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Meiotic Study of Intersectional Hybrids between *Arachis hypogaea*, *A. duranensis* and *A. diogoi* with *A. glabrata*

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Wild species, which are compatible and closely related to cultivated groundnut (*Arachis hypogaea*) are diploid and are classified into section *Arachis*. The tetraploids in the genus *Arachis* are *A. hypogaea*, the cultivated groundnut, *A. monticola*, a wild species belonging to section *Arachis*, and *A. glabrata*, belonging to section *Rhizomatosae*. There are very few reports on intersectional hybrids between members of section *Arachis* and *A. glabrata* (Shen et al. 1995, Mallikarjuna 2002, Mallikarjuna and Sastri 2002). This article reports meiotic analysis of the hybrids between *A. duranensis* and *A. diogoi* (= *A. chacoense*) (section *Arachis*) and tetraploid *A. glabrata* and the backcross progeny of the hybrid between *A. hypogaea* and *A. glabrata*. It corroborates the assumption that one genome of *A. hypogaea* and the A genome of section *Arachis* is closely related to R genome of *A. glabrata*.

Immature flower buds of hybrids (*A. hypogaea* × *A. glabrata*) × *A. hypogaea*, *A. duranensis* × *A. glabrata* and *A. diogoi* × *A. glabrata* were fixed in Carnoyís II mixture (6:3:1 alcohol : acetic acid : chloroform) at 4∞C for meiotic analysis. After 24 h in Carnoysís II, buds were transferred to Carnoyís I (3:1 alcohol : acetic acid). Buds were squashed and stained in 2% acetocarmine and meiotic analyses were made on suitable preparations. Pollen fertility counts were made on well stained pollen grains.

The details regarding crossability and introgression of DNA from *A. glabrata* into *A. duranensis*, *A. diogoi* and *A. hypogaea* have been dealt in detail by Mallikarjuna (2002). The hybrid between *A. duranensis* and *A. glabrata* was a triploid and had 8ñ11 bivalents with a mean of 10 bivalents per meiocyte (Table 1). Ten bivalents were observed in 30% of the cells analyzed. Formation of 10 bivalents could be due to the homology between the diploid genome (A genome) of *A. duranensis* and the R genome of *A. glabrata*. Trivalents were rarely observed. The occurrence of a mean of 9 univalents in the hybrid may be the non-homologous R chromosomes of *A. glabrata*.

Forty-eight percent of the pollinations formed pegs when *A. duranensis* × *A. glabrata* was pollinated with *A. hypogaea* pollen. Morphologically the hybrid had erect growth habit and resembled *A. hypogaea*. Flower buds had short hypanthium and flowers were pale yellow as seen in *A. duranensis.* Of the 485 pegs formed, 3 pods were obtained. Two of the pods had large but immature seeds and one pod had a mature seed. One BC_1 hybrid plant was obtained.

Triploid hybrid *A. diogoi* × *A. glabrata* was obtained when *A. diogoi* was crossed with *A. glabrata*. Bivalent formation in the hybrid ranged from 7 to 10 with a mean of 9 per meiocyte. The number of univalents ranged from 10 to 16 with a mean of 12 per meiocyte (Table 1). Both ring (4 per cell) and rod (6 per cell) bivalents were present. The occurrence of more number of rod than ring

Table 1. Chromosome configuration in the hybrids *Arachis hypogaea* (A) × *A. glabrata* (G), *A. duranensis* (D) × *A. glabrata* (G), *A. diogoi* (C) × *A. glabrata* (G), and (*A. hypogaea* × *A. glabrata*) (A × G) × *A. hypogaea* (A).

	A × G		D × G		C × G		(A × G) × A	
Chromosome association	Range	Mean	Range	Mean	Range	Mean	Range	Mean
Pentavalent	0ñ1	0.04	0	0	0	0	0	0
Tetravalent	0ñ2	0.6	0	0	0	0	0ñ1	0.1
Trivalent	0ñ2	0.6	0ñ1	0.1	0	0	0ñ1	0.1
Bivalent	9ñ19	15.3	8ñ11	10	7ñ10	9	10ñ20	15
Univalent	1ñ12	05.0	8ñ18	9	10ñ16	12	9ñ14	11

bivalents and of 12 univalents in 30% of the cells showed that there was some restriction in chromosome pairing in the hybrid *A. diogoi* × *A. glabrata.*

Meiotic pairing in *A. hypogaea* was normal with 20 ring bivalents in more than 95% of the meiocytes analyzed. Although tetravalents (2.3 per cell), univalents (1.13 per cell) and occasionally trivalents (0.2 per cell) are observed in *A. glabrata*, 20 bivalents in a cell was not an uncommon feature. Chromosome association in BC_1 hybrid (*A. hypogaea* × *A. glabrata*) × *A. hypogaea* was more stable than its F_1 hybrid (Mallikarjuna and Sastri 2002). Occurrence of 20 bivalents was rare in F_1 hybrid whereas 7% of the meiocytes analyzed showed the occurrence of 20 regular bivalents (Table 2) and regular anaphase separation of chromosomes. The number of bivalents in *A. hypogaea* × *A. glabrata* ranged from 9 to 19 with a mean of 9.8 ring and 5.5 rod bivalents. In the BC_1 hybrid the number of bivalents ranged from 10 to 20 with a mean of 11 ring bivalents and 4 rod bivalents. The occurrence of more number of ring bivalents in BC_1 hybrid showed greater homology compared to *A. hypogaea* × *A. glabrata*. This is an expected phenomenon as more of *A. hypogaea* chromosomes have had the opportunity to pair with the genome of *A. hypogaea* × *A. glabrata*. Hence, majority of the cells analyzed showed 14ñ15 bivalents per cell (Table 2). Only 4% of the cells analyzed showed bivalent formation of less than 13 per cell. Trivalents and tetravalents were more in *A. hypogaea* × *A. glabrata* than in its BC_1 hybrid (Table 1). The number of univalents in BC_1 was more than in *A. hypogaea* × *A. glabrata*. This may be due to preferential pairing of modified A genome of *A. hypogaea* × *A. glabrata* with A genome of *A. hypogaea* and non-homology between B genome of *A. hypogaea* and R genome of *A. glabrata* (Mallikarjuna and Sastri 2002). According to Stalker and Simpson (1995) one of the genomes of *A. hypogaea* (made up of A and B genomes) (Smartt et al. 1978) is related to the R genome of *A. glabrata*. Efforts to cross *A. batizocoi* and *A. ipaensis* (B genome species) with *A. glabrata* were not successful thus suggesting that A genome is closely related to R genome than the B genome.

Production of 15 bivalents in 23% of the meiocytes and more than 15 bivalents in 24% of the meiocytes in the hybrid (*A. hypogaea* × *A. glabrata*) × *A. hypogaea* show that there is some amount of homology between the genomes of *A. hypogaea* and the R genome of *A. glabrata*. The hybrid *A. duranensis* × *A. glabrata* had 10 bivalents in 30% of the meiocytes analyzed while the hybrid *A. diogoi* × *A. glabrata* had 10 bivalents in 50% of the meiocytes analyzed. These configurations can only be obtained when A and R genomes are closely related. Thus it further proves that A genome of section *Arachis* is homologous with R genome of *A. glabrata*. Crossing the hybrid *A. duranensis* × *A. glabrata* with *A. hypogaea* gave rise to the hybrid plant with 58% pollen fertility. This is possible only if the genome of the hybrid *A. duranensis* × *A. glabrata* has homology with the genome of *A. hypogaea*. Cytological information on close relationship between A and R genomes was lacking, which is provided by this study.

Table 2. Chromosome association in the backcross hybrid (*Arachis hypogaea* × *A. glabrata*) × *A. hypogaea*.

Chromosome association				No. of cells
II	I	III	IV	(%)
20	0	0	0	9 (7)
19	2	0	0	4 (3)
18	4	0	0	1 (1)
17	6	0	0	1 (1)
16	8	0	0	16 (12)
15	10	0	0	29 (23)
14	12	0	0	54 (43)
13	14	0	0	8 (6)
11	11	1	1	2 (2)
10	13	1	1	2 (2)

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