

Cytogenetics of Brazilian species of Bromeliaceae

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Received 2 October 2006; accepted for publication 12 November 2007

This paper presents the mitotic chromosome numbers of 18 species of Bromeliaceae. The diploid number $2n = 50$ was observed in *Aechmea comata*, *A. caudata*, *A. correa-araujoi*, *A. recurvata*, *A. marauensis*, *A. bicolor*, *A. pine-liana*, *Hohenbergia cattingae*, *H. blanchetti*, *Alcantarea imperialis*, *Al. nahoumi*, *Neoregelia tenebrosa*, *Nidularium lyman-smithii*, *N. scheremetiewii*, *N. innocentii* var. *innocentii*, and *N. innocentii* × *Neoregelia johannis* hybrid, whereas $2n = 34$ was observed in *Cryptanthus maritimus* and *C. warren-loosei*. All of the determinations presented in this study are previously unpublished, except *A. comata* and *H. cattingae*. These results confirm $x = 25$ as the basic number for the family and $x = 17$ as a secondary basic number probably generated by decreasing dysploidy. © 2008 The Linnean Society of London, *Botanical Journal of the Linnean Society*, 2008, 158, 189–193.

ADDITIONAL KEYWORDS: *Aechmea* – *Alcantarea* – chromosome numbers – *Cryptanthus* – dysploidy – *Hohenbergia* – *Neoregelia* – *Nidularium* – polyploidy.

INTRODUCTION

The family Bromeliaceae occurs in the tropical and subtropical zones of the American continent, with about 50% of the known species found in Brazil. A large majority of the Brazilian species grow in the Atlantic Coastal Forest, although the family has adapted to a great variety of ecosystems ranging from humid to arid, with terrestrial, rupicolous, and epiphytic habits.

Although the family has significant horticultural and decorative importance, cytogenetic analyses have been performed on only about 12% of the species (Lindschau, 1933; Gauthé, 1965; Weiss, 1965; Marchant, 1967; Sharma & Ghosh, 1971; McWilliams, 1974; Brown, Varadarajan & Gilmartin, 1984; Varadarajan & Brown, 1985; Brown & Gilmartin, 1986, 1989; Lin, Ritschel & Ferreira, 1987; Brown, Palací & Luther, 1997; Cotias de Oliveira *et al.*, 2000, 2004; Ramirez-Morillo & Brown, 2001; Palma-Silva *et al.*, 2004; Bellintani, Assis & Cotias de Oliveira, 2005). Some of the pioneering work on the cytogenetics of Bromeliaceae

revealed a large variation in the numbers of chromosomes, and disagreement on their basic number. Lindschau (1933) reported chromosome counts for 47 species, many with $2n = 54$, and suggested a basic number of $x = 9$. Weiss (1965) later reported a series of counts that established basic numbers of $x = 8, 9$ and 25, and suggested that many of the species analysed were allohexaploids. Marchant (1967) analysed the chromosome numbers of 70 species, finding (with the exception of *Cryptanthus* with $n = 17$) $n = 25$ and 75 and $2n = 50$ and 100, indicating a basic number of $x = 25$ for most of the family. The analyses of Sharma & Ghosh (1971) revealed chromosome numbers of $2n = 34, 36, 46, 48, 50, 52, 98$ and 100, suggesting the existence of variable basic numbers of $x = 7, 8, 9$ and 25. More recent work agrees with a basic number of $x = 25$ (Brown & Gilmartin, 1986, 1989).

The present work attempts to fill some of the gaps in the knowledge of the cytogenetics of this family and its chromosomal evolution by reporting the chromosome numbers for 16 species of Bromeliaceae belonging to the subfamily Bromelioideae (*Aechmea*, *Cryptanthus*, *Hohenbergia*, *Neoregelia*, and *Nidularium*) and two species from the subfamily Tillandsioideae (*Alcantarea*).

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MATERIAL AND METHODS

Most of the material was collected from natural habitats, with some from specimens in cultivation (Table 1). The plants were kept in xaxim to encourage rooting. Root tips were pretreated with 0.002 M of 8-hydroxyquinoline at 18 °C for 4 h and fixed in Carnoy (absolute ethanol–acetic acid, 3 : 1) overnight, transferred to 70% alcohol, and stored at 4 °C until use. They were then hydrolysed in 1 M HCl for 8 min at 60 °C and stained in Feulgen (Sharma & Sharma, 1980). Squash preparations were made in 1% acetocarmine. The slides were mounted in Entellan. Chromosome counts were made from 5–20 metaphases of one to four plants of each species. Chromosome size was estimated from the metaphases using a micrometer scale.

RESULTS AND DISCUSSION

All of the chromosome counts reported in this work concern species that have not been examined previ-

ously, except for *Aechmea comata* (Lindschau, 1933) and *Hohenbergia cattingae* (Cotias de Oliveira *et al.*, 2000). The examined species of the genera *Aechmea*, *Alcantarea*, *Hohenbergia*, *Neoregelia*, and *Nidularium* had $2n = 50$, whereas those of *Cryptanthus* had $2n = 34$ (Table 1). Supernumerary chromosomes (in addition to those comprising the normal karyotype) were observed in *Aechmea bicolor*, *A. caudata*, *A. recurvata*, *A. comata*, *A. correia-araujoi* and *Cryptanthus warren-loosei*. The existence of these is well documented for a number of species of angiosperms, and may be responsible for some of the numerical discrepancies amongst the published chromosome counts in Bromeliaceae.

In general, the chromosomes of the species of *Cryptanthus* varied from 0.71 to 1.25 µm in length, whereas those of the species with $2n = 50$ varied from 0.25 to 1.5 µm.

Aechmea correia-araujoi, *A. caudata*, *A. comata*, *A. recurvata*, *A. pineliana*, *A. bicolor* (Figs 1–6), and *A. marauensis* had $2n = 50$, in agreement with earlier reports for the genus (Marchant, 1967; Brown &

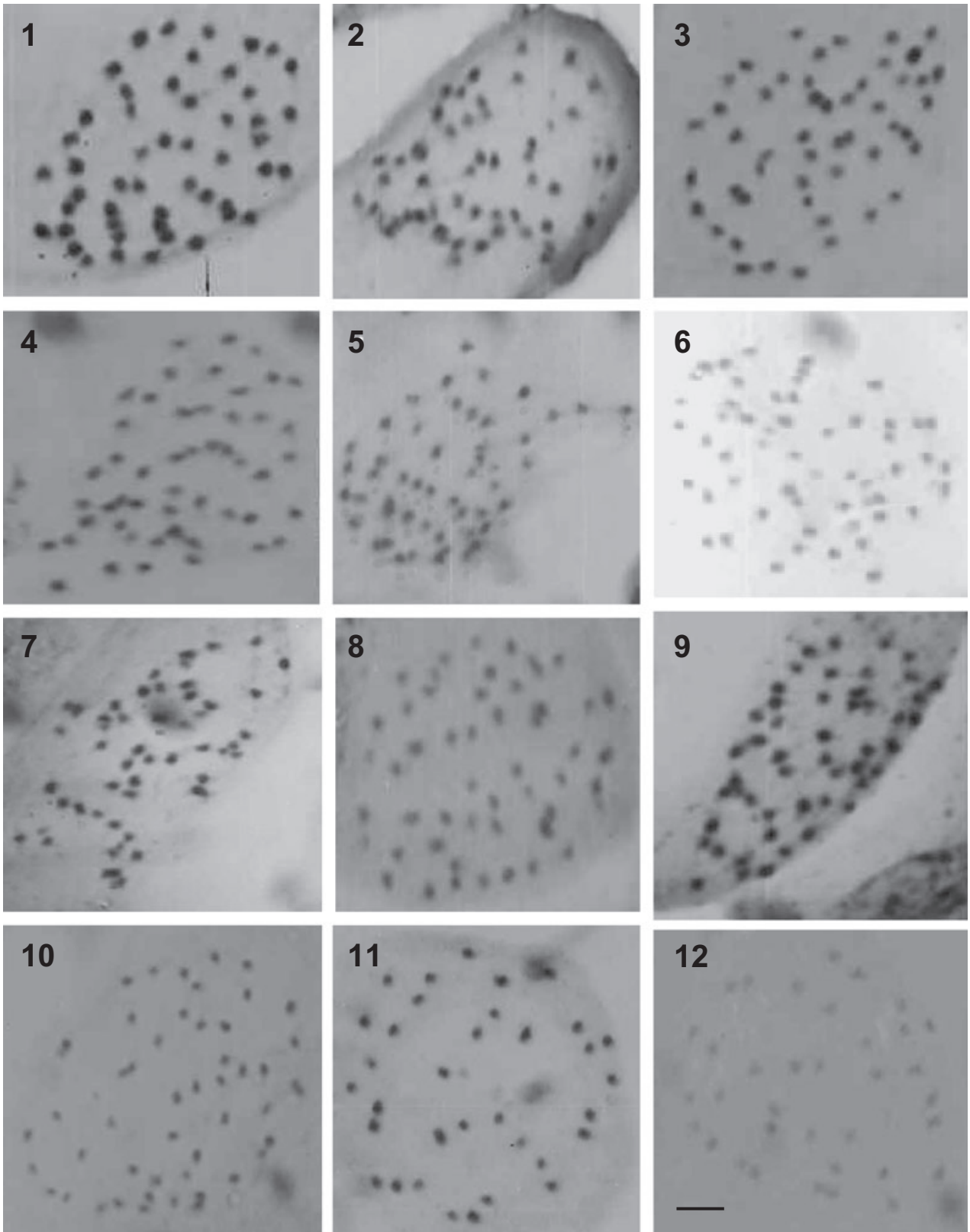
Table 1. List of species of Bromeliaceae analysed, with respective chromosome numbers and provenance or collection

Subfamily/species	Provenance	2n
Tillandsioideae		
<i>Alcantarea nahoumi</i> (Leme) R. Grant*	BA†, Santa Teresinha	50
<i>Al. imperialis</i> (Carrière) Harms*	RJ†, Rio de Janeiro (cultivated)	50
Bromelioideae		
<i>Neoregelia tenebrosa</i> Leme*	Leme collection 2218	50
<i>Nidularium lyman-smithii</i> Leme*	Leme collection 1871	50
<i>N. scheremetiewii</i> Regel*	Leme collection 048	50
<i>N. innocentii</i> var. <i>innocentii</i> Lemaire*	BA†, Jaguaripe	50
<i>N. innocentii</i> × <i>Neoregelia johannis</i> *	Leme collection	50
<i>Hohenbergia cattingae</i> Ule	BA†, Morro do Chapéu	50
<i>H. blanchetti</i> (Baker) E. Morren ex Mez*	BA†, Camaçari	50
<i>Aechmea comata</i> (Gaudichaud) Baker	RJ†, Rio de Janeiro (cultivated)	50
<i>A. caudata</i> Lindman*	RJ†, Rio de Janeiro (cultivated)	50
<i>A. recurvata</i> (Klotzsch) L.B. Smith*	RJ†, Rio de Janeiro (cultivated)	50
<i>A. correia-araujoi</i> Pereira & Moutinho*	RJ†, Rio de Janeiro (cultivated)	50
<i>A. pineliana</i> (Brongniart ex Planchon) Baker*	RJ†, Rio de Janeiro (cultivated)	50
<i>A. marauensis</i> Leme*	BA†, Camaçari	50
<i>A. bicolor</i> L. B. Smith*	BA†, Jaguaripe	50
<i>Cryptanthus warren-loosei</i> Leme*	BA†, Salvador	34
<i>C. maritimus</i> L.B. Smith*	BA†, Entre Rios	34

*First chromosome number report for the species.

†Brazilian states: BA, Bahia; RJ, Rio de Janeiro.

Figures 1–12. Mitotic metaphases in Bromeliaceae species. Fig. 1. *Aechmea correia-araujoi*, $2n = 50$. Fig. 2. *Aechmea caudata*, $2n = 50$. Fig. 3. *Aechmea comata*, $2n = 50$. Fig. 4. *Aechmea recurvata*, $2n = 50$. Fig. 5. *Aechmea pineliana*, $2n = 50$. Fig. 6. *Aechmea bicolor*, $2n = 50$. Fig. 7. *Alcantarea imperialis*, $2n = 50$. Fig. 8. *Alcantarea nahoumi*, $2n = 50$. Fig. 9. *Hohenbergia blanchetti*, $2n = 50$. Fig. 10. *Hohenbergia cattingae*, $2n = 50$. Fig. 11. *Cryptanthus maritimus*, $2n = 34$. Fig. 12. *Cryptanthus warren-loosei*, $2n = 34$. Scale bar, 5 µm.



Gilmartin, 1986, 1989; Brown *et al.*, 1997; Cotias de Oliveira *et al.*, 2000, 2004; Palma-Silva *et al.*, 2004). However, Marchant (1967) found $n = 21$ for *A. tillandsioides*. This suggests that dysploidy has occurred in species of some genera with $2n = 50$, reducing the number of chromosomes with the previous transfer of genetic material to the remaining chromosomes.

The counts presented here for species of the genera *Neoregelia* and *Nidularium* agree with the $2n = 50$ observed in other species analysed previously within the same genera (Marchant, 1967; Cotias de Oliveira *et al.*, 2004). However, Lindschau (1933) recorded $2n = 54$ for *Nidularium innocentii* var. *lineatum*. The genus *Nidularium* is endemic to Brazil, occurring in the states of Bahia and Rio Grande do Sul. *Nidularium innocentii* is the most widely distributed species within this range. The hybrid form analysed in this work (*Nidularium innocentii* × *Neoregelia johannis*) showed $2n = 50$, as did *Nidularium lyman-smithii*.

The genus *Alcantarea* was considered by Smith & Downs (1977) to be a subgenus of *Vriesea*, but was resurrected as a genus by Grant (1995). It is endemic to Brazil and comprises 15 species distributed in Bahia, Rio de Janeiro, Minas Gerais and Espírito Santo (Grant, 1995). The species analysed here, *Al. imperialis* and *Al. nahoumi*, have $2n = 50$ (Figs 7, 8), with chromosomes relatively uniform in size. This size uniformity contrasts with other species of *Vriesea* analysed previously by Marchant (1967) and Cotias de Oliveira *et al.* (2004), who demonstrated a bimodal karyotype, with two distinctly different size classes. These chromosomal differences strengthen the case for treating *Alcantarea* as a genus distinct from *Vriesea*.

Hohenbergia blanchetti and *H. catingae* analysed here were diploid, also with $2n = 50$ (Figs 9, 10). This observation is in agreement with earlier reports for other species in the genus (Brown *et al.*, 1997; Cotias de Oliveira *et al.*, 2000; Bellintani *et al.*, 2005).

The genus *Cryptanthus* is endemic to Brazil and comprises 45 species. It is found in areas of Atlantic coastal forest and caatinga dry lands, from the state of Paraíba south to Rio de Janeiro and Goiás. The greatest diversity of species is found in the states of Minas Gerais, Espírito Santo and Rio de Janeiro (Ramírez, 1998). More than 60% occur in the Atlantic Coastal Forest, a biome recognized widely for its high percentage of endemic species.

Cryptanthus, with $2n = 34$ (Figs 11, 12), demonstrates chromosome numbers distinct from all other genera of Bromeliaceae. The pattern for the majority of the genera is $2n = 50$, reflecting a basic number of $x = 25$. Brown & Gilmartin (1989) suggested a model of chromosome evolution for Bromeliaceae that fits the chromosome numbers already recorded. This suggests that the basic number $x = 25$ could be derived

from hybridization between palaeo-diploids with $x = 8$ and 9, with chromosome doubling to produce a palaeo-tetraploid with $x = 17$. Later hybridization of this palaeo-tetraploid and a palaeo-diploid with $x = 8$ could have resulted in an allohexaploid with $x = 8 + 8 + 9 = 25$, which now forms the basis of the entire family. They suggested two alternative hypotheses that could explain the basic number of $x = 17$ in *Cryptanthus*. It could represent the palaeo-tetraploid level ($x = 8 + 9$) or could be the result of a recent series of aneuploid reductions from $x = 25$, although no intermediate chromosome number has been found. The second alternative seems to be more likely, because of the fact that the genus exhibits numerous features considered to be derived within the subfamily (Brown & Gilmartin, 1989).

Additional chromosomal analyses in species of *Cryptanthus* have been undertaken by other authors. Marchant (1967) recorded $n = 17$ for *C. bahianus*, *C. acaulis* and *C. zonatus* and $2n = 34$ for *C. beuckeri*. Brown & Gilmartin (1986) recorded $2n = 34$ and 36 for *C. acaulis* and *C. zonatus*. Sharma & Ghosh (1971) reported $2n = 34$ for *C. bromelioides* and *C. praetextus*, and $2n = 36$ for *C. bivittatus*. Lindschau (1933), by contrast, reported $2n = 54$ for *C. beuckeri*, a number atypical for this genus. This may reflect faulty identification of the specimens, in the light of the fact that Marchant (1967) and Bellintani *et al.* (2005) reported $2n = 34$ for this species.

Cytogenetic analyses of Bromeliaceae reveal an almost universal homogeneity of basic chromosome number, which is atypical in comparison with most other families of monocotyledons, many of which demonstrate significant heterogeneity in basic number between genera, and even among species of the same genus (Guerra, 2000). As such, more investigations are necessary in order to improve the characterization of the chromosome complement of Bromeliaceae, to provide more information that may reinforce existing hypotheses, and/or raise others that might help to explain the evolution of the karyotype of the family.

ACKNOWLEDGEMENTS

We are grateful to Elton Leme and Rogério Alves, who kindly supplied plants, and Ervene Barreto for technical support. G. O. Ceita was supported by a graduate fellowship from Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq).

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