An Explanatory message from the author

Plant Conservation: A Natural History Approach by Krupnick and Kress (eds.) was published in 2005 by University of Chicago Press.

The Chapters are divided into sections and each Chapter has a literature cited that includes the references for all of the sections of that chapter. The Press did not provide PDF's of the papers. We have scanned in the four sections for which I am a co-author and included the literature cited for the entire Chapter. There are, therefore, many extraneous references in the Literature Cited for each paper and the page numbers for the literature cited and the actual paper are not sequential in three of the four papers. Color plates follow the chapters and like the literature cited contain extraneous material. This presentation is not perfect but it appears to be our only option. - Vicki

The four papers included are as follows:
Chapter 4.3. *The Guiana Shield* by V. A. Funk and P. E. Berry, article pages76-79, literature 89-92
Chapter 5.7 *Daisies and Sunflowers: Family Asteraceae* by V. A. Funk and H. E. Robinson, article pages 115-124, literature 130-137.
Chapter 10.1 *Herbarium Collections, Floras and Checklists* by W. J. Kress and V. A. Funk, article pages 209-218, literature at end of next section.
Chapter 10.3 *Phylogenetic Considerations* by M. A. Jaramillo and V. A. Funk, article pages 223-229, literature 229-235.
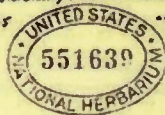
PLANT CONSERVATION

A NATURAL HISTORY APPROACH

Edited by Gary A. Krupnick and W. John Kress

With a foreword by Daniel H. Janzen

near two artificial lakes, the Laguna Negra and the Laguna de Los Cedros. Both are located on the northwestern edge of the park, and both have large numbers of introduced and adventive plant species. As yet, few foreign tourists visit Guaramacal National Park. Those who do, however, seem most interested in birds. Ecotourism could probably be expanded with negligible impact on the park's biodiversity.

It is likely, given the enormous human pressure being exerted on all tropical forests, that relatively well studied natural areas such as Guaramacal National Park will become increasingly important as isolated exemplars of entire biomes. Our obligation is therefore not only to protect them, but also to understand them.

4.3 THE GUIANA SHIELD

Vicki A. Funk and Paul E. Berry

THE GUIANA SHIELD underlies the northeastern corner of South America and includes much of the area east and south of the Río Orinoco and east and north of the Rio Negro and Rio Amazonas. The area includes Bolívar, Amazonas, and Delta Amacuro states in Venezuela; most of Guyana, Surinam, and French Guiana; parts of northern Brazil; and parts of southeastern Colombia. The area, which includes the famous tepuis of Sir Arthur Conan Doyle's *Lost World*, is known to be rich in species diversity; for many groups, including some plant families, it serves as a center of species diversity. The Venezuelan portion of the Shield is the subject of a detailed flora (families A–M have been published), with the first volume dedicated to extensive background information on the Guiana Shield and its flora (Steyermark et al. 1995–present). The *Flora of the Guianas* (Guyana, Surinam, and French Guiana) is in progress, and a number of volumes have been published (Görts–van Rijn 1989–present).

The Guiana Shield refers to an ancient craton that was formed well before the breakup of the supercontinent of Gondwana. The Shield's igneous-metamorphic basement was laid down in several events from 0.8 to 3.6 billion years ago (Mendoza 1977; Schubert and Huber 1990). This granitic basement is easily observed in the many black "hills" of granite that dot the landscape across the Guiana Shield and is exposed on some of the mountains and massifs. Between 1 and 1.6 billion years ago, sedimentary covers of sand were successively laid down and cemented during thermal events (Huber 1995). The resulting quartzite and sandstone rocks are known today as the Roraima Formation. Some recent work has suggested that the eastern rocks are the oldest (Huber 1995), so this would make the Pakaraima Mountains and the eastern parts of Venezuela older than the rest of the Roraima Formation.

Over the last 200 to 600 million years, intrusions of diabases and granite have penetrated both the granitic basement and the quartzite sedimentary rocks.

The most distinctive feature of the Guiana Shield is the tepuis, the steep-walled table mountains prominently featured in photos and films. For many groups of organisms, they support a unique flora and fauna. Tepui elements begin to appear in the biota at around 300–1,000 m elevation, but predominate above 1,500–1,800 m. The easternmost peaks that reach heights of 2,000 m include Mount Ayanganna and Mount Wokomong in Guyana. The highest tepui, Sierra de la Neblina, just exceeds 3,000 m elevation and occurs in the western part of the Shield on the border of Venezuela and Brazil. Many of the remaining Venezuelan tepuis have summits between 2,000 and 2,400 m. There is a large, midelevation, sandy plateau between 400 and 1,500 m called La Gran Sabana that occupies southwestern Venezuela and adjacent parts of Guyana, and there are variously sized areas of lowland white-sand savannas scattered in different parts of the Shield.

The Guiana Shield is located slightly north of the equator and is affected by trade winds blowing off the Atlantic Ocean. The trade winds bring moisture and collide with other masses of air in what is known as the intertropical convergence zone (ITCZ). Over the course of the year, the ITCZ migrates north and south, leading to distinct wet and dry seasons in different parts of the equatorial zone of South America. The rainy part of the year in the Venezuelan part of the Guiana Shield is from May to August, and the driest part is from January to March (earlier to the south, later to the north). As one moves to the east, a second rainy season develops from December to January. This second rainy season is shorter, is less intense, and does not penetrate as far inland from the Atlantic Ocean. As a whole, the Guiana Shield has a tropical climate characterized by a high mean annual temperature exceeding 25°C at sea level (but decreasing with elevation); a diurnal range of temperature exceeding the annual range; and an annual temperature range of less than 5°C. Most of the Shield area is covered by evergreen forest, but scrub or savanna predominates in some lowland areas, particularly when soil conditions are extremely poor or clay hardpans prevent penetration by tree roots and lead to flooding during the rainy season. Slopes of mountains that face the incoming trade winds usually have higher precipitation than the leeward sides (Clarke et al. 2001).

Only a few parts of the Guiana Shield have well-known floras, such as Mount Roraima (Venezuela), Iwokrama–Mabura Hill and Kaieteur (Guyana), Tafelberg (Surinam), and Saül (French Guiana). Most areas, such as the lowland forests and tepui slopes in Venezuela, the Pakaraima Mountains and New River Triangle in Guyana, and southern Surinam and French Guiana, are very poorly known. Hollowell et al. (2001) recently published a checklist for about half the flowering plants of the Guiana Shield (families from A to L). Using this publication and subsequent online updates (see Biological Diversity of the Guiana Shield 2004) as a guide, we estimate there are 12,500 species of flowering plants currently known for the Guiana Shield (excluding Brazil and Colombia). The ten largest groups are the Fabaceae (sensu lato), ferns or pteridophytes (all families), Orchidaceae, Rubiaceae, Poaceae,

Cyperaceae, Melastomataceae, Euphorbiaceae, Myrtaceae, and Asteraceae. The Venezuelan portion of the Shield includes about 9,000 species, Guyana 6,200, Surinam 4,500, and French Guiana 5,000 (these species partially overlap between countries). If the southern part of Surinam were better explored, the number of species for that country would surely increase. The Venezuelan Guayana includes 672 species of ferns and fern allies (Berry et al. 1995), while there are 638 species in the three Guianas. The estimated overlap of these two areas is 74%, so that the total number of ferns is predicted to be close to 1,000 species (not including the Brazilian and Colombian parts of the Shield). Thus, a conservative estimate of the total number of vascular-plant species from the Guiana Shield is 13,500 species, perhaps closer to 15,000 with the Colombian and Brazilian parts of the Shield included. Berry et al. (1995) calculated that 40% of the plant species occurring in the Guiana Shield do not occur outside this area. A closer analysis of the flora of Kaieteur Falls, Guyana (Kelloff and Funk 2004; plate 4.2), shows that 42% of the plant species are endemic to the Guiana Shield. Consequently, we can conclude that about 6,000 species of vascular plants are restricted to the Guiana Shield. Considering just the plants of the Pantepui area (over 1,500 m elevation), Berry et al. (1995) found that the percentage of endemics increases to 65%. Notable families with high levels of endemism include Asteraceae, Bonnetiaceae, Bromeliaceae, Eriocaulaceae, Podostemaceae, Rapateaceae, Rubiaceae, Tepuianthaceae, and Xyridaceae. This level of endemism must be one of the highest for noninsular floras, and documents the existence of a "Guiana Shield flora" that is separate from other floras such as the Andean, Amazonian, and Brazilian Shield floras.

With a few exceptions, such as cities along the Río Orinoco, the Rupununi savanna (Guyana), and the coastal areas of the Guianas, the Guiana Shield has benefited from its isolation and low population density, and much of the vegetation is still relatively undisturbed by human activities. This has led to its designation as a "tropical wilderness" (Mittermeier et al. 1998). Unfortunately, the pace of disturbance has accelerated greatly in recent times because of logging by Asian and local companies, gold and diamond mining, oil drilling, bauxite mining, dams for hydroelectric power, wildlife trade, burning, grazing, and agriculture. If this pace of activity continues, the Guiana Shield will lose its place as part of one of the three remaining "tropical wilderness" areas in the world.

Efforts to conserve this interesting and unique region vary by country. Since 1962, Venezuela has set up 7 national parks, 29 natural monuments, and 2 biosphere reserves covering 142,280 km², or almost 31% of the Shield that lies in the country, and about 15% of the country. In Guyana the totals are much less, with only one major national park, the expanded Kaieteur National Park (627 km² or about 3% of the country). Several other areas have been proposed, but the boundaries are ambiguous and no legislation has been passed. Surinam has 18 areas of nature or forest reserves or national parks that total 7,290 km² (1,310 km² of which is proposed; Lindeman and Mori 1989) and that make up 4.4% of the country. French Guiana has no designated protected areas, but there are 18 proposed sites that total 6,710 km² and make up 7.5% of the country (Lindeman and Mori 1989). However, just be-

cause an area is marked on a map as a park or reserve does not mean that the area is actually protected. As with many countries in the tropics, areas that are designated as parks are often only "paper" parks because they lack the infrastructure and financial backing to effectively protect the areas. As a result parks often host gold miners, hunting, wildlife trade, and other disruptive activities. Currently, Venezuela and Guyana have the most pressure being put on their respective biodiversities, while French Guiana is probably the least threatened of the countries and therefore has the best chance to protect its environment.

The Guiana Shield encompasses parts of five countries, each with a different administrative structure and official language; there are a number of border disputes, and the borders are porous to drug, gold, and wildlife trafficking; and there are serious issues concerning native peoples. All of these issues will have to be overcome before a viable reserve system for the Guiana Shield can be designed and maintained.

4.4 PACIFIC OCEANIC ISLANDS

Warren L. Wagner, Denise Mix, and Jonathan Price

THE PACIFIC OCEAN is the earth's largest feature, covering about one-third of the surface in an expanse of 155,000,000 km². It is interspersed with thousands of islands totaling roughly 1,250,000 km² of land, which is equal to the size of Peru and about one-half the size of Greenland. Many of the islands are situated on the Pacific plate, where the land arises from volcanic activity and has never been connected to a continental landmass. These islands are considered to be truly oceanic. The remainder of the Pacific Islands, which make up a greater proportion of the land area, are on the Indo-Australian plate. These islands generally have a continental origin with some volcanic composition, and will not be addressed here. Fiji is included, although it formerly was considered to have originated on the northeastern edge of the Indo-Australian plate. More recent syntheses of data suggest that Fiji's origin was on the Pacific plate and that it is an oceanic island that made contact with a fragment of Gondwana, now part of Tonga.

Two types of islands can be distinguished throughout the Pacific oceanic islands:

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5.7 DAISIES AND SUNFLOWERS:
FAMILY ASTERACEAE

Vicki A. Funk and Harold E. Robinson

THE COMPOSITAE (Asteraceae) family contains the largest number of described species of any plant family, approximately 25,000 distributed in over 2,200 genera, and they occur on all continents except Antarctica. Estimates vary, but assuming that there are 200,000–300,000 species of flowering plants, then one out of every 8–12 species of flowering plants is in the Compositae (about 10%). The family is monophyletic, characterized by florets arranged on a receptacle in heads (plate 5.7) and by anthers fused in a ring with the pollen pushed out by a style that acts as a plunger (fig. 5.4). Although the family is well-defined, there is a great deal of variation among the members. The habit varies from annual and perennial herbs to shrubs, vines, or trees, although a few are true epiphytes. The heads can have 1 to more than 1,000 florets. Chromosome numbers range from $2n = 4$ to high-level polyploidy with $2n = 228$. Species grow in just about every type of habitat from forests to páramo and puna; however, they are less common in tropical wet forests and more common in open areas. They can be showy or obscure, fragrant or foul, breathtakingly beautiful or nondescript. However, the general perception of this family as "weedy" is not correct. Certainly some members benefit from disturbance, such as a few species of dandelions, goldenrods, and thistles, but most species have a restricted distribution, and just about every "at risk" habitat in the world contains members of this family that are an important part of the flora. In fact, the 1997 IUCN Red List of Threatened Plants (Walter and Gillett 1997) lists 2,553 species of Compositae. Particularly vulnerable are previously unappreciated epiphytic members of the family in tropical forests, island floras, and the páramo and puna floras of the Andes.

That the family is monophyletic has never been in question. Every early worker in plant classification recognized the Compositae as a group at some level. The compound inflorescence with florets, often found in the striking ray/disk arrangement (plate 5.7), enabled everyone to accurately delimit this family (e.g., Bentham in Bentham and Hooker 1873). There are several general references that treat the family (Bremer 1994; Heywood et al. 1977; Hind 1996); the most up-to-date is the Kubitzki volume (in press) that provides keys to and descriptions for all the genera of every tribe. In every molecular analysis that contains more than one member of this family, the results show that the family is monophyletic (i.e., Jansen and Palmer 1987; Bremer et al. 1992; Hansen 1992). Within the family, however, things are not as clear-cut. The family is traditionally divided into three subfamilies: Barnadesioideae, Cichorioideae, and Asterioideae (fig. 5.5). The Cichorioideae has been
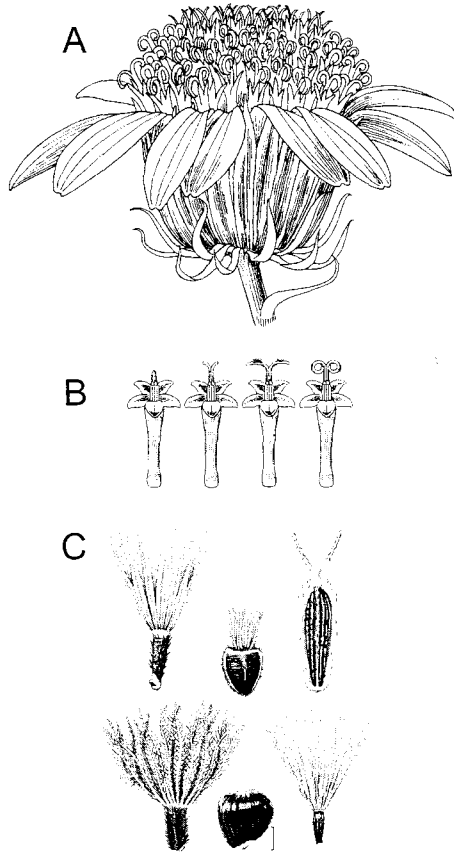
Figure 5.4 Characters of the Compositae. A, The head with ray florets arranged around the perimeter, disk florets in the center, and involucral bracts surrounding the outer florets. B, The pollen is released when the style pushes out through the anthers, which are fused at the margins. C, A few of the achene (cypsela) and pappus types found in the Compositae. The scale bar in C is 1 mm long.

divided into additional subfamilies (Panero and Funk 2002); for this treatment three of these are used. The Asterioideae is subdivided into two supertribes; each of these is divided into tribes (Baldwin et al. 2002). The tribes are the subunits of the family used in most treatments.

Most tribes contain some useful and noxious species as well as some that are common and some that are rare. No simplistic answers are available for management or protection of these types of plants in the various tribes other than the preservation of ample representations of the richest overall habitats.

The subfamily Barnadesioideae lacks the complex chemistry and twin hairs that characterize most of the rest of the family: their terpenoids are mostly diterpenes. Most members have paired axillary spines. The pollen lacks the characteristic form
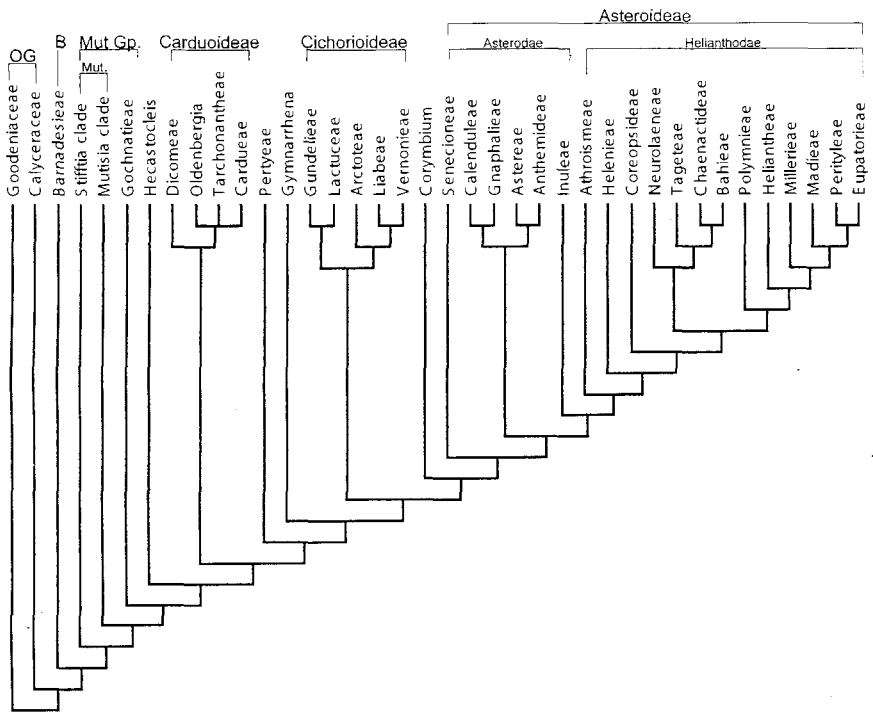
Figure 5.5 Relationships among the major tribes and subfamilies in the Compositae. The basal group, the monophyletic subfamily Barnadesioideae, contains less than 1% of the species in the family. The monophyletic terminal subfamily, the Asterioideae, contains ca. 65% of the species in the family. This large and diverse subfamily contains many of the tribes that are widespread and easily recognized, as well as several smaller ones. The third subfamily, the Cichorioideae (ca. 35% of the species in the family), vary in their morphological and molecular characters. Current thinking on the number of tribes ranges from 17 to 22; here 19 tribes are recognized (Funk et al., in press). B, subfamily Barnadesioideae; Mut., tribe Mutisieae; Mut. Gp., mutisioid group.

of higher Asteraceae. There is only one tribe, Barnadesieae, consisting of 9 genera and 90–95 species. Members are restricted to the Andes except for *Dasyphyllum* Kunth, which extends into southern Brazil, and the monotypic *Schlechtendahlia* Less. in lowland southern South America. Their habit ranges from small herbs to trees. Although many of the species are rare, most of them grow in habitats that are relatively inhospitable, and only a few of these habitats are threatened.

The former paraphyletic subfamily Cichorioideae can be divided into three groups: the complex and variable Mutisieae, called the mutisioid group, and two monophyletic subfamilies, the Carduoideae and Cichorioideae. In addition there are several genera that do not fit in any of these groups, and they have been placed in subfamilies of their own (Panero and Funk 2002).

The paraphyletic mutisioid group is notable for its variable floret structure, gen-

erally showy involucral bracts, absence of much of the specialized chemistry of higher Compositae, and a nonspecialized pollen type. Members of the former large tribe Mutisieae are now found at the base of the Carduoideae and between the Mutisieae and Carduoideae and the Carduoideae and Cichorioideae.

The tribe Mutisieae sensu strictu consists of ca. 70 genera and nearly 1,000 species. The members occur mainly in Central America and South America. Most are Andean, on the Brazilian Shield, or on the Guiana Shield; however, there are also genera in Africa and Madagascar, Asia, and one monotypic genus in Australia, *Amblysperma* Benth. Numerous members of the tribe are of limited distribution and at risk of extinction because of habitat destruction, such as several species of the rare small tree *Wunderlichia* Riedel ex Benth. from the Brazilian *planalto*. This tribe includes some of the most interesting plants found in the unusual tepui flora found on the Guiana Shield in northeastern South America.

Two unusual dioecious genera that used to be in the Mutisieae from southern and tropical Africa and Madagascar (*Tarchonanthus* L. and *Barchylaena* R. Br.) have been placed in their own tribe, Tarchonantheae (Keeley and Jansen 1991). They are now in the Carduoideae.

The tribe Cynareae (Cardueae) has 74 genera and ca. 2,500 species. Centers of distribution are primarily Eurasia and North Africa; some are successful weeds. Notable members are the thistles (*Cirsium* L.), the artichoke (*Cynara* L.), and various *Centaurea* L. (e.g., bachelor's button). These often spiny-leaved plants are sometimes appreciated horticulturally, but can be unwelcome invaders outside of their normal range, as in western North America, the pampas of Argentina, and the fallow fields of Australia. Some taxa are restricted in their distribution, and most of these are endangered by habitat destruction and invasive species. For instance, *Centaurodendron* Johow and *Yunquea* Skottsb. are endemic to the Juan Fernandez islands, with the latter known only from a few plants from one summit. There are many small endemic genera in the Middle East (*Centaurothamnus* [Forssk.] Wagenitz & Dittrich), Central Asia (*Schmalhausenia* C. Winkl.), and Iran (*Aegopordon* Cass., *Karvandarina* Rech. f., *Myopordon* Cass.), all of which are difficult to find. Many endemic species of various genera, such as *Stemacantha australis* (Gaud.) M. Dittrich in Australia, *Cirsium* in the western United States, and *Centaurea* in the Mediterranean region, are rare and often endangered.

The subfamily Cichorioideae contains tribes with specialized asteraceous pollen, echinate or often lophate, and style branches with undivided areas of stigmatic papillae on their inside surfaces. The tribe Arctoteae is a small group of 15 genera almost totally restricted to southern Africa; one outlying genus, *Cymbonotus* Cass., is endemic to Australia, where it is rare. A number of the species are used in horticulture, especially members of *Gazania* Gaertn. and *Arctotis* L. Many of the species found in the ephemeral flora of Namaqualand (a recognized conservation hot spot) are in this tribe.

Vernonieae have nearly 120 genera with ca. 1,400 species. It is widespread in North America and South America, Africa south of the Sahara, and areas around the Indian Ocean. A few species are invasive weeds such as *Cyanthillium cinereum*

(L.) H. Rob. of Africa. The widespread *Struchium sparganophorum* (L.) Kuntze of possible American origin invades agricultural fields in Africa and India. *Baccharoides anthelmintica* (L.) Moench of Asia and Africa, and *Gymnanthemum amygdalinum* (Del.) Sch. Bip. ex Walp. of Africa have some medicinal value and have been introduced in a limited way into America. *Lychnophora* (Candelabra) is restricted to rocky outcrops in the Brazilian Shield and is endangered, even within the protected areas, by fire and grazing. Many species from Africa and Asia are threatened, such as the species of *Distephanus* in Madagascar and Reunion Islands. In addition, the Tanzania genus *Hystrichophora* Mattf. is still known from only one collection that was destroyed in Berlin; a fragment exists at the British Museum. Located at the base of the Vernonieae is the small tribe Moquineae (Robinson 1994).

The tribe Liabeae contains 15 genera and ca. 180 species. Many genera are like the Cichorieae in having milky sap. Members of the Liabeae are found in Mexico, Central America, the Greater Antilles, and the Andes; however, the greatest diversity is in Ecuador and northern Peru. A few taxa are common, but most genera, such as *Pseudonoseris* H. Rob. & Brettell and *Chionopappus* Benth., are characterized by species that are difficult to find. One rare Peruvian genus, *Bishopanthus* H. Rob., is still known from only one collection, and the pygmy *Microliabum humile* (Cabrera) Cabrera of the Andes of northern Argentina has been collected only twice.

The tribe Cichorieae (Lactuceae) includes nearly 100 genera and several thousand species. Members of the tribe have milky sap and unusual ligulate florets. Distribution is nearly worldwide, but is concentrated in Eurasia and western North America. Notable members are lettuce (*Lactuca* L.) and *Cichorium* L., used as food and flavoring, and the dandelion, *Taraxacum* Weber, which is usually considered a weed, can be used as a salad green and for making wine. More localized and endangered elements are found in restricted habitats around the world such as California and Eurasia, and some are island endemics, such as *Dendroseris* D. Don of Juan Fernandez with 11 species, 2 of which are extinct and another which is known from only three specimens.

The tribe Gundelieae contains a single genus with one to two species distributed from Turkey to the Middle East and Iran. *Gundelia tournefortii* L. is believed to have supplied the pollen and the plant images found on the shroud of Turin, and it has been suggested that it was the "crown of thorns." In spite of its distribution, the species may be threatened because its leaves, stems, roots, and undeveloped flower buds are edible and it is harvested from the wild before it sets seed.

The subfamily Asteroideae is notable for the familiar echinate, tricolporate, asteraceous pollen and the stigmatic papillae of the style branches often separated into two separate bands. When rays are present, they are "true" rays, and the disk florets often have short lobes. It is divided into two supertribes, one paraphyletic, Asterodae, and one monophyletic, Helianthodae. The supertribe Asterodae has tribes without phytomelanin in the walls of their achenes. Six of the seven tribes in the supertribe Asterodae are discussed below (Panero and Funk 2002; Funk et al., in press).

The tribe Astereae has ca. 190 genera and nearly 3,000 species; it is nearly world-

wide in distribution. Included are the common asters (e.g., *Aster* L.) and goldenrod (*Solidago* L.), the widespread *Erigeron* L., the weedy *Conyza* L., *Amellus* L. of South Africa, and the Bellidinae (the true daisies) of Europe. Some genera are very local and endangered, such as the tree genera *Commidendron* DC. and *Melanodendron* DC. of St. Helena, *Remya* Hildebr. ex Benth. of Hawaii, *Pleurophyllum* Hook. f. of the Subantarctic islands near New Zealand, *Pacifigeron* Nesom of Rapa Island, and the small bromeliad-like *Novenia* Freire of Peru and Bolivia. There are also a fairly high number of substrate endemics in the Andes and the western United States, particularly in *Townsendia* Hook. and *Erigeron* L., a number of which are threatened by mining and grazing.

The tribe Gnaphalieae (187 genera, 1,250 species) has a nearly cosmopolitan distribution, and has an especially rich diversity in Australia and the southern Africa–Madagascar region. It is notable for *Antennaria* Gaertn. (pussytoes), *Anaphalis* DC. (pearly-everlasting), and *Leontopodium* R. Br. ex Cass. (edelweiss). Most species have a restricted distribution; however, a few taxa such as *Gamochaeta* Wedd. turn up in sidewalks around the world. *Calocephalus* in Australia is restricted to one vulnerable area in Canberra. Two more recently described small-statured Andean genera, *Cuatrecasasiella* H. Rob. and *Jalcophila* Dillon & Sagást., may or may not be endangered.

Inuleae (including Plucheeae) seem to be a monophyletic group with 66 genera and over 700 species with a nearly cosmopolitan distribution but concentrated in Eurasia and the Neotropics. Cultivated members include *Inula helenium* L. (elecampane) and *Buphthalmum salidifolium* L. (yellow ox-eye). There are several weedy taxa, but most genera have only a few species nearly all of which have restricted distributions. Some are endemic to islands (Canary Islands: *Allagopappus* Cass.; Mauritius: *Monarrhenus* Cass.; Madagascar: *Neojeffreya* Cabrera), or Namibia (*Antiphiona* Merxm.), or Australia (*Allopterigeron* Dunlop). *Cylindrocline* Cass. has two very rare species on Mauritius, one of which is known from ten specimens at a single locality.

The tribe Senecioneae contains 138 genera and over 3,000 species in both the Eastern and Western Hemispheres (Nordenstam, personal communication). It is on record as the largest tribe, with *Senecio* L. alone containing over 1,000 species, particularly in Eurasia and America. The horticultural cineraria (actually *Pericallis* D. Don in Sweet), native to the Canary Islands, is now widely introduced; the South African true *Cineraria* L. is distinguished in the tribe by its obcompressed achenes. One narrowly endemic genus is *Dendrosenecio* (Hauman ex Hedberg) B. Nord., whose members are trees in the mountains of tropical east Africa. Other groups of particular interest are the Jamaican genus *Odontocline* B. Nord., which is still known mostly from 18th-century collections of Swartz, and *Hoehnephytum* Cabrera, a rare genus from Brazil. There are two remarkable trees on St. Helena, both very important for conservation efforts, *Lachanodes arborea* (Roxb.) B. Nord., which is critically endangered, twice thought to be extinct, and *Pladaroxylon leucadendron* (G. Forst.) Hook. f., also critically endangered with fewer than 50 plants (Cronk 2000). *Robinsonia* DC. has seven species endemic to the Juan Fernandez is-

lands; two are extremely rare or possibly extinct, and the monotypic *Lordhowea* B. Nord. from Lord Howe Island is endemic and known only from a small population. The Mascarene Islands have two small genera as well, *Faujasiopsis* C. Jeffrey and *Parafaujasia* C. Jeffrey.

The tribe Anthemideae has over 100 genera and ca. 1,750 species that are found mostly in the Northern Hemisphere, especially in the Mediterranean region and Central Asia, with an additional center of diversity in South Africa. The chrysanthemums and daisies (*Chrysanthemum* L. with a conserved type and *Leucanthemum* Miller, respectively) are widely cultivated, as is *Tanacetum* L., which includes the tansies and pyrethrum. A few taxa, such as *Matricaria matricarioides* Porter ex Britton, *M. recutita* (L.) Rauschert, and the yarrow, *Achillea* L., are weeds. Members of the tribe are rich chemically, and are the source of the important insecticides named pyrethrins. *Artemisia* (sensu lato) is one of a handful of anemophilous genera in Asteraceae (Faegri and van der Pijl 1979), and its species are a major cause of allergies in humans (Lewis et al. 1983). All *Artemisia* (sensu lato) species produce aromatic oils, and several are culinary herbs or used as flavorings, hallucinogens, vermifuges, and pharmaceuticals (Lee and Geissman 1970; Heinrich et al. 1998; Burrows and Tyrl 2001). The habitats of the Mediterranean and South African Anthemideae are severely threatened.

The tribe Calenduleae is credited with 8 genera and ca. 110 species. Its native range is almost completely restricted to Africa. Today, genera such as *Calendula* L. and *Dimorphotheca* Moench are often planted in gardens or on maintained roadsides. The tribe is most notable for extreme differences in the form of the ray and disk achenes. A few of the species are local and potentially endangered.

The supertribe Helianthodae contains tribes that usually have phytomelanin in the walls of their achenes. There are 12 tribes in this supertribe; here 5 are discussed. The tribe Tageteae is an American group of ca. 16 genera and 250 species. *Pectis* L. is widespread, and one species of *Porophyllum* is weedy, but most species of this genus have restricted distributions and some are narrowly endemic. Some species of *Tagetes* L. are rare and local, and the Peruvian type species of *Schizotrichia* Benth. has been very rarely collected. Most notable in horticulture is the marigold (*Tagetes*), which is often planted among other garden plants that would benefit from its insect-repelling monoterpene chemistry.

The tribe Helenieae includes 900 species in 130 genera. It occurs prominently in western North America with some interesting disjunctions of some of the species in Chile and Argentina. The tribe contains the horticultural *Gaillardia* Foug., the weedy *Schkuhria* Roth, and *Helenium* L. (sneezeweed). Many of the North American species are rich in terpenoids, and they are problems in range management. The tarweeds (e.g., *Madia* Molina) of California and their relatives, including the 19 species of the Hawaiian silversword alliance (*Argyroxiphium* DC., *Wilkesia* A. Gray, and *Dubautia* Gaudich.) are especially important not only because of their distinctive natural habitats but because they are threatened and endangered. *Lasthenia* Cass. and *Perityle* Benth. contain many isolated species in California or Mexico that are subject to extinction.

The tribe Coreopsideae contains ca. 18 genera and over 300 species. It is basically American; some species of *Bidens* L. have become pantropical with the help of the retrorse barbs on the pappus awns. Horticultural genera include *Coreopsis* L., *Cosmos* Cav., and *Dahlia* Cav. One particularly interesting Pacific endemic is the tree-like *Fitchia* Hook. f. with liguliform corollas, and a potentially endangered monotypic genus is the St. Helena endemic *Petrobium* R. Br. known only from ca. 250 plants.

The tribe Heliantheae has nearly 150 genera and 2,400 species. The tribe rather characteristically has the combination of persistent pales on the receptacles of the heads and slowly maturing achenes (Robinson 1981). It is almost wholly American, with some pantropical elements such as *Melanthera* L. and *Wedelia* Jacq. Crop plants include the sunflower (*Helianthus* L.) from North America and *Guizotia* Cass. (niger seed) of Africa and India. Horticultural plants include *Tithonia* Desf. (Mexican sunflower), *Rudbeckia* L. (black-eyed Susan), and *Echinacea* Moench (coneflower). Among the noxious weeds are *Xanthium* L., the cocklebur, and *Acanthospermum* Kunth, both of which have fruits with hooked or straight spines, and ragweed (*Ambrosia* L.), the source of allergenic pollen. Some genera are rare endemics such as *Faxonia* Brandeg., collected once in southernmost Baja California, *Espeletia* Mutis ex Humb. & Bonpl., providing a special forested aspect to the páramo habitats of the northern Andes, and *Exomiocarpon* Lawalrée, endemic in Madagascar. In spite of the appearance of great numbers in some species, the habitat is at risk, and many more-narrowly ranging species could easily become extinct. Some genera and species of restricted distribution, such as *Scalesia* Arn. and *Trigonopterum laricifolium* (Hook. f.) W. L. Wagner & H. Rob. of the Galápagos, may be more vulnerable than others.

The tribe Eupatorieae consists of ca. 173 genera and 2,400 species. It is almost exclusively American, with main centers of diversity in Mexico, the Andes, and Brazil. Members include the well-known *Ageratum* L., *Liatris* Gaertn. ex Schreb. (blazing star), and *Eupatorium* L. (bonesets and joe-pye weeds). Their chemistry prevents them from being used as food, and a number of species (e.g., *Chromolaena odorata* [L.] R. M. King & H. Rob.) have become weeds when introduced to Hawaii, Asia, Africa, or Australia. Many of the more than 2,000 species have narrow distributions, and one monotypic forest genus from Costa Rica, *Standleyanthus* R. M. King & H. Rob., known from one stem, may already be extinct. There are a number of narrow endemics from eastern Brazil, such as *Agrianthus* Mart. ex DC. The tribe has many genera of pygmy plants known mostly from only one or two collections such as *Iltisia* S. F. Blake from Costa Rica and Panama, *Monogerion* G. M. Barroso & R. M. King and *Cavalcantia* R. M. King & H. Rob. from the south edge of the Amazon basin, *Piqueriopsis* R. M. King from southwest Mexico, *Ferreyrella* S. F. Blake from northern Peru, *Piqueriella* R. M. King & H. Rob. from northeast Brazil, *Siapaea* Pruski from the Guayana Highland area of southern Venezuela, *Ciceronia* Urban and *Antillia* R. M. King & H. Rob. from Cuba, *Parapiqueria* R. M. King & H. Rob. from Pará in Brazil, and *Teixeiranthus* R. M. King & H. Rob. from the São Francisco area of eastern Brazil. Some of these have not been re-collected for more

than a century, and they may be extinct. Others like them may remain to be discovered or become extinct without ever having been known to science.

OVERVIEW

Two characteristics of the family bear examining in the context of conservation: chemistry and pollination. The Compositae is notable for having a diverse secondary metabolite chemistry based especially on the presence of unique structural types, sesquiterpene lactones, and a variety of types of polyenes (= polyacetylenes) (Mabry and Bohlmann 1977; Hegnauer 1977). This chemistry is considered a major factor in the success of the family. The basal element in the family, the Barnadesieae, lacks complex polyenes and sesquiterpene lactones, but has secondary metabolite chemistry based mostly on triterpenes. Most of the widespread weeds are not in these lower branches, so the chemistry may play an important role in the success of the more common taxa. Concerning pollination, insect and wind are the most common vectors for the Compositae. Bird pollination also occurs, however, being most common in the Barnadesioideae and Mutisieae and sporadic in tribes such as Cardueae, although there is bird pollination scattered in other tribes such as the Heliantheae and Senecioneae (Leppik 1977). The Barnadesioideae, Mutisieae, and Cardueae are the basal branches of the Compositae phylogeny (fig. 5.5), and one can surmise that the ancestor of the extant Compositae was bird pollinated. In addition, one could say that most of the species in these basal groups are rare and at-risk taxa, and so one might surmise that it was the switch from bird pollination to insect pollination, along with the chemistry, that led to the diversification and success found in the higher branches of the phylogeny.

Endemicity in the family can also be examined from a habitat standpoint. For instance, within the area of rich diversity mentioned in the tribe Liabeae is a smaller and even more critical area of endemism. This recently noticed area is in the eastern foothills of the Andes in Morona-Santiago and Zamora-Chinchipe Ecuador and in closely adjacent northern Amazonas Peru. The area remains moist and mostly forested to this day, although areas not far to the west and south are now deforested and desertified. Rarities in the area include *Stenopadus andicola* Pruski (Mutisieae), the only member of that genus outside of the Guiana Shield; *Munnozia luyensis* H. Rob. (Liabeae); three recently described species of *Piptocarpha* (Vernonieae), including one that has very unusual heads; *Pentacalia tilletii* H. Rob. & Cuatrec. (Senecioneae); and some rarely recollected older species such as *Ayapanopsis mathewsii* (B. L. Rob.) R. M. King & H. Rob. (Eupatorieae). The most inexplicable endemic is the recently described new genus *Holoschkuhria* H. Rob., whose closest relatives are all from drier areas of North America and Mexico or from southern South America.

Around the globe various habitats contain rare and at-risk members of the Compositae. From the tree senecios of east Africa (*Dendrosenecio* [Hauman ex Hedberg] B. Nord., Senecioneae), to the *Espeletia* Mutis ex Humb. & Bonpl. of the northern Andes (Heliantheae), the hummingbird-pollinated trees of the tepuis of

the Guiana Shield (e.g., *Stenopadus* S. F. Blake, Mutisieae) and the *planalto* of Brazil (*Wunderlichia* Riedel ex Benth., Mutisieae), the daisy trees of Mexico to northern South America (*Montanoa* Cerv., Heliantheae), and the silverswords of Hawaii (*Argyroxiphium* DC. and *Wilkesia* A. Gray, Helenieae), members of the Compositae are threatened, endangered, or extinct. Numerous habitats that are dominated by the Compositae are also under threat, such as the fields of spring flowers in Namaqualand (South Africa), Western Australia, California, and the Mediterranean. While it is true that some members of the family are well-known weeds, the majority of species in the family are restricted in their distributions, and many are headed toward extinction. Clearly, this family does not deserve its reputation as "weedy," and indeed it might be used as an indicator of importance for many areas of the world that are not heavily forested.

5.8 AFRICAN VIOLETS: FAMILY GESNERIACEAE

Láurence E. Skog

THE GESNERIACEAE, commonly known as the African violet family, is a moderately sized family of herbs, subshrubs, shrubs, lianas, and epiphytes, and mainly tropical. The family has over 2,500 species in about 135 genera usually grouped by seedling morphology and geography into two subfamilies of nearly equal size, the Gesnerioideae from the Neotropics and the Cyrtandroideae from the Paleotropics, and a small subfamily of few species in southern South America and the southwestern Pacific, the Coronantheroideae. Closely related to the Scrophulariaceae and distinguished from that family by placentation characters, the Gesneriaceae are commonly found in humid habitats, often in wet or cloud forests at upper elevations, and are relatively uncommon in low-elevation rain forests and drier habitats. The plants, particularly those in the Neotropics, sometimes have modified storage stems, such as tubers (e.g., *Sinningia* spp.), or aerial and subterranean rhizomes (e.g., *Gloxinia* spp.), or stolons (e.g., *Episcia* spp.), all of which allow them to be propagated vegetatively, as well as from leaves and other plant parts. This ease of propagation, in addition to the attractiveness of the flowers, has made the plant family especially popular with amateur and commercial plant growers (e.g., the florists' gloxinia [*Sinningia speciosa* cultivars] and the African violet [*Saintpaulia* spp. and cultivars]). Other than in horticulture and for folk uses for food and medicine, the plants have little economic importance.

Among the approximately 135 genera there a few monotypic genera (e.g., *Lembocarpus, Titanotrichum* [plate 5.8]), as well as a few large genera with 100 species

or insufficiently known while others are common. The following genera have their only species listed as vulnerable by the IUCN Red List (Hilton-Taylor 2000): *Athyana* Radlk., *Euchorium* Ekman & Radlk., *Eurycorymbus* Hand.-Mazz., *Gloeocarpus* Radlk., *Gongrospermum* Radlk., *Haplocoelopsis* Davis, and *Sinoradlkofera* F. G. Meyer. To this list, the genera *Bizonula* Pellegr., *Blighiopsis* van der Veken, *Chonopetalum* Radlk., *Handeliodendron* Rehder, *Pentascyphus* Radlk., *Pseudopancovia* Pellegr., *Scyphonychium* Radlk., and *Tsingya* Capuron should be added, as they are rare or known from a single collection.

A few monospecific genera are not considered vulnerable or threatened because they are common, widespread, or cultivated. These include *Amesiodendron* Hu, *Arfeuillea* Radlk., *Beguea* Capuron, *Blomia* Miranda, *Cubilia* Blume, *Euphorianthus* Radlk., *Hippobromus* Eckl. & Zeyh., *Hypelate* P. Browne, *Magonia* A. St.-Hil., *Schleichera* Willd., *Tristira* Radlk., and *Ungnadia* Endl. Some genera, although local or narrowly endemic, need further evaluation of their conservation status. These include *Bridgesia* Cambess., *Castanospora* F. V. Mueller, *Delavaya* Franch., *Dipteronia* Oliv., *Erythrophysopsis* Verdc., *Eurycorymbus* Hand.-Mazz., *Gloeocarpus* Radlk., *Gongrospermum* Radlk., *Hornea* Bak., *Loxodiscus* Hook. f., *Otonephelium* Radlk., *Pavieasia* Pierre, *Phyllotrichum* Lecomte, *Sisyrolepis* Radlk., *Smelophyllum* Radlk., *Stocksia* Benth., and *Tripterodendron* Radlk.

Elucidation of the conservation status of species requires a solid taxonomic knowledge that can be attained only through monographic studies. Species concepts depend on the knowledge level that we have of the organisms under study. The greater the knowledge, the better chance our hypotheses will stand the test of time. Anybody who has been involved in the monographic studies of a group knows very well the difficulties of this multidisciplinary endeavor. Expeditions are increasingly expensive, and the logistics for exploring remote areas are complicated. In the end, it will not be possible to gather all the necessary pieces of the puzzle, since habitat destruction is usually faster than current exploration efforts. As a result, monographs are written based on data that are less than ideal. It is not uncommon for monographs to contain species known only from one or a handful of collections. These species are thus interpreted as extremely rare or in some cases as extinct.

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CHAPTER 10

MAPPING BIOLOGICAL DIVERSITY

Many natural history scientists are concerned with understanding the extent and distribution of organismic diversity as well as using this knowledge for conservation purposes. It is clear that only a portion of the remaining forested areas can be preserved unless a considerable change takes place in the current social, political, and economic priorities of the world. If only a portion of these habitats can be maintained, it is imperative that, given a level of available resources and budget, areas be identified that maximize the amount of diversity from the genome level to the biome level. A number of approaches have been advocated for defining what constitutes an area or set of areas of maximum diversity, including those that use species diversity (i.e., total species richness, endemic species richness, complementary richness) and phylogenetic diversity as their basic criterion.

The underlying assumption of all conservation planning is that one must use the best available data at any given time. However, what constitute the best data? Unfortunately, a database that describes the full distribution of all biodiversity is never available. This absence of complete data requires the use of surrogates, such as vegetation maps, modeled distributions, or numerical classifications of environmental variables, to quantify biodiversity. None of these surrogates, however, is robust enough on its own to be heralded as optimal. The most convincing biodiversity surrogates come from a combination of environmental variables and species data that are always limited by the availability of information about a specific region.

The first two sections of this chapter explore the use of species data from herbarium collections and published floras to identify conservation priority regions; the third section discusses how the evolutionary history of species is used to rank geographic regions when setting conservation priorities.

10.1 HERBARIUM COLLECTIONS, FLORAS, AND CHECKLISTS

W. John Kress and Vicki A. Funk

AN ESTIMATED 3 billion specimens of organisms, including plants, animals, and microorganisms, are housed in the world's natural history collections (Edwards et al. 2000). These collections are a crucial subset of systematic data that can

be used for conservation planning. Each of these specimens contains a suite of information about the organism, including name, rank, and the locality where it was collected. Taken together, these data constitute a rich library about life on earth, providing important information about the distribution of individual species, genera, and families by region, country, and habitat. They also supply crucial information on the recent history of a species as they constitute a permanent species record at a given location and at a specific time. A record attached to a specimen housed in a herbarium is considered "vouchered," which means it can be checked by experts at any time in the future for accuracy of the information and proper identification. As environmental degradation continues around the world, the analyses of biological information derived from museum collections will provide a wide array of information that will assist in preserving the earth's biodiversity.

The limitations to using collections data for conservation decision making are that they can be (1) geographically biased, favoring more easily accessed areas; (2) taxonomically incomplete, including only easy-to-study species thus giving undue weight to a few taxa; and (3) temporally biased, that is, based on a single survey in a single season (Faith and Walker 1996; Ferrier 1997; Funk et al. 1999). Several techniques have been developed to deal with these limitations. Some exclude the use of collections data altogether, for example, techniques that use abiotic surrogates of biodiversity including land classifications, vegetation maps, numerical classification of environmental variables, and ordination of environmental variables (Mackey et al. 1988; Mackey et al. 1989; Belbin 1993, 1995; Pressey and Logan 1995; Faith and Walker 1996; Wessels et al. 1999; Faith et al. 2001). The problem with these techniques is that they are not informed by the biological data, which means that the resulting conservation decisions are made without regard to what species may or may not be in those areas. As a baseline, collections data serve as the only direct evidence of species distributions.

Most conservation planners accept that a network of conservation sites needs to be complementary, where each site complements the biodiversity of other sites (Vane-Wright et al. 1991; Pressey et al. 1993; Pressey et al. 1994; Margules and Austin 1994). Incorporating the concept of "complementarity" ensures that sites are selected to maximize the representation of different species. Recently the concept of complementarity has been enhanced by the introduction of "irreplaceability" (Pressey et al. 1993; Ferrier et al. 2000). *Irreplaceability* refers to a measure of uniqueness, where the irreplaceability value of a site reflects the relative importance of that site for achieving an explicit conservation target (Ferrier et al. 2000). Although the political decision to designate a site for conservation may depend upon additional analyses of economic, political, and other potential land uses, and the methods depend on comparable lists of taxa, this complementarity-irreplaceability approach has been used successfully to select areas of high biodiversity priority in Australia, South Africa, and the United States (Pressey et al. 1993; Rebelo 1994; Pressey 1994; Lombard et al. 1997; Lombard et al. 1999; Davis et al. 1999).

In this section two examples of the use of collections data in biodiversity and conservation studies in South America are provided. In the first example, taxo-

nomic data documented directly from museum collections are used alone to determine areas of high species diversity and endemism in the Amazon Basin. These results are then compared to field-based "ad hoc" estimates, and the limitations of these approaches for assessing biodiversity are discussed. In the second example, taxonomic data from museum specimens collected in Guyana are combined with environmental factors to predict total distributions of the organisms that are then used to identify areas for conservation.

THE AMAZON REGION

The Amazon region of tropical South America contains the largest remaining expanse of pristine forest on the planet. Yet with over 100 years of collecting data on species diversity and distribution in the Amazon Basin, until the 1990s only scattered information on the areas of greatest species concentrations was available, and hence baseline data for conservation purposes were lacking (Nelson et al. 1990; Voss and Emmons 1996). In 1990 a group of taxonomic specialists and conservationists made an attempt to identify high species-diversity regions for conservation priority areas in Amazonia based on their individual field experience with various groups of organisms (Workshop 90 1991). They outlined five levels of priority areas for conservation based on a qualitative synthesis of species diversity and endemism criteria.

In response to this initial identification of diversity areas based on qualitative assessment, scientists in the Neotropical Lowlands Research Program at the National Museum of Natural History utilized quantifiable specimen data, although recognizably incomplete, to verify these centers of biodiversity (for details of the analyses, see Kress et al. 1998; Heyer et al. 1999). Before specimen localities were mapped, the geographic area of Amazonia (as defined by Ab'Sáber 1977) was divided into 472 one-degree (latitude by longitude) grid cells. Distributional data from five main taxonomic groups found in Amazonia, that is, plants, arthropods, fishes, amphibians, and primates, were selected for study. Any species with a significant portion of its distribution within the Amazonian domain (and below 350 m) was included. In total 3,991 records of 421 species in 33 genera were included in the analysis (table 10.1). These collections, which provide a repeatable and reliable data set for analyzing the distribution of biological diversity, are housed at museums and universities distributed throughout the world and in some cases are an exhaustive record for a particular species. Although other taxa could have been selected for the analyses, these genera exemplify a cross section of both rare and common species found in Amazonia and represent one of the most extensive taxonomic samples currently available for this geographic region. A geographic information system (GIS) analysis was then used to determine the distribution in Amazonas of each species by pinpointing the exact locality of each specimen record in a specific grid cell on the map. Both total species richness (i.e., maximizing the number of species) and endemic species richness (i.e., maximizing the concentration of rare species) were calculated.

Table 10.1 Taxa used in the analyses of Amazonian biodiversity distribution

Taxon	Number of species	Number of records
Plants		
Heliconia	30	440
Phenakospermum	1	17
Talisia	35	198
Total for plants	66	655
Arthropods		
Agra	101	122
Batesiana	21	79
Deinopis	6	16
Geballusa	2	4
Gouleta	3	28
Hemiceras	108	342
Total for arthropods	241	591
Amphibians		
Leptodactylus	14	536
Total for frogs	14	536
Fishes		
Boulengerella	5	112
Caenotropus	3	55
Copeina	1	25
Copella	3	38
Cyphocharax	2	6
Lebiasina	1	15
Nannostomus	15	123
Pyrrhulina	2	17
Steindachnerina	33	419
Total for fishes	65	810
Primates		
Alouatta	2	152
Aotus	3	104
Ateles	3	43
Cebuella	1	41
Cacajao	3	50
Callicebus	2	191
Callimico	1	27
Callithrix	2	58
Cebus	2	19
Chiropotes	2	108
Lagothrix	1	74
Pithecia	5	187
Saguinus	7	236
Saimiri	1	109
Total for primates	35	1,399
Total	421	3,991

Table 10.2 Species diversity and endemism in Amazonia

Identifying locality within grid	Latitude, longitude (NW corner of grid cell)
a. Tambopata, Peru*	12°S, 70°W
b. Cocha Cashu–Manu, Peru*‡	11°S, 72°W
c. Iquitos, Peru*	3°S, 74°W
d. Along upper Rio Solemoes, Brazil*‡	3°S, 69°W
e. Tefé, Brazil*‡	3°S, 65°W
f. Manaus–Ducke Reserve–INPA, Brazil*	3°S, 60°W
g. Santarém, Brazil*	2°S, 55°W
h. Parimaribo Region, Surinam*‡	6°N, 55°W
i. Georgetown, Guyana*‡	7°N, 59°W
j. Cayenne, French Guiana‡	5°N, 53°W
k. Moyobamba, Peru‡	6°S, 77°W
l. Rio Ucayali, Peru‡	5°S, 75°W
m. Pôrto Velho, Brazil‡	8°S, 64°W

Notes: Areas with highest species diversity (43–67 species) are marked with *; areas with highest concentrations of endemism (4–13 endemic species) are marked with ‡. Identifying letters correspond to grid cells marked in plates 10.1 and 10.2.

The distribution of species across all taxa within the 472 one-degree grid cells in Amazonia comprised six categories between 0 and 66 species per grid cell (plate 10.1). Over one-fourth of the grid cells had no representative species of the groups under study, that is, no collections. Only 2.0% of the total grid cells had high species diversity (45–66 species) and 57.8% had low species diversity (1–11 species). The nine areas with highest diversity are scattered throughout the region and in general correspond to well-known and historical collection localities (e.g., Tambopata Reserve, Iquitos, Tefé, Manaus, Cayenne, etc.; table 10.2). There was no obvious species-diversity gradient between east and west or north and south.

For endemic species, 64 grid cells in Amazonia contained from 1 to 13 endemic taxa (plate 10.2). Nine areas composed the three highest categories (4–13 endemic species); the remaining 55 grid cells contained from 1 to 3 endemic species. Five of the nine grid cells with the highest endemicity corresponded to areas with the highest species diversity (45–66 species). The overall distribution of endemic species was significantly associated with the distribution of total species number.

With respect to numbers of records of species, individual grid cells ranged from 0 (129 cells) to 143 records (1 cell). Of the grid cells with records present, 64.2% had 27 or fewer records. The remaining 40 grid cells with more than 27 records had an average of 49.3 records per cell. If individual taxonomic groups are considered separately, insects are the least collected, with nearly 84% of grid cells with 0 records,

and primates are the most evenly sampled, with over 53% of the grid cells with at least 1 record.

As previously noted (Williams et al. 1996), little correspondence exists between the high-priority areas of the Workshop 90 report and the actual specimen-based data (plates 10.1 and 10.2). Of the total area of Amazonia, 25.3% (120 grid cells) over-lapped in part with the Workshop 90 high-priority areas. The highest species areas (45–66 species) identified by the specimen data corresponded with only 2.5% of the Workshop 90 high-priority areas, whereas 52.5% of their priority areas had low spe-cies diversity for the actual taxa studied (less than 11 species). Of the nine highest areas of endemicity identified by specimens, only four fell within the high-priority areas of Workshop 90; the two grid cells with the highest endemicity based on specimens (13 endemic species) were not identified as high-priority areas by Work-shop 90.

The centers of high diversity identified with actual specimen data (plate 10.1; table 10.2) correspond to many areas that historically have been the focus of mu-seum collectors, for example, areas around Iquitos, Manaus, Santarém, and Cayenne (Nelson et al. 1990). The nine highest species grid cells in Amazonia all corresponded to the most intensively collected areas. If total number of species is accepted as the only criterion for determining genetic diversity, one might recom-mend that the top nine most diverse regions identified here, and especially those five areas that overlap with high levels of endemism, be considered high-priority areas for conservation.

This study based on museum collections demonstrated that in most cases no areas in Amazonia have been thoroughly or even adequately sampled. It is clear that the perceived species diversity of any area in Amazonia is a direct function of how many collections have been made in that area and not necessarily the absolute level of diversity. In general very few localities have more than a single collection per spe-cies even in the areas with high numbers of collections. It is therefore likely that all areas will prove more diverse when additional collections are made. It is remarkable that even after a century of inventory and collecting efforts by museum scientists in this super-high-diversity region, adequate distributional data are lacking for most organisms. A coordinated plan to intelligently sample Amazonia is clearly in order.

The museum-based collection data supported the recognition of at least a sub-set of the high-priority areas of Workshop 90 as regions of exceptional biodiversity. However, it is noteworthy that the majority of the Workshop 90 high-priority areas lack significant collection data to verify the recommendations for conservation. Such recommendations should be treated as hypotheses of centers of diversity and not as conservation planning mandates. Areas of high diversity that are docu-mented with collection data should be given conservation priority over areas of sus-pected diversity that lack supporting collection-based data. Additional biological information about species, which can be provided by systematists, field biologists, and local naturalists, also must be taken into account when identifying high-diversity regions. This investigation of biodiversity in the Amazon region demon-strated that collections information as currently available is necessary but not

always sufficient for identifying priority areas for conservation. Reliable taxonomic data should be complemented with data on multiple environmental factors (as discussed in the next section) to provide a baseline upon which conservation recommendations can be formulated.

GUYANA

Many of the problems facing other tropical countries are not an issue in Guyana: it is not a large country (215,000 km^2); it has a large amount of its land intact or only marginally damaged (ca. 70%); and it has a small human population that is concentrated along the coast (ca. 800,000 in 10% of its territory). In addition, although previously poorly known biologically, exploration in the last 20 years has generated a wealth of information for some organisms in some parts of the country. Most importantly, although there are few protected areas in Guyana, the government is interested in developing a national protected-area system. Based on this initiative, several preliminary studies on how existing data might be used in the development of such a system have been conducted (see Ter Steege 1998; Funk et al. 1999; Richardson and Funk 1999; Ter Steege et al. 2000), but no final decisions have yet been made.

The Biological Diversity of the Guianas Program (BDG) of the Smithsonian Institution (Hollowell et al. 2004) has had an active field program in Guyana for the last 18 years. The BDG has developed a database from historical collections made in Guyana and now housed at museums and herbaria around the world as well as from recent field collections. These collections data have been used in investigations to identify sampling gaps, to improve survey design, and to reduce collecting biases (Funk and Richardson 2002). Two aspects of conservation assessment using collections data are considered here: (1) building richness, restricted range (endemicity), and distribution maps; and (2) selecting priority biodiversity sites for possible conservation. Distributions were examined using 25,111 records representing 5,123 species of plants and animals from Guyana. Data on climatic variables and vegetation types were assembled from various sources (see Funk and Richardson 2002).

Building Distribution and Species-Richness Maps

Sites with greater species richness have generally been considered more important for conservation than the sites deemed "species-poor" (Myers 1988, 1990; Mittermeier and Werner 1990). Given that complete inventories of species are impractical, particularly in species-rich tropical areas, the utility of species richness and other species-based approaches depends on the extent to which results from limited data sets can be generalized. In this example, known locality data and potential distribution data from modeled distributional maps were used to enhance species-richness maps (Funk and Richardson 2002). Other studies have examined how well certain taxonomic groups act as indicators for other taxonomic groups (Pearson and Cassola 1992; Prendergast et al. 1993; Williams et al. 1996; Moritz et al. 2001).

Modeling of species' distributions assumes that differences in species composition and abundance at any given location can largely be explained by differences in environmental factors, such as temperature, moisture, nutrients, and evaporation (Nix 1982; Busby 1986; Margules et al. 1988; Belbin 1995). The following steps were taken to model the potential distributions of each species: (1) The digital elevation model, vegetation map, lithology map, and mean monthly rainfall of the driest month (October) were selected as the variables to model species distributions. (2) Using the selected variables, each species was modeled with the program DOMAIN (a presence-only data modeling technique; Carpenter et al. 1993; for an example, see plate 10.3). (3) A similarity map that was produced for each species showed the likelihood of the species' being present in a given area (a similarity value of 95% or greater was chosen as a conservative cutoff point). (4) The modeled distributions were then used to improve upon the species-richness map (Funk and Richardson 2002).

A map of the restricted range values, which is a measurement of endemism, was calculated in the same manner, using an index of restricted range. Species with very restricted ranges had higher scores, with the most restricted species (found only in one grid cell) scoring 1.0 on the restricted range scale. Both the known locality data and the modeled data were used to calculate restricted range values and to produce the resulting map of restricted range.

The species-richness maps of only the known locality data and of the known locality and modeled distribution data reveal differences in both the number of species in a given grid cell and the distribution of the sites with the highest species richness. In the analysis of species richness for Guyana using only the known locality data, only 0.15% of the total grid cells had high species richness, and 42% had low species richness. Using the known locality and modeled distribution data, species richness increased to 8.5%. Areas of estimated high species richness are Kaieteur Falls and the Potaro River gorge; Kurupukari and the central Essequibo; Bartica and the lower Cuyuni, Mazaruni, and Essequibo rivers; the Pakaraima Mountains including Mounts Ayanganna, Roraima, and Wokomong; the upper Cuyuni and Mazaruni rivers; the Kanuku Mountains and the Rewa River; the upper Berbice River, and a few scattered areas in the Rupununi savannas, disregarding the sites in the far southeast of the country where virtually no collecting has taken place and very little abiotic data are available. Interestingly, the overlap between areas of high species richness and areas of very restricted species was found to be quite high (71.4%). This may indicate that certain species-rich areas in Guyana are also centers of endemism and that these areas have similar biogeographic features.

Location of Priority Biodiversity Sites

One of the main drawbacks with using only species-richness or restrictedness data to select priority biodiversity sites for conservation is that they do not provide any means of ensuring that different species in an area are conserved. For instance, a grid cell might be relatively species-poor, but if it adds the most species not already represented in an existing network of conservation sites, then it may be the most

important in terms of conservation (Flather et al. 1997). However, it is possible to represent many more species in a network of sites if decisions are made to use endemism-richness, species-richness, or restricted-range values and the complementarity principle to select sites (in this case an index of summed irreplaceability) (Vane-Wright et al. 1991; Pressey et al. 1993; Margules and Austin 1994).

The known and modeled data of 320 species were used to select priority sites for biodiversity conservation using a grid size of 8 km × 8 km (3,553 grid cells across the country; Funk and Richardson 2002). This grid size was chosen for demonstrative purposes only. Although the size of the grid is arbitrarily set in most conservation planning exercises, the size may influence the quantity and location of priority biodiversity sites (Flather et al. 1997; Reid 1998; R. Richardson and V. A. Funk, unpublished data). Excluded from the analyses were 157 grid cells representing urban areas and cultivated fields and 418 grid cells from the southeast corner of the country where very little information has been collected due to logistical and political problems.

Priority biodiversity sites were selected using an interactive software package, C-Plan (New South Wales National Park Service 1999), that runs as an extension in ArcView (version 3.2; ESRI 2000). Sites were selected to maximize the rate of species accumulation, using an iterative process based on estimated summed irreplaceability, defined as the sum for all species of the likelihood that a site would be required as part of a network of sites to achieve a set target: in this instance the representation of each species within at least three sites (Pressey et al. 1993; Ferrier et al. 2000). The minimum set of sites needed to satisfy the target was calculated using an interactive stepwise algorithm that selected sites based on their highest summed irreplaceability. For Guyana, in order to capture each species at least three times in a network of sites, 33 grid cells of a possible 2,978 were required (plate 10.4). These 33 sites were selected to maximize the complementarity of species between the sites and the relative irreplaceability value of each site. A few sites are in the northwest both near the Venezuelan border and the coast, and quite a number are in the Pakaraima Mountains, including the vicinity of Kaieteur, Mount Ayanganna, and the upper reaches of the Mazaruni River. In the northeast corner there are three sites, the Essequibo River between Bartica and Kurupukari has three sites, and the Berbice River has several. Below the fourth parallel there are four sites, two in the Kanuku Mountains, one near the border with Surinam, and one in the far south just north of Gunn's. No doubt additional data from southern Guyana would change the results. The rate of species accumulation for plants and animals shows that 80% of the plants species (95% of animals species) are represented in 19 grid cells; however, it requires a further 14 grid cells to capture all species at least three times.

CONCLUSIONS

Analyses of biological data derived from museum collections can provide predictive tools for identifying critical biodiversity regions for conservation. Collections

data may not be the perfect surrogate of biodiversity; however, they can be used to assist in the identification of areas with high endemism and species diversity as well as the prioritization of conservation areas. Yet the acquisition of biological information is only the first step in a many-tiered process for determining conservation areas that includes social, political, and economic factors as well. In order to take this first step, it is clear that our current knowledge of the distribution and diversify of the biota in such areas as Amazonia and Guyana must be greatly expanded. A renewed and structured effort to inventory with vouchered collections the various habitats of the tropics is imperative if informed decisions on conservation priorities are to be made in the near future.

10.2 HOT SPOTS AND ECOREGIONS

Gary A. Krupnick

THE NUMBER OF SPECIES threatened with extinction due to human activities is at an all-time high (Pitman and Jørgensen 2002; see also chapters 3 and 11 in this volume). Actions by conservation biologists, politicians, and land managers are urgently needed to prevent further extinctions. In a just world, conservation biologists would be able to focus their efforts on protecting all species, habitats, and ecosystems on the planet. However, with limited funds, time, and human resources, this is not an easy option. Conservation biologists should thus focus on areas that maximize biodiversity, thereby protecting the highest proportion of species and the most evolutionarily unique species at the lowest necessary cost.

Since resources for conservation are limited, it is essential to establish priorities to maintain earth's biodiversity. One tool that is used in setting priorities is a detailed map of the total species diversity. There have been several approaches to creating maps of biodiversity. The data upon which these maps are based come from different sources ranging from detailed species distribution maps to the expert opinions of taxonomic specialists. Here a variety of approaches that have been used in mapping out conservation priorities are compared.

CREATING MAPS

Identifying the areas that maximize biodiversity is the first step in setting conservation priorities. To many people, biodiversity is simply a count of the number of species within a given area. Yet biodiversity can be defined more elaborately—a measure of spatial variation and turnover (beta diversity), or a count of species rarity and endemism. Other criteria may also be used when setting conservation pri-

Even though practical conservation priorities can be based on partial measures of biodiversity, it is imperative that we push forward to assemble the enormous amount of data found in the world's biological collections and ultimately complete an inventory of all organisms on earth. Accurate measures of species diversity and distribution should be the first goal when setting conservation priorities.

10.3 PHYLOGENETIC CONSIDERATIONS

M. Alejandra Jaramillo and Vicki A. Funk

PRESERVING BIODIVERSITY is the most important goal of conservation biology. Biodiversity defined as "the total complexity of life" is not measurable. As a result, species numbers are used as the default surrogate or proxy for biodiversity. In an effort to preserve the maximum diversity, some conservation biologists have focused on saving the largest number of species by setting goals based on species richness or by concentrating on areas with high levels of endemism (e.g., hot spots; Myers et al. 2000). Relying on species counts and numbers of endemics to establish a value for diversity depends on a large number of assumptions, two of which relate particularly to systematics: the assumption that taxonomic knowledge (including distributions) is adequate for most regions of the world and for most groups of organisms, and the assumption that all species are equivalent. However, many systematists would argue that neither of these two assumptions is correct. There is much we do not know about species distributions—many species await description, and many more species are unknown to science. The second assumption, that all species are equivalent, will be discussed in this section. It is clear that species are indeed nonequivalent; some have argued that more divergent species (genetically, taxonomically, or ecologically) make a larger contribution to the overall biodiversity than closely related species (Vane-Wright et al. 1991; Faith 1992). Therefore, whenever possible, it is essential to consider the evolutionary history of the taxa (species, genera, etc.) in order to rank geographic regions, taxa, or populations according to their conservation priority. Phylogenies can contribute in four ways: diversity indexes, vicariant histories, evolutionary process, and predicting hybridization risk after translocation.

DIVERSITY INDEXES

An appropriate measure is needed in order to identify areas of highest importance—a measure that is different from species totals, a way to measure diversity that is not based on simple numbers. Such diversity measures should quantify not

only the numbers of species (or other taxa), but also their evenness—how the individuals are distributed among species, and their disparity—how varied are the species in the sample. Some argue that measures based on biological attributes, such as ecology and genes, are more desirable because they are better indicators of biological diversity (Noss 1990). Because the goal is to quantify evolutionary history rather than the amount of differentiation, however, this option does not fulfill the need. We seek not only to conserve current biodiversity but also future diversity, and so it is important to maximize the amount of information preserved and to select carefully which taxa might be the most important for the future evolution within a group. Modern systematics offers a number of analytical tools that permit measures of phylogenetic distinctiveness among the species and that allow us to identify a set of taxa or geographic regions that include the greatest biodiversity (Vane-Wright et al. 1991). Several phylogenetic diversity indexes have been proposed, falling into three categories: node-based or cladistic estimates (CD: Vane-Wright et al. 1991; Nixon and Wheeler 1992), genetic-distance estimates (GD: Crozier 1992), and feature-based or phylogenetic estimates (PD: Faith 1992). All of these indexes include information about the relatedness of the species in the sample (CD, PD) or level of genetic divergence among them (GD, PD), aiming to maximize the total diversity preserved. These indexes prioritize the uniqueness of the taxa being considered. Feature-based estimates have the advantage of including both aspects of a phylogenetic tree—topology and divergence among taxa—giving priority to highly divergent taxa that are either on basal or long branches (fig. 10.2). Given the relative scarcity of phylogenetic data available for specific regions and taxa, only a few studies have used these measurements (Crandall 1998; Virolainen et al. 1999; Whiting et al. 2000; Polasky et al. 2001; Posadas et al. 2001; Virolainen et al. 2001; Pérez-Losada et al. 2002; Sechrest et al. 2002; Jaramillo 2001). As the number of phylogenies available increases and as analytical and technical tools improve, the pace and accuracy of these studies will increase.

Phylogenetic diversity measures were illustrated from both the theoretical and practical viewpoint by the early proponents of phylogenetic diversity indexes (Vane-Wright et al. 1991; Faith 1992). The best-known example is the bumblebees in the *Bombus sibiricus* group, where the number of species and phylogenetic diversity (Vane-Wright 1991; Faith 1992) were estimated and three different reserve areas were compared using PD and the total number of species. The analyses showed that the area with the least number of species had the maximum PD because the species in that area were well-distributed across the phylogeny (Faith 1992). Another well-known example is that of the tuatara (*Sphenodon*). If all species of reptiles are equally weighted, the two species of *Sphenodon* represent only 0.03% of all extant reptiles, but they represent 50% of their evolutionary history (May 1990), given that the tuataras are the sister clade to all other reptiles. These two cases exemplify how species counts, when used alone, are a poor representation of phylogenetic diversity.

Some studies have used morphological phylogenies and taxonomic classifications to obtain an estimate of cladistic diversity (CD) and compare the efficiency of the CD index to "species richness" and "endemism" in selecting conservation re-
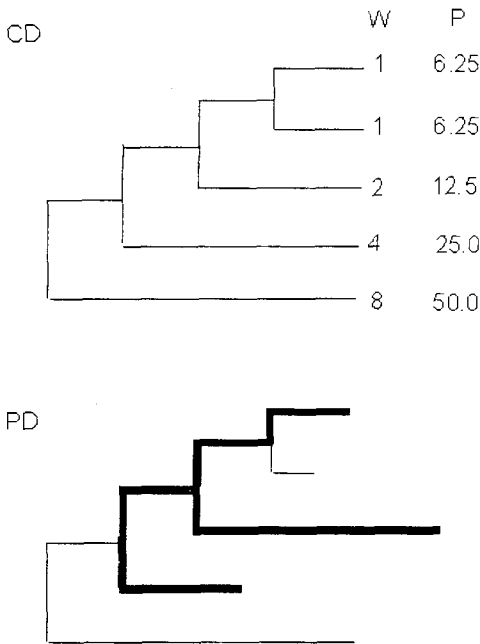
Figure 10.2 Cladistic diversity (CD, upper panel) applies equal weighting (W) to sister clades. Based on the W values, the percentage contribution of each taxon (P) can be calculated (Vane-Wright et al. 1991). Phylogenetic diversity (PD, lower panel) is calculated as the sum of branch lengths across the minimum spanning path (in bold; Faith 1992).

serves. An analysis of 177 species of plants in the herb-rich boreal-lake forests in Finland compared the efficiency of different measures (species richness, phylogenetic diversity, and restricted-range diversity) in selecting a reserve network representing total diversity. The authors emphasized that phylogenetic diversity was a poor predictor of total species richness because it does not take into account rare and sparsely distributed species if they are not phylogenetically distinct (Virolainen et al. 1999; Virolainen et al. 2001). A morphological phylogenetic analysis was used to compare the importance of endemisms and phylogeny in the conservation of South African orchids (Linder 1995). This study suggests that conserving "metaspecies," taxa that form unresolved assemblages with monophyletic clades imbedded in them (Donoghue 1985), may be better than choosing recent endemics growing on ephemeral habitats. Metaspecies have been able to speciate into other habitats in the past and have great potential of doing so in the future. In another attempt to take into account rare species, Posadas et al. (2001) proposed a measure that includes taxon distinctness and endemicity. In their analysis of southern South America, the authors considered 115 species of arthropods and angiosperms, distributed in 12 biogeographic regions. They found that the most important region when taxa distinctness and endemicity were considered, Santiago (in the central portion of Chile), was also the region of highest species richness. These studies both

illustrate that CD can be important and complementary to species-richness data. However, they tried to maximize the number of species preserved by using CD as an indicator of species richness, which minimizes the use of CD and misses the point that CD is an important index for determining areas for conservation.

Molecular phylogenetics has burst upon the systematic scene in the last ten years with the use of the polymerase chain reaction (PCR) techniques that immensely facilitate the acquisition of molecular sequence data. Since the speed of production has greatly increased, the number of molecular phylogenies has surpassed the number previously prepared by using morphological characters, and molecular techniques are the leading provider of cladograms. In the past five years some studies have used genetic information in the estimation of phylogenetic diversity indexes. For instance, Crandall and his collaborators have used molecular phylogenetics of the crayfish in the Ozark plateaus (Crandall 1998) and Australia (Whiting et al. 2000) to establish conservation priorities. In both studies the crayfish data suggested that the conservation priorities selected using maximum PD were very similar to those chosen using species-richness indexes. Similarly, a molecular phylogeny of the plant genus *Piper* (Piperaceae, black pepper and its allies) was used to determine areas of high diversity in the Chocó region of Colombia (Jaramillo 2001). This study showed that PD was positively correlated with species richness but negatively correlated with endemism. The *Piper* analysis concluded that species richness can be a surrogate for PD as was shown by the crayfish studies. It also suggested that focusing on endemic species as conservation targets cannot be the main goal in biodiversity conservation, because endemics do not always make a large contribution to the phylogenetic diversity of an area. The broadest application of these methods is a study using carnivore and primate molecular phylogenies and their worldwide distribution to test the importance of biodiversity hot spots for conservation (Sechrest et al. 2002). The authors found that the taxa from these regions represent more than 70% of the evolutionary history of the groups evaluated.

From this small sample of cases that used phylogenetic measures, we can see how data from evolutionary histories is very important in determining conservation areas, because they are estimates of feature or information diversity. These studies also indicate that in some cases species richness can be a good surrogate for CD and PD, which is encouraging, given the scarcity of phylogenetic data, the high costs of generating it, and the little time we have for making conservation decisions. Some authors still give great importance to endemic and rare species (Virolainen et al. 1999; Posadas et al. 2001; Virolainen et al. 2001). However, two studies (Linder 1995; Jaramillo 2001) seem to suggest that endemicity is not invariably the most important factor, because endemic species do not always make a large contribution to feature diversity. It was hypothesized that the relatively low importance of endemics on the coast of South Africa and the Chocó region is a product of the recent speciation in the region, making most endemics young and closely related to each other. For an area that has relictual endemics, however, we predict that endemic species would make a larger contribution to the total diversity of the locality. The difference in the relative importance of endemics in the feature-based indexes depends on the evolutionary history of the biota of each region. Therefore one cannot a priori dis-

miss CD or PD and use only species richness as a surrogate. For the record, a recent study has shown that PD and the alternative ED (environmental distance) do not function well in some situations (Araújo et al. 2001).

IDENTIFICATION OF AREAS OF SHARED VICARIANT HISTORY

The intraspecific phylogeographies of codistributed species can be used to identify areas that share common vicariant history. One identifies evolutionarily distinct communities or areas and searches for repeating patterns among these areas in different groups of taxa (Nelson and Platnick 1981). Rosen (1978) illustrated how this could be accomplished using poeciliid fish genera, but he did not suggest that such areas should be the basis for conservation planning. Phylogenies were generated for many lineages of organisms endemic to the Hawaiian islands. Each island was treated as a separate area(s). The repeated pattern observed among the islands revealed the importance of the different areas for conservation (Wagner and Funk 1995).

The search for groups of species that share the same geographic distribution has been extended by the concept of evolutionarily significant units, within single species (Moritz 1994). Using congruence among haplotype phylogenies (mostly cpDNA or mtDNA, for plants and animals respectively), it is possible to identify recent vicariance events that have segregated the communities into distinct geographic units. A good example of this method comes from the tropical forest of northeast Queensland, Australia. Moritz and his collaborators have studied a large number of animal taxa from the region, showing that several species have similar geographic structures, with distinct northern and southern populations (Moritz and Faith 1998; Joseph et al. 1995). In order to prioritize among those areas, Moritz and Faith used a PD approach and proposed that if only two areas can be conserved, a subregion from the north and another from the south should be selected in order to maximize preserved genetic diversity. There are no similar examples in the plant literature, although some phylogeographic studies in northern Europe and northwestern North America have shown that most diversity is derived from Pleistocene refugia (Soltis et al. 1992; Manos et al. 1999). However, they have not discussed conservation issues explicitly. This approach can be extended to different areas to organisms of restricted and extended distribution that can be undergoing geographic differentiation that we need to take into account when making conservation decisions.

PRESERVING THE COMPONENTS OF EVOLUTIONARY PROCESSES

Phylogenies can also be enlightening about evolutionary processes and can provide information about how to preserve the potential for evolutionary change at either the population level or the species level. At the population level, phylogeographic studies can be useful in understanding the bridge between intra- and interspecific evolution and in inferring speciation events. Phylogenies can distinguish among

three major factors that can spatially differentiate the lineages: restricted gene flow, range expansion (i.e., colonization), and past fragmentation (Templeton 1998). At the species level, tree-shape information can help distinguish different diversification processes and their correlation to extinction rates (Heard and Mooers 2000).

Intraspecific phylogenies reflect population histories, helping to reconstruct the processes that have shaped the current distribution of genetic diversity. Information about evolutionary processes is essential in making judicious conservation decisions. In a study of African bovids, it was found that while the populations of impala and wildebeest were fragmented by the Rift Valley in Tanzania, this barrier was not important for the buffalo populations that presented recurrent gene flow (Templeton and Beorgiadis 1996). According to these results there is no genetic rationale to stop the translocation of buffalos for repopulation. Translocation of impala and wildebeest individuals should be avoided, however, because it can disrupt local adaptation. These conclusions were not possible without the genetic analysis.

Phylogenies at the species or supraspecific level can provide information about diversification and extinction processes. Heard and Mooers (2000) demonstrated that the loss of diversity is associated with two factors: the diversification processes that produced the clades in consideration and the patterns of extinction risk across species. Given that phylogenetic trees are often unbalanced because of the differences in speciation rates across lineages (Guyer and Slowinski 1991), conservationists are better off selecting priorities guided by a minimum-loss algorithm (Heard and Mooers 2000). Additionally, given that extinction is not random, organisms belonging to certain clades or with particular biological conditions are more vulnerable. In the case of bird species, it has been shown that extinction risk depends on family affiliation, body size. and fecundity (Bennett and Owens 1997). In many plant groups there is no comparative study that evaluates extinction risk.

RISK OF HYBRIDIZATION WITH INVASIVE SPECIES

Species introductions into nonnative habitat impose a big danger to biodiversity conservation. Most studies have emphasized the ecological effects of invasions; however, the diversity lost by hybridization poses a great risk that is largely underestimated. Species introduced from different continents, in general distantly related to local taxa, produce ecological effects like competition, predation, and parasitism. Closely related taxa are prone to hybridize with local species and erode the genetic diversity of a population. Given these conditions, phylogenies are the best tool to predict the probability of hybridization after species translocation.

A recent review of invasions in freshwater habitats in North America showed that phylogenetic relationships are perhaps the best way to predict hybridization (Perry et al. 2002). Recent genetic studies using molecular markers confirmed that hybridization has occurred for more than a decade between the rusty crayfish (*Orconectes rusticus*) and the resident species *O. propinquus* in northern Wisconsin and Michigan lakes (Perry et al. 2001). Although this hybridization had been suggested by earlier morphological studies (Smith 1981), only molecular markers can test the

extent of hybridization and its consequences. Although only one case has been documented genetically, the observation of intermediate phenotypes suggest that hybridization may be occurring in at least another five pairs of crayfish species, all of it among closely related species (Crandall and Fitzpatrick 1996).

A recent example in the plant kingdom shows the potential of invasive species. Consider the uproar over the possibility of transgenic DNA from genetically modified maize in local varieties of the crop in Oaxaca, Mexico (Quist and Chapela 2001). Corn is wind-pollinated, and so cross-pollination among fields is common. The appearance of genes from the genetically engineered maize in native varieties has many worried. Mexico is the center for native varieties of corn and seeds; the contamination of the genome of the native species has dire implications for the future of native maize. There is some controversy over the report (Butler 2002), but should this introgression prove to be true it would bear out the worst fears of the opponents of genetically altered crops and illustrate the danger of such crops as they are introduced into cultivation.

Four different scenarios have been presented where phylogenetic information is critical to conservation efforts. One of the largest barriers to making phylogenetic (especially molecular phylogenetics) methods more widely used is time and cost of obtaining the data. The speed of producing molecular phylogenies is increasing, however, and once the phylogenies are available, they are invaluable as conservation tools. For instance, in diversity indexes where the number of species can, in some cases, be a good surrogate of PD, a phylogeny is important in choosing priorities. Phylogenies illustrate the patterns of diversification of organisms at different taxonomic levels; thus they are helpful in understanding the ecological and geologic processes that have been responsible for the generation of diversity and as such should be preserved. Most examples presented here are from animals; it is clear that there is a real need to conduct similar studies in plants and to use these to compare evolutionary histories of the flora and fauna of different regions of interest.

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Plate 4.2
Kaieteur Falls, Guyana,
in the Guiana Shield.
Photograph by Carol Kelloff.

Plate 4.3
Hatiheu Valley on the
north coast of Nuku Hiva,
Marquesas Islands.
Photograph by K. R. Wood.

Plate 4.4
The Gaoligong Mountains at
3,000 m in Yunnan, China.
Photograph by Bruce
Bartholomew.

Plate 5.6 *Pachystachys spicata* (Acanthaceae).
Photograph by Dieter Wasshausen.

Plate 5.7 *Gazania krebsiana* (Asteraceae).
Photograph by Vicki Funk.

Plate 5.8 *Titanotrichum oldhamii* (Gesneriaceae).
Photograph by Richard Dunn.

Plate 5.9 *Lophostigma plumosum* (Sapindaceae).
Photograph by Pedro Acevedo-Rodríguez.
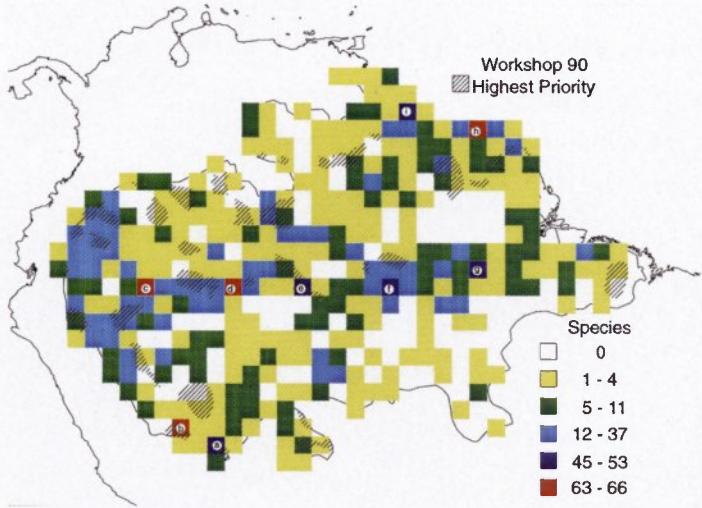
Plate 10.1 Geographic distribution in Amazonia of species diversity for all taxa combined. The number of species is indicated for each of the 472 one-degree grid cells. The Workshop 90 high-priority conservation areas are also shown. Grid cells with the highest number of species are indicated by lowercase letters (for localities see table 10.2; after Kress et al. 1998).
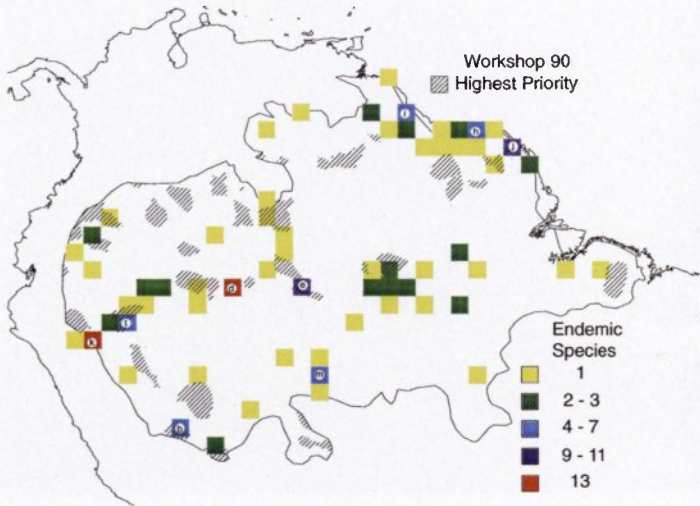

Plate 10.2 Geographic distribution in Amazonia of endemic species diversity for all taxa combined. The number of endemic species is indicated for each of the 472 one-degree grid cells. The Workshop 90 high-priority conservation areas are also shown. Grid cells with the highest concentration of endemic species are indicated by lowercase letters (for localities see table 10.2; after Kress et al. 1998).
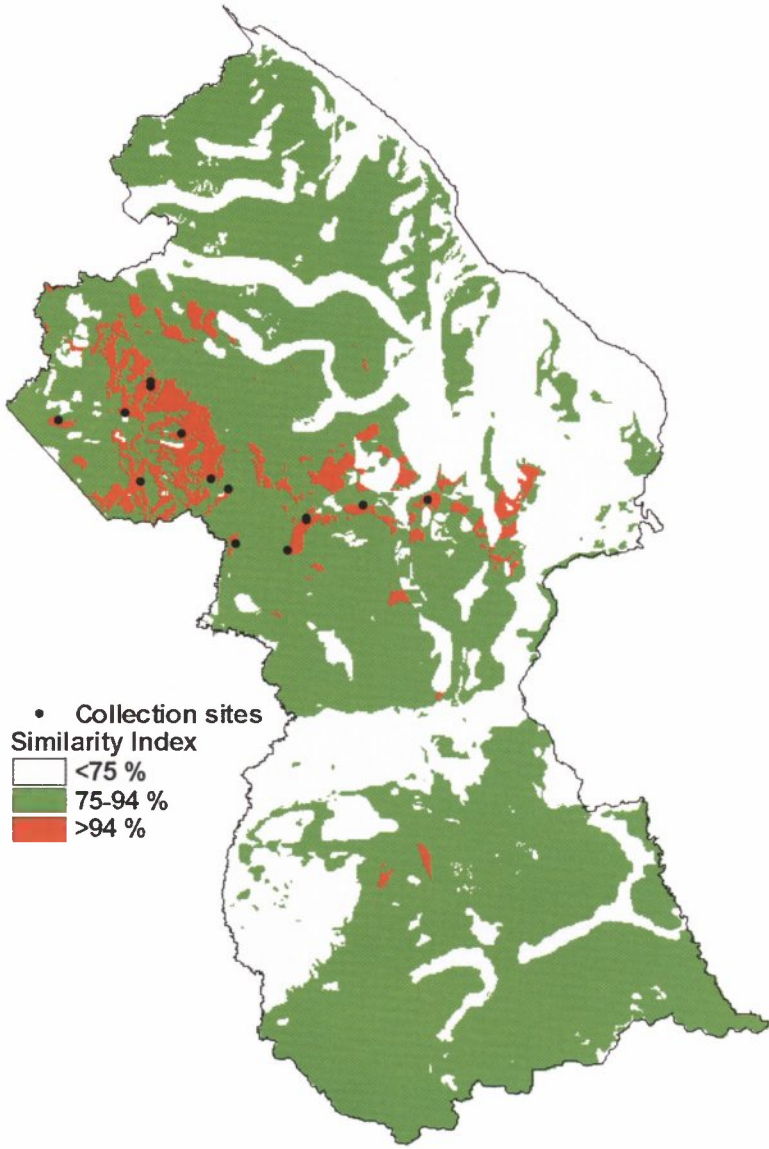
Plate 10.3 A map of Guyana illustrating the known distribution of a plant species (Melastomataceae, *Leandra purpurea* Gleason: black dots) and the distribution of the same species (shaded gray areas) based on DOMAIN modeling of the known localities with four abiotic factors. Three levels of similarity are shown; only a similarity index of 95% or more was used in the analysis (after Funk and Richardson 2002).
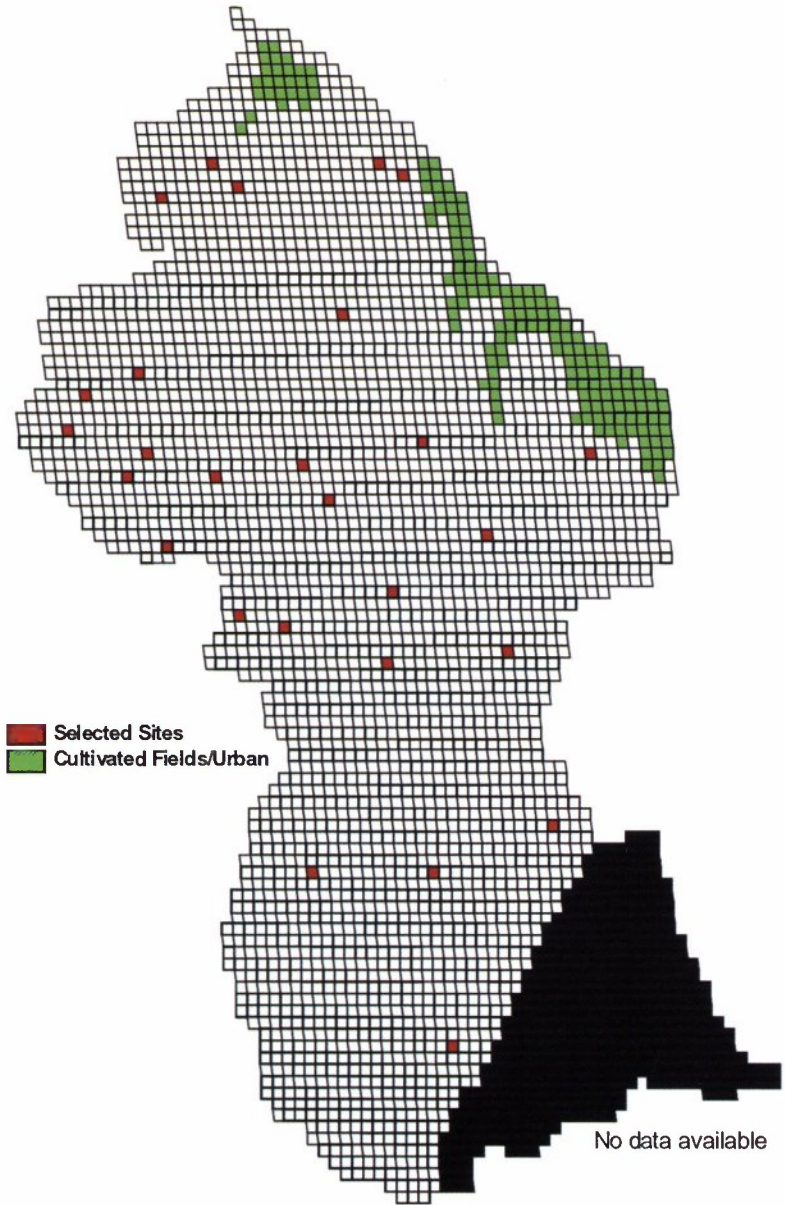
Plate 10.4 Map of Guyana with a grid showing 27 of the 33 cells that would capture each species at least three times (after Funk and Richardson 2002).