Arachis hoehnei, the Probable B Genome Donor of *Arachis hypogaea* Based on Crossability, Cytogenetical and Molecular Studies

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Cultivated groundnut (*Arachis hypogaea*) is made up of two genomes, A and B. It is presumed that polyploidization event between diploid A and B genome species gave rise to cultivated tetraploid groundnut some 3500 years ago (Singh and Simpson 1994). There is no ambiguity regarding *A. duranensis* as the A genome donor of *A. hypogaea* (Gregory and Gregory 1979, Singh 1988, Kochert et al. 1991, Paik-Ro et al. 1992, Stalker 1992). Different species from the B genome pool have been proposed as the B genome donor. According to Singh (1998), *A. batizocoi* is the B genome donor. Based on RFLP (restriction fragment length polymorphism) studies, Kochert et al. (1991) have suggested *A. ipaensis* as the B genome donor. According to Paik-Ro et al. (1992), *A. batizocoi* is not closely related to *A. hypogaea* and hence cannot be the B genome donor. Karyotype studies of Fernandez and Krapovickas (1994) support *A. duranensis* and *A. ipaensis* as the A and B genome donors of *A. hypogaea*.

We studied the crossability relationship between *A. hypogaea* and six B genome species. Cultivated groundnut was crossed with *A. hoehnei*, *A. benensis*, *A. valida*, *A. magna*, *A. batizocoi* and *A. ipaensis*. *Arachis hoehnei* when crossed with *A. hypogaea* set bold seeds without the application of growth regulators. Majority of the seeds germinated in vitro and hybrid plants were obtained and a few (5%) mature seeds were obtained. Fertility in the hybrids ranged from 14 to 21%, whereas *A. benensis*, *A. valida*, *A. magna* and *A. ipaensis* set immature seeds, when crossed with *A. hypogaea*. The seeds were less than 3 mm in size. This indicated that the hybrid embryos aborted early. Embryo rescue technique was necessary to obtain hybrid plants if *A. benensis*, *A. valida*, *A. magna* and *A. ipaensis* were used as pollen donor. *Arachis batizocoi* set mature seeds with *A . hypogaea*, but pollen fertility was low (7%). Singh and Moss (1984) reported that in the crosses involving *A. batizocoi* and diploid A genome wild species from section *Arachis*, mean bivalents ranged from 3.2 to 6.9 with pollen fertility ranging between 3 and 7%. When *A. hypogaea* was crossed with *A. batizocoi*, the survival of the seedlings was poor.

Crosses were also carried out between *A. duranensis* and *A. hoehnei* (Fig. 1a). Large number of seeds (15%) was obtained. Cytogenetical study of the hybrid between *A. duranensis* and *A. hoehnei* showed 10 bivalent formation in 30% of the pollen mother cells analyzed (Fig. 1b). Amongst the bivalents, 4–6 were ring bivalents. The formation of large number of bivalents and in ring formation shows that there is homeology between the genomes of *A. duranensis* and *A. hoehnei*. For a hybrid between A and B genomes to survive in nature, greater degree of homeology between the genomes would be a contributory factor and would play a major role in the perpetuation of the hybrid. Such a hybrid could have doubled its chromosome number to give rise to the amphidiploid groundnut.

Simple sequence repeat (SSR) analysis of *A. duranensis*, *A. hoehnei* and the hybrid between *A. duranensis* and *A. hoehnei* was carried out. The SSR 4F07 profile of *A. duranensis* was different from that of *A. hoehnei*. The hybrid had the DNA profile with bands from both the parents. The interesting feature of the hybrid DNA profile was that it resembled the DNA profile of *A. hypogaea* with some differences (Fig. 1c). This shows that the hybrid, which has the genomes of both *A. duranensis* and *A. hoehnei*, has close resemblance to the genome of *A. hypogaea*. The difference between the hybrid *A. duranensis* × *A. hoehnei* and *A. hypogaea* may be due to ploidy difference and the synthesis of *A. hypogaea* which took place some 3500 years ago.

Based on crossability between *A. duranensis* and *A. hoehnei*, cytogenetical data and molecular analysis of the hybrid between *A. duranensis* and *A. hoehnei*, we propose *A. hoehnei* as the probable B genome donor of cultivated groundnut.

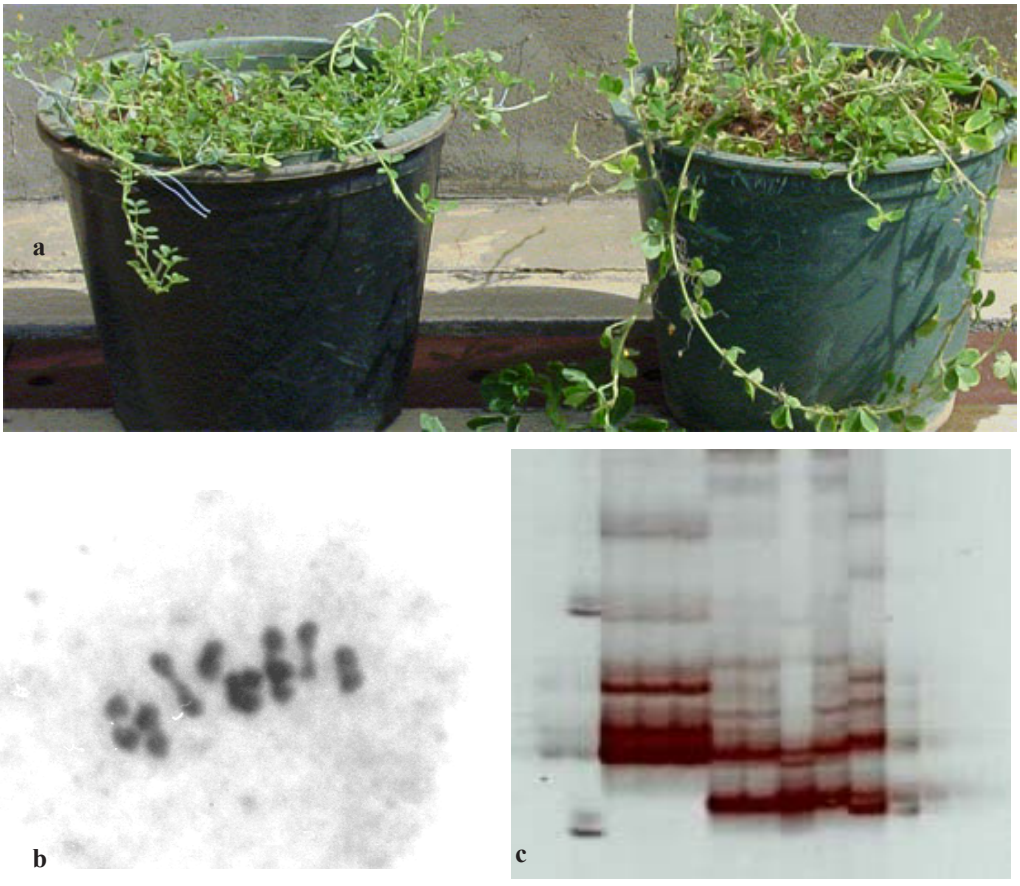

Figure 1. *Arachis hoehnei* as the B genome donor of cultivated groundnut *A. hypogaea*: (a) *Arachis duranensis* (left) and *A. hoehnei* (right); (b) metaphase plate of *A. duranensis* × *A. hoehnei* (note the presence of 10 bivalents); and (c) SSR marker 4F07 profile: Lane 1- 100 base pair ladder, Lanes 2–4 - *A. duranensis*, Lanes 5, 6 & 8 - hybrid between *A. duranensis* and *A. hoehnei*, Lane 7 - *A. hoehnei*, Lane 9 - *A. hypogaea*.

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