# Karyotype differentiation in *Pancratium hirtum* A. Chev. complex (Amaryllidaceae) in Nigeria.

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**Resumen:** Se estudió un conjunto de poblaciones de nueve taxa de *Pancratium hirtum* usando preparaciones en metafase. La diferenciación cariotípica incluye rupturas cromosómicas, cambios en la ubicación de los centrómeros y diferencias en la longitud total de material de cromátidas por núcleo. El complemento semático en cada grupo contiene 22 autosomas, excepto en  $C_n$  y  $C_f$  en los cuales hay uno adicional y cuatro cromosomas acsesorios, respectivamente. Posiblemente se trata de una especie dinámica (un conjunto de "sibs") y hay más especies en vias de formación.

Key words: nucleous, karyotype, chromosomes, sibs.

Cytological studies have been extensively utilized for information to elucidate the taxonomy of various taxa of angiosperms (Lakey 1980, McDonald 1980, Oyewole 1988). Sindhu *et al.* (1983) emphasized the usefulness of karyotype data in complementing taxonomic information from other areas of study. Karyotypic analysis of *P. hirtum* is here attempted with a view to resolving taxonomic relationship among the various populations and to supplement or complement the morphological data with a view to rationalizing its taxonomy.

Nine morphs designated  $C_1$ ,  $C_2$ ,  $C_3$ ,  $C_4$ ,  $C_5$ ,  $C_5$ ,  $C_h$ ,  $C_f$  and  $C_n$  were used for the purpose of this study and the method of Oyewole (1988) was employed.

Tables 1 and 2 contain summary of the karyotype data. Counts of 2n = 22 autosomes were obtained for all the cells examined in all the groups, confirming earlier works both on the genus and West African species (Oyewole 1988). Each genome consists of a graded series of chromosomes with centromere placement ranging from median to terminal. Chromosomal length in each group varies as well as the total length of chromatin material.

Despite the outward similarity of karyotypic configuration of the nine groups and the constancy in chromosome numbers, there is evidence that a number of centromeric shifts have occurred in their separate evolutionary histories. The amount and pattern of karyotypic diversity among the groups appear typical. Although the nine groups have different karyotypes, they have a common basic plan in which the longest two and the shortest pairs have centromere in the median to submedian regions. C<sub>1</sub> has little chromosomal changes and is probably closest to the ancestral stock (s). Karyotypie differentiation is therefore similar to what Coates and James (1979) and Coates (1979) reported for *Stylidium crossocephalum*, and it also confirms Oyewole (1988).

Karyotype differentiation may therefore be said to have involved;

- (i) loss of chromosome segments from certain members of the complements, thus rendering homologous members dissimilar in length and morphology;
- (ii) variation in the length of chromatin per complement;
- (iii) most probably, chromosome changes involving rearrangement of genes and/or gene-blocks in translocation and inversions, and
- (iv) the situation may have been compounded by natural hybridizations between the different cytotypes.

## TABLE 1

## The Karotype data of Pancratium hirtum

Homologues	C <sub>1</sub>	C <sub>2</sub>	C <sub>3</sub>	C <sub>4</sub>	C5	Cs	Ch	Cf	Cn
Chrom. lenghth (µm) 1-r-value Centromere	34.63 1.29	41.79 1.36	32.46 1.33	24.91 1.07	48.21 1.22	49.02 1.10	19.13 1.53	40.17 1.32	40.01 1.25
location	m	m	m	m	m	m	m	m	m
Chrom. length (µm) 2 re-value Centromere	29.00 1.29	37.77 1.35	25.71 1.13	24.11 1.10	38.89 1.02	40.17 1.08	18.24 1.65	30.54 1.23	36.16 1.50
location	m	m	m	m	m	m	m	m	m
Chrom. length (µm) 3 r-value Centromere	22.50 2.49	32.94 2.06	21.37 2.33	23.37 2.70	28.93 2.07	30.54 2.80	13.66 4.27	26.83 6.45	27.00 2.78
location	sm	sm	sm	sm	sm	sm	st	st	sm
Chrom. length (µm) 4 re-value Centromere	20.09 11.48	28.45 16.67	19.28 23.10	20.37 11.65	24.11 13.97	24.11 6.48	13.60 2.43	17.68 9.98	20.45 11.44
location	t	t	t	t	t	st	sm	t	t
Chrom. length (µm) 5 r-value Centromere	17.68 4.14	19.13 10.88	18.00 11.41	14.68 28.92	18.72 10.63	21.46 9.91	12.86 5.97	16.39 9.18	20.09 5.24
location	st	t	t	t	<b>t</b>	t	st	t	st
Chrom. length (µm) 6 r-value Centromere	16.07 15.74	18.68 8.43	17.68 9.98	13.66 7.48	17.27 9.74	21.01 9.66	11.25 7.72	13.50 7.38	18.08 10.27
location	t	t	ς t	t	t	t	t	t	t
Chrom. length (µm) 7 r-value Centromere	14.46 10.27	17.68 8.43	16.07 0	12.86 6.14	16.07 6.69	20.89 11.97	8.84 10.50	12.86 7.90	17.28 13.78
location	t	t	Т	t	t	t	t	t	t
Chrom. length (µm) 8 r-value Centromere	13.66 11.20	17.20 7.91	15.27 8.48	12.85 9.79	15.91 7.25	20.08 11.52	8.52 2.53	11.61 0	16.88 2.00
location	t	t	t	t	t	t	sm	Т	sm
Chrom. length (µm) 9 r-value Centromere	12.86 11.00	16.47 9.23	12.86 8.89	11.88 9.51	15.75 8.78	15.67 8.73	8.36 0	11.25 13.05	15.67 13.79
location	t	t	t	t	t	t	Т	t	t
Chrom. length (µm) 10 r-value Centromere	11.25 15.74	15.91 8.88	8.84 8.11	11.06 12.85	13.90 1.16	15.27 8.48	8.36 11.86	11.25 1.60	14.14 8.36
location	t	t	t	t	t	t	t	m	t
Chrom. length (µm) 11 r-value Centromere	8.36 1.36	8.04 1.27	8.03 1.27	8.36 1.09	12.86 1.35	15.27 1.21	7.71 1.40	8.60 1.15	11.41 1.22
location	m	m	m	m	m	m	m	m	m
Accessory Chromosomes lengths (µm)	-	-	-	-	-	-	1.93	1.92 1.92 1.92 2.08	



Fig. 1. Metaphase of P. hirtum. Bars: 10 mm

#### TABLE 2

Centromeric location differentiation

Taxa	М		m	sm	st	t	Т
C <sub>1</sub>	-		3	1	1	6	-
$C_2$	-	3		1	-	7	-
$\tilde{C_3}$	-	3		1	-	6	1
C₄	-	3		1	1	6	-
Cs	-	4		1	-	6	-
C <sub>s</sub>	-	3		1	1	6	_
Ch	-	3		2	2	3	1
C <sub>f</sub>	-		3	-	1	6	1
C <sub>n</sub>	-	3		2	1	5	-
		T t st sm m		Terminal point Terminal region Subterminal region Submedian region Median region			
		Μ	=	Median	point		

A number of groups appears to differ considerably in number of median and submedian, terminal and subterminal chromosomes. This further strengthens the suggestion that karyotype differentiation may involve chromosomal rearrangement. Morphological and karyotypic data suggested that  $C_1$ ,  $C_5$ ,  $C_8$ ,  $C_h$  and  $C_f$  may be hybrids between *P. hirtum* and *P. trianthum*. If hybridization occurred between *P. hirtum* and *P. trianthum* as claimed by Morton (1965), there may have been introgression of the hybrid swarms into *P. hirtum*, leading to karyotypic segmentation in the species.

Differences in climate or soil, or even the flora with which the species is competing may be sufficient to initiate divergence of the population. Changes in the genetic regulatory apparatus may also play an important role in evolution. At the level of gross chromosomal reorganization, there is little evidence that chromosomal divergence has proceeded at a rapid rate

Fig. 2: Karyotypes of P. hirtum

among the groups except in  $C_h$ . All the groups appear to be characterized by general conservatism in karyotype evolution.

All the groups exhibit differences in total length of chromatin material though some are close in value. In *P. hirtum*, the direction of the differences exhibited, and their relation to actual process of speciation, is obscure, but it is conceivable that they may lead to speciation events.

The various factors that have been examined cannot as of now be used to establish concreto differences among the groups until investigations of meiotic behaviour and chromosome banding pattern are carried out. All that can be said with certainty is that the species is dynamic and that more species formation may be on the way. For the present, the taxon can be regarded as a complex of sibs.

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