

Microsatellite diversity and population structure associated with geographical factors in *Epimedium koreanum* populations in China

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Introduction

Epimedium koreanum has highly commercial importance and served as a famous and important traditional medicinal plant. In the past several decades, wild populations of *E. koreanum* declined and become fragmented due to over-exploitation and unreasonable harvest. Basic research on the conservation biology of medicinal plants using principles and methods of conservation genetics is essential for the security of Chinese medicinal resources and the sustainable development of traditional Chinese medicines.



Fig. 1 The morphology of the *Epimedium koreanum*.

On the other hand, genetic diversity of both plant and animal is not randomly distributed but is intimately linked to ecosystem function and evolution, which may associated with certain ecogeographical factors (temperature, water availability and latitude), ecological factors (water, temperature and geography). The clinal variation in genetic diversity can provide compelling evidence for spatially varying selection across an environment gradient. Many studies have addressed the latitudinal or longitude gradients in genetic diversity both for European and Asia taxa.

Material and method

A total of 466 *E. koreanum* adult individuals were collected from 10 populations from Changbai Mountains of Liaoning and Jilin provinces representing the geographic distribution of *E. koreanum* in China. Individuals were sampled exceed 1 m from each other and hence it is unlikely that the same clone would be sampled twice. Microsatellite diversity at nine highly polymorphic loci was examined in all 466 individuals.

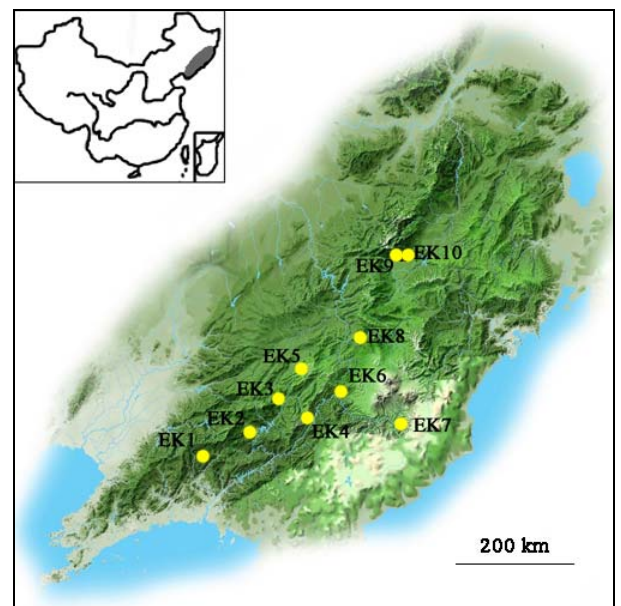


Fig.2 Geographical location and distribution of sample locations of the study site in Changbai Mountains.

Results I

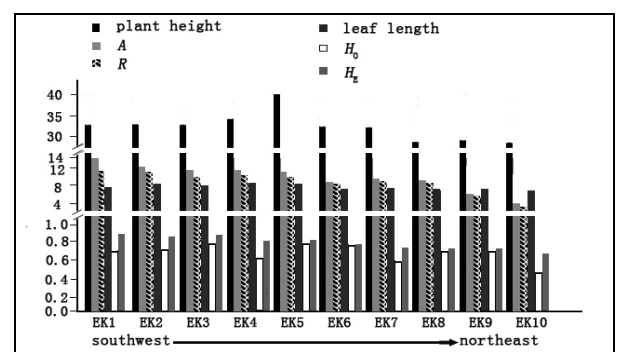


Fig. 3 Population genetic and morphology characteristic of 10 populations of *Epimedium koreanum*. A, number of alleles per locus; R , corrected allelic richness; H_O , observed heterozygosity; H_E , expected heterozygosity.

Results II

The mantel test did not reveal a significant relationship between geographic and genetic distances ($r = 0.1203$, $P = 0.1550$ for F_{ST} and $r = 0.1053$, $P = 0.1800$ for $F_{ST}/(1 - F_{ST})$).

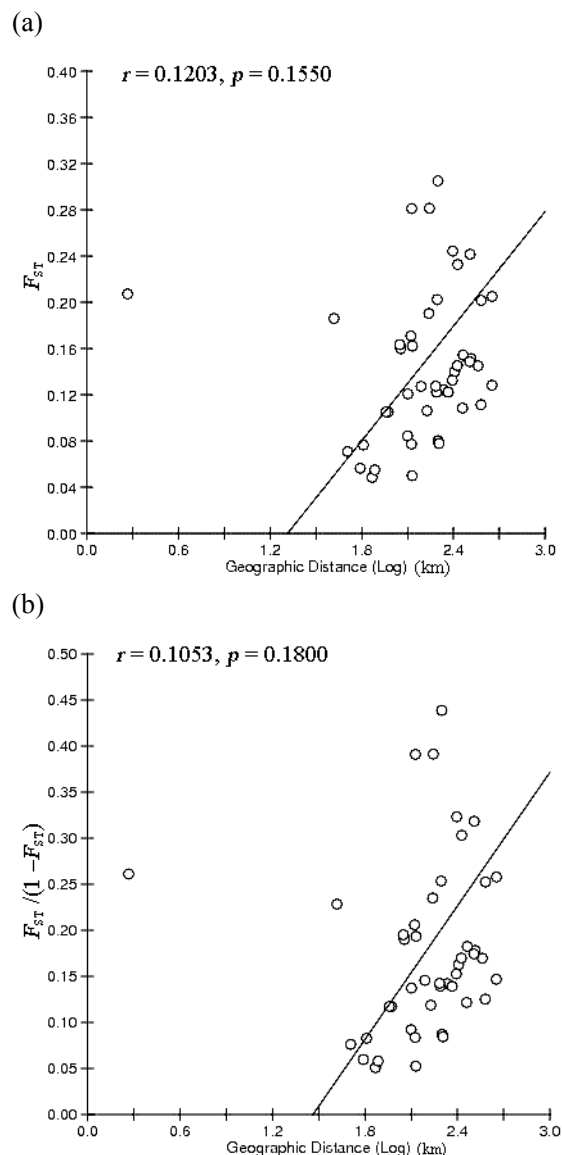
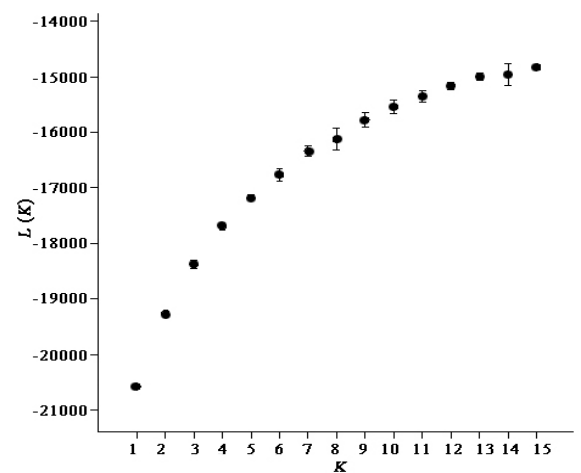


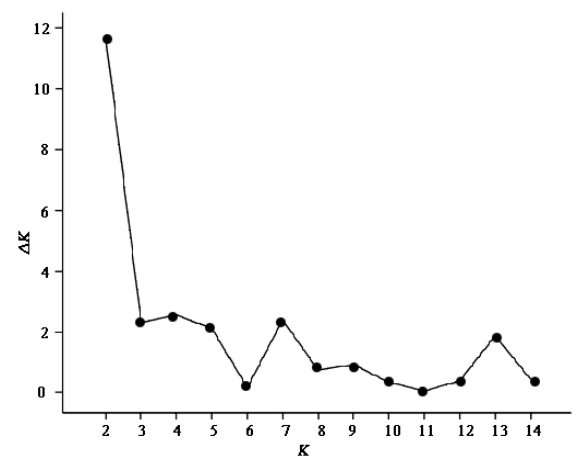
Fig. 4 Isolation by distance pattern in the distribution area. Regression of genetic distance against logarithm of geographical distance (km) for all pairs of sampled populations. (a) the genetic distance estimated by F_{ST} and, (b) estimated by $F_{ST}/(1 - F_{ST})$.

Results III

(a)



(b)



(c)

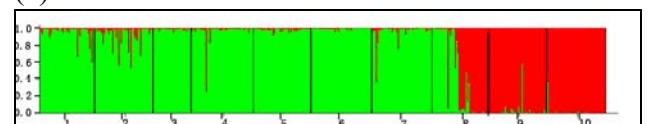
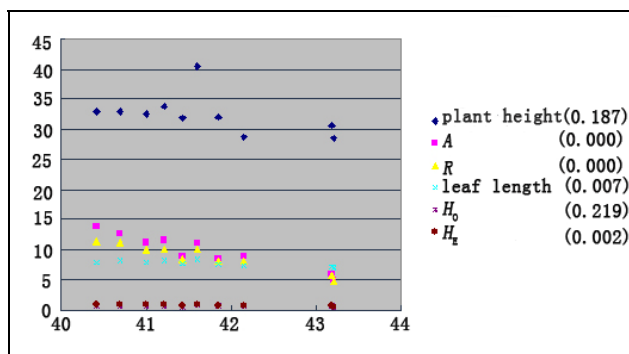


Fig. 5 Result of Bayesian clustering of *E.koreanum*. (a) Mean of $\ln \Pr(X | K)$ ($\pm$ SD) for each value of K . The plot illustrates the difficulty in inferring the optimal number of cluster, (b) ad hoc statistic ΔK , showing a peak at the uppermost level of structure at the true value of K , here two clusters, and (c) individuals from EK1-EK7 populations, were grouped together in the cluster 1, populations EK9 and EK10 grouped in cluster 2, while. population EK8 showed admixture between clusters 1 and 2.

Results IV

(a)



(b)

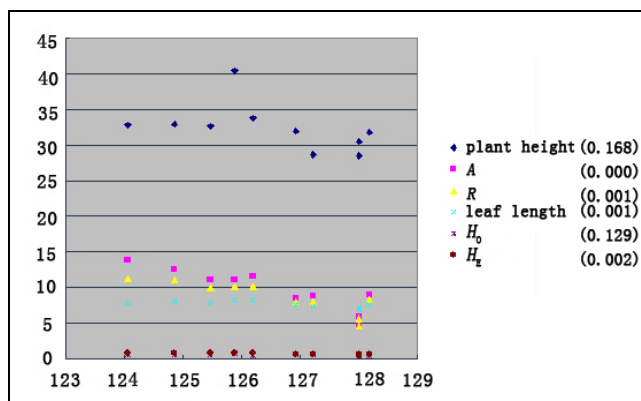


Fig. 6 Regression analysis between genetic diversity measures (A , R and H_E), the latitude and longitude of populations (p values in parenthesis). (a) significant and negative associations between genetic diversity measures (A , R and H_E) and the latitude of population. The latitude was also negatively correlated with the mean leaf length of corresponding population, and (b) similar and significant trends were also detected between the plant height and the genetic diversity and the longitude of the population.

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