Discussion

Tribe Hibisceae :

On the basis of cytological observations, the 4 genera of the tribe Hibisceae studied can be arranged in the following evolutionary sequence.

The genus Thespesia with low chromosome number, longer chromosomes and more or less symmetrical nature of the karyotype indicates a very primitive nature. The complement of T. populnea contains 28 chromosomes, which is the multiple of 7. The chromosomes range from 6.04 μ to 2.55 μ in length with a mean length of 4.33 μ.

The chromosome number of Azanza lampas is also 2n = 28. The chromosome length ranges from 2.72 u to 1.28 u with a mean length of 1.92 u. Both the genera Thespesia and Azanza resemble each other in chromosome number, and in having more or less equal number of chromosomes with nearly median and nearly sub-median centromeres (Fig. 158). Since Azanza lampas has shorter chromosomes, lesser TF% and a pair of secondarily constricted chromosomes in its complement (Table IX), it

Fig. 158 - Idiograms of :

Thespesia populnea, *Azanza lampas*, *Hibiscus panduraeformis*, *H. ovalifolius*, *H. cannabinus* and *H. caesius*.

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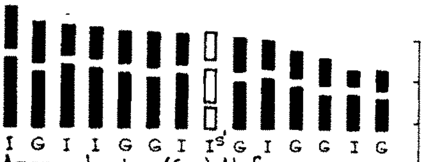
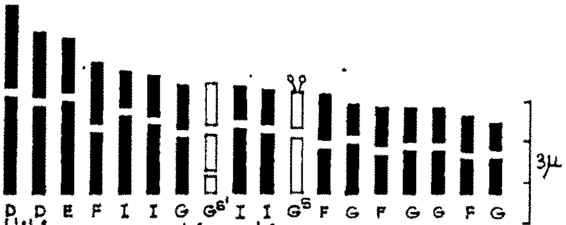
Thespesia populnea Soland. COLL.NO.49



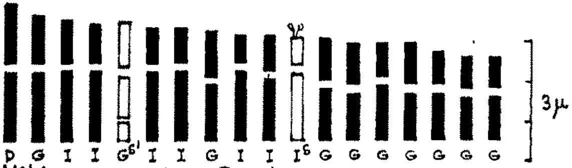
Azanza lampas (Cav.) Alef. COLL.NO.10

H. panduraeformis Burm. COLL.NO.26

H. ovalifolius (Forsk.) Vahl COLL.NO.56



Hibiscus cannabinus Linn. COLL.NO.14



Hibiscus caesius Garcke COLL.NO.55

seems to be more evolved than *Thespesia*.

The chromosome numbers recorded for the genus *Hibiscus* in the present work as well as in the earlier investigations (viz. Davie, 1933; Skovsted, 1935; 1941; Medvedeva, 1936; Nakajima, 1936; Narasingarao, 1935; Rao, 1941; Menzel and Wilson, 1961; 1963; Sharma and Sharma, 1962; Hazra and Sharma, 1971; Kachecheba, 1972) show a wide range from 2n = 22 to 2n = 225. Among the species investigated presently, the lowest number 2n = 24 in *H. panduraeformis* and the highest number 2n = 120 in *H. mutabilis* are recorded. All the somatic numbers 24, 34, 36, 56, 64, 72 and 120 met-with are the multiples of 6, 7 and 8. Multiple of 6 is more common in the genus *Hibiscus*, suggests that the number 6 is more deep seated in the genus. However, 2n = 34 found in *H. vitifolius* must have been derived through aneuploidy and polyploidy from one of the basic numbers mentioned for the genus. The occurrence of high chromosome number in majority of the species indicates the significant role of polyploidy in speciation within the genus.

A detailed analysis of the karyotypes of different species reveals a gross similarity in the related species. On the basis of gross morphological characters a number of chromosome types are seen to be common in most of them. A critical analysis, shows that different combinations of these chromosome types, together with the minor structural alterations, may be regarded as the criteria for differentiating the different species and varieties. In general, the karyotypes of most of the species show a graded nature of the chromosomes. Present study pertains to 11 species and 5 varieties(of *H. sabdariffa*).

H. panduraeformis appears to be the most primitive among the species studied for the present work. The primitive nature of the karyotype is exhibited by low chromosome number (viz. $2n = 24$), comparatively longer chromosomes (range - 5.44 μ to 2.38 μ) and more number of median and nearly median types of chromosomes (Fig. 158). The more symmetrical nature of the karyotype is reflected by high TF% value i.e. 40.45 (Table IX).

In *H. ovalifolius* the chromosome number recorded is $2n = 32$. As the complement has higher chromosome number, shorter chromosomes (range - 3.06 μ to 1.45 μ), absence of median types and less TF% (38.97), the species can be considered more evolved than the preceeding one (Table IX).

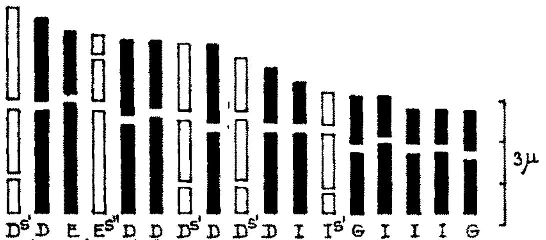
The somatic complement of *H. cannabinus* and *H. caesius* resemble in many respects, such as chromosome number (2n = 36) and in having a pair of SATs and a pair of secondarily constricted chromosomes (Fig. 158). The complement of *H. cannabinus* has chromosomes with median (4 pairs), nearly median (9 pairs) and nearly sub-median (5 pairs) centromeres. In contrast to this, *H. caesius* lacks median types of chromosomes in its complement, but contains only nearly median (11 pairs) and more number of nearly sub-median (7 pairs) types of chromosomes (Table IX). The chromosomes of *H. cannabinus* are longer (range 4.20 μ to 1.51 μ) than the chromosomes of *H. caesius* (range 3.15 μ to 1.87 μ). TF% of both the species are almost the same (Table IX). Except for the slight abruptly graded nature of the karyotype, other characters show the advanced nature of *H. caesius* over *H. cannabinus* (Fig. 158).

2n = 34 have been found in the somatic complement of *H. vitifolius*. Except for the longer chromosomes

Fig. 159 - Idiograms of :

H. vitifolius, *H. trionum*, *H. hirtus*, *H. lobatus*, *H. sabdariffa* and *H. mutabilis*.

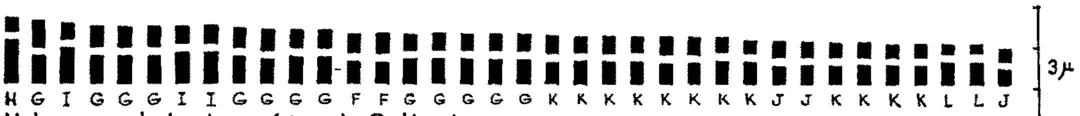
Contd.........



Hibiscus vitifolius Linn. COLL.NO.33

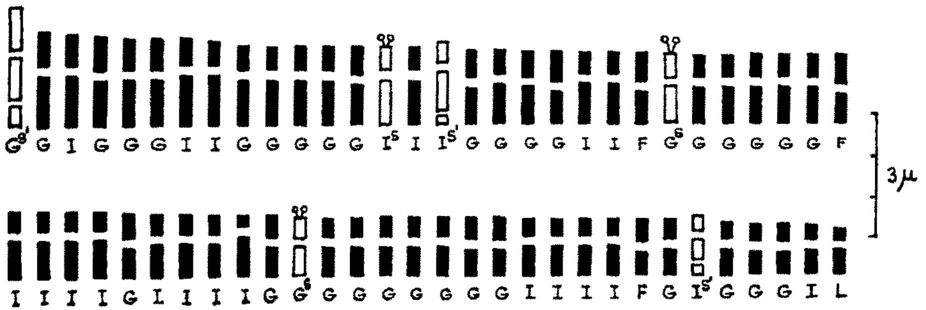
Hibiscus trionum Linn. COLL.NO.47

Hibiscus hirtus Linn. var. *hirtus* COLL.NO.54



Hibiscus lobatus (Murr.) O. Kuntze COLL. NO. 15

Hibiscus sabdariffa Linn. var. *sabdariffa* COLL. NO. 7



Hibiscus mutabilis Linn. COLL. NO. 44

(range 4.63 μ to 2.31 μ) the species shows a gross similarity with the two preceeding species (Fig. 159). The presence of only two types of chromosomes i.e. nearly median (10 pairs) and nearly sub-median (7 pairs) shows more resemblance with *H. caesius*. The more number (3-5 pairs) of secondarily constricted chromosomes in complements of *H. vitifolius* show the evolved nature of the karyotype, though the TF% is more (40.78 Table IX).

The chromosome number 2n = 56 is observed in *H. trionum*. The chromosomes are of medium size ranging from. 3.32 μ to 1.53 μ in length. Absence of chromosomes with median centromeres, presence of 2 pairs of SATs and 1 pair of secondarily constricted chromosomes coupled with higher ploidy indicate the evolved nature of the species (Fig. 159).

The chromosome number of *H. hirtus* is 2n = 64. The advanced nature of the karyotype is evidenced by high chromosome number, absence of chromosomes with median centromeres, shorter chromosomes (range 2.38 μ to 1.02 μ Fig. 159) and less TF% (i.e. 38.25), though the complement has only 1 pair of SATs and 1 pair of secondarily constricted chromosomes (Table IX).

In *H. lobatus*, two chromosome numbers 2n = 36 and 72 are observed in the different populations. The karyotypes of these populations show notable differences in chromosome size and number of median, nearly-median, nearly sub-median types of chromosomes (Table V). This shows that the genome of these two populations are not closely related. The populations with 36 chromosomes come near *H. cannabinus* in evolutionary sequence, as they have same chromosome number (2n = 36). However, chromosomes with satellites or secondary constrictions were not observed in any of the populations.

The population of *H. lobatus* with 2n = 72 is advanced over all the preceeding species in having high chromosome number and shorter chromosomes (range 1.36 µ to 0.68 µ; mean length 1.01 µ Fig. 159).

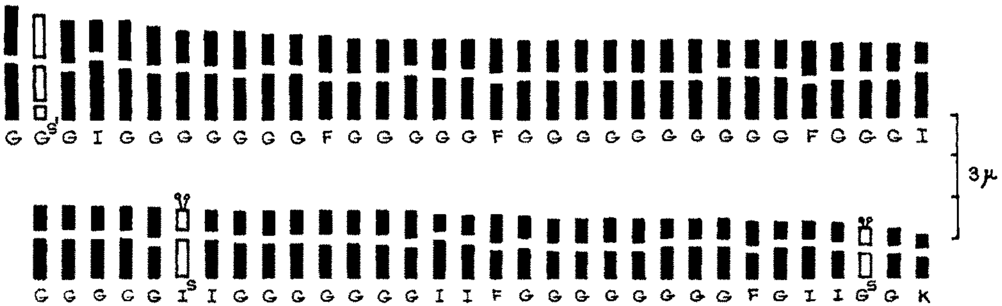
H. sabdariffa also contains 72 chromosomes in its complement. The chromosomes are a little longer in size (range 2.25 µ to 0.78 µ; mean length 1.54 µ) than the chromosomes of *H. lobatus*. The presence of two pairs of SAT-chromosomes and low TF% (39.50) shows the evolved nature of the karyotype.

Amongst all the species of *Hibiscus* studied presently, H. mutabilis exhibits the most advanced type of karyotype (Fig. 159), since it has highest chromosome number 2n = 120, and 3 pairs of SAT chromosomes and 3 pairs of secondarily constricted chromosomes (Fig. 159). However, the TF% is 39.22 .

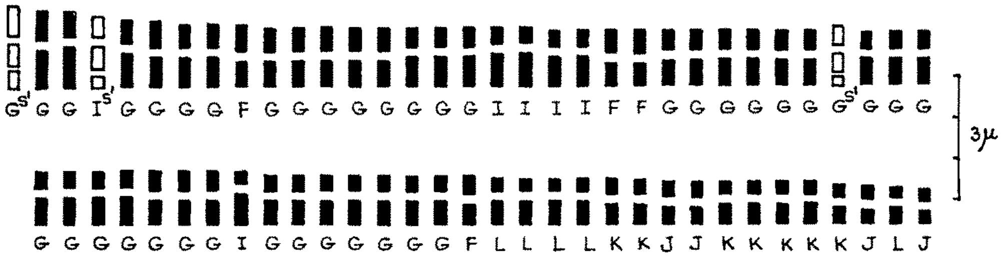
The cytological studies made in the genus Abelmoschus by quite a few workers (viz. Skovsted, 1935; 1941; Medvedeva, 1936; Purewal and Randhawa, 1947; Joshi and Hardas, 1953) show different chromosome numbers. They vary from 2n = 66 to 2n = 132. The two species studied presently under the genus Abelmoschus exhibit 2n = 130 chromosomes, which is a multiple of 13. Both the species show a graded nature of the karyotype. Since TF% is more (42.75 in A. angulosus and 42.08 in A. manihot), the karyotypes are symmetrical in both the species. However, short chromosomes and high chromosome number revealed the evolved nature of the genus. As complement of A. manihot contains comparatively shorter chromosomes (range 1.80 μ to 0.68 μ; mean length - 1.13 μ) than that of A. angulosus (range 2.55 μ to 0.94 μ; mean length 1.60 μ) and more number of chromosomes with nearly sub-median centromeres, it can be considered more evolved than A. angulosus (Fig. 160).

Fig. 160 - Idiograms of :

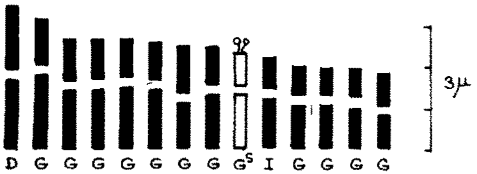
Abelmoschus angulosus, A. manihot,
Pavonia patens, P. zeylanica,
Urena lobata and Malachra capitata.



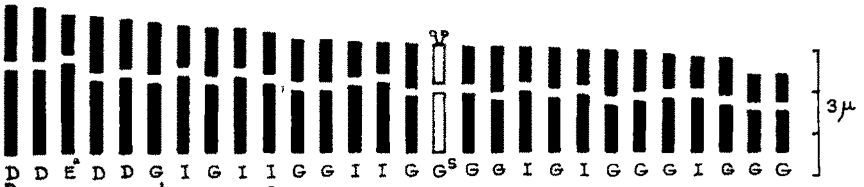
Abelmoschus angulosus Wt. & Arn. COLL. NO. 52



Abelmoschus manihot (Linn.) Medic. COLL. NO. 8

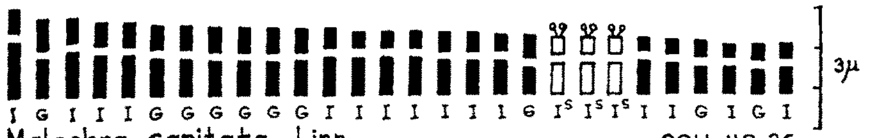


Pavonia patens (Andr.) Chiov. COLL. NO. 16



Pavonia zeylanica Cav. COLL. NO. 40

Urena lobata Linn. COLL. NO. 29



Malachra capitata Linn. COLL. NO. 36

Tribe Ureneae :

Homogeneity in the chromosome numbers of different genera under the tribe is noticed in the present work as well as in the earlier investigations (Skovsted, 1935; 1941; Bates, 1967; Kootin-Sanwu, 1969; Hazra and Sharma, 1971). Three genera studied here show multiple of 7 chromosome numbers.

The 2 species of *Pavonia* studied show different chromosome numbers viz. $2n = 28$ in *Pavonia patens* and $2n = 56$ in *P. zeylanica*. The karyotypes of both the species resemble each other in their gross morphology and in having a pair of chromosomes with satellites (Fig. 160). *P. zeylanica* appears more advanced than that of *P. patens* due to the higher ploidy level and less TF% (39.38 - Table X).

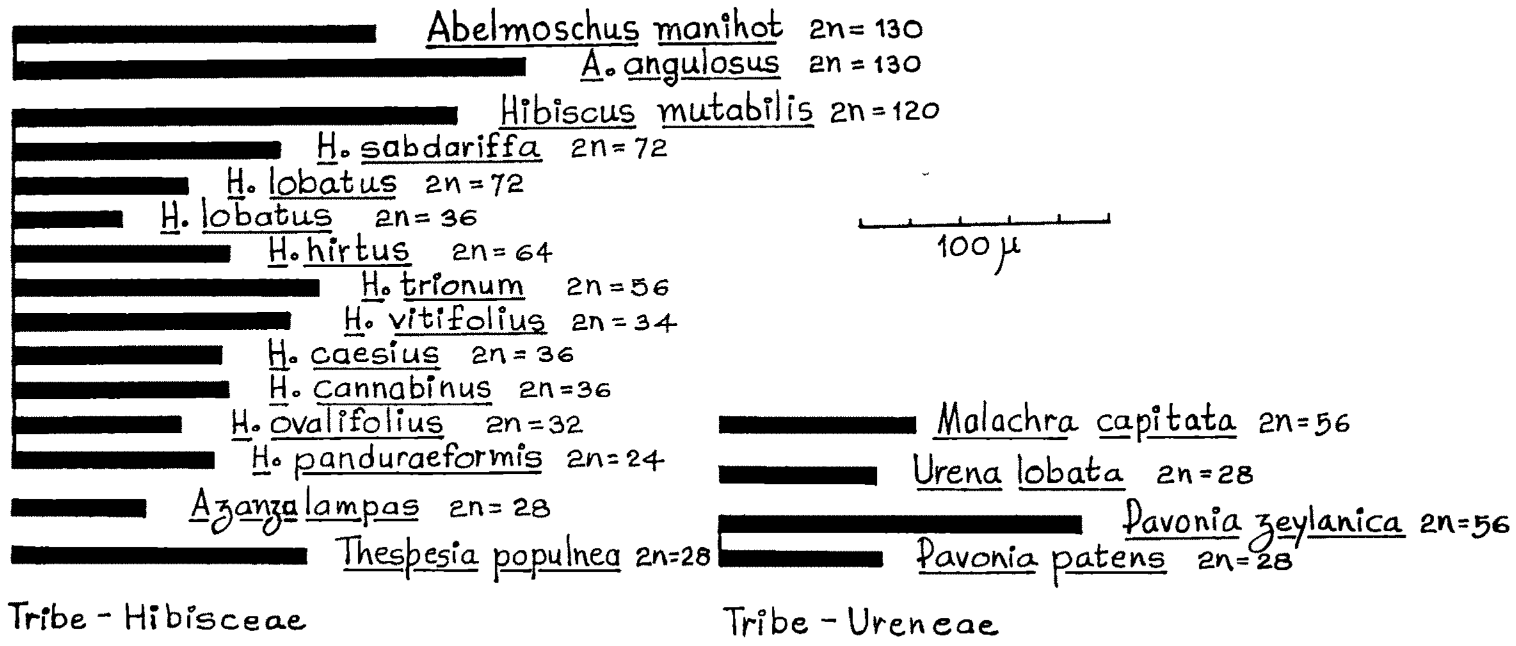
The somatic complement of *Urena lobata* also contains 28 chromosomes. The karyotype of this species resemble with that of *Pavonia patens* in having the same chromosome number and size. The advanced nature of *Urena lobata* is evidenced by the presence of a pair of SAT-chromosomes and a pair of secondarily constricted chromosomes. Occurrence of β-chromosomes in *Urena lobata*

(Coll. No. 29) further showsthe evolved status of the species.

The chromosome number of *Malachra capitata* is 2n = 56. As the karyotype has more number of nearly sub-median types, 3 pairs of SATs (Fig. 160), low TF% (36.89 - Table X) and comparatively shorter chromosomes, the species can be considered most evolved than other members studied presently under the tribe Ureneae.

Both the tribes show differences in the chromosome number, morphology and represent primitive to advanced type of karyotypes. In the tribe Hibisceae, the primitive nature is seen in the genus *Thespesia* (*I. populnea* Fig. 158) and evolved nature in the genus *Abelmoschus* (*A. manihot* Fig. 160). In the tribe Ureneae, the primitive nature is exhibited by the genus *Pavonia* (Viz. *P. patens* Fig. 160) and evolved nature by *Malachra* (*M. capitata* (Fig. 160). Thus, by karyomorphological observations, it is apparent that both these tribes must have diverged very early in the course of evolution. The members of the tribe Ureneae show karyotypes, which are less evolved than those of the tribe Hibisceae, as they have lesser chromosome

Fig. 161 - Histograms of different species showing absolute length of the chromosomes.


Abelmoschus manihot 2n= 130
A. angulosus 2n = 130
Hibiscus mutabilis 2n=120
H. sabdariffa 2n=72
H. lobatus 2n=72
H. lobatus 2n= 36
H. hirtus 2n= 64
H. trionum 2n=56
H. vitifolius 2n=34
H. caesius 2n= 36
H. cannabinus 2n=36
H. ovalifolius 2n=32
H. panduraeformis 2n=24
Azanza lampas 2n= 28
Thespesia populnea 2n=28
100 μ
Malachra capitata 2n=56
Urena lobata 2n=28
Pavonia zeylanica 2n=56
Pavonia patens 2n=28
Tribe - Hibisceae
Tribe - Ureneae

HISTOGRAMS

numbers in their somatic complements (viz. 2n = 28 and 56). It is probable that, polyploidy has not played that significant role in the tribe Urenae as in the case of Hibisceae, in the evolution of various taxa of the tribe.

The total chromatin length of different species of the tribes Hibisceae and Ureneae are shown in histograms (Fig. 161).

The meiosis is regular in most of the taxa analysed. However, a few irregularities like laggards in anaphase and telophase I and II, irregular distribution at anaphase I and non-congressional bivalents, secondary association of bivalents at metaphase I are noticed in a few species. Secondary association of bivalents was observed in *H. sabdariffa* (Fig. 20); *H. panduraeformis* (Fig. 92); *H. vitifolius* (Fig. 38) and *H. ovalifolius* (Fig. 75) under the tribe Hibisceae and in *Urena lobata* (Fig. 145) under the tribe Ureneae. The secondary association of bivalents commonly observed are the groups of 5, 6, 7 and 8. If the theory of secondary association with the maximum grouping is considered a reliable check of the phylogeny of the species, then the ancestral form of these genera and species would be supposed to contain 5, 6, 7 and 8 chromosomes in the haploid set from which further evolution might have taken place by polyploidy. The presence of secondary association and absence of multivalent formation in the species studied, indicate that they represent ancient polyploids.

Regarding the basic number for the family Malvaceae, different workers, working with different genera and species have expressed their views which are not unanimous.

Davie (1933) visualised divergent line of origin of different genera and species from a common ancestral type with a basic number of 7. This was supported by Wanscher (1934). Skovsted (1935) also supported the polyphyletic course of evolution of the family. He believed that the evolution of different members in the family has taken place not from a common ancestral type as suggested by Davie, but from more than one prototype and chromosome numbers 5, 6 and 7 all must have taken part in the evolution of polyploidy. The five series of chromosome numbers (7, 5, 6, 11 and 13) recognized by him have originated from the different prototypes.

Hazra and Sharma (1971) also consider, 7 to be deep seated in many genera of the family. According to them this basic number 7 is presumably derived from the basic set of 6 (Thespesia populnea), which was then adopted for evolution in different directions in the family and as such X = 7 has become the most prevalent number. Other numbers found within the family have been derived from secondary basic number of 7.

According to Bates and Blanchard (1970) the significant basic number in the tribe Malveae are X = 7, 6 and 5, which must have originated through aneuploidy reduction from basic set of X = 8. From these basic numbers, once established, further course of evolution is followed through euploidy and aneuploidy. Thus, the polyphyletic view point is also supported by this work. Further these basic numbers are supported by Gajapathi (1962) in Abutilon (X = 7 and 8) and Adhikari (1963) in Sida (X = 7). According to Hazra and Sharma (1971 a) of the three basic numbers observed (X = 7, 8 and 9) in the genus Sida, number 7 is more deep seated.

Sharma and Sharma (1962) based on the study of 27 species of the genus Hibiscus, have opined that the existence of all series of chromosome numbers, so far reported are closely related to each other and none of them can be regarded as representing a distinct series. Of the different chromosome numbers, 7, 8 and 15 are more adopted and found in majority of the species.

Menzel and Wilson (1963) based on meiotic studies of the genus Hibiscus - Sect.Furcaria, have suggested 18 as the effective basic number, which has been also observed by Bates (1965) and Kachecheba (1972). The ancestral base number of which could be 6 (Skovsted, 1941) or 9 (Darlington and Wylie, 1955). Of the two, 6 has been supported as an ancestral basic number by the pachytene analysis of H. cannabinus by Menzel (1966).

In the present work, varied chromosome numbers are metwith in different genera and species. All the three genera of the tribe Ureneae and 2 genera (Thespesia and Azanza) and 1 species of Hibiscus (H. trionum) in the tribe Hibisceae studied, show multiple of 7, while in other species of the genus Hibiscus, multiple of 6 and 8, and in the genus Abelmoschus multiple of 13 are noticed. As multiple of 7 is observed in genera of both the tribes, number 7 can be considered more deep seated in the family.

The other numbers are presumably derived from the basic set of 7 by aneuploid, reduction or duplication. The number 2n = 24 in the complement of *H. panduraeformis* is multiple of 6. The karyotype of this species also exhibit a primitive nature. This observation raises a feeling about considering 6 as the basic number, which might have been derived from basic set of 7 by aneuploid reduction (7-1). However, further investigation in this direction can only clarify the situation.

Part of this work is published in a paper entitled "Cytotaxonomy of Malvaceae I. Chromosome number and karyotype analysis of *Hibiscus*, *Azanza* and *Urena*". Cytologia 41 : 207 - 217, 1976.

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