

# Spatial analysis of wild peanut distributions and the implications for plant genetic resources conservation

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## Summary

### Spatial analysis of wild peanut distributions and the implications for plant genetic resources conservation

Domesticated crop plants and their related wild species represent the biological foundation upon which world food security is based, yet these important components of biological diversity are imminently threatened by genetic erosion *in situ*. Spatial analyses are used to assess three key issues for the conservation and use of wild peanut genetic resources: (1) spatial analyses at the genomic level to elucidate the geographic origin of the cultivated peanut, (2) climatic adaptation analysis for each species, and (3) prioritization modeling for conservation. The analyses were conducted using a data-set of 397 geo-referenced records of wild peanuts (genus *Arachis* section *Arachis*), including accessions conserved in *ex situ* genebanks and herbarium specimens. These species are close relatives of the cultivated peanut, *Arachis hypogaea*, and contain traits of importance for crop improvement, as well as their potential usefulness as tropical forages. The results show clustering of climatic adaptation in species considered potential progenitors of the cultivated peanut. Paraguay is suggested to be another possible place of origin for *Arachis hypogaea*. Finally, a priorities model for *ex situ* conservation was produced to target a number of areas in Bolivia for future germplasm collecting missions.

**Key words:** *Arachis*, Bolivia, conservation, geographic information systems (GIS), Paraguay, peanut

## Introduction

IUCN's Red List of Threatened Plants (Walter and Gillett 1998) suggests that 34 000 plant species are threatened globally (equivalent to some 12.5% of the estimated world flora). Some estimates suggest that 25–35% of plant genetic diversity could be lost in the next 20 years. The need to act quickly is clear, but

## Résumé

### Analyse spatiale des distributions d'arachide sauvage et implications pour la conservation des ressources phylogénétiques

Les plantes cultivées domestiquées et les espèces sauvages apparentées constituent la base biologique sur laquelle repose la sécurité alimentaire mondiale. Cependant, ces éléments importants de la biodiversité sont fortement menacés par l'érosion génétique *in situ*. Des analyses spatiales ont été utilisées pour évaluer trois points clés de la conservation et de l'exploitation des ressources génétiques d'arachide sauvage : (1) analyses spatiales au niveau génomique pour élucider l'origine géographique de l'arachide cultivée, (2) analyse des adaptations climatiques pour chaque espèce et (3) hiérarchisation des priorités en vue de préserver la biodiversité. Ces analyses ont été réalisées à l'aide d'une base de données constituée de 397 sites géo-référencés où pousse l'arachide sauvage (genre *Arachis* section *Arachis*), incluant des accessions conservées dans des banques de données *ex situ* et des spécimens d'herbier. Ces espèces sont étroitement apparentées à l'arachide cultivée, *Arachis hypogaea*, et présentent des caractéristiques importantes pour l'amélioration des plantes cultivées. Elles constituent également des ressources potentielles pour les cultures fourragères en zone tropicale. Les résultats font apparaître des groupes correspondant à des adaptations climatiques parmi les espèces considérées comme ancêtres possibles de l'arachide cultivée. Le Paraguay est évoqué comme autre centre d'origine d'*Arachis hypogaea*. Enfin, des priorités ont été définies pour la conservation *ex situ* afin de cibler un certain nombre de zones en Bolivie pour de futures missions de collecte de matériel génétique.

## Resumen

### Análisis espacial de las distribuciones de cacahuete silvestre e implicaciones para la conservación de recursos fitogenéticos

Las plantas cultivadas y sus parientes silvestres son la base biológica en la que se asienta la seguridad alimentaria mundial, pero estos importantes componentes de la diversidad biológica están gravemente amenazados por la erosión genética *in situ*. Se utilizan análisis espaciales para estudiar tres cuestiones fundamentales para la conservación y el uso de los recursos genéticos de cacahuete silvestre: 1) análisis espaciales a nivel genómico para dilucidar el origen geográfico del cacahuete cultivado, 2) análisis de la adaptación climática para cada especie, y 3) modelos prioritarios de conservación. Los análisis se realizaron mediante una serie de datos de 397 registros con referencias geográficas de cacahuetes silvestres (género *Arachis*, sección *Arachis*), incluyendo accessiones conservadas en bancos de genes *ex situ* y especímenes de herbarios. Estas especies son parientes cercanos del cacahuete cultivado, *Arachis hypogaea*, y contienen características de importancia para la mejora de los cultivos, así como para su utilidad potencial como forrajes tropicales. Los resultados muestran grupos de adaptación climática en especies consideradas como posibles progenitoras del cacahuete cultivado. Se sugiere Paraguay como otro posible lugar de origen del *Arachis hypogaea*. Por último, se produjo un modelo de prioridades para la conservación *ex situ* con miras a varias zonas de Bolivia para futuras misiones de recolección de germoplasma.

as funds for conservation are likely to remain limited, interventions must be carefully targeted to have maximum impact. Conservationists, therefore, need methods for the identification of action priorities, both in geographical space and biological importance.

This paper describes a geographical approach to identifying biodiversity hotspots, and prioritizing regions for conservation action, using peanut wild relatives as a case study. Guarino et al. (2001) gives a thorough literature review of the uses of GIS in plant genetic resource conservation and use. The paper also provides a conceptual framework for the application of GIS to the processes of plant exploration, conservation, and subsequent use and impact.

The cultivated peanut, *Arachis hypogaea* L., is the most widely cultivated grain legume in the world and is one of the five most important oilseeds, with total world production in 1990–1991 reaching some 23 086 000 mt (Carley and Fletcher 1995). Among the outstanding nutritional qualities of peanut are a protein content of up to 30% and a fat content of up to 50% that is nearly 80% unsaturated. Moreover, various wild *Arachis* species have been used successfully as high-quality tropical forages (Valls et al. 1994).

The closest relatives of the peanut include some 26 described and several still undescribed diploid wild species of the genus *Arachis*, section *Arachis* (Krapovickas and Gregory 1994; Singh and Simpson 1994), all endemic to south-central South America (Bolivia, Argentina, Brazil, Paraguay and Uruguay). Some of these wild species have already been used successfully for breeding improved peanut varieties. A recent example of this is found in Simpson and Starr (2001), where germplasm from three wild relatives (*A. cardenasii* Krapov. & W.C. Gregory, *A. diogoi* Hoehne, *A. batizocoi* Krapov. & W.C. Gregory) contributed resistant genes that have helped reduce the infestation of root-knot nematodes by >90%. It is important to note that there are just 17 conserved germplasm accessions of *A. cardenasii*, five for *A. diogoi* and 12 for *A. batizocoi*. Several other species regarded to be some of the closest peanut relatives are represented by even fewer accessions. Additional genetic material will be necessary if breeders are to continue responding to the ever-changing needs of peanut farmers and consumers. The center of origin of the cultivated peanut is generally thought to lie in the area of northern Argentina and southern Bolivia (Stalker and Simpson 1995), but numerous key questions remain unanswered regarding the evolutionary history and domestication of this important crop.

The cultivated peanut is an allotetraploid ( $2n=4x=40$ ), while its closest wild relatives are essentially all diploids ( $2n=2x=20$ ). The species is postulated to have arisen from a fortuitous natural crossing of two diploid species that produced an interspecific tetraploid hybrid with noticeably larger plants and fruits. Neolithic hunters and gatherers probably discovered and propagated the anomaly and, after many generations of co-evolution, emerged as sedentary farmers and the peanut became a fully domesticated cultigen. Numerous attempts by breeders to identify the peanut's progenitor species and experimentally recreate the original interspecific hybrid using combinations of known species as parents have thus far been unsuccessful.

Efforts to determine the origin of the cultivated peanut have focused around the genomic makeup of the crop and its progenitor species. Cytogenetic and experimental crossing studies have identified and confirmed genomic differences among the species in the section *Arachis* (Krapovickas and Gregory 1994; Simpson and Faries 2001). In many species in this section, a distinctive small pair of chromosomes has been identified and designated as 'chromosome A'. On the other hand, *A. batizocoi*, *A. cruziana* Krapov., W.C. Gregory & C.E. Simpson, *A. ipaënsis* Krapov. & W.C. Gregory, *A. magna* Krapov.,

W.C. Gregory & C.E. Simpson, and *A. williamsii* Krapov. & W.C. Gregory do not have the small pair but instead have a chromosome pair with secondary constriction and a satellite, which has been designated as 'chromosome B' (Smartt et al. 1978). These chromosomes serve as markers for the genomic complements of the tetraploid *A. hypogaea* that Smartt et al. (1978) first designated as the A and B genomes. Most of the diploid species in the section *Arachis* have the small set of chromosomes and are said to possess the A genome (AA). To date, only seven (including two still-undescribed) wild species are known to possess the B genome (BB), with the exception of the wild tetraploid, *A. monticola* Krapov. & Rigoni. *Arachis monticola* has the same AABB genome as the cultigen *A. hypogaea*, with which it is highly interfertile. While specialists may argue that *A. monticola* is either the wild tetraploid from which the cultigen was domesticated, or that it is instead merely a feral descendent of the cultigen (Stalker and Simpson 1995), the fact remains that *A. monticola* possesses the same ploidy level and genomic makeup as the cultigen and ultimately must have arisen from the same amphidiploid hybridization event involving the same two unidentified diploid progenitor species. Experimental crosses between *A. batizocoi* (BB) and various AA species from the section *Arachis* produced some synthetic AABB amphidiploids but were not successful in producing plants with the genomic configuration or morphological characteristics of the cultigen (Stalker and Simpson 1995). Experimental crosses between the cultigen and likely diploid progenitor species, with synthetic AABB amphidiploids, and with synthetic autotetraploids, all showed varying degrees of incomplete chromosome pairing (Stalker and Simpson 1995). These results have led scientists to conclude that either the diploid ancestors or the cultigen have diverged genetically over time, or that one or both of the true progenitor species were missing from the experiments conducted. Given the incomplete exploration of these species' natural range and the fact that new species in the section *Arachis* continue to be discovered as plant collectors penetrate the more inaccessible areas where they occur, it is not unreasonable to suspect that the actual progenitors of *A. hypogaea* may still exist but have yet to be collected (Singh and Simpson 1994). In light of the above, the most logical places to look for undiscovered wild peanut progenitors would be those areas where populations of both A and B genome species are believed to occur sympatrically, these areas being potential cradles of origin of the cultivated peanut. Figure 1 shows the areas where FloraMap predicts that both genomes may be sympatric.

Beyond the academic problem surrounding the origin of a major crop, there is also a practical reason behind the keen interest in identifying the peanut's progenitor species. The peanut is increasingly susceptible to a long list of diseases and pests that can significantly reduce yields (Porter et al. 1982; Smith and Barfield 1982), particularly affecting those farmers who are unable to afford the expensive pesticides used by most commercial farmers. For many important peanut diseases and pests, few good sources of resistance have been found within the crop species itself, while many of the related wild species screened for those same diseases show high levels of resistance (Stalker and Simpson 1995; Bertoli 2001). However, interspecific fertility barriers and differences in genomic composition prevent the easy transference of this resistance to the crop (e.g. Simpson 2000). The progenitor species, if identified, could serve either as direct gene donors or as 'bridge'



**Figure 1.** Potential evolutionary origin of the cultivated peanut.

species through which agronomically desirable traits found in other *Arachis* species could be transferred to the cultigen using conventional breeding methods. The progenitor species could be instrumental in achieving major advances in peanut improvement and significantly benefit peanut farmers and consumers worldwide.

Recent collecting missions in Bolivia have continued to discover new species closely related to the cultigen (Krapovickas and Gregory 1994; Valls 2001), giving real hope to the possibility that the wild progenitor species may still exist. Unfortunately, intensive recent development activities in the remote, fragile environments of eastern Bolivia, Paraguay and southwestern Brazil threaten to extirpate populations of wild peanuts, and may even destroy the progenitor

species before they can be collected, described, conserved, or used.

Three specific spatial analyses are presented in this paper in an attempt to address some of these issues:

Spatial analyses of the distribution of genomes to help elucidate the evolutionary origin of *A. hypogaea*.

Analysis of the climatic adaptation of each wild *Arachis* species.

Prioritization of geographic areas for wild *Arachis* conservation interventions in Bolivia.

### Materials and methods

- A total of 397 geo-referenced germplasm accessions and herbarium specimens were used in this study. The germplasm accessions data were obtained from the System Wide Information Network for Genetic Resources (SINGER—<http://singer.cgiar.org>) and the USDAs Genetic Resources Information Network (GRIN—<http://www.ars-grin.gov/npgs>). The data from herbarium specimens were compiled from herbaria in Argentina and Paraguay, visited during a project to inventory the wild crop relatives of Paraguay, and from specimens cited in the taxonomic monograph of the genus *Arachis* (Krapovickas and Gregory 1994). This study was limited to the section *Arachis*, which roughly corresponds to the secondary gene pool of the cultigen (Singh and Simpson 1994) and is therefore a priority for genetic resources conservation. Section *Arachis* includes the cultigen plus 26 wild species described to date. The wild species are listed in Table 1, with the number of geo-referenced accessions used for each.

- In this case study a computer tool called FloraMap (Jones and Gladkov 1999) was used to develop climatic models for predicting the distribution of genomes and species of section *Arachis* within

**Table 1.** PCA details for each species (number of non-unique accessions indicates the number of geographically indistinct accessions)

Species (genome)	Number of accessions	Number of non-unique accessions	Number of components used in PCA	Variance (%)
<i>A. batizocoi</i> (B)	29	15	3	95.97
<i>A. benensis</i> (A)	12	4	1	94.11
<i>A. cardenasii</i> (A)	38	13	3	99.27
<i>A. correntina</i> (A)	15	7	2	91.44
<i>A. cruziana</i> (B)	4	3	N/A	N/A
<i>A. decora</i> (A)	16	15	3	94.98
<i>A. diogoi</i> (A)	17	9	3	97.96
<i>A. duranensis</i> (A)	66	32	4	95.29
<i>A. glandulifera</i> (D)	11	6	2	97.99
<i>A. helodes</i> (A)	19	10	2	95.75
<i>A. herzogii</i> (A)	4	2	N/A	N/A
<i>A. hoehnii</i> (A)	7	6	2	99.37
<i>A. ipaënsis</i> (B)	4	2	N/A	N/A
<i>A. kempff-mercadoi</i> (A)	24	13	2	95.49
<i>A. kuhlmannii</i> (A)	37	26	3	94.87
<i>A. magna</i> (B)	14	9	2	93.86
<i>A. microsperma</i> (A)	2	2	N/A	N/A
<i>A. monticola</i> (AB)	8	4	1	100
<i>A. palustris</i> (A)	4	4	2	99.38
<i>A. praecox</i> (A)	3	2	N/A	N/A
<i>A. simpsonii</i> (A)	12	8	2	95.71
<i>A. stenosperma</i> (A)	33	25	2	95.60
<i>A. trinitensis</i> (A)	2	1	N/A	N/A
<i>A. valida</i> (A)	10	6	1	98.13
<i>A. villosa</i> (A)	3	2	N/A	N/A
<i>A. williamsii</i> (B)	2	1	N/A	N/A

the study area. Jones and Gladkov (1999) developed FloraMap for the prediction of the distribution of organisms in the wild, when little or nothing is known of the ecology of the species involved. The model assumes that the climate at the points of observation and/or collection of a species is representative of the environmental range of the organism. The climate at these points is used as a calibration set to compute a climate probability model. FloraMap uses 36 climate surfaces (monthly values of rainfall, mean temperature and diurnal temperature range) with a grid resolution of 10 arc minutes (approximately 18 km at the equator) for all of Latin America. A thorough description of FloraMap is presented by Jones et al. (in press). Further discussion is given on the theoretical background of FloraMap in Jones (1991), Jones and Thornton (1999), Jones et al. (1997) and the FloraMap manual Jones and Gladkov (1999), which is available online at <http://www.floramap-ciat.org>.

- FloraMap was used for each species in section *Arachis* to map a probability distribution across a geographical range spanning all of central South America. Table 1 shows the number of accessions and principal components used for the generation of each species probability surface. The dearth of accessions (less than five) in eight of the species meant that it was not possible to carry out a sensible principal components analysis (PCA), so these species were omitted from the analysis (*A. cruziana*, *A. herzogii* Krapov., W.C. Gregory & C.E. Simpson, *A. ipaënsis* Krapov. & W.C. Gregory, *A. microsperma* Krapov., W.C. Gregory & Valls, *A. praecox* Krapov., W.C. Gregory & Valls, *A. trinitensis* Krapov. & W.C. Gregory, *A. villosa* Benth., and *A. williamsii* Krapov. & W.C. Gregory). Ironically, some of these undercollected species have been identified as possible progenitors of the cultigen, underlining the need for further collecting and conservation efforts.

- Whilst the climatic potential for a species may be widely distributed (e.g. Cuba is climatically very suitable for many of the species, none of which occur there naturally), in many cases the collection records show a much more limited distribution. This can be partially explained by the slow rate of migration characteristic of the genus, causing restriction of populations to a smaller range than its climatic potential would suggest. It is generally recognized that, due to their particular reproductive biology and dispersal mechanism, wild *Arachis* species can migrate at a maximum rate of about 1 m per year, given no fluvial transport of seeds, dispersal by animals or human intervention (Krapovickas and Gregory 1994). For these reasons, the predicted distribution must be in some way limited to a feasible area. Each distribution map was subsequently limited to a 300 km buffer around the existing observations of the species. This distance of 300 km was chosen based on an analysis of the geographic gaps in the collections and of the system of road accesses in central South America. Areas in the Bolivian and Paraguayan Chaco are sufficiently lacking in infrastructure that accessible areas for collecting lie as much as 300 km apart. This is an indication of the inaccuracy that the existing collections might represent in defining the species distributions as most collection locations are concentrated along roadsides (Hijmans et al. 2000).

- The raw climatic data for the 36 climatic variables mentioned above were extracted from FloraMap for each of the accessions in the data-set and subjected to discriminant function analysis, using

species as the *a priori* groups. The STATISTICA software package was used for all analyses. The scores of each accession along the first and second discriminant function were calculated and used for further analysis.

- These individual species' distribution maps were then combined to give a map of species richness. If the probability of finding a species in an individual grid square was 0.5 or greater, then it was assumed to be present. The results of this analysis are used in prioritizing locations for a collecting mission, and are displayed in Figure 4.

- To produce a map of the areas where wild A and B genome species are potentially sympatric, the FloraMap species probability surfaces were again used. Table 1 outlines the genome of each species in section *Arachis* concurrent with the present state of knowledge. Surfaces for each of the 14 A genome species (excluding five species for which there were insufficient accessions or passport data) were superimposed to identify those areas where at least one A genome species is likely to exist. The presence of a species is assumed if  $p > 0.5$ . This resulting A genome probability surface was combined with the probability surface for the two B genome species with sufficient datapoints for analysis (*A. batizocoi* and *A. magna*), producing a map of areas where there is a probability greater than 0.5 of finding both an A and a B genome species growing sympatrically (Figure 1).

## Results and discussion

### Locating the peanut's progenitors

As can be seen in Figure 1, two main areas are highlighted, one in the southern part of the Department of Santa Cruz in eastern Bolivia, and the other lying across the border in north-western Paraguay. The main highlighted areas fall within a geographically unique region corresponding to the low continental divide between the massive Amazon and Paraná river basins. This semi-arid region is characterized by chaco thorn forest vegetation interspersed with patches of natural savanna where populations of wild *Arachis* are most often found. The germplasm collection locations are overlaid on this map, and show that no (geo-referenced) accessions exist from the region of interest in Paraguay, underscoring the need for further collecting in that country. Moreover, the predicted high probability of sympatric populations of A and B genome species suggests that this area of Paraguay also be considered as a possible place of origin for the cultigen.

### Climatic characteristics of each species

Detailed climatic information corresponding to a germplasm accession is often not available to, or recorded by, the plant explorer at the time the germplasm is collected. Nevertheless, climatic information from other sources can be correlated with geo-referenced accessions and can be extremely useful for determining the climatic adaptation of a species and hence its usefulness for agriculture. For example, a few wild *Arachis* species (e.g. *A. glabrata* Benth., *A. kempff-mercadoidi* Krapov., W.C. Gregory & C.E. Simpson, *A. pintoii* Krapov. & W.C. Gregory, and *A. repens* Handro) are already being cultivated extensively as tropical forages and ground covers (Valls et al. 1994). Climatic data corresponding to the natural

distribution of other *Arachis* species can help scientists identify those with forage potential adapted to specific conditions such as drought, frost or flooding. For those species closely related to the cultigen, their associated climatic data can be used to target adaptive traits such as drought tolerance, earliness and pest resistance for crop improvement. Moreover, species-specific climatic characteristics will become important for devising novel *in situ* conservation measures (such as relocating threatened populations) that may become necessary to avert extinctions and mitigate genetic erosion caused by global climate change that is predicted to proceed at a rate significantly faster than the slow-moving wild peanut species can keep pace with (Williams et al. 2001).

Figure 2 plots the species scores along the first and second discriminant functions against each other (accounting for a total of 59% of the total variance). Figure 3 shows the mean and standard deviation for each species along the first discriminant function, which accounted for 39% of the total variance.

Most of the species had very similar climatic adaptations, with overlapping variation along discriminant functions 1 and 2. However, four species (*A. diogeni* Hoehne, *A. kempff-mercadoii*, *A. kuhlmannii* Krapov. & W.C. Gregory and to some extent *A. cardenasii*) had somewhat higher scores than the others along discriminant function 1. This reflects adaptation to higher April and May rainfall, higher January, March and July temperature and a greater September

temperature range; and lower October rainfall, lower May and September temperatures and a lower March and October temperature range. Four other species (*A. magna*, *A. monticola*, *A. cruziana*, and *A. glandulifera* Stalker) had somewhat lower scores than the others along discriminant function 2, reflecting adaptations to higher rainfall in the early part of the year (until July) and lower rainfall later, and higher May, July and December temperatures with lower April, June and August temperatures. *A. glandulifera* showed particularly wide adaptation along discriminant function 1.

Interestingly in the scatterplot of *Arachis* spp. means, *A. valida* Krapov. & W.C. Gregory, *A. ipaënsis*, *A. williamsii*, and *A. batizocoi*, comprising most of the strongest candidates for peanut progenitor species, are clustered. The scatterplot also groups *A. magna* and *A. monticola*, the two most *hypogaea*-like wild species, closely together and clearly separated from the rest. *A. glandulifera* (D genome) is predictably off on its own, accompanied only by *A. cruziana* whose affinity with the rest of the section is still not clear.

### Conservation prioritization

Limited human and financial resources available for conservation activities necessitate careful prioritization so that these interventions can be better targeted and have the greatest conservation impact. By conducting spatial analysis of species distributions and diversity hotspots, combined with geo-referenced data on socioeconomic and anthropocentric variables that contribute to habitat loss, areas where wild crop relatives are at most risk of genetic erosion can be predicted and prioritized in a more objective and precise manner than was previously possible. The areas identified as being at highest risk can be targeted for collecting missions so that the endangered material can be conserved *ex situ* (in genebanks) as a safeguard against its possible extirpation *in situ*. In preparation for a proposed collecting mission in eastern Bolivia, a case study was conducted to determine the relative threat of genetic erosion of wild *Arachis* populations *in situ*. Four factors were chosen for prioritizing areas in Bolivia where wild *Arachis* is most in need of *ex situ* conservation:

1. Species richness as defined by the FloraMap predictions of individual species distributions. Highest priority was given to those areas potentially high in species richness.
2. Proximity to existing accession points. Highest priority was given to areas most distant from existing collections, thus targeting geographical gaps in existing collections.
3. Proximity to protected areas. Those areas most distant from protected areas were given the highest priority. The Ministerio de Desarrollo Sostenible y Planificación in Bolivia provided the data, and covers all nationally recognized protected areas.
4. Genetic erosion risk assessment. Areas with the greatest risk of genetic erosion were given priority. Risk data were obtained from two sources. Synthesized data on infrastructural developments and population pressures on habitat change came from the Environmental Assessment of the San Miguel-Cuiaba Pipeline Project (FAN 1999). In addition, data on soil degradation was obtained from the Global Assessment of the Status of Human Induced Soil Degradation (GLASOD) database.

Each of the four factors was transformed into an index varying between zero and one. The separate indices were then combined to produce a single index of prioritization. Double weighting was given

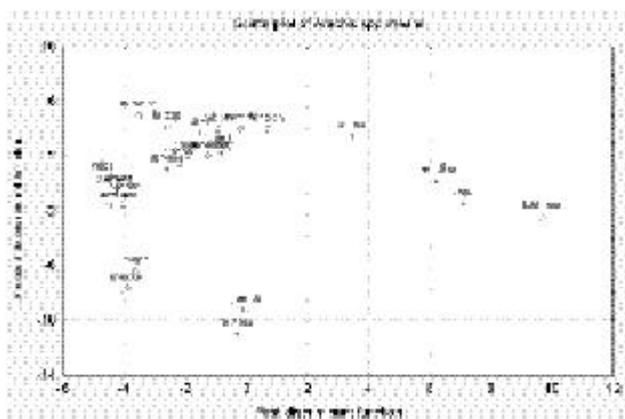


Figure 2. Scatterplot of *Arachis* section *Arachis* species scores along first and second discriminant function.

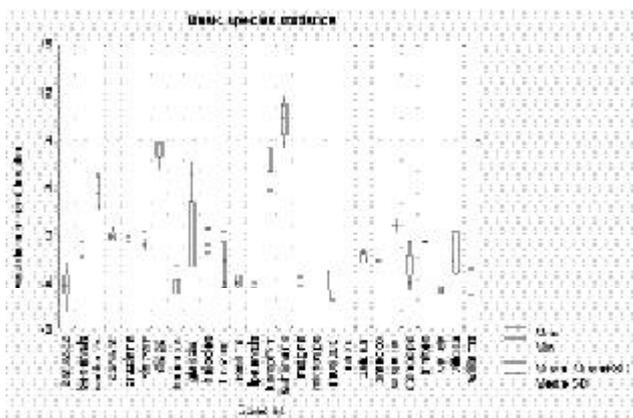


Figure 3. First discriminant function species means and standard deviation based on 36 climate variables.

to two factors, for risk of genetic erosion and probability of high diversity, which were deemed of greater importance in the prioritization of conservation intervention. Only those areas where wild peanuts are likely to occur were included in the calculation (i.e. where species richness is one or greater). The individual factors are shown in Figure 4, and the final priority model is shown in Figure 5.

A number of areas are highlighted for attention. Those areas where wild *Arachis* populations are most at risk follow the recently constructed gas pipeline from Santa Cruz to Cuiabá, and along the Andean fringe in the south of the Department of Santa Cruz. The total area of Bolivia where wild peanuts potentially grow is 328 000 km<sup>2</sup> (24.7% of the total land mass). Some 400 km<sup>2</sup> of land potentially harbors five different species growing sympatrically. The areas of highest species richness lie along the Brazilian border in the far eastern edge of the Department of Santa Cruz, and in the region around the town of San José de Chiquitos.

The highest priority areas for germplasm collecting and/or *in situ* conservation efforts lie along the Santa Cruz–Puerto Suarez road around the town of San José de Chiquitos. The area surrounding

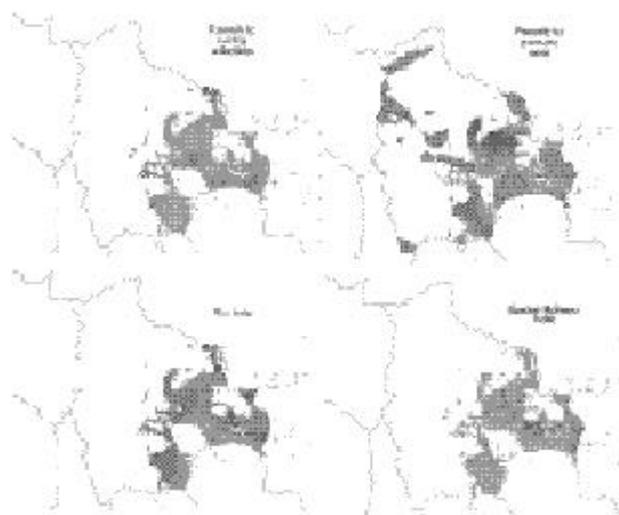
the town of Puerto Suarez on the Brazilian border is also highlighted as an important target for conservation action.

## Acknowledgements

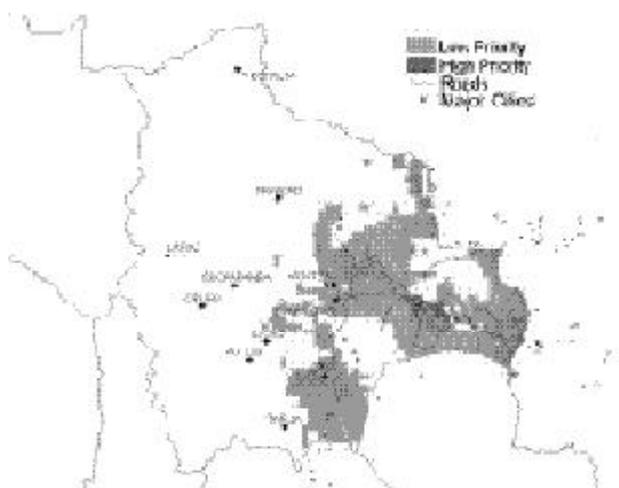
FloraMap is one of the first truly user-friendly GIS software-cum-data tools to be aimed at the plant conservationist, and we would like to thank its developer, Peter Jones (CIAT), for showing the way. The protected areas data-set came from the CD-ROM Mapa de Áreas Protegidas y Reservas Forestales—República de Bolivia, Ministerio de Desarrollo Sostenible y Planificación, Viceministerio de Medio Ambiente, Recursos Naturales y Desarrollo Forestal, April 2000; and soil degradation from Global Assessment of the Status of Human-induced Soil Degradation (GLASOD). The authors would like to thank FAN for permission to use their datasets on conservation threats for Bolivia, and the anonymous reviewer for their constructive comments.

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**Figure 4.** Priority mapping for targeting collecting missions in Bolivia for *ex situ* conservation of wild *Arachis*.



**Figure 5.** Final map of priorities for conservation intervention in *Arachis* section *Arachis* in Bolivia.

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