Variation in important seed constituents among various chickpea genotypes

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Chickpea (Cicer arietinum L.) is the third most important pulse crop and an excellent source of protein in the human diet (Garg et al., 2011). However, the presence of anti-nutritional factors like the raffinose family oligosaccharides (RFO) restrains its acceptability as food and feed (Olimedilla Alonso et al., 2010). Higher concentration of RFO in chickpea seeds affects human health negatively and plays an important physiological role in plants (Martinez-Villaluenga et al., 2008). Hence, there is a need to reduce RFO concentration in seeds without affecting plant growth. To achieve this objective, it is imperative to understand the biochemical mechanism and genetic basis of the RFO biosynthetic pathway. As a first step, we studied the variation in RFO concentration along with starch and protein in a germplasm collection of 152 genotypes. These genotypes were grown in the field for two consecutive years 2009 and 2010 at ICRISAT in India and in greenhouse in 2010 at the University of Saskatchewan, Canada. Enzymatic methods using commercial kits (Megazyme International) were used to determine starch and total RFO concentration. Protein concentration was determined by FP-526 Protein/Nitrogen Analyzer (Leco). To determine individual RFO profiles, we have developed a new high performance anion exchange chromatography based gradient method. Results showed that lentil genotypes from greenhouse cultivation had significantly lower (1.58–4.67 mmole/100 g−1) concentration of total RFO than that of their field grown counterparts. Stachyose was identified as a major RFO in chickpea seeds followed by raffinose and verbascose. Individual RFOs (raffinose, stachyose and verbascose) showed higher concentration in the ICRISAT 2009 set than that of the ICRISAT 2010 and greenhouse sets. An obvious strong positive correlation was found among total RFO and individual members of the family. Starch concentration in chickpea genotypes ranged from 25.7 to 50.7% of total seed weight. ICRISAT 2009 set (29.4–50.7%) had a higher amount of starch than that in ICRISAT 2010 (25.7–44.5%) and the greenhouse set (28.2–44.4%). Starch concentration showed a positive correlation with total RFO. The chickpea seeds have 13.5–31.7% protein. Genotypes in the ICRISAT 2010 set had a higher amount of protein (17.92–31.73%) compared to the ICRISAT 2009 and greenhouse sets. A significant negative correlation was observed between protein and starch concentration. Analysis of variance revealed a significant effect (P < 0.001) of genotype, environment and genotype x environment on chickpea seed constituents. This study has revealed the RFO variation in chickpea genotypes and its correlation with other important seed constituents. These findings will be helpful in genotype screening for contrasting RFO concentration and in exploring the RFO biosynthetic pathway.

Keywords
chickpea; anti-nutrients; raffinose family oligosaccharides.

References