The enigmatic genus *Craterispermum* (Rubiaceae): state of the art

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After a taxonomic revision of the genus *Craterispermum* in continental Africa 19 taxa (16 species and three varieties) were recognized. Eight new species and three varieties were described. The most important distinctive characters are vegetative (stipules, young branches, leaves) and inflorescence characters (Fig. 3) The characteristic yellow colour of dried *Craterispermum* material is typical for aluminium accumulating species. Pollen of *Craterispermum* are (2-)3(-4)-zono-colporate or –porate (Fig.1 C, D).

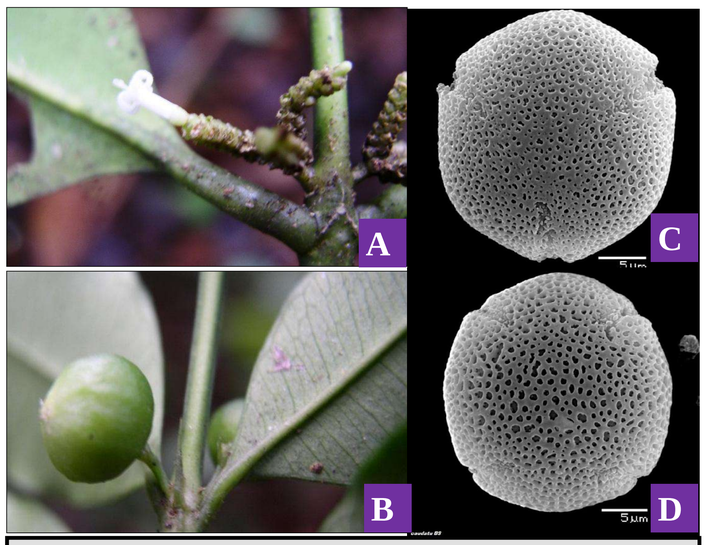

Fig. 1: A. *C. robbrechtianum* (new species); **B**. C. *parvifolium* (new species); **C**. 3- zono-colporate pollen from a longistylous flower of *C. caudatum;* **D.** 4- zono-colporate pollen from a bevistylous flower of *C. caudatum*

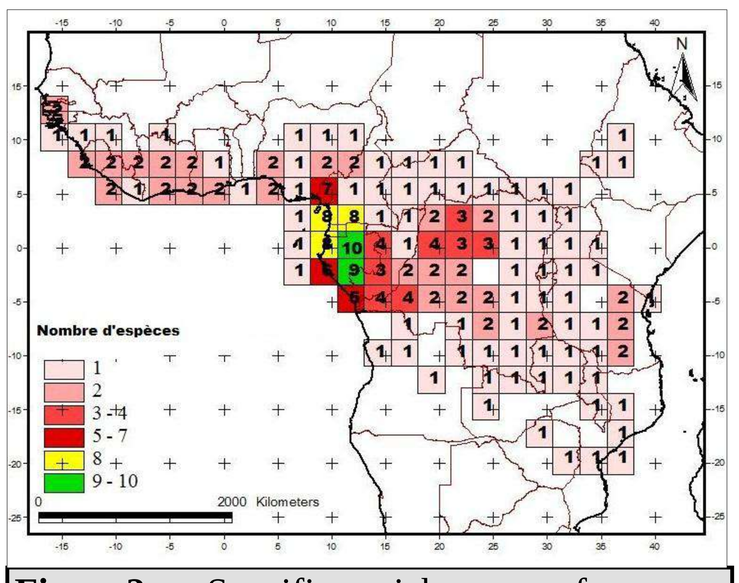

Fig. 2: Specific richness of genus *Craterispermum* on continental Africa

Craterispermum is distributed in continental Africa from Senegal to Mozambique with the Lower Guinea Domain its principal center of diversity and endemism (Fig.2).

Craterispermum shows a collapse of species boundaries in Central Africa for the complex *C. cerinanthum*, *C. laurinum* and *C. schweinfurthii*. While easily distinguished in the rest of their distribution area, in Cameroon and R.D. Congo they show widely overlapping morphological characters and identification is nearly impossible. Morphometric analysis of the complex shows that *C. laurinum* is rather well delimited, as well by its characters as by its distribution strictly confined to the Upper Guinea Domain. However, taxonomic overlap between *C. cerinanthum* and *C. schweinfurthii* is high in Central Africa, where "typical" specimens mix with atypical ones (Fig.3 B, C).

Molecular studies may provide a solution for this problem. Therefore, conception of genetic markers was undertaken. Methods, approaches and tools developed for the Rubiaceae genera *Hedyotis* and *Coffea* were tested on the genome of *Craterispermum*: 14 microsatellite markers derived from coding sequence libraries (EST) of *Coffea* and *Hedyotis* were proven useful in genetic diversity analyses in *Craterispermum* (Fig.5). The estimated values of the genome sizes in the genus vary between 1.03 pg and 1.64 pg (Fig.4).

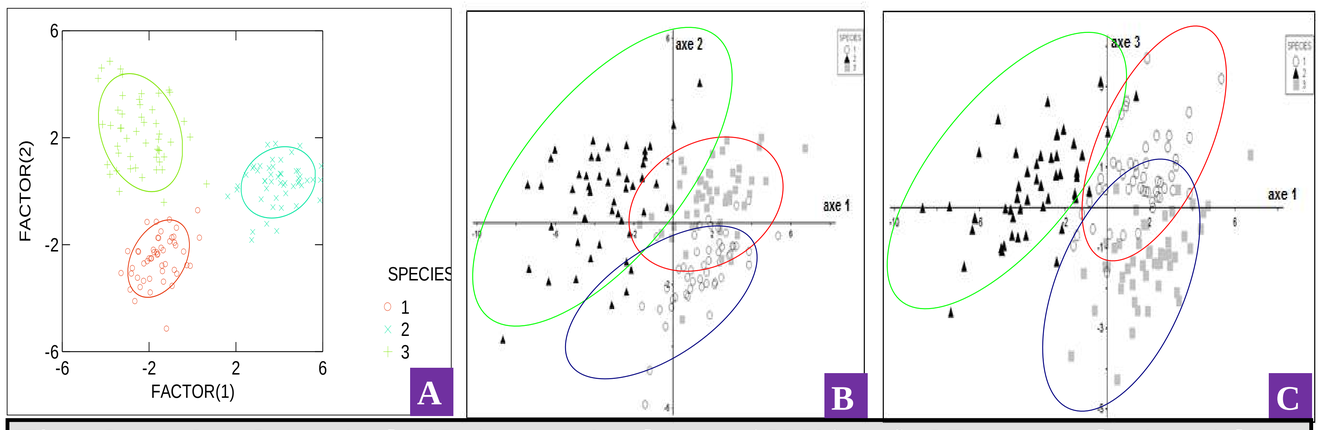

Fig. 3 : A. Canonical Variance Analyses (CVA) of 27 most distinguishing standardized morphological characters scored for 150 specimens (50 specimens per *a priori* group: **1**: *C. cerinanthum*, **2**: *C. laurinum*, **3**: *C. schweinfurthii*). **B and C**. Principal Component Analysis (PCA) (27 characters, 150 specimens); **B**, axes 1 & 2 and **C**, axes 1 & 3

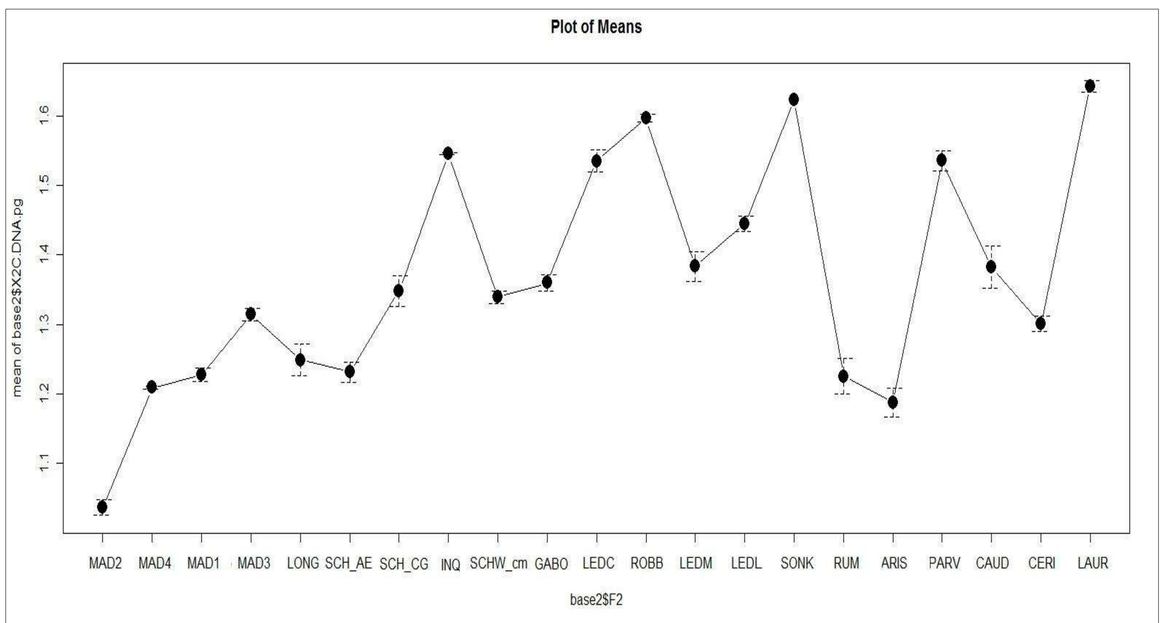

Fig. 4: Variation of genomes size in genus *Craterispermum* in continental Africa

ID	Motif repet	Séquence des amorces	%GC	optimal T° C d'hybrid.	T° C applied	Awaited size of PCR products (pb)	Size of PCR products (pb)
ES68	(CAG)28	*F* AACGGTGGAGATTTGACGAG	-	60-55	50 ° C	256	500 -1500
		R GCGGCTGTGGTTGATAGAGT	-				-
ES83	(AGG)8	*F* CACCTCTCTCTCCGACACC	-	60-55	50 ° C	196	500-750
		R TCACCAACTCCCTCACCTTC	-				-
CB076507	(CT)20	*F* ATGGATGAACCCACATCAGG	50	50-60	53 ° C	200	250-1500
		R GCTGCCATATGCATGAGAGA					-

Fig. 5: Some microsatellites markers (3/14) from *Coffea* and *Hedyotis* transferable to *Craterispermum* (ES from *Coffea* and CB from *Hedyotis*)

We need to clarify the phylogenetic relationships between the species (African continent and Madagascar) and to carry out a genetic diversity analyses to propose an evolutionary hypothesis for the genus.

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