Identifying Tree Populations for Conservation Action through Geospatial Analyses

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Rapid development of information and communication technologies has made it possible to easily collect georeferenced information on species and their environment, and to use it for analyzing biological diversity, its distribution and threats to it. Such analyses can importantly inform development of conservation strategies and priorities, especially across countries or species distribution ranges (Guarino *et al.* 2002).

Data for spatial analyses on species or genetic diversity and its distribution are collected in specifically designed studies, obtained from existing records of species occurrence, or both. Observations may be complemented by species distribution modelling, where the potential occurrence of a species is predicted based on its documented geographic distribution and climate in those areas. Results on the distribution of diversity, documented or modelled, can then be compared, for example, with existing protected areas, rates of forest degradation, threats of environmental changes, or socio-economic indicators, to identify priority tree populations and tailor strategies for their conservation and sustainable use (Pautasso 2009).

In this paper recent case studies on spatial biodiversity analyses across the tropics are presented, demonstrating how such analyses can help to identify most unique or most threatened populations of a tree species for conservation actions. Insights on initiating collaborative research on diversity and distributions of important Asian tree species are also discussed.

Analysis of species distributions

Conservation status of 100 woody plant species of socio-economic importance that are native to Latin America and the Caribbean are being evaluated in a regional initiative called MAPFORGEN (www.mapforgen.org). It is a joint project of Bioversity International and CIFOR-INIA, Spain, in close collaboration with the Latin American Forest Genetic Resources Network (LAFORGEN) and with financial support of INIA, Spain. Georeferenced observations or records of occurrence of the study species were obtained from national information systems and herbaria, literature, members of LAFORGEN, and the Global Biodiversity Information Facility (GBIF, www.gbif.org) which provides free and open access to hundreds of millions of biodiversity records. Observation points per species ranged between 21 and 6527. Potential distribution of each species was estimated by species distribution modelling. The distributions were then compared with protected areas, and with maps of short-term and long-term threats, including accessibility, conversion to agriculture, and fires (Jarvis *et al.* 2010). Specific threat profiles were developed for each species. A regional MAPFORGEN platform and a website are being developed for promoting information sharing among scientists and policy makers about the diversity, geographical distribution, biology and conservation status of the species.

Pinus kesiya and *Pinus merkusii* are economically important species of the natural pine forests of Southeast Asia. Van Zonneveld *et al.* (2009) used species distribution modelling to estimate the

potential occurrence of the two species and analyze how their distributions might change as a result of climate change. Data on the locations of 46 and 50 natural populations of *P. kesiya* and *P. merkusii*, respectively, was obtained from literature, seed collection and *in situ* conservation programmes, and the GBIF. Distribution modelling revealed several areas in the Southeast Asian mainland where the species could naturally occur although they have not yet been recorded there. Comparison of the current potential distribution with the climate projections for the year 2050 indicated that increasing temperatures and decreasing precipitation may make several current pine populations vulnerable to degradation, especially in lowland areas.

Species distribution modelling can provide a rapid first assessment of the species occurrence in current and future climates. The results need to be compared e.g. with the suitability of soil types, plant community composition and competition in the predicted species distribution areas, connectedness of the existing populations, and provenance trials, to evaluate the validity of the predictions and the ability of the populations to survive under changing conditions (van Zonneveld *et al.* 2009, Pearson and Dawson 2003).

To evaluate the availability of data for collaborative studies on species distributions in Asia, information on selected priority species of the Asia Pacific Forest Genetic Resources Programme (APFORGEN, www.apforgen.org) was extracted from the GBIF (Table 1). Data on some important species in the region seem to be readily available for spatial analyses, and it could be further complemented from literature, national information systems or individual research groups. Data on other important species in the GBIF is surprisingly scanty. For instance, no records are available on *Tectona grandis* (teak) within its natural distribution range.

Table 1. Availability of records on the occurrence of some important tree species in Asia from the Global Biodiversity Information Facility. The data may include non-natural populations. (GBIF, www.gbif.org)

Species	No. of specified locations	No. of countries	Countries [1]
Chukrasia tabularis	17	7	Ca, Ch, Ind, Lao, Ma, Th, Vi
Dipterocarpus alatus	22	7	Ca, Ind, Ins, Lao, Mya, Th, Vi
Fagraea fragrans	55	7	Ca, Ind, Ins, Lao, Ma, Th, Vi
Hopea odorata	7	6	Ca, Ind, Ins, Lao, Mya, Th
Pterocarpus macrocarpus	99	5	Ca, Lao, Mya, Th, Vi
Tectona grandis	1	1	Ph

[1] Ca=Cambodia, Ch=China, Ind=India, Ins=Indonesia, Lao=Lao, Ma=Malaysia, Mya=Myanmar, Ph=Philippines, Th=Thailand, Vi=Vietnam

Analysis of the distribution of genetic variation

Cherimoya (*Annona cherimola* Mill.) is a neotropical fruit tree species. It is known for its taste and nutritious value, and it has an excellent market potential to which a very high local diversity further contributes. An international collaborative project called CHERLA, funded by the European Commission, analyzed the genetic diversity of cherimoya at its origins of diversity (van Zonneveld *et al.* 2012). Samples from 1504 cherimoya trees were collected from georeferenced stands in Ecuador, Peru and Bolivia. The samples were used for molecular analysis using microsatellite markers, and spatial analyses then conducted with DIVA-GIS (www.diva-gis.org). Geocluster analysis showed that populations in each country clearly differ from each other. Reserve networks for cherimoya were identified according to the principle of complementarity, i.e. by selecting a combination of reserves that best captures both the areas of highest diversity and those with possibly lower but unique diversity. The results show the highest allelic richness (number of alleles) and locally common alleles in the cherimoya populations in Southern Ecuador and Northern Peru. These areas should be priority when establishing in situ conservation measure. Structure analysis shows that although in Bolivia and

southern Peru lower levels of diversity were observed, the allelic composition in those areas is very different from that of Ecuador and Northern Peru. To maintain these unique compositions, some sites from these areas should, thus, also be prioritized for conservation (van Zonneveld *et al.* 2012).

Bark of the valuable *Prunus africana* tree yields medicinal products for treating benign prostatic hypertrophy (BPH). The collection and processing of the bark has created economic opportunities for indigenous peoples, especially in countries where the commercial exploitation is most significant, such as Cameroon, Madagascar and Kenya. A study funded by the Austrian Development Agency collected georeferenced chloroplast and nuclear markers data of *P. africana* to evaluate allelic richness and composition of its populations across the species distribution range (B. Vinceti *et al.* in prep.). The data collected represent the most significant, extensive sampling of an Afromontane tree investigated in genetic studies. The DIVA-GIS software was used to calculate and map the allelic richness of 32 populations of *P. africana* from 9 countries. A cluster analysis was performed to assess the allelic composition of the populations to gain insight on the genetic structure of the species. Reserve selection analysis was conducted to identify a combination of priority conservation sites which would conserve the largest proportion of genetic diversity (measured through microsatellite markers). Use of spatial analysis could be expanded in future studies e.g. by applying spatial analysis tools to markers of adaptive significance, and to derive insight on how to improve the current management practices of the species in the face of climate change (e.g. identifying highly adapted germplasm or monitoring the most vulnerable populations). Spatial analysis tools can also support the interpretation of complex G x E interactions which determine the observed variation in useful traits.

Regional collaboration in diversity distribution analyses

Predictions of species distributions or diversity analyses are based on field observations, and their accuracy directly depends on the amount and quality of available data. Figure 1 demonstrates how adding observation data from different countries affects the predicted distribution of a species. Collaboration among countries to collect and compile data along species distribution ranges can greatly enhance the usefulness of spatial analyses and facilitate identification, conservation and sustainable use of species of common interest and their genetic resources.
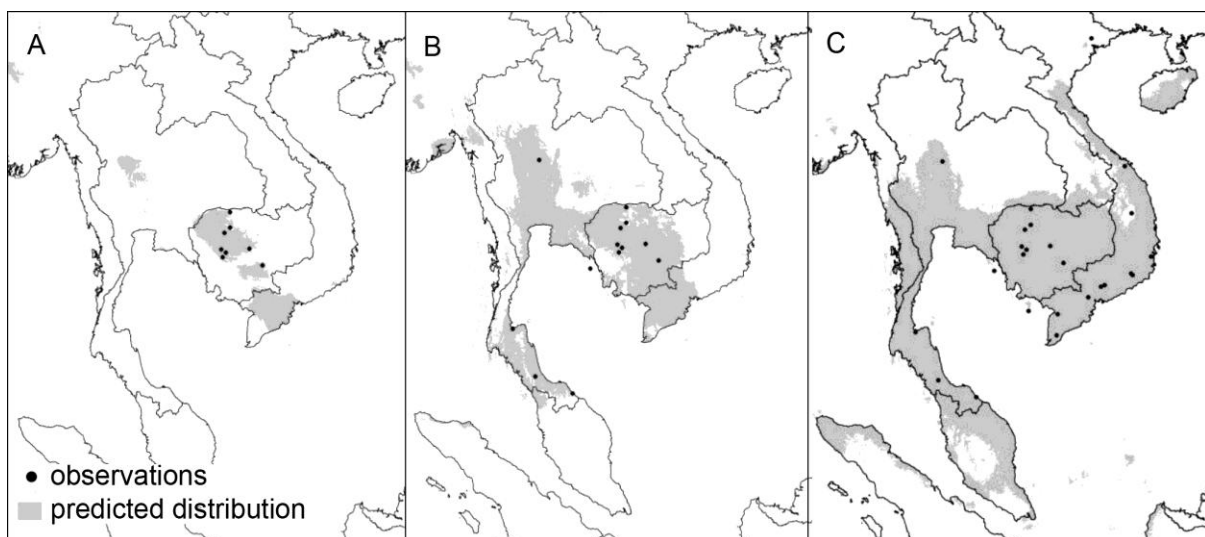

Figure 1. Effect of adding observations from different countries on the predicted distribution of *Fagraea fragrans*. (a) one country, (b) two countries, (c) three countries. Data from the Global Biodiversity Information Facility (GBIF) and the WORLDCLIM database (Hijmans *et al.* 2005) was analyzed using DIVA-GIS and the species distribution modelling program Maxent (Phillips *et al.* 2006).

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