International Journal for Multidisciplinary Research (IJFMR)
E-ISSN: 2582-2160 ● Website: www.ijfmr.com ● Email: editor@ijfmr.com

Phytocomparative Omics, Antimicrobial Dynamics, and Biotechnological Conservation of Gloriosa Species: Implications for Novel Drug Discovery

Juhi Nagar[1], Abhilasha Dwivedi[2]

[1,2]School of Sciences, Sage University Bhopal, Madhya Pradesh, 462043, India

Abstract

Gloriosa species, particularly *Gloriosa superba*, have long been recognized as medicinal plants due to their wealth of bioactive compounds that include colchicine and have multiple pharmacological uses. In this review we will explore how phyto-comparative Omics (Genomics, Transcriptomics, Proteomics, Metabolomics), can help to explain the complex molecular mechanisms responsible for the biosynthesis of important metabolites from the plant and other biological functions of the plant. Additionally, this review highlights how Omics technologies can be used to identify and characterize new compounds with antimicrobial properties and how they may serve as lead drugs to combat emerging microbial resistance. The importance of Biotechnological Conservation Paradigms (in vitro culture and genetic diversity assessments) is also emphasized as they provide sustainable methods of protecting endangered Gloriosa populations and conserving their genetic diversity. Additionally, these Biotechnological conservation methods offer sustainable alternatives to enhance the production of the desired secondary metabolites. This review integrates the existing literature to emphasize the great potential of Gloriosa as a source for developing new drugs and to advocate for the use of an integrated conservation strategy to sustainably utilize Gloriosa.

Keywords: Gloriosa; Phytocomparative Omics; Secondary Metabolite Biosynthesis; Antimicrobial Phytochemicals; Conservation Biotechnology; Medicinal Plant Genomics

1. Introduction

The Flame Lily (*Gloriosa*) is a flowering plant within the family Colchicaceae that has been used for generations in traditional medicine, particularly in African and Asian communities, because of its bright, unique flower; the medicinal effects of this plant can be attributed to the bioactivity associated with the compounds found within the plant, specifically the alkaloids. Alkaloids are pharmacologically active compounds that include one or more nitrogen atoms. One example of these alkaloids is colchicine, which has anti-inflammatory and anti-gout properties and has also shown promise in treating certain types of cancers.

Omics technology has transformed plant research through genomics, transcriptomics, proteomics and metabolomics by allowing researchers to explore the complex biology behind how plants grow and develop, as well as biosynthesize numerous secondary metabolites that are economically valuable. By

providing an overall picture of biological systems, high throughput techniques enable identification of the genes, proteins and metabolites associated with a particular pathway, which enhances our ability to discover new compounds and understand the mechanisms of those compounds. Omics analysis of Gloriosa species will allow researchers to deconstruct the biochemical machinery that enables production of Gloriosa's diverse array of chemicals, many of which have potential as antibiotics.

Beyond their use as therapeutics, Gloriosa species are subject to severe conservation problems. Therefore, because of over-exploitation from wild populations, habitat destruction and slow natural propagation rates many Gloriosa species have been classified as endangered or vulnerable. Biotechnological approaches such as tissue culture and genetic diversity assessment offer a promising avenue for sustainable propagation, conservation and genetic improvement of these plants that will provide valuable resources for production of desired metabolites.

This review aims to provide a comprehensive overview of the current understanding of *Gloriosa* species through the lens of phytocomparative omics and their antimicrobial dynamics. We will explore how omics technologies contribute to the identification and characterization of bioactive compounds, particularly those with antimicrobial properties, and their implications for novel drug lead discovery. Furthermore, we will discuss the critical role of biotechnological conservation paradigms in safeguarding *Gloriosa* species and ensuring their sustainable utilization for future pharmaceutical and agricultural applications. This article synthesizes recent research to highlight the immense potential of *Gloriosa* as a source of new therapeutic agents and emphasizes the urgent need for integrated conservation strategies.

2. Phytocomparative Omics of Gloriosa Species

The application of omic technologies have greatly increased the amount of knowledge about the complex biological systems of the Gloriosa species, specifically regarding how these species biosynthesize the unique secondary metabolite compounds they produce. These high-throughput techniques offer a complete view of all the genes, transcripts, proteins and metabolites that are present in a plant as well as how they function together.

2.1. Genomic and Transcriptomic Insights

Genomic and transcriptomic studies in *Gloriosa* species are crucial for unraveling the genetic basis of their medicinal properties. While a complete genome sequence for *Gloriosa superba* is still emerging, significant progress has been made in identifying genes involved in the biosynthesis of colchicine and related alkaloids. For instance, recent research has identified several key genes from *Gloriosa superba* that are responsible for the biosynthesis of N-formyldemecolcine, a direct precursor to colchicine (Nett et al., 2020). These discoveries are pivotal, as they pave the way for metabolic engineering strategies to enhance colchicine production.

Transcriptomic analyses, which involve studying the entire set of RNA transcripts in a cell or organism, provide dynamic insights into gene expression patterns. By analyzing transcriptomes from different tissues or developmental stages of *Gloriosa*, researchers can identify genes that are actively involved in specific metabolic pathways or responses to environmental stimuli. Integrated metabolome and transcriptome analyses have been particularly insightful in understanding the mechanisms underlying the formation of diverse floral colors in *Gloriosa* tepals and anthocyanin accumulation (Sun et al., 2023; Sun et al., 2025). Such studies not only contribute to our understanding of plant development but also help in identifying potential regulatory genes that could influence the production of other valuable compounds.

2.2. Proteomic and Metabolomic Profiling

Proteomics, the large-scale study of proteins, complements genomic and transcriptomic data by providing information on the functional molecules within the plant. While specific proteomic studies on *Gloriosa* are less abundant compared to transcriptomics, the general approach involves identifying and quantifying proteins to understand their roles in various biological processes, including stress responses and secondary metabolism. The identification of enzymes involved in alkaloid biosynthesis pathways is a key application of proteomics in *Gloriosa* research.

Metabolomics, the comprehensive analysis of all metabolites in a biological sample, offers a direct snapshot of the plant's biochemical state. For *Gloriosa* species, metabolomic profiling has been instrumental in identifying and quantifying a wide range of primary and secondary metabolites, including various alkaloids, flavonoids, and phenolic compounds (Mondal & Chandra, 2023). These studies help in understanding the metabolic diversity within different *Gloriosa* accessions and identifying novel compounds with potential pharmacological activities (Figure 1). Integrated approaches, combining metabolomics with transcriptomics, have proven powerful in elucidating complex metabolic pathways, such as those involved in colchicine biosynthesis (Nett et al., 2020). This integration allows researchers to correlate gene expression with metabolite accumulation, providing a more complete picture of the underlying biochemical processes. An overview of omics investigations conducted in *Gloriosa* species, encompassing genomic, transcriptomic, and metabolomic analyses, is presented in Table 1.

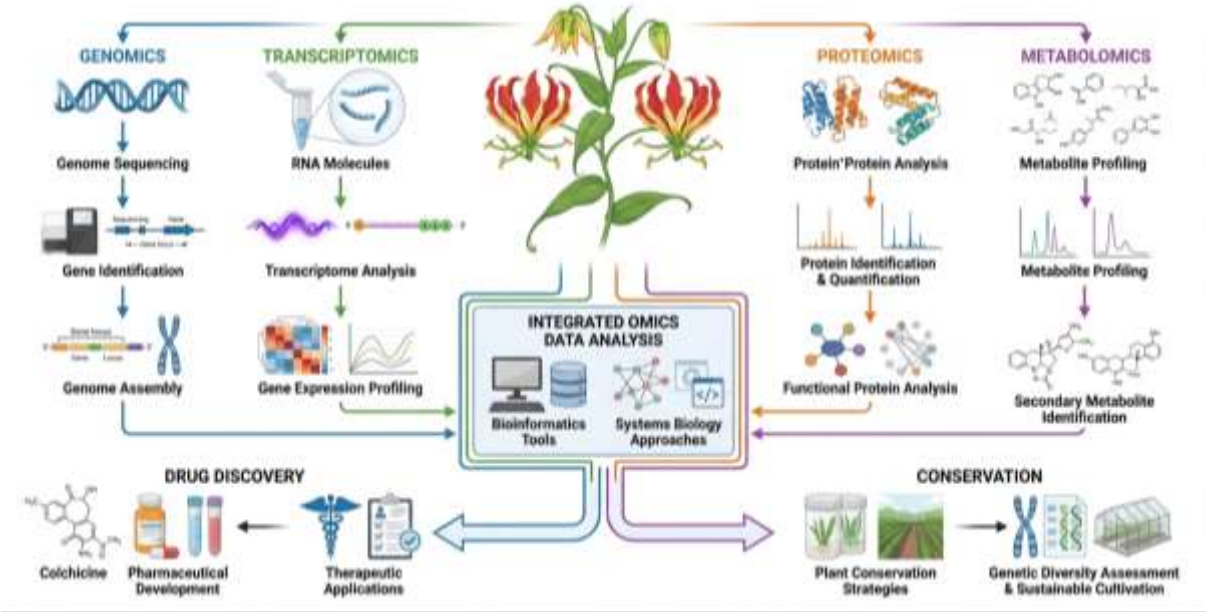

Figure 1: Integrated omics framework in Gloriosa research*: a flowchart showing the synthesis of genomics, transcriptomics, proteomics, and metabolomics data. The diagram illustrates the transition from genetic information to metabolites, highlighting their critical applications in advancing drug discovery (e.g., colchicine) and informing species conservation strategies.*

Table 1: Summary of Omics Studies in *Gloriosa* Species

Omics Type	*Gloriosa* Species/Part Studied	Key Findings	Ref.
Transcriptomics & Metabolomics	*G. superba* 'Rothschildiana' (petals)	Anthocyanin accumulation mechanisms during flower development; 59 anthocyanins identified with color-transformation-linked gene expression.	(Sun et al., 2023)
Metabolomics	*G. superba*, *G. lutea*, *G. rothschildiana* (tubers)	Comparative quantification of colchicine; anti-gout activity validated; significant interspecific alkaloid variation.	(Misra et al., 2022)
Metabolomics & Proteomics	*G. superba* (leaves)	Elicitor-induced metabolic reprogramming; 500+ metabolites identified, including 15 key secondary metabolites.	(Gandra et al., 2022)
Transcriptomics	*G. superba* (leaves, multiple ecotypes)	De novo transcriptome assembly; 6,102 EST-SSR markers developed for genetic diversity studies.	(Das et al., 2020)
Genomics	*G. superba* (chromosomes)	Karyotype analysis via FISH; localization of 5S/45S rDNA and telomeric repeats.	(Zhao et al., 2024)
Metabolomics	*G. superba* (rhizomes/leaves)	Endophyte-enhanced colchicine/gloriosine production; metabolic profiling of elite chemotypes.	(Semwal et al., 2023)
Transcriptomics	*G. superba* (rhizomes/leaves/roots)	Tissue-specific reference genes validated; differential expression of colchicine-biosynthesis genes.	(Johnson et al., 2023)
Genomics & Metabolomics	*G. superba* (tubers/leaves, 50 accessions)	Genetic and metabolic diversity linked to colchicine content; ISSR markers correlate with chemotype variation.	(Mahajan et al., 2022)

Omics Type	*Gloriosa* Species/Part Studied	Key Findings	Ref.
Multi-Omics†	*G. superba* (leaves)	Biosynthetic pathway engineering: 4-hydroxydihydrocinnamaldehyde production via monolignol pathway.	(Xiong et al., 2024)

† *Combines transcriptomic reconstruction and metabolomic validation.*
***Abbreviations**: FISH = Fluorescence in situ hybridization; EST-SSR = Expressed Sequence Tag-Simple Sequence Repeat.*

3. Antimicrobial Dynamics in Gloriosa Species

Gloriosa species have long been recognized in traditional medicine for their diverse therapeutic properties, including their potential as antimicrobial agents. Modern scientific investigations have begun to validate these traditional claims, revealing that various extracts and isolated compounds from *Gloriosa* exhibit significant activity against a range of pathogenic microorganisms.

3.1. Bioactive Compounds with Antimicrobial Activity

The antimicrobial efficacy of *Gloriosa* species is attributed to the presence of a rich array of bioactive compounds, primarily alkaloids, but also flavonoids, phenolics, and other secondary metabolites. A summary of key bioactive compounds identified in *Gloriosa* species and their reported antimicrobial activities is presented in Table 2. While colchicine is the most well-known alkaloid, other compounds contribute to the plant's broad-spectrum antimicrobial activity. Studies have shown that crude extracts and various fractions from *Gloriosa superba* demonstrate antibacterial and antifungal properties (Khan et al., 2008). For instance, chloroform fractions have displayed high antibacterial sensitivity against *Staphylococcus aureus*, and methanol extracts have shown promising activity against a variety of bacteria and fungi (Khan et al., 2008; Nikhila et al., 2014).

The mechanisms of action of these compounds are diverse, often involving disruption of microbial cell membranes, inhibition of essential enzyme activities, or interference with microbial genetic material. The synergistic effects of multiple compounds present in the plant extracts may also contribute to their overall antimicrobial potency, making the whole plant extract more effective than isolated compounds in some cases.

Table 2: Key Bioactive Compounds from Gloriosa Species and Their Antimicrobial Activities

Compound/Extract	Source	Class	Antimicrobial Activity	Ref.
Ethyl acetate fraction (non-alkaloidal compounds)	Tubers	Flavonoids, Terpenoids, Phenolics	Antibacterial: Significant inhibition of *Staphylococcus aureus* and *Escherichia coli*; moderate activity against *Bacillus*	(Kiros et al., 2023)

Compound/Extract	Source	Class	Antimicrobial Activity	Ref.
			subtilis and *Pseudomonas aeruginosa*	
Methanol extract	Rhizomes	Polyphenolics	Antifungal: 78–90% inhibition of *Candida albicans*, *C. glaberata*; 80% inhibition of *Microsporum canis*; Antibacterial: Broad-spectrum activity against Gram-positive and Gram-negative bacteria	(Khan et al., 2008)
Ethanol extract	Tubers	Alkaloids, Flavonoids	Strongest antimicrobial activity among solvents tested; effective against fungi (*Aspergillus niger*) and bacteria (*E. coli*, *S. aureus*)	(Chimahali et al., 2019)
Pyocyanin-like compound	Endophytic *Pseudomonas aeruginosa* (rhizosphere)	Bacterial metabolite	Antifungal: Inhibits *Fusarium oxysporum*, *Rhizoctonia solani*; potential for agricultural biocontrol	(TALUKDAR et al., 2023)
Asperpyrone derivatives (A–C)	Endophytic *Aspergillus* spp. (seeds)	Dimeric naphtho-γ-pyrones	Antibacterial: Activity against *Bacillus cereus*; Antifungal: Inhibits *Candida* spp.	(Budhiraja et al., 2013; Khazaal et al., 2023)
Colchicine	Tubers	Alkaloid	Indirect antimicrobial: Enhances host immune response; synergistic effects in combinatorial therapies (literature notes)	(PEELE et al., 2022)

3.2. In Vitro and In Vivo Antimicrobial Studies

Numerous *in vitro* studies have confirmed the antimicrobial potential of *Gloriosa* extracts against a wide range of human and plant pathogens. These studies often involve testing different plant parts (e.g., tubers, leaves, seeds) and various extraction solvents (e.g., methanol, ethanol, chloroform, aqueous) to determine the most effective preparations. For example, tuber extracts have consistently highlighted effective antibacterial and antifungal activities compared to shoot and flower extracts (Jasmine et al., 2020).

The antimicrobial activity has been observed against both Gram-positive and Gram-negative bacteria, as well as various fungal strains. Some studies have reported activity comparable to standard antibiotics and antifungals, suggesting *Gloriosa* as a promising source for novel antimicrobial drug leads (Kamna Bhatnagar & Anirudha Rishi, 2012). While *in vitro* evidence is substantial, more *in vivo* studies are needed to fully ascertain the therapeutic potential and safety of *Gloriosa*-derived antimicrobial agents in living systems. Such studies would provide crucial data on pharmacokinetics, toxicity, and efficacy in complex biological environments.

4. Novel Drug Lead Discovery from Gloriosa Species

The rich phytochemical diversity of *Gloriosa* species, particularly the presence of unique alkaloids, positions it as a significant source for the discovery of novel drug leads. While colchicine remains the most prominent compound, ongoing research is exploring other bioactive molecules and their therapeutic potential.

4.1. Colchicine and its Derivatives

Colchicine, a potent alkaloid found abundantly in Gloriosa species, has a long history of medicinal use, primarily for the treatment of gout due to its anti-inflammatory properties. Its mechanism of action involves binding to tubulin, thereby inhibiting microtubule polymerization, which affects various cellular processes including cell division and inflammatory responses. Beyond gout, colchicine has shown promise in treating other inflammatory conditions and has been extensively investigated for its anticancer properties, particularly in inhibiting cancer cell proliferation and inducing apoptosis (Goel et al., 2022).

The biosynthesis of colchicine in Gloriosa is a complex pathway that has been increasingly elucidated through omics approaches (see Figure 2). This pathway involves the enzymatic conversion of primary amino acid precursors (phenylalanine and tyrosine) into the final alkaloid product through a series of intermediate metabolites. Key enzymatic transformations—including hydroxylation, methylation, and cyclization reactions—drive the stepwise assembly of colchicine's distinctive tropolone ring structure. Recent discoveries have identified key enzymes and genes involved in the pathway, offering opportunities for metabolic engineering to enhance colchicine production or to produce novel derivatives with improved pharmacological profiles or reduced toxicity (Nett et al., 2020).

The development of new colchicine derivatives, often with modifications to the basic molecular structure, aims to optimize their therapeutic efficacy and expand their application in various diseases, including neurodegenerative disorders and fibrotic diseases.

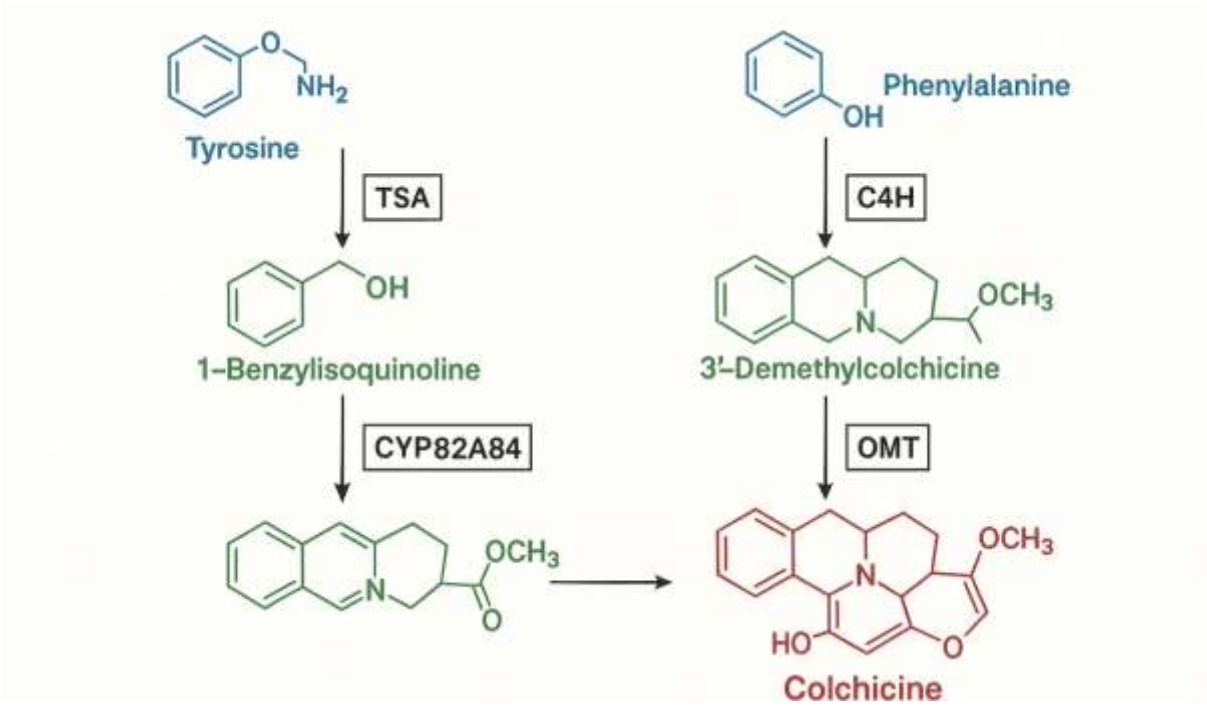

Figure 2. Biosynthesis of Colchicine in Gloriosa *: Colchicine production from amino acids (blue) via enzymatic steps (marked), showing intermediates (green) and final product (red), with tropolone ring formation highlighted.*

4.2. Beyond Colchicine: Other Bioactive Compounds

While colchicine is dominant in research on Gloriosa, numerous secondary metabolites with various pharmacological activities have been identified in the plant. Alkaloids such as gloriosine; flavonoids and phenolic acids; and various steroidal compounds also contribute to the overall medicinal value of the plant. For example, gloriosine, an alkaloid similar to colchicine, demonstrates significant antiproliferative activity, making it a candidate compound for the development of new anticancer drugs (Nett & Sattely, 2021).

Additionally, studies have shown that extracts and isolated compounds from Gloriosa exhibit a variety of pharmacologically active properties including anti-inflammatory, analgesic, antipyretic, antioxidant and antivenom activities (Ashokkumar, 2015; Mahajan et al., 2024). This suggests that Gloriosa may serve as a source of multi-target drugs or of compounds that can be developed into treatments for complex diseases where multiple pathways are involved. Thus, the identification and characterization of additional compounds present in Gloriosa, as well as their modes of action, will be necessary for extending the therapeutic use of this plant.

4.3. Omics-Guided Drug Discovery

Omics technologies play a pivotal role in accelerating the drug discovery process from natural products like those found in *Gloriosa*. By integrating genomic, transcriptomic, proteomic, and metabolomic data, researchers can gain a comprehensive understanding of the biosynthetic pathways of various compounds, identify novel enzymes, and pinpoint potential drug targets. This integrated approach, often referred to as systems biology, allows for the rapid identification of promising compounds and the elucidation of their pharmacological mechanisms.

For example, transcriptomics can reveal genes upregulated under conditions that favor the production of specific metabolites, guiding the isolation and characterization of new compounds. Metabolomics can provide a direct chemical fingerprint of different *Gloriosa* accessions, enabling the selection of chemotypes rich in desired bioactive molecules. Furthermore, computational approaches, leveraging omics data, can predict potential drug-target interactions, streamlining the drug development pipeline and reducing the time and cost associated with traditional screening methods. This omics-guided strategy is particularly valuable for complex plant species like *Gloriosa*, where a vast array of secondary metabolites exists, and their individual contributions to therapeutic effects need to be systematically explored.

5. Biotechnological Conservation Paradigms for Gloriosa Species

Gloriosa species, despite their immense medicinal value, face significant threats to their natural populations due to over-exploitation, habitat degradation, and slow natural propagation. Biotechnological approaches offer powerful tools for the conservation, sustainable utilization, and genetic improvement of these endangered plants.

5.1. In Vitro Propagation and Micropropagation

The use of tissue culture and specifically micropropagation has proven to be an essential tool for the fast and mass multiplication of the Gloriosa species which is causing less pressure on the wild population and a steady supply of plant materials for medicinal purposes. The use of various explant types (shoot tip, nodal segment, tuber) to create in vitro cultures (Akter et al., 2014; Hassan & Roy, 2005) has allowed for the creation of a significant amount of genetically identical plantlets in a relatively short time span with minimal seasonal variability.

Different techniques (callus induction, direct and indirect organogenesis and somatic embryogenesis) have been developed to produce efficient regeneration of the Gloriosa species. For example research has focused on developing standardized protocols for in vitro callus induction and indirect organogenesis to aid in the efficient regeneration of plants (Mosoh et al., 2024b). In addition to providing a method of conservation, micropropagation allows researchers to study plant growth and metabolite production under sterile conditions in a controlled manner and can provide a base for genetic transformation.

5.2. Genetic Diversity and Conservation

The understanding of the level of genetic diversity that exists within Gloriosa populations is critical to developing and implementing effective conservation strategies. Molecular marker techniques, including RAPD (Random Amplified Polymorphic DNA) and ISSR (Inter Simple Sequence Repeat), have been used to measure levels of genetic diversity among individual accessions (Yadav et al., 2013) of Gloriosa. These types of assessments allow for the identification of genetically distinct populations of Gloriosa, that will be useful for both maintaining biodiversity and for choosing appropriate germplasms for both ex-situ (e.g. gene banks) and in-situ (e.g. habitat preservation) conservation efforts.

Biotechnology has an essential role in conserving the genetic material of Gloriosa. Conservation through in vitro methodologies, including the use of slow-growth storage or cryo-preservation of seeds, pollen, or tissue culture, provide viable alternatives for the long term conservation of valuable genotypes. These types of conservation methods are especially important for endangered species such as *Gloriosa superba*, as natural reproduction is limited and genetic loss is becoming a growing concern (Mosoh et al., 2024a).

5.3. Enhanced Metabolite Production through Biotechnology

Beyond conservation, biotechnology offers avenues to enhance the production of valuable secondary metabolites, such as colchicine, in *Gloriosa* species. Various strategies have been explored, including:

- **Elicitation:** Applying biotic or abiotic elicitors to *in vitro* cultures can stimulate the plant's defense mechanisms, leading to increased production of secondary metabolites. For example, studies have investigated the effect of different elicitors on colchicine accumulation in *Gloriosa* cell cultures.
- **Metabolic Engineering:** With the increasing knowledge from omics studies about the colchicine biosynthetic pathway, metabolic engineering approaches can be employed to overexpress key enzymes or silence competing pathways, thereby redirecting metabolic flux towards colchicine synthesis. This involves genetic modification to optimize the plant's metabolic machinery.
- **Optimized Culture Conditions:** Manipulating *in vitro* culture conditions, such as nutrient media composition, plant growth regulators, light, and temperature, can significantly influence the yield of desired compounds. Optimized micro-tuber production *in vitro* has been shown to enhance colchicine concentration (Subiramani et al., 2019).

These biotechnological interventions provide sustainable alternatives to wild harvesting, ensuring a consistent and high-quality supply of medicinal compounds while simultaneously contributing to the conservation of *Gloriosa* species *(Figure 3)*.

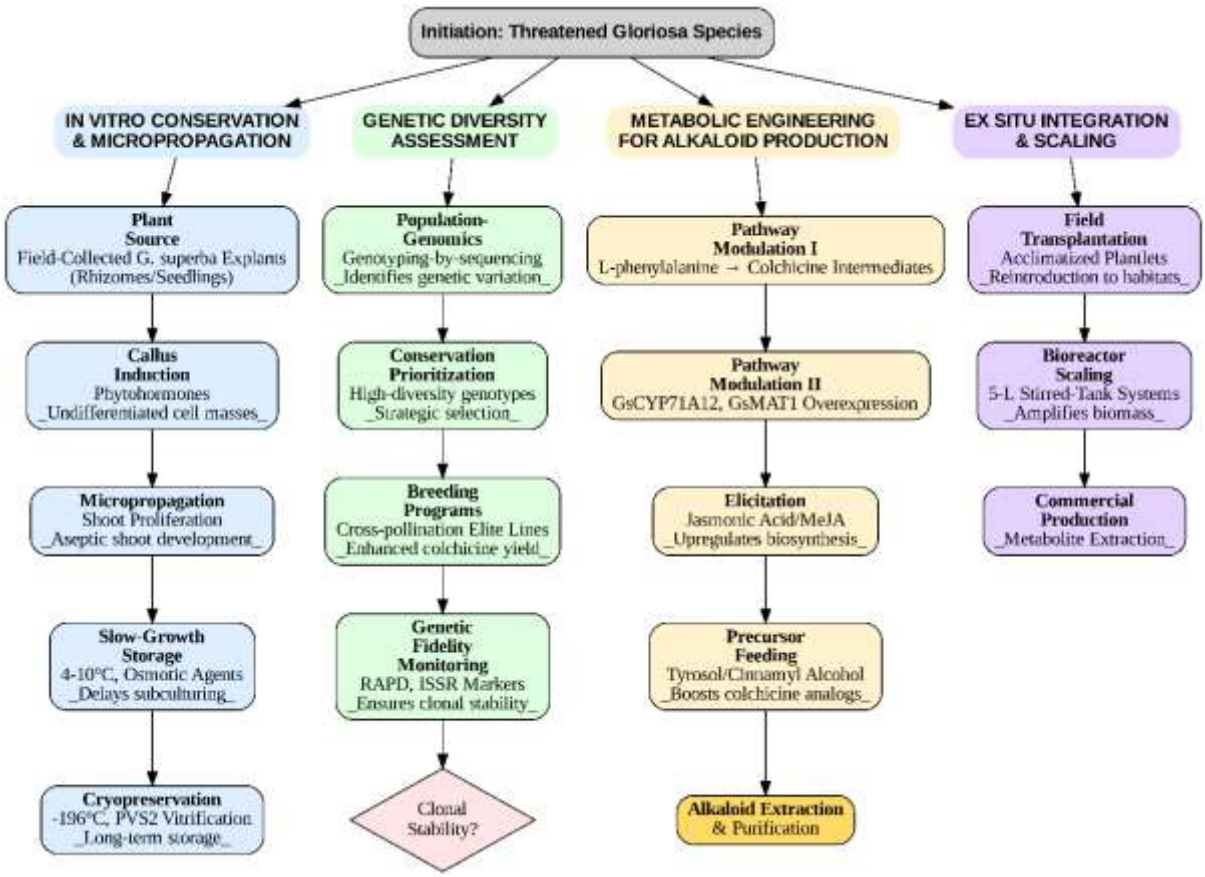

Figure 3: Biotechnological Strategies for Gloriosa Conservation and Improvement

6. Conclusion and Future Perspectives

In addition to being an example of a plant with significant medicinal importance due to its bioactivity and wealth of bioactive compounds (especially colchicine) with diverse pharmacologic uses, Gloriosa is a model for the application of phytocomparative omic technologies to identify the molecular mechanisms that govern the synthesis of bioactive compounds and other biological functions of the plant. Utilizing

advanced technology has not only led to the discovery of novel antimicrobially active compounds but it has also identified them as drug leads. Gloriosa species' antimicrobial dynamics, supported by both traditional knowledge and current scientific evidence, support their potential use to combat increasing antimicrobial resistance. Additionally, the discovery of new antimicrobially active compounds beyond colchicine will add additional therapeutic options derived from the Gloriosa genus. Ultimately, the utilization of omics-based drug discovery methods will expedite the identification, evaluation, and development of new drug leads from plants, thus facilitating a more rapid and focused transition from the plant to the pharmaceutical.

The preservation of Gloriosa species is critical to preserving genetic resources that will allow for continued access to valuable drugs. The application of biotechnology (in vitro propagation, assessment of genetic diversity, and cryopreservation) offers viable options for protecting endangered populations of Gloriosa. Additionally, biotechnology may be used to produce large quantities of secondary metabolites; which could help reduce dependence on wild harvesting and support the responsible use of Gloriosa.

The next step for researchers is to identify several key areas for research. There are many ways to integrate multi-omics data using advanced bioinformatics and systems biology techniques. The ultimate goal of this type of research is to develop a complete understanding of the biological and metabolic processes associated with Gloriosa. Through the application of systems biology techniques, it is likely that additional novel compounds will be identified along with an increased understanding of their mechanisms of action. Clinical trials are also needed to convert promising lead compounds derived from Gloriosa into therapeutics for humans. Additional research is required to develop biotechnologies to conserve Gloriosa populations and produce them sustainably. If we adopt an integrated approach to study Gloriosa and other plants similar to Gloriosa, they can remain as a source of new lead compounds for therapeutics and a model for conserving biodiversity threatened by multiple environmental factors.

References

1. Akter, S., Roy, P., Mamun, A., Islam, M., Kabir, M., & Jahan, M. (2014). In vitro regeneration of Gloriosa superba L-an overexploited medicinal plant in Bangladesh. *Nuclear Science and Applications*, *23*(1), 55-59.
2. Ashokkumar, K. (2015). Gloriosa superba (L.): a brief review of its phytochemical properties and pharmacology. *Int J Pharmacogn Phytochem Res*, *7*(6), 1190-1193.
3. Budhiraja, A., Nepali, K., Sapra, S., Gupta, S., Kumar, S., & Dhar, K. (2013). Bioactive metabolites from an endophytic fungus of Aspergillus species isolated from seeds of Gloriosa superba Linn. *Medicinal Chemistry Research*, *22*, 323-329.
4. Chimahali, J., Jebamalar, A., Duraikannu, G., & Thirumal, S. (2019). Phytochemical analysis and evaluation of antimicrobial activity in the whole plant extracts of Gloriosa superba. *Asian J Pharm Clin Res*, *12*(6), 245-249.
5. Das, M., Sahu, S. P., & Tiwari, A. (2020). De novo transcriptome assembly and mining of EST-SSR markers in Gloriosa superba. *Journal of Genetics*, *99*, 1-15.
6. Gandra, J., Patel, H. K., Kumar, S. A., Doma, M., Deepthi, Y., Bhalothia, P.,…Katam, R. (2022). Metabolomic and proteomic signature of Gloriosa superba leaves treated with mercuric chloride and phenylalanine, a precursor of colchicine alkaloid. *Industrial Crops and Products*, *178*, 114557.

7. Goel, B., Dey, B., Chatterjee, E., Tripathi, N., Bhardwaj, N., Kumar, S.,…Jain, S. K. (2022). Antiproliferative potential of gloriosine: A lead for anticancer drug development. *ACS Omega*, *7*(33), 28994-29001.
8. Hassan, A., & Roy, S. K. (2005). Micropropagation of Gloriosa superba L. through high frequency shoot proliferation. *Plant Tissue Cult*, *15*(1), 67-74.
9. Jasmine, J., Sundari, T., & Balakrishnan, V. (2020). Phytochemical analysis of Gloriosa superba L. using GC-MS from five different ecotypes of Tamil Nadu State, India. *Current Botany*, *11*, 01-06.
10. Johnson, N., Rodriguez Diaz, D., Ganapathy, S., Bass, J. S., Kutchan, T. M., Khan, A. L., & Flavier, A. B. (2023). Evaluation of reference genes for qRT-PCR studies in the colchicine producing Gloriosa superba L. *Plant Biotechnology Reports*, *17*(4), 561-571.
11. Kamna Bhatnagar, K. B., & Anirudha Rishi, A. R. (2012). Antimicrobial efficacy of an endemic plant species (Gloriosa superba Linn.).
12. Khan, H., Ali Khan, M., Mahmood, T., & Choudhary, M. I. (2008). Antimicrobial activities of Gloriosa superba Linn (Colchicaceae) extracts. *Journal of enzyme inhibition and medicinal chemistry*, *23*(6), 855-859.
13. Khazaal, H. T., Khazaal, M. T., Abdel-Razek, A. S., Hamed, A. A., Ebrahim, H. Y., Ibrahim, R. R.,…Soliman, H. S. (2023). Antimicrobial, antiproliferative activities and molecular docking of metabolites from Alternaria alternata. *AMB Express*, *13*(1), 68.
14. Kiros, T., Eswaramoorthy, R., Mohammed, S., Dekebo, A., & Melaku, Y. (2023). Non-Alkaloidal Compounds from Tubers of Gloriosa superba and their In vitro and In silico Antibacterial and Antioxidant Activities. *Current Bioactive Compounds*, *19*(8), 2-15.
15. Mahajan, Y. A., Shinde, B. A., Mulani, F. A., Gade, A. B., Kasodekar, A. K., Thulasiram, H.,…Nikam, T. D. (2022). Diversity assessment of Gloriosa superba accessions from Western Ghats of India based on morphological traits, ISSR markers and metabolite content. *Journal of Applied Research on Medicinal and Aromatic Plants*, *30*, 100388.
16. Mahajan, Y. A., Shinde, B. A., Shirke, H. A., Gandra, J., Suravajhala, P., Kishor, P. K.,…Nikam, T. D. (2024). Unlocking the genetic and biotechnological potential of Gloriosa superba to enhance its alkaloid production. *Industrial Crops and Products*, *211*, 118144.
17. Misra, A., Kumar, B., & Srivastava, S. (2022). A comparative pharmacognostical evaluation and simultaneous HPTLC quantification of bioactive alkaloids in three species of gloriosa, collected from natural habitat in India. *Pharmacognosy Magazine*, *18*(79).
18. Mondal, M., & Chandra, I. (2023). Organ specific phytochemical changes and antioxidant activities of in vivo and in vitro grown Gloriosa superba L. *South African Journal of Botany*, *152*, 1-10.
19. Mosoh, D. A., Khandel, A. K., Verma, S. K., & Vendrame, W. A. (2024a). Multi-explant and multiplex applications of plant growth regulators: A critical analysis of direct organogenesis in Gloriosa superba (L.). *Tropical Plants*, *3*(1).
20. Mosoh, D. A., Khandel, A. K., Verma, S. K., & Vendrame, W. A. (2024b). Standardizing in vitro callus induction and indirect organogenesis of Gloriosa superba L. leaf explants using exogenous phytohormones. *Journal of Plant Biotechnology*, *51*(1), 237-252.
21. Nett, R. S., Lau, W., & Sattely, E. S. (2020). Discovery and engineering of colchicine alkaloid biosynthesis. *Nature*, *584*(7819), 148-153.
22. Nett, R. S., & Sattely, E. S. (2021). Total biosynthesis of the tubulin-binding alkaloid colchicine. *Journal of the American Chemical Society*, *143*(46), 19454-19465.

23. Nikhila, G., Sangeetha, G., & Swapna, T. (2014). Antimicrobial screening of a medicinally potent plant—Gloriosa superba. *CIB Tech J Microbiol*, *3*, 48-57.
24. PEELE, K. A., INDIRA, M., SIBY, L., PALLAVI, G., LAVANYA, D., KRUPANIDHI, S.,…PRABHAKAR, K. V. (2022). PHYTOCHEMICAL AND BIOACTIVE POTENTIAL OF GLORIOSA SUPERBA L.
25. Semwal, P., Misra, S., Misra, A., Kar, S., Majhi, B., Mishra, S. K.,…Chauhan, P. S. (2023). Endophytic Bacillus strains enhance biomass and bioactive metabolites of Gloriosa superba. *Industrial Crops and Products*, *204*, 117296.
26. Subiramani, S., Sundararajan, S., Govindarajan, S., Sadasivam, V., Ganesan, P. K., Packiaraj, G.,…Narayanasamy, J. (2019). Optimized in vitro micro-tuber production for colchicine biosynthesis in Gloriosa superba L. and its anti-microbial activity against Candida albicans. *Plant Cell, Tissue and Organ Culture (PCTOC)*, *139*(1), 177-190.
27. Sun, Y., Hu, P., Jiang, Y., Li, J., Chang, J., Zhang, H.,…Zhou, Y. (2023). Integrated metabolome and transcriptome analysis of petal anthocyanin accumulation mechanism in Gloriosa superba 'Rothschildiana'during different flower development stages. *International journal of molecular sciences*, *24*(20), 15034.
28. Sun, Y., Hu, P., Jiang, Y., Wang, Z., Chang, J., Zhou, Y., & Shao, H. (2025). Comprehensive analysis of metabolomics and transcriptomics reveals varied tepal pigmentation across Gloriosa varieties. *BMC Plant Biology*, *25*(1), 66.
29. TALUKDAR, J., BARTHAKUR, M., & GOSWAMI, N. (2023). Antifungal Activity of Pyocyanin like Compound of Pseudomonas aeruginosa JT25 Isolated from Gloriosa superba L. *Biopesticides International*, *19*(2).
30. Xiong, Z., Ding, Z., Sun, J., Jiang, X., Cong, H., Sun, H., & Qiao, F. (2024). In vivo assembly in tobacco cells to elucidate and engineer the biosynthesis of 4-hydroxydihydrocinnamaldehyde from Gloriosa superba. *Plant Cell Reports*, *43*(10), 235.
31. Yadav, K., Aggarwal, A., & Singh, N. (2013). Evaluation of genetic fidelity among micropropagated plants of Gloriosa superba L. using DNA-based markers—a potential medicinal plant. *Fitoterapia*, *89*, 265-270.
32. Zhao, H., Wang, D., Li, H., Li, S., Wang, Y., Xu, A.,…Zhang, L. (2024). Fluorescence in situ hybridization analysis of Oligonucleotide 5S rDNA, 45S rDNA, and (TTTAGGG) 3 locations in Gloriosa superba L. *Cytogenetic and Genome Research*, 1-14.