

## Genetic diversity of cultivated and wild Tartary buckwheat (*Fagopyrum tataricum* Gaert.) accessions in East Asia revealed by AFLP analyses

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Buckwheat (*Fagopyrum spp.*) is consumed in many countries, including Korea, China, Japan, Nepal, Bhutan and many European countries. There are two cultivated species of buckwheat i.e., common (*F. esculentum* Moench) and Tartary (*F. tataricum* Gaertner). Common buckwheat is widely utilized worldwide, whereas Tartary buckwheat is utilized in limited region including China, Nepal and Bhutan. In view of some of beneficial effects for human health, such as beneficial effects on blood pressure and on cholesterol metabolism, increased attention has been currently paid to Tartary buckwheat as a functional food. Some factors, e.g., rutin is thought to be involved in such a beneficial effect. Thus, various Tartary buckwheat products, including noddles, roasted grain tea and buckwheat sprouts, may be available in Korea, such as common buckwheat. To ensure the long-term success of breeding programs and maximize the use of the germplasm resources in East Asia, knowledge of genetic diversity among cultivated and wild Tartary buckwheat accessions must be pursued. This study was intended to clarify the genetic diversity among cultivated and wild Tartary buckwheat accessions in East Asia generated by AFLP markers.

The 50 accessions of cultivated and wild Tartary buckwheat were surveyed with eight AFLP primer combinations. The levels of polymorphism detected with each primer combination in Tartary buckwheat accessions are reported in Table 1. With eight AFLP primer combinations, the obtained numbers of bands were 334 among which 121 were polymorphic in the 50 Tartary buckwheat accessions. The number of polymorphic bands per primer combination varied from eight for E-AC/M-GAC to 22 for E-CG/M-CTC with an average of 15.1 (Table 1). The cluster dendrogram constructed by UPGMA is presented in Fig. 1. The 50 accessions of cultivated and wild Tartary buckwheat showed comparatively high levels of similarity indices ranging from 0.40 to 1.00. The phylogenetic tree recognized two major groups at 81% genetic similarity (Fig. 1). Group I was

included all most of cultivated Tartary buckwheat accessions and two wild Tartary buckwheat accessions, and Group II was included only wild Tartary buckwheat accessions. In addition, Group I was subdivided into three subclusters at 83% genetic similarity. The first subcluster contained two wild Tartary buckwheat accessions. The second subcluster contained 32 cultivated Tartary buckwheat accessions and one wild Tartary buckwheat accession. The third subcluster contained 10 cultivated Tartary buckwheat accessions. Most wild Tartary buckwheat accessions with several exceptions, are situated far away from the main cluster of cultivated Tartary buckwheat. While several accessions of wild Tartary buckwheat could not be discriminated with cultivated Tartary buckwheat accessions by the AFLP analyses. According to our results, the AFLP markers provide a powerful tool for the studying genetic relationship and genetic variation among cultivated and wild Tartary buckwheat accessions. The assessment of genetic diversity and genetic relationships among Tartary buckwheat accessions in this study will be helpful to the studies of Tartary buckwheat breeding programs.

Table 1. Number of AFLP fragments generated with eight primer combinations among cultivated and wild Tartary buckwheat accessions

Primer combination	Total no of fragments	Number of polymorphic bands detected										% of polymorphic fragments	
		Cultivated Tartary buckwheat											Total
		Wild (8)*	Chi (19)	Paki (1)	India (4)	Nepal (9)	Bhu (3)	Lux (1)	Jap (2)	Slo (3)	(50)		
E-AC-M-CAC	43	12	8	6	7	7	8	6	6	6	13	30.2	
E-AC-M-GAC	34	8	7	6	6	7	7	6	6	5	8	23.5	
E-AC-M-GAA	33	12	8	5	7	9	6	5	6	5	12	36.3	
E-AC-M-CTA	40	18	13	8	11	11	11	10	11	10	18	45.0	
E-AI-M-GAF	48	12	10	7	9	11	8	6	8	6	13	27.1	
E-AI-M-GTG	45	17	12	7	9	11	8	8	10	9	18	40.0	
E-CG-M-CTC	50	22	19	16	17	17	16	17	17	16	22	44.0	
E-CG-M-GTC	41	13	11	5	7	9	6	7	8	7	17	41.5	
Total	334	114	88	60	73	82	70	65	72	64	121		
Avg		14.3	11	7.5	9.1	10.3	8.8	8.1	9.0	8.0	15.1	36.2	
% of polymorphism		34.1	26.3	18.0	21.9	24.6	21.0	19.5	21.6	19.2	36.2		

\* Number of accessions

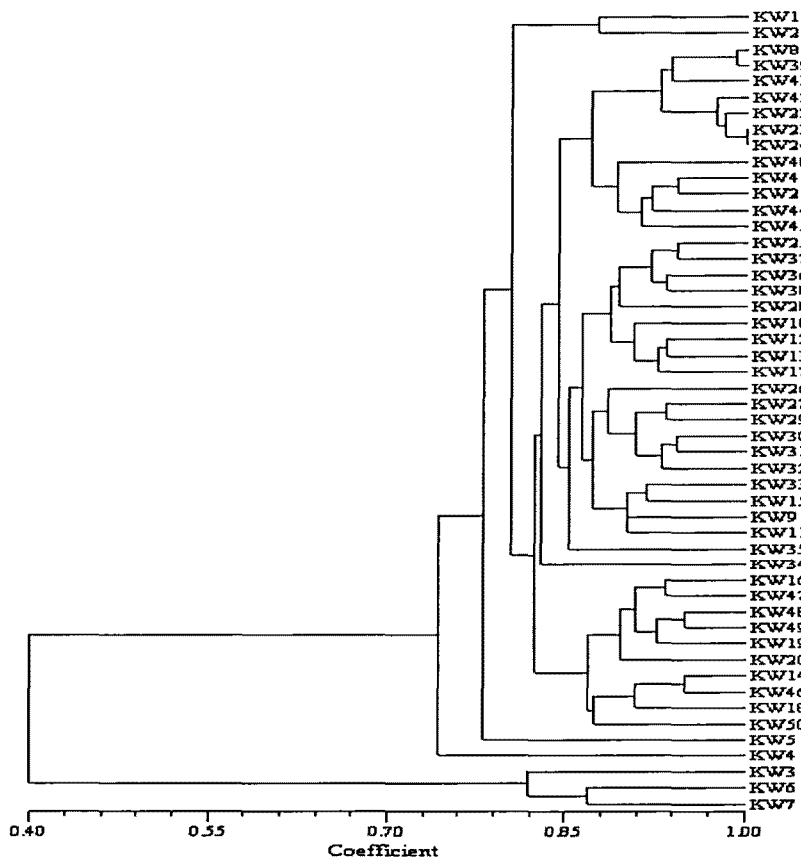


Fig. 1. Cluster dendrogram of 50 Tartary buckwheat accessions based on AFLP markers obtained with eight primer pairs.