Global legume diversity assessment: Concepts, key indicators, and strategies

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Abstract While many plant species are considered threatened under anthropogenic pressure, it remains uncertain how rapidly we are losing plant species diversity. To fill this gap, we propose a Global Legume Diversity Assessment (GLDA) as the first step of a global plant diversity assessment. Here we describe the concept of GLDA and its feasibility by reviewing relevant approaches and data availability. We conclude that Fabaceae is a good proxy for overall angiosperm diversity in many habitats and that much relevant data for GLDA are available. As indicators of states, we propose comparison of species richness with phylogenetic and functional diversity to obtain an integrated picture of diversity. As indicators of trends, species loss rate and extinction risks should be assessed. Specimen records and plot data provide key resources for assessing legume diversity at a global scale, and distribution modeling based on these records provide key methods for assessing states and trends of legume diversity. GLDA has started in Asia, and we call for a truly global legume diversity assessment by wider geographic collaborations among various scientists.

■ INTRODUCTION

While plants support many ecosystem services such as food provisioning, mitigating floods and droughts, carbon sequestration, primary production, and cultural inspiration (Daily & al., 2000; Millennium Ecosystem Assessment, 2005), plant natural habitats such as forests and wetlands are being rapidly lost. Thus, many plant species are also being lost, but it remains uncertain at what rate we are losing plant species diversity (Butchart & al., 2010; Rivers & al., 2011; Yahara & al., 2012). To reduce this uncertainty, we need to assess states and trends of as many plant species as possible at the global scale (GEO BON, 2010). Here, we propose the legume family (Fabaceae or Leguminosae, hereafter called Fabaceae)—one of the largest and most economically vital plant families—as a target for a global plant diversity assessment project which aims at clarifying uncertainties in and improving the understanding of biodiversity loss. The purpose of this paper is to introduce concepts and strategies of the global legume diversity assessment by reviewing literature relevant to the legumes, methods of assessing states and trends, and data availability.

The idea of the global legume diversity assessment (GLDA) has been developed through discussion in (1) the bioGENESIS core project of DIVERSITAS (Donoghue & al., 2009) which aims at providing an evolutionary framework for biodiversity science, conservation and policy in a rapidly changing world (Hendry & al., 2010) and (2) Working Group 1 (Genetics/phylogenetic Diversity) of GEO BON (Group on Earth Observations Biodiversity Observation Network) that was organized in February 2008 to contribute to the efficient and effective collection, management, sharing, and analysis of data on the status and trends of the world's biodiversity (Scholes & al., 2008; GEO BON, 2010). As a trial for applying evolutionary approaches to biodiversity monitoring and conservation practice, bioGENESIS is promoting global genetic/phylogenetic diversity observation in collaboration with GEO BON in which GLDA is the first project under this framework. GLDA aims to employ taxonomic and ecological approaches such as species distribution modeling as well as rapidly developing genetic and phylogenetic approaches. GLDA also hopes to incorporate new developments of genome science technologies such as next-generation sequencing (Yahara & al., 2010). Future progress would also benefit from extending in-depth approaches of genome science from "model organisms" such as *Arabidopsis thaliana* (L.) Heynh. to some "model groups" for which the Fabaceae makes an excellent candidate.

Fabaceae ("legumes") is the third-largest family of angiosperms, including ca. 730 genera and ca. 19,400 species (Lewis & al., 2005). Fabaceae has the following advantages as a target group of global plant diversity assessments in comparison to Asteraceae (23,000 spp.), Orchidaceae (22,000 spp.), and other large plant families: (1) Fabaceae includes many useful plants such as crops, vegetables, timber, ornamentals and medicinal plants (Van der Maesen & Somaatmadja, 1992; Gepts & al., 2005; Brink & Belay, 2006; Saslis-Lagoudakis, 2011); (2) Habitat diversity of Fabaceae is extremely high; legumes occur from tropics to arctic zones, from the seashore to alpine habitats, and

in rain forests, mangroves, peat swamp forests, seasonal forests, savannas, and deserts (e.g., Prado, 1993; Prado & Gibbs, 1993; Pennington & al., 2000; Prado, 2000). In addition, Fabaceae show high diversity in all of three main tropical vegetation types including tropical rain forests, dry forests and woody savannas (Sheil, 2003; Ter Steege & al., 2006; Sarkinen & al., 2011), while other families have comparable diversity, if at all, in just one of these vegetation types; (3) Plants of Fabaceae harbor many specific herbivorous insects and support characteristic food webs (Southgate, 1979; Harmon & al., 2009); (4) Many legume species are symbiotic with nodule-forming bacteria with nitrogen fixation ability, and as such support important ecosystem functions (Sprent, 2009); (5) Fabaceae includes many invasive species, presenting serious economic threats and costs (Bradshaw & al., 2008); (6) Fabaceae harbors extremely diversified life forms, including annuals, shrubs, canopy trees, vines, and aquatic plants (Lewis & al., 2005); (7) Fabaceae are highly diversified in functional traits of leaves, stems, flowers, fruits and seeds (Lewis & al., 2005; Kleyer & al., 2008; Kattge & al., 2011a, b); (8) Fabaceae display a range of rarity, from extreme endemics only known from small local areas, which are exceedingly vulnerable to threats (Raimondo & al., 2009), to widespread and even cosmopolitan species; (9) Flowers of Fabaceae are generally animal-pollinated and thus sensitive to pollinator loss (Proctor & al., 1996); (10) Fabaceae contains many unique chemicals, especially in the seeds, for which a rich database is available (Bisby, 1994; Dixon & Sumner, 2003); (11) Legume taxonomy and phylogeny is well-studied by an active global legume systematics research community that resulted in the ten volumes of the *Advances in Legume Systematics* series, and (12) Whole-genome sequences of four species of Fabaceae, *Medicago truncatula* Gaertn. (http://www.medicago .org/genome), *Lotus japonicus* (Regel) K. Larsen (http://www .kazusa.or.jp/lotus), *Glycine max* (L.) Merr. (http://www.phyto zome.net/soybean, Schmutz & al., 2010) and *G. soja* Siebold & Zucc. (Kim & al., 2010) are already available with several more underway.

In this paper we describe the concepts, approaches and strategies of GLDA as comprehensively as possible. With this purpose in mind, we introduce three sections in this paper. First, we characterize legume diversity as an introduction for non-legume specialists. Second, we describe the concepts, strategies, key methods and key indicators that are required to achieve the goals of the assessment. In addition, we review available data for assessing states and trends of key indicators. Third, we describe strategies for acquisition of new data for key indicators. The approach proposed here can be applied to other families of flowering plants.

■ AN OVERVIEW OF LEGUME DIVERSITY

Phylogenetic relationships of legumes. — There is a substantial body of evidence from morphological and molecular phylogenetic studies to support the Fabaceae as a monophyletic family (Wojciechowski & al., 2004; Bruneau & al., 2008). It traditionally has been divided into three subfamilies

Caesalpinioideae, Mimosoideae, and Papilionoideae (Polhill & al., 1981), on the basis of morphological differences, particularly in floral characters. On the basis of molecular phylogenetic studies, Mimosoideae (with the possible exclusion of *Dinizia* Ducke) and Papilionoideae have both been resolved as monophyletic, nested within a paraphyletic Caesalpinioideae (Fig. 1, modified from Wojceichowski & al., 2004). The paraphyletic subfamily Caesalpinioideae comprises a diverse assemblage of "caesalpinioid" legumes that mostly diverged early in the history of the family and lack distinctive floral features used to group genera into the other two families. The caesalpinioid tribe Cercideae is suggested to be one of the earliest diverging lineages in the family. However, in a phylogenetic study where sequences of *matK* and the *trnL* and 3′-*trnK* introns of Caesalpinioideae were used, relationships among the first branching lineages of the legumes are still not well supported, with Cercideae, Detarieae and the genus *Duparquetia* Baill. alternatively resolved as sister group to all other legumes (Bruneau & al., 2008). A clade including many other genera of Caesalpinioideae is sister to the subfamily Mimosoideae, and a clade comprising these two groups is sister to the subfamily Papilionoideae.

In the subfamily Papilionoideae, several major groups have been identified based on molecular phylogenies (summarized by Lewis & al., 2005; for further studies, see Torke & Schaal, 2008; Boatwright & al., 2008; LPWG, 2013). The dalbergioid clade is a large group of 45 genera and ca. 1270 species that includes the peanut (*Arachis hypogaea* L.) (Lavin & al., 2001). The genistoid clade includes the genus *Lupinus* L., as well as other diverse genera. The millettioid group comprises the strongly supported millettioid and phaseoloid clades including many important crop species such as the cultivated soybean (*Glycine max*) and common bean (*Phaseolus vulgaris* L.)

(Doyle & Luckow, 2003). Hologalegina (an informal name) is the largest of the well-supported major clades of Papilionoideae, split into two major clades, the robinioids (*Robinia* L. spp., e.g., black locust; and *Sesbania* Scop. spp., of interest because of stem-nodulation in some species) and the inverted repeat-loss clade (IRLC; Wojciechowski & al., 2000) that is marked by the loss of one copy of the large (approximately 25 kb) inverted repeat commonly found in the chloroplast genome of angiosperms. The IRLC is dominated by temperate, herbaceous genera, including familiar plants such as *Pisum* L. (pea), *Vicia* L. (vetch, broadbean), *Cicer arietinum* L. (chickpea), *Medicago* L. (alfalfa), and *Trifolium* L. (clovers).

The largest papilionoid subgroup in number of genera is the phaseoloid/millettioid group, which, like Hologalegina, includes a number of domesticated taxa such as *Glycine* L. (soybean), *Phaseolus* L. (common bean), *Vigna* Savi (cowpea, mungbean), *Cajanus cajan* (L.) Millsp. (pigeon pea), and *Psophocarpus* Neck. ex DC. (winged bean). Relationships in the group are complex and include elements of several tribes (e.g., Kajita & al., 2001; Hu & al., 2002). As an example, the closest relatives of *Glycine*, the soybean genus, still remain unknown with several candidates suggested by various molecular studies including the pantropical genus *Teramnus* P. Browne (Lee & Hymowitz, 2001), Amphicarpaea, the tribe Psoraleeae (Stefanovic & al., 2009) or a combination thereof (Egan & Doyle, unpub. data). Further details of our current knowledge on phylogeny of Fabaceae will be reviewed by the Legume Phylogeny Working Group (LPWG, 2013).

Biogeography of legumes. — Fabaceae hava a nearly cosmopolitan distribution and the diverse habitats in which they grow have been grouped by Schrire & al. (2005b, 2009) into four major biomes: succulent (a semi-arid, fire-tolerant, succulent-rich and grass-poor, seasonally dry tropical forest,

Fig. 1. Summary of phylogenetic relationships in Fabaceae based on molecular analyses (*matK*). Modified from Wojciechowski & al. (2004). Some well-known genera for certain groups are listed.
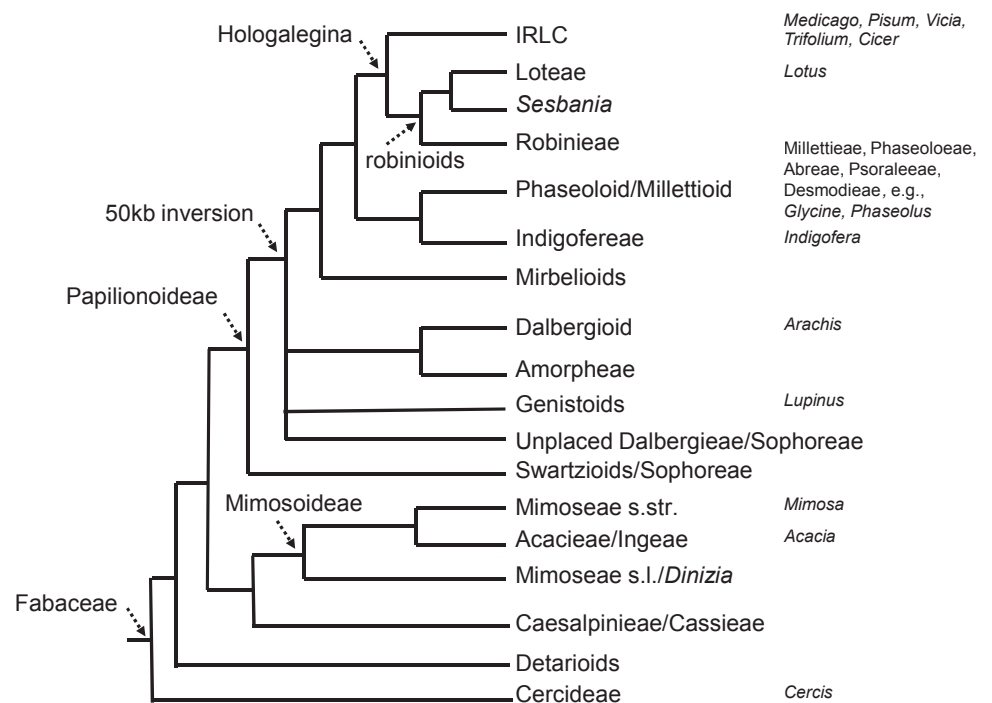
Table 1. Numbers of genera and species of Caesalpinioideae, Mimosoideae, and Papilionoideae in each biome from Schrire & al. (2005b).

	No. gen./sp.	No. (%) gen. present				No. (%) sp.			
		Af/Mad	As/Pac/Aus	New World	Eur/Med	S-biome	G-biome	R-biome	T-biome
Caesalpinioideae	171 (2251)	93 (54)	43 (25)	70 (41)	2 (1)	907 (40)	468 (21)	855 (38)	21 (1)
Mimosoideae	82 (3271)	29 (35)	25 (30)	50 (61)	3 (4)	1040 (32)	1050 (46)	724 (22)	3 (<1)
Papilionoideae	478 (13,805)	167 (35)	214 (45)	176 (37)	68 (14)	1946 (14)	3655 (26)	1084 (8)	7120 (52)

No. (%), number and percentages of genera and species; gen./sp., genera/species; S, Succulent biome; G, Grass biome; R, Rainforest biome; T, Temperate biome.
Four continental regions: Af/Mad, Africa-Madagascar; As/Pac/Aus, (tropical) Asia-Pacific-Australia; New World, Neotropics and temperate North and South America; Eu/Med, (temperate) Eurasia-Mediterranean (including Africa north of the Sahara)-Macaronesia.

thicket and bushland biome), grass (a fire-tolerant, succulent-poor, and grass-rich woodland and savanna biome), rainforest (a tropical wet forest biome), and temperate (a temperate biome in both the Northern and Southern Hemispheres). The paraphyletic subfamily Caesalpinioideae is relatively rich in Africa and approximately 40% of the species are found in the two contrasting biomes, grass and rainforest (Table 1). The subfamily Mimosoideae is relatively richer in the New World and in the grass biome. The subfamily Papilionoideae is relatively richer in the Asia-Pacific region including Australia and in the temperate biome. Schrire & al. (2005a) suggested that lineages confined to the semi-arid succulent biome gave rise to sublineages occupying all other biomes, based on a cladistic reconstruction of ancestral biome states in the basal branches of the legume phylogenetic tree.

The proportion of legumes in a plot or in an area largely varies among biomes and also among continents, providing a useful indicator of ecosystem composition. For forest ecosystems, many permanent plots have been established in various places across the world and continuous monitoring has been carried out in these locations (Condit, 1995; Rees & al., 2001). The Center for Tropical Forest Science of the Smithsonian Tropical Research Institute maintains 47 large-scale forest plots in 21 countries in which 4.5 million trees of 8500 species have been monitored (Burslem & al., 2001). This dataset provides an outlook for global patterns of woody legume proportion in forest ecosystems and its determinants (Table 2). The dataset reveals that the proportion of woody legumes is highest in

Table 2. Proportion of legumes in African, American, and Asian forest plots under the network of the Center for Tropical Forest Science, Smithsonian Tropical Research Institute.

	Africa	Americas	Asia
Plots	5	5	17
Mean % trees	11.1	4.7	2.6
Min % trees	5.8	0.9	0.0
Max % trees	14.5	12.5	12.1
Mean Basal Area	49.0	7.4	2.5
Min Basal Area	8.6.	0.3	0.0
Max Basal Area	78.1	15.0	9.2
% of all species	8.0	11.5	3.0

Central and South America, somewhat lower in Africa, and much lower in Asia.

Ecosystem functions of legumes. — Fabaceae is a dominant family in terms of species-richness and biomass in many forests of the Neotropics and Africa (including Madagascar). For example, Ter Steege & al. (2006) demonstrate the dominance of legumes in the Amazon rain forest (see also Du Puy & al., 2002), and legumes are the most species-rich family in both Neotropical dry forests (Pennington & al., 2006; Sarkinen & al., 2011) and savannas (Ratter & al., 2006). Legume abundance is a significant factor that influences the rate of carbon and nitrogen accumulation in ecosystems (Knops & Tilman, 2000; Knops & al., 2002). The presence of legumes often has a positive effect on ecosystem nitrogen pools which can significantly increase above-ground biomass (Spehn & al., 2002). In addition, nitrogen-fixing leguminous trees (Sprent, 2009) are key invaders on several continents (Archer, 1994; Lewis & al., 2009) and oceanic islands (Caetano & al., 2012), having strong impacts on savanna and grassland ecosystems (Scholes & Archer, 1997; Chaneton & al., 2004). On the other hand, there are many Fabaceae trees that grow slowly and produce very heavy wood such as *Dalbergia* L. f. Such heavy wood has slow decomposition rate and contributes to carbon storage in ecosystems (Weedon & al., 2009).

Economic value of legumes. — Seeds (grains) and fruits of Fabaceae are major food sources. According to FAOSTAT, 262 million tons of soybeans, 18 million tons of common beans, and 16 million tons of green peas were produced in 2010. These are particularly important as a major source of proteins and oils; grain legumes provide about one-third of all dietary protein nitrogen and one-third of processed vegetable oil for human consumption (Graham & Vance, 2003). As a resource of proteins, legumes are complementary to cereals; cereal seed proteins are deficient in lysine, and legume seed proteins are deficient in sulfur-containing amino acids and tryptophan (Wang & al., 2003). Grain legumes also provide essential minerals required by humans (Grusak, 2002a) and produce health promoting secondary compounds that can protect against human cancers (Grusak, 2002b; Madar & Stark, 2002). Legumes are also valuable in agroforestry, in industrial and medical sectors, and for biological nitrogen fixation (Graham & Vance, 2003). Some species of legumes are important in horticulture where they are typically grown for their beautiful flowers and sometimes as foliage plants. Multi-purpose

trees and shrubs have long been selected and refined by local communities for shade, ornament, forage, fodder, fuel wood, bee forage for honey production, and soil enrichment (Lewis & al., 2005). Regional favorites include *Butea* Roxb. ex Willd. and *Dalbergia* in India, *Calliandra* Benth. and *Inga* Mill. in Central America (Polhill, 1997), *Prosopis* L. in southern South America and *Acacia* Mill. and *Faidberbia* A. Chev. in Africa. Legume timber and wood from many species have long been put to a multitude of uses, ranging from heavy construction (house and boat building, railway sleepers, cart wheels), to paper and plywood manufacture, and fine furniture production, carpentry, marquetry, and veneer work. Some species (e.g., *Dalbergia nigra* (Vell.) Allemão ex Benth., *Kalappia celebica* Kosterm.) are now rare and endangered due to over-exploitation for their commercially valuable timbers (Lewis & al., 2005).

Genetics and genomics of legumes. — Fabaceae includes a diverse array of genome sizes. Crop and model legumes differ greatly in their C-value (the amount of DNA per haploid genome), base chromosome number, and ploidy level (Fig. 2). The crop legume soybean experienced a polyploidy event about 12 million years ago (Innes & al., 2008) and has a genome about twice as large as the model legumes *Medicago truncatula* and *Lotus japonicus*. The genome of *M. truncatula* and *L. japonicus* is about one-tenth the size of the pea genome and more than three times that of *Arabidopsis thaliana* (125 Mbp).
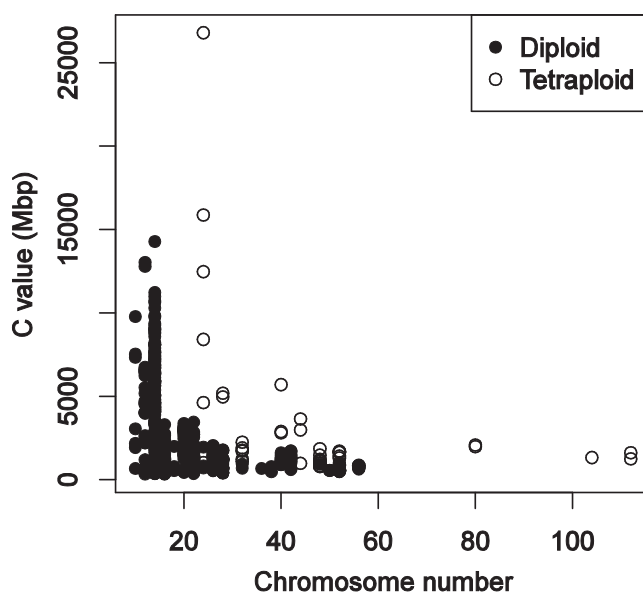
On 25 July 2012, a search of the Royal Botanic Gardens, Kew, Plant DNA C-value database for Fabaceae returned 676 records, ranging from ~300 to over 26,000 Mbp/1C (data.kew .org/cvalues/). The smallest legume genome (with accompanying chromosome number), at 336 Mbp, belongs to *Trifolium ligusticum* Balb. ex Loisel. (Ligurian Clover), a member of the IRLC clade. *Trifolium* and *Prosopis* make up the majority of species with genomes smaller than the model legumes

Fig. 2. 1C/Mbp values for all legume records in the Royal Botanic Gardens Kew Plant. C-value DNA database as of 25 July 2012 and this database was based on 676 records.

M. truncatula and *L. japonicus* (465 Mbp/1C). Although *Medicago* and *Lotus* L. are often considered the primary legume biological models, it may be more helpful to think of many models, each making critical contributions to a body of knowledge about legumes as a semi-unified genetic system. *Medicago* and *Lotus* serve as effective models for the legumes adapted to temperate climate and soybean for the many crop species in the Phaseoleae that are better adapted to more tropical climates (Cannon & al., 2009). The largest diploid genome represented in the database is *Lathyrus vestitus* Nutt. (a wild pea, $2n = 2x = 14$) with a size of 14,279 Mbp/1C. Diploid *Vicia faba* L. (the broad bean, $2n = 2x = 12$) is not far behind with a genome size of 13,032 Mbp/1C. The largest legume genome listed is for the tetraploid *Vicia faba* ($2n = 4x = 24$) with a size of 26,797 Mbp/1C.

■ CONCEPT, STRATEGIES AND KEY INDICATORS OF THE ASSESSMENTS

Goal of the assessment. — The goal of GLDA is to provide the largest, integrative and extensive assessment on the global state and trends in key biodiversity indicators for a major group of vascular plants. By focusing on Fabaceae as the first effort for global plant diversity assessment, we aim also to develop a series of standardized approaches that can be applied to other plant families. Some efforts for global assessments of biodiversity have been made as a response to the sad fact of rapid biodiversity loss. These include the Global Biodiversity Assessment (Heywood, 1995; Watson & al., 1995), the Millennium Ecosystem Assessment (2005), and the Global Biodiversity Outlook 3 (Leadley & al., 2010; Secretariat of the Convention on Biological Diversity, 2010). However, these assessments have been made on a very limited proportion of vascular plant diversity. Kreft & Jetz (2007) modeled and mapped global patterns of vascular plant species richness but did not carry out any assessment of trends (species decline/loss). In GLDA, we intend not only to model and map the global states of legume diversity but also to assess trends of legume diversity using various time series records available. As for the current states of legume diversity, we intend to assess not only species richness but also phylogenetic diversity and phylogenetic endemism (Faith, 1992; Faith & al., 2004; Rosauer & al., 2009), and functional diversity (Faith, 1996; Petchey & Gaston, 2006; Díaz & al., 2011). We will also examine the relationships between species richness and phylogenetic or functional diversity (Devictor & al., 2010; Safi & al., 2011), plus some additional key indicators at the within-species level, described below. As for the trends, we will assess loss of diversity under land-use change, climate change and other changes in environmental drivers (e.g., Wearn & al., 2012), biological invasion including contemporary evolution of invasive species, and response of legume distribution and ecosystem composition to climate change under proposed scenarios.

Strategies: modeling and mapping. — Maps provide broad, clear and intuitive communication tools on states and trends of biodiversity not only among scientists but also between scientists and policy makers. Distribution maps have

been used since the first stages of research in taxonomy and biogeography and now the sophisticated methodology of distribution modeling (Guisan & Zimmermann, 2000; Guisan & Thuiller, 2005; Elith & al., 2006; Franklin, 2009) can be used to draw maps of biodiversity indicators. This methodology is complementary to molecular phylogenetic methodology that reconstructs evolutionary history. It is critical for the success of GLDA to integrate the two modeling approaches, one on spatial patterns and another on temporal patterns.

Forest plot records provide presence/absence data and specimen records presence-only data, and both of these sources can be used for modeling and mapping spatial patterns of diversity. While most methods of distribution modeling require presence/absence data, several methods to model presence-only data have been developed. First, the maximum entropy model (Maxent; Phillips & al., 2006) provides one of the most useful models among distribution modeling methods (Elith & al., 2006; Graham & al., 2008; Wisz & al., 2008). Second, several studies (e.g., Elith & Leathwick, 2007; Phillips & al., 2009) have shown that various modeling methods for presence/absence data can be applied to presence-only data by using presence data of related species as pseudo-absence data.

In a pioneering work, Raes & al. (2009) used 44,106 specimen records to model distributions of Borneo plant species belonging to 102 revised families. After excluding non-significant species distribution models, 1439 plant species were used to identify hotspots of species richness and endemicity. Using the same method, Van Welzen & al. (2011) projected changes of plant distribution in Thailand under a climate change scenario for 2050, and Zhang & al. (2012) prioritized areas for conservation in Yunnan. This method is useful to assess states and trends of Fabaceae both on regional and global scales.

Species richness and distribution records. — Indicators of current states will help to quantify biodiversity patterns and processes, and sometimes act as a lens to interpret changes in land use. One of the most widely used indicators for the states of biodiversity is Species Richness (SR) that simply counts taxonomic species (e.g., Queiroz, 2007). The areas where SR (endemic and/or threatened SR in particular) is higher often are considered to have higher conservation value (Orme & al., 2005). One of the goals of GLDA is to determine those SR hotspots for Fabaceae. By determining those hotspots and by considering complementarity (degrees of non-overlap) of species distribution, we can develop systematic conservation planning (Margules & Pressey, 2000; Watts & al., 2009).

Species level taxonomy is the basis of SR assessment. Among flowering plant families, the taxonomy of legume species is relatively well studied. The International Legume Database & Information Service (ILDIS; http://www.ildis.org/) provides a world list of legume species, though in some cases it has not been updated to reflect recent taxonomic monographs. Owing to the well-studied species taxonomy, taxonomic monographs and local Floras provide us a reliable list and description of species in a particular area by which we can identify species and accumulate distribution records.

Distribution records of virtually all legume species can be obtained from herbarium specimen records, plot data, and additional field work. Each dataset has its own advantages and disadvantages. Herbarium specimen labels, ideally captured into digital databases that can be shared and interrogated, provide the most extensive and accurate distribution data available, but provide only historical presence records (as opposed to absence records). Specimen-based distribution records have been accumulated in GBIF as well as in the databases of the Chinese Virtual Herbarium (CVH; http://www.cvh.org.cn/cms/), the Kew Herbarium Catalogue (http://apps.kew.org/herbcat/navigator .do), speciesLink (http://splink.cria.org.br), Plants of Southern Africa (http://posa.sanbi.org/searchspp.php), TROPICOS of the Missouri Botanical Garden (http://www.tropicos.org/), and many other herbaria (http://www.virtualherbarium.org/vh/other systems.html). Plot data obtained from ecological studies can provide presence/absence data but plot studies may not detect rare species that have very low densities. Plot data also often cover only tree species and lack records of herbaceous species. Additional field work in areas poor in data or high in endemism are critically important to improve the prediction power of distribution models (Yahara & al., 2012), but those are time-consuming and costly. The envisaged data-collecting strategy will be optimized by integrating advantages of all three data sources (herbarium specimen records, plot data, records from field work).

Species loss rate, extinction risks and threat status. — In addition to describing states of SR, we will quantify deterministic trends of diversity, including the rate of species loss. Using scenarios of climate change or land use change, we can project future species loss. Van Vuuren & al. (2006) projected that a loss of global vascular plant diversity by 2050 would be 7% to 24% relative to 1995, and Malcolm & al. (2006) projected that climate change would result in extinctions of endemic plant and vertebrate species in biodiversity hotspots ranging from 1% to 43%. However, these projections depend on crude estimates of species–area relationships and it is desirable to obtain more reliable estimates of species loss using distribution models developed for as many species as possible (see also Mendenhall & al., 2012; Wearn & al., 2012).

Species loss could be caused not only by deterministic factors but also by stochastic factors and thus we need to calculate extinction risk by considering various sources of stochasticity. Stochastic extinction risk is particularly significant for rare species having a small population size and/or a narrow distribution range. This risk can be assessed by repeating stochastic simulations based on minimal assumptions even if detailed demographic data are not available (Matsuda & al., 2003).

Many of these approaches will be useful also for assessing the conservation status of species using the IUCN Red List criteria (IUCN, 2001; Rivers & al., 2011). In the latest version of the IUCN Red List (IUCN, 2012), 837 species of Fabaceae were assessed and 75% are assigned to the categories: Extinct (EX, 6 spp.), Extinct in the Wild (EW, 1 sp.), Critically Endangered (CR, 74 spp.), Endangered (EN, 165 spp.), and Vulnerable (VU, 378 spp.). Only 4% "(837/19400)" of all legume species have been assessed. GLDA would contribute to fill this gap by organizing a project for assessing most legume species in the world under IUCN criteria.

In Japan (Yahara & al., 1998) and South Africa (Raimondo & al., 2009), the entire floras of the countries have been assessed for Red Lists. In Japan, of 170 legume species, 17 are Critically Endangered, eight Endangered, four Near Threatened, six Vulnerable, one Extinct in Wild, and one Extinct. The remaining 133 species are Least Concern. In South Africa, of 1595 indigenous legume species, 36 are Critically Endangered, 85 Endangered, 128 Vulnerable, 36 Near Threatened, 61 Data Deficient. In addition, another 103 species are of conservation importance, being listed as Critically Rare, Rare, or Declining (Victor & Keith, 2004). Eight species have been listed as Extinct, and a further nine are possibly extinct. The remaining 1129 species are Least Concern. Thus, almost 30% of all indigenous Fabaceae in South Africa are threatened or are of conservation concern. There are an additional 433 species in the country that are exotic or naturalized and therefore listed as Not Evaluated.

Phylogenetic diversity. — While SR is frequently used as a measure of biodiversity, taxonomic species are not equivalent in terms of their evolutionary histories. They are related with each other to various degrees and thus SR and other indicators using taxonomic species violate a fundamental statistical assumption that data are independent and randomly sampled (Felsenstein, 1985). In addition, taxonomic species often include some cryptic phylogenetic lineages (Purvis & Hector, 2000), making SR an underestimate of the number of lineages. To overcome these drawbacks, Phylogenetic Diversity (PD; Faith, 1992), the sum of branch lengths of a molecular phylogenetic tree for a given set of species, is a useful measure.

Compared to conventional SR, PD arguably may better reflect the current state of biodiversity at different spatial scales (Faith, 1992; Rodrigues & al., 2011). While PD is usually correlated with SR, their spatial patterns often show mismatches with spatial pattern of SR (Forest & al., 2007; Slik & al., 2009; Devictor & al., 2010). In grassland experiments, PD was a better predictor of ecosystem function than SR (Cadotte & al., 2009; Cardinale & al., 2012). Also, Davies & Buckley (2011) concluded that "the loss of PD, quantified in millions of years, provides a resonant symbol of the current biodiversity crisis".

Phylogenetic diversity, through its link to features, provides phylogenetic analogues not only to SR but also to other species-level measures, including complementarity, endemism, and community dissimilarity. The PD complementarity of a species is measured by the additional branch length it represents, relative to that spanned by a reference set of species (Faith, 1992). PD-complementarity values are also the basis for measures of loss of phylogenetic diversity (e.g., Thuiller & al., 2012). A PD-based measure of phylogenetic endemism of an area or region is the amount of branch length (PD) or "evolutionary history" uniquely represented by a given area—calculated when the reference set corresponds to the set of species found in all other areas (Faith & al., 2004; see Rosauer & al., 2009 and Faith, 2011 for the extension of this index to grid cells where a cell on its own may not strictly have endemic elements but does gain credit for having elements found in few other cells).

PD also provides a phylogenetic dissimilarity among areas or communities (so measuring "phylogenetic beta diversity";

for discussion see, Faith & al., 2009). This approach has been developed particularly in microbial ecology (Lozupone & al., 2006; Lozupone & Knight, 2008) and has gained further support by Swenson's (2011) finding that "environmental distance rather than spatial distance is the best correlate of phylogenetic dissimilarity". This parallels findings of microbial ecologists, and supports use of special regression models (Ferrier & al., 2007) that can predict the PD-dissimilarities for unsampled sites, allowing mapping of phylogenetic beta diversity patterns for an entire region.

These PD-based analyses will be useful for the assessment of loss of PD and evolutionary history based on changes in IUCN red list ratings and other indicators of changes in extinction probabilities. Here, refinements in some proposed phylogenetic approaches are needed. The EDGE (Evolutionarily Distinct and Globally Endangered) of Existence program measures species' phylogenetic distinctiveness through simple scores that assign shared credit among species for evolutionary heritage represented by the deeper phylogenetic branches. The logic is that a species with high distinctiveness plus a high extinction probability deserves high conservation priority. However, the existing probabilistic framework based on PD better takes into account the status of close relatives through their extinction probabilities, and better allows for updated priorities based on changes in species threat status (Faith & al., 2008). A modified EDGE program could continue to promote a list of top species conservation priorities through application of probabilistic PD, combined with simple estimates of current extinction probability (Collen & al., 2011; Kuntner & al., 2011). The global legume assessment will provide an opportunity to apply the improved approaches, including associated phylogenetic risk analyses (Faith & al., 2008).

A molecular phylogeny of the legumes, a basis for computing PD, is relatively well studied; for example, a super tree for 2228 papilionoid legumes (McMahon & Sanderson, 2006) and a 3-gene 1276-taxon tree for the whole family (LPWG, 2013) are available. Thus, PD can be computed using available data in many geographical regions because PD is more sensitive to basal divergence than to terminal divergence. However, availability of phylogenetic data is relatively poorer in particular areas, such as tropical Asia, and assessments using PD endemism and EDGE need a phylogenetic tree for a nearly complete set of species including threatened and rare species for which DNA sequence data are frequently lacking. Thus, we need more efforts to generate DNA sequences for unsampled taxa. As has been recommended for plant DNA barcodes (Kress & al., 2009), a multi-locus approach using two coding loci (conservative *rbcL* and less conservative *matK*) with a more rapidly evolving intergenic spacer is mostly optimal to get well-resolved phylogenetic trees for a local assemblage of species. We intend to focus on these markers because they provide adequate resolution at the genus level (e.g., Lavin & al., 2005) in legumes and are well represented in publicly available databases such as GenBank. It will be necessary in some species-rich genera to sequence more rapidly evolving regions such as chloroplast introns (e.g., *trnK* introns flanking the *matK* gene) and spacers, and the nuclear ribosomal internal transcribed spacer region.

To improve the availability of phylogenetic data, we will collaborate with the Legume Phylogeny Working Group (LPWG). LPWG (2013) proposed the construction of a phylogeny that samples all 751 accepted genera of legumes and listed 83 genera in which DNA sequence data are not available. Generic under-representation is most acute in SE Asia, where we will carry out targeted field work.

Functional diversity. — Taxonomic species vary in morphological and physiological traits such as size, longevity, nutrient concentration and dispersal mechanism. Vascular plants, for example, range from small annual herbs to tall canopy trees. To consider these differences, we need to measure Functional Diversity (FD; Petchey & Gaston, 2002). FD is the degree to which species communities differ in terms of their functional traits. Functional traits are those traits that are important for plant performance such as growth, survival and reproduction, and often these traits influence ecosystem functions (Díaz & Cabido, 2001; Isbell & al., 2011).

Over the past decade, there has been a growing body of interest in FD among ecologists (Cadotte & al., 2011). This is partly because many experiments and meta-analyses have shown that FD is a better predictor of ecosystem function than SR or the number of functional groups (Petchey & Gaston, 2006; Hoehn & al., 2008; Griffin & al., 2009). In addition, knowledge of costs and benefits in functional traits enables us to elucidate key trade-offs that determine vegetation changes along climatic gradients (Westoby & Wright, 2006). In fact, functional traits and FD are known to covary with climatic variables at regional and global scales (Swenson & al., 2012) and thus trait maps are useful to develop global vegetation models to predict vegetation changes under climate changes (Van Bodegom & al., 2012).

There are a wide variety of functional diversity measures (Villéger & al., 2008; Cadotte & al., 2011; Pla & al., 2012). Among them, one of the most commonly used is Petchey & Gaston's (2002) FD such that it is calculated as the total branch length of a dendrogram obtained from functional trait distance among species, in a similar manner to PD. The choice of the distance and the clustering method remain controversial and Mouchet & al. (2008) recommended using all combinations of them. Other useful measures include functional richness (Cornwell & al., 2006) and Rao's quadratic entropy (Rao, 1982; Ricotta, 2005). Another approach is to compute the Environmental Diversity (ED)-based functional diversity measure (Faith, 1996). This method allows tracking of loss of functional diversity linked to estimated extinction probabilities (thus, the same IUCN ratings may be used in estimating loss of both phylogenetic and functional diversity).

Taxonomic publications (e.g., Floras and monographs) are a good source for some key functional traits such as plant height, growth form, leaf size, flower characters and seed size. Some information of legume traits is already summarized (Bradshaw & al., 2008). Phenology and growth habits of tropical trees including some species of legumes are reported by Hatta & Darnaedi (2005). For woody Fabaceae species, wood density data are available for 2735 records including 1098 species (Zanne & al., 2010). More detailed physiological

and morphological traits, such as leaf N content, photosynthesis etc., are available from the global database initiative for plant trait ecology, TRY, which stores almost three million trait entries for 69,000 plant species (Kattge & al., 2011a). Additional databases of plant traits are listed in Kattge & al. (2011b).

In recent ecological studies on functional traits and FD, chemical traits except for N and P have been mostly neglected. However, many legume species are known to produce unique chemicals that are often toxic (Wink & Mohamed, 2003). It has been suggested that those are defense chemicals against specific herbivorous insects (Southgate, 1979; Harmon & al., 2009) and seed predators (see below). Recently, Kursar & al. (2009) documented for Neotropical *Inga* that coexisting species are highly diverged in anti-herbivore defense chemicals compared with non-defense traits, suggesting that niche differentiation between species may occur via differences in anti-herbivore defenses, rather than differences in resource use, pollination, or dispersal. This example illustrates the importance of chemical trait diversity as a determinant of ecosystem functions, especially of food web structure. Thus, it is desirable to compare patterns of chemical and non-chemical trait diversity when we quantify FD.

Interaction diversity. — Food web structure is determined not only by abundance and functional traits of plant species but also by those of animal species or other interacting organisms. Thus plant traits alone often show a low predictive power of food web structure. For example, a particular set of floral traits called a "pollination syndrome" is often only weakly associated with a particular group of pollinators (Ollerton & al., 2010). Thus, to describe spatial patterns of biotic interaction such as pollination and herbivory, it is desirable to develop another indicator for "interaction diversity" (ID), such as the number of links in pollination food webs (Sabatino & al., 2010). Methods to describe ID are reviewed by Vazquez & al. (2009). For the pollination food web, Olesen & al. (2007) analyzed 51 total pollination networks encompassing almost 10,000 species of plants and flower-visiting animals using their own data and data extracted from published literature. This dataset will provide an outlook for global patterns of the role of legumes in pollination food webs.

In Fabaceae, two other unique systems of biotic interaction are known: food webs of legume-bruchine system and the symbiotic system of legumes and nitrogen-fixing bacteria (Sprent, 2009). Thus, decline or loss of legume species in a local ecosystem may result in changes of food webs and nitrogen cycling. Studies of these changes will contribute to deepen our understanding of the relationship between biodiversity and ecosystem functions. In GLDA, we will review updated knowledge about the relationship between legume species richness with the above two interaction systems. Below is a short summary of our contemporary understanding of these systems.

Many legumes are associated with bruchine beetles (Coleoptera: Chrysomelidae: Bruchinae) that have diversified from an endophagous group of chrysomelids (Farrell, 1998; Gómez-Zurita & al., 2008). Food webs of the legume-bruchine system have been studied in various geographic areas (Johnson, 1981a; Udayagiri & Wadhi, 1989; Kergoat & al., 2007a); Asia

(Chujo, 1937; Arora, 1977; Tuda & al., 2005, 2006), the Middle East (Johnson & al., 2004), Europe (Hoffmann, 1945; Jermy & Szentesi, 2003; Delobel & Delobel, 2006; Kergoat & al., 2007b), Africa (Johnson & al., 2004; Kergoat & al., 2005), Russia (Luk'yanovich & Ter-Minasyan, 1957) and the New World (North and Central America, Johnson, 1970, 1983; Kingsolver, 2004; Kato & al., 2010; South America, Johnson, 1990). Native bruchines are absent in arctic areas and Pacific islands and scarce in Australia (Borowiec, 1987). Most species of bruchines are oligophagous, i.e., feeding only on a few related legumes (Johnson, 1981a; Delobel & Delobel, 2006), with the exception of stored legume pests (Tuda, 2007) and post-dispersal seed predators (Morse & Farrell, 2005). Predation by bruchines is considered to affect the pattern of seed dispersal, evolution of various resistance traits in legumes and counter-evolution in bruchines (Janzen, 1969; Rosenthal & al., 1977; Johnson, 1981b).

Many legumes are also associated with symbiotic nitrogen-fixing bacteria (root nodule bacteria). However, some legumes are not symbiotic with nitrogen-fixing bacteria, and nitrogen-fixing efficiency of symbiotic bacteria varies among legume species. Among the three subfamilies of legumes, nodulation has long been known to be rare in paraphyletic Caesalpinioideae, common in Mimosoideae, and very common in Papilionoideae (Allen & Allen, 1981; Doyle & al., 1997; Sprent & James, 2007; Sprent, 2007, 2009). The majority of legumes form symbioses with members of the genus *Rhizobium* and its relatives which belong to α-Proteobacteria, but some legumes, such as those in the large genus *Mimosa* L., are nodulated predominantly by *Burkholderia* and *Cupriavidus* of β-Proteobacteria (Gyaneshwar & al., 2011). In the genus *Lebeckia* Thunb., some species are nodulated by α-Proteobacteria and others by β-Proteobacteria (Phallane & al., 2008). It is likely that groups of genes required for symbiotic nodulation are horizontally transferred from α-Proteobacteria to β-Proteobacteria (Sprent & James, 2007).

Within-species genetic diversity. — The goal of GLDA is to provide an extensive assessment of the state and trends of ca. 19,400 species of Fabaceae as a representative of flowering plants, using SR, PD and FD as key indicators of states and focusing on species loss rate and extinction risks as key indicators of trends. Thus, we intend to assess these indicators for as many species as possible, with a goal to assess all 19,400 species, rather than focusing on a particular fraction of species. However, this strategy is not applicable to within-species genetic diversity, another key indicator associated with adaptability and persistence of species, because assessment of within-species genetic diversity is much more time-consuming. On the other hand, within-species genetic diversity is rapidly being lost in many species under population decline and habitat reduction driven by forest loss and other environmental changes. Thus, developing adequate strategies for assessing within-species genetic diversity is another important mission of GLDA.

A feasible approach for assessing within-genetic diversity of legume species is to develop reasonable criteria for selecting target species. We will employ the following criteria proposed by GEO BON (2010). (1) Rapidly declining species, including those listed as Critically Endangered on the IUCN Red List, and EDGE; (2) Rapidly increasing species, including invasive alien species; and (3) Other species as a control, including keystone species that have a large influence on ecosystem functions, flagship species that attract high social attention, commercially important species (crops, horticultural plants, domesticated animals, etc.) and their wild relatives, economically important wild species (e.g., timber species), wild populations of model species (e.g., *Lotus japonicus*, *Medicago truncatula*) and their relatives, and species having good historical records.

Multiple genetic studies have been carried out on crop legumes and their wild relatives including soybean (*Glycine max*; Vaughan & al., 2006; Li & al., 2010), peanut (*Arachis hypogaea* L.; Varshney & al., 2009), common bean (*Phaseolus vulgaris*; Mensack & al., 2011), lima bean (*Phaseolus lunatus* L.; Martínez-Castillo & al., 2006), pea (*Pisum sativum* L.), mungbean (*Vigna radiata* (L.) R. Wilczek, Sangiri & al., 2007; Vaughan & al., 2007). However, the geographic sampling of the wild species in most of these previous studies is limited to certain countries and/or regions, and most used accessions from seed banks. GLDA will promote surveys on genetic diversity of those species covering their full ranges.

Another possible approach to assess within-species genetic diversity is to use range size as a surrogate of population size and model the relationship between range size and within-species genetic diversity (Faith & al., 2008; GEO BON, 2010). Rauch & Bar-Yam (2005) proposed a general relationship between them and argued that habitat loss causes a dramatic loss of genetic diversity relative to species diversity. Of course, observed relationships between range size and within-species genetic diversity are often more complicated, reflecting breeding system, hybridization, population subdivision and history of bottleneck and/or range expansion. Thus, we need to carry out further genetic studies of more legume species based on the target species criteria given above. Then, meta-analysis will enable us to develop a more realistic model for assessing the relationship of within-species genetic diversity and range size.

The rapid development of genomic studies has enabled us to carry out much deeper studies of within-species genetic diversity using many genetic markers (Siol & al., 2010; Yahara & al., 2010). Employing these new techniques, there is a growing body of population genetic studies on functional genes (e.g., nodulation signaling gene; De Mita & al., 2007). These studies will hopefully be linked with studies on FD. It has been documented that many of the functional traits can vary approximately as much within species as they do between species (Albert & al., 2010; Hulshof & Swenson, 2010; Messier & al., 2010), and at least part of this variation is considered to be genetic. Although in-depth studies on a few species are not the main task of GLDA, we will encourage studies on critically endangered species, rapidly increasing species and economically important wild species to deepen our understanding of the role of within-species genetic variation on ecological processes under anthropogenic pressure.

Range size. — It is well known that some species are widespread, while others are restricted to narrow ranges. Generally,

species having narrower ranges are more vulnerable to anthropogenic pressure and more prone to extinction. Thus, determining range size is critically important for GLDA. Traditionally, range sizes have been compared among species using distribution maps. Now, we can determine range size quantitatively with distribution models based on digital databases of georeferenced distribution records. Then, we can obtain the Range Size Frequency Distribution (RSFD; Morin & Lechowicz, 2011) for a particular set of species. RSFD can be calculated at various scales from a set of species found in a forest plot to national or regional scales. It has been documented that RSFD is strongly right-skewed, with the majority of species having small distribution ranges both in animals (Orme & al., 2006) and in plants (Morin & Lechowicz, 2011). The more right-skewed RSFD is, the more unique a community is. An area having extremely right-skewed RSFD is considered to be a hotspot of endemic species. Recently, Hubbell & al. (2008) developed a model for estimating RSFD based on the neutral theory of community ecology. This model is useful to interpret empirical patterns of RSFD and to determine extinction risks associated with small distribution ranges.

We will pay attention to the fact that the majority of plant species are rare (Yahara & al., 2012) in terms of range size among various forms of rarity (Rabinowitz, 1981; Gaston, 1997). In the case of legume species in tropical SE Asia, 806 species (66%) among the 1220 total for which specimen records are georeferenced by the Naturalis Biodiversity Center, section National Herbarium of the Netherlands (NHN), had five or less records (Fig. 3). It is difficult to develop distribution models for those rare species. On the other hand, narrow range is one of the indicators for the IUCN Red List Category and we need to assess the states and trends of rare species. Facing these challenges, how can we work on rare species in the assessment? First, we can increase distribution records by

georeferencing more specimen data in various herbaria. As a test case, we checked 31 species of *Desmodium* Desv. that are among the 806 species having five or fewer records in NHN with the monograph of Ohashi (1973). As a result, we could obtain five or more specimen records mainly from Asian herbaria for 21 species, two species are taxonomically doubtful, two species are introduced from America and only six species remained recorded in five or less localities. Thus, it is critically important to make further efforts to digitize specimen records in various herbaria to carry out more accurate assessments of rare species. Second, we can model the distribution of rare species by using a hierarchical Bayesian approach with information of related or ecologically similar species as a prior. To employ this approach, it is highly desirable to obtain a complete phylogenetic tree including all rare species.

Spatial models act as the "lens" for assessing the loss of rare species. As noted above, the model uses ED (Environmental Diversity)-type methods to infer the relative amount of species loss for the loss of different sites or areas. This indirect approach (which complements but does not replace estimating distributions for selected rare species) relies on the general model for the relative numbers of species with different range sizes in a region (see also Hubbell & al., 2008). The ED method can be adjusted to integrate different assumptions about the relative numbers of range-restricted versus widespread species in a region (e.g., a common log-normal distribution of range sizes may be assumed; Faith & Walker, 1996). While the initial lens model (for example using the methods of Ferrier & al., 2007) may be derived using available (mostly common) species, the integration of the log-normal or similar model allows the losses of areas to be interpreted in terms of estimated losses over all species—including rarer species. This indirect approach requires testing and evaluation within the global legume project.

Fig. 3. The "rank–abundance" relationship in 1220 SE Asian legume species for which georeferenced records are available for specimens kept in the National Herbarium of the Netherlands. Vertical axis is the number of records and horizontal axis is the rank of species in the number of records. Among the 1220 total, 806 species (66%) had five or fewer specimen records.
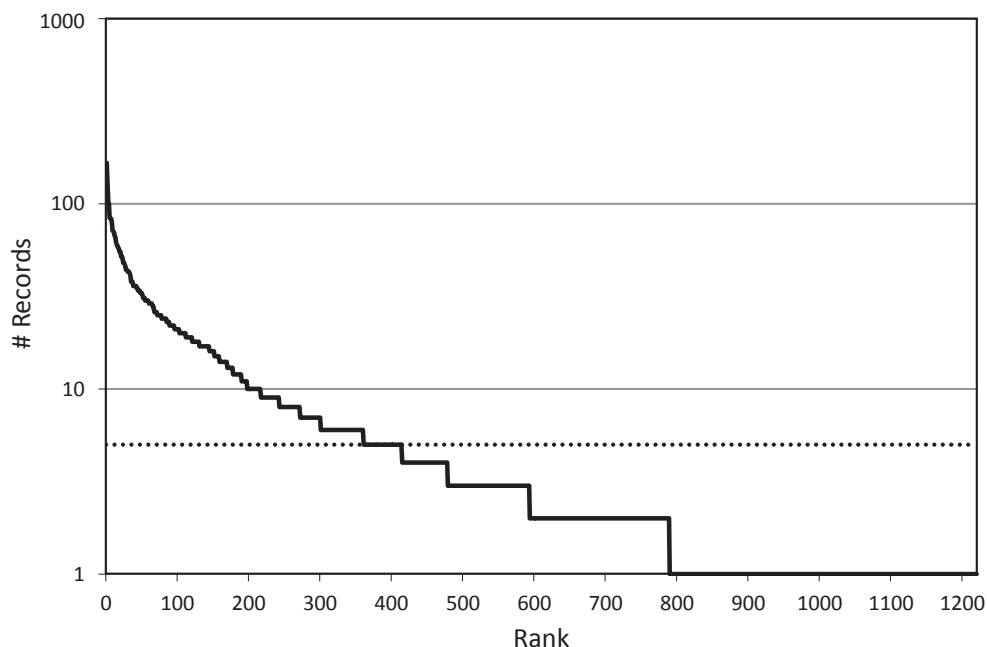
■ STRATEGIES FOR GATHERING NEW DATA FOR KEY INDICATORS

The legume diversity assessment project is being carried out in Asia from 2011 to 2015 as a project of Asia-Pacific Biodiversity Observation Network (AP-BON) sponsored by the Ministry of Environment, Japan, and we hope to extend the assessment to the global scale within the term of this project, though this in part will depend upon seeking further funding. The seven major tasks of the five-year assessment are as follows.

(1) Collecting distribution records of all legume species of Asia from specimen databases, herbaria and from many inventory plots. The accumulated distribution data will be used for modeling distribution probabilities of most species and identifying geographic patterns in species richness and endemism. From other parts of the world, current projects aim to collect inventory data of 1100 woody legume species from South America (Royal Botanic Garden Edinburgh and University of Leeds, U.K.) and of 600 species from inventory data of Madagascar (Buerki, unpub.).

(2) Carrying out extinction risk analyses by using predicted distribution probabilities and trends of land use and climate changes, and identifying threatened taxa and hotspots of threats (Carpenter & al., 2005; Foley & al., 2005; Van Vuuren & al., 2006; IPCC, 2007; Jetz & al., 2007; Stibig & al., 2007; Alkemade & al., 2009; Gonzalez & al., 2010; Corlett, 2011). The 1100 species from South America and 600 species from Madagascar will be analyzed in the same way.

(3) Estimating phylogenies that sample as many legume species from Asia as possible, calculating PD per mapped grid cells, and identifying hotspots of PD. Phylogenetic work will focus first at the generic level in Asia; *Bauhinia* L., *Dalbergia*, *Desmodium*, *Mucuna* Adans., and *Vigna* will be further studied with detailed data as representative case studies. For other parts of the world, most genera have been sampled for loci such as *matK* and *rbcL*, and efforts are underway, co-ordinated by the Legume Phylogeny Working Group, to produce family-wide phylogenetic estimates (LPWG, 2013).

(4) Developing a database of functional traits for Asian legume species using Bradshaw & al. (2008) for an initial dataset. Analyses will be performed to elucidate relationships among SR, PD and FD, and assessing FD loss in association with SR/PD loss. Comparative studies of SR, PD and FD in forest plots are being conducted by many projects, and we will collaborate with them.

(5) Developing a database of traditional use of Asian legume species by local people, expanding the basal information of PROSEA (in Asia) and PROTA (in Africa). This database will enable us to assess loss of provisioning and cultural services in association with loss of SR, PD or FD.

(6) Determining within-species genetic diversity for some wild species and assessing genetic changes under various human impacts using many genetic markers. Target species include critically endangered species, invasive alien species (e.g., *Pueraria lobata* (Willd.) Ohwi, "Kudzu"), and wild relatives of commercially important species.

(7) Developing a biodiversity informatics platform to facilitate international cooperation of data management and data cleaning, to encourage new observations and regional field surveys of legume species, to deposit new primary field data, and finally bring some models and assessment procedures working online to real time update the results with latest dataset.

■ CONCLUSIONS

There is an urgent need to assess states and trends of approximately 250,000 species of vascular plants in the world. Although it requires enormous efforts to assess the majority of plant species, time has come to call a global plant diversity assessment by organizing collaborative networks of plant diversity scientists in the world. In this paper, we proposed to promote GLDA as the first step of a global plant diversity assessment and discussed its feasibility by reviewing relevant approaches and data availability. We conclude that Fabaceae are a good proxy for overall angiosperm diversity in many habitats and countries and that much relevant data for GLDA are available. Although legumes amount to only 8% of the whole diversity of vascular plants, they proved one of the best candidates for the first assessment of global plant diversity, because the family is comparably large, its species are found in many habitat types, there is great diversity of life forms and functional traits, many species have a crucial function in ecosystems (mainly N fixation), and they are often useful for humans. Specimen records and plot data provide key resources for assessing legume diversity at the global scale, and distribution modeling based on these records provides key methods for assessing states and trends of legume diversity. As indicators of the assessment, we propose to compare taxonomic diversity with phylogenetic and functional diversity to obtain an integrated picture of diversity. One of the major difficulties we are facing for the global assessment is that the majority of plant species have too few specimen records to model their ranges using common approaches of distribution modeling. This difficulty can be overcome by coordinating collaboration of local herbaria and by developing a new modeling approach in which phylogenetic relationships between common and rare species are taken into consideration (see Mi & al., 2012). GLDA has started under grant support from the Japanese Government. Now we call for a truly global legume diversity assessment by wider geographic collaboration among various scientists and additional financial support for a global project.

■ ACKNOWLEDGEMENTS

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