

Chontira Sangsiri 2009: Genetic Diversity of the Mungbean (*Vigna radiata*, Leguminosae) Genepool Based on Microsatellite Analysis.
Doctor of Philosophy (Agricultural Biotechnology), Major Field:
Agricultural Biotechnology, Interdisciplinary Graduate Program.
Thesis Advisor: Professor Peerasak Srinives, Ph.D. 142 pages.

A large representative collection of mungbean [*Vigna radiata* (L.) Wilczek] consisting of 415 cultivated, 189 wild and 11 intermediate accessions were analyzed using 19 SSR primers. These primers were developed from azuki bean [*V. angularis* (Willd.) Ohwi & Ohashi], and showed polymorphism in wild and cultivated mungbean. One or more SSR locus from each azuki linkage group was used. In total, 309 alleles were detected and of these about twice as many were detected in wild (257 alleles) compared to cultivated accessions (138 alleles). The number of alleles per primer ranged from 2 in CEDG174 to 37 in CEDG304 primers. The average diversity values for each locus was 0.59, ranging from 0.06 in CEDG269 to 0.92 in CEDG304. The results show that cultivated mungbean has its greatest diversity in South Asia, which supports the view that South Asia is the region where this crop was domesticated. SSR marker allelic diversity for cultivated mungbean has a distinct regional distribution with high variation in South and West Asia. Wild Australia and New Guinea represent a distinct center of diversity for wild mungbean. Based on Bayesian algorithm, the entire population was separated into two subgroups with largely belong to two subspecies. Each subspecies was further subdivided into three sub-subgroups. Wild mungbean has a rather clear geographical genetic structure, as compare to the cultivated mungbean. Based on the SSR marker diversity 106 accessions were selected for a useful core collection. This study represents the first comprehensive analysis of cultivated and wild mungbean germplasm diversity. It also highlights specific genetic diversity that might be used to broaden the genetic base of currently grown mungbean cultivars.

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Thesis Advisor's signature

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