

polyphylla and related taxa can generate forms that are difficult to distinguish morphologically, which disrupts seed-based breeding and weakens the uniformity of medicinal raw materials. Marker studies also show that cultivated materials often carry high admixture and mixed ancestry. EST-SSR analysis found low differentiation among cultivated populations but high diversity among individuals, with populations likely derived from two ancestral groups and with evidence of cross-pollination among cultivars (Gao et al., 2022). AFLP results likewise showed that cultivated populations can have high variation, probably because they originated from mixed provenances, which means provenance screening is still urgently needed before artificial germplasm can be treated as genetically standardized breeding material (Huang et al., 2019).

Quality evaluation is similarly underdeveloped because medicinal value is not determined by survival alone, but by stable biomass and saponin accumulation across propagules, growth stages, and lineages. One recent study had to select elite wild accessions and then clone them as candidate cultivars on the basis of biomass production and polyphyllin content, showing that quality-assured artificial germplasm is still being built from screened wild founders rather than from mature breeding pools (Wang et al., 2023). Developmental-stage effects further complicate evaluation, because extraction yield, antioxidant activity, phenolics, flavonoids, and diosgenin content all change with plant age, and reproductive-stage rhizomes can differ substantially from juvenile or vegetative materials (Kumar et al., 2025). At the molecular level, researchers still emphasize that marker resources are limited, complete genomes are unavailable, EST resources are scarce, and the lack of marker information has constrained collection, conservation, and utilization of *Paris* germplasm (Gao et al., 2022). Although SSR, AFLP, SCoT, and SRAP studies now provide an emerging basis for diversity analysis and genetic improvement, these tools are still being established as foundational resources rather than functioning as a fully integrated quality-control system for artificial germplasm development (Zhao et al., 2020).

4 Key Technical Pathways for Artificial Germplasm Restoration of *Paris* spp.

4.1 Conservation of wild germplasm resources and selection of elite germplasm

Artificial germplasm restoration of *Paris* spp. should begin with the protection and systematic evaluation of wild germplasm, because wild populations remain the original reservoir of genetic diversity, adaptive traits, and medicinal-quality variation (Gao et al., 2022). Current evidence indicates that in situ conservation should remain the fundamental strategy even when ex situ cultivation and artificial propagation are expanding (Huang et al., 2019). Population genetic and phylogeographic studies show clear geographic structure in wild *P. polyphylla* var. *yunnanensis*, with Guizhou, western Yunnan, and parts of southern Sichuan retaining high conservation value and therefore deserving priority protection and restricted harvesting (Zhao et al., 2021). Wild populations in Guizhou appear especially important because they showed richer genetic diversity than those in Yunnan and were explicitly proposed as priority areas both for protection and for provenance selection. Broader regional work in Nepal and the Dabie Mountains similarly found substantial within-population variation and geographic clustering of germplasm, supporting region-based conservation sampling rather than random collection (Zhao et al., 2020; Oliya et al., 2023).

Elite germplasm selection should therefore combine ecological provenance, genetic diversity, and medicinal-quality screening instead of relying only on morphology or yield (Gao et al., 2022). This is especially necessary because cultivated populations often originate from mixed provenances and show admixture, gene flow, and weak domestication differentiation from wild sources, which can obscure genetic background and reduce breeding precision. Several studies now support using molecular markers such as AFLP, cpDNA haplotypes, SSR, EST-SSR, SCoT, and SRAP to define core germplasm, identify superior provenances, and guide conservation-oriented breeding (Zhao et al., 2020; Zhao et al., 2021). At the applied level, elite wild accessions have already been selected and clonally reproduced as candidate cultivars on the basis of biomass and saponin content, showing that restoration can move from passive conservation to targeted domestication when representative wild founders are first secured (Wang et al., 2023). Reasonable interventions in protected habitats, such as improving seed germination before sowing back into wild sites, may also strengthen renewal of effective wild populations and link conservation directly with germplasm recovery (Huang et al., 2019).