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RESEARCH ARTICLE

Characterization of groundnut (*Arachis hypogaea* L.) collection using quantitative and qualitative traits in the Mediterranean Basin

Engin Yol¹, Seymus Furat², Hari D Upadhyaya³, Bulent Uzun¹



¹ Department of Field Crops, Faculty of Agriculture, Akdeniz University, Antalya 07058, Turkey

² West Mediterranean Agricultural Research Institute, Antalya 07058, Turkey

³ International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Telangana 502324, India

Abstract

This study was conducted to determine the genetic diversity and relationship among 256 groundnut genotypes of which 132 belong to subsp. *hypogaea* (*Arachis hypogaea* L.) and 124 to subsp. *fastigiata* (*Arachis fastigiata* L.). The collection was evaluated for eight quantitative and five qualitative traits during three consecutive years under Mediterranean climate conditions. Coefficient of variation (CV) significantly differed among the genotypes for all the studied quantitative traits ranged from 9.10 to 33.98%, while the highest CV was recorded for seed yield. The subspecies of *hypogaea* and *fastigiata* displayed significant differences for quantitative traits except for numbers of pods per plant and seed yield. Principal component analyses showed that the first three principal components accounted for 68.14% variation for quantitative traits. Major traits that accounted for the variation by the three principal components (PCs) include days to the first flowering, days to 50% flowering, number of pods per plant and shelling percentage. The groundnut collection also offers wide seed coat color diversity which affects the crop marketability. The information on variations in quantitative and qualitative traits identified in the present investigation provided useful genotypes which would be serving parents. These parental genotypes can be used in groundnut breeding programs to develop desirable cultivars in Mediterranean Basin and globally.

Keywords: evaluation, genetic diversity, peanut, agronomic selection

1. Introduction

Groundnut, also known as peanut, is an annual allotetraploid crop ($2n=4x=40$) and belongs to Fabaceae family. The genus, *Arachis* contains about 80 species including *Arachis monticola*, which is another tetraploid species.

Differing from other flowering plant genera, this genus produces fruits below the ground but flowers, leaves and stems form above ground (Krapovickas and Gregory 1994). Groundnut is a native crop of South America (Gregory and Gregory 1976) and spreads worldwide from Chaco Region between southern Bolivia and northwestern Argentina after a long journey (Upadhyaya *et al.* 2005). Systematic nomenclature of *Arachis hypogaea* L. shows that it is divided into two subspecies based on the presence/absence of flowers on the main axis and branching pattern (Krapovickas and Gregory 1994), subsp. *hypogaea* is divided into two botanical varieties, var. *hypogaea* and var. *hirsuta*, while subsp. *fastigiata* includes four varieties, var. *fastigiata*, var. *vulgaris*, var. *aequatoriana* and var. *peruviana*.

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Correspondence Bulent Uzun, E-mail: bulentuzun@akdeniz.edu.tr

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Worldwide, groundnut was produced 45.22 million tons from 25.44 million ha with an average yield of 1.77 t ha⁻¹ (FAO 2013). The crop is the second most important cultivated food legume and the fourth largest edible oilseed crop in the world (Shilman *et al.* 2011). The seeds have palmitic, oleic and linoleic acids accounting for about 90% of total fatty acids at seed maturity (Sekhon *et al.* 1972; Young and Waller 1972). Groundnut seeds with high oleic acid provide lower rate of oxidation and less painty flavor in storage causing higher acceptability for marketing (Mozingo *et al.* 2004). Groundnut is also a valuable source of vitamins E, K, and B (the richest source of thiamine and niacin) and other essential minerals (Kassa *et al.* 2009). Groundnut cake after oil extraction is especially used for animal feeding with high protein content (Savage and Keenan 1994). Studies indicated that consuming groundnut at least four times a week showed a 37% reduced risk of coronary heart disease (Suchoszek-Lukaniuk *et al.* 2011) and anticancer activity with 50% inhibition of the proliferation of related leukemia cells (Hwang *et al.* 2008).

Improving the genetic potential of groundnut for qualitative and quantitative traits is one of the major objectives in most groundnut breeding programs (Upadhyaya *et al.* 2005). Wide genetic diversity for these traits is necessary for crop improvement. Commonly, the use of only few elite germplasm lines and/or cultivars in breeding programs reduces the genetic variation, leading to a narrow genetic base in the groundnut gene pool (Gupta *et al.* 2015). Sustainable groundnut improvement programs, therefore, need to discover and incorporate genes from germplasm with high genetic variability for desired traits. Many genetic diversity studies have been conducted in groundnut for different regions (Holbrook *et al.* 1993; Swamy *et al.* 2003; Upadhyaya *et al.* 2003, 2005, 2006; Holbrook and Dong 2005; Kassa *et al.* 2009; Bishi *et al.* 2013; Jiang *et al.* 2014; Garba *et al.* 2015). New desirable traits and genotypes have been revealed in these studies to select specific cultivars for growing in the target regions of the crop.

Mediterranean areas offer suitable climate regimes for both vegetative and reproductive growth of groundnut (Caliskan *et al.* 2008b). Especially under irrigated conditions groundnut production could be remarkably increased (Smartt 1994). Wheat is a very common crop traditionally planted in fall or spring and harvested in summer in Mediterranean areas and groundnut is an important alternative crop for second-crop production (Isik and Gul 2004). However, genetic diversity of cultivated gene pools of groundnut is narrow especially for these regions (Caliskan *et al.* 2008b). Thus, there is a need for the studies to determine useful groundnut variability for the Mediterranean conditions. The evaluation of morphological traits for economic importance could be useful for choosing the appropriate initial materials for crop improvement in these areas. Therefore to better understand and effectively utilize groundnut germplasm in Mediterranean Basin, it is important to evaluate global collections for desirable agronomic traits such environment. From this perspective, this present study was conducted to (i) assess the agro-morphological diversity of groundnut collections, which includes the mini core collection (Upadhyaya *et al.* 2002), breeding lines, local landraces, and registered cultivars, (ii) determine the relationship of important yield traits, and (iii) select desirable genotypes from different botanical varieties useful for breeding in Mediterranean areas and similar environments elsewhere.

2. Materials and methods

2.1. Genetic materials, experimental area and climate conditions

The plant materials included 256 groundnut (*A. hypogaea* L.) genotypes representing over 25 countries across Asia, America and Africa (Appendix A). The field trials were set up at the West Mediterranean Agricultural Research Institute (36°52'N, 30°50'E, and altitude 15 m) during 2011, 2012, and 2013 growing seasons in Antalya, Turkey (Fig. 1). The experimental area has a coastline of the Mediterranean Sea



Fig. 1 Map of the Mediterranean Basin.

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