

Advances in Arachis
Through Genomics & Biotechnology

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Integration of rapid phenotyping and genotyping tools for peanut genetic improvement

D.J. O'Connor^{1*}, R.C.N. Rachaputi¹, R.J. Henry¹, A. Furtado¹, G.C. Wright²

¹Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, QLD, 4072; ²Peanut Company of Australia, Kingaroy, QLD, 4610
*oconnor@uq.edu.au

Blanchability, propensity of the testa to be removed from the kernel following rapid heat treatment, is a key breeding trait for the cultivated peanut (*Arachis hypogaea*). Blanchability is an ideal candidate for marker assisted selection (MAS) as it is difficult to phenotype, highly heritable, genotype specific and has a low genotype by environment interaction. Currently, due to the existing phenotyping technique, many undesirable lines are well progressed in a breeding program, only to be discarded after exhibiting poor blanchability at the F5 or F6 generation. Progress of MAS in the cultivated peanut has been slow due to its large genome size, 2800Gbp, complex nature, it is an allotetraploid, and low genetic diversity in the domesticated species. The reference genome for the cultivated peanut is still in development but annotated references have been released for the two diploid progenitors, *Arachis duranensis* and *Arachis ipaensis*. 99 lines from the US peanut minicore collection have been phenotyped for blanchability with significant variability identified, between 95% and 45%. A pooled DNA sample from a selection of excellent and poor blanching accessions has been developed. These two DNA pools have been enriched using probes developed from the annotated diploid reference, in collaboration with Roche Nimblegen. The enriched DNA has then been next generation sequenced using the Illumina platform in order to develop functional DNA markers for the trait. It is expected this novel protocol will increase the efficiency of peanut breeding programs to select for other difficult to phenotype breeding traits.

Evaluation of intensity and duration of seed dormancy in a recombinant inbred population derived from Spanish bunch genotypes

Y.B. Naganagoudar^{1*}, P.V. Kenchangoudar¹, B.N. Motagi^{1,2}, M.V.C. Gowda¹, H.L. Nadaf¹, S. Pujer¹

¹Oilseeds Scheme, Main Agricultural Research Station, University of Agricultural Sciences, Dharwad-580 005, Karnataka, India; ²ICRISAT, Kano, Nigeria
*yallurajgouda@gmail.com

Pre-harvest sprouting in groundnut (*Arachis hypogaea* L.) seeds belonging to subspecies *fastigiata* (Spanish bunch) is undesirable. Since it leads to *in vitro* germination resulting in substantial loss of seeds, both in quantity and quality. A short period of dormancy is therefore desirable in the sub-species to reduce such losses. Evaluation of fresh seed dormancy was conducted for two seasons to determine the intensity and duration of dormancy in recombinant inbred population with 268 RILs developed from crosses involving moderately dormant (GPBD-4) and non-dormant (TAG-24) parents. The intensity of dormancy ranged from 0 to 100% in summer season while 0 to 90% in *khariif* season. There was large variation in the intensity of dormancy which could be related to genetic differences between the entries tested. RIL nos. 165, 259, 160, 172, 209, 254, 213, 247, and 248 recorded very high values (> 70 %) of intensity of dormancy in both the seasons. The variation for dormancy in terms of duration as revealed by germination of 70% (G 70 estimates) was subsequently large as compared to the intensity of dormancy among the RILs. The RIL nos. 5, 40, 84, 165, 183, 209, 213, 248, 254, 259 and 265 were found to have more than two weeks of dormancy (based on G70 count) in both the seasons. These dormant lines can be utilized in breeding for fresh seed dormancy under Spanish background.