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Systematic Study of Genus *Malus* Using ITS SequencesMin Ug Jung, Man Kyu Huh and Ji Seon kwon<sup>1</sup>

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*Malus*, the apples, is a genus of about 30–35 species of small deciduous trees or shrubs in the family Rosaceae, including most importantly the domesticated Orchard or Table Apple (*M. domestica*, derived from *M. sieversii*). The other species are generally known as "wild apples", "crab apples", "crabapples" or "crabs", this name being derived from their small and sour, unpalatable fruit. The genus is native to the temperate zone of the Northern Hemisphere, in Europe, Asia and North America. ITS (nuclear ribosomal DNA internal transcribed spacer sequences) and *rbcL* gene (the gene encoding a large subunit of ribulose-1,5-bisphosphate arboxylase/oxidase) have been widely used in plant molecular phylogenetics of genera, subfamilial taxa and families (Martins et al., 2003). Although it is important to gain knowledge of the genetic variation for conservation purposes, detailed information on the levels and distribution of this variation, as well as population structure, are not available for most woody taxa in Korea. Therefore, the objectives of this study were to estimate how much genetic diversity is maintained in genus *Malus* and to describe how Species-specific markers, which may be useful in germ-plasm classification are distributed among species. *Malus sieboldii* and *Malus baccata* was similar to *Malus asiatica*, while *Malus micromalus* taxa were more distinct the other. The phylogenetic tree clearly distinguished two clades. Species-specific markers, which may be useful in germ-plasm classification and agricultural process.

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Evolution of Parental ITS Regions of Nuclear rDNA in Allopolyploid Genus of *Acanthopanax* and Structure of ITS2 Region

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ITS (nuclear ribosomal DNA internal transcribed spacer sequences) and *rbcL* gene (the gene encoding a large subunit of ribulose-1,5-bisphosphate carboxylase/oxidase) have been widely used in plant molecular phylogenetics of genera, subfamilial taxa and families (Martins et al., 2003). Although it is important to gain knowledge of the genetic variation for conservation purposes, detailed information on the levels and distribution of this variation, as well as population structure, are not available for most woody taxa in Korea (Huh and Huh, 2001). Genus of *Acanthopanax* is a long lived woody species that is primarily distributed throughout Asia and Europe. This Many species of this genus are regarded as medically and ecologically important in the world. We evaluated a representative sample of the seven taxa with nuclear ribosomal DNA internal transcribed spacer sequences (ITS) to estimate genetic relationships within genus. As some Korean populations were isolated and patchily distributed, they exhibited a low level of genetic diversity. Genus of *Acanthopanax* is divided with two group. One group, genetic distances of *Acanthopanax* of *Acanthopanax sessiliflorus* Seem and *Acanthopanax chisanensis* is bound together from about 35. And the other group is bound together from about 95. This group is *Acanthopanax seoulense* Nakai, *Acanthopanax senticosus* (Rupr. Et Max.) Harms, *Acanthopanax sieboldianum* and *Acanthopanax sessiliflorus* for. *inermis*. The longest genetic distances of *Acanthopanax koreanum* Nakai and the other species by MEGA3 analysis appear to 174. Therefore, the objectives of this study were to estimate how much genetic diversity is maintained in genus *Acanthopanax* and to describe how species-specific markers, which may be useful in germ-plasm classification are distributed among species.