(Fig. 2). The pollen sterility was higher in tetrasomics than trisomics. Two tetrasomic types had fruits with normal size and shape, with much reduced seed size (75%) and the seed number of each fruit was half of the diploid cultivar.

Fruit shape was mostly deformed in hyper-triploid, hypo-triploid and triploid types, probably because of high ovule sterility. It was found that tolerable limit of extra chromosome in case of guava was four, beyond this limit seed fertility and fruit shape was found to be adversely affected.

As guava is vegetatively propagated, the aneuploid types can very well be maintained, unlike annual crop plants. The addition of two chromosomes to diploid number has shown a great promise in guava improvement. This method of breeding can very well be adopted in tree fruits where numerous seeds decrease the fruit value.

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A NOTE ON THE CYTOGENETIC STATUS OF *NICOTIANA AMPLEXICAULIS* BURBIDGE

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WHILE assigning taxonomical positions for the five new Australian species of *Nicotiana*, Burbidge (1960) fixed *N. amplexicaulis* ($2n = 36$) between *N. gossei* ($2n = 36$) and *N. maritima* ($2n = 32$). Morphologically, *N. amplexicaulis* may well be regarded as a mini copy of *N. gossei* but bears little resemblance to *N. maritima*. Distributionally, the three species are widely separated, *N. gossei* in Central Australia, *N. amplexicaulis* in Queensland and *N. maritima* in South Australia. According to Goodspeed (1954) almost all the Australian species had their origin through amphidiploidy followed by chromosomal and genetic reorganisation. Aneuploidy through loss of chromosomes played an important part in the evolution of the Australian species in particular. In this context, the cytogenetic position of *N. amplexicaulis* was investigated to determine its relationship to the older species. For this purpose, inter- and intrasectional crosses between *N. amplexicaulis* and certain species of *Nicotiana* were done and the cytology of the hybrids followed. Since *N. amplexicaulis* is similar to *N. gossei* in chromosome number and also in morphology, comparison of chromosome behaviour of crosses between *N. gossei* and the same species involved in *N. amplexicaulis* crosses was made. The trend of cytogenetic behaviour of *N. gossei* and *N. amplexicaulis* is almost similar.

The chromosome pairing of *N. gossei* and *N. amplexicaulis* is given in Table I. From Table I it may be seen that a high degree of pairing between *N. amplexicaulis* as well as *N. gossei* with the species is evident. This points to a close genotypic homology between *N. gossei* and *N. amplexicaulis*. This is further proved by the complete pairing and fertility of the hybrids between the two species. The pairing relationship between *N. amplexicaulis* and the other species, as listed in Fig. 1,

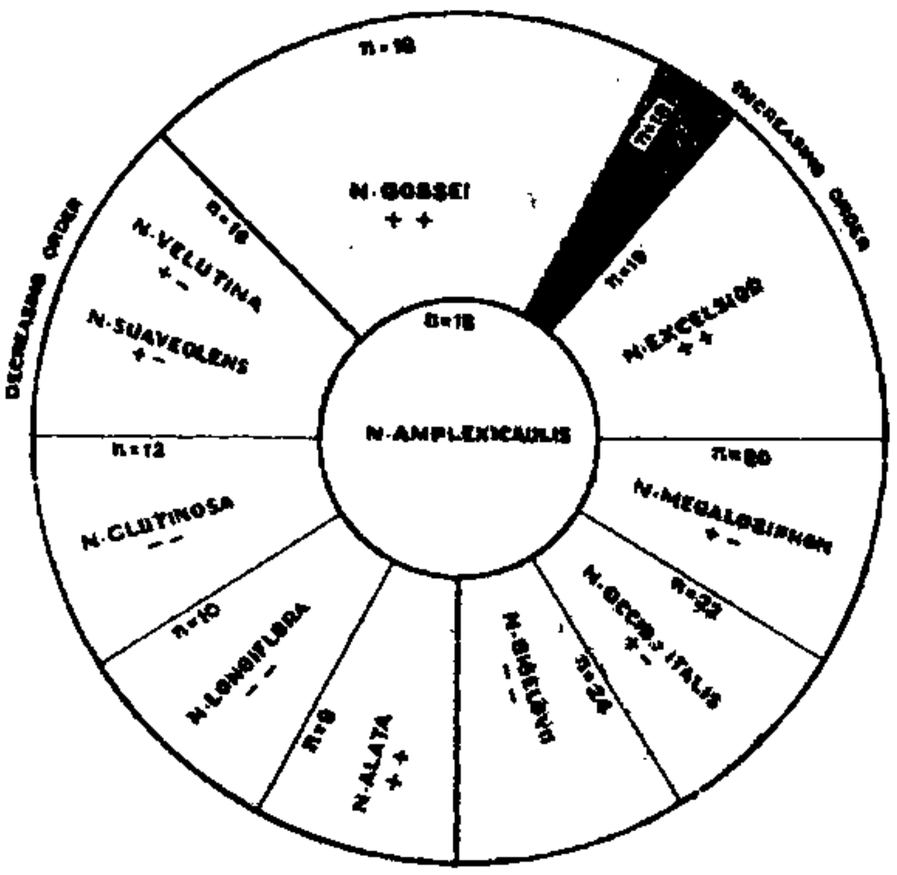

FIG. 1. Chart indicating *N. amplexicaulis* crosses with other species of *Nicotiana*. + indicates goodness and − indicates failure. First symbol for chromosome pairing and second symbol for pollen and seed fertility. The striped portion will be the cytogenetic location for *N. amplexicaulis*.

reveals another interesting feature. With certain species, the chromosome pairing was excellent but genetic abortion resulted in complete sterility both on the male and female sides. This is indicated in Fig. 1. The symbol + or − below the specific name indicates the chromosome pairing or its failure. The first symbol indicates pairing while the second symbol, goodness or failure of pollen and seed fertility as a consequence thereof. It may be seen from Fig. 1 that besides *N. gossei*, both pairing and fertility was obtained only in crosses with *N. excelsior* and *N. alata*. In the case of *N. excelsior*, no morphological similarity can be seen with *N. amplexicaulis*. Consequently, the derivatives from this cross looked quite different from either of the parents. Based on the inclusion or elimination of the extra *excelsior* chromosome, F_2 and F_3 generation also threw out different type of segregants.

With regard to the cross between *N. amplexicaulis* and other members of the Suaveolentes section, namely, *N. megalosiphon*, *N. occidentalis*, *N. velutina* and *N. suaveolens*, though chromosome pairing was excellent, fertility of the hybrids had been completely impaired. Considering all these facts of cytogenetic interest, it may not be improbable to fix *N. amplexicaulis* cytogenetically between *N. gossei* and *N. excelsior* as represented in Fig. 1. With regard to the complete pairing and fertility of the hybrid between *N. amplexicaulis* and *N. alata*, it is quite intriguing that a distant inter-sectional species, like *N. alata*, should have a very close affinity with *N. amplexicaulis*. Morphologically, these two species are poles apart. However, *N. gossei* and *N. alata* do not show such affinity (*vide* Table I). So it can be inferred that in the origin of *N. amplexicaulis* genotype, a greater expression of chromosomal homology derived from *N. alata* is amply evident. In this respect only, *N. amplexicaulis* differs from *N. gossei*. With species of other section, the hybrids were always sterile (Table I).

TABLE I

Chromosome pairing in interspecific hybrids involving either N. gossei *or* N. amplexicaulis *as one of the parents*

	Cross*	Range of bivalent formation during meiosis in the hybrids	
		N. gossei†	*N. amplexicaulis*‡
1.	*N. velutina* ($n=16$) ..	15 to 16	15 to 16
2.	*N. suaveolens* ($n=16$) ..	13 to 15	15 to 16
3.	*N. excelsior* ($n=19$) ..	17 to 18	17 to 18
4.	*N. megalosiphon*($n=20$)	13 to 17	17 to 18
5.	*N. occidentalis* ($n=21$)	13 to 15	17 to 18
	Inter-sectional hybrids:		
6.	*N. glutinosa* ($n=12$) ..	..	3 to 7
7.	*N. alata* ($n=9$) ..	0 to 3	12 to 13
8.	*N. longiflora* ($n=10$) ..	0 to 3	0 to 3
9.	*N. bigelovii* ($n=24$) ..	..	4 to 10

* The direction of cross not indicated.
† Reference : Goodspeed (1954).
‡ Reference : Gopinath *et al.* (1965).

As for the origin of *N. amplexicaulis*, it is found very difficult to determine through chromosome homology since the chromosomes of *N. amplexicaulis* freely paired with most of its sectional species. So test crosses did not give any clear indication. Overlapping as they do in geographical distribution, *N. gossei* and *N. excelsior* might have also hybridised and given rise to *N. amplexicaulis* type of plants. But the contrasting leaf and flower characters of the above species would scarcely support such an assumption. Further, flowers of *N. amplexicaulis* have little similarity with those of *gossei* or *excelsior*. Taxonomically *N. excelsior* is far below *N. amplexicaulis* in classification. The discovery of *N. amplexicaulis* as late as 1960 might indicate that it would have arisen as a hybridised product of the modern Australian species.

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