



Genetics, evolution and conservation of Bromeliaceae

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Abstract

Bromeliaceae is a morphologically distinctive and ecologically diverse family originating in the New World. Three centers of diversity, 58 genera, and about 3,140 bromeliad species are currently recognized. We compiled all of the studies related to the reproductive biology, genetic diversity, and population structure of the Bromeliaceae, and discuss the evolution and conservation of this family. Bromeliads are preferentially pollinated by vertebrates and show marked variation in breeding systems, from predominant inbreeding to predominant outcrossing, as well as constancy in chromosome number ($2n = 2x = 50$). Autogamous or mixed mating system bromeliads have a high inbreeding coefficient (F_{IS}), while outcrossing species show low F_{IS} . The degree of differentiation among populations (F_{ST}) of species ranges from 0.043 to 0.961, which can be influenced by pollen and seed dispersal effects, clonal growth, gene flow rates, and connectivity among populations. The evolutionary history of the Bromeliaceae is poorly known, although some studies have indicated that the family arose in the Guayana Shield roughly 100 Mya. We believe that genetic, cytogenetic, and reproductive data will be essential for diagnosing species status and for assisting conservation programs.

Keywords: bromeliads, cytogenetics, genetic diversity, population structure, reproductive biology.

Introduction

The Bromeliaceae is one of the morphologically and ecologically most diverse flowering plant families native to the tropics and subtropics of the New World (Givnish *et al.*, 2011). Its geographical distribution ranges from the states of Virginia, Texas, and California in the USA (latitude 37° N) to northern Patagonia in Argentina (latitude 44° S). The family is known for its recent adaptive radiation. Bromeliads have different habits, varying from terrestrial to epiphytical, and are found from sea level to altitudes above 4,000 m, in both desert and humid regions, as well as in soils subject to regular floods and in places with very low or high luminosity. They can thrive on scalding sands and rocks, and withstand temperatures near 0 °C (Benzing, 2000).

Traditionally, the family has been divided into three subfamilies, Bromelioideae (~650 spp.), Pitcairnioideae (~890 spp.), and Tillandsioideae (~1000 spp.), based on

Smith and Downs (1979); this classification is adopted in the present study. However, in a recent phylogeny based on eight plastid regions, with representatives from 46 of 58 genera, Givnish *et al.* (2011) confirmed the eight-subfamily classification advanced by Givnish *et al.* (2007). The new classification splits the paraphyletic Pitcairnioideae into six subfamilies and proposes that they are related to each other as follow: (Brocchinioideae, (Lindmanioideae, (Tillandsioideae, (Hechtioideae, (Navioideae, (Pitcairnioideae, (Puyoideae, Bromelioideae)))))).

Bromeliads are especially appreciated for their ornamental value, but some species have proven medicinal properties (*e.g.*, *Bromelia antiacantha*) or are cultivated as tropical fruits (*e.g.*, pineapple: *Ananas comosus*). Here, we review the main genetic and evolutionary topics concerning Bromeliaceae, from a conservation standpoint.

Pollination and Reproductive Biology

Among the plant families, Bromeliaceae is the one with the highest diversity of pollination modes (ornithophily, chiropterophily, entomophily, mixed/unspecific, and autogamy) throughout its geographic distribution (Kessler

and Krömer, 2000; Canela and Sazima, 2005; Wendt *et al.*, 2008; Schmid *et al.*, 2010). Bromeliads have evolved floral displays with a great diversity of colors, shapes, and scents, which are related to pollinator attraction, with nectar being the usual reward (Benzing, 2000). The presence of Bromeliaceae in the New World has provided an important resource base, largely absent in the Old World, for small, hovering vertebrate pollinators (Fleming and Muchhala, 2008). A recent study (Krömer *et al.*, 2008) strongly supports the hypothesis that the composition of nectar sugars in Bromeliaceae is correlated with the pollinator syndrome (lepidopterophilous, trochilophilous, or chiropterophilous). Although the majority of bromeliads are pollinated by vertebrates, mainly hummingbirds and bats, bees are among the most frequent visitors to some short-corolla species with ornithophilous features. Nevertheless, few studies have identified insects as effective pollinators of these bromeliads (Kamke *et al.*, 2011).

Simultaneously with the divergence of bromeliad subfamilies (see “Evolution” below), the first split of modern hummingbird lineages appears to have occurred in the Andes about 13 Mya, with several other Andean lineages diverging during the Pliocene and Pleistocene (Givnish *et al.*, 2011). This might have contributed to the rapid expansion of the range of bromeliads and pollinators throughout the Neotropics. However, plant-pollinator interactions, seed dispersal, and the mechanisms promoting or constraining species diversification via these interactions are complex and poorly studied in the Neotropics (Antonelli and Sanmartín, 2011).

Bromeliads possess specialized floral features such as herkogamy and dichogamy, which prevent spontaneous self-fertilization and facilitate animal-mediated outcrossing (Benzing, 2000; Martinelli G, 1994, PhD Thesis, University of St. Andrews). Floral morphology, hand-pollination experiments, and population genetics studies have shown that selfing and mixed are the most common mating systems in a large part of the family (Bush and Guilbeau, 2009; Matallana *et al.*, 2010; Table 1), although self-incompatibility systems can be found in all of the subfamilies (Pitcairnioideae: Vosgueritchian and Buzato, 2006; Bromelioideae: Canela and Sazima, 2003, 2005; Schmid *et al.*, 2010; Kamke *et al.*, 2011; Tillandsioideae: Hietz *et al.*, 2006; Ramírez-Morillo *et al.*, 2009). The Tillandsioideae subfamily has a particularly high frequency of selfing and mixed systems in various genera, including *Alcantarea*, *Guzmania*, *Racinea*, *Tillandsia*, *Vriesea*, and *Werauhia* (Benzing, 2000; Lasso and Ackerman, 2004; Paggi *et al.*, 2007, 2012; Matallana *et al.*, 2010; Martinelli G, 1994, PhD Thesis, University of St. Andrews; Table 1). Clonality is another reproductive strategy present in the family (Murawski and Hamrick, 1990; Izquierdo and Pinero, 2000; Sarthou *et al.*, 2001; Sampaio *et al.*, 2002; Sgorbati *et al.*, 2004; Cascante-Marín *et al.*, 2006; Barbará *et al.*, 2009), with important ecological and evolutionary consequences

(Gonzales *et al.*, 2008) such as recruitment and population maintenance (Villegas, 2001).

We studied the mating systems of two bromeliad species. *Vriesea gigantea* presented a high natural production of flowers, fruits, and seeds, with high rates of viable seeds, with an average germination rate of 94% (Paggi *et al.*, 2007, 2010). Furthermore, the species showed regular chromosome segregation and high pollen viability (84-98%, Palma-Silva *et al.*, 2008), which indicated that the populations analyzed were fertile. Manual hand-pollination indicated that *V. gigantea* is self-compatible (Paggi *et al.*, 2007) and showed low to moderate levels of inbreeding depression ($\delta = 0.02$ to 0.39 ; Sampaio *et al.*, 2012). In a study with *Vriesea friburgensis* we highlighted that it is pollinated by hummingbirds and produces high flower, fruit, and seeds together with high seed and pollen viability. We concluded that the wild populations studied were fertile. Self-sterility was observed from spontaneous selfing and manual self-pollination treatments, which may be a consequence of late-acting self-incompatibility. We proposed that this self-sterile species depends on pollinator services to maintain its population fitness and viability through cross-pollination (Paggi *et al.*, 2012).

Diversity and Genetic Structure

The genetic diversity of only a few species of Bromeliaceae has been studied. We compiled data from all diversity and genetic structure studies published before June 2011 (Table 1). Of the 58 genera and about 3,140 bromeliad species (Givnish *et al.*, 2011), only 20 species of the following nine genera have been previously evaluated: *Aechmea*, *Alcantarea*, *Bromelia*, *Dyckia*, *Encholirium*, *Pitcairnia*, *Puya*, *Tillandsia*, and *Vriesea*. Most of the studied species are endemic to the Atlantic rainforest in southeastern Brazil.

The use of co-dominant markers has been the preferred method for studying bromeliad population genetics, with nuclear microsatellite markers being the most frequently used molecular markers (nine species), followed by allozymes (eight species). Dominant markers such as amplified fragment length polymorphisms have been used in only one study of one species, and random amplified polymorphic DNA was applied in another study of three species (Table 1). A comparison of genetic diversity parameters among such studies is difficult, as the highly polymorphic SSRs usually show higher observed and expected heterozygosity (H_O and H_E , respectively) compared with other markers. For example, populations of *Pitcairnia geyskesii* have been evaluated using allozymes (Sarthou *et al.*, 2001) and SSRs (Boisselier-Dubayle *et al.*, 2010). With allozymes, H_O and H_E were 0.188 and 0.246, respectively; with SSRs, H_O and H_E were 0.293 and 0.324, respectively.

We found low inbreeding coefficient indices (F_{IS}) in almost all species with outcrossing mating systems. The ex-

Table 1 - Bromeliads studied: Mating system, genetic diversity and population structure descriptors, molecular markers used and geographical distribution.

| Species | Mating system | Marker | H_O mean/all | H_F mean/all | F_{IS} mean | F_{ST} mean | Geographical distribution | Reference |
|---|---------------|----------|----------------|----------------|---------------|--------------------|---|---|
| <i>Aechmea magdalenae</i> | ND | Allozyme | 0.099/- | 0.084/- | - | 0.356 ^a | Mexico to Ecuador | Murawski and Hamrich, 1990 |
| <i>Aechmea tuitensis</i> | ND | Allozyme | 0.061/- | 0.12/- | 0.631 | 0.196 | Endemic to Mexico | Izquierdo and Piñero, 2000 |
| <i>Alcantarea geniculata</i> | Out | SSR | 0.356/0.357 | 0.380/0.429 | 0.094 | 0.1111 | Rio de Janeiro, Brazil | Barbará <i>et al.</i> , 2007 |
| <i>Alcantarea glaziouana</i> | Out | SSR | 0.259/0.299 | 0.334/0.472 | 0.156 | 0.217 | Rio de Janeiro, Brazil | Barbará <i>et al.</i> , 2009 |
| <i>Alcantarea imperialis</i> | Out | SSR | 0.357/0.362 | 0.398/0.615 | 0.099 | 0.434 | Rio de Janeiro, Brazil | Barbará <i>et al.</i> , 2007 |
| <i>Alcantarea Regina</i> | Out | SSR | 0.479/0.484 | 0.458/0.523 | -0.051 | 0.195 | Rio de Janeiro, Brazil | Barbará <i>et al.</i> , 2009 |
| <i>Bromelia antiacantha</i> | Out | SSR | 0.326/- | 0.559/- | 0.431 | 0.224 | southeastern Brazil | Zanella <i>et al.</i> , 2011 |
| <i>Dyckia ibiramensis</i> | Mix | Allozyme | 0.055/0.064 | 0.098/0.219 | 0.436 | 0.674 ^b | Endemic to southern Brazil | Hmeljevski <i>et al.</i> , 2010 |
| <i>Encholirium biflorum</i> | ND | RAPD | - | - | - | 0.160 ^c | Cadeia do Espinhaço, Brazil | Cavallari <i>et al.</i> , 2006 |
| <i>Encholirium pedicellatum</i> | ND | RAPD | - | - | - | 0.084 ^c | Cadeia do Espinhaço, Brazil | Cavallari <i>et al.</i> , 2006 |
| <i>Encholirium subsecundatum</i> | ND | RAPD | - | - | - | 0.012 ^c | Cadeia do Espinhaço, Brazil | Cavallari <i>et al.</i> , 2006 |
| <i>Pitcairnia albiflos</i> | Out | SSR | 0.383/- | 0.429/- | 0.109 | 0.336 | Rio de Janeiro, Brazil | Palma-Silva <i>et al.</i> , 2011 |
| <i>Pitcairnia geyskesii</i> | ND | SSR | 0.293/- | 0.325/- | 0.125 | 0.156 | French Guyana and Suriname | Boisselier-Dubayle <i>et al.</i> , 2010 |
| <i>Pitcairnia geyskesii</i> | ND | Allozyme | 0.185/0.188 | 0.183/0.246 | -0.037 | 0.266 | French Guyana and Suriname | Sarthou <i>et al.</i> , 2001 |
| <i>Pitcairnia staminea</i> | Aut | SSR | 0.347/- | 0.452/- | 0.240 | 0.336 | Rio de Janeiro, Brazil | Palma-Silva <i>et al.</i> , 2011 |
| <i>Puya raimondii</i> | Aut | AFLP | - | - | - | 0.961 ^a | Peru | Sgorbati <i>et al.</i> , 2004 |
| <i>Tillandsia achyrotachys</i> ^d | ND | Allozyme | 0.127/- | 0.210/- | 0.433 | 0.391 | Mexico | González-Astorga <i>et al.</i> , 2004 |
| <i>Tillandsia ionantha</i> | ND | Allozyme | 0.064/- | 0.069 | 0.056 | 0.043 | Central Mexico to Nicaragua | Soltis <i>et al.</i> , 1987 |
| <i>Tillandsia recurvata</i> | ND | Allozyme | 0/- | 0.01/- | 1.000 | 0.906 | USA to Argentina | Soltis <i>et al.</i> , 1987 |
| <i>Vriesea friburgensis</i> | Mix | Allozyme | -0.234 | -0.226 | -0.035 | - | Rio Grande do Sul to Pernambuco, Brazil | Alves <i>et al.</i> , 2004 |
| <i>Vriesea gigantea</i> | Mix | SSR | 0.431/- | 0.579/- | 0.273 | 0.211 | Brazil (south and southeast) | Palma-Silva <i>et al.</i> , 2009 |

ND = Not determined; Out = Outcrossing; Mix = Mixed; Aut = Autogamous; AFLP = Amplified Fragment Length Polymorphism; RAPD = Random Amplified Polymorphic DNA; SSR = Microsatellite.

^a G_{ST} (Nei, 1973, 1977).

^b G'_{ST} (Hedrick, 2005).

^c θ_{ST} (Excoffier *et al.*, 1992).

^d*Tillandsia achyrotachys* var *achyrotachys*.

ceptions were *B. antiacantha* ($F_{IS} = 0.431$), possibly due to the Wahlund effect and/or null alleles, and *Alcantarea glaziouana* ($F_{IS} = 0.156$), owing to biparental inbreeding. *Pitcairnia staminea*, which is autogamous, had a high inbreeding coefficient ($F_{IS} = 0.240$; Table 1). *V. gigantea* and *Dyckia ibiramensis*, which have a mixed mating system, also showed high inbreeding coefficients ($F_{IS} = 0.273$ and 0.436 , respectively; Table 1). The degree of differentiation among populations (F_{ST}) of species evaluated ranged from 0.043 to 0.961. These differences in plant population structure can be influenced by pollen and seed dispersal effects, clonal growth (Gliddon *et al.*, 1987), gene flow rates, and connectivity among populations. Compared with species from continuous forest habitats, species restricted to inselberg habitats (Barbará *et al.*, 2007, 2009; Palma-Silva *et al.*, 2011; Table 1) showed more highly structured populations, with extremely high population differentiation and isolation based on the distance among inselbergs. Thus, rock outcrops could be highly useful venues for studies regarding the molecular ecology and genetics of continental radiations.

Cytogenetics

Few cytogenetic studies of Bromeliaceae are available. Chromosome numbers have been determined for nearly 12% of the known species (Cotias-de-Oliveira *et al.*, 2004), most of which are horticulturally important as ornamentals or fruit producers. Owing to the scarcity of cytogenetic data, the chromosomal evolution of the family has not been completely elucidated. The major hindrances to cytogenetic studies are probably the very small size and poor staining ability of the chromosomes, together with a marked cytoplasmic content (Sharma and Ghosh, 1971; Brown and Gilmartin, 1986).

Billings (1904) was the first to determine the chromosome number of a bromeliad, using *Tillandsia usneoides*, after which several studies were carried out. The first reports revealed a great variety of diploid numbers ($2n = 16, 34, 36, 46, 48, 50, 52, 54, 56, 64, 96, \text{ and } 100$) and basic numbers ($x = 5, 8, 9, 16, 17, \text{ and } 25$; Brown and Gilmartin, 1986; Bellintani *et al.*, 2005). In contrast, most of the 72 bromeliad species studied by Marchant (1967) showed a basic number of $x = 25$ (except *Cryptanthus*: $x = 17$). Since then, studies in several different species have generally found the basic chromosome number to be a multiple of $x = 25$, corroborating Marchant's finding (Brown and Gilmartin, 1989; Cotias-de-Oliveira *et al.*, 2000, 2004; Palma-Silva *et al.*, 2004; Gitaí *et al.*, 2005; Ceita *et al.*, 2008; Louzada *et al.*, 2010). Polyploidy of this base number ($2n = 4x = 100$ and $2n = 6x = 150$) has been observed in all subfamilies, but with low frequency (Brown and Gilmartin, 1989; Gitaí *et al.*, 2005; Louzada *et al.*, 2010).

Brown and Gilmartin (1989) have proposed a model to explain the evolution of the chromosome base number. In their model, two paleodiploids ($x = 8$ and $x = 9$) hybrid-

ized, resulting in a paleotetraploid lineage ($x = 17$), which in turn hybridized with the $x = 8$ paleodiploid, and the poliploidization stabilized at the hexaploid level of $x = 25$. Electrophoretic data (Soltis *et al.*, 1987) suggest that a "diploidization" of the dibasic paleohexaploid occurred. The dibasic model could explain the origin of the distinctive chromosome number in *Cryptanthus*, which may represent a paleotetraploid with $2n = 34$. One alternative hypothesis is that *Cryptanthus* evolved from $x = 25$ via aneuploidy (Brown and Gilmartin, 1989). Flow cytometric results obtained by Ramírez-Morillo and Brown (2001) indicated that the *Cryptanthus* chromosome number originated by descending aneuploidy.

Bromeliaceae chromosomes are usually exceedingly small (0.21–2.72 μm), although the size varies widely among species. According to Gitaí *et al.* (2005), larger chromosomes are usually found at lower ploidy levels, with diploids exhibiting a higher contrast between maximal and minimal chromosome sizes compared with polyploids. Chromosome banding and triple staining with CMA₃/Actinomycin/DAPI has revealed that bromeliads have relatively little heterochromatin, with only one or two CMA⁺/DAPI terminal bands corresponding to nucleolus organizing regions. B chromosomes have been reported in three Bromelioideae species (Cotias-de-Oliveira *et al.*, 2000, 2004; Bellintani *et al.*, 2005).

Evolution

Recently, Givnish *et al.* (2011) reinforced the *i.e.* of Smith (1934) that bromeliads arose in the Guayana Shield roughly 100 Mya during the Cretaceous Period, with the extant subfamilies beginning to diverge only about 19 Mya. Givnish *et al.* (2011) also suggested that about 15.4 Mya, bromeliads began to spread from that hyper-humid, extremely infertile center to other parts of tropical and subtropical America, and probably arrived in tropical Africa about 9.3 Mya, in a recent long-distance dispersal event. During the evolution of this family, events such as climatic oscillations throughout the Pleistocene have resulted in the dispersion of some clades, including Bromelioideae (Givnish *et al.*, 2011). As of the current time, *V. gigantea* has survived glaciation periods in two fragmented refugia in southeastern Brazil (Palma-Silva *et al.*, 2009).

The "bromeliad revolution" probably occurred after the uplift of the northern Andes and shift of the Amazon to its present course (Givnish *et al.*, 2007). Some morphological and physiological adaptations, including crassulacean acid metabolism (CAM) photosynthesis and the formation of rosettes and leaf absorptive scales, might have been crucial to the adaptive radiation of bromeliads (Benzing, 2000; Crayn *et al.*, 2004).

An ecological peculiarity of Bromeliaceae, compared with other families of the order Poales, is their epiphytic habit (Linder and Rudall, 2005). Based on plastid loci,

Crayn *et al.* (2004) proposed that the epiphytic habit of bromeliads evolved a minimum of three times, most likely in response to geological and climatic changes in the late Tertiary.

The more than 3,000 bromeliad species that currently occupy the Neotropical region have evolved to fill numerous niches, with an incredible diversity of adaptations. Some aspects of the complex evolutionary history of this family are still unclear, indicating the need for further molecular studies, in combination with paleontological data, to explain the evolutionary gaps in the wide diversity of bromeliad forms and adaptations.

Conservation

Bromeliads are widely distributed in the Neotropics, with three centers of diversity: the Brazilian Atlantic rainforest; the Andean slopes of Peru, Colombia, and Ecuador; and Mexico and adjacent Central America (Zizka *et al.*, 2009). Many species are presently distributed in endangered biomes, are endemic, or have a relict distribution, threatening the survival of many members of this family. For example, the Brazilian Atlantic rainforest is a diverse biome with multiple extremely endangered vegetation types occupying only 7.91% of the extent of their original distribution (Fundação SOS Mata Atlântica and Instituto Nacional de Pesquisas Espaciais, 2009; Carnaval and Moritz, 2008). As the Atlantic rainforest contains at least 803 bromeliad species, 653 of which are endemic and 40% of which are endangered, the preservation of the Atlantic rainforest is vital for the conservation of Bromeliaceae (Martinelli *et al.*, 2008).

Few studies of Bromeliaceae connect genetic data and conservation planning. All of the works cited in the above section “Diversity and genetic structure” contain data that could be used in making conservation decisions. Considerations of the clonal and sexual reproduction, demography, genetic structure within and among populations, gene flow, and mating systems of Bromeliaceae are of primary importance in developing successful conservation strategies (Bizoux and Mahy, 2007).

Our group has studied mainly Brazilian bromeliads, and our field records show a significant reduction in the current distribution of species, compared with the first records in the literature. We believe that genetic, cytogenetic, and reproductive data will be essential for diagnosing species status and for assisting conservation programs and will help to elucidate aspects of evolution and environmental and climate change for Bromeliaceae and the Brazilian Atlantic rainforest.

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