Table 2. Salient features of male sterile mutant Girnar 1 ms and its parent Girnar 1[1].

Salient characteristics	Girnar 1 ms	Girnar 1
Height of main axis (cm)	6.50	25.30
Maximum branch height (cm)	8.20	29.00
Number of primary branches	4.00	4.07
Number of secondary branches	1.30	1.30
Number of nodes on main axis	9.70	9.90
Number of leaves plant[1]	42.00	43.00
Internode length (cm)	0.60	2.55
Leaflet length (cm)	1.03	3.50
Leaflet width (cm)	0.48	1.70
Petiole length (cm)	2.16	4.40

1. Observations are based on 100 plants in Girnar 1 ms and 50 plants in Girnar 1.

these F_1 plants was done. The pods harvested from each plant were kept separately. The inheritance studies based on the F_2 results will be studied in rainy season 2000.

Quantitative observations were recorded on 100 male sterile plants and on 50 plants in parent Girnar 1 (Table 2). The male sterile mutant Girnar 1 ms was dwarf having small and rounded leaves. The number of nodes on the main axis was same in both mutant and parent; internodes were shorter in mutant plants and hence resulted in short stature.

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Quantitative Studies on Mating System of Groundnut

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The amount and nature of genetic variability in a population depend in part on its mating system. In addition to self-fertilization, autogamous species undergo varying degree of intermating. Allard and Workman (1963) and Harding and Tucker (1964) have given methods for estimating outcrossing when selection is present and/or equilibrium gene frequencies cannot be assumed. These methods are based on estimates of the frequency of dominant individuals appearing in the progeny of recessive individuals taken at random from the population. Groundnut (*Arachis hypogaea*) is mainly a self-pollinated species. The extent of natural cross-pollination in this species was highly variable (Hammons and Leuck 1966, Culp et al. 1968, Coffelt 1989, Nigam et al. 1990). Whether cross-pollination is random or not has not been studied so far. The purpose of the present investigation was to study the mating system involved in certain artificial population of this species using different markers and seasons and years.

True breeding "golden yellow leaf" and "puckered leaf" mutants were planted with TAG 24 (homozygous dominant) in alternate rows in separate plots. The spacing in all the plots was 30 cm × 10 cm. The experiment was conducted at the National Research Centre for Groundnut, Junagadh, India, in rainy season (kharif) and summer crop season of 1997 and rainy season of 1998. Since mutants and the homozygous normals (TAG 24) were equally frequent in both the artificially constructed populations, the gene frequency 'q' in both the cases was assumed to be 0.5.

The estimation procedure developed by Harding and Tucker (1964) was adopted. Let 'a' and 'b' denote the number of heterozygotes and recessive homozygotes respectively in the offsprings generated by recessivse homozygotes of a population. The maximum likelihood (ML) estimate of the outcrossing proportion is then given by:

$$\hat{T} = \frac{a}{a+b}$$

with variance:

$$var(\hat{T}) = \frac{ab}{(a+b)^3}$$

However, since not all the crosses will be observed, and as homogeneous matings will give rise to homozygotes, an adjusted ML estimate of total outcrossing, $\hat{\alpha}$, given below, should instead be used:

$$\hat{\alpha} = \frac{\hat{T}}{(1-q)}$$

where q is the gene frequency of selected homozygote. Provided q is known, the ML estimate of var ($\hat{\alpha}$), the variance of α, can be computed from:

$$var(\hat{\alpha}) = \frac{\alpha(1-\alpha q)}{Np} = \sigma^2(\hat{\alpha})$$

where p+q = 1 and N = a+b. Since, q=p=0.5 is known and $\hat{T}$ did not exceed 0.15 in the present study, the above formula was utilized for computation of variance of $\hat{\alpha}$.

Table 1 presents the frequencies of heterozygotes (a), total offsprings (N), estimates of outcrossing ($\hat{\alpha}$), and their standard deviations [$\sigma(\hat{\alpha})$] for five artificially constructed populations of two different leaf markers in two different seasons and years. The estimates of outcrossing, pooled over years and seasons, for golden yellow leaf (0.0116) and puckered leaf (0.0330) were heterogeneous as revealed by χ^2 test ($\chi^2_{1df} = 102.8$; $P<0.001$). Seasonal variation in outcrossing rates in puckered leaf mutant was negligible ($\chi^2_{1df} = 0.7691$; $P>0.05$) while it was considerable

in golden yellow leaf mutant ($\chi^2_{1df} = 23.2$; $P<0.001$). The differences in degree of seasonal fluctuations in outcrossing rate among the two mutants might be the expression of variable genotype × environment interaction in these two mutants. The experiments with both the mutants were conducted in a common experimental field in both the seasons. Hence, the observed degree of seasonal fluctuations of outcrossing in them cannot be ascribed to differences in insect (pollinator) populations available in the experimental plots. However, the preferential visit of insects to selected flower forms cannot be ruled out and possible differences in the flower form in the mutants are supposed to be genetically controlled. The outcrossing during rainy season in two years in golden yellow leaf was homogeneous ($\chi^2_{1df} = 0.0059$; $P>0.05$).

The composite estimate of outcrossing ($\hat{\alpha}$) for puckered leaf (0.0330) was almost three times higher than that in golden yellow leaf (0.0116). The approximate expected range [$\alpha \pm 2\sigma(\alpha)$] due to random fluctuation leaf was −0.0062 to 0.0294 for golden yellow and was −0.0106 to 0.0766 for puckered leaf. But if the observed fluctuations were used the approximate range [$\alpha \pm 2s(\alpha)$] for golden yellow leaf and puckered leaf was −0.0010 to 0.0242 and 0.0182 to 0.0478 respectively where $s^2(\hat{\alpha})$ was computed as $s^2(\hat{\alpha}) = [1/(n-1)][\Sigma\alpha_i^2-(1/n)(\Sigma\alpha_i)^2]$; n = 3 for golden yellow leaf and n = 2 for puckered leaf. The observed fluctuation in α for golden yellow leaf was approximately 1.5 times less than the fluctuations expected on the basis of random chance alone [$\sigma(\alpha)/s(\alpha) = 1.41$]. Similarly for puckered leaf $\sigma\alpha$ /sα was 4.45. In both the mutants, the observed fluctuations were less than the fluctuations expected due to chance alone. Hence, it could be concluded that the outcrossing in all the populations was a random event.

Table 1. Estimation of outcrossing ($\hat{\alpha}$) in groundnut using golden yellow leaf and puckered leaf mutants as markers at Junagadh, India[1].

Marker	Year/Season	a	N	q	$\hat{\alpha}$	$\sigma\hat{\alpha}$
Golden yellow leaf	1997 rainy season	8	1147	0.5	0.0139	0.0416
	1997 summer crop season	9	5822	0.5	0.0031	0.0185
	1998 rainy season	126	17714	0.5	0.0142	0.0105
Total		143	24683	0.5	0.0116	0.0089
Puckered leaf	1997 summer crop season	12	619	0.5	0.0388	0.0563
	1998 rainy season	56	3506	0.5	0.0319	0.0237
Total		68	4125	0.5	0.0330	0.0218

1. a = Frequency of heterozygotes; N = Total offsprings; q = Gene frequency; $\sigma\hat{\alpha}$ = Standard deviation.

The mating system is commonly considered to be the chief factor determining the genetic structure and evolutionary potential in a population. The mating system of present populations of *A. hypogaea* was a mixed system of random mating and self-fertilization. One of the important features of the variability in inbreeding species is genetic differentiation between populations within the species. Clinal variation is frequently observed in association with progressive changes in rainfall, temperature, and other factors of the physical environment and such local differentiation appears to provide the scope of massive storage of genetic variability. It is true that population structure in inbreeding species is much more complicated than has been commonly supposed and probably it does not take the same form in all inbreeding species or even in different populations of the same species. For example, in *Phaseolus lunatus*, heterozygotes and homozygotes of *S/s* locus were equal in fitness when all three genotypes were equally frequent in population (Harding et al. 1966). However, when heterozygotes were rare in the population, their fitness increased to homozygotes. Thus, the maintenance of stable nontrivial polymorphism depends on a complex set of interaction between genetic factors, mating systems, and ecological factors. The observed variability of outcrossing in groundnut under different ecological conditions (different years and seasons) in different marker stocks may well contribute to a complex population structure. Workman (1964) and Allard et al. (1968) have discussed in detail the evolutionary consequences and significance of such a mating system.

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Genetics and Interrelationship of Oil and Protein Contents in Crosses Involving Confectionery Genotypes of Groundnut

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With the changing scenario in the global trade in general, and in agriculture in particular, the emphasis in the groundnut breeding program in India is shifting towards the development of large-seeded genotypes with low oil, high protein, and high sugar contents to meet the standards for international trade. An understanding of relationship and genetic control of oil and protein contents should facilitate the breeding strategies to select for improved seed quality traits. Hence genetic analysis was carried out on 28 non-reciprocal diallel crosses involving large-seeded confectionery virginia genotypes of groundnut following Hayman's (1954) approach. The F_1s and F_2s of these crosses were grown in a randomized block design with three replications.

Data on protein and oil contents were recorded on twenty randomly selected plants in F_1 and F_2 generations for each cross. Protein content was estimated based on total nitrogen content of seed by microKjeldahl method (Jackson 1967), and oil content was estimated following specific gravity method (Misra et al. 1993). Correlation coefficients and heritability estimates (in narrow sense) were estimated.