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Biosystematics and Cytological Studies of Some West African Species of Commelina

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ABSTRACT
Biosystematics studies of some West African species of Commelina were investigated during this study. Samples for the study were collected from South Eastern part of Nigeria. The four species used were identified as Commelina congesta, C. diffusa, C. erecta and C. lagosensis. C. diffusa and C. congesta were diploid with 2n=2x =30 chromosomes; C. erecta was a polyploidy with 2n=4x=60 chromosomes and C. lagosensis had 2n=26 chromosomes. Both morphological and cytological studies point to the fact that C. congesta is ancestral to all other species. Karyotype studies showed wide variation in chromosome arm ratio of the species. Total volume of chromosome also differed significantly (P<0.05) between species. Karyotype differences were also observed between subspecies of C. diffusa. Cytological studies suggest that C. congesta is the probable ancestor of other species and had undergone a number of cytological changes such as; gross increase in chromosome size which led perhaps to the evolution of C. diffusa; reduction in chromosome number led to the evolution of C. lagosensis; while allopolyploidy led to the evolution of C. erecta.
Keywords: *Biosystematics, Commelina, Chromosome, Karyotype, Morphology*

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INTRODUCTION

Commelina is one of the commonest and most prevalent weedy plants in the south eastern Nigeria, located in the equatorial rainforest zone of West Africa. Wilson [1] recognized them as weed of the moist places. They grow best on road side drains, irrigation ditches, swampy or flooded areas and also on cultivated lands where they affect the yield of crops adversely. The plants are sprawling or straggling herbs. They root at the nodes and possess fibrous root systems. According to Bhattacharya [2] the distinguishing feature of these plants is the foliaceous spathe. In some cases these spathes contain mucilage especially in the rhizomatous types. With about 100 species, *Commelina* is the largest genus of Commelinaceae in Africa. At least 65 species occur in the combined areas of the Flora of Tropical East Africa (Kenya, Uganda, and Tanzania) and Flora Zambesiaca (Malawi, Mozambique, Zambia, Zimbabwe, and Botswana). About 19 species have been identified in Ethiopia and Eritrea including 2 undescribed species that are endemic to Ethiopia. *Commelina* is one of the genera of plants that has offered excellent material not only to the weed scientist for the study of weed problems but also to cytologists, taxonomists and evolutionists for the study of variation and speciation [3]. In Kenya, the mucilage in *C. benghalensis* is used for the treatment of burns and sterility in women and investigations are being carried out to see water content of the plant could be reduced in order to make them useful as forage crops. Some of the commonest members of the genus are *C. erecta, C. diffusa, C. lagosensis* and *C. congesta* of these four species, *C. diffusa* and *C. lagosensis* are the most prevalent types found on cultivated lands which cause major problem to farmers. In Ibibio, commelina are commonly called 'ikpa-ikpa-ikpa' meaning 'can never die. This is apparently because the plants adapt to varied environments and survive adverse conditions such as drought and bush fire [1]. Wilson [1] reported that Commelina had recently extended from tropics and subtropics, where they originated, to temperate zones in Europe and America. The aim of the study was to examined the possible difference in the morphology and chromosomes of different species of Commelina.

MATERIALS AND METHODS

Collection of plant samples

Four distinct species of Commelina and some of their subspecies were collected from Calabar and the nearby towns of Itu and Odukpani and were given accession numbers. They were cultivated at the University of Calabar, Botanical Garden. The plants were watered during the dry season.

Morphological studies

The morphological characters studied were the shapes of the leaves, spathes, the types of hairs on the leaf sheaths and the spathes, colour of petals and internodes and also the shape of the fruits. Measurements were carried out to determine the length of internodes, leaf sheaths, spathes, peduncle and pedicels. The areas of leaves, spathes, petals were also determined. At least ten observations for each character were made for each species and the subspecies.

Cytological studies

Root tips were collected between 8.00am and 11.00am from uprooted plants. This time range gave maximum number of cells at dividing stages.

Pretreatment

The root tips were placed in small samples bottles containing 0.002 molar solution of hydroxiquinoline [4] and kept in the refrigerator at about 10^0C for three to four hours.

Fixation

The root tips were removed from the pretreatment solution, washed for two to four times in distilled water and fixed in 1:3 acetic alcohols. The sample bottles were kept in the refrigerator for at least 24 hours.

Hydrolysis and staining

After fixing, the root tips were washed thoroughly with distilled water, then transferred into test tubes containing 1NHCl. The test tubes were then placed in a water bath at 60^0C for 20minutes. After the hydrolysis, the root tips were again washed thoroughly in tap water and then placed in small sample bottles containing Feulgen stain. These were kept in the dark for at least 2-3 hours. By this time the meristematic regions of the root tips had stained pink.

Squashing

With a pair of forceps the root tips were removed from Feulgen stain and 1-2mm of the tips were cut off and placed on a clean slide. A drop of aceto-orcein was placed on the root tip. This was then left for about a minute before a clean cover-slip was placed on it. With a match, the cover slip was tapped gently to spread the cells. The slide was then put within the fold of a filter paper and gentle thumb pressure was applied to spread the cells further and to keep the chromosomes on the same plane. The edges of the cover-slip were sealed with rubber solution and the slide was examined under the microscope. This gave the temporary slide.

Cells found to contain well spread chromosomes were drawn, the chromosomes in them numbered arbitrarily. The chromosomes were measured with the help of ocular micrometer and later calibrated with stage micrometer. This was done to determine the total length, the length of long and short arms of the chromosomes. The cells were finally photographed with Ashai Pentax camera on the Dialux 20 Leitz microscope. Ax3 magnifying lense was used during photography for greater magnification of the chromosomes. The volume of chromosomes was determined according to the method of Seal [5]. Seal measured the length and width of pachytene chromosome of Festuca for the determination of chromosome volume. Analysis of variances was carried out on the total length, volume and the arm ratio of the chromosomes to determine whether there were significant differences at 5% probability level between the strains, and species while least significant difference test was used to separate significant mean.

RESULTS

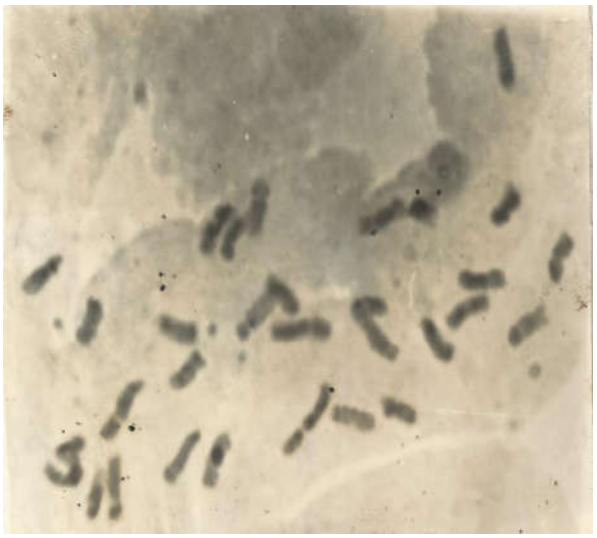
Table 1: Mean values of different characters of different strain of *C. diffusa*

Characters	Subsp. *aquatic* EK/002	Subsp. *montana* EK/003	Subsp. *diffusa* EK/011	Subsp. *diffusa* EK/017	Subsp. *montana* EK/018	Subsp *diffusa* EK/023	LSD 5%	1%	0.1%
Length of penduncle	1.16±0.03	1.57±0.01	1.59±0.02	1.54±0.04	1.33±0.01	1.50±0.01	0.008	0.23	0.408
Length of spathe	2.83±0.04	1.94±0.01	2.26±0.02	2.10±0.01	1.94±0.01	2.03±0.08	0.286	0.746	1.324
Length of internode	6.65±0.40	5.38±0.96	5.18±0.30	5.4±0.53	6.5±0.67	5.01±0.576	0.45	1.18	2.09
Length of leaf sheaths	1.74±0.01	1.49±0.01	1.69±0.01	1.9±0.03	1.81±0.01	1.51±0.01	0.076	0.19	0.35
Area of leaves	21.92±2.14	15.0±9.7	16.0±4.7	17.83±4.93	15.0±9.35	19.84±2.89	1.58	4.12	7.30
Area of spathe	8.84±0.96	3.06±0.04	3.15±0.08	6.88±0.24	3.17±0.13	6.90±0.28	0.35	0.93	1.65
Length of pedicels	1.86±0.05	1.50±0.01	1.61±0.01	1.50±0.01	1.64±0.01	1.53±0.01	0.077	0.2	0.35
Area of petals	0.69±0.01	0.76±0.01	0.66±0.01	0.69±0.01	0.86±0.02	0.01±0.04	0.052	0.13	0.24

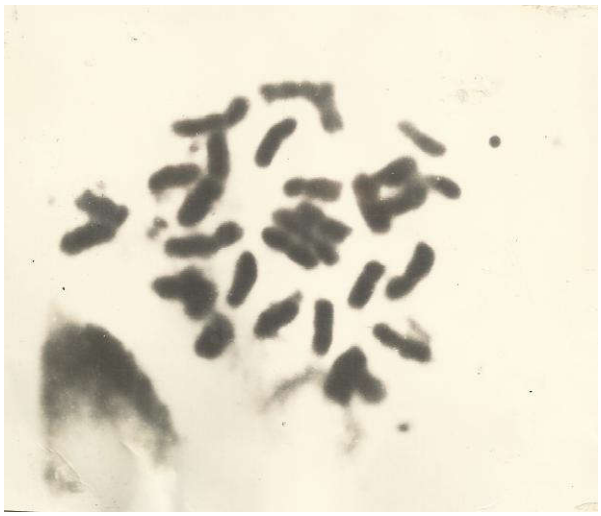
Table 2: Mean value for different Commelina species other than *C. diffusa*

Characters	*C. congesta*	*C.lagosensis*	*C. erecta*	*C. maritime*	LSD 5%	1%	0.1%
Length of penduncle	$0.39^{b}\pm0.01$	$0.51^{a}\pm0.01$	$0.57^{a}\pm0.01$	$0.48^{a}\pm0.01$	0.083	0.128	0.195
Length of spathe	$1.20^{c}\pm0.01$	$0.72^{d}\pm0.01$	$1.94^{a}\pm0.05$	$1.59^{b}\pm0.01$	0.263	0.4048	0.6166
Length of internode	$4.74^{a}\pm0.17$	$6.73^{a}\pm0.74$	$5.43^{a}\pm0.44$	$5.9^{a}\pm0.77$	1.265	1.948	2.96
Length of leaf sheaths	$1.69^{b}\pm0.01$	$1.40^{c}\pm0.01$	$1.78^{a}\pm0.01$	$1.39^{c}\pm0.01$	0.014	0.0224	0.033
Area of leaves	$11.17^{c}\pm0.25$	$14.15^{c}\pm1.72$	$36.48^{a}\pm2.82$	$22.46^{b}\pm6.81$	5.43	8.369	12.74
Area of spathe	$5.31^{b}\pm0.19$	$4.91^{b}\pm0.13$	$8.02^{a}\pm0.32$	$7.68^{a}\pm0.17$	0.811	1.248	1.900
Length of pedicels	$0.72^{a}\pm0.22$	$0.58^{b}\pm0.01$	$0.76^{a}\pm0.01$	$0.85^{a}\pm0.01$	0.087	0.134	0.204
Area of petals	$0.51^{c}\pm0.01$	$1.67^{b}\pm0.01$	$1.73^{b}\pm0.03$	$2.07^{a}\pm0.01$	0.090	0.139	0.210

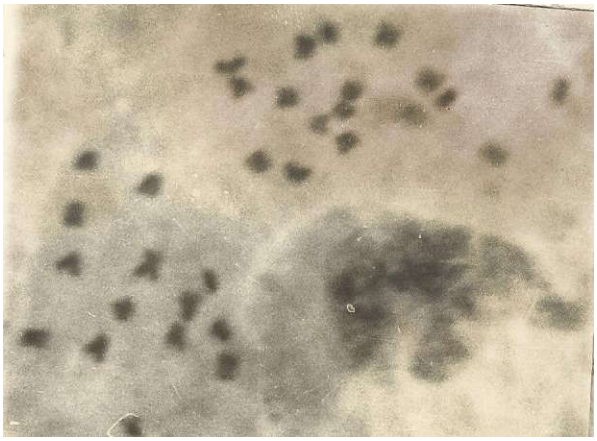
Means with the same case letters along the horizontal array indicates no significant difference (p>0.05).



Mitotic chromosome of strain EK/017, 2n=30



Mitotic chromosomes of strain EK/023 *C. diffusa* 2n=30



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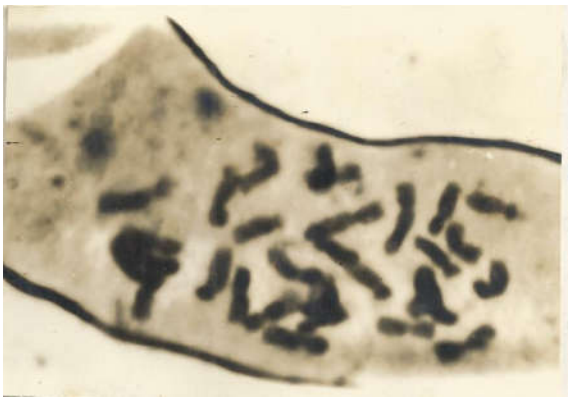
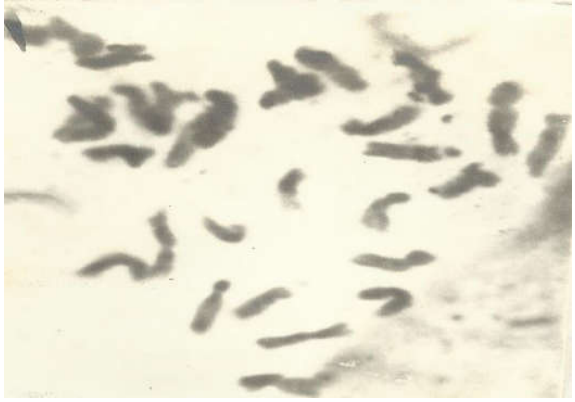
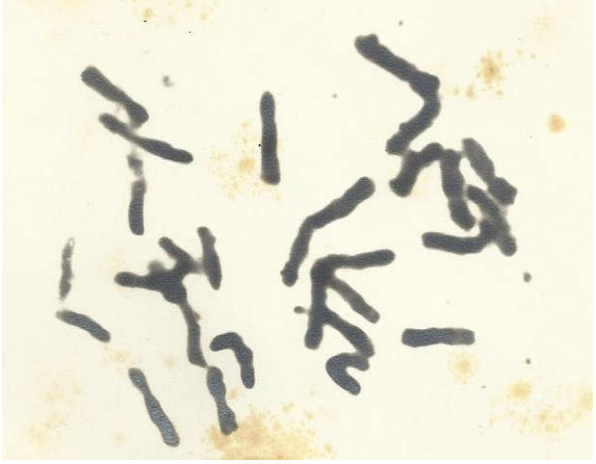


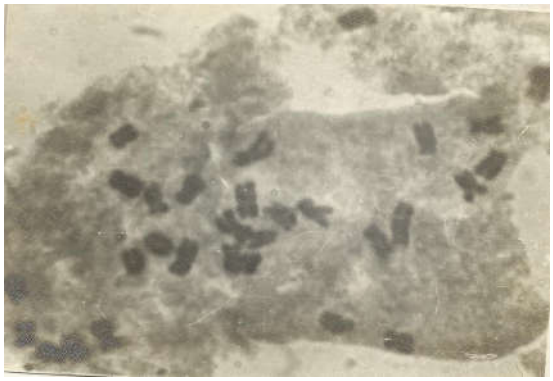
Mitotic chromosomes of strain EK/018, *C. diffusa* subsp. *montana* 2n=30



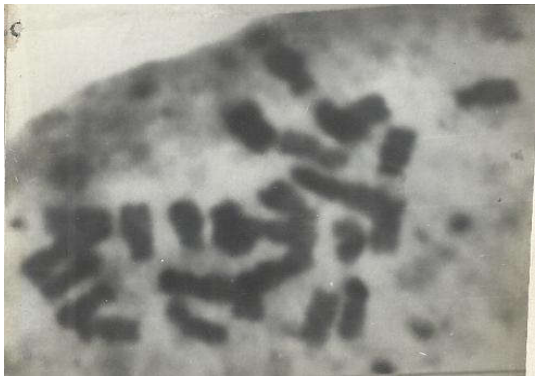
Mitotic chromosomes of strain EK/003, *C. diffusa* subsp. *montana* 20=30



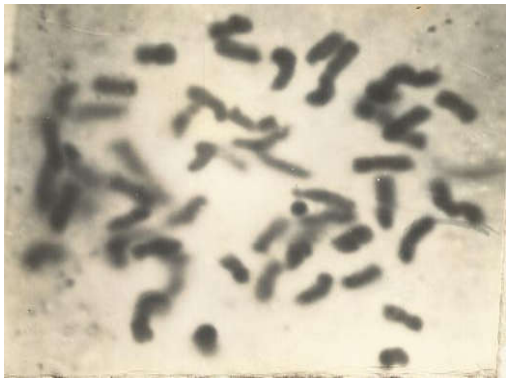
Mitotic chromosome of strain EK/002 *C.diffusa* subsp. *Aquatica*



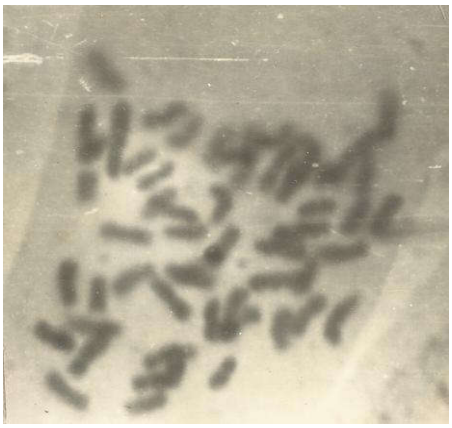
Mitotic chromosome of *C. congesta* 2n=30



Mitotic chromosomes of *C. lagosensis* 2n=26



Mitotic chromosomes of *C. erecta* subsp. *maritina* 2n=4x=60



Mitotic chromosome of *C. erecta*, subsp *erecta* 2n=4x =60

Table 3: Karyotype data of strain EK/017 including volume of chromosome in μ³ subspecies diffusa 2n=30

CHR.No	Long arm	Short arm	Total length	Arm ratio	Volume
1	2.3	1.2	3.5	2.0	5.085
2	2.03	1.2	2.23	1.7	3.25
3	2.6	0.58	3.18	4.5	4.619
4	2.03	0.58	2.4	3.5	3.486
5	1.5	0.9	2.4	1.7	3.486
6	1.5	0.9	2.4	1.7	3.486
7	1.5	0.9	2.4	1.7	3.486
8	1.2	0.7	1.9	1.7	3.050
9	1.2	0.6	1.8	2.0	2.615
10	1.2	0.6	1.8	2.0	2.615
11	1.2	0.6	1.8	2.0	2.615
12	1.2	0.6	1.8	2.0	2.615
13	1.2	0.6	1.8	2.0	2.615
14	1.2	0.6	1.8	2.0	2.615
15	0.9	0.6	1.5	1.5	2.179
Totals			32.91	30.9	47.79
Means			2.194	2.06	3.186

Table 4: Karyotype data of strain EK/023 including chromosome volume in μ³ subspecies diffusa 2n=30.

CHR.No	Long arm	Short arm	Total length	Arm ratio	Volume
1	2.3	1.2	3.5	2.0	6.776
2	2.03	1.5	2.53	1.4	4.898
3	1.74	1.2	2.94	1.5	5.692
4	1.74	1.2	2.94	1.5	5.692
5	1.5	1.5	3.0	1.0	5.808
6	1.74	1.2	2.94	1.5	5.692
7	1.74	1.2	2.94	1.5	5.692
8	1.74	0.6	2.34	3.0	4.530
9	1.74	0.6	2.34	3.0	4.530
10	1.74	0.6	2.34	3.0	4.530
11	1.74	0.6	2.34	3.0	4.530
12	1.74	0.6	2.34	3.0	4.530
13	1.74	0.6	2.34	3.0	4.530
14	1.2	0.6	1.8	2.0	3.485
15	1.2	0.6	1.8	2.0	3.485
Totals			38.43	32.4	74.400
Means			2.56	2.16	4.96

Table 5: Karyotype data of strain EK/011 including volume of chromosome in μ³ subspecies diffusa

CHR.No	Long arm	Short arm	Total length	Arm ratio	Volume
1	1.5	0.87	2.73	1.72	6.703
2	1.2	0.58	1.78	2.0	4.369
3	1.2	0.58	1.78	2.0	4.369
4	1.2	0.58	1.78	2.0	4.369
5	1.2	0.58	1.78	2.0	4.369
6	1.2	0.58	1.78	2.0	4.369
7	1.2	0.58	1.78	2.0	4.369
8	1.2	0.58	1.78	2.0	4.369
9	0.9	0.6	1.5	1.5	3.682
10	0.9	0.6	1.5	1.5	3.682
11	0.9	0.6	1.5	1.5	3.682
12	0.6	0.6	1.5	1.5	3.682
13	0.6	0.6	1.2	1.0	2.946
14	0.6	0.6	1.2	1.0	2.946
15	0.6	-	0.6	-	1.473
Totals			24.19	23.73	59.37
Means			1.612	1.58	3.95

Table 6: Karyotype data strain EK/018 including volume of chromosome μ³ subspecies Montana 2n=30

CHR.No	Long arm	Short arm	Total length	Arm ratio	Volume
1	3.0	1.2	4.2	2.5	10.312
2	2.7	1.5	4.2	1.8	10.312
3	2.4	1.2	3.6	2.0	8.838
4	2.0	1.2	3.2	1.7	7.856
5	1.5	1.5	3.0	1.0	7.365
6	2.0	0.87	2.87	2.3	7.045
7	1.7	1.2	1.9	1.4	4.66
8	2.3	0.58	2.88	4.0	7.070
9	2.0	0.58	2.58	3.5	4.38
10	2.0	0.58	2.58	3.5	6.333
11	2.0	0.58	2.58	3.5	6.33
12	2.0	0.58	2.58	3.5	6.33
13	1.7	0.58	2.28	2.9	5.59
14	1.5	0.9	2.4	1.6	5.89
15	0.9	0.58	1.5	1.5	2.54
Totals			42.35	36.7	100.85
Means			2.82	2.4	6.72

Table 7: Karyotype data of strain EK/003 including volume of chromosome subspecies *montana* 2n=30

CHR.No	Long arm	Short arm	Total length	Arm ratio	Volume
1	3.0	0.9	3.9	3.3	9.57
2	2.7	0.9	3.6	3.0	10.02
3	2.0	1.2	3.2	1.7	7.856
4	2.3	1.5	3.8	1.5	9.329
5	2.0	2.0	4.0	1.0	9.82
6	1.7	1.7	3.4	1.0	8.347
7	1.7	1.2	2.9	1.4	7.119
8	2.3	0.58	2.9	4.0	7.119
9	2.0	0.9	2.9	2.3	7.119
10	1.5	0.9	2.4	1.6	5.89
11	1.5	0.9	2.4	1.6	10.46
12	1.7	0.6	2.3	2.8	5.64
13	1.2	1.2	2.4	1.0	5.89
14	1.2	1.2	2.4	1.0	5.89
15	1.5	0.6	2.1	2.5	5.15
Totals			44.6	29.7	115.219
Means			2.97	1.98	7.68

Table 8: karyotype data of strain EK/002 including volume of chromosome in μ³ subspecies *aquatica* 2n=30

CHR.No	Long arm	Short arm	Total length	Arm ratio	Volume
1	3.5	1.7	5.2	2.0	12.76
2	3.2	1.5	4.7	2.1	11.53
3	3.5	1.2	4.7	3.0	11.53
4	3.0	1.2	4.2	2.5	10.311
5	3.0	0.9	3.9	3.3	9.57
6	3.0	0.9	3.9	3.3	9.57
7	3.0	0.9	3.9	3.3	9.57
8	3.0	0.9	3.9	3.3	9.57
9	2.7	1.2	3.9	2.2	9.57
10	1.7	1.7	3.4	1.0	8.34
11	2.0	1.7	3.7	1.2	9.08
12	2.0	1.2	3.2	1.6	7.856
13	2.3	0.9	3.2	2.6	7.856
14	2.3	0.6	2.9	3.3	7.119
15	2.0	0.6	2.6	3.3	6.363
Totals			57.3	38.5	140.6
Means			3.82	2.56	9.37

Table 9: Karyotype data of strain EK/008 including volume of chromosomes in µ³ *C. congesta* 2n=30

CHR.No	Long arm	Short arm	Total length	Arm ratio	Volume
1	1.74	1.02	2.76	1.7	6.77
2	1.2	0.9	2.1	1.3	5.15
3	1.2	0.9	2.1	1.3	5.15
4	1.2	0.9	2.1	1.3	5.15
5	1.2	0.9	2.1	1.3	5.15
6	1.2	0.6	1.8	2.0	4.41
7	1.2	0.6	1.8	2.0	4.41
8	1.2	0.6	1.8	2.0	4.41
9	0.9	0.6	1.8	1.5	4.41
10	0.9	0.6	1.8	1.5	4.41
11	0.9	0.6	1.8	1.5	4.41
12	0.9	0.6	1.8	1.5	4.41
13	0.9	0.3	1.2	3.0	2.00
14	1.5	-	1.5	-	3.68
15	1.5	-	1.5	-	3.68
Totals			27.96	21.9	62.52
Means			1.86	1.46	4.46

Table 10: Karyotype data of strain EK/022 including chromosome volume in µ³ *C. lagosensis* 2n=26

CHR.No	Long arm	Short arm	Total length	Arm ratio	Volume
1	2.03	2.03	4.06	1.0	9.96
2	1.5	1.2	2.7	1.25	6.62
3	1.5	0.6	2.1	2.5	5.15
4	1.5	0.6	2.1	2.5	5.15
5	2.03	0.3	2.33	6.7	5.70
6	1.5	0.6	2.1	2.5	4.41
7	1.5	0.6	2.1	2.5	4.41
8	1.5	0.3	1.8	5.0	4.41
9	1.5	0.3	1.8	5.0	4.41
10	1.5	0.3	1.8	2.0	4.41
11	1.2	0.6	1.8	2.0	4.41
12	1.2	0.3	1.5	4.0	3.68
13	1.2	0.3	1.5	4.0	3.68
Totals			27.69	43.95	66.43
Means			2.13	3.38	5.11

Morphological attributes of Commelina

The result obtained shows that there were significant difference ($p<0.05$) in the length of penduncle of the Commelina plant. It was observed that *C. diffusa* (EK/011) had the highest length of penduncle followed by *C. montana* (EK/003), *C. diffusa* (EK/017), *C. diffusa* (EK/023), *C. montana* (EK/018) and *C. aquatica* (EK/002) respectively (see Table 1). The length of the internode of *C. aquatic*a and *C. montana* (EK/018) had no significant difference ($p>0.05$) but significantly higher than the internode length of *C. montana* (EK/003), *C. diffusa* (EK/011), *C. diffusa* (EK/011), *C. diffusa* (EK/017) and *C. diffusa* (EK/023) thus having no significant difference ($p>0.05$). *C. aquatic* had significantly high length of spathe followed by *C. montana* (EK/003), *C. diffusa* (EK/011), *C. diffusa* (EK/017), *C. montana* (EK/018) and *C. diffusa* (EK/023) indicating no significant difference ($p>0.05$). It was observed that *C. diffusa* (EK/017) had the highest length of leaf sheaths followed by *C. montana* (EK/018), *C. aquatica*, *C. diffusa* (EK/011), which was also followed by *C. diffusa* (EK/023) and *C. montana* (EK/003). *C. aquatica* had the highest area of leaf followed by *C. diffusa* (EK/023) also followed by *C. diffusa* (EK/017) while *C. montana* (EK/003), *C. diffusa* (EK/011), and *C. montana* (EK/018) had the smallest area of leave with no significant difference ($p>0.05$) between them. *C. aquatica* had the highest area of spathes followed by *C. diffusa* (EK/017), *C. diffusa* (EK/023) also followed by *C. montana* (EK/003), *C. diffusa* (EK/011) and *C. montana* (EK/018). It was

observed that *C. aquatica* had a significantly higher ($p<0.05$) length of pedicels followed by other accessions that indicated no significant difference ($p>0.05$). It was observed from the result obtained that *C. montana* (EK/018) had the highest area of petals followed by *C. montana* (EK/003), which was also followed by *C. aquatic* (EK/002), *C. diffusa* (83/011), *C. diffusa* (EK/017) while *C. diffusa* (EK/023) had the smallest area of petals.

Cytological features of all the strain and/or species of commelina

The chromosome lengths for all the strains showed that the mean chromosome length of *C. diffusa* EK/011 was the shortest and this mean was significantly lower ($P<0.05$) than the mean chromosome lengths of *C. congesta* EK/008. But the mean chromosome length of other strains of subspecies *diffusa* were significantly higher ($P<0.05$) than the mean length of *C.congesta* EK/008. These strains were EK/017 and EK/023 belonging to subspecies *diffusa*. *C. lagosensis* EK/022 had mean chromosomes length significantly higher ($p<0.05$) than that of *C. congesta* EK/008. The data on all the karyotype show that subspecies *diffusa diffusa* (EK/017, EK/011, EK/023) and *C.congesta* (EK/008) show high symmetrical chromosomes. For instance the mean arm ratio for strain EK/011 of *diffusa* was 1.58 and for strain EK/008 of *C. congesta* was 1.46. Low mean arm ratio and many pairs of chromosomes with same arm ration are not common in subspecies *montana*, sub-species aquatic and in *C. lagosensis*. The results also shows that *C. lagosensis* (EK/022) chromosomes were most asymmetrical. It was also observed that the arm ratio is significantly higher ($p<0.05$) than that of other strains. The mean arm ratio of subspecies *aquatica* was significantly higher ($p<0.05$) than those of subspecies *diffusa* (EK/011, EK/017, EK/023) and *C. congesta* (EK/008), but was not significantly higher ($p<0.05$) than the arm ratio of subspecies *montana* EK/018. In *C. lagosensis* (EK/022) chromosomes 1 and 2 were metacentric and submetacentric respectively and larger than the rest of the chromosomes. All other chromosomes for the strain were acrocentric with arm ratio varying from 2.0 to 5.0. There was only one pair which was subtelocentric. It was also observed that the volume of chromosomes for eight strains of commelina shows that the mean volume of *C. congesta* (EK/008) chromosomes was significantly higher ($p<0.05$) than those of subspecies *diffusa* (EK/011 and EK/017 respectively). But the mean volume of chromosomes of the strain EK/023 of subspecies *diffusa* (EK/023) was higher than the mean volume of chromosomes of *congesta* (EK/008). Also the mean volume of subspecies *montana* (EK/018 and EK/003) were significantly higher ($p<0.05$) than that of C. congesta (EK/008). The mean chromosome volume of *C. lagosensis* (EK/022) was siginificantly higher (0.01) than the chromosome volume of *C. congesta*. The chromosome volume of the strains of subspecies *montana* (EK/018 and EK/003) were significantly higher ($p<0.001$) than that of *C. lagosensis* (EK/022). The two strains for the subspecies *montana* showed significant difference ($p<0.05$) in their volume of chromosomes, with EK/003 higher than EK/018. The volume of the chromosome of subspecies *aquatica* EK/002 was significant higher ($p<0.01$) than that of *montana* strains EK/003

DISCUSSION

The chromosome number for *C. congesta* and *C. diffusa* was observed to be 2n=30 ansd that of *C. erecta* was 2n=60. These results support the view of earlier workers as the basic chromosome number for this genus. The exception is in *C. lagosensis* with 2n=26. Since the majority of the five, it is therefore safe to conclude that the basic number for this genus is 5. The karyotype data for all the strains examined show that acrocentric and submetacentric chromosomes dominate over metacentric, subtelocentric and telocentric chromosomes. Bhattacharya [2] reported that the chromosomes of this genus are mostly metacentric and submetacentric. Jones [6] stated that chromosome evolution is a continuous process. The differences obtained in the present study in karyotypes within the same species even subspecies are in line with the results of Bhattacharya [2]. Morton [7] and Sharma and Sharma [8] had associated polypoid forms of *C. diffusa* and *C. erecta* with montane habitats. In the present investigation, however, polypoid form of *C. diffusa* has not been encountered. The chromosome lengths ranged from very short as in subspecies *diffusa* strain 83/011 with chromosome length of 0.6u to medium sized as in subspecies aquatic with chromosome length of 5.2u. This result is similar to that of Bhattacharya [2]. This cytological result also agrees with Brenan's [9] placement of commelina in the 10^{th} position in the phylogenetic classification of the genera within the family commelinaceae. In his phylogenetic classification Tradescantia with longer chromosomes than commelina was placed at the 11^{th} position while zebrine with longer chromosomes than Tradescantia (10u-13. 0u range) occupies the 12^{th} position. The present study showed an increased in size of chromosome and increase in asymmetry of chromosomes from *C. congesta* to *C. diffusa*. Also of particular interest was the increased asymmetry of chromosomes of *C. lagosensis*.

Changes in the chromosome size

In the present investigation *C. congesta* had the smallest chromosomes size and had primitive morphological characters. The highest chromosome volume and length were observed in *C. diffusa* subspecies aquatic. The subspecies with the second highest chromosome volume and length was subspecies *montana*. These subspecies show phylogenetic advancement mostly in floral parts and adaptation to environment as compared to *C. congesta*. *C. lagosensis* had less total chromosome volume and length, very close to *C. congesta* but it showed phylogenetic advancement in terms of its high asymmetry of chromosomes and reduction in chromosome number. Increase in the absolute chromosome size with phylogenetic advancement had been reported by many workers in many Cruciferae [10]. Narayan [11] reported that an increase in the chromosome volume is accompanied by an increase in DNA content of Lathyrus. A similar result was reported by Seal (1982) in Festuca and Lolium that there is a direct correlation between the chromosome size, DNA content and phylogenetic advancement. Jones [6] also reported that where size differences are associated with variation in DNA content, they can be confidently ascribed to lengthwise amplification (or dimunition) of particular chromosome segments and often the amplified segments consist of repetitive DNA. It is not certain whether the increased chromosome size in *C. diffusa* is due to repetitive DNA or not. However, the adaptive radiation in *C. diffusa* with numerous variant types and advanced floral characters indicated that a *diffusa* is likely to have more functional DNA than *C. congesta*. It seems also that *C. congesta* with small chromosome volume has low DNA content and this is associated with less advanced floral characters and less adaptive capability especially in open habitats as compared to *C. diffusa*.

Chromosome symmetry versus asymmetry

According to Stebbins (1950), a karyotype consisting of chromosomes all essentially similar to each other in size and with median or submedian centromeres, may be termed a symmetrical karyotype. Asymmetrical karyotypes posses many chromosomes with subterminal centromeres or greater differences in size between the largest and the smallest chromosomes or both. The result of the present investigation showed that *C. congesta* and *C. diffusa* subspecies *diffusa* showed the highest degree of chromosome symmetry. Subspecies Montana and subspecies aquatic of species *C. diffusa* showed greater differences in their chromosome sizes and centromeric position while *C. lagosensis* showed the greatest mean arm ratio.

Morphological studies of the three species, *C. congesta*, *C. diffusa* (subspecies *montana* and *aquatica*) and *C. lagosensis* showed that *C. congesta* is primitive and least adaptive to open habitats. On the contrary subspecies *montana* and subspecies aquatic showed advanced morphological characters and possessed many variant types which are highly adaptive to different ecological conditions. *C. lagosensis*, in addition to the possession of advanced morphological characters, appears to be spreading rapidly in different habitat.

Reduction in number of chromosome

Karyotype asymmetry is closely related to reduction in chromosome number. Stebbins [12] reported that increasing karyotype asymmetry is associated with decreasing chromosome number and with respect to specialized morphological characters. Morton (1967) reported 2n=28 chrome for *C. lagosensis*. From the present study *C. lagosensis* was found to have 2n=26 in the genus Commelina. A closer look on the karyotype data of this species showed that chromosome 1 and 2 are metacentric and submetacentric respectively and these are the two largest chromosomes of the remaining chromosomes, all are acrocentric (chromosomes 8, 9 and 10 have higher arm ratio of 5.0) except chromosome number 5 which is a subtelocentric chromosome. This means that the karyotype of *C. lagosensis* is highly asymmetrical. At the peak of asymmetry, all the chromosomes can be acrocentric and/ or telocentric. If four of such chromosomes are fused in twos this will give two large metacentric or submetacentric chromosomes and thereby reduce the basic number from n=15 to n=13. It is difficult to say how highly asymmetric karyotype could have occurred. One possibility can however, be discussed. The meiotic chromosome of *C. diffusa* strains (2n=30) are characterized by many translocation complexes indicating a high degree of chromosome instability. From these translocations, an asymmetric karyotype, as mentioned above, might have occurred in which two independent centric fusion took place giving rise to n=13. Jones [6] reported that acrocentric or telocentric chromosomes are the necessary starting point for the fusion process and that metacentric chromosomes are the end. Chromosome 1 and 2 which are metacentric and submetacentric respectively might have resulted from centric fusion. Centric fusion of Robertsonian fusion is a type of interchange which joins almost all the genetic material of two chromosomes to a single centromere [6]. Reduction in chromosome number by Robertsonian fusion seems to be relatively common in the family of Commelinaecae, Gibasis and Zebrina of the family Commelinaecae. Up until now, *C. diffusa* appears to be the dominant species of commelina invading different ecological niches including crop fields, bushes, marshy places, high lands and even waste rocky places. In contrast *C. lagosensis* did not appear to be common as C. diffusa until recently. However, in Calabar area it appears that *C. lagosensis*

is invading rapidly all kinds of ecological niches and it is increasingly becoming a problem for farmers. Its stout rhizomatous roots apparently have helped in its colonization in areas where *diffusa* failed because of its subtteranean nodal root system. The adaptive radiation of *C. lagosensis* by which it dominates over other weeds, crops in fields and waste land or even bushes suggest that the reduction in chromosome of *C. lagosensis* has contributed to its adaptive capabilities.

Polyploidy

Polyploidy has been observed in the two strains of *C. erecta*, subspecies *erecta* and subspecies maritime. Both of them have 2n=60 chromosomes. The chromosomes of these strains were mainly metacentric and submetacentric. This has provided yet another type of change i.e in the chromosome number in Commelina. The close morphological resemblance of *C. congesta* to these two subspecies of *C. erecta,* especially in their shapes of spathes, possession mucilage in the spathe, peduncle, pedicels, number of staminodes and their capsule suggest that *C. congesta* is one probable ancestor of these two strains. The probable line of origin is apparently through hybridization of *C. congesta* with some other species (likes *C.diffusa*) followed by chromosome doubling. The spathes of subspecies maritime aborted soon after flowering. Therefore no fruit was developed. Whereas subspecies erecta produced fruits which were dehiscent. The inability to produce fruits in maritime might be due to chromosomal or genic instability of maritime.

The picture given by both morphological and cytological changes of the four species studied suggest that *C. congesta*, a forest taxon in tropical forest zones, had utilized three types of cytological changes to give rise to other species which have achieved adaptive radiation to various ecological conditions. Increase in chromosome size led to the evolution of *C. diffusa*., Reduction in chromosome number (probably through *C. diffusa*) led to the evolution of C. lagosensis while hybridization followed by polyploidy had led to the evolution of *C. erecta*. It may be concluded that Commelinaeceae and its genus Commelina had shown enormous differences in chromosome, size pattern and number in their component species. These cytological differences contributed immensely to morphological differences and the great success of this genus.

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