

quality control, but comparative genomic mini-barcodes can now separate them, providing a needed basis for taxon-specific breeding and deployment (Wang et al., 2026).

The broader breeding literature indicates that marker-assisted selection, genomic resources, and genome editing can sharply improve breeding precision, especially when traits are difficult to assess phenotypically or are strongly affected by environment. DNA markers improve the productivity and accuracy of classical breeding and can shorten the time required to release improved varieties (Hasan et al., 2021). Genomics-assisted breeding further expands this framework by integrating genotyping, phenotyping, and envirotyping, while genomic markers, reference genomes, transcriptomes, and expression profiles support genotype-phenotype analysis, trait mapping, and faster selection (Tyagi et al., 2024). However, the breeding literature also cautions that marker-assisted selection is most straightforward for simpler traits, whereas polygenic traits require new strategies, stronger genomic infrastructure, and more innovative selection schemes. For *Paris* spp., this means that future breeding should first prioritize development of reference genomes, denser diagnostic markers, and phenotype-linked quality traits such as polyphyllin content, stress adaptation, and dormancy behavior before genome editing or genomic selection can be applied effectively (Su et al., 2022; Kumar et al., 2024).

6.3 Establishment of long-term resource restoration mechanisms

The third challenge is that germplasm restoration will not be durable unless it is embedded in long-term ecological and management mechanisms rather than isolated propagation projects. Across the Himalayan and Chinese literature, the same pressures recur: wild populations are vulnerable, slow-growing, destructively harvested, and affected by habitat degradation, illegal trade, and weak management guidelines (Kunwar et al., 2020). Reviews therefore converge on the need for combined in situ and ex situ conservation, while field studies add that local participation, awareness, and large-scale cultivation can reduce pressure on wild populations and support rural livelihoods (Thakur et al., 2023). Long-term mechanisms should also be spatially explicit. Nepal modeling predicted 51 suitable mid-hill and mountainous districts for future growth, and recent ensemble modeling in China showed that the suitable zones of var. *chinensis* and var. *yunnanensis* differ, are shaped by climate and human disturbance, and will change under future emissions scenarios. These results support restoration mechanisms that combine protected wild refugia, taxon-specific ecological cultivation zones, and long-horizon climate adaptation planning (Zhao et al., 2021; Wang et al., 2026).

A durable restoration model should therefore link policy, community, propagation, and monitoring into a continuous renewal system. Socio-ecological work in Nepal explicitly argues that sustainable production depends on understanding distribution, use, trade, and conservation together, while trade control requires stronger harvesting guidelines and more active community involvement (Kunwar et al., 2020). Studies from India likewise recommend placing *P. polyphylla* on priority cultivation lists, promoting rhizome and seed propagation, ecological niche modeling, and awareness programs, and maintaining long-term conservation through both field protection and cultivation support (Singh et al., 2026). Practical restoration infrastructure can include field gene banks, clonal trials, and seed production systems, as exploratory resource work in Northeast India reported conservation of distinct forms, vegetative clonal trials, and establishment of seed production systems for medicinal plant restoration programs. At the information level, PPDP already provides the first dedicated biomolecular database for *Paris*, integrating transcriptome, chloroplast, SSR, and functional analysis resources, and it is intended to expand further, making it a useful base for long-term germplasm documentation, trait mining, and restoration monitoring (Su et al., 2022).

7 Conclusions and Perspectives

Wild resource conservation remains the foundation of *Paris* spp. restoration because wild populations still contain the primary reservoirs of geographic, ecological, and genetic diversity needed for future breeding and provenance selection. This importance is reinforced by population studies showing clear geographic structuring in wild germplasm, with Guizhou, western Yunnan, and related regional groups retaining especially valuable diversity for protection and source selection. Wild *Paris* populations also form part of understory forest biodiversity, because it is an understory species associated with forest biodiversity and ecosystem stability. Yet these populations are