Iron deficiency tolerance in mungbean was studied in an F$_2$ population derived from the cross between tolerant line, NM10-12 and susceptible variety, Kamphaeng Saen 1 (KPS1). The F$_2$ population and parents were grown in calcareous soil at Nakhon Sawan Field Crops Research Center. Correlation between total chlorophyll content and SPAD index was measured and analyzed. KPS1 and NM10-12 showed average SPAD index of 11.5 and 39.7, respectively. F$_2$ population displayed segregation of SPAD index in a range of 5.7-47.9. Average total chlorophyll content of KPS1 and NM10-12 were 0.085 and 0.323 g/m$^2$, respectively and showed high correlation with SPAD index ($r = 0.97$).

Screening for iron deficiency tolerance mungbean was carried out using half-Hoagland nutrient solution. The seedlings of three mungbean varieties, KPS1, KPS2 and NM 10-12 were grown in the solution. After 14 days, SPAD index was measured. It was found that the solution supplemented with 2 µM Fe-EDTA, 5 g/l CaSO$_4$ at pH 9 could distinguish the susceptible genotypes (KPS1 and KPS2) from the tolerant (NM10-12) one. When F$_2$ population of KPS1 x NM10-12 was grown in this solution, it was found that iron deficiency tolerance in mungbean is controlled by a single dominant gene which is in agreement with the field testing.

Bulked segregant analysis of two DNA two pools from 10 plants each of tolerant and susceptible F$_2$ individuals was done using AFLP technique. Marker ACC/CTG, AAC/AAC, ACC/CAA, ACT/CTA and ACT/CTA gave the combined phenotypic variation explained of 81.41%. Whereas the markers ACC/CTG and ACT/CTA were closely linked to the gene controlling to iron deficiency in mungbean.