

match cultivar origin to future cultivation environments (Qiang et al., 2020). Rhizosphere engineering also appears promising: *Pseudomonas palleroniana* P6 increased root biomass, polyphyllin I, II, and VII content, and soil available potassium, indicating that industrial germplasm systems can be strengthened by microbe-assisted cultivation (Wu et al., 2025). Taken together, the renewal-utilization model should connect elite germplasm screening, marker-based authentication, clonal renewal, ecological site matching, and traceable downstream cultivation so that *Paris* spp. production shifts from wild-resource mining to adaptive, quality-controlled industrial regeneration (Oliya et al., 2023; Wang et al., 2026).

## 6 Challenges and Future Directions in *Paris* spp. Germplasm Restoration

### 6.1 Further improvement of germplasm evaluation systems

A central challenge in *Paris* spp. germplasm restoration is that evaluation systems remain incomplete, especially for linking population identity, geographic origin, genetic diversity, and medicinal quality into a single usable framework. Current studies show that molecular evaluation has advanced, but remains fragmented across marker types and regions. EST-SSR work in cultivated *P. polyphylla* var. *yunnanensis* found high polymorphism, high within-population diversity, low differentiation among cultivated populations, and clear admixture from two ancestral groups, indicating that existing cultivated materials are genetically mixed rather than standardized breeding stocks (Gao et al., 2022). SSR analysis in Nepal similarly showed that 74% of variation occurred within individuals in populations and only 26% among populations, while germplasms from similar geographic origins clustered together, supporting evaluation systems that combine individual-level diversity with provenance structure rather than relying on morphology alone (Oliya et al., 2023). AFLP studies in China reached a similar conclusion, with most genetic variation occurring within populations and with wild populations showing clear geographic structure, especially in Guizhou, Yunnan, and Sichuan, which supports region-prioritized germplasm assessment and provenance selection (Huang et al., 2019). Additional AFLP analysis from Yunnan also found that inter-population differentiation was relatively small and that gene flow among groups was limited, reinforcing the need to sample broadly while still preserving local lineages in evaluation programs.

The future direction is therefore not simply to add more markers, but to build a multi-dimensional germplasm evaluation system that integrates genetics, phylogeography, traceability, and source-level quality control. Phylogeographic work based on chloroplast trnL-trnF sequences detected 15 haplotypes, including wild-unique and cultivated-unique haplotypes, and identified Guizhou and western Yunnan as likely historical refugia that should be included in protection zones and core germplasm construction (Zhao et al., 2021). SCoT and SRAP markers also produced very high polymorphism in Dabie Mountain materials and were explicitly proposed as suitable tools for diversity analysis, genetic improvement, and conservation (Zhao et al., 2020). Beyond DNA markers, source-traceability systems are becoming feasible: a multi-block MIR/NIR platform distinguished seed germplasm from six Yunnan origins with 96.03% test accuracy, offering a practical route for rapid screening of excellent germplasm and source-based quality control (Li et al., 2022). At the time of the cited marker studies, complete genome and EST resources remained limited, and the field still required expanded molecular databases (Su et al., 2022).

### 6.2 Potential application of molecular breeding technologies

The second major future direction is the application of molecular breeding technologies to overcome the slow growth cycle, long seed dormancy, mixed genetic background, and unstable quality that limit conventional *Paris* improvement. Current evidence suggests that the species is well positioned for marker-assisted and genomics-assisted breeding, but the enabling resources are still emerging. The most direct *Paris*-specific evidence comes from EST-SSR markers related to polyphyllin backbone biosynthesis, which were developed specifically to characterize cultivated populations and were proposed as tools to facilitate marker-assisted breeding (Gao et al., 2022). That need is strengthened by the fact that cultivated populations show admixture, cross-pollination among cultivars, and little deep domestication differentiation from wild sources, which complicates parent selection and makes phenotype-only breeding inefficient (Huang et al., 2019). Recent assessment work also shows that accurate distinction between *P. polyphylla* var. *chinensis* and var. *yunnanensis* remains a practical issue for cultivation and