

P020

Relationship between Genetic Diversity and Transformation in Korean Wheat Varieties

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Objectives

The objective of this study was to quantify the genetic relationship of Korean wheat cultivars using random amplified polymorphic DNA (RAPD), which was used to assessment a correlation between genetic relationship and transformation of Korean varieties.

Materials and Methods

Plant materials : RAPD - 18 Korean wheat cultivars (cvs. Fig. 1)

Transformation - Six genotypes (cvs. Alchanmil, Geurumil, Gobunmil, Keumkangmil,
Tapdongmil, Urimil)

Agrobacterium strain / plasmids : KYRT1, EHA105 / pCAMBIA1305.1

PCR primers : A total of 56 operon random primers (20 primers of each OPB and OPC series, and 8 primers of
OPD series, and 4 primers of each OPI and OPG series)

Treatments : sonication, vacuum infiltration, and the combination of sonication and vacuum infiltration

Analysis : RAPD - the unweighted pair group of arithmetic means (UPGMA)

Transformation efficiency - GUS assay

Results and Discussion

DNA was isolated from the young leaves of 18 Korean wheat cultivars for RAPD analysis. Thirty-two polymorphisms were generated across the 18 cultivars of Korean wheat. These similarity coefficients were used to construct a dendrogram (Fig. 1) by UPGMA analysis to determine grouping of the wheat cultivars and had ranging from 0.98 to 0.66. The cultivars were clustered into one major cluster (A) and two small clusters (B and C). The major cluster (A) comprised of nine cultivars. The (B) cluster was contained five cultivars. The third cluster (C) was constituted two cultivars; Olgeurumil and Urimil, while Olmil and Dahongmil did not hold in any group. Efficiency of *Agrobacterium*-mediated transformation was determined by GUS gene expression in immature embryos of wheat. Expression of GUS gene was first observed 2-3 days post-infection and was consistently shown four patterns of GUS stain, and we were determined a grade of transient GUS expression (Fig. 2). In experiments described here, the frequency of GUS expression observed clearly difference among the Korean wheat cultivars. Geurumil and Keumkangmil was showed high GUS expression efficiency compared with other cultivars (Table 1). The dendrogram clustered Korean wheat cultivars accessions into three groups and that was been observed a narrow genetic base. In selected six cultivars, group A contained three cultivars (cvs. Alchanmil, Gobunmil and Tapdongmil) and group B contained two cultivars (cvs. Geurumil and Keumkangmil), while group C contained Urimil. These results suggest that the efficiency GUS expression among the cultivars was inherited a genetic property of Geurumil.

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Table 1. The effects of *Agrobacterium* strains, treatments and cultivars on GUS expression in immature embryos of Korean wheat.

Plasmid/ strain	Treatment	Proportion of explant with GUS expression (%) ^a	
		Alchanmil	Keumkangmil
pCAMBIA1305.1/ NT ^b		100.00 +++ ^c	87.50 +++
KYRT1	30sec	0.00 -	35.29 +
	60sec	10.00 +	30.00 +
	0.5h	100.00 ++++	35.00 ++
	1h	100.00 ++++	50.00 +
	30sec + 0.5h	100.00 ++++	100.00 +++
	60sec + 0.5h	100.00 ++	85.00 +++
	30sec + 1h	50.00 +	75.00 ++
	60sec + 1h	100.00 +++	25.00 +
	pCAMBIA1305.1/ NT		75.00 +
EHA105	30sec	85.00 ++	25.00 +
	60sec	10.00 +	0.00 -
	0.5h	100.00 +++	5.00 +
	1h	75.00 +	15.00 +
	30sec + 0.5h	100.00 ++	95.00 +++
	60sec + 0.5h	100.00 ++	90.00 +++
	30sec + 1h	10.00 ++	0.00 -
	60sec + 1h	85.00 ++	5.00 +

a: Number of GUS expression immature embryos / Number of immature embryos × 100

b: No treatment.

c: GUS expression in immature embryos of wheat (Same as Fig. 2).

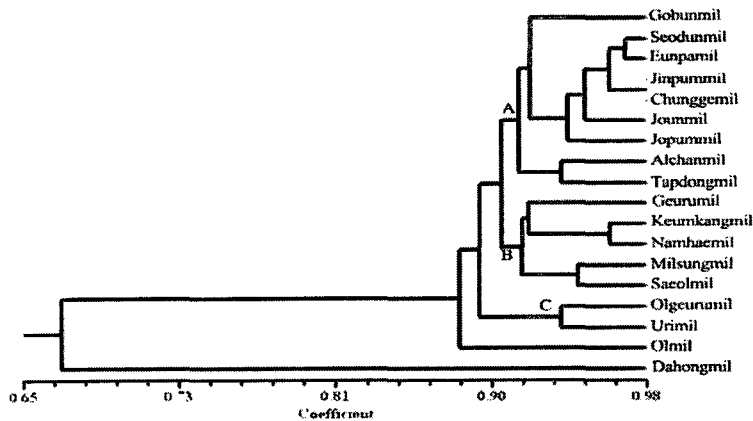


Fig. 1. Dendrogram of 18 wheat cultivars developed from RAPD data using unweighted pair group of arithmetic means (UPGMA).

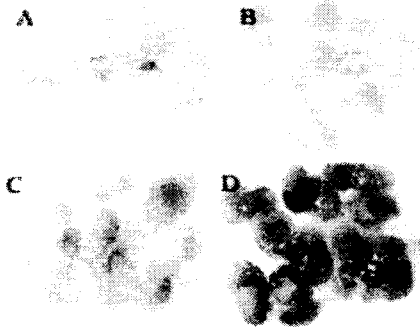


Fig. 2. Grades of transient GUS expression in wheat immature embryos. (A) + : Individual blue spots, (B) ++ : GUS expressing cells grouped, (C) +++ : Many GUS expressing cells grouped, (D) ++++ : GUS expressed as a whole.