

Cowpea is a tropical legume contributing significantly to food security in developing countries, especially in Africa. This research project was motivated by the upcoming introduction of Bt cowpea in Africa, likely to disturb the genetic equilibrium existing between wild and cultivated cowpea. The objectives of this study were to assess the genetic relationship between wild and cultivated cowpea, to determine how inbred and how differentiated are cowpea populations as well as gene flow, to estimate the mating system parameters in cowpea and their relation to ecological agents. In order to achieve these goals, wild and cultivated cowpea individuals were electrophoretically analysed using isoenzymes and PCR-RFLP techniques. Isozyme analysis revealed 61 alleles within wilds, 30 in cultivated and 29 common while chloroplast DNA variation was evident with two distinct haplotypes, the two within wilds, one in cultivated and one common. Very little genetic variation was found within accessions. Cultivated cowpea was found to be less diverse compared to its wild progenitor. Within wilds, genetic diversity indices decreased significantly from Southern to Western Africa via Eastern and Central Africa. Cultivated cowpeas were highly characterised by three markers (cpDNA haplotype I, Amp²¹⁰² and Fle³⁰⁹⁶). Positive and significant correlations were found between any pair of these markers within wilds. Wild cowpeas from West Africa region and especially Ghana at the country level displayed significantly most of these markers. Nei's genetic distances indicated wild accessions from western Africa more close to the domesticated taxa. These results indicate a possible centre of domestication of cowpea in West Africa. Populations of cowpea showed high level of genetic differentiation, suggesting a low level of gene flow between populations. Gene flow estimation between populations based on the level of population differentiation and private allele's frequencies were confirmed to be low. The inbreeding coefficients were significantly high, highlighting a significant departure from Hardy-Weinberg expectations. Genetic investigation of the mating system in the region indicated up to 97% self-fertilization. Most of the genetic variation (65.8%) was found between populations. Isolation by distance either based on the level of population differentiation or genetic distance was positive and significant, ($r = 0.142$, $P < 0.001$) and ($r = 0.2318$, $P < 0.001$) respectively. Outcrossing rates were high in Kenya (East Africa) (32.7%) compared to West Africa (3.4%). The monthly outcrossing rate estimates over two years showed the same tendency in coastal Kenya, although a significant difference in mean was found between the two years. Significant level of crossing was found between relatives. The results indicate that wild cowpea have a mixed mating system primarily inbred. The monthly specific outcrossing rate was inversely correlated ($r = -0.68$, $P < 0.001$) with rainfall distribution and positively correlated with flower density ($r = 0.44$, $P = 0.069$) and temperature ($r = 0.50$, $P < 0.050$). These data point out the dynamics of the mating system in cowpea through time. Implications of all these results in the light of releasing genetically modified cowpea, genetic conservation management and breeding programs in cowpea are discussed