

Conservation and restoration of the plants in the Three Gorges Reservoir - a case study of *Myricaria laxiflora*

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The construction of the Three Gorges Dam (TGD) has had an important impact on the biodiversity and ecosystems in the Three Gorges Reservoir Area (TGRA). The construction will disrupt the natural hydrochory regime of the Yangtze River and alter the evolutionary processes of the existing biodiversity. Many species will lose their natural habitats and become endangered or disappear in the wild. Up to now, many conservation efforts have been taken for rescuing those endangered plants and great progress in understanding the biology and ecology of those species have been made (Liu et al., 2006). The results of those studies are valuable information for formulating conservation guidelines to successfully conserve and reintroduce those plants within TGRA.

Myricaria laxiflora is narrowly distributed along riverbank of Yangtze River valley and will be completely lost due to the Three Gorges Dam construction. It belongs to the genus *Myricaria* Desv. of the family Tamaricaceae which comprised four genera and has occurred in Paleo-Mediterranean sea region since the Tertiary period. Thirteen species are identified in the genus *Myricaria* and ten species naturally occur in China (Zhang and Zhang, 1984). Except *M. laxiflora*, all species are distributed in the Qinhai-Tibet Plateau and adjacent regions. Himalayas is considered the centre of origin. A recent review also suggested that ancestral populations of *M. laxiflora* possibly originated in the Paleo-Mediterranean sea region and the subsequent geological formation of the Himalayas and Yangtze River gorges forced the current pattern of natural distribution (Wang et al., 2003). However, little is known about the genetic diversity and structure of this species. Also, the phylogeographic origin and evolutionary history of *M. laxiflora* is ambiguous. In this study, we will investigate the population genetic structure of *M. laxiflora* and the origin of this species based on species-level phylogeography. Nine natural and one *ex situ* populations of *M. laxiflora* were investigated using AFLP markers (Figure 1). A moderate level of gene diversity was found in natural populations, while the *ex situ* population exhibited the highest (Figure 2). The F statistics by different approaches consistently revealed a high genetic differentiation among natural populations, attributing > 45% of total gene diversity. The Bayesian approach-based analysis demonstrated existence of nine independent populations in accordance with the sites they sampled. Estimates of gene flow by F_{ST} and coalescent-based simulation analysis indicated a restricted recurrent gene exchange among populations ($Nm=0.290-0.401$), whereas genetic distance-based clustering and coalescent-based assignment analyses revealed significant genetic isolation among populations. Tero et al. (2003) have introduced five basic models for the linear migration pattern among natural populations for plants. Compared with those introduced patterns, the migration pattern in *M. laxiflora* is best explained by classical-metapopulation model, but with a unique unidirectional direction underlined by hydrochoric force that drove dispersal of seeds and asexual propagules from upstream toward downstream populations (Figure 3). The previous efforts in preserving genomic integrity in *ex situ* conservation were evaluated and results provide valuable information to formulate conservation guidelines for the practice of successfully reintroducing *M. laxiflora* to the wild.

In order to investigate the special species status for *M. laxiflora* in *Myricaria* genus, we conducted species-level phylogeography of *Myricaria* populations in native China with the cpDNA haplotypes analysis. cpDNA genetic lineages indicated a clearly clustering pattern based on their species boundaries, except *M. Paniculata*, *M. bracteata* and *M. squamosa* which showed a mixed genetic lineages distribution and indicated potential shared ancestral genetic diversity and interspecies introgressive hybridization. Also, four major distinctly monophyletic clades have been identified from 41 *Myricaria* haplotypes and some species such as *M. platyphylla* showed incongruences between species phylogeny and morphology. The phylogeographic patterns among Chinese *Myricaria* populations have been shaped by both the uplifting of Qinghai-Tibet plateau and Quaternary glacial climates. Besides the previous proposition of the Himalayas as the center of origin (Zhang and Zhang, 1984), larger distributed areas for ancient *Myricaria* populations have been identified such as the eastern area of the Sichuan basin. Biogeographic analyses provided support for the maintenance of south mountains refugia during the last glacial maximum, and have responded to glacial expansion by shifting *Myricaria* plant ranges to south refugia and recolonizing northward to north-temperate regions. Finally, we highlighted the origin and colonization history for *M. laxiflora*. Estimation of molecular clock and biogeographic inferences suggested this species may derive from an ancient *Myricaria* lineage, but with recent limited range expansions following the eastward water-flow in Yangtze River after Three Gorges river sector had been established. Ancient vicariance events were the key factors for the origin of this endemic species and, possibly, the Hubei-Hunan-Chongqing mountain refugium reinforced the potential for *M. laxiflora* to survive the ice.

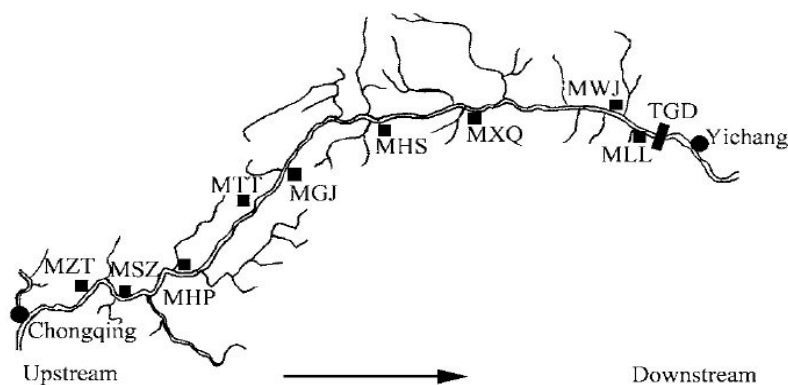


Figure 1 Map of the Yangtze River valley in China and population sampling sites for *Myricaria laxiflora*

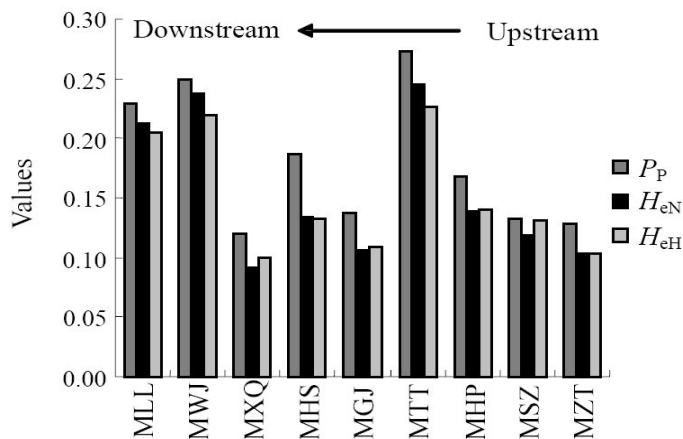


Figure 2 Percentage polymorphic loci (P_p) and gene diversity (H_{eN} and H_{eH}) of *Myricaria laxiflora* populations from the Yangtze River valley

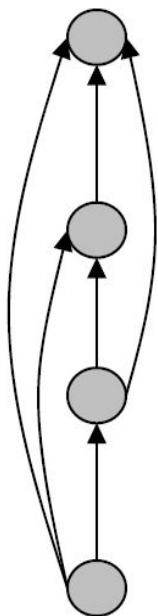


Figure 3. Diagram of the proposed unidirectional linear migration pattern and metapopulation model for *Myricaria laxiflora*

References

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