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Genetic Variation and Population Structure of Wild Lentil Tare, *Vicia tetrasperma*

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Genetic variation and population structure of seventeen populations of *Vicia tetrasperma* (Leguminosae) in Korea and Japan were investigated at 32 allozyme loci. The percent of polymorphic loci was 50.0%. Genetic diversity was high at both species and population levels ($H_{ES} = 0.171$; $H_{EP} = 0.158$), whereas the extent of the population divergence was relatively low ($G_{ST} = 0.116$). In the hierarchical analysis, the great amount of variance was exhibited among populations with respect regions ($F_{XY} = 0.266$) and a large component of the value was explained by variance among regions with respect to the total ($F_{XY} = 0.132$). The results consistent with the strong geographic effect indicated by UPGMA and Mantel's test. The correlation between genetic distance and geographic distance by Mantel's test was high and significant ($r = 0.597$). F_{IS} , a measure of the deviation from random mating within populations, was 0.503. It indicates that *V. tetrasperma* is an inbreeding species. An indirect estimate of the number of migrants per generation ($Nm = 1.90$) indicated that gene flow was high among populations. Nearly 88.4% of the total genetic diversity in *V. tetrasperma* was apportioned within populations. Wide geographic ranges, wild condition of the species nature and high fecundity are proposed as possible factors contributing to high genetic diversity.