



# Genetic improvement of peanut in Argentina between 1948 and 2004: Seed yield and its components



Ricardo J. Haro<sup>a,\*</sup>, Jorge Baldessari<sup>a</sup>, María E. Otegui<sup>b</sup>

<sup>a</sup> Instituto Nacional de Tecnología Agropecuaria (INTA), Estación Experimental Agropecuaria Manfredi, Argentina

<sup>b</sup> Instituto de Fisiología y Ecología Vinculado a la Agricultura del Consejo Nacional de Investigaciones Científicas y Tecnológicas (IFEVA-CONICET), Facultad de Agronomía, Universidad de Buenos Aires, Argentina

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## ABSTRACT

In Argentina, peanut (*Arachis hypogaea* L.) breeding has been based on seed yield *per se* plus defensive and seed quality traits. An important milestone was the shift from cultivars with erect growth habit (CEGH) to cultivars with procumbent (CPGH) growth habit that took place in the 1970s. However, there is no information on the genetic gain obtained for seed yield and related secondary traits (numerical and physiological determinants of seed yield), or on the effect of growth habit shift on these traits. Field experiments were performed to compute this gain and the relationships between traits in potential growing conditions. Eight cultivars released between 1948 and 2004 were evaluated. Introduction of the procumbent habit in 1975 produced a mean increase of 52% in seed yield, which was related to year of cultivar release (YOR) only for CPGH (mean genetic gain of  $0.43\% \text{ y}^{-1}$ ). This trend was driven by seed weight, a trait that registered a mean genetic gain of  $0.29\% \text{ y}^{-1}$  ( $P=0.026$ ) only among procumbent cultivars (56% increase with habit change between 1973 and 1975). No genetic gain was computed for seed numbers, and only a 10% difference was registered between growth habits (CPGH > CEGH). Seed number was related to crop growth rate between R3 and R6.5 ( $r^2=0.55$ ,  $P<0.001$ ). This rate was higher for CPGH than for CEGH. Breeding increased the number of flowers per plant ( $0.86\% \text{ y}^{-1}$ ), and the number of pods per plant and pod set (CPGH > CEGH). Breeding had a clear effect ( $P<0.001$ ) on the determinants of seed weight, and a genetic gain of  $0.52\% \text{ y}^{-1}$  was estimated for pod growth rate. Introduction of CPGH enhanced pod growth duration (37% increase). No trade-off was detected between seed number and seed weight because there was no source limitation to seed filling. Therefore, peanut seed yield might be further increased by improving the determinants of seed numbers and seed weight simultaneously.

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## 1. Introduction

During the past six decades, yield performance of many crops has been greatly improved, and this progress can be attributed to genetic improvement as well as enhanced cultural and management practices (Datt et al., 2011; Ramteke et al., 2011; Ci et al., 2012; Manès et al., 2012; Sadras and Lawson, 2013). These trends were also observed for peanut (*Arachis hypogaea* L.), but information on yield gains for this species have not been updated as for other crops and last reports date from the 1980s (Mozingo et al., 1987). During most part of the 20th century, peanut breeders aimed

almost exclusively at developing cultivars with enhanced seed yield (Holbrook and Stalker, 2003). Consideration of other traits is relatively recent in breeding programs of this species, and includes physical and chemical seed quality required by the market, and enhanced tolerance to abiotic and biotic stresses (Isleib et al., 1994; Holbrook and Stalker, 2003). This process produced an increase in total flower numbers and reproductive efficiency (percentage of flowers resulting in pods or seeds) of new cultivars as compared to the old ones (Coffelt et al., 1989; Seaton et al., 1992), as well as an improved partitioning of assimilates to reproductive structures (Coffelt et al., 1989; Wells et al., 1991).

In Argentina, peanut genetic improvement has been based on the same general criteria. Selection focused on yield *per se* in trials conducted at sites representative of the target environment, a common practice in extensive grain crops (Austin, 1993; Betran et al., 2004; Orf et al., 2004). However, an important shift occurred in the middle of the 1970s. Up to then, cultivars of the subspecies *fastigiata* were released; these cultivars had a growing cycle of 120–135 days, predominantly erect growth habit and seeds with  $48 \pm 1\%$

**Abbreviations:** Exp, experiment; CGR, crop growth rate; PGR, pod growth rate; SSR<sub>SE</sub>, source–sink ratio during the effective seed-filling phase; CEGH, cultivars with erect growth habit; CPGH, cultivars with procumbent growth habit; YOR, year of release.

\* Corresponding author at: Estación Experimental Agropecuaria INTA Manfredi, CC 5988 Córdoba, Argentina. Tel.: +54 3572493053; fax: +54 3572493058.

E-mail address: [ricardoharo@manfredi.inta.gov.ar](mailto:ricardoharo@manfredi.inta.gov.ar) (R.J. Haro).

oil content. Since then, with the release of genotypes of the subspecies *hypogaea*, on-farm yield increased substantially, whereas seed oil content remained unchanged (Giandana, 2006). The new genotypes were also characterized by longer cycles (ca. 140–145 days from sowing to harvest) and a procumbent growth habit. Currently, evaluation of peanut genotypes is based on final pod yield and seed grades.

It is well recognized that selection for yield *per se* has several constraints (Reynolds et al., 1996; López Pereira et al., 1999; Peng et al., 1999; Araus et al., 2002), because yield is characterized by low heritability and high genotype  $\times$  environment interaction (Wallace et al., 1993; Jackson et al., 1996; Richards et al., 2001). Up to the present, however, the inclusion in breeding programs of traits representative of the physiological determinants of grain yield (e.g. crop growth rate during critical periods and source/sink relationships) has not been significant for any species, probably due to difficulties for assessing those related to biomass production on a large number of genotypes and environments (Araus et al., 2001). Consequently, a better understanding of the impact of these traits on genetic gains in seed yield has become essential for assisting conventional (Jackson et al., 1996; Boote et al., 2001; Araus et al., 2002) and molecular (Mifflin, 2000) breeding approaches for hastening yield improvement. An effective approach to the analysis of physiological determinants is achieved by dissecting yield into component traits (Yin et al., 2004; Lee and Tollenaar, 2007). Crop yield is often viewed as the product of seed number and seed weight, two variables for which there are evidences of a negative association in some crops but not in others (Slafer et al., 1996; López Pereira et al., 1999; Luque et al., 2006; Gambín and Borrás, 2010). There is no evidence on the trends caused by peanut breeding on this topic.

Starting with the work of Austin et al. (1980), comparing cultivars released in different eras became a useful method to estimate the contribution of genetic improvement to crop yield and its determinants. Richards (1997) highlighted the value of identifying yield determinants by comparing historical sets of cultivars because any increase in yield potential must have a physiological basis. Accordingly, Richards (1997) proposed that, by targeting the components contributing to greater yield, we should be able to select for them more easily and efficiently and to identify the most appropriate germplasm to be used as parents. This comparative approach has been applied to a number of species (Wells et al., 1991; Slafer, 1994; López Pereira et al., 1999; Luque et al., 2006), but no previous attempt has been made to elucidate the physiological differences that account for the large increase in on-farm yield among Argentine peanut genotypes over the years. As mentioned previously, a clear breakpoint occurred in the 1970s, when Spanish and Valencia genotypes of predominantly erect habit were substituted by procumbent runner varieties that were better suited for exporting as hand picked and selected peanuts to Europe. Additionally, the harvest work of digger-shaker-inverter machines was facilitated by the shift in growth habit because procumbent plants were inverted easily (too many pods remained in contact with the soil among machine-harvested erect genotypes). So far, no information was produced on how this shift affected seed yield determination from the physiological point of view. A better understanding of the differences among genotypes and how these differences relate to their yield potential may contribute to the selection process and future yield improvement in peanut.

The objective of our study was to investigate the genetic gain in seed yield and seed yield components among peanut cultivars of contrasting growth habit (erect and procumbent) released between 1948 and 2004 in Argentina. For this purpose we used the analytical framework proposed by López Pereira et al. (1999) for the study of sunflower breeding. We evaluated (i) the relationship between seed yield and yield components, (ii) the relationship between seed

number and seed weight, and (iii) the response of seed number and seed weight to their physiological determinants (e.g. crop and pod growth rates, source/sink relationships).

## 2. Materials and methods

### 2.1. Experimental design and crop husbandry

Field experiments were conducted during the 2009–2010 (Exp1), 2010–2011 (Exp2 and Exp3), and 2011–2012 (Exp4) growing seasons at the research station of the National Institute of Agricultural Technology (INTA), located in Manfredi (31°49'S, 63°46'W), Córdoba province, Argentina. The soil is silty loam Typic Haplustoll (USDA Soil Taxonomy). The experiments included eight cultivars (Table 1) of contrasting growth habit developed for this region and released between 1948 and 2004. The cultivars employed for the experiments were representative of the most widely used by Argentine peanut farmers at their time of release. The fact that all cultivars corresponded to the breeding program of INTA (used in 90% of the land cropped with this species in the country) allowed us to better understand effects of breeding, which is not always possible when cultivars from completely different breeding programs are tested (Luque et al., 2006). Sowing was performed on November 10 (Exp1), October 19 (Exp2), November 10 (Exp3) and November 1 (Exp4). Exp1 and Exp2 were aimed to understanding breeding effects at the crop level, for this reason seeds were hand-planted in rows 0.7 m apart using a stand density of 14 plants  $m^{-2}$ . In these experiments, treatments (cultivars) were arranged in a completely randomized block design with three replicates and plots were four rows wide and 15 m long. Exp3 and Exp4 were developed for the analysis of traits at the individual plant level, and for this reason they were grown with almost no interference among them (ca. 1.5 m between plants) and treatments were arranged in a completely randomized block design with five replicates (i.e. each experimental unit had one plant).

Experiments received drip irrigation to keep the uppermost 1 m of the soil near field capacity throughout the growing season. Experimental units were maintained free of weeds by frequent hand removal, and received periodical applications of 125  $mL ha^{-1}$  of tebuconazole ( $\alpha$ -[2-(4-chlorophenyl) ethyl]- $\alpha$ -(1,1-dimethylethyl)-1*H*-1,2,4-triazole-1-ethanol) to prevent foliar diseases. Daily mean air temperature was measured within 10 m from the experimental plots to calculate thermal time. Thermal unit calculations (in  $^{\circ}Cd$ ) were linearly accumulated from a base temperature of 11  $^{\circ}C$  (Williams and Boote, 1995).

### 2.2. Measurements

In Exp1 and Exp2, crop phenology (Boote, 1982) was followed in each plot on three plants tagged at R1 (first flower visible in at least 50% of the plants). Starting from initial pod growth (R3) and fortnightly, all plants in samples of 0.35  $m^2$  were harvested from the two central rows (i.e. between 6 and 7 sampling dates along the cycle). Plants were separated into leaves plus stems (vegetative biomass) and pods (reproductive biomass), and dried at 70  $^{\circ}C$  until constant weight. At final harvest (R8), total seed number was counted manually and seeds were weighed for quantification of final seed yield. Seed weight was computed as the quotient of seed yield and seed number. Crop growth rate (CGR, in  $g m^{-2} d^{-1}$ ) and pod growth rate (PGR, in  $g m^{-2} d^{-1}$ ) at different growth stages were estimated by linear interpolation. CGR between R3 and R6.5 (CGR<sub>R3–R6.5</sub>) was taken as representative of the critical period for pod and seed set (Haro et al., 2007). PGR between R3 and R8 was used as indirect estimator of seed growth. The source–sink ratio during the effective seed-filling phase (SSR<sub>sf</sub>, in  $mg seed^{-1}$ ) was

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