Locating coconut genetic diversity

V Ramanatha Rao[1], T Hodgkin[2] and R Bourdeix[3]

[1]Senior Scientist, International Plant Genetic Resources Institute - Regional Office for Asia, the Pacific and Oceania (IPGRI-APO), Serdang, Selangor, Malaysia

[2]Principal Scientist, International Plant Genetic Resources Institute (IPGRI), Rome, Italy

[3]Coconut Breeder, Centre de cooperation internationale en recherché agronomique pour le developpement (CIRAD), Cedex 5, Montpellier, France

Introduction

Cocos is a genus in the family Arecaceae (Palmaceae), subfamily Cocoideae, which includes 27 genera and 600 species. Distributed mainly in coastal regions between 20° N and 20° S, from sea level to 1000 m asl, the coconut – *Cocos nucifera* L. (2n = 2x = 32) – the only species in the genus, is an important perennial tropical plantation crop with no known truly wild forms.

The variability of local coconut types is reported to be highest in Southeast Asia (Whitehead 1976). However, it has not been possible to establish either a true centre of diversity or centre of origin for the species. These simple but basic factors are of great importance for understanding the extent and distribution of coconut genetic diversity and for locating useful variation.

In 1992, the International Plant Genetic Resources Institute (IPGRI), with the endorsement of the Consultative Group on International Agricultural Research (CGIAR) and its donors, established the International Coconut Genetic Resources Network (COGENT) with the aim of promoting an international collaborative programme on the conservation and use of coconut genetic resources. Collecting, conserving, evaluating and enhancing coconut germplasm of member countries, and locating and characterizing genetic diversity using morphometric and molecular biology techniques, have been some of COGENT's major concerns (http://www.ipgri.cgiar.org/networks/cogent). Under the auspices of COGENT, the activities related to genetic resources collection and genetic diversity in coconut have been streamlined and significant progress in these areas has been made.

Genetic diversity

Genetic diversity is usually thought of as the amount of genetic variability among individuals of a variety, or population of a species (Brown 1983). It results from the many genetic differences between individuals and may be manifest in differences in DNA sequence, in biochemical characteristics (e.g. in protein structure or isoenzyme properties), in physiological

properties (e.g. abiotic stress resistance or growth rate) or in morphological characters such as flower colour or plant form (Ramanatha Rao and Hodgkin 2001). Four components of genetic diversity can be usefully distinguished; the number of different forms (alleles) ultimately found in different populations (sometimes referred to as 'richness'), their distribution (or 'evenness'), the effect they have on performance (related to population density) and the overall distinctness between different populations. The variation that underpins genetic diversity arises from mutation and recombination. Selection, genetic drift and gene flow act on the alleles present in different populations to cause variation in them. The selection can be natural or it can be artificial, as is the case with much of the variation present in crop species (Suneson 1960; Frankel 1977; Nevo *et al*. 1984; Brown 1988; Hamrick *et al*. 1992). It allows species and populations to adapt to changing conditions and provides the basis for the observed differences between different ecotypes, populations or cultivars of coconut.

It is generally accepted that the genetic variation in plant populations is structured in space and time (Loveless and Hamrick 1984). The description of the extent and distribution of the different aspects of genetic diversity in a species, and of the way in which it is structured, is an essential prerequisite to determining what to conserve, and where and how to conserve it. To date, most conservation efforts, either *in situ* or *ex situ*, have proceeded with little information on the genetic diversity that was being conserved and on what part of the total genetic diversity of a species this constituted. There is an urgent need to remedy this situation by describing the variation observed and identifying the factors likely to affect its distribution. Such factors often include climatic, edaphic and biotic ones as well as those specific to the populations (e.g. population size, selection) or to the species (e.g. ploidy, breeding system, linkage).

Where data is available at the genetic level, e.g. from DNA or isozyme studies, direct measures of richness, evenness and distinctness may be obtained (Nei 1973). However, when dealing with morphological data, direct estimates of numbers and distributions of genes or alleles are hardly obtained and analyses of diversity are based on statistical parameters such as means, ranges, standard deviation and variance. Nonetheless, descriptions of morphological characteristics and reactions to pests and diseases of a population, local cultivar or accession remain the most useful information for plant breeders, agronomists and other users. Although these are often obtained in ways that make formal analyses of the extent and distribution of genetic diversity difficult, the information can often provide useful guidance on location of variation of particular characteristics. It can also be combined with other more formal analyses

to provide an overall view of the ways in which different components of diversity are distributed.

Coconut genetic diversity: General considerations

Coconut is one of the few major crop species that has no closely related wild relatives. Coconut belongs to the palm family (Palmae or Arecaceae), which has about 2800 species of 190 genera. The Cocoeae tribe with 27 genera and nearly 600 species includes several economically important plants such as *Cocos nucifera* (coconut), *Elaeis guineensis* (African oil palm), *Attalea cohune* (babacu) and *Bactris gasipaes* (peach palm). Palm species most related to the coconut palm are found in Colombia (Cook 1901). However, there appears to have been no possibility of mating or gene exchange with any related species and all coconut cultivars constitute a single potentially freely intermating genepool. Since coconut is an ancient species and has been under cultivation for several thousand years, it is reasonable to presume that early humans, while developing habitats in coastal areas, must have slowly domesticated any wild form that was present. Current theories mainly suggest that it must have originated in the Indonesian Islands and later spread to become pantropical, although the date of its spread to the Pacific has been under considerable debate (Harries 1990; 1995). It is also reasonable to presume that the spread of coconuts was based on small initial sample size, considering the bulk of the seed material. If the theory about its spread by flotation is true, then the sample size might be limited to one or two nuts and this is especially so in coconut populations found on the mostly uninhabited small islands and atolls. Thus, the bottleneck processes through which the coconut must have undergone through its world-wide spread, either human-assisted or otherwise, may well have resulted in considerable genetic drift in the founding populations. These observations have a significant bearing on the current genetic structure of the coconuts. In order to understand the process of spread, further studies on the historical and pre-historical knowledge of coconut are needed. Current knowledge appears to be weak in many countries and there has been no attempt to carry out a thorough check of the world literature relevant to this subject as suggested by Bourdeix *et al*. (1999).

Although it has been generally agreed that humans must have domesticated the coconut in pre-historical time, it is not clear what was the domestication process involved and how the species evolved under domestication, as there are no 'wild' coconuts for comparison. The nature of selection pressure that farmers might have applied is difficult to comprehend taking account of the perennial character of the species. In many cases, there could be more than one human generation in the life

of a coconut palm. This leads to difficulties in trying to determine the farmer practices and their effect on the constitution and characteristics of local populations. This is further complicated by the fact that farmers are unlikely to have replaced individual coconut trees in their prime, let alone a whole orchard or population, with another crop or improved genotype, unless such substitution brought enormous benefits or they were forced to take such measures by external circumstances. This suggests that complex evolution of the different types or genotypes of coconut (with more and less desirable coconut types occurring together) may have been a quite common feature of coconut populations. This would lead to highly heterogeneous populations in which there could have been substantial. Thus the genetic structure of coconut could be fairly complex even if the frequent bottlenecks might result in populations with reduced genetic diversity in individual populations than what occurs in other perennial species that have undergone similar process of evolution, with less stringent bottlenecks.

Guarino *et al*. (1998) suggested that the key features of coconut evolution might be summarized as follows:

- Populations initially established by few individuals (founder effect, genetic bottleneck), but often from a variety of sources.
- Low but continuing levels of gene migration among wild-type, feral or semi cultivated populations.
- High levels of outcrossing within populations.
- Selection by local communities, and movement of domesticated germplasm to Africa and the New World.
- Continuing introgression of selected local varieties with wild-type populations and hybridization among domesticated varieties.

The result, as revealed by genetic diversity studies using a range of morphological, physiological, agronomic, biochemical and DNA characters (see below), is that every region or large island has more or less distinctive populations, (commonly described as ecotypes). Tall ecotypes are highly variable (about 60% of the total diversity is found within Tall ecotypes in the Pacific), while Dwarfs are less variable, probably reflecting the fact that they are autogamous. The distinction between Tall and Dwarf types (which is really a difference in precocity) is sometimes formalised into botanical varieties *typica* and *nana*, but the taxonomic validity of this is not universally recognized. Although variation among ecotypes is basically continuous, regional Afroindian, Southeast Asian and Polynesian groupings can be recognized. Sub-groupings are also recognized within the Polynesian germplasm, in particular South Pacific, Northeast Pacific and Marquesas-Hawaii groupings, with the Rennell Island population relatively isolated.

Morphometric studies of diversity

A description of the morphological characteristics and reaction to pests, diseases and stresses of an accession are the most useful information to plant breeders and other users. Such data (in conjunction with locality data) can be used in identifying especially diverse areas and those where specific traits can be found, and in exploring the relationship among accessions. However, using morphological characterization data for locating diversity has a number of limitations. Differential heritabilities, pleiotropic and epistatic effects, polygenic control and genotype x environment (G x E) interactions that are often associated with morphological characters can make estimation of genetic variation difficult. In many cases, long-term crossing and inheritance studies will be needed for precise estimation. There is also the problem that most genetic variation is hidden and is not apparent at the phenotypic level, so that morphologically similar material may in fact be genetically quite different. Despite these drawbacks, morphometric methods have been used to advantage in coconut as well as other crops (N'cho *et al.* 1993; Akpan 1994; Sugimura *et al*. 1997; Ashburner *et al*. 1997).

The first publications comparing a large amount of data gathered from coconut accessions came from Africa. The description of most of the accessions from the collection at the Marc Delorme Station (Ivory Coast) has been reported in numerous publications (Nuce de Lamothe and Rognon 1977; Nuce de Lamothe and Wuidart 1979 and 1981; Le saint *et al*. 1983; Sangare *et al*. 1984; N'Cho *et al*. 1988). However, each of these publications produced in a series covered only a limited number of accessions, generally four to six, always compared with West African Tall (for Tall types) or Malayan Yellow Dwarf (for Dwarfs) used as reference controls. Using the same data, 17 Tall coconut ecotypes were assessed taking a biometric approach with the use of 24 major morphological descriptors. A discriminant analysis revealed the relations existing between ecotypes. The resulting dendrogram groups together accessions to the extent of their similarity into nine groups of 1 to 3 (N'cho *et al*. 1993).

Sugimura (1997) carried out a genetic diversity study using botanical and agronomical traits on 39 cultivars of coconut palms which were mainly collected in the Philippines, and statistically analyzed to clarify the variation between and within cultivar groups (*typica*, *nana* and *javanica*). Although there were broad variations in all the traits except for several male flower characters, significant differences among the three cultivar groups were found in a dozen of traits. The variation within a cultivar group was higher in *typica* and *javanica*. *Nana* was noted as an aggregate group, which was distantly far from *typica*. *Javanica* was

characterized as the intermediate group having overlapping boundaries with other groups. As noted earlier, although these are not valid taxonomic classes, they seem to be useful for morphological groupings of cultivars.

Zizumbo-Villarreal (1998) studied the pattern of morphological variation of coconut in Mexico. They analyzed 41 populations using 17 morphological fruit characters. Principal component and cluster analyses indicated four main groups of coconut populations that showed high similarity with four different genotypes recently imported into Mexico from areas that could be the origin of Mexican coconut populations. These four genotypes were evaluated with regard to lethal yellowing disease in Jamaica and showed a differential susceptibility. Based on the difference in susceptibility of the Mexican genotypes, the analysis of correlation between morphological and geographical distances showed a high positive correlation that supports: 1) historical evidence that indicates early introductions of coconut from different regions of the world, and 2) that on both coasts of Mexico two different patterns of dispersal were involved - continuous and in jumps. It was concluded that collectively these results suggest that the impact of the lethal yellowing disease on coconut populations will vary depending on the specific area and the origin of its coconuts, although it is not very clear how this conclusion could be drawn. This will require some level of follow up.

Vargas (2000) evaluated Tall coconut cultivars from the Pacific coast of Costa Rica and the Philippines (San Ramón, Tagnanan and Laguna), for fruit characteristics. Most of the introduced cultivars showed extremely large heterogeneity. A cluster analysis, based on the Ward method (Ward and Neel 1970), classified the palms into four groups with high internal homogeneity. Some of the evaluated coconut palms from the Costa Rican Pacific area had nut characteristics similar to San Ramon (Group 1: large and elongated nuts) and Tagnanan palm (Group 4: heaviest fruits and nuts) groups but not with the Laguna group (Group 3: rounded and small-sized nuts). At the association level used (semipartial R2 = 0.10), another group (Group 2: small size and mildly elongated nuts) that included the remaining palms sampled from the Costa Rican Pacific Coast (Group 2: small-sized mildly elongated nuts) was constituted, thus showing that the Costa Rican types were different from the established cultivars (for detailed treatment, see Baudouin and Santos, Chapter 4).

Use of Isozymes

This method of genetic variability evaluation is barely developed for coconut. The initial study, undertaken with pollen involved nine enzyme systems (Benoit and Ghesquiere 1984; 1989). After several technical difficulties, only four systems were used to compare eight ecotypes:

Malayan Yellow Dwarf (MYD); Cameroon Red Dwarf (CRD); Pumilla Green Dwarf (PGD); Niu Leka Dwarf (NLA); West African Tall (WAT); Malayan Tall (MLT); Tahiti Tall (TAT) and Vanuatu Tall (VTT). The eight ecotypes showed a weak enzyme polymorphism, few polymorphic loci per system, and never more than two alleles per locus. The intra-ecotype variability was low for autogamous Dwarfs, higher for the Niu-Leka Dwarf and the Talls, with the exception of the West African Tall, which was monomorphic for the four enzyme systems tested. The low enzyme polymorphism of coconut contrasts with the morphologic diversity within the species and suggests that the marked phenotypic differences could hide homologous genetic structures. The apparent absence of variability in WAT is possibly due to successive bottlenecks in its spread that have led to a high level of consanguinity. Other studies of patterns of isozyme variation were also conducted in Sri Lanka (Fernando 1995) and Indonesia (Asmono *et al.* 1993) with rather similar results.

Villareal *et al*. (2002) studied the diversity of 22 populations of Mexican coconut and six imported populations using 15 enzymatic systems and the allele frequencies in: peroxides, endopeptidase, glucose 6-phosphate dehydrogenase. They observed very low polymorphism, not more than two alleles per locus. The Wright fixations indices, F(it)= 0.62, F(is) = 0.40 and F(st) =.036, indicated low total heterozygosity and low heterozygosity within populations suggesting inbreeding and genetic drift and a high diversity among populations due to differentiation between Pacific and Gulf of Mexico coastal populations. The phylogenetic tree with values for genetic distance, indicated three groups on the Pacific coast related to Rennell Tall and Polynesian Tall, and two groups on the coast of the Gulf of Mexico, one related to the West African Tall and the other to Mexican Pacific coast populations. This corroborated historical antecedents and morphological and physiological patterns. The Dwarf coconuts were related to the Pacific Tall populations, Rennell Tall and Polynesian Tall. There was no difference between local and imported Dwarf populations.

Cardeña *et al*. (1998) determined electrophoretic patterns of leaf peroxidases, endopeptidases, and Coomassie blue stained proteins were analyzed in four cultivars (West African Tall, Rennell Tall, Malayan Yellow Dwarf, Cameroon Red Dwarf), and in the hybrids PB121 (MYD x WAT) and PB111 (CRD x WAT). Polymorphisms were detected for the expression of two alleles of a dimeric peroxidase, two alleles of monomeric endopeptidase, and a pair of active null alleles of a dimeric peroxidase, two alleles of Coomassie blue stained protein. Four distinctive genotypes were identified, one for each of the Tall cultivars, another for both of the Dwarf cultivars, and the last for both of the hybrids.

Use of polyphenols

The analysis of the polymorphism based on the analysis of leaf polyphenol using High Performance Liquid Chromatography (HPLC) provided an original approach to the study of genetic diversity in numerous plant species. The first analysis on coconut has involved the measurement of 16 sufficiently individualized peaks or major items of chromatographic information, each corresponding to a molecule or a few molecules of strong structural affinity (Jay *et al*. 1989). From 32 ecotypes, 171 palms were sampled in the collection of the Marc Delorme Station in Côte d'Ivoire. The data were subjected to multivariate analysis. The first discriminant analysis showed a clear distinction between Dwarfs and Talls. Only 19 out of 171 individual palms showed atypical behaviour. Certain Tall trees of various ecotypes behaved like Dwarfs: AGT, MLT, RGT, TAGT, RIT, TAT, WAT, PNTO1; while one NLAD tree behaved like a Tall. Most Dwarfs presented common characteristics that clearly distinguished them from Talls as shown in the morphologic and polyphenol analyses.

The second analysis consisted of a canonical analysis per ecotype. Data analysis favoured the differences between ecotypes at the expense of intra-ecotype variability. Classification within this analysis was not based on geographic groups; the image obtained, however, permits such an interpretation. Five groups were recognized to classify the collection of the Marc Delorme station: Pacific, Far East, Indian Ocean, Africa and America, the last one being represented by only one ecotype. Among the Tall ecotypes, the representation permitted the determination of three distinct groups corresponding to the Pacific, the Far East and Africa. The ecotypes of the Indian Ocean may be divided between the African and the Far East groups. Certain points precisely strengthen the historical hypothesis. The Ghana Yellow Dwarf (GYD) and Malayan Yellow Dwarf (MYD) are very close, confirming the old hypothesis that the Yellow Dwarf was introduced from Malaysia into Africa during the time of the British colonial rule. Anyway, with the advent of DNA marker technology, the characterization of genetic diversity in coconut germplasm at the DNA level has recently begun to substitute other strategies like isozyme or leaf polyphenol analysis.

Molecular studies of diversity

The use of molecular techniques in studying genetic diversity in recent years has contributed to better understanding of the genetic diversity of some species (Karp 2002; Hodgkin *et al*. 2001). The increase in the use of molecular techniques in genetic diversity studies is based on the facts that:

- Appropriate molecular markers can provide direct estimates of gene and allele frequencies and can detect whether plants are homozygous or heterozygous for given markers;
- Molecular techniques make it possible to analyze numerous and independent characters, whereas morphological analysis provides fewer characters, often of dubious homology;
- Morphology is prone to considerable convergence while most DNA regions are less so and even if there is some convergence, the genetic basis of convergence in molecules is better understood; and
- Molecular markers are relatively independent of the environment (Beckmann and Soller 1986).

It has been argued that molecular markers provide a particularly powerful approach to understanding patterns of distribution of genetic diversity that can be used to adjust collecting, evaluating and breeding strategies so as to obtain maximum variation from any given wild population (Morikawa and Leggett 1990). However, it has also been noted that molecular methods should not be used on their own. Thus, Ashburner (1994) emphasized that DNA analysis should not replace currently used characterization methods, but should be used as adjunct when formulating conservation and crossing strategies. Analysis of data can distinguish similarities or differences between coconut populations and thus can be used to prevent duplication in conservation blocks and crossing programmes. However, if two populations appear similar, major adaptive genes may still exist and these may not be picked up by molecular studies. Therefore, collecting priorities should still take account of the need to sample unique environments. Where differences are detected by molecular techniques, there is a greater probability of the presence of different genes resulting from genetic drift, and priority should also be given to their collection.

The information from molecular marker studies can also help improve utilization of diversity in coconuts. The data can assist in setting priorities for crossing programmes allowing breeders to maximize genetic distance and take advantage of any heterosis that may occur. Markers can also be used to tag important genes and allow the use of marker-assisted selection.

For details on use of molecular markers, see Lebrun *et al*., Chapter 4.

Improving location of diversity

A molecular marker kit for COGENT partners

Sampling, collecting and maintaining coconuts have always raised substantial logistical problems. The development of *in vitro* collecting

techniques helps deal with the physical problems of collecting large nuts but the logistical requirements still remain labour intensive and expensive. Currently, fruit component analysis coupled with observing a few other characteristics at the time of collecting are used to get some idea on the population variability at the time of collecting (see Bourdeix *et al*. in Chapter 2). However, this approach does not really give a measure of the genetic diversity that is being sampled.

It was argued that molecular methods based on field collected tissue samples (Adams 1992) provided an efficient way of optimising the diversity collected and minimizing the numbers of new samples that had to be maintained in field gene banks. For this reason, over the last few years, COGENT and a number of other donors have supported the development of a molecular marker kit for coconut.

The Bureau for the Development of Research on Tropical Perennial Oil Crops (BUROTROP) and IPGRI/COGENT supported the research by Centre de Cooperation Internationale en Researche Agronomique pour de Developpment (CIRAD) France, with participation from IACR Long Ashton (UK), on developing a microsatellite marker kit and dedicated software for developing countries. As a result, the kit, consisting of 14 microsatellite loci, was developed and tested on 681 coconut palms representing a large range of diversity. A statistical method was devised to identify any small set of individual palms of the same, unknown origin. The method allows the user to compare this sample with a set of reference populations and to rank these populations in order of decreasing probabilities of being the origin of the sample. It is a very efficient tool for diversity studies and identification of germplasm accessions. The transfer of this technology to the countries where the coconut germplasm collections are located will improve efficiency and reduce the cost of conserving, characterizing, managing and utilizing germplasm accessions for breeding improved varieties (see also Chapter 4 by Lebrun *et al*.).

To downstream this technology to developing countries, 18 trainees from Brazil, India, Indonesia, Papua New Guinea, Mexico, Côte d'Ivoire, the Philippines, Portugal and Tanzania participated in a workshop on "Coconut Genetic Resources Management Using a Microsatellite Kit and Dedicated Software" held at CIRAD in Montpellier, France on 15-24 April 2002. Specialists from CIRAD managed the workshop while other specialists from partner institutions, consisting of nine molecular biologists and nine collection managers (representing a team of two participants per country) participated in the activity. The workshop was supported by IPGRI/COGENT, Common Fund for Commodities (CFC), the European Union, BUROTROP and CIRAD.

Thus, there is now a tool kit available for estimating the genetic diversity prior to collecting to facilitate the locating of germplasm and

make appropriate conservation decisions including the identification of on-farm conservation sites.

Using GIS tools

A Geographic Information System (GIS) may be defined as a database management system which can simultaneously handle spatial data in graphics form - i.e., maps, or the 'where' - and related, logically-attached, non-spatial, attribute data - i.e. the labels and descriptions of the different areas within a map, or the 'what' (Guarino *et al*. 2001). It is a tool for managing information of any kind according to where it is located (Treweek 1999). The main elements of a GIS are as follows (Guarino 1995; Guarino *et al*. 1999):

- Data input, verification and editing
- Data storage, retrieval and management
- Data manipulation and analysis
- Output

If we have georeferenced information on some level of genetic diversity of coconut based on the characterization and evaluation, including molecular evaluation of the available genetic resources, it would be possible to predict where additional genetic diversity could exist using GIS tools. GIS tools will not be able to measure genetic diversity but will be able to help locate new areas where coconut diversity might exist or the areas for extension of coconut cultivation. This is somewhat a refined way of using pre-existing information. To support this type of analysis, IPGRI and the International Potato Centre (CIP) have collaborated in the development of a software called DIVA-GIS, which calculates diversity indices for all the cells in a user-defined grid given latitude, longitude and characterization data for a set of accessions, and maps the results. They have recently trained a number of plant genetic resources (PGR) workers using this technology. It is expected that new areas of coconut genetic diversity would be located using this technology in the near future. Preliminary studies, using existing data in the Coconut Genetic Resources Database (CGRD) and the specialized GIS tools (FloraMap and DIVA-GIS), have been carried out to map the diversity collected, from different COGENT member countries as well as for diversity analysis for certain important morphological traits and for prediction of similar sites where similar diversity may exist or the sites for coconut cultivation (Prem Mathur 2003, pers. comm). Using these GIS tools, one can also generate climatic database for individual collecting sites and the climatic grids for temperature, precipitation and elevation. Some of the examples are presented in Figures 1 and 2.

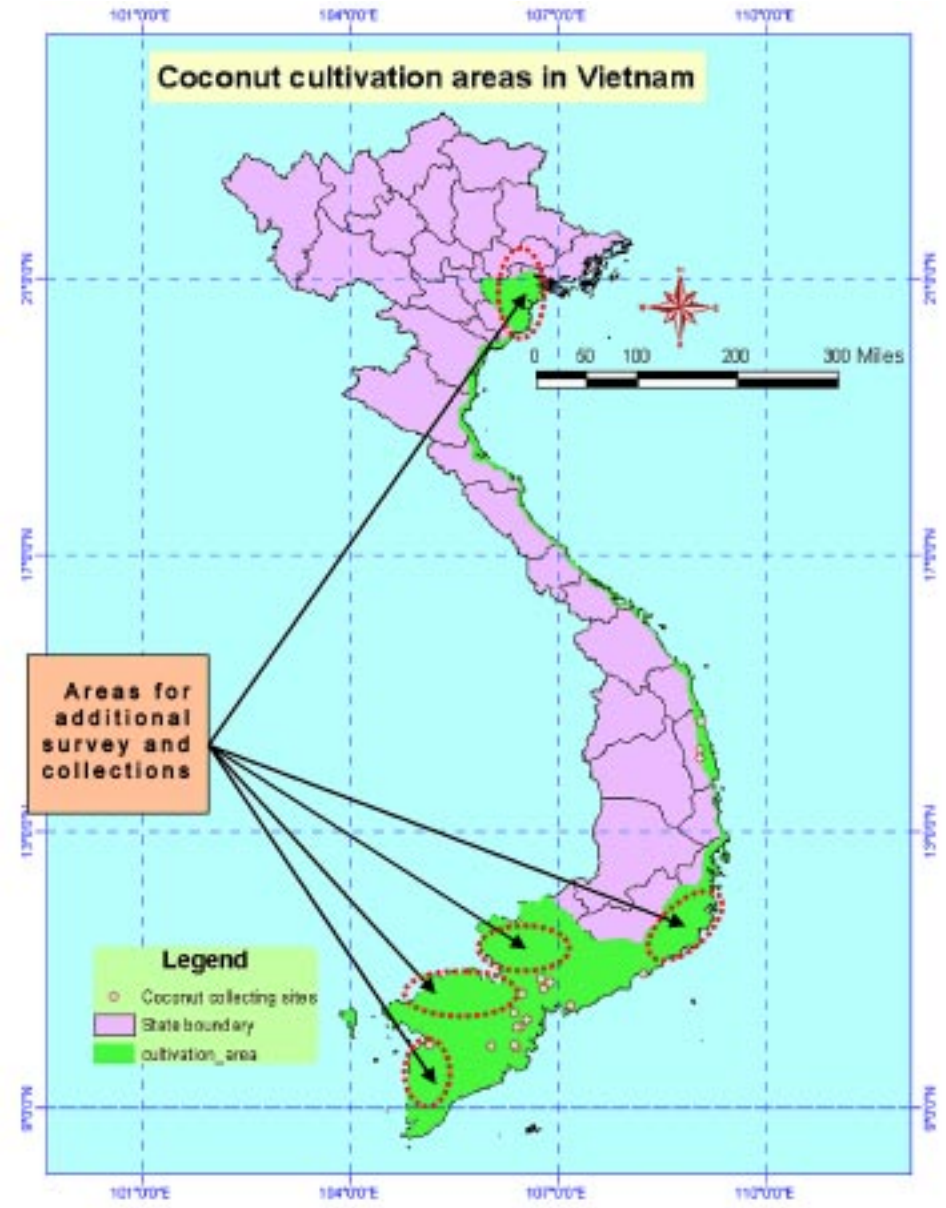

Figure 1. Mapping of major coconut cultivation areas, coconut collecting sites and gaps identification in coconut collections in Vietnam

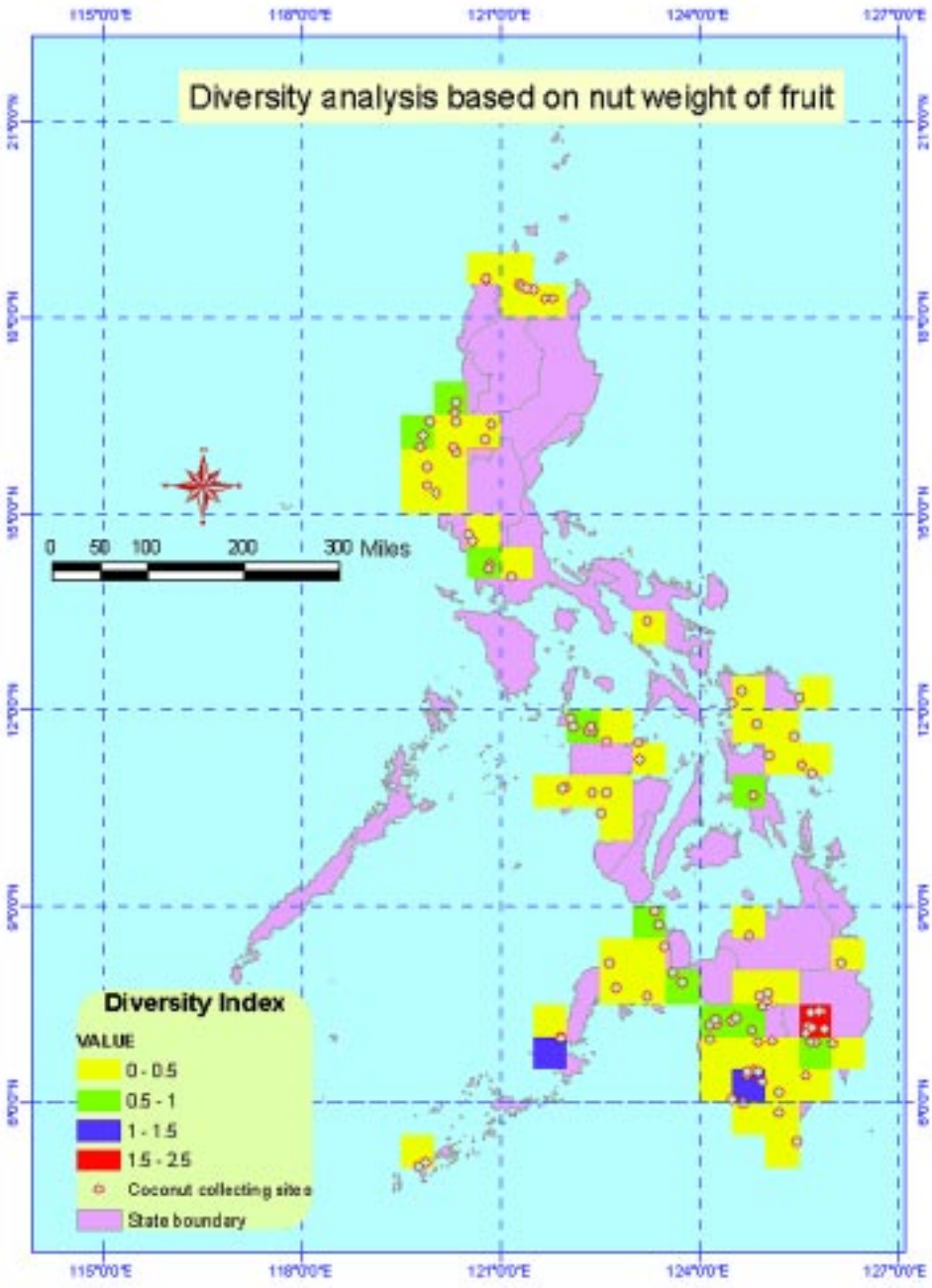

Figure 2. Mapping coconut diversity for nut weight in the Philippines

Figure 1 presents the mapping of major coconut growing areas and the coconut collecting sites in Vietnam, from which one can easily visualize where the gaps are in their coconut collections and can plan accordingly for more collections from those areas, which have not been surveyed earlier.

In Figure 2, using GIS tools to calculate trait location-specific diversity, enabled the identification of sites with high diversity grids where recollecting could be done.

Additional historical information on the movement of people, especially ethnic minorities, could provide additional information on genetic diversity as agricultural practices followed (including farmers' selection) are closely linked to ethnic origins of a community. Quite often, the ethnic composition of the population is a very important factor to be taken in account for locating diversity. For instance, the islands of Rennell, Bellonna and Rotuma are the only 'Polynesian' Islands of the 'Melanesian' archipelago (Solomon and Fiji) and these islands have provided very important coconut varieties. Bourdeix *et* al. (1999) recommended that the Farmer Participatory Method (FPM) be used by following a grid based not only on the geographical aspect but also the ethnic aspect. For example, People of Ko Samui Island in Thailand came long time ago from Hainan (China) which is famous for its coconuts and it would be possible that this community in Thailand could be maintaining coconut growing tradition. Additional survey or FPM should be conducted also in Ko Samui Island.

Conclusion

Locating, maintaining and using genetic diversity of coconut present substantial challenges given the wide dispersal of the species, the limited knowledge of the history of that dispersion and of the current extent and distribution of diversity. The logistical problems conservers and users face when dealing with a perennial species with large recalcitrant seeds added to the complexity of managing coconut germplasm. However, in recent years, substantial progress has been made, at least in part, through the strong support of COGENT partners by establishing an effective framework of knowledge on which to base their activities.

Certain general features of the species seem to be important in understanding the picture that is emerging from recent studies. These include the lack of a related wild genepool, small founding populations, human involvement in the selection and spread of the species/cultivars, outbreeding and intercrossing among populations of Talls and low but continuing gene migration among wild type or distant populations. These characteristics provide a general framework for analyzing the data that

are currently coming from molecular studies. Clear differences are emerging between groups of ecotypes and populations from different areas and expected patterns of migration and transfer are being better described and understood.

Further, detailed studies are needed, particularly in high diversity areas. These should focus on ecogeographic aspects of the distribution of diversity and on the location of populations and ecotypes with unique useful traits such as resistance to biotic and abiotic stresses. The use of general, commonly agreed procedures that COGENT has developed and made available will be important to maximize the value of this new information for users and to safeguard the resources needed by poor farmers who still depend for coconut for much of their livelihood.

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