SUMMARY AND CONCLUSION

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Seven genera, eighteen species and five varieties of H. sabdariffa belonging to tribes Hibisceae and Urenea of the family Malvaceae are included in the present work.

The taxonomic position of the family and the genera studied have been discussed in brief. The genera and the species are classified following Schumann's treatment as modified by Hutchinson (1967). The different species of Hibiscus studied, are kept under different sections following Hochreutiner (1900). For presenting morphological and karyomorphological observations the above mentioned treatments have been followed throughout.

Different populations of Hibiscus lobatus, Azanza lampas and Urena lobata showed marked morphological variations among themselves. A study of these morphological variations by polygraphic method, revealed the existence of consistent differences amongst the populations of a species. Even in case of H. sabdariffa the closely related varieties could be morphologically distinguished by subjecting them to a polygraphic study.

Cytological observations include the karyotypic study and the meiotic behaviour of chromosomes of different populations of the species studied presently. The comparison of the karyotypes of different taxa, yielded informations concerning the evolutionary status of a genus, phylogenetic relationships and the probable course of evolution followed for speciation.

Comparison of exomorphological and karyomorphological data of different populations of *Hibiscus lobatus* and *Azanza lampas* revealed the presence of 3 ecotypes each in both of them. Two species of *Urena* viz. *U. lobata* and *U. sinuata* recognized by Linnaeus (1753) were merged into one i.e. *U. lobata*, by Hochreutiner (1900). The present study supports the maintainance of two distinct species as they show consistent morphological as well as cytological differences between them. In contrast to these, in *H. panduraeformis*, *H. cannabinus* and *H. vitifolius* the different populations, though morphologically similar showed presence of 3, 2 and 2 cytotypes respectively.

The karyotypes of the four genera of the tribe Hibisceae studied show the following evolutionary sequence, i.e. *Thespesia*; *Azanza*, *Hibiscus* and *Abelmoschus*. However, in Hutchinson's treatment (1967), the genus *Thespesia* is placed after *Abelmoschus*. On the basis of karyotypic study, Rakshit and Kundu's suggestion (1971) of placing the problematic genus *Azanza* inbetween *Thespesia* and *Hibiscus* is validated. Passing from more primitive to more advanced, the different species of *Hibiscus* under consideration, may be placed in the following sequence i.e. *H. panduraeformis*, *H. ovalifolius*, *H. cannabinus*, *H. lobatus*, *H. caesius*, *H. vitifolius*, *H. trionum*, *H. hirtus*, *H. sabdariffa* and *H. mutabilis*. It is quite evident that different levels of ploidy (aneuploidy and euploidy) accompanied by structural alterations in chromosomes might have played a significant role in the speciation of the genus *Hibiscus*. Medikus (1787) separated the genus *Abelmoschus* from *Hibiscus* on morphological grounds and the same is supported by the present cytological observations. Between the two species studied, *A. manihot* shows evolved nature of the karyotype as compared to that of *A. angulosus*.

On the basis of karyotypic study, the three genera of the tribe Ureneae studied can be arranged in the following evolutionary sequence i.e. *Pavonia*, *Urena* and *Malachra*. It is just the reverse of Hutchinson's treatment (1967). Of the two species of *Pavonia* studied, the karyotype of *P. zeylanica* having 2n = 56 appears more evolved than that of *P. patens* having 2n = 28. Between the two karyotypes of *Urena*, one of *U. lobata* having more number of nearly sub-median types of chromosomes, appears slightly more evolved than that of *U. sinuata*. The evolved nature of the karyotype of *Malachra capitata* is pronounced in having higher number (2n = 56) and shorter chromosomes.

On the basis of morphological criteria (the stylar branches) Davie (1933) and Hutchinson (1967) have subscribed a view of considering the tribe Ureneae more advanced than the tribe Hibisceae. As the primitive and advanced type of karyotypes are observed in the taxa of both the tribes, it is reasonable to consider that the two tribes must have diverged early showing parallel course of evolution.

Different primitive basic numbers proposed for the family are 7 (Davie, 1933), 5, 6 and 7 (Skovsted, 1935) and 6 (Hazra and Sharma, 1971). All the workers are unanimous regarding the polyphyletic course of evolution of different genera and species within the family. As multiple of 7 is metwith in the majority of the genera of the two tribes studied, number 7 can be considered more deep seated in the family. Other numbers observed are presumably derived from the basic number 7. H. panduraeformis having 2n = 24 and comparatively primitive nature of the karyotype among the species of Hibiscus, raises a feeling about considering 6 as the base number. However, a more primitive nature of the karyotype is metwith in Thespesia populnea having 2n = 28, suggesting that the number 6 also must have been derived from the basic set of 7 through aneuploid reduction.

Of the two tribes, the tribe Ureneae is very homogenous in having chromosome numbers which are simple multiple of 7. In contrast to this, members of the tribe Hibisceae, have chromosome numbers, which are multiples of 6, 7, 8 and 13. In the genus Hibiscus a wide range of chromosome numbers (2n = 24 to 2n = 120) representing multiples of 6, 7 and 8 have been observed in different species. The stray number 2n = 34 observed in H. vitifolius must be the result of aneuploidy and polyploidy of one of these basic numbers.

In meiotic study, the occurrence of distinct bivalents in majority of the taxa studied, indicate that they represent ancient polyploids. However, along with other abnormalities the secondary associations of bivalents were recorded in few cases such as *Urena lobata* (7 groups), *Hibiscus vitifolius* (8 groups) and *H. panduraeformis* (6 groups). If the theory of secondary associations of bivalents holds good, these groupings of 6, 7 and 8 also support the contention of considering 6, 7 and 8 as the basic numbers of ancestral types from which further evolution might have progressed.

The genus *Hibiscus* has been further sub-divided into different sections by Hochreutiner (1900). The grouping made on evident morphological characters, is coherent in some respects with the present cytological findings. The chromosome numbers in the somatic complement of the species, belonging to different sections, studied in the present work are as follows.

Section - Furcaria DC.

1. *H. sabdariffa* 2n = 72
2. *H. cannabinus* 2n = 36 x 18

Section - Pterocarpus Garcke

3. *H. vitifolius* 2n = 34 x 17

Section - Trionum DC.

4. *H. mutabilis* 2n = 12 x 12
5. *H. trionum* 2n = 56 x 14

Section - Solandra Hochr.

6. *H. lobatus* 2n = 36
2n = 72 x 18

Section - Hibiscus Borss.

7. *H. hirtus* 2n = 64
8. *H. ovalifolius* 2n = 32 x 16

Section - Trichospermum Hochr.

9. *H. panduraeformis* 2n = 24 x 12

Section - Ketmia DC.

10. *H. caesius* 2n = 36 x 18

These numbers represent the multiple of different secondary basic numbers in different sections. In Hochreutiner's grouping, the two sections viz. Trichospermum and Ketmia are kept last as 9th and 10th sections. But the comparative study of the karyotypes of different species of *Hibiscus* show, that the karyotypes of *H. panduraeformis* and *H. caesius* belonging to sections Trichospermum and Ketmia respectively, appear more primitive than those of other species.

The results obtained from the study of limited taxa, can not be considered sufficient to draw a definite conclusions concerning the delimitations of genera, tribe and species of the family. A thorough investigation on the line suggested above, of the remaining taxa of the family can further clarify the situation.

However, the data concerning the karyomorphology and the comparison of the karyotypes are useful for checking the existing groups based solely on morphological (phenotypic) criteria. On occasions, when conventional taxonomy failed, this approach has provided solutions in reorganization of taxa at various levels of classification and also served as an indicator suggesting the probable phylogenetic relationships.

It has been rightly emphasized by Davie (1933) that from purely cytological evidences it is difficult to assemble the genera in a phylogenetic sequence. Since chromosome number and morphology are not absolutely diagnostic. The broad cytological data are of more value for sectional relations than for the alignment of the species. Chromosome difference is not necessarily a measure. Chromosome difference between the complements of two taxa, do not necessarily signify a great difference in their external morphology, and the converse is also true (ecological races i.e. ecotype, cytotypes and ecads within the circumscription of a species). Workers like Darlington (1956), Stebbins (1959) and Löve (1960) have opined that, too much emphasis on such characters and comparing them with morphological traits would be a serious misunderstanding of the principle of evolutionary biology.

As it stands at present the traditional descriptive taxonomy should be considered to be the basic foundation and other approaches (Anatomy, Cytology, Palynology, Physiology etc.) should be profitably used by modern taxonomists (Omega taxonomy, Turrill, 1938) in realization of the envisaged phylogenetic system of classification.