A Simple Method for Analysis of the Heritability with Plant Chloroplast Genome

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In developing and breeding system of crop sciences, heritability of genetic traits is one of fundamental features but its research requires some time-consuming, costly, and labor intensive. So, we developed a simple method to infer heritability of the genetic trait using chloroplast genomes and our method uses phylogenetic distance and statistic correlation. When testing our method, we used nine genetic traits—days to flowering, days to maturity, period from flowering to maturity, the number of seeds per pod, 100-seeds weight, and four contents such as crude protein, crude oil, crude fiber, and dietary fiber—using 455 homologous chloroplast gene sets of six species of legumes. In results, correlation analysis between genetic trait differences and phylogenetic distance of homologous gene sets revealed that days to flowering, the number of seeds per pod, and crude oil content were influenced by genetic factors rather than environmental factors by 62.86%, 69.45%, 57.14% of correlated genes (P-value ≤ 0.05) and days to maturity showed intermediate genetic effects by 62.42% (P-value ≤ 0.1). But some genetic traits such the period from flowering to maturity and 100-seeds weight showed different results compared to those of some previous studies, which may be attributed to highly complicated internal (epistatic or additive gene effects) and external effects (cultural environment and human behaviors). Despite being slightly unexpected, our method can widely contribute to analyze heritability by including genetic information on mitochondria, nuclear genome, and single nucleotide polymorphisms. [This work was supported by a project grant from "Improvement of Information Management Framework and Development of Agrobiodiversity System" (RDA Project No. PJ017274)].