Abstract

Hymenaea and Guibourtia are part of the Hymenaea clade and they present interesting taxonomic challenges and biogeographical patterns. This work presents karyotype data from representatives of these genera and some preliminary evidences for an improvement of taxonomy and biodiversity knowledge of the group.

Key words: Cytogenetic, CMA/DAPI, Systematic.

Introduction

Hymenaea L. and Guibourtia Benn. are included in the Detarieae tribe (Leguminosae, Caesalpinioideae) and, together with the genus Peltogyne Vogel, they form the Hymenaea clade. Representatives of this clade are mainly recognized by their arboreal size, bifoliolate leaves and capability of producing resin. Due to a vegetative similarity between these genera, it is common to find mixed materials in herbarium collections and even misidentification data in some species lists. Hymenaea and Guibourtia currently comprises about 14 species each, nevertheless, the distribution of these species presents a curious pattern, since Hymenaea has most of its diversity in the Neotropical region, with the exception of H. verrucosa Gaert., which is restricted to East Africa and Madagascar, while Guibourtia has most of its diversity on the African continent with the exception of G. hymenaeifolia (Moric.)J.Léonard, restricted to South American continent. Even with an evident difficulty in the delimitation of taxa and an interesting biogeographical pattern, the knowledge on cytological characteristics for the group is still scarce. Thus, this work aims to provide karyotype data for representatives of Hymenaea clade, helping further taxonomic and evolutionary studies.

Results and Discussion

The species Hymenaea courbaril L., H. stigonocarpa Hayne and H. parvifolia Huber presented chromosome counts of 2n=24, following previously studies and two pairs of CMA bands (GC-rich sites). The species G. hymenaeifolia presented a chromosome count of 2n=10 and one pair of CMA bands. The chromosome number presented by G. hymenaeifolia stands out by escaping from the range presented by other caesalpinioideas legumes (2n=22 to 2n=24). Moreover, this Neotropical species differs from the existing data for the African species G. ehie (A. Chev.) J. Leonard, which presented the count of 2n=24².

Conclusions

With the data obtained until now, we conclude that representatives from Hymenaea clade present predominantly a chromosome number of 2n=24. Moreover, the chromosome number presented by the Neotropical species G. hymenaeifolia can be an indicative of isolation and that this species do not belongs to genus Guibourtia. Further studies are being conducted to evaluate if this taxon can be treated as a new legume genus. We intend to obtain data from more taxa, including Peltogyne species and associate these data with phylogenetic and taxonomic studies that are being carried out in the DBV-IB for a better understanding of the biogeography and diversification of the Hymenaea clade.

Acknowledgement

GMS thanks FAPESP for IC scholarship. RBP thanks CNPq for DR scholarship. AMGAT thanks CNPq (proc.563550/2010-4) and FAPESP (proc. 2010/52488-9). VFM thanks CNPq (proc. 312766/2009-2) and FAPERJ (E-26/111.581/2014). ERFM thanks CNPq (proc. 306142/2011-2).

References


DOI: 10.19146/pibc-2015-38084 XXIII Congresso de Iniciação Científica da UNICAMP