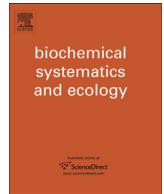




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The phylogeographic history of the self-pollinated herb *Tacca chantrieri* (Dioscoreaceae) in the tropics of mainland Southeast Asia

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ABSTRACT

The geological and climatic oscillations influenced the geographic distribution and demography of most present-day species, but few studies have investigated evolutionary history of species adapted to the tropical regions of Southeast Asia. Here, using sequence datasets obtained from three chloroplast DNA fragments (*trnH-psbA*, *trnS-trnG*, and *trnL-F*) from 320 individuals belonging to 24 natural populations, we investigated the phylogeographical history of *Tacca chantrieri*, which inhabits Southeast Asian tropical forests. Although relatively high level of differentiation among the populations were observed, mismatch distribution and neutrality tests showed no evidence of recent demographic population expansion. Phylogenetic inference exhibited two identified population groups showing a disjunctive distribution of dominant haplotypes. The split in cpDNA was largely consistent with the Tanaka line and Red River geographically. Molecular clock estimations revealed that the two lineages diverged during Pleistocene approximately 1.16 Ma. Therefore, the disjunct distribution of *T. chantrieri* could be explained by both the vicariance caused by Red River as well as ecological barriers caused by the different monsoon climates (Southwest monsoon vs. Southeast monsoon) that developed during the Pleistocene. The Tanaka line can be considered as a climatically driven barrier that influenced present-day plant dispersal.

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1. Introduction

The current geographical distribution of living organisms were influenced by both present and past ecological or historical factors (Cheng et al., 2005) such as climatic oscillations of the Quaternary (Avice, 2000; Hewitt, 2000, 2004) and various geographical barriers (Demesure et al., 1996; Taberlet et al., 1998; Hiramatsu et al., 2001). Mainland Southeast Asia, is one of the 25 global biodiversity “hotspots” (Myers et al., 2000), which contains several important biogeographical boundaries and harbors high levels of biodiversity. Yunnan is a special region of complex geological history in southwestern China because it located at a sutural zone between Gondwana and Laurasia (Audley-Charles, 1987; Jin, 2002; Metcalfe, 2006). Location in this transitional zone between tropical south-east Asia and temperate east Asia allows for the high biodiversity in the region

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(Takhtajian, 1978; Wu and Wu, 1996). The origin and evolution of the Yunnan flora is considered to be largely influenced by several factors including the uplift of the Himalayas, the formation of the east Asian monsoon climate and the extrusion of the Indochina block into tropical Southeast Asia since the later Tertiary period (Zhu, 2012, 2013).

Many studies focused on the flora of Yunnan and its relationship to biogeography and climate of the neighboring areas. Among these, three main studies stand out. First, Li et al. (1999) pointed out that the formation of the tremendous physical and climatic changes were associated with the vertical displacement of Shan-Malay Plate. The complex movements of the tectonic plates resulted in many important biogeographical boundaries in Yunnan and neighboring areas, which could facilitate the vicariance and speciation of plants in this region. For example, the Tanaka line (TKL) (Fig. 1; Tanaka, 1954). Indeed, strong genetic differentiation across southern and northern parts of the TKL has been reported previously (Qiu et al., 2009; Guan et al., 2010). Second, Mitsui et al. (2008) ascribed the evolutionary history of Yunnan plants to both geological diversity as well as the climate in the distribution area of these species. The development of the Himalayas drove a large amount of rainfall by forming a monsoon system in East Asia (Sun and Wang, 2005). Southwest China is the geographical meeting place for the southeast (SE) monsoon and southwest (SW) monsoon providing climatic diversity to this area (Gao et al., 1962).

Third main idea that explores the Yunnan flora and its relationship to the biogeography and climate of the neighboring areas is the Red River hypothesis (Clark et al., 2004). The Red River, also known as the Hồng Hà or Sông Cái in Vietnamese and the Yuan River in Chinese, is a river that flows from Yunnan in southwest China through northern Vietnam to the Gulf of Tonkin (Fig. 1). Clark et al. (2004) proposed that the Jinshajiang (Upper Yangtze) and its tributaries (Yalongjiang, Daduhe, Jialingjiang), as well as the Salween (Nujiang), Mekong (Lancangjiang), and Brahmaputra (Yarlung Tsangpo), were all once tributaries to the paleo-Red River. Moreover, the past changes in paleo-drainage systems of ancient Red River could influence the phylogeographic structure of Yunnan flora (e.g. *Terminalia franchetii*; Zhang et al., 2011b).

Plant phylogeographical studies are capable of examining the distribution of genealogical lineages and assessing the relative importance of different historical events, such as range expansion/contraction, fragmentation, and migration from refugia (Taberlet et al., 1998; Hewitt, 2000; Morris et al., 2010). Qiu et al. (2011) reviewed the current literature about plant molecular phylogeography in China and adjacent regions and documented the population histories of temperate plant species. However, studies on phylogeography have most often been directed at woody plants (Wang and Ge, 2006; Yu and Nason, 2013; Zhao et al., 2013). Herbaceous plants may have been more sensitive to quaternary (historical) climatic oscillations than woody plants because of their short life cycles, and would therefore be ideal candidates to illustrate the evolutionary history of the flora (Meng and Zhang, 2011). However, very few studies have investigated the phylogeographic patterns of herbaceous plants in the tropical rain forests of Southeast Asia.

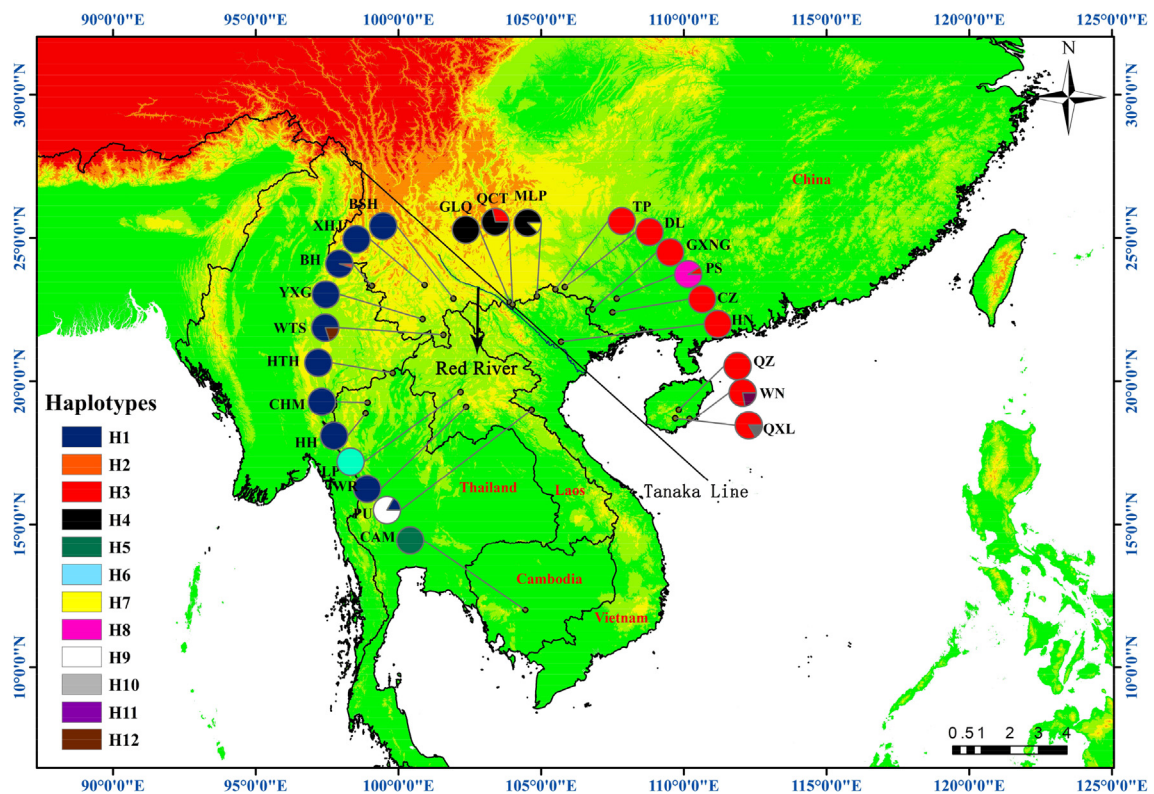


Fig. 1. Distribution of cpDNA haplotypes detected in 24 populations of *T. chantrieri*. Pie charts show the frequencies of haplotypes in each population.

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