

Genetic Diversity between Red Rice Accessions from Korea and the USA

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Objectives

The aim of the present study was to evaluate genetic diversity among red rice accessions from Korea and the U.S.A using RAPD (random amplified polymorphic DNAs) profiles.

Materials and Methods

○ Plant materials and DNA isolation

A total of eighteen red rice accessions from Korea and the U.S.A., and 6 varieties (three each from Korea and the U.S.A.) were tested. Grain types and origins of the materials analyzed in this study are given in Table1. Total genomic DNA was isolated and purified from fresh leaves of 20-day-old seedlings using the plant DNA isolation kit (Qiagen, USA).

○ RAPD analysis and Data analysis

Radom 10-mer RAPD primers were obtained from Operon technologies Inc. (Kit A, OPA 1~20). RAPDs were performed in capillaries of 10 μ l total volume containing about 10 ng template DNA, 1 μ M of each primer, 50 mM Tris-HCl (pH.8.3), 2 mM MgCl₂, 0.5 U *Taq* polymerase, and 0.2 mM of each dNTPs. RAPD fragments were separated in 1.4% agarose gels and stained with ethidium bromide. Only clear and unambiguous bands were scored. RAPD profiles were scored for the presence and absence of the corresponding bands, and analyzed for their genetic relationships using NTSYS-pc program.

Results and Discussion

A total of 105 reproducible bands were produced from 20 primers. Sixteen of them were polymorphic among red rice accessions from Korea and the U.S.A., and nine of them were between the red rice accessions and the U.S.A. cultivars. In association analysis, Korean and the U.S.A. accessions were clearly classified into two groups. One major group (cluster A) consists of the three subgroups, the one for the short grain red rice accessions including the three Korean cultivars, the one for the long grain Korean red rice accessions, and the one for the U.S.A. cultivars. The other major group (cluster B) included only the red rice accessions from the U.S.A. These results indicate a considerable genetic differentiation between the red rice accessions from the two regions.

Table 1. Accessions used to investigate their phylogenetic relationships.

No.	Acessions	Ecospecies ^{a)}	Sources	No.	Acessions	Ecospecies	Sources
1	Newbonet	Long	USA	13	Dongjinbyeo	Jap.	Korea
2	Legrwe	Medium	USA	14	Nampyeongbyeo	Jap.	Korea
3	Bengal	Medium	USA	15	ShinDongjinbyeo	Jap.	Korea
4	16B	Long	USA	16	Kyongjuaengmi	Short	Korea
5	2B	Long	USA	17	Kyunggishare	Short	Korea
6	7C	Long	USA	18	Buanaengmi	Short	Korea
7	Blakhull	Long	USA	19	Gochangaengmi	Long	Korea
8	20E	Long	USA	20	Galsacshare	Short	Korea
9	14F	Long	USA	21	Chunpoaengmi	Long	Korea
10	LA3	Long	USA	22	Samryeaengmi	Medium	Korea
11	TX4	Long	USA	23	Sangjuaengmi	Long	Korea
12	12B	Long	USA	24	Kimjeaengmi	Long	Korea

^a Jap. : Japonica cultivars, Short : Short grain type, Long : long grain type

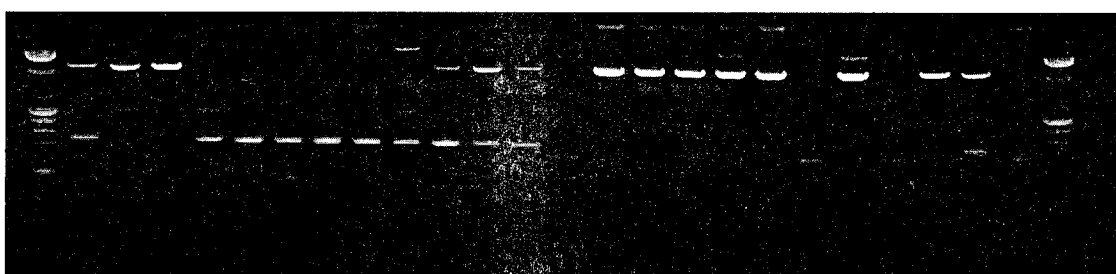


Fig. 1. A typical RAPD profile of red rice accessions and cultivars from Korea and U.S.A. Genomic DNA was amplified using the primer OPA 19.

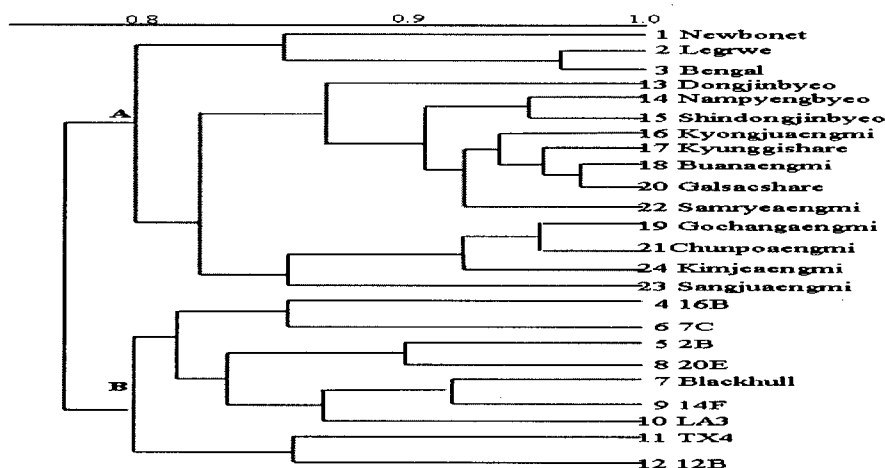


Fig. 2. Dendrogram showing phylogenetic relationship among the red rice accessions and cultivars from Korea and U.S.A. based on RAPD polymorphisms.