CYTOGENETICS AND UTILIZATION OF *ARACHIS* SPECIES

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I. INTRODUCTION

Groundnut *(Arachis hypogaea* L) is the most widely cultivated grain legume in the world and is one of the five most important oilseeds in India. It has important nutritional qualities, containing approximately 50% high quality unsaturated fats and 30% digestible proteins. Besides, a few wild *Arachis* species (*A. glabrata, A. kempff-mercadoi, A. pintoi and A. repens*) are being cultivated extensively as tropical forages and ground covers (Valls *et al.*1994).

The species has been cultivated for nearly four centuries in Western Africa, the East Indies, India, China and Japan, however, not known to occur in wild state in these regions. Archeological evidences proved pre-Columbian (before 600 AD) cultivation of groundnut in Peru, South America and distributed in eastward of Andes Mountains from the Amazon River to the La Plata River. The center of origin of cultivated groundnut thought to lie in northern Argentina and southern Bolivia (Stalker and Simpson 1995). Recent evidence indicates northwest Peru may be another possible site for the origin of the cultivated groundnut (Simpson *et al*. 2002).

II. TAXONOMY OF *ARACHIS SPECIES*

A. Wild species

The genus *Arachis* is morphologically well defined and clearly delineated from its closest relatives by the presence of geocarpic peg. *Arachis* is placed with its relatives *Stylosanthes, Chapmannia, Arthrocarpum and Pachecoa* in the subtribe *Stylosanthinae* of the tribe *Aeschynumeneae* on the basis of the shared morpological characters of a staminal tube with alternately attached basal and dorsal anthers, flowers in terminal or axillary spikes or small heads (which are sometimes raceme-like), pinnate leaves, and leaflets without stipules.

The only member of the genus known to science till 16th century was *A. hypogaea* described by Linnaeus (1753). About a century later, Bentham (1841) described 5 more wild species namely, *A. glabrata*, *A. pusilla*, *A. villosa*, *A. prostrata*, and *A. tuberosa*. So far, 69 species have been reported under 9 sections namely, *Trierectoides, Erectoides, Extranervosae, Triseminatae, Heteranthae, Caulorrhizae, Procumbentes, Rhizomatosae* and *Arachis* (Krapovickas and Gregory 1994) (Table 1). However, recently Valls and Simpson (1997) recognized 11 new species, which still have not been formally described, with which the species number of the genus would increase to 80 (Lavia 2000). Hence, taxonomic revision of the genus is one of the highest priorities for documentation and utilization since new accessions of wild species are adding up.

B. Cultivated species

The cultivated groundnut has been classified based on growth habit, branching pattern, type of inflorescence, pod and seed characters, seed dormancy etc. Based on sub specific nomenclature and the varietal associations proposed by Krapovickas and Gregory (1994), two sub-species and six botanical varieties are recognized which exchange genes within and between them freely (Table 2). The sub-specific classification in this genus would remain inconclusive on account of wide variations and intermediate forms observed among the *Arachis* germplasm as well as in the breeding populations. Hence, the classification restricting to the botanical types of erect, semi-spreading and spreading would be much more practical and applicable.

C. Groundnut gene pools

Based on the cross compatibility relationships, the *Arachis* gene pool has been classified into primary, secondary, and tertiary gene pools. *Arachis hypogaea* and *A. monticola* are two tetraploid species of section *Arachis* grouped under primary, while all other diploid species of section *Arachis* fall in secondary gene pool. Species that belong to section other than *Arachis* are grouped under tertiary gene pool. The gene flow among different gene pools and between different sections within tertiary gene pool is generally limited.

III. CHROMOSOMES OF *ARACHIS* SPECIES

A. Number

Badami (1928) reported a chromosome number of 2n=20 in the cultivated species. Husted (1931,1933, 1936) reported a chromosome number of 2n=40. Ghimpu (1930) and Kawakami (1930) were the first to determine the true chromosome number of *A. hypogaea* to be 2n=40.

The first chromosome count reported for a wild species was 2n = 40 for *A. glabrata* (Gregory 1946). Subsequently, many have reported the chromosome number both in cultivated and wild species. Most species in the genus are diploid (2n=20). However, tetraploid species with chromosome numbers 2n=40 are also reported in sections *Arachis* and *Rhizomatosae* and are highly cross-incompatible, This indicates that polyploidy may have apparently arisen at least twice in the section *Arachis* and *Rhizomatosae* independently in this genus.

Table 1. Taxonomic summary of the genus *Arachis*

Section	species	Section	species
Arachis	*A. glandulifera*	**Extranervosae**	*A. setinervos*
(27 species)	*A. cruziana*	(9 species)	*A. macedoi*
	A. monticola		*A. marginata*
	A. magna		*A. prostrata*
	A. ipaensis		*A. lutescens*
	A. valida		*A. retusa*
	A. williamsii		*A. burchelii*
	A. batizocoi		*A. pietrarellii*
	A. duranensis		*A. villosulicarpa*
	A hoehnei		
	A. stenosperma	**Triseminatae**	*A. triseminata*
	A. praecox	(1 species)	
	A. palustris	**Heteranthae**	*A. giacomettii*
	A. benensis	(4 species)	*A. sylvestds*
	A. trinitensis		*A. pusilla*
	A. decora		*A dardani*
	A. herzogii		
	A. microsperma	**Erectoides**	*A. martii*
	A. villosa	(13 species)	*A. brevipetiolata*
	A. helodes		*A. oteroi*
	A. correntina		*A. hatschbachii*
	A. simpsonii		*A. cryptopotamica*
	A. cardenasii		*A. major*
	A. *kempff-mercadoi*		*A. benthamii*
	A. *diogoi*		*A. douradiana*
	A. kuhlmannii		*A. gracilis*
	A. hypogaea L.		A. *hermannii*
			A. archeri
Trierectoides	*A.guarantica*		*A. stenophylla*
(2 species)	*A. tuberosa*		*A. paraguariensis*
Caulorrhizae	*A. repens*	**Procumbentes**	*A. lignosa*
(2 species)	*A. pintoi*	(8 species)	*A. kretschmeri*
			A. rigonii
Rhizomatosae	*A. burkartii*		*A. chiquitana*
(3 species)	*A. glabrata*		*A. matiensis*
	A. pseudovillosa		*A. appressipila*
			A. vallsii
			A. subcoriacea

Lavia (1996, 1998) reported a chromosome number of x=9 for *A. palustris* and *A. praecox* (section *Arachis*), which was also found for *A. décora* (section *Arachis*) by Penaloza *et al.* 1996. It reveals that there are two series of chromosome numbers that appear to occur in the genus (2n=2x=20 and 2n=4x=40). Lavia (1998) was of the opinion that since the diploid forms are more predominant, the basic chromosome number is believed to be x=10 and proposed that basic chromosome number x=9 in species *A. palustris* and *A. praecox* might have originated by loss of a chromosome from the other species having n=10. On the other hand, Bera *et al.* (2002b) described that reverse may be true and species with chromosome number x=10 might have originated by selective duplication of chromosome. The presence of two basic chromosome number (x=9 and x=10) and less existence of polyploid species indicate that aneuploidy has played a key role in the evolution and speciation of *Arachis* species rather polyploidization. Therefore, the species diversity of *Arachis* may be mainly due to structural chromosomal rearrangements. This observation thus supports the hypothesis that section *Arachis* represents the most advanced traits within the genus.

Table 2. Botanical classification of *Arachis hypogaea*

Varieties	Market type	South American Location	Characteristics
Sub-species ***hypogaea***			No floral axes on main stem; alternating pairs of floral & reproductive axes on branches; branches short; less hairy
hypogaea	Virginia Runner	Bolivia, Amazon	Less hairy; large seeded
hirsuta	Peruvian runner	Peru	More hairy, small seeded
Sub-species ***fastigiata***			Floral axes on main stem; alternating pairs of floral & vegetative axes on branches
fastigiata	Valencia	Brazil,Guranian, Goias Minas gerais ,Paraguay Peru ,Uruguay	Less branches, long upright branches, hairy leaf
peruviana		Peru N.W. Bolivia	Less hairy; deep pod reticulation
aequatoriana		Ecuador	Very hairy; deep pod reticulation; purple stems; more branched, erect
vulgaris	Spanish	Brazil, Guranian, Goias ,Minas Gerais Paraguay, Uruguay	More branched; upright branches

B. Aneuploidy

Aneuploid complements have been reported in *A. hypogaea* sporadically. Husted (1936) first reported a plant showing 2n=41 plus a chromosome fragment. The most extensive reports of aneuploidy in the genus has arisen as a result of interspecific hybridization. Kumar and D'Cruz (1957) obtained a plant with 2n=41 from the backcross (*A. hypogaea* x *A. villosa*) x *A. hypogaea*. Other naturally occurring aneuploids were observed by Spielman *et al*. (1979), Singh and Joshi (1981) and Stalker (1985). Bera *et al*. (2002b) reported aneuploids (2n=38) from F_1 population of *A. hypogaea* x *A. paraguariensis*. Eight different trisomics or doubled trisomics (2n+1+1) were reported by Stalker (1985). Chemical treatments (Ashri *et al*. 1977) or ionizing radiation (Patil and Bora 1961; Patil 1968; Menon *et al*.1970) have also produced aneuploid plants. In addition, aneuploids are commonly observed when interspecific hybrids involving *A. hypogaea* are treated with colchicine (Smartt and Gregory 1967; Spielman *et. al.* 1979; Company *et al.* 1982). Davis and Simson (1976) reported chromosome numbers ranging from 32 to 48 in hexaploid derivatives of *A. hypogaea* x *A. cardenasii* hybrid.

Cytologically, the extra chromosome behaved as a trisomic. Smartt (1965) and Smartt and Gregory (1967) reported material with aneuplold complements ranging from 2n=38 to 60 arising from *A. hypogaea* x section *Arachis* diploid species hybrids. Davis and Simpson (1976) reported aneuploid chromosome complements ranging between 32-43 and 32-48 in the F_7 generation of allohexaploids derived from the F_1 hybrids of *A. hypogaea x A. cardenasii* (Smartt 1965). In general, the origin of the aneuploids is unclear. They could have arisen through interspecific crosses involving cultivated groundnut, the meiosis of which would tend to produce aneuploids. Alternatively, they may arise through erosion of the chromosomes in the natural/ doubled hexaploids of interspecific crosses involving tetraploid and a diploid species. Cytologically, univalent or multivalent formation and unequal chromosome segregation in meiosis of such hexaploids may throw aneuploid progenies. Aneuploidy in *A. hypogaea* can be found by selecting small seeds (Spielman *et al.* 1979) and can also arise from the effects of ionizing radiation on cells in division (Menon *et al*. 1970; Patil 1968; Patil and Bora 1961).

C. Chromosome morphology and genomic complements

The chromosomes of groundnut are small, ranging from 1.3 to 6.0 µm in length, mostly metacentric and are difficult to karyotype. Genomes of most species are symmetrical with median chromosomes. Husted (1933, 1936) analyzed somatic chromosomes of several cultivars and distinguished a pair of a small chromosome, termed as "A" chromosome and another pair with a secondary constriction, termed as

"B" chromosomes. Babu (1955) reported several types of secondary constriction in chromosomes of *A. hypogaea*, and cultivars can be distinguished on the basis of karyotype differences (D'Cruz and Tanskasale 1961; Stalker and Dalmacio 1986). Stalker and Dalmacio (1986) were able to distinguish at least 15 of the 20 chromosome pairs based on arm ratios and chromosome lengths and able to separate members of different botanical varieties based on somatic chromosomes morphology. The meiotic chromosomes of *A. hypogaea* pair mostly as 20 bivalents, but a few multivalents occasionally have also been observed (Husted 1936). Hybrids among subspecific accessions have mostly bivalents at metaphase I, but univalents also exist at a low frequency. Husted (1936), Raman (1976), and Stalker (1980) concluded that chromosomal structural differences exits between the subspecies *hypogaea* and *fastigiata.* Further, Gregory *et al*. (1980) observed reduced fertility in hybrids between subspecies, and Krapovikas (1973) reported genetic differences between the subspecies *hypogaea* and *fastigiata.* Only a few Karyotype studies have been reported and that to restricted mostly to the section *Arachis* (Stalker and Dalmacio 1981; Singh and Moss 1982; Stalker 1991). Small chromosome pair designated as chromosme "A" were present in most species of the section *Arachis* (Table 3) while *A. batizocoi* , *A. cruziana, A. magna, A. williamsii and A. ipaensis* do not have the small pair but instead have a chromosome pair with secondary constriction and a satellite, designated as chromosome "B" (Smartt *et al*. 1978a). There are very few reports on Karyotype of different species (Lavia 2000, 2001) (Table 4). However, ten different types of SAT chromosomes were identified on the basis of arm ratio (Farnandez and Krapovikas 1994). Lavia (2000) reported a new SAT chromosome 3B, which closely resembles the first, described type-3. Cytogenetical and experimental crossing studies have confirmed genomic differences among the species within the section *Arachis* (Krapovicas and Gregory 1994; Simpson and Faries 2001). These chromosomes served as markers for the genomic complements of the tetraploid *A. hypogaea* and Smartt *et al*. (1978b) first designated the genome of cultivated groundnut as "AB" genome. Based on the cumulative cross-compatibility of interspecific hybrids by several workers different genomes were proposed (Smartt and Stalker 1982 and Stalker 1985) for the various species in the sections (Table 5).

Pachytene analysis of *Arachis* chromosomes indicated the presence of six well-differentiated chromosomes, a nucleolar organizing chromosome, and three heterochromatic short armed chromosomes. Proximal region of centromere of each chromosome is heterochromatic while distal end is euchromatic (Murty *et al.* 1982; Bharati *et al.* 1983; Kirti *et al.* 1983; Jahnavi and Murty 1985a). Although pachytene analysis is tedious and time consuming, the length of the chromosomes (1.3-6.0 μm) offers excellent scope to better understand the morphology of chromosomes of various species. Kirti *et al.* (1983) and Janavi and Murty (1985a) analysed the pachytene chromosomes of species in sections *Arachis*, *Erectoides, Extranervosae, Rhizomatosae* and *Triseminatae* and distinguished the chromosome pairs. Although chromosomes did not stain well, Jahnavi and Murty (1985a) concluded that six different chromosomes, three specialized chromosomes and one nucleolus organizing chromosome are present in the species of different groups.

Table 3. Chromosome number and presence of "A" chromosomes in the species of section *Arachis*

Species	2n	Pair "A"	Species	2n	Pair "A"
A. batizocoi	20	-	*A. kuhlmannii*	20	+
A. benensis	20	-	*A. magna*	20	-
A. cardenasii	20	+	*A. microsperma*	20	+
A. correntina	20	+	*A. monticola*	40	+
A. cruziana	20	-	*A. palustris*	18	-
A. diogoi	20	+	*A. praecox*	18	-
A. duranensis	20	+	*A. simpsonii*	20	+
A. decora	18	-	*A. stenosperma*	20	+
A. glandulifera	20	-	*A. trinitensis*	20	+
A. helodes	20	+	*A. villosa*	20	+
A. herzogii	20	+	*A. valida*	20	-
A. hoehnei	20	-	*A. williamsii*	20	-
A. ipaensis	20	-	*A .hypogaea*	40	+
A. kempff-mercadoi	20	+			

+ =Presence of "A" chromosome - =Absence of "A" chromosome

Table 4 *Arachis* species with karyotype formula and SAT chromosome

Species	2n	Karyotype Formula	SAT
A. palustris	18	16m+2sm	3-par 7
A. praecox	18	16m+2sm	3-par 9
A. tuberosa	20	20m	8
A. duardina	20	18m+2sm	2
A. subcoriacea	20	18m+2sm	9
A. appressipila	20	14m+6sm	9
A. vallsii	20	18m+2sm	3B
A. villosa	20	10m+8sm+2smsc	3
A. cardenasii	20	2m+16sm+2smsc	9
A. correntina	20	8m+10sm+2smsc	3
A. chacoense	20	6m+12sm+2smsc	3
A. stenosperma	20	6m+12sm+2msc	5
A. kuhlmannii	20	6m+12sm+2smsc	7
A. duranensis	20	10m+8sm+2smsc	2
A. batizocoi	20	2m+14sm+2st+2smsc	4
A. glandulifera	20	14m+4sm+2st.	2,3,4

Table 5 Genomic constitution in the genus *Arachis*

Genome	Section	Species
A	*Arachis*	Perennials and most annuals
B	*Arachis*	*A. batizocoi*
D	*Arachis*	*A. glandulifera*
AB	*Arachis*	*A. hypogaea*
AM	*Ambinervosae*	-
C	*Caulorrhizae*	*A. repens*
E	*Erectoides*	*A .paraguariensis*
Ex	*Extranervosae*	*A. villosulicarpa*
T	*Triseminatae*	*A. pusilla*
R	*Rhizomatosae*	*A. burkartii*

D. Chromosome behaviour

1. Meiosis in cultivated groundnut

Meiosis of intervarietal crosses of cultivated groundnut indicated formation of 20 bivalents during meiosis. However, occasionally, a quadrivalent and 1-2 trivalents were also observed. The low frequency of multivalent configurations in these crosses indicate that the cultivated groundnut is an effectively dipioidized tetrapioid. Multivalent association can also be due to homeologous pairing (the formation of quadrivalents or a trivalent plus a univalent) between chromosomes of the 2 genomes and when pairs of trivalents or hexavalents were observed, the probability of segmental interchanges having occurred in the differentiation of the genomes is high.

2. Meiosis in wild species

Meiotic studies in wild species have been reported by Raman (1976) for both tetraploid and diploid wild species. The behavior of *A. monticola* is comparable to that of *A. hypogaea* with normally 20 bivalents but occasionally with 18 bivalents and 1 quadrivalent. In a polyploid of section *Rhizomatosae* species, Raman (1976) reported up to four quadrivalents. A second accessions reported by Stalker (1985) averaged 19.92 bivalents and only 0.04 quardrivalents per pollen mother cell (PMC). The high frequency of quadrivalents in this section indicates the homeology between the genomes. The analysis of PMC indicates that chromosomes of diploid species pair mostly as bivalents (Raman 1976; Resslar and Gregory 1979; Smartt *et. al.* 1978a, b; Stalker and Wynne 1979; Singh and Moss 1982) but quadrivalents have also been observed at a low frequency in the diploid species *A. villosa* and *A. spegazzinii*

(Singh and Moss 1982). However, less frequent, secondary associations of bivalents were also observed in this section leading to suspicion of secondary polyploid origin of the species.

3. Meiosis in interspecific hybrids

Cytology of the sterile triploid hybrids between *A. hypogaea* and the diploid wild species has been frequently reported because of the interest emulated in identifying the putative parents of groundnut. Usually 6-10 bivalents, 2-3 trivalents and 1-2 quadrivalents were reported in different cross combinations. Segregation was irregular and percentage of stainable pollen grains varied in size. Hexaploids, pentaploids and tetraploids progenies were recovered from these triploids either through natural chromosomal doubling or with colchicine treatment. Meiosis in hexaploid hybrid derivatives was highly irregular. A maximum of twenty univalents have been reported (Company *et al.* 1982). In addition, several workers reported 1-2 hexavalents, 2-3 quadrivalents plus trivalents and 20-25 bivalents in the progenies of various crosses.

Meiosis of species hybrids or amphidiploids involving diploid *Arachis* species indicated the formation of 10 regular bivalents except in the crosses involving *A. batizocoi* where meiosis was highly irregular. Chromosomal associations in the intersectional hybrids also exhibited low frequency of univalents and multivalents indicating their genomic homologies (Stalker 1985).

IV. INTERSPECIFIC HYBRIDIZATION

Interspecific cross-compatibilty both between and within sections of this genus helped, to a certain extent, to understand the phylogeny. Interspecific hybridization in this genus has been attempted as early as 1938 by Hull and Carver between *A. hypogaea and A. glabrata* but with no success. Similarly, attempts to cross *A. hypogaea* x *A. villosulicarpa* and *A. hypogaea* x *A. diogoi* were also unsuccessful (Gregory 1946).

First successful interspecific hybrids involving *A. hypogaea* and diploid wild species were produced by Krapovickas and Rigoni (1951) between *A. hypogaea and A. villosa* var. *correntina*. The hybrid was triploid and sterile. Subsequently, interspecific hybrids between *A. hypogaea* and several species of section *Arachis* have been reported by several workers, with limited success in their respective reciprocal crosses. These hybrids were usually vigorous, flowered profusely and were mostly sterile (Smartt and Gregory 1967; Raman 1976; Gregory and Gregory 1979; Seetharam *et al*. 1973). Although triploids are usually sterile, seeds were produced by several hybrids of different cross-combinations of interspecific *A. hypogaea* hybrids (Simpson and Davis 1983; Singh and Moss 1984a).

Raman and Kesavan (1962) reported the first hybrids among wild species in the genus between *A. duranensis* and *A. villosa* var. *correntina*. Since then, hundreds of interspecific crosses among intra and inter sectional wild species and between cultivated and wild species have been reported to introgress alien gene for different agronomic traits of interest and disease resistance to cultivate groundnut (Kumar *et al.* 1957; Smartt and Gregory 1967; Gregory and Gregory 1979; Singh 1985; Singh and Moss 1984b; Ouedoraogo *et al*. 1994; Vindhiyavarman 1999; 2001 Simpson and Starr 2001).

In India, Kumar *et al.* (1957) produced the hybrid of *A. hypogaea* and *A. villosa* var. *correntina* and obtained hexaploids by treating it with colchicine. A naturally occurring allohexaploid of *A. hypogaea* x *A. villosa* var. *correntina* has also been reported by D'cruz and Chakravarty (1961). Interspecific hybrids involving *A. hypogaea* x *A. glabrata* var *hagenbeckii* were first produced by Nair *et al*. (1964). Subsequently, Raman (1976) and Varisai Muhammad (1973 a, b, c, d) reported hybrids between *A. hypogaea* x *A. diogoi* and *A. glabrata* x *A. villosulicarpa*).

International Crop Research Institute for Semi Arid Tropics, Pattancheru, India (1988, 1989) and George *et al.* (1989) at National Research Center for Groundnut reported interspecific hybrids involving *A. hypogaea* with *A. sp* PI 276233 (*Rhizomatosae*) and *A. hypogaea* with *A. paraguariensis* (*Erectoides*). Two more species, *A.sp* KSSC 36025-1 and *A. otavioi* of the section *Erectoides* were found to be freely crossable with *A. hypogaea* (George *et al.* 1989). Raman (1988) and Muralidharan (1988) have reported free exchange of genes between *A. hypogaea* and a spontaneous stabilized autotetraploid of *A. villosulicarpa.* Successful intersectional hybrids were depeloped between *A. hypogaea* and *A. oteroi* (Bera *et al.* 2003). Similarly, successful intrasectional hybrids were developed between *A. hypogaea* and different accessions of *A. kretschmeri, A. pusilla, A. correntina, A. diogoi, A. helodes, A. kempff-mercadoi, A. cardenasii, A. appressipila A. duranensis* and *A. batizocoi* at National Research Center for Groundnut, Junagadh, Gujarat (Murthy *et al*. 1987, 1989, 1990; Bera unpublished data). International Crop Research Institute for Semi Arid Tropics (ICRISAT), Hyderabad reported successful crossing between *A. duranensis* and *A. hypogaea* of section *Arachis* with *A. glabrata* of section *rhizomatosae* (ICRISAT 2002a). ICRISAT also reported successful hybrids between *A. hypogaea* with species from other sections of *Arachis* such as *Procumbentes, Heteranthae, Erectoides* and *Rhizomatosae* (ICRISAT 2002a).

A. monticola is a tetraploid in series Amphiploids of section *Arachis* and is the only wild *Arachis* taxon which can readily be crossed with *A. hypogaea* to produce fertile progeny. Though, the species has been given specific status, but it is a member of the same biological species as *A. hypogaea* and logically could be considered as a subspecies of the cultivated groundnut. For all practical purposes, *A. monticola* can be considered a wild form of groundnut, which does not need species manipulatios for its utilization in breeding programs.

Arachis hypogaea is cross compatible with almost all diploid species of secondary gene pool but either partially or completely sterile. The intrasectional hybrids are much easier to produce than intersectional ones, but low frequencies of success are still observed for many hybrid combinations within groups. Reasons for this, include incompatibilities among species, especially when the wild species is used as female parent; hybrid sterility due to differences in ploidy level; genomic differences among species; irregular meiosis in colchicine treated hybrids; and difficulties encountered during back cross generations when sterile aneuploid or pentaploid plants are obtained. Ploidy manipulations may be used to bypass the sterility of triploids and difficulties of back crossing hexaploids, by producing tetraploid derivatives of the wild species which can be then crossed with A. *hypogaea*. Further, these crosses have the advantage of producing wild x cultivated hybrids with a range of genome formulas (AABB, AAAB, or ABBB) which encourage intergenomic "AB" pairing.

V. EVOLUTION OF THE CULTIVATED GROUNDNUT

Arachis hypogaea is an allopolyploid (Stalker 1992; Raina and Mukai 1999). There are several theories put forth for the evolution of groundnut. Direct amphidiploid origin (Krapovickas and Rigoni 1957); evolution from pre-existing wild allotetraploid (Smart and Gregory 1967) and lastly of the annual x perennial hybrid combination within section *Arachis* were considered important in the evolution of groundnut with the later theory being most favoured.

One of the "A" genome species among *A. cardenasii, A. chacoense, A. correntina, A. duranensis, A. villosa* and "B" genome species, *A. batizocoi* have been hypothesized as possible progenitors of cultivated *A. hypogaea* (Stalker and Moss 1987*;* Singh and Smart 1998*).* However*,* Paik-Ro *et al.* (1992) reported that *A. batizocoi* is not closely related to *A. hypogaea* and hence cannot be the "B" genome donor. Kochert *et al.* (1991) suggested *A. ipaensis* as the "B" genome donor based on RFLP studies. Fernandez and Krapovikas (1994) support *A. duranensis* and *A. ipaensis* as the "A" and "B" genome donors respectively, of *A. hypogaea.* Based on crossability and molecular data, ICRISAT reported *A. hoehnei* as the "B" genome and *A. duranensis* as "A" genome donor of cultivated groundnut (ICRISAT 2002b)**.** However, till date no cross combinations between "A" and "B" species produced *A. hypogaea* like species. Molecular studies (Kochert *et al.* 1991; Halward *et al.* 1991a, Stalker 1991) at DNA levels (RFLP, PCR, Isozymes and seed storage proteins) have indicated that a large amount of genetic differentiation had already taken place in 'A' and 'B' genomes as reported earlier (Stalker and Dalmicio 1981, Singh and Moss 1982). On the other hand either one or both putative genome donor of *A. hypogaea* is missing in the experiment conducted or yet to explore.

VI. GERMPLASM EVALUATION IN THE GENUS *ARACHIS*

Arachis species have been evaluated for protein, oil content, fatty acids, nitrogen fixing ability, forage potential, seed dormancy, earliness and other agronomic traits. But the greatest potential lies in imparting disease and insect resistance in *A. hypogaea*. Many *Arachis* species have been evaluated for various diseases and pests (Subrahmaniam *et al.* 1985; Amin 1985). A list of multiple resistances found in various *Arachis* species has been summarized in Table 6.

However, there is not much success in introgression of these disease resistance genes to the cultivated background due to poor understanding of genome relationship, cross incompatibility, and non availability of true progenitor species. It appears from the literature that the resistance is mostly found in species belonging to section *Arachis and Rhizomatosae.* Several species of the section *Arachis* like *A. chacoense* and *A. cardenasii* exhibits multiple resistances against leaf spot, tomato spotted wilt virus. rust, nematode, thrips, earworm, and leaf hoppers.

VII. PATHWAYS AND STRATEGIES TO UTILIZE *ARACHIS* GERMPLASM

Wild *Arachis* gene pool is a mine to harvest especially for resistance to different diseases and pests which is either not simply available or not too enough in cultivated background. The desire to transfer genes from wild *Arachis* species into cultivated groundnut has burned brightly since the 1940s without much success. However, with constant effort and diligence success rate has improved over next five decades (Gregory and Gregory 1979; Krapovikas and Gregory 1994).

Recent success story in this direction is the transfer of root knot nematode from three wild diploid species to cultivated background (Simpson and Starr 2001) and introgression of resistance against Helicoverpa from *A. kempff-mercadoi* to cultivated species (ICRISAT 2002a). Several strategies have been used to introgress desirable genes from wild species for improving the cultivated groundnut. Three most effective and successful strategies used by the groundnut breeders are mentioned here.

Table 6 Multiple disease and insect-pests resistance in wild *Arachis sp.*

Speces	EL	LL	RT	SP	HE	TH	JA	AP	PM	PSt	PS
A. sp GK 12934	-	-	-	-	HR	HR	1	-	-	-	-
A. sp. GK 12946	-	-	-	-	HR	HR	HR	-	-	-	-
A. stenosperma HLK 410	HR	HR	HR	-	HR	HR	HR	R	-	-	-
A. duranensis K 7988	R	-	1	-	HR	S	1	R	-	-	1
A. spegazzinii GKP 10038	HR	-	1	-	HR	R	HR	-	-	-	R
A. batizocoi K 9484	S	-	1	-	HR	1	HR	R	-	-	-
A. khulmanii GK 30035	HR	R	1	-	-	-	-	R	-	-	-
A. correntina GKP 9530	HR	R	1	-	HR	HR	HR	R	R	-	R
A. chacoense GKP 10602	HR	HR	1	R	HR	HR	HR	R	R	R	S
A. cardenasii GKP 10017	HR	HR	1	-	HR	HR	HR	R	R	1	S
A. villosa BU 22585	R	R	1	-	-	-	HR	-	-	-	1
A. sp. GK 30017	HR	HR	1	-	-	-	HR	-	-	-	-
A. paraguariensis GKP 96-46	R	MR	1	R	S	-	R	R	-	R	R
A. appressipila GKP 9990	HR	R	1	R	HR	HR	R	-	-	-	R
A. sp GKP 105773	HR	R	1	R	HR	1	R	-	-	-	R
A. repens GKP 20538	S	S	-	-	HR	1	HR	-	-	-	1
A kempff-mercadoi GKP 10127	R	-	-	R	HR	1	1	R	-	-	-
A. villosulicarpa	HR	HR	1	-	-	-	-	-	-	-	-
A. glabrata GKP 9830	HR	HR	1	R	HR	1	HR	-	-	R	R
A. hagenbeckii HL 436	1	HR	1	R	HR	R	1	-	-	R	-
A. pusilla GKP 12922	HR	HR	1	R	HR	1	1	-	R	S	-

EL=Early leaf spot, LL=Late leaf spot, RT=Rust, AP=Aphids, JA=Jassid, TH=Thrips
PS=Peanut stunt virus, SP=Spodoptera HE=Heliothis PM=Peanut mottle virus PSt= Peanut stripe virus
HR= Highly resistant, S= Susceptible, I=Immune

A. Hexaploid pathway

A. *hypogaea* x *Arachis* sp.
2n=4x=40 ↓ 2n=20
F1 hybrid 2n=3x=30
↓
Colchicine treatment
↓
A. *hypogaea* x Amphidiplid hybrid 2n=6x=60
↓
Several back crossing with
A. *hypogaea* to lose chromosome
↓
A. *hypogaea* x Tetraploid hybrid 2n=4x=40

Attempts at crossing A. *hypogaea* with diploid species with "A" or "B" genome, produced hybrids although the success varied depending on the parental species employed. The resultant hybrids are mostly triploids and usually remain sterile. However, seeds were produced on few hybrid combinations involving *A. hypogaea* (Singh 1985). The selfed progenies of such triploids consisted of hexaploids, tetraploids and triploids. Upon back crossing the hexaploids with the cultivated types several tetraploid like derivatives were obtained. Several progenies involving A. *hypogaea* and *A. cardenasii* and *A. chacoense* have been obtained (Singh and Moss 1982).

Hexaploids, whether produced by colchicine treatment or from selfing of partially fertile triploids have many undesirable characters associated with wild species and none have been considered suitable as the basis of developing hexaploid groundnut crop. To utilize these hexaploids in crop improvement programmes the ploidy must be lowered to 40 chromosomes either through '6x' x '2x' crosses or through '6x' x '4x' crosses. But this will be difficult to obtain because of complete embryo abortion (Stalker1992). However, success in obtaining a stable tetraploid with desirable recombination through hexploid route is rather scanty.

B. Tetraploid pathway

Arachis sp. 2n=20 (A) — *Arachis* sp. 2n=20 (B)
↓ ↓
Colchicine (Double chromosome) Colchicine
↓ ↓
4x=40 x 4x=40
↓
A. hypogaea x Tetraploid hybrid
↓
Backcross to A. *hypogaea* untill
desired character is recovered

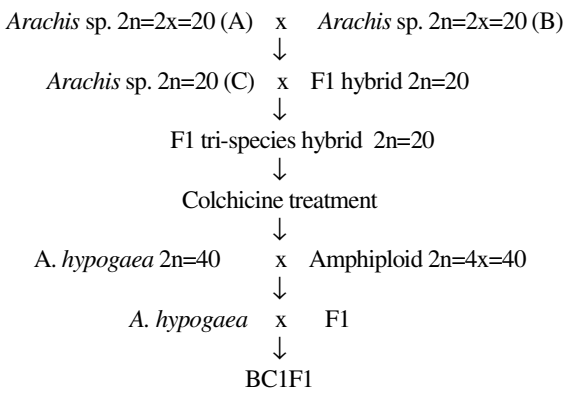
Autotetraploids and amphidiploids of *Arachis* species can be produced before hybridizing them with A. *hypogaea*. This pathway has certain advantage over the others in that the intervening sterile triploid, hexaploid and pentaploid generations can be circumvent as the crosses are at same ploidy level. Theoretically, Mendelian genes can be rapidly incorporated. Usually the amphidiploids involving "A" and "B" genome species are more readily crossable with *A. hypogaea* and are generally more sterile than when single genome species are used. Several auto and amphidiploid derivatives of A. *hypogaea* have been reported in the literature possessing resistance to *Cercospora arachidicola* and tomato spotted wilt virus (Gardener and Stalker 1983; Singh 1985 Murthy et al. 1989). However, the problem of identifying polyploid hybrids due to low vigour and seed set in them and restricted recombination between the autopolyploids/amphidiploids and *A. hypogaea* restricts the ease of gene transfer.

C. Diploid/tetraploid pathway

1. Two-way cross

Arachis sp.2n=20 (A) x *Arachis* sp.2n=20 (B)
↓
F1 hybrid 2n=20
↓
Colchicine
↓
A. hypogaea 2n=40 x Amphiploid 2n=4x=40
↓
Back cross to A. *hypogaea* until
desired character is recovered

2. Three-way cross



Two and three way cross of diploid/tetraploid pathway are also successful in some cross combinations. It is effective while parents are closely related and appreciable level of homologous/homeologous pairing is expected due to crossing in same ploidy level. However, breeder would be the best judge to choose the right pathway based on parents used, characters of interest and its genetic control to get the success.

VIII. PROBLEMS AND PROSPECTS IN UTILIZING OF *ARACHIS* GENE POOL FOR GROUNDNUT IMPROVEMENT

Number of germplasm accessions has increased in the recent years (>11,000), which includes species from all the three gene pools. Several species in different sections have been found to possess desirable agronomical, pests and disease resistance and quality traits. Attempts have also been made to utilize them for groundnut improvement. However, the pace of utilization and the economic end of product, the cultivar does not commensurate.

So far, by using the wild species only a few cultivars were released for general cultivation. In India, only one variety GPBD 4 has been released which involves *A. cardenasii* in its pedigree. Very recently, a stem rot resistant interspecific advanced line (CS-19) has been reported from National research Center for Groundnut, Junagadh, Gujarat. Although several advanced and stable lines have been developed but their performance when compared to the local elite varieties remain either at par or even below.

In spite of difficulties, looking in to the narrow genetic base, lack of stable and high level of resistance for diseases and pests in the cultivars, land races and cultivated germplasm of groundnut, the wild *Arachis* gene source still offers unparalleled mine to explore. At least in the near future introgression of useful genes from species of section *Arachis* will certainly find a priority in the era of high cropping intensity, growing use of pesticides and declining trend of agricultural lands. For which the suitable pre-breeding pathways integrated with available different parasexual techniques have to be exploited. Similar to sugarcane, hotspots for enhanced natural seed set in interspecific hybrids may be identified and crosses effected. In addition of parents, suitable bridging species, which combine better for fertility and seed set should be identified to introgress more and more wild gene source to the cultivated back ground. Conventional breeding and molecular marker based selection may go in hand to hand for priority specific and directed exploitation of large wild gene pool cutting the time and resources. Collaborative long term and multidisciplinary efforts in utilizing wild gene source would be crucial for the success.

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