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GENETIC IMPROVEMENT OF *Arachis* THROUGH SYNTHETIC AMPHIDIPLOIDS

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ABSTRACT

In order to serve as a bridge species, three wild diploid species of the section *Arachis viz., A.cardenasii A.duranensis* and *A.stenosperme* were crossed in all possible combinations and amphidiploids were induced from the resultant F_1s. The results revealed the presence of reciprocal differences in the crossability of the different species. Cytological studies in F_1s of diploid species indicated the presence of genomic similarities while in the hybrids between the *A.hypogaea* cultivars and theamphidiploids showed the presence of not only intragenomic pairing but also high degree of intergenomic pairing. The studies resulted in the identification of *A.hypogaea* like derivatives possessing rust resistance.

KEY WORDS: *Arachis*, Genetic Improvement, SyntheticAmphidiploids

Many of the wild relatives of *A.hypogaea* are potentially useful in groundnut improvement. The diploid wild species of the section *Arachis* have a number of desirable attributes like resistance to foliar diseases. Ploidy differences are the major barriers for interspecific gene transfer. A basic understanding of the genomic structure, relationship and cytogenetic mechanism in *Arachis* has helped to overcome the barriers for transferring wild germplasm. In this paper, an attempt was made for transfer of wild genes for rust resistance through induction of amphidiploids

MATERIALS AND METHODS

Three wild diploid species of the section Arachis viz., *A.stenosperma* Krap.et Greg, *A.duranensis* krap et Greg.nom.nud and *Arachis cardenasii* Krap et Gerg. nom. nud., all of them having AA genome were crossed in all possible combinations. For induction of amphidiploid the procedure of Singh, 1986 was adopted.

Only treated meristems were allowed to grow. These plants were transferred to field to study the morphological and cytological behaviour. These F1s were crossed with *A.hypogaea* cultivars utilising the cultivars as ovule parent. For cytological studies, young flower buds were collected between 06.00 - 08.00 h and fixed in Carnoy Fluid II for 24 h. They were then transferred to Carnoys Fluid containing a drop of ferric chloride (5%) solution. The buds were dissected and anthers squashed in acetocarmine solution (1%) and stained pollen grains were counted as fertile.

RESULTS AND DISCUSSION

The data on crossability of the wild species showed the presence of reciprocal differences in the crossability between the species. *A.duranensis* was not affected in its crossing ability while. *A.cardenasii* as female parent had reduced crossability. The differences in the female crossability are often associated with the habits and are explained by faster evolutionary divergence of the annual species compared to the perennial (Stebbins, 1971)

Further the differences in pod set in the case of *A.cardensaii* as a male and female parent suggest the possible cytoplasmic effect on the crossability of the species. Similar results on crossability differences were reported in the species *A.chacoense* (Singh and Moss, 1984) Morphologically, the F_1 hybrids between the diploid species show either intermediate or increased values for the different characters studied.

The chromosome association in the hybrids between the diploid species (Table 1) indicated the presence of univalents, bivalents and multivalents at different frequencies. The high frequency of bivalents (8.6) in the hybrids between *A.duranensis* and *A.cardenasii* suggests a strong genomic relationship between the species. Singh and Moss (1984) observed similar results in the crosses

Table 1. Chromosome association in the hybrids of diploid species

Cross	Chromosome Association								Pollen fertility
	I		II		III		IV		
	Range	Mean	Range	Mean	Range	Mean	Range	Mean	
A. stenosperma x *A. cardenasii*	3-5	3.8	6-10	7.8	0-1	0.2	-	-	26
A. stenosperma x *A. duranensis*	3-5	3.2	7-9	8.0	-	-	0-1	0.2	32
A. cardenasii x *A. stenosperma*	4-7	4.4	6-9	7.1	0-1	0.2	0-2	0.2	22
A. cardenasii x *A. duranensis*	2-5	6.0	5-7	6.3	0-2	0.2	0-1	0.1	16
A. duranensis x *A. stenosperma*	2-7	3.6	7-9	7.8	0-1	0.2	0-1	0.2	33
A. duranensis x *A. cardenasii*	0-4	2.1	7-10	8.6	0-1	0.1	0-1	0.1	39

Table 2. Chromosome association in amphiploids

Cross	Chromosome Association				Pollen fertility
	I	II	III	IV	
A. stenosperma x *A. cardenasii*	2.39	13.2	0.19	2.66	26
A. stenosperma x *A. duranensis*	3.31	14.5	0.75	1.36	31
A. cardenasii x *A. stenosperma*	2.04	12.3	0.72	2.80	17
A. cardenasii x *A. duranensis*	2.71	12.2	0.51	2.84	28
A. duranensis x *A. stenosperma*	1.73	14.2	0.61	2.01	35
A. duranensis x *A. cardenasii*	4.55	13.0	0.23	2.19	12

Table 3. Chromosome association pollen and pod fertility in the hybrids between *A. hypogaea* x amphidiploid

Amphidiploid (0)	Chromosome Association				Pollen fertility (%) Range	Pods formed	
	I	II	III	IV		Range	Total
A. stenosperma x *A. cardenasii*	9.8	11.4	1.4	0.8	18-32	1-2	23
A. stenosperma x *A. duranensis*	11.5	11.1	1.3	0.6	35-55	1-3	31
A. cardenasii x *A. stenosperma*	9.6	11.6	0.8	1.2	17-28	1-2	18
A. cardenasii x *A. duranensis*	3.6	16.5	0.6	0.4	41-62	1-4	42
A. duranensis x *A. stenosperma*	7.6	14.5	0.6	0.4	36-59	1-4	52
A. duranensis x *A. cardenasii*	4.8	15.2	0.8	0.6	40-69	1-4	60
A. hypogaea (VRI 2)					79-94		

involving the same two species. In the amphidiploids, the bivalent association follows a similar pattern as that of the hybrids of the species (Table 2).

The results of cytological studies on chromosome association, pollen fertility and pod fertility are furnished in Table 3. The formation of more than 10 bivalents in the hybrids between the *A. hypogaea* cultivars and amphidiploids (AAAA) indicate not only a high intragenomic pairing within the 'A' genome but also intergenomic pairing with 'B' genome of *A. hypogaea*. There were no marked differences as regard to seed set in the hybrids between *A.hypogaea* and the amphidiploids. The hybrids are spreading in habit. The predominent features of the wild species such as stem pigmentation, leaflet shape, margin and resistance to rust were expressed in the hybrids. The fertility of the hybrids and strong intergenomic pairing shows the possible production of viable gene combinations through the amphidiploid route.

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