Arachis hypogaea L, the cultivated peanut, is a believed to be an allotetraploid and the evolution of the crop dates back to the tertiary era (Gregory and Gregory, 1979). Cultivated peanut is comprised of two genomes A and B (Simpson and Stalker, 1995). Gregory and Gregory (1976) were the first to suggest that A. duranensis is one of the putative genome donor of A. hypogaea. Cytogenetical and molecular data support A. duranensis as the female parent and the A genome donor of A. hypogaea (Simpson and Stalker, 1995), and there is no ambiguity about it. The problem has long been the B genome donor. Different species from the B genome pool have been proposed. According to Singh and Smartt (1998) A. batizocoi is the donor. Kochert et al., (1991) based on RFLP studies, suggested A. ipaensis as the 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. Inter-relationships of twenty-five species of Arachis, of which thirteen were from section Arachis, were studied by Randomly Amplified Polymorphic DNA (RAPD)-cluster analysis. It was interesting to note that most of the species from different sections grouped together as per the classification of Arachis. The B genome species formed two groups placed away from each other. One group comprised of A. batizocoi, A. ipaensis and A. magna. The other group comprised of A. hoehnei, A. benensis and A. valida. The A. hoehnei group showed closer relationship to cultivated species A. hypogaea, whereas the A. batizicoi group showed a distant relationship. Crossability between A. hoehnei and A. hypogaea produced bold seeds without the application of growth regulators, indicating lack of barriers. A few mature seeds were obtained. Majority of the seeds were bold but immature and were germinated in vitro to obtain plants. Fertility in the hybrids was promising and ranged from 14-21%. Cytological analysis showed 86% of the PMCs with more than 10 bivalents and a mean of 4 univalents per PMC. Trivalents ranged from 1-3 with a mean of 3 per PMC. Based on crossability studies, cytogenetics and the molecular data, we propose A. hoehnei as the B genome donor.