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Studies on the cytotaxonomy of a few important medicinal plants of Ranchi, Jharkhand

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Abstract : Karyotype analysis has been widely employed in cytotaxonomy in describing the phylogeny, evolution and interrelationships of taxa. The present study provides karyotype analysis on various medicinally important plants of Ranchi. Some of the medicinal plants showed uniformity in their diploid chromosome content. They also differed from each other in their total chromatin length, arm ratio and position of centromere.

Key words: . Cytotaxonomy, Phylogeny, Chromatin length.

INTRODUCTION

Jharkhand, a state of India is a treasure of flora, fauna and mineral wealth. The state has 27% of forest area which is a rich source of medicinal plants. The forest area cover more than 600 valued medicinal plant species out of which about 150 are of greater medicinal importance. Medicinal plants are the local heritage of Jharkhand with global importance. The people of villages of this state are mainly dependent on the herbal medicines, which are prepared by different parts of the plants. Traditional medicines which includes Ethno-medicine (WHO 1978) is important and it provides health services to 75% to 80% of the world's population.[1] Many plant derived drugs employed in modern medicine were discovered through ethno-botanical investigations.

The study of chromosome is important as it has advanced far from the initial stages of chromosome counts after a laborious processing. Since the chromosomes are bearer of genes, the ultimate units of heredity, a study of gene expression necessarily involves the handling and observation of chromosomes. The contribution of cyto-genetics and breeding to human welfare are rooted in the knowledge of their chromosomes. The study of structural and behavioural pattern of chromosomes has eliminated most of the pitfalls in the tedious process of breeding leading to revolution in food, fodder and fodder production.

Karyotype analysis is widely employed in cyto-taxonomy in describing the phylogeny, evolution and interrelationships of taxa in plant kingdom. The effect of different physical and chemical agents on chromosomes are utilized in various ways. Applications of chromosome study are of use in breeding practices, raising new forms, monitoring for environmental mutagens identifying syndromes due to chromosomal abnormalities, identifying carriers of such diseases. The study of karyotype is of great value in modern taxonomy. Its importance as a taxonomic character of a plant species has been very well established. The concept has been reviewed[1] and connected with karyotypes and their evolution. In a large number of plant species karyotypic data have been effectively employed to resolve taxonomic status and for authentic genotypic identification.

MATERIALS AND METHODS

During the prepration of chromosome atlas of medicinal plants of Jharkhand (UGC's minor research

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project) following important plants were selected for cytological studies and karyotype analysis : *Allium cepa* L. (onion,pyaaz), *A.cepa* L. var. desi white, *A.cepa* var. white round, *Allium sativum* L,(garlic), *A. sativum* L. var. large clove garlic, *Allium ascalonicum* L. var. single clove garlic, different important species of *Aloe* Grithakumari—*A. abyssinica* Lam. *A.barbadensis* Mill. *A. plicatalis* (Sensu Bose and chowdhury,1991), *A. harlana* (Sensu Bose and Chowdhury, 1991), *A. distance* Haw. *A. variegata L. Asparagus plumosus* Baker (*Asparagus* fern), *Asparagus racemosus* Willd (satawar), five ecotypes of *Acorus calamus Catharanthus roseus* (sadabahar),*Chlorophytum* (safed musli), *Cymbopogon flexuosus, C. flexuosus* var. RRL-16, *C. flexuosus* var. Local, *C. martini* var. Motia, *C. martini* var. Sofia, *Iberis amara* (bitter candytuft) *Lycopersicon esculentum* Mill var. Pusa Early Dwarf, *L. esculentum* Mill var. Local variety, *L. esculentum* Mill var. Selection 22, *L. esculentum* Mill. var. Pusa Ruby, *L. esculentum* Mill. var. Punjab Kesari, *L. esculentum* Mill. Var. Selection 18, *Stevia rebaudiana* Bertoni var. 123, var. 128, var. 512, *Trigonella foenum-graecum* var. *Zea mays* L. var. Pop corn, *Z. mays* L. var. KH-9451, *Z. mays* var. Shanker, *Z. mays* L. var. K-51, *Z. mays* L. var. DMH-849, *Z. mays* L. var. Baby corn, *Z. mays* L. var. K-99, *Z. mays* L. var. Proagro-4212, *Z.. mays* var. Super gold-651, *Z. mays* L. var. Ganga safed-2, *Z. mays* L. var Sweet corn.

The mitotic studies were performed by fixing the root tips. The roots were taken either from the germinating seeds or from the bulbs or rhizomes or from the ovary wall. The slides were prepared by standard squash technique. Well separated metaphase stages were photographed by Digital SLR camera. The data were analysed statistically.

RESULTS AND DISCUSSION

The stability of the genus depends upon its consistency in the chromosome number. The chromosome numbers of the above medicinal plants are almost constant except different species of *Aloe, Chlorophytum* and *Cymbopogon* (table1, fig 1- 12). The uniformity in diploid chromosome complement (2n =16) was recorded in all the species and varieties of *Allium cepa* and *Allium sativum*. This indicates the stability of the genus. The interrelationships among the species and varieties are determined on the basis of total chromatin length. Maximum TLC recorded in *Allium cepa* L. Desi white considers it most primitive and lowest TLC shown by *Allium ascalonicum* L.considers it most advanced among those investigated, because of tailoring of the superfluous chromatin material, reciprocal translocation as wellas para and pericentric inversions in these species.[2-3]

The constancy in the chromosome number of *Aloe* have not been reported. The three species *Aloe abyssinica* Lam., *A.barbadensis* Mill. and *A.plicatalis* showed symmetry in the chromosome complement whereas, *A.harlana, A. distance* exhibited auto triplody whereas, *A. variegata* L. reported autotetraploidy. Thus there was asymmetry in the chromosome number (fig-). Earlier scientists have reported polyploidy and aneuploidy in this genera.[4-9]

The greatest diversity of karyotypes are found in a single family of plants, that is the Liliaceae.[2] *Aloe* comprises eight long and six short chromosomes. Centromere of all the species investigated are sub terminal to sub median showing that these species had highly asymmetrical and bimodal karyotype.[10,3,11] In the present investigation *Aloe harlana* is primitive having greatest chromatin length and *Aloe.distance* Haw. is advanced having the lowest chromatin length.

Two species of *Asparagus, A.racemosus* Willd *and A.plumosus* baker exhibited the uniform chromosome number 2n = 20 indicating that they are stable and not show any polyploidy series. Though the two species have the same chromosome number, but their karyotypes are different. *Asparagus plumosus* Baker had ten long chromosomes and ten short chromosomes. All of them were nearly sub-terminal except one, which was nearly sub median. The two species under consideration having the same chromosome number differ in karyotype, indicating that structural changes have played a significant role in evolution of these species. The greater chromatin length in *A. racemosus* Willd. confers to be primitive than *A.plumosus* Baker.[2]

Acorus calamus L. of family Acoraceae with 5 ecotypes were taken. The basic chromosome number varied from $x = 7$ and $x = 9$ and thus the genus *Acorus* was unstable. The changes in the normal haploid

chromosome number of chromosomes indicates that aneuploidy have played a major role in evolution. Different varieties of *A. calamus* L. having asymmetrical karyotypes were considered advanced which confirms the previous findings.[12] In the above ecotypes of *Acorus calamus* L. the karyotypes were analysed for the first time and the chromosome numbers are in confirmity with the previous reports.

The chromosome number of different varieties of *Catharanthus roseus* and *C.pusillus* have been reported as 2n = 16 and the basic chromosome number 2n = 8. This indicated that all of them were highly stable.[13-18] All the varieties of *Catharanthus roseus* except two and *Catharanthus pusillus* consisted nearly median and nearly submedian chromosomes which bring them to the line of nearly asymmetrical karyotypes. The assessment of evolutionary tendencies indicated that *Catharanthus pusillus* was more primitive than others as here all the eight chromosomes were nearly median type and it had maximum total chromatin length.

The six species and varieties of *Chlorophytum* investigated for cytological analysis. All the six species and varieties of *Chlorophytum* were noticed with same tetraploid chromosome number 2n = 4*x* = 28 having the basic chromosome number *x* = 7. It exhibited a high tendency of polyploidy and therefore, polyploidization have played a significant role in evolution of this genus. The chromosomes were long and medium in size based on their relative lengths and geographical distribution. The karyotype of all the six species and varieties showed nearly median, nearly sub median and nearly sub terminal chromosomes. It appears that there is over all symmetry in majority of chromosomes. In the present investigation since sub metacentrics were very high in number, they did not generate sub telocentrics or telocentrics through fusion and fission of chromosome segments. This helps us to believe that structural alterations of chromosomes have played little role in speciation and evolution of the genus.

The satellite chromosomes were observed in both the varieties of *Chlorophytum borivilianum* and *C.tuberosum.* Secondary constrictions are good markers which enables to understand the morphology of chromosomes. The number of nucleoli present are proportional to number of SAT regions of the cell.[19] On the basis of total chromatin length *Chlorophytum borivilianum* var. white flowers was considered most primitive as it consists maximum total chromatin length. Whereas, *Chlorophytum laxum* was considered most advanced having minimum total chromatin length.

Variation in total chromatin length might be due to loss of translocated segments formed due to asymmetrical changes. The increase in total chromatin length might be due to large amount of DNA with "non sense" sequences having no adaptive value.[2] Asymmetrical karyotypes are considered advanced over symmetrical karyotypes.[20] Among all the species and varieties of *Chlorophytum* under consideration, the lowest gradient value (12.87) was recorded in *Chlorophytum laxum* which may be considered most advanced. The detailed cytotaxonomical studies of all the species and varieties of *Chlorophytum* under consideration are being reported for the first time from Ranchi, Jharkhand. Earlier findings also confirms the results.[21,22]

All the species and varieties of *Cymbopogon* under consideration showed a different chromosome number. *C. fiexuosus, C. flexuosus* var. RRl-16, *C. flexuosus* var. Local and *C. martinii* var. Motia showed are diploid chromosome numbers 2n = 2*x* = 20 and *C. martinii* var. sofia showed tetraplod chromosome number 2n = 4*x* = 40 having the basic chromosome number x = 10.[23] The chromosomes were smaller in size in all the species and varieties but little variation existed in shape and size of individual chromosomes. The karyotypes of species and varieties of *Cymbopogon* showed nearly median, nearly sub-median chromosomes in high proportion while sub-median chromosomes were very few in number.[24] Presence of nearly median and sub median chromosomes in high proportion indicates the symmetrical nature of the karyotype. The species and varieties of *Cymbopogon* having greater number of meta centrics and telocentrics chromosomes should be considered as more advanced than those in which there are lesser number of sub metacentric and telocentric chromosomes.[3]

Studies indicate that *C. flexuosus* var. Local was more advanced having sub median and nearly sub median chromosomes, while *C. martini* var. Motia was considered more primitive since it consisted the highest number of

nearly median chromosomes. Secondary constrictions were present only in *C. martinii* var. Motia and was absent in rest of the species and varieties of *Cymbopogon*.[23]

Total chromatin length was found maximum in *C. martini* var. Sofia thus considering it most primitive whereas, *C. flexuosus* was considered most advanced having minimum total chromatin length. Variation in total chromatin length among the species and varieties of *Cymbopogon* might be due to the loss of translocated segments found during asymmetrical exchanges.

Somatic chromosome number and detailed karyotype analysis were carried out in two varieties of *Iberis amara* var. Hyacinth flowered and var. Iceberg. The basic chromosome counts observed 2n = 2*x* = 14 in the ovary wall were very small and the total chromatin length was 2.07 in var. Hyacinth flowered and 1.33 in the variety Iceberg. The haploid chromosome complement consisted only median, nearly submedian and subterminal chromosomes. The earlier findings also confirms the chromosome number as well as smaller size of the chromosomes.[25,26] This indicates their symmetrical nature.[2,24] Among the two varieties Iceberg contained moderately asymmetrical karyotype thus it was considered advanced than Iceberg.[20]

The karyo morphological data of the six varieties of *Lycopersicum esculentum* Mill is a cytological assemblage with a basic chromosome complements n = 12. This indicates that all the varieties under consideration were highly stable. However in the var. Selection 22 some of the cells with triploid chromosomes were observed. A review of literature indicated that the genus *Lycopersicon* exhibited lesser tendency of polyploidy and therefore polyploidization have not played any significant role in evolution. The lowest chromatin length observed in the variety Pusa Early Dwarf was considered most primitive and the variety Selection 18 was considered most advanced having lesser chromatin length. The variation in total chromatin length in different varieties of *Lycopersicon esculentum* Mill may be caused due to the loss or gain of translocated segments formed during changes. However,[27] the increase or decrease in total chromatin length cannot be considered a criteria for primitiveness and advancement but the amount of DNA per genome can increase or decrease during the course of evolution. The karyotypic difference among the varieties were quite distinct. The chromosomes were smaller in size and all the varieties under consideration showed nearly sub median type of chromosomes. The varieties having greater number of sub median chromosomes should be considered advanced than those in which there are lesser number of sub meta centrics.[2]

Karyotype analysis in many genera and species of compositae have been reported earlier but the detailed karyo morphological analysis for the three varieties of *Stevia rebaudiana* Bertoni var. SRB-123, var. SRB-128, var. SRB-512 is being reported for the first time from Ranchi, Jharkhand. The genus *Stevia* shows much variation in chromosome number. But the data from the present findings indicate that all the three varieties of *Stevia rebaudiana* Bertoni were diploid with 2n = 2*x* = 22 chromosomes. Cytological investigations on the genus *Stevia* from different countries reported[28] its basic chromosome number as *x* = 11, 12, 17.

The constancy in the diploid chromosome complements indicate that these varieties were highly stable. The chromosomes of all the three varieties were very small and proportion of nearly median chromosomes were higher than nearly submedian. This indicates the relatively symmetrical nature of the karyotype. The above parameter in the assessment of evolutionary tendencies indicates that var. SRB-123 was more advanced than rest of the varieties since it consisted highest number of nearly submedian type of chromosomes.

Satellite chromosomes were completely absent in all the three varieties. Maximum total chromatin length was observed in the variety SRB-123 thus considering it most primitive and the variety SRB-128 as advanced because it was reported with minimum total chromatin length.

The analytical data of *Trigonella foenum-graecum* L. shows that all the twelve varieties under consideration[17,29] have 2n = 16. This indicates that all the varieties under consideration were highly stable so far the chromosomes were considered. The constancy in chromosome number observed is suggestive that aneuploidy changes have not played any major role in evolution of varieties. The chromosome of twelve varieties of *Trigonella foenum-graecum* L were long and medium sized, based on their length. There were nearly median and nearly sub terminal

chromosomes in most of the varieties. Presence of median and subterminal chromosomes indicates the symmetrical nature of karyotype. The varieties of *Trigonella foenum-graecum* L.containing greater number of nearly subterminal and submetacentric chromosomes should be considered more advanced than those where there are lesser number of sub metacentrics and telocentric chromosomes. Maximum total chromatin length was observed in the variety South local thus considering it most primitive among the twelve varieties under consideration. These findings have been confirmed earlier.[30-32]

The essential uniformity in the gross features of the karyotype of eleven different varieties of *Zea mays* are clearly evident by the comparative karyo morphological studies. The ten pairs of chromosomes of maize can be distinguished from each other by the combination of their relative lengths, arm ratio and cytological markers such as satellite on the chromosomes. The data from the present finding indicate that all the varieties under consideration were diploid 2n = 2*x* = 20. All the varieties were stable and tendency of polyploidy has not been reported. The chromosomes of all the varieties were of medium and small size based on their relative length. The haploid chromosome complement reported were nearly median and sub median in high proportion whereas, sub telocentrics were rare. This indicates the symmetrical nature of the karyotype.[2] The assessment of evolutionary tendencies indicated that *Zea mays* var. Shanker was more advanced than rest of the varieties since it consisted maximum number of nearly sub median and nearly sub terminal chromosomes while *Zea mays* var. Pop corn and var. Proagro-4212 was considered most primitive as there were eight chromosomes of nearly median type. These alterations take place through different chromosomal aberrations. Satellite chromosomes were absent in all the varieties of *Zea mays* under consideration which might be due to subsequent loss during evolution. Considering the total chromatin length it was reported that the maximum TLC was observed in *Zea mays* var. Pop corn and it was considered most primitive while the variety K-99 depicted minimum TLC and was considered most advanced. The variation in total chromatin length might be due to the loss or gain of translocated segments formed during asymmetrical changes.

Table-1 : Data related to karyotype of a few important medicinal plants of Ranchi

Species and varieties under consideration	TCL (μ)	Chromosome number	Karyotypic formula
1. *Allium cepa* L.	99.86	2n = 2*x* = 16	1 mc + 4 smc + 3 tc
A. cepa L. var. Desi white	99.97	2n = 2*x* = 16	1 mc + 5 smc + 2 tc
A. cepa L. var. White round	66.95	2n = 2*x* = 16	7 smc + 3 tc
2. *Allium sativum* L.	99.98	2n = 2*x* = 16	1 mc + 5 smc + 2 tc
A. sativum var. Large clove garlic	99.96	2n = 2*x* = 16	1 mc + 3 smc + 4 tc
A. ascalonicum var. Single clove garlic	63.46	2n = 2*x* = 16	1 mc + 3 smc + 4 tc
3. *Aloe abyssinica* Lam.	67.97	2n = 2*x* = 14	8L + 6S – 4L (nsm) + 4L (nst) + 6S (nsm)
A. barbadensis Mill.	74.37	2n = 2*x* = 14	8L + 6S – 2L (nsm) + 6L (nst) + 4S (nsm) + 2S (nst)
A. plicatalis	74.40	2n = 2*x* = 14	8L + 6S – 2L (nsm) + 6L (nst) + 4S (nsm) + 2S (nst)
A. harlana	88.27	2n = 3*x* = 21	12L + 9S – 12L (nst) + 9S (nsm)
A. distance Haw.	59.33	2n = 3*x* = 21	12L + 9S – 12L (nsm) + 3S (nst) + 6S (nsm)
A. variegata L.	72.80	2n = 4*x* = 28	16L + 12S – 8L (nsm) + 8L (nst) + 12S (nsm)
4. *Asparagus plumosus* Baker	21.04	2n = 2*x* = 20	2 nsm + 18 st
A. racemosus Willd	23.77	2n = 2*x* = 20	2 nm + 10 nsm + 8 nst
5. *Acorus calamus* L. var. Palandu I	9.92	2n = 2*x* = 14	6 nsm + 1 nst
A. calamus L. var. Palandu II	11.93	2n = 2*x* = 18	2 nm + 3 nsm + 2 nst + 2 t
A. calamus L. var. Palandu III	12.80	2n = 2*x* = 14	1 sm + 2 nsm + 2 nst + 2 t
A. calamus L. var. Palandu IV	7.65	2n = 2*x* = 14	4 nsm + 3 t
A. calamus L. var. Namkum Collection	13.40	2n = 2*x* = 14	1 nm + 4 nsm + 2 nst

Table 1 continued....

Table 1 continued....

Species and varieties under consideration	TCL (µ)	Chromosome number	Karyotypic formula
6. *Catharanthus roseus* var. White flower	21.25	2n = 2*x* = 16	2 nst + 10 nsm + 4 nm
C. roseus var. Deep pink flower	21.23	2n = 2*x* = 16	2 nsm + 12 nm + 4 m
C. roseus var. Pink flower with yellow eye	17.12	2n = 2*x* = 16	4 nsm + 10 nm + 2 m
C. roseus var. Pink flower	16.84	2n = 2*x* = 16	14 nsm + 2 nm
C. roseus var. Light pink flower	15.77	2n = 2*x* = 16	4 nsm + 12 nm
C. roseus var. White flower with red eye	14.54	2n = 2*x* = 16	6 nsm + 10 nm
C. pusillus	28.07	2n = 2*x* = 16	16 nm
7. *Chlorophytum borivilianum* var. White flowers	91.56	2n = 4*x* = 28	6 nm + 20 nsm + 2 sm
C. borivilianum var. Purple flowers	59.64	2n = 4*x* = 28	4 nm + 20 nsm + 2 sm + 2 nst
C. tuberosum	74.76	2n = 4*x* = 28	4 nm + 22 nsm + 2 nst
C. comosum var. Green leaves	62.28	2n = 4*x* = 28	16 nm + 12 nsm
C. comosum var. Striped leaves	60.64	2n = 4*x* = 28	14 nm + 14 nsm
C. laxum	41.64	2n = 4*x* = 28	14 nm + 14 nsm
8. *Cymbopogon flexuosus*	9.02	2n = 2*x* = 20	5 nm + 4 nsm + 1 sm
C. flexuosus var. RRL-16	36.75	2n = 2*x* = 20	6 nm + 4 nsm
C. flexuosus var. Local	24.75	2n = 2*x* = 20	8 nsm + 2 sm
C. martini var. Motia	40.30	2n = 2*x* = 20	10 nm
C. martini var. Sofia	42.65	2n = 4*x* = 40	7 nm + 1 nsm + 2 sm
9. *Iberis amara* L. var. Hyacinth flowered	2.07	2n = 2*x* = 14	2 nm + 5 nsm
I. amara L. var. Iceberg	1.33	2n = 2*x* = 14	1 nm + 4 nsm + 2 nst
10. *Lycopersicon esculentum* Mill var. Pusa early dwarf	30.05	2n = 2*x* = 24	12 nsm
L. esculentum Mill. var. Local variety	28.01	2n = 2*x* = 24	12 nsm
L. esculentum Mill. var. Selection 22	27.85	2n = 2*x* = 24	12 nsm
L. esculentum Mill. var. Pusa ruby	24.48	2n = 2*x* = 24	11 nsm + 1 sm
L. esculentum Mill. var. Punjab kesari	24.42	2n = 2*x* = 24	12 nsm
L. esculentum Mill. var. Selection 18	20.92	2n = 2*x* = 24	12 nsm
11. *Stevia rebaudiana* Bertoni var. 123	26.05	2n = 2*x* = 22	14 nm + 8 nsm
S. rebaudiana Bertoni var. 128	19.50	2n = 2*x* = 22	12 nm + 10 nsm
S. rebaudiana Bertoni var. 512	23.85	2n = 2*x* = 22	10 nm + 12 nsm

Table 1 continued....

Species and varieties under consideration	TCL (μ)	Chromosome number	Karyotypic formula
12. *Trigonella foenum-graecum* L. var. Pant Ragini	30.95	2n = 2*x* = 16	4 nm + 3 nsm + 1 nst
T. foenum-graecum L. var. Hisar Mukta	28.15	2n = 2*x* = 16	3 nm + 5 nsm
T. foenum-graecum L. var. Hisar Suvarna	24.12	2n = 2*x* = 16	3 nm + 4 nsm + 1 nst
T. foenum-graecum L. var. Hisar Madhavi	21.81	2n = 2*x* = 16	4 nm + 4 nsm
T. foenum-graecum L. var. Lam Selection	19.32	2n = 2*x* = 16	1 nm + 6 nsm + 1 nst
T. foenum-graecum L. var. Hisar Sonali	24.66	2n = 2*x* = 16	4 nm + 4 nsm
T. foenum-graecum L. var. Co-1	23.12	2n = 2*x* = 16	4 nm + 4 nsm
T. foenum-graecum L. var. RMT-1	21.53	2n = 2*x* = 16	1 nm + 6 nsm + 1 sm
T. foenum-graecum L. var. GM-1	19.08	2n = 2*x* = 16	4 nm + 4 nsm
T. foenum-graecum L. var. NRCSS AM-1	23.71	2n = 2*x* = 16	2 nm + 5 nsm + 1 nst
T. foenum-graecum L. var. North Local	30.63	2n = 2*x* = 16	5 nm + 3 nsm
T. foenum-graecum L. var. South Local	36.27	2n = 2*x* = 16	4 nm + 4 nsm
13. *Zea mays* L. var. Pop corn	37.92	2n = 2*x* = 20	4 nm + 4 nsm
Z. mays L. var. KH-9451	27.18	2n = 2*x* = 20	12 nm + 6 nsm + 2 nst
Z. mays L. var. Shanker	25.20	2n = 2*x* = 20	6 nm + 12 nsm + 2 nst
Z. mays L. var. K-51	26.64	2n = 2*x* = 20	4 nm + 16 nsm
Z. mays L. var. DMH-849	24.58	2n = 2*x* = 20	8 nm + 12 nsm
Z. mays L. var. Baby corn	25.38	2n = 2*x* = 20	6 nm + 14 nsm
Z. mays L. var. K-99	21.66	2n = 2*x* = 20	2 m + 8 nm + 10 nsm
Z. mays L. var. Proagro-4212	26.76	2n = 2*x* = 20	16 nm + 4 nsm
Z. mays L. var. Super gold-651	23.40	2n = 2*x* = 20	6 nm + 14 nsm
Z. mays L. var. Ganga safed-2	29.46	2n = 2*x* = 20	12 nm + 8 nsm
Z. mays L. var. Sweet corn	23.88	2n = 2*x* = 20	6 nm + 14 nsm + 2 B's

Plate - I

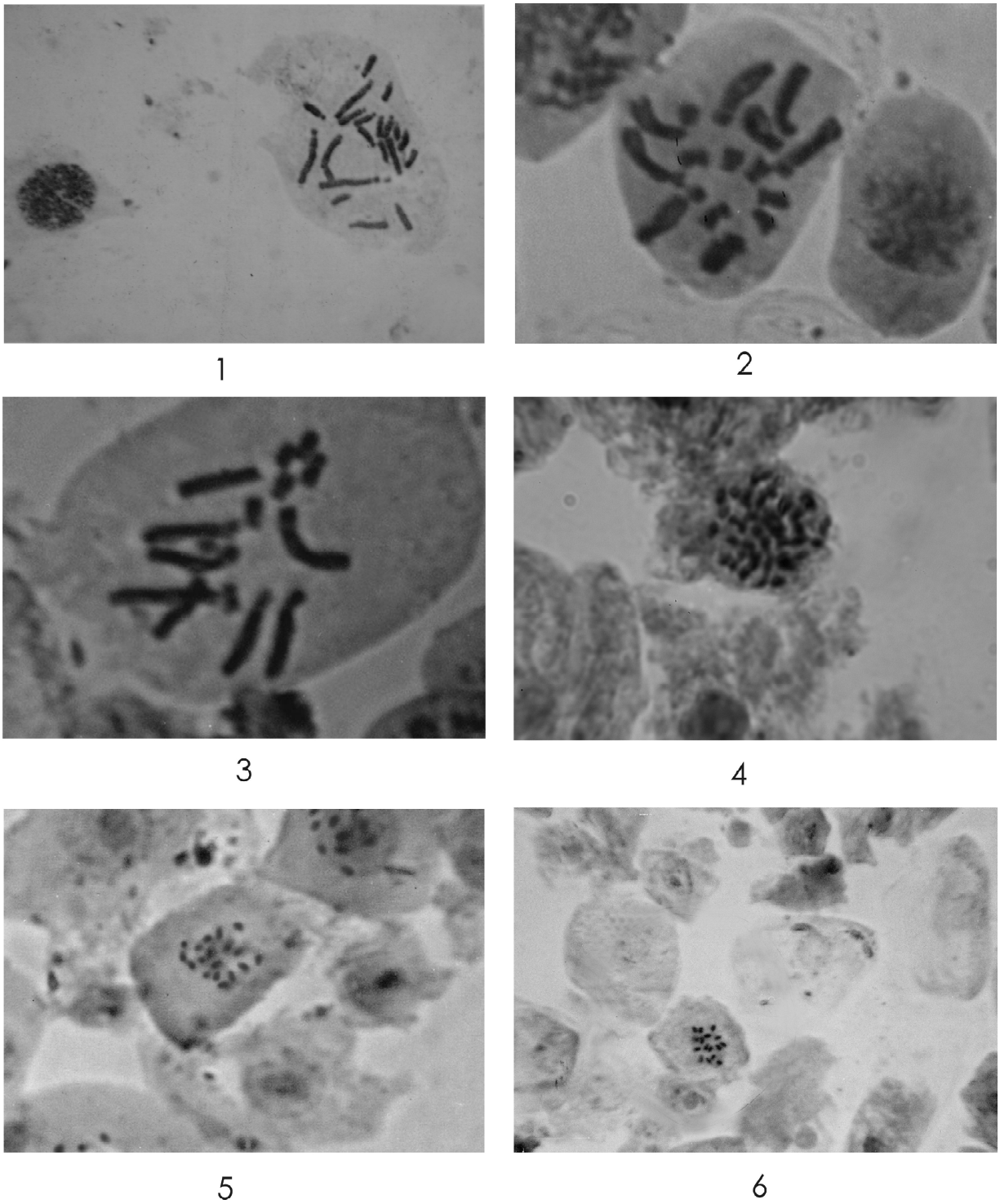

Fig.1-6 Microphotographs showing mitotic metaphase chromosomes of 1. Allium ascalonicum, 2. Aloe abyssinica 3. A.plicatalis, 4.Acorus calamus l.Palandu II, 5. Catharanthus pusillus 6.Catharanthus roseus Pink Flower.

Plate - II

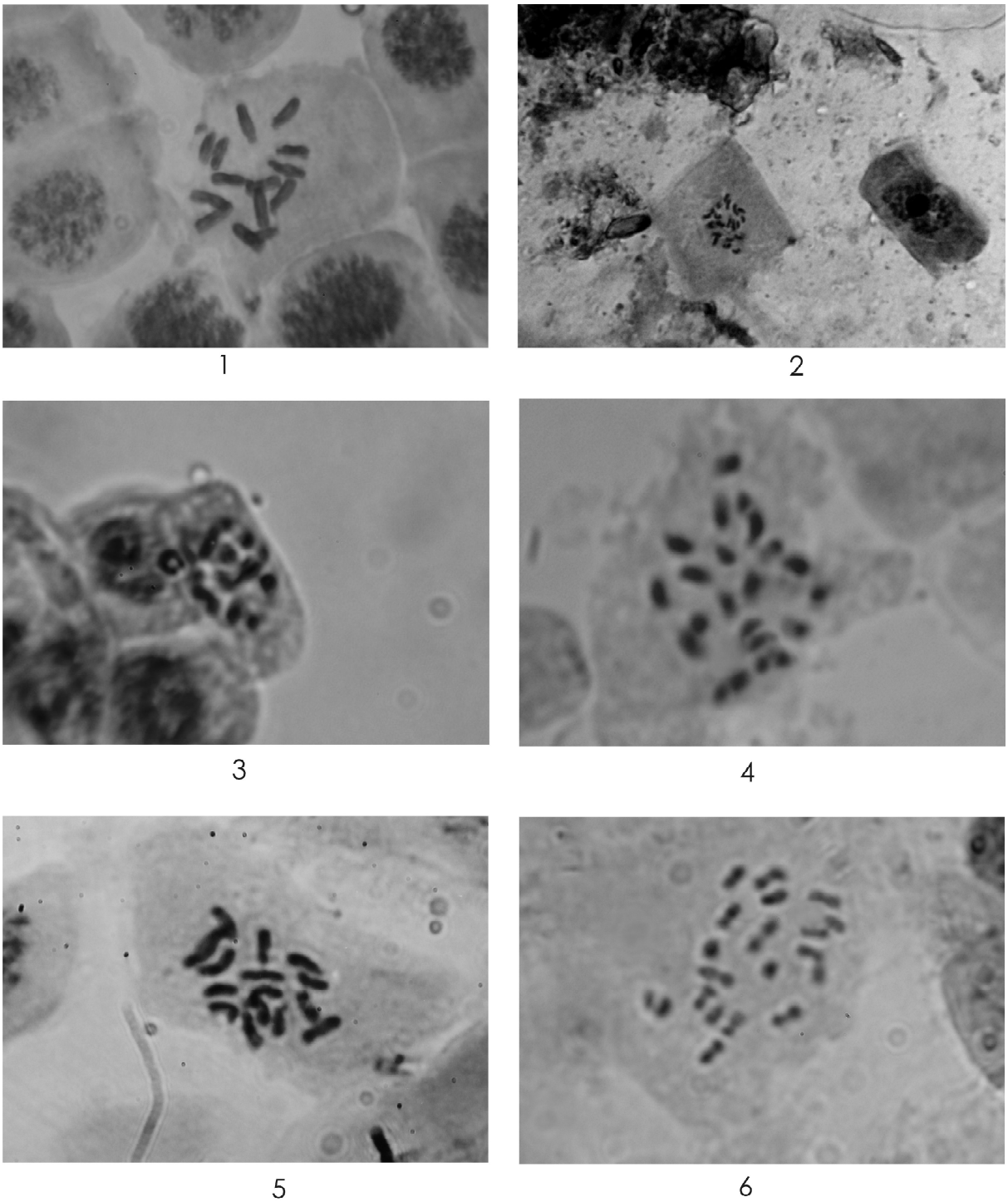

Fig.7-12. 7.Chlorophytum borivilianum White Flower, 8.Cymbopogon flexuosus var. local, 9. Iberis amara L. Var. Iceberg, 10. Stevia rebaudiana Bertoni var. SRB-123, Trigonella foenum graecum L.var. Hisar Mukta, 12.Zea mays L. Var. Pro agro.

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