

Population genetic diversity of *Potania mongolica* Maxim

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Introduction Research of genetic diversity provides important information for analyzing why some species become rare and endangered, and it provides information that can be used for protecting a species. (Greef et al, 1997). We used Amplified Fragment Length Polymorphism (AFLP) to study *Potania mongolica* Maxim in different regions, in order to explore the genetic background and evolutionary processes of these populations.

Materials and methods In the present paper, we studied the genetic diversities of eight wild *P. mongolica* Maxim. Populations (No. 1—No. 8), selected on the Western Ordos and Eastern Alax plateau. We collected thirty random samples in each population and extracted the total DNA in the lab. PCR selective amplifications were performed with eight primer combinations of 2 EcoR I and 4 Mse I. The AFLP data were analyzed with PopGen32.

Results Genetic diversity and differentiation among eight populations (240 samples) were studied using AFLP analysis with 8 informative primer pairs. 397 unambiguous bands (Figure 1) were created between 65-530bp, 286 of which were polymorphic. One pair of AFLP primers has detected a mean of 35.75. The result indicated a relatively high level of genetic variation in this species. According to the genetic distance matrix shown in attached Table 1. It is shown by the dendrogram (Figure 2) that the 8 populations can be categorized into 4 groups. A low degree of population differentiation existed among the eight populations with GST values of 0.13.

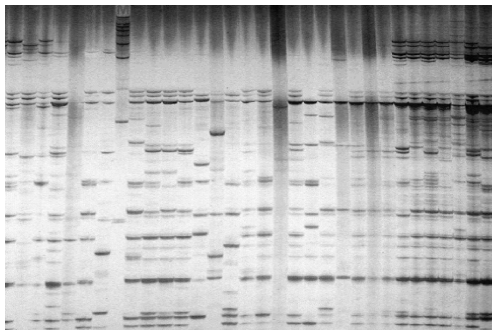


Figure 1 AFLP fingerprinting of *P. Mongolica* Maxim. M: Marker

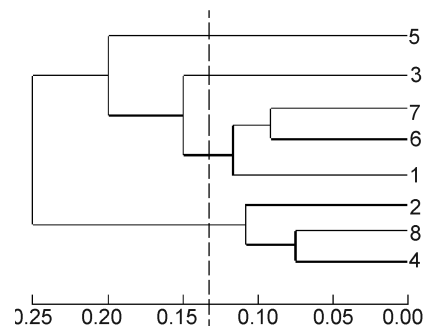


Figure 2 Dendrogram based on Nei's genetic distance of all *P. Mongolica* Maxim. populations

Discussion The capabilities of evolutionary potential and resisting severe environments rests with variation and genetic structure of populations (Arise & Hamrick, 1996). The genetic structure of *P. Mongolica* Maxim reflected its evolutionary history of population and determined adaptive potential for the future. Genetic diversity of *P. Mongolica* Maxim. populations shows clear regional relativity and similar genetic style, it shows they have a common origin. The random genetic vagrancy and inbreeding decline aren't affecting genetic diversity.

Table 1 Nei's genetic identity of all *P. Mongolica* Maxim. populations

Population	1	2	3	4	5	6	7	8
1	-							
2	0.13	-						
3	0.12	0.14	-					
4	0.13	0.12	0.17	-				
5	0.13	0.14	0.19	0.20	-			
6	0.11	0.12	0.14	0.14	0.14	-		
7	0.09	0.12	0.12	0.13	0.13	0.08	-	
8	0.13	0.12	0.14	0.07	0.16	0.14	0.15	-
Average	0.13							

References

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