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## Screening of elite cowpea genotypes for zinc, iron, protein and yield attributes

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Cowpea (*Vigna unguiculata*) with chromosome number 2n=22 is a multipurpose grain legume crop grown throughout sub-tropical areas of the world. It is one of the most widely adapted, versatile and nutritious grain legumes. It's a good source of protein, carbohydrate, fat, vitamins and phosphorous. Cowpea is a cheapest source of vegetarian protein; development of high yielding cowpea varieties with high zinc, iron and protein will help fight against malnutrition. Introduction of bio-fortified agricultural products and crop varieties with superior nutritional value are a prime low-cost crop improvement strategy for increasing the food sustainability. Though several options are available for augmenting mineral deficiencies of the soil, development of nutrient efficient genotypes seems be eco-friendly and long sustaining option to fight malnutrition. Keeping these aspects in mind, present investigation was carried at Department of Genetics and Plant Breeding, University of Agricultural Sciences, Bengaluru. Two hundred (200) cowpea genotypes obtained from different sources were field screened for their phenotypic performance and also screened for zinc, iron and protein. Iron and zinc contents in seeds of elite cowpea genotypes were analyzed using atomic absorption spectrophotometry (AAS). The seed protein content was estimated using Kjeldahl method described in AOAC (1984). The analysis of variance (ANOVA) indicated significant difference for all the characters under consideration justifying the selection of genotypes for the study. Genetic variability estimates, phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) were high for plant height, clusters per plant, pods per plant, pod yield per plant and seed yield per plant, indicating the predominance of additive gene action and these traits offer scope for direct selection. High heritability estimates coupled with high genetic advance as per cent of mean was observed for days to first flowering, days to fifty per cent (50%) flowering, plant height, primary branches per plant, clusters per plant, pods per plant, pod length, pod yield per plant, 100-seed weight and seed yield per plant suggesting that these characters are under the control of additive genes and phenotypic selection for these characters may be effective. Twenty-two (22) lines were found to be rich in zinc, iron and protein. Considering yield also, 18 genotypes were found to be most promising. The micronutrient range was found to be 15.8-48.6 ppm, 49.6-150.2 ppm and 22.03 ppm to 26.21% for zinc, iron and protein, respectively. Genotype, PGCP-6 scored high zinc content of 48.6 ppm, high iron of 137.2 ppm and 23.85% protein. Genotype KBC-6 was found to be rich in zinc 41.8 ppm, iron 150.2 ppm and 23.11% protein. Local check KM5 scored zinc of 15.8 ppm, iron 83.6 ppm and protein 24.5%. The genotypes which showed high zinc were also associated with stay green color even after maturity thus serving as phenotypic markers. Biochemical components associated with this trait needs to be identified which serve as marker to tag genotypes as zinc efficient. Molecular markers associated with stay green phenotype with high zinc needs to be identified. The two genotypes viz., PGCP-6 and KBC-6 were found to be most promising in terms of yield and also could be used for further confirmation of their results and then used in crop improvement programs.

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