspecific variation, and understand adaptive responses to a variety of habitats. Anatomical research has therefore become a crucial part of contemporary plant systematics, biodiversity studies and conservation biology, especially of plants growing in harsh ecosystems (Carlquist, 2013).

The availability of water, temperatures, light, soil properties, and humidity of the atmosphere affect the development of tissues like the epidermis, mesophyll, vascular bundles, sclerenchyma, and xylem. So anatomical traits are often found to be related to ecological pressures and hereditary traits. Thus, anatomical characters are useful in assessing the phenotypic plasticity and environment adaptations in natural populations of plants (Esau, 1977).

General xeromorphic features, like thick cuticles, serve as background information on adaptation, while *tecomella undulata* exhibits specific traits suited to arid environment. These structural changes are all desirable morphological traits that combine to create drought tolerance, by limiting transpiration, reducing the exposure of photosynthetic tissue to excessive solar radiation, and maintaining hydraulic conductivity under conditions of long droughts (Fahn, 1988). Such anatomical modifications may be present or absent in different populations, and if present, may be more or less intense depending on the conditions of their environment, and may serve as useful indicators of ecological differentiation.

Leaves being the most important interface between plants and their environment have attracted a good deal of attention in leaf anatomy. The study of ecological adaptation and taxonomic relationships is often addressed by investigating the following anatomical traits: epidermal cell morphology, stomatal frequency, stomatal index, cuticle thickness, palisade and spongy mesophyll organization, trichome distribution and vascular bundle arrangement. it has been shown that populations of plants which are exposed to high temperatures and high and low rainfall generally show higher cuticle thickness, lower stomatal densities, and tighter mesophyll than plants that are exposed to relatively favorable environments (Dickison, 2000). Such anatomical changes help minimize transpiration and yet ensure adequate photosynthetic productivity under environmental stresses (Dickison, 2000).

Stem anatomy likewise provides valuable information regarding plant adaptation and systematic relationships. The differences in the features of the bark, development of the secondary xylem, diameter of the vessels, distribution of fibers, characteristics of rays, and lignification patterns are often due to both genetic differentiation and to environmental influences. In the woody plants of arid regions the vessels in the xylem are generally small and numerous, thus minimizing the possibility of embolism during dry periods and still allowing for sufficient water movement (Carlquist, 2013). Mechanical tissues (sclerenchyma) develop more,

increasing the rigidity and resistance to water loss in the stems. Such morphology plays an important role in the ecological success of xerophytic trees of arid environments (Carlquist, 2013).

Anatomical traits of roots are also important in plant adaptation to drought affected soils. The changes, such as thickening of the cortex, better suberization of endodermis cells, good development of vascular cylinder and deeper root system, are responsible for better water absorption and soil water resistance. Root anatomy has been dealt with in large numbers of xerophytes, but little information is available on the anatomical variation in the root system of *Tecomella undulata*, an important subject for future research.

Anatomical markers have been especially useful in taxonomic identification as many microscopic features are relatively constant within species, which has been influenced by environmental changes. Patterns of epidermal cells and stomatal structure, organization of vascular bundles and wood anatomy have been used for a long time to distinguish closely related taxa and to identify medicinal plants (Metcalfe & Chalk, 1950). Anatomical evidence is particularly important when there is a possibility of species misidentification or commercial adulteration as in some cases (Metcalfe & Chalk, 1950).

Several studies relate anatomical variations within desert tree populations to altitude. Recently, Wang *et al*., (2026) noted that in lower-elevation deserts, shrubs invest more in stem conductive tissues (enlarged central cylinders and thicker xylem) to support a hydraulic reinforcement strategy adapted to high temperature and elevated evaporative demand. Further they identified a strategy associated with high elevation that exhibits reinforced leaf protective structures (cuticle and epidermal thickness) consistent with tolerance to high radiation and low-temperature stress. The warm-adapted genotypes from the relatively warm Sonoran Desert ecoregion exhibit lower wood densities and xylem vessels with higher hydraulic mean diameters than genotypes from the cooler Mogollon Rim ecoregion, indicating differences in hydraulic architecture (Blasini *et al*., 2022). Further, stomatal density variation in warm-adapted genotypes is higher compared to the cool-adapted ecotypes, representing a difference in leaf anatomy and regulation (Blasini *et al*., 2022). While Peng *et al*., (2026) claim that anatomical traits like vessel density, cell wall reinforcement, and wood density in *Tamarix ramosissima* varied significantly across the different arid sites, while other hydraulic traits remained stable. In arid regions of Australia, Dörken *et al*., (2020) examined the morpho-anatomical features of photosynthetic organs of three tree species (*Callitris* spp.) and four shrub species to identify tissue formation patterns related to xeromorphy.

Although, *Tecomella undulata* is ecologically and medicinally significant, its intera-population anatomical studies are not found as compared to the molecular and phytochemical study. The majority of the published work is of a descriptive botanical nature, analyses of the wood anatomy, or a pharmacognostic identification of the stem bark while detailed studies of leaf, stem and root anatomy of geographically separate natural populations are few. Previous research has focused on diagnostic anatomical characteristics for plant medicinal authentication, but not on intraspecific anatomical variation related to environmental adaptation.

There is a lack of anatomical data in particular, about populations in Pakistan and especially in the arid areas of Sindh. The species is found naturally in the Thar Desert and its neighboring dry areas, but there is no systematic anatomical study to check if there are any changes in anatomical structure in response to environmental changes in different populations. This is a substantial knowledge gap as anatomical variation can have fundamental meaning to local adaptation, ecological plasticity and population differentiation.

Environment and genetics play a major role in the anatomy of plants. Anatomical features include:

- Stomatal density
- Cuticle thickness
- Xylem vessel structure

Leaf epidermal patterns
are frequently used in ecology and taxonomy.
However, in the case of *T. undulata*, there are extremely limited studies available on its anatomy in Pakistan, particularly, in the Sindh region, showing a significant research gap.

Phytochemical Diversity in *Tecomella undulata:* Naturally occurring bioactive compounds produced by plants as a result of primary (and secondary) metabolic processes are called phytochemicals. Secondary metabolites are not involved in the normal growth and development of plants but play a major role in plant defence, ecological interaction and adaptation to environmental stress. The compounds provide plants with defense against herbivores, pathogenic microorganisms, UV radiation, oxidative stress and unfavorable environmental conditions and they also play a role in the medicinal and pharmacological properties of plants. Phytochemicals have been the subject of interest in several fields of research, such as pharmaceutical studies, conservation biology and medicinal plant studies, due to their varied biological activities (Wink, 1999).

The nature and abundance of phytochemicals in a plant species is determined by complex interactions of the genetic makeup and environmental conditions. External factors such as temperature, rainfall, soil fertility, altitude, water availability, salinity and solar radiation have a strong impact on the production of secondary metabolites, although it is genetically regulated. Plants under divergent environmental situations, therefore, often show significant differences in their phytochemical profile in terms of

both quality and quantity. This variation is useful as biochemical indicators of population diversity, ecological adaptation and evolutionary responses to environmental stress (Verpoorte *et al*., 2006). Bhandari *et al*., (2026) explain that differences in phenolic and flavonoid content of *T. undulata* may be attributed to biological, environmental, and methodological factors, specifically mentioning geographical location, climate, soil composition, and stress conditions as playing a significant role in regulating the biosynthesis of bioactive compounds.

The various parts of the plant, such as leaves, stem bark, flowers, fruits, roots and seeds are used since long in traditional medicine for the treatment of liver disorders, diabetes, inflammatory diseases, skin infections, wounds, obesity and different gastrointestinal diseases (Kalia *et al*., 2014). The advent of therapeutic applications in the broad range is reflected by the extensive phytochemical studies to identify the compounds responsible for the above pharmacological activities (Thanawala & Jolly, 1993; Vats *et al*., 2025).

Phytochemical screening of *T. undulata* has indicated the presence of different classes of secondary metabolites such as flavonoids, phenolic acids, alkaloids, terpenoids, quinones, steroids, glycosides, tannins, saponins and coumarins. Several of these compounds are potent antioxidants, antimicrobials, hepatoprotective, anti-inflammatory, anticancer, antidiabetic and immunological. The presence of several classes of bioactive constituents suggests the medicinal potential of *T. undulata* is due to the synergistic effect of many phytochemicals instead of a single compound (Riaz *et al*., 2022; Vats *et al*., 2025).

Some of these metabolites have been highlighted because of their strong antioxidant properties, including phenolic compounds and flavonoids. Phenolic compounds can effectively reduce the production of reactive oxygen species, block the process of lipid peroxidation and prevent the oxidation of cells. Flavonoids also play a role in antimicrobial defense through damaging the microbial cell walls, blocking enzyme activity, and blocking nucleic acid synthesis. The antioxidant activity of *T. undulata* showed a positive correlation with total phenolic metabolites, and thus phenolic metabolites appear to be among its main therapeutic sources according to several pharmacological studies (Rita *et al*., 2014).

The other bioactive compounds found in *T. undulata* are called ‘alkaloids'. These secondary metabolites containing nitrogen are known to have various biological activities, such as antimicrobial, anti-inflammatory, analgesic, cytotoxic and anticancer. Laghari *et al*. (2014) have isolated eleven structurally different alkaloids from the stem bark of *T. undulata*, some of which showed excellent biological activity. Their results greatly increased the phytochemical profile of the species and revealed the potential of this plant as a source for new pharmaceutical compounds. As this led to the identification of a number of structurally different alkaloids, this again highlights the medicinal value of maintaining natural populations of diverse genetic types. In recent biochemical studies it has been determined that *T. undulata* has highly potent antioxidant and cytoprotective properties.

Biochemical characterization and molecular docking analyses revealed that Riaz *et al*. (2022) possess significant antioxidant, cytotoxic, antimutagenic and anticancer potential. Their study showed that extracts of *T. undulata* possessed potent antioxidant activity and also exhibited noteworthy inhibitory activity against the selected cancer cell lines indicating its significant potential in pharmaceutical application. This has led to a renewed interest in the scientific community about this endangered medicinal tree and the need for its preservation of its phytochemical diversity.

The amount and type of secondary metabolites in medicinal plants is determined by the environmental factors. Oxidative stress can be triggered by drought, salinity, high temperatures, nutrient levels and light intensity, which can result in activation of metabolic pathways leading to the biosynthesis of secondary metabolites. It is well established that plants tend to produce more phenolics, flavonoids and terpenoids in dry conditions as a response to stress. As a result, populations of *T. undulata* from different ecological regions may be quite different in terms of their phytochemical composition, depending on their environment (Verpoorte *et al*., 2006).

Various researches on medicinal plants from different geographical areas have consistently shown that environmental heterogeneity significantly affects the phytochemical contents. Otho *et al*. (2022) indicated that the abundance and variety of secondary metabolites in medicinal plants species were influenced by climatic variation, soil characteristics and geographical location. A similar effect on the production of antioxidant metabolites has been reported for many xerophytic plants, which are often highly sensitive to drought stress. The results indicate that the differences in phytochemical may be adaptive to the local environment, and can be used as biochemical markers for diversity assessment in *T. undulata* natural populations.

Although great efforts are being made in the identification of the main phytochemicals of *T. undulata*, several key points are still unanswered. Although many investigations have been published so far, most of them have concentrated on the qualitative phytochemical screening or pharmacological evaluation of the plant extracts, while comparatively less research has been taken up to evaluate the phytochemical variation within geographically separated natural populations. Data on the effects of environmental gradients on accumulation of metabolites, especially for populations found in

Pakistan, is scarce. Moreover, comparative phytochemical research, that encompasses biochemical profiling, molecular and anatomical studies are virtually non-existent.

The Sindh region of Pakistan is a perfect natural system to investigate the phytochemical diversity of *T. undulata* due to the presence of significant differences in soil texture, salinity, rainfall and temperature among various desert habitats. The opposing environmental conditions may affect the production and accumulation of secondary metabolites and thus create different phytochemical profiles between populations. The variation is of great significance for the conservation biology, as well as for the identification of elite chemotypes with better medicinal and pharmaceutical properties.

Elemental Composition and Environmental Influence: Elemental composition is a key part of plant physiology because mineral nutrition plays a key role in controlling virtually every aspect of plant growth, development, metabolism and response to environmental stress. Macroelements like nitrogen (N), phosphorus (P), potassium (K), calcium (Ca), magnesium (Mg) and sulfur (S) and microelements like iron (Fe), zinc (Zn), manganese (Mn), copper (Cu), boron (B) and molybdenum (Mo) are essential for normal cellular functions. These mineral elements serve as activators of enzymes, are involved in photosynthesis, respiration, osmotic mechanisms, nucleic acid synthesis, protein metabolism, and antioxidant defense mechanisms. The elemental composition of plants therefore can be affected by plant growth condition as well as by the environmental conditions in which the plants grow (Marschner, 2011).

Mineral elements are not produced by plants but rather are acquired from the soil environment in which they grow, and are extracted by highly regulated physiological processes. Several interacting factors that influence uptake, translocation and accumulation of these elements include soil texture, mineral composition, pH, salinity, organic matter content, moisture availability, microbial activity, and climatic factors. Thus, between different ecological regions, species often vary greatly in their mineral content, even though they are the same species. This variation can be useful to get information on ecological adaptation and environmental heterogeneity (White & Brown, 2010).

For medicinal plants elemental composition has drawn more scientific attention since minerals not only affect plant growth, but also play an important role in the biosynthesis of secondary metabolites of medicinal importance. A number of essential elements are co-factors of enzymes in biosynthetic pathways of flavonoids, phenolics, alkaloids and terpenoids. Therefore, certain mineral nutrient deficiencies or excesses can significantly change the phytochemical profile, and consequently the medicinal properties and therapeutic value of medicinal plants. A knowledge of the variation of the mineral components is therefore necessary for the standardization of medicinal plants and conservation of medicinal plant resources (Marschner, 2011).

Tecomella undulata is naturally occurring in areas of low soil fertility, dry or semi-dry conditions with high water availability fluctuations. Under these harsh environmental circumstances, the species has evolved striking physiology, which could facilitate efficient acquisition and utilization of nutrients. The extensive root system is used to take up water and mineral nutrients in the deeper soils and makes the plant survive in a very long drought. Mineral nutrition is therefore likely to be important for ecological success of *T. undulata* in the various desert habitats it inhabits, based on these adaptations. The concept of integrated approaches in diversity analysis is introduced

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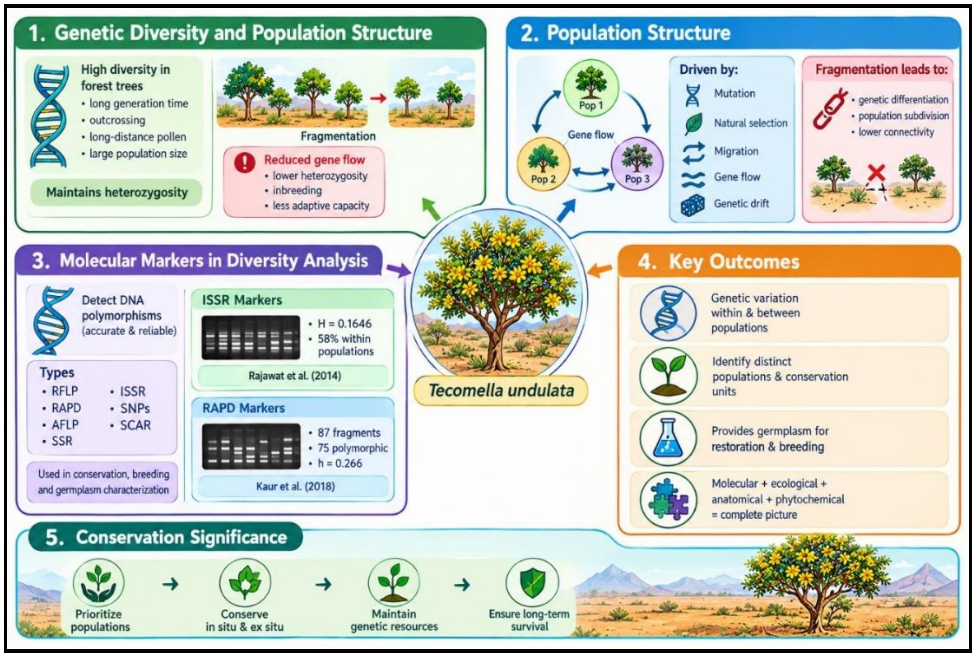


Figure 4: Molecular diversity analysis of *Tecomella undulata*, highlighting ISSR and RAPD markers and their role in assessing genetic variation and conservation.

Integrated Approaches in Diversity Analysis: The many different analytical techniques that can be used to assess biological diversity are complementary and are required to fully capture the diversity of natural plant populations, which is a complex pattern of variation. In the past, species identification and diversity evaluation were mainly based on morphological traits, however, morphological traits are environmentally influenced and are age dependent thereby limiting their use in distinguishing genetically related populations. With the progress in plant biology, there is an increasing necessity for a multi-disciplinary approach where anatomical, phytochemical, biochemical, cytological and molecular data are integrated to gain a holistic understanding of plant diversity, evolution and adaptive variation (Kalia *et al*., 2011; Shankarnarayan and Nanda, 1963).

Integrated diversity analysis is based on the assumption that the different biological markers are indicators of different aspects of plant variation. Anatomical traits are those that can be explained by the combination of genetic control and environmental factors, the phytochemical profile outlines the metabolic diversity related to physiological and environmental processes, while molecular markers give direct information on the level of DNA polymorphism and evolutionary relationship which are not significantly affected by environmental changes. These are independent data which, when considered together, provide a more complete and scientifically sound assessment of biodiversity, than any one technique can offer by itself (Frankham *et al*., 2018).

Of the different elements of integrated diversity studies, molecular markers allow the most direct estimation of genetic variation since they focus on polymorphisms at the DNA level. Marker systems like ISSR, RAPD, SSR, AFLP and SNPs allow for an accurate assessment of genetic diversity, population structure, phylogenetic relationships and gene flow between populations. These molecular approaches are essential tools in conservation genetics as they help in identification of genetically distinct populations, estimation of inbreeding levels and selection of priority germplasm for conservation and breeding programmes (Kalia *et al*., 2011). However, there is a need for complementary approaches since the expression of genetic variation in terms of structural or physiological traits is not explained by molecular markers alone.

Anatomical investigations give valuable data on structural adaptations that were made in response to a particular environment. Changes in the organization of the epidermis, the thickness of the cuticle, stomatal characteristics, arrangement of vascular tissue, xylem structure, and mechanical tissues frequently indicate adaptation to water availability, temperature, salinity and other environmental conditions. Anatomical traits reflect a combination of the effects of environment and genetics, and are therefore good evidence of phenotypic plasticity and adaptive evolution. It is therefore possible to use anatomical data in conjunction with molecular data to differentiate environmental-induced structural changes from genetically determined variation (Carlquist, 2013).

Another important aspect of integrated diversity assessment is the phytochemical profiling, since secondary metabolites are biochemical responses to environmental factors and expressions of genetic potential. Frequently, fluctuations in phenolics, flavonoids, alkaloids, terpenoids, tannins and other

bioactive compounds are related to the difference in genotype, habitat conditions, physiological status and ecological interactions. Comparative phytochemical analyses are therefore important biochemical markers that could be useful in identifying elite medicinal genotypes, assessing adaptive responses to environmental stress and understanding metabolic diversity in natural populations (Wink, 1999). A combination of the molecular data and the anatomical data with the phytochemical information greatly facilitates the interpretation of population diversity.

Integrated diversity analysis has the great benefit that it can separate genetic variation from phenotypic plasticity. Differences in morphology or anatomy between populations could be due to differences in their genetic makeup or due to environmental effects on the same genetic makeup. Molecular markers can give independent evidence that there is a difference in DNA, which in turn can be used to assess if the difference is seen in the structure or in biochemical processes, and whether this is genetic or environmentally induced response. These complete assessments significantly enhance the precision of biodiversity assessments and minimize the potential of false conclusions from morphological observations (Frankham *et al*., 2018).

Conservation biology has been gaining importance as an integrated approach because endangered plant species frequently show complex patterns of variation which are only poorly suited to individual analytical approaches. Populations that have an ecological niche which is different from the rest of the species may be overlooked in conservation decisions due to molecular diversity. Conservation decisions based solely on molecular diversity may exclude populations with ecologically distinct adaptations or useful phytochemical properties. Likewise, relying on anatomical and/or phytochemical characteristics alone may underestimate the genetic diversity that is not phenotypically expressed. Accordingly, a multidisciplinary approach will invariably give a more scientific background to the identification of the evolutionarily significant units, conservation priority and germplasm selection for restoration programmes (Kalia *et al*., 2011).

In the last twenty years there has been a significant increase in the use of integrated methodologies in research on medicinal plants, forest trees and threatened species. Many studies have been successful in using DNA marker analysis together with anatomical observations, phytochemical profiles, ecological data, and geographical information systems to analyze population structure, to identify elite genotypes, and to assess adaptive variation along environmental gradients. These multidisciplinary studies have always yielded a more reliable and biologically meaningful interpretation than those based on any single type of evidence, and have highlighted the need for complementary data sets when investigating biodiversity (Rao & Hodgkin, 2002).

In case of medicinal plants it further has the added benefit of identifying better chemotypes with improved pharmacological properties through integrated diversity analysis. Genetically diverse populations do not always yield higher levels of medicinal compounds, and genetically similar populations under different environmental conditions can have significant biochemical differences. A combination of molecular markers, phytochemical composition and anatomical adaptations is therefore possible to evaluate simultaneously to identify populations that have desirable genetic traits and medicinal quality. This information is of great importance for pharmaceutical research, conservation of germplasm and sustainable commercial use.

By synthesizing available molecular anatomical, and phytochemical findings on *T. undulata,* we demonstrate how multidisciplinary data complements our understanding of genetic distinctiveness and structural adaptation, offering a more comprehensive assessment of population diversity than single marker estimates alone.

In Pakistan there is a lack of comprehensive studies evaluating the combined molecular, anatomical and phytochemical diversity of *T. undulata*, populations. Addressing this information gap is essential for understanding local environmental adaptation and developing effective conservation strategies.

Research Gap: Despite the growing scientific interest in the species due to its ecological, medicinal and economic importance, there is a lack of an integrated literature that covers all of these aspects. In the past, its ethno-medicinal uses, phytochemical constituents, pharmacological activities, molecular diversity and general botanical features have been the focus of the study. The studies have improved our knowledge of the species to a great extent, but they have mostly focused on one aspect of research at a time, and thus so far have not integrated an overall picture of the biological diversity and adaptive variation found in natural populations.

Molecular studies with ISSR and RAPD markers have confirmed that there is high genetic variability among the populations of *T. undulata* and so conserving genetically diverse germplasm is important. Likewise, phytochemical studies have unveiled a number of bioactive compounds underlying the antioxidant, antimicrobial, hepatoprotective, anti-inflammatory and anticancer properties of the species. However, such studies have been mostly qualitative phytochemical screening or pharmacological studies without taking genetic diversity into consideration and its relationship with the variability of phytochemicals between geographically separated populations. Therefore, the linkage of molecular diversity to biochemical variation has not been investigated well. 1

Similarly, no extensive anatomical studies have been made on *T. undulata* and only a few have been conducted for general taxonomic observations or pharmacognostic descriptions. Good comparative studies of anatomy of natural populations are nearly nonexistent. Specifically, there is limited knowledge of how environmental conditions can affect leaf, stem and vascular anatomy which could be associated with drought tolerance and ecological adaptation. This anatomical evidence will enable us to understand the phenotypic plasticity and identify adaptive structural characteristics linked to habitat.

The other important drawback of the current literature is the lack of multi-disciplinary studies that combine molecular, anatomical and phytochemical data. Most studies published thus far have been based on a single analytical approach and have not enabled the establishment of relationships between genetic variation, structural adaptations and biochemical diversity. These biological attributes are each part of a plant's diversity so measuring them individually gives only a part of the picture of population differentiation. Therefore, integrated analyses are needed to elucidate the relationship between environmental conditions, genetic variation and anatomical traits as well as secondary metabolite production.

This absence of data at the regional level restricts effective conservation strategies to address local environmental conditions. To address this, a systematic literature review was conducted across databases like Scopus and Google scholar, analyzing studies from 2000 to 2026.

The other big gap in research is the capacity to identify elite populations with improved medicinal and adaptive qualities. So far, few studies have tried to combine biochemical, anatomical and molecular data to identify genetically valuable populations for conservation, restoration and/or future breeding programs. The integrated evaluations are of great significance for endangered species to guide the conservation planning and sustainable use of valuable genetic resources.

-This review study involves anatomical characterization and phytochemical profiling of the populations, along with molecular marker analysis, to gain a comprehensive understanding of the diversity within the populations; to analyses the relationships between the structural, biochemical and genetic variations; and to determine the populations with desirable adaptive and medicinal properties.

CONCLUSION

Tecomella undulata shows considerable genetic, anatomical and phytochemical variation across its arid South Asian range, but these three dimensions have almost always been studied in isolation, and never together for populations in Sindh. These matters because genetic distinctiveness, structural adaptation and medicinal chemistry do not necessarily coincide a population valuable on one measure may be unremarkable on another so conservation decisions based on a single type of evidence risk protecting the wrong populations or missing the ones that matter most. Given the rapid decline of *T. undulata* from habitat loss, overharvesting and climatic stress, an integrated study combining molecular markers, comparative anatomy and phytochemical profiling in the same Sindh populations is urgently needed. This review synthesizes the current understanding of *T. undulata* genetic, anatomical, and phytochemical diversity. It highlights the species adaptive mechanisms and emphasizes the importance of multidisciplinary approaches in informing effective conservation and management strategies.

CONFLICT OF INTEREST

The author declares no conflict of interest.

AUTHOR CONTRIBUTION

S.A: Conceptualization, methodology, investigation, data collection, data analysis, and original manuscript preparation. S.A.A: Supervision, scientific guidance, and critical review. N.S: Manuscript writing, editing, and proofreading.

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