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## CYTOGENETIC CHARACTERISTICS OF THE HYMENAEA CLADE (LEGUMINOSE, DETARIOIDEAE) REVEAL PHYLOGENETIC SIGNALS

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### Abstract

Study citotaxonomic of Hymenaea clade using chromossomes number, Multivariate Analyses and Molecular phylogenetics.

### Key words:

Chromosome number, Hymenaea clade, Multivariate Analyses.

### Introduction

The here called Hymenaea clade is a lineage of the Detarioideae subfamily of Leguminosae. The clade is currently composed of three genera: *Guibourtia* Benn. with ca. 15 species, one in the Neotropics and 13 in Africa; *Hymenaea* L. with ca. 20 species in the Neotropics and one in Africa; and *Peltogyne* Vogel with ca. 21 Neotropical species. Representatives of this clade are mainly recognized by their resin production capability and the bifoliolate leaves.

Even with this biogeographical pattern, and an evident difficulty in the delimitation of some taxa, especially at the infrageneric level, the knowledge on cytological characteristics for the group is scarce and restricted only to chromosome number. In the last year, we were contributing to unprecedented cytogenetics date in Hymenaea clade. We also used literature data aiming to investigate the potential of chromosomal characteristics in taxonomy and in phylogenetic studies.

### Results and Discussion

After cataloging data available in the literature and collecting some samples we observed that apparently, the predominant chromosome number in the Hymenaea clade is  $2n = 24$ , such as for most of the representatives of the subfamily. The seeds of 11 taxa (three *Guibourtia*, seven *Hymenaea* and one *Peltogyne*) were collected in several Brazilian regions. We observed some variations in chromosome numbers, CMA<sup>+</sup> bands and rDNA sites. The exception for chromosome number was *G. coleosperma* with  $2n = 48$ . Most taxa present two pairs of CMA<sup>+</sup> bands (except *G. coleosperma* and *G. conjugata* with one pair, and *H. altissima* Ducke with three pairs), one pair of rDNA 5S (except *P. pauciflora*, with two pairs), and one pair of rDNA 45S.

In order to evaluate the karyological relationship among the studied taxa, a principal component analysis (PCA) was carried out with the data gathered from representatives of 10 taxa of the Hymenaea clade. Cumulative variance of the components PC1 and PC2

explained 90.1% of the total information. The formation of PC1 was due to mean centromeric asymmetry (MCA), the coefficient of variation of centromeric index (CVCI) and number of 5s rDNA sites, which had a discriminant power of 53.9%. The multivariate analyses pointed out the formation of three groups: one with *Hymenaea* and the only neotropical species of *Guibourtia* [*G. chodatiana* (Hassl.) J.Leonard], other with the African species of *Guibourtia* and the last one with *Peltogyne* species.

To molecular phylogenetics, DNA samples were obtained from 20 representatives of the Hymenaea clade for the amplification of the plastid *trnK* gene. Additional 54 sequences from other representatives of Detarioideae subfamily (including some of the Hymenaea clade) were obtained from GenBank®. *trnK* data set included 73 terminals and 1754 bp. Bayesian analyses of this cpDNA data set recovered a clade containing the genera *Guibourtia*, *Hymenaea* and *Peltogyne* with maximum support. The genera *Hymenaea* and *Peltogyne* were also supported as monophyletic but the genus *Guibourtia* presented a polytomy that indicates a recovering of two different clades.

### Conclusions

The multivariate results (chromosome data) and phylogenetic analyses (molecular data) presented congruent hypothesis of group formation. Both discriminated the African *Guibourtia* from the monophyletic Neotropical genera *Hymenaea* and *Peltogyne*. They also suggested a closer relationship between the neotropical *Guibourtia chodatiana* with *Hymenaea* representatives, such as it has been demonstrated in other phylogenetic studies with different markers.

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