Quality Assurance and Safety of Crops & Foods

ICC MoniQA

Quality Assurance and Safety of Crops & Foods 2012, **4**, 136–158 *Abstracts*

Variation in important seed constituents among various chickpea genotypes

M. Gangola[1], Y. Khedikar[1], P. Gaur[2], M. Båga[1], R. Varshney[2] & R. Chibbar[1]

1 Department of Plant Sciences, College of Agriculture & Bioresources, University of Saskatchewan, Saskatoon, SK, Canada
2 International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad, Andhra Pradesh, India

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 (Olmedilla 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-528 Protein/Nitrogen Analyzer (Leco). To determine individual RFO profiles, we have developed a new high performance anion exchanged chromatography based gradient method. Results showed that lentil genotypes from greenhouse cultivation had significantly lower (1.58–4.67 mmoles/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

Garg R., Patel R.K., Tyagi A.K., Jain M. (2011) *De novo* assembly of chickpea transcriptome using short reads for gene discovery and marker identification. *DNA Research*, **18**, 53–63.

Martinez-Villaluenga C., Frias J., Vidal-Valverde C. (2008) Alpha-galactosides: antinutritional factors or functional ingredients? *Crit Rev Food Sci Nutr*, **48**, 301–316.

Olmedilla Alonso B., Farré Rovir R., Asensio Vegas C., Martín Pedrosa M. (2010) The role of pulses in the present-day diet. *Actividad Dietetica*, **14**, 72–76.