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# VARIATION AND ASSOCIATION ANALYSIS AMONG PROTEIN QUALITY TRAITS IN CHICKPEA

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## ABSTRACT

**The study revealed sufficient variation among genotypes for protein content, methionine and tryptophan content along with various protein fractions. Globulin was the major protein fraction. Protein, methionine and tryptophan contents were independent of each other. Albumin protein fraction was positively associated with methionine and tryptophan amino acids. Various protein fractions were positively associated with protein content but had no association among themselves. Thus, it is suggested that improvement for nutritional quality of protein content in chickpea would be effective and economical if selection is carried out for albumin content alone rather than individual amino acids.**

**Key words:** Chickpea, proteins, methionine, tryptophan, albumin, globulin.

Chickpea, one of the important pulse crops of India, provides a good and cheap source of protein in cereal mixed diets [1], but when consumed alone has low nutritive value due to deficiency of methionine and tryptophan content. The development of cultivars with well balanced amino acid composition will improve their nutritional quality. In the past, little efforts had been laid on to develop protein quality cultivars. Keeping in view that various protein fractions having their own characteristic amino acid profiles [2, 3] can be better manipulated than the individual amino acids. The present study has been undertaken to assess variation and nature of association of protein content with methionine and tryptophan content along with protein fractions.

## MATERIALS AND METHODS

The experimental material comprised 36 genotypes of chickpea including ten varieties released for cultivation in various parts of India. Each genotype was raised in randomized block design during rabi 1991–92 in 3 m long rows with 30 cm row-to-row spacing and 10 cm plant-to-plant spacing with three replications so as to nullify soil heterogeneity effects.

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Healthy, disease-free, mature seeds harvested from all the three replications were bulked, crushed to a fine powder and defatted with cold acetone. The defatted flour was divided into three equal parts; each part treated as a repeat for the estimation of biochemical traits. Protein content was worked out by multiplying a factor 6.25 to nitrogen per cent [4]. Methionine [5] and tryptophan [6] contents were measured on Spectronic-20 at 515 nm and 545 nm, respectively. Protein fractionation was based on solubility characteristics [7]. Albumin and globulin-A were the supernatant and precipitate of water soluble fraction, respectively. Globulin-B and glutelin were salt soluble and alkali soluble fractions, respectively.

## RESULTS AND DISCUSSION

Analysis of variance (Table 1) revealed significant differences among genotypes for all the protein quality parameters indicating presence of sufficient variation for these traits. The results are in agreement with earlier reports [8, 9]. Range of variation also confirmed it. It is interesting to note that the range was quite broad for albumin and globulin-B fractions alongwith that for protein content. Segregates of the cross GGC 61 x GGC 31 may have adequate protein content coupled with favourable proportion of protein fractions.

Mean values for various protein quality traits (Table 1) revealed that methionine and tryptophan contents were 1.80 and 0.83 mg/g flour which was equivalent to 684.93 and 315.82 mg/100 g protein, respectively. Both the amino acids were much below than the

**Table 1. ANOVA, mean, range and high ranking genotypes for protein quality traits in chickpea**

| Character | Mean squares | Mean ± SE | Range | Top genotypes |
|---|---|---|---|---|
| Protein content (%) | ** | 26.28 ± 0.44 | 18.4–32.26 | GGC 55, GGC 61 |
| Methionine content (mg/g flour) | ** | 1.80 ± 0.05 | 1.40–2.25 | GGC 10, GGC 31 |
| Tryptophan content (mg/g flour) | ** | 0.83 ± 0.04 | 0.41–1.85 | GGC 30, GGC 31 |
| Albumin content (%) | ** | 6.47 ± 0.24 | 3.20–11.00 | GGC 31, GGC 59 |
| Globulin-A content (%) | ** | 1.54 ± 0.08 | 1.0–2.24 | GGC 2, GGC 31 |
| Globulin-B content (%) | ** | 11.51 ± 0.29 | 7.10–15.80 | GGC 55, GGC 68 |
| Glutelin content (%) | ** | 4.21 ± 0.21 | 2.22–5.80 | GGC 9, GGC 59 |

**Significant at 1% level.

standard recommended levels by WHO/FAO [10]. Therefore, like other chickpea cultivars, methionine and tryptophan were limiting amino acids in the present material [11]. Genotypes GGC 10, GGC 87 and GGC 93 had high protein, high tryptophan content.

Genotype GGC 31 had high methionine, tryptophan and protein content. Protein quality can be improved by developing cultivars with high tryptophan and methionine contents along with high protein content following hybridization among these genotypes. However, studies in the past had shown that it is difficult to manipulate individual amino acids being components of complex polypeptides.

Protein fractionation analysis revealed that among various protein fractions, globulin-B fraction was maximum: 11.51% being 43.79% of protein, followed by albumin protein fraction: 6.47% equivalent to 24.62% of protein. Protein to albumin ratio was 1:4, protein to globulin ratio 1:2 and protein to glutelin ratio 1:6. Albumin to globulin ratio was 1:2. The results corresponds with earlier studies [2, 12] for globulin protein fraction being maximum, but albumin to globulin ratio was higher than the earlier germplasm studied and thus is desirable from nutritional point of view. These genotypes can be extensively used. Genotype GGC 31 had high protein, methionine, tryptophan, albumin and globulin-A content. Therefore, this is the most desirable donor from nutritional point of view.

The association analysis (Table 2) revealed protein, methionine and tryptophan content to be independent of each other, indicating feasibility of combining high protein content with high methionine and tryptophan content in chickpea. The results were in agreement

**Table 2. Correlation among protein quality characters of chickpea**

| Character | Methionine content | Tryptophan content | Albumin content | Globulin-A content | Globulin-B content | Glutelin content |
|---|---|---|---|---|---|---|
| Protein content | 0.13 | 0.17 | 0.66** | 0.40** | 0.75** | 0.33** |
| Methionine content | | 0.05 | 0.32** | 0.27* | 0.10 | 0.07 |
| Tryptophan content | | | 0.36** | 0.16 | -0.16 | 0.09 |
| Albumin content | | | | 0.19 | 0.22 | 0.11 |
| Globulin-A content | | | | | 0.25 | 0.01 |
| Globulin-B content | | | | | | 0.01 |

*,**Significant at 5 and 1% levels, respectively.

with earlier observation [8] and in partial agreement with report [13]. The association of methionine and tryptophan content with albumin content was significantly positive, indicating that the albumin protein fraction is rich in methionine and tryptophan, as observed earlier [8]. This means that simultaneous screening for methionine and tryptophan content can be done by screening for albumin content alone. Globulin-A content also showed significant positive association with methionine content. Another desirable feature

of present study was that various protein fractions had significant positive association with protein content but nonsignificant association among themselves suggesting that various protein fractions can be manipulated independent of each other. In simple words, although it is natural that total protein content increases with increased proportions of its fractions, but high albumin content can be incorporated in high protein low albumin content genotypes by recurrent crossing with high protein high albumin content genotypes (GGC 31, GGC 65, GGC 93). Crossing among high protein high albumin content genotypes may also throw transgressive segregates for both of them. Theoretically, high protein–low globulin content genotypes can also be developed on similar lines and then intercrossing among high protein high albumin and high protein low globulin content genotypes is expected to throw transgressive segregates for high protein, high albumin and low globulin contents.

It can be concluded that the present status of chickpea protein quality can be improved by selecting genotypes with high albumin fractions because this will take care of limiting amino acids as well as albumin/globulin ratio which is the primary criterion for assessing nutritional quality.

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