Progress report
Data improvement and analysis of the Coconut Genetic Resources Database (CGRD6)
R. Bourdeix, 15 March 2013

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Introduction

In 1999, the COGENT Steering Committee took the decision to release the Coconut Genetic Resources Database (CGRD) into the public domain, in order to make accessible and disseminate this useful information, and to create public awareness about coconut genetic resources (source: minutes of the 8th COGENT Steering Committee held in Ho Chi Minh City, Vietnam 20-22 September 1999).

The CGRD project was initiated in 1994. Until 2002, the project was funded by the French Government and implemented by CIRAD (French Agricultural Research for Development), in collaboration with COGENT member countries and Bioversity International. Its objective is to facilitate data storage and exchange among the members of the COGENT network. This will enable coconut breeders to access data on coconut cultivars.

Thanks to the project “Upgrading international coconut genebanks and evaluating accessions” funded by the Global Crop Diversity Trust, the Coconut Genetic Resources Database has been updated and improved to comply with international standards. **Here is the test new version (CGRD6.0) of the software, available from June 2012.** Users are strongly recommended to download this new version, although the previous one (CGRD5.1) in still available on COGENT Website.

In COGENT’s Coconut Genetic Resources Database, data about coconut cultivars are divided in two main parts: passport data and priority characterization, and evaluation data. It takes into account the standardized descriptors for the coconut palms and the methods detailed in the STANTECH manual. Presently 24 genebanks from 23 COGENT member-countries are conserving 725 unique populations with 1374 living accessions.

The database GCRD5.0 have 202 fields, while CGRD6.0 have 210 (8 more). Table A.1 in annex compare the structure of the two databases. This document presents the work conducted[1] on the software CGRD6.0 during the Year 2013.

---

[1] The work was conducted on the following folders :

C:\roland2011\Cocotier\Texte\RAPPORT\MISSION\2012\2012-12 Cote d Ivoire\CGRD 2013\version travail CGRD6

The original data, as available on internet the t5th January 2013, are in the folder :

C:\roland2011\Cocotier\Texte\RAPPORT\MISSION\2012\2012-12 Cote d Ivoire\CGRD 2013\version internet

A. Towards a new approach of data management

Germplasm information systems provide efficient tools for an appraisal of coconut ex situ conservation at global level.

Curators generally do not pay enough attention to the completion of the Database. More than 60% of the actual content of the database was obtain during the fields missions conducted by database experts (Dr R. Bourdeix, J.P. Labouisse, and L. Baudouin) or by managers of the database (C. Hamelin, F. Bonnot, and R. Bourdeix).

For the strategy, the idea is to value , in monetary terms, the content of the database for each genebank ; and to fund the countries accordingly to the evolution of the content of the database.

Each set of data will be valued for one accession, to a maximum of USD 50. **Then, when a country will increase the quantity of data, it will be paid accordingly to the increase of data,** taking account the date of releasing the data and the yearly budget available.

Presently the maximum value of the 1680 accessions is 84,000 USD (50 USD each). It can be expected that this approach will generate a 20% maximum yearly increase of the data, so the budget requested to pay the countries can be estimated at 20,000 USD per year.

So, we need a small procedure to value the content of the database in real time. Table 1 give an estimation of the values for completion of the data for each field of the database.

Table 1. Budget (3 years)

Activities	USD
Management of the data (including a field visit per year)	20000
Maximum funds released to countries	60000
Overheads	20000
Total	100000

B. Points to be improved in the CGRD6.0 software.

Table 2. Points to be improved in CGRD6.0

Section	**Sub-section**	**Fields**	**To be corrected**	**Status**
File/ send data to the centralized intitute	Send data by disquette		Export of data is not working because the new windows 64 bit version do not accept the included version of the PKzip software	
File/ send data to the centralized intitute	Send data by Email		Say « Function argument value, type or count is invalid » and force to quit the software.	
Accession/ Data management	Passport/ accession Data/ page 1/4		When clicking one time on « cultivar name », and then on « population », and then again on « cultivar name », the value of cultivar name dissappear on the top (window in yellow part).	
Accession/ Data management	Passport/ accession Data/ page 4/4	Present accession status	This field must not have blank values. Blank values must be replaced by « unknown ».	Suggestion : to replace the accession status by « Unknown » each time that the trees were counted more than 10 years ago ;
Accession/ Data management			Negative Sign missing for GIS	
Accession/ Data management				

C. New fields useful for data management

1. The new field ‘REJUV’ for managing rejuvenations

On 19 August 2013, we added a new field indicating with the value given in the following table. It was also an opportunity to update the field “country” and “COLL_SRCE”.

Table 3. Values of the field REJUV

Values of the field REJUV	Count at 29/05/2013
’R’: regeneration in the same Genebank	402
’T’: transfer between ex Situ Genebanks	273
’F‘: taken from farmer’s field	1005
Total	1680

Calculation method:

Brow field site, cult_name, access_nb, rejuv, country

```
Sele distinct rejuv, count(*) group by rejuv from access.dbf
```

Message to be sent to India:
- could you please confirm that the following varieties where collected in India:
Hanimaadhoo Tall – collected in India or in another country? Taken from Farmers fields
Kaadedhdhoo Tall
Chinashukhania Tall From Bangladesh, taken from genebank or from farmers fields?

D. KML files in Google Earth for checking and video making

1. Creating KML files from Foxpro

Calculation method: a FoxPro procedure was written to generate a file in KML format for visualisation under Google Earth, improved by interaction with Cyril Bernard.

```
* Procedure KML.prg
* R. Bourdeix, M. Ruas and C. Bernard, 14th March 2013
* create a file CGRD_KML.KML for Google Earth
* une fois le fichier créé
* enlever la ligne blanche au début
* et la petite flèche à la fin du document

Close all
Use access
Dele file CGRD_KML.KML
Set alter to CGRD_KML.KML
Set alter on
?'<?xml version="1.0" encoding="UTF-8"?>'
?'<kml xmlns="http://www.opengis.net/kml/2.2">'
?' <Document>'
* Rajout des styles de points
 ?’<Style id="Ypaddle">’
 ?’<IconStyle>’
 ?’<Icon>’
 ?’http://maps.google.com/mapfiles/kml/paddle/ylw-blank.png’
 ?’</Icon>’
 ?’</IconStyle>’
 ?’</Style>’
*Fin rajout des styles de points
*ici on filtre éventuellement les données
set filter to coll_lat*coll_long>0
Do while.not. eof()
 ?' <Placemark>'
* indique ici le style de point
 ?”<styleUrl>#Ypaddle</styleUrl>”
* fin indication style de point
 ?' <name>'+alltrim(access_nb)+'</name>'
 ?' <Point>'
 ?' <coordinates>',coll_long,',',coll_lat,', 0 </coordinates>'
 ?' </Point>'
```

```
 ?' </Placemark>'
 Skip
Enddo
 ?'</Document>'
 ?'</kml>'
Set alter off
Set alter to
modi comm CGRD_KML.kml
```

Comments from Cyril Bernard:

De : Cyril BERNARD
Date d'envoi : mercredi 6 mars 2013 18:14
À : Roland BOURDEIX
Objet : RE: Données cocotier

```
<Style id="Ypaddle">
<IconStyle>
<Icon>
http://maps.google.com/mapfiles/kml/paddle/ylw-blank.png
</Icon>
</IconStyle>
</Style>
```

http://maps.google.com/mapfiles/kml/paddle/ylw-blank.png

Bonjour Roland,
J'ai jeté un coup d'œil à ton KML.
Voici en pièce jointe un kml corrigé au niveau des coordonnées, avec de la couleur pour les points du Brésil (BRA) et du Bengladesh (BG)
Pour les coordonnées, il semble que la donnée altitude soit obligatoire. Généralement on met 0 (sauf pour les vols de vautours) et le point va se mettre tout seul au ras du sol.
Pour les symboles il faut définir au début du KML les symboles que tu vas utiliser (nom et url du symbole : le plus pratique est d'utiliser l'url des symboles google que tu peux trouver sur cette page http://kml4earth.appspot.com/icons.html#pushpin) .
Exemple :

```
<Style id="punaise_verte">
<IconStyle>
<Icon>
<href>http://maps.google.com/mapfiles/kml/paddle/grn-circle.png</href>
</Icon>
</IconStyle>
</Style>
```

Puis au niveau de chaque point tu met une référence au symbole que tu as défini.
Exemple :

```
<Placemark>
<styleUrl>#punaise_verte</styleUrl>
<name>BG0013</name>
<Point>
<coordinates> 92.21670 , 23.63330 , 0 </coordinates>
</Point>
</Placemark>
```

Ce tuto est également utile:
https://developers.google.com/kml/documentation/kml_tut?hl=fr#placemarks
Cyril

Exemple d'un point dans le fichier de Cyril:

```
<Placemark>
 <name>CCRI MVT</name>
 <Point>
 <coordinates> 146.01670 , -6.11670 , 0 </coordinates>
 </Point>
 </Placemark>
```

We used this example to improve the procedure KML.prg

2. Ideas for videos on CGRD for COGENT communication

Two video ideas concerning the CGRD database and which can be used for communication for COGENT:

1. A video no longer than one minute showing the earth slowly rotating. First round normal land, second round land with the areas where the coconut tree grows (in green main cultivation area, in orange marginal cultivation areas); second round with the 39 COGENT countries (outlines or shaded purple); third round with the geographical location of the 24 collections (large red dots for the 5 international collections, medium dots for the other collections); fourth round with the geographical location of all accessions collected from farmers (small yellow dots). Then, possibly, the countries in which the coconut tree grows but no accession has been collected light up.
2. A video showing the international movement of plant material over time. For example, if an accession was transferred from Côte d'Ivoire to Tanzania in 1980, a trait "grows" from Côte d'Ivoire to Tanzania during the second which corresponds to 1980.

E. Improving the data in CGRD database

1. Latitudes and longitudes

There are 8 values of latitudes and longitudes in the file access.dbf :

- COLL_LAT, CO_LAT_OLD, COLL_LONG, CO_LAT_OLD refer to the location where the parent palms of the accession are located. It can be a farmer field or and ex situ genebank.
- RI_LAT, RI_LAT_OLD, RI_LONG, RI_LON_OLD refer to the location where the accession is planted.

When transferring the data, a mistake was done and the negative signs of some longitudes and longitude were forgotten. This was corrected using the following instructions:

```
brow field site, access_nb, acq_date, cult_name, population, abbrev, country, province, dept, coll_lat, coll_long, co_lat_old, co_lon_old
repla all coll_lat with -coll_lat for substr(co_lat_old,6,1)='S'
repla all coll_long with -coll_long for substr(co_lon_old,6,1)='W'
repla all Ri_lat with -Ri_lat for substr(co_lat_old,6,1)='S'
repla all Ri_long with -Ri_long for substr(co_lon_old,6,1)='W'
```

Table 4. Latitudes and longitudes in CGRD

	Old name in CGRD5		Present name in CGRD6				
44	COLL_LAT	LATITUDE OF COLLECTION SITE in hexadecimal minute and degrees	CO_LAT_OLD	Character	8		Old format.This field does not appear in the software CGRD6.
45		LATITUDE OF COLLECTION SITE in Decimal format	COLL_LAT	Numeric	9	5	Change from Hexa to decimal
46		LONGITUDE OF COLLECTION SITE in hexadecimal minute and degrees	CO_LON_OLD	Character	8		Old format.This field does not appear in the software CGRD6.
47	COLL_LONG	LONGITUDE OF COLLECTION SITE in decimal format	COLL_LONG	Numeric	9	5	Change from Hexa to decimal
88	RI_LAT	Latitude in hexadecimal format	RI_LAT_OLD	Character	8		Old format.This field does not appear in the software CGRD6.
89		Latitude in decimal format	RI_LAT	Numeric	9	5	Change from Hexa to decimal
90		Longitude in hexadecimal format	RI_LON_OLD	Character	8		Old format.This field does not appear in the software CGRD6.
91	RI_LONG	Longitude in decimal format	RI_LONG	Numeric	9	5	Change from Hexa to decimal

2. Latitudes and longitudes of collection sites

The “collection site” corresponds to the location where are planted the parent palms of the accessions – it can be either farmer’s field or the same or another *ex situ* genebank.

Les champs latitudes et longitudes dans le fichier Access.dbf ont été passés de 9 à 10 en longueur totale.

Remise à jour des champs fem_acc_nb, mal_acc_nb pour les accessions de l’OPRI Ghana introduites de Côte d’Ivoire et repassage du programme. 151 remplacements.

Position de SMD GOA3 et SMD GOA4, SMD NJG corrigées

Accessions from the Philippines

ZRC TBOT (6.58330; 6.58330): they keyboarded 2 times the latitude, so longitude is fake. Collection site= ‘T'boli Village, Koronadal, South Cotabato’. Tboli (6.049526°; 124.911863°) ; Koronadal (6.220122°; 125.058716°). At this stage, I took 125.058716° but ask to the Phillipines.

ZRC GAT: (0.000000°; 7.033300°); inversion latitude and longitude ? I reversed and took 126.331006 as longitude, but ask to the Philippines

Accessions from Côte d’Ivoire

Pour l’instant, pour les champs Coll_lat et coll_long, on a positionné toutes les accessions venant de la station Marc Delorme en Côte d’Ivoire à:

- Latitude= 5.274716°
- Longitude: -3.842083°

Ceci correspond au milieu des parcelles 092, 102, 091, 101 qui regroupent l’essentiel de la collection. 137 remplacements.

- brow field site, access_nb, rejuv, fem_acc_nb, mal_acc_nb, coll_LAT, co_lat_old, coll_long, co_lon_old, ri_lat, ri_long
- set filter to fem_acc_nb='SMD'
- repla all coll_lat with 5.274716 for fem_acc_nb='SMD'
- repla all coll_long with -3.842083 for fem_acc_nb='SMD'

Accessions from Samoa

WS001 various site of collection in the island, including this one (-13.862974°; -172.043442°)
WS002 various site of collection in the island, including this one (-13.911125°; -172.023815°)
WS003 various site of collection in the island, including this one (-14.035133°; -171.683704°)
WS006 various site of collection in the island, including this one (-13.818358°; -171.808497°)

3. Latitudes and longitudes of collection sites after Internship of P. Komba

This study is in the directory:

C:\roland2011\Cocotier\Cogent\Methodology\SIG\2013 data\3013-09-17

We conducted an analysis on the file “2013-09-17 cocoglobal.xls”, containing 1784 data of which **609** from CGRD. This file contains 18 records with oridata=’ Bbiblio’, we do not know if it is mistake.

Data from CGRD in cocoglobal.xls

We checked the data coming from CGRD. From the file cocoglobal.xls, we create a Foxpro file GISnew.dbf. This file has well 1784 data. Then this file was compared to the main file of CGRD access.dbf.

Calculation method:

```
close all
Sele 2
```

```
Use access
dele file temp.idx
index on access_nb to temp
Sele 1
use GISNEW
set filter to oridata='CGRD'
go top
Do while.not. eof()
Store access_nb to maccess
sele 2
seek maccess
  if found()
  store coll_lat to mlat
  store coll_long to mlon
  sele 1
  repla incgrd with 'o'
  repla cgrd_lat with mlat
  repla cgrd_long with mlon
  endif
sele 1
Skip
Enddo
brow
1 Set filter to oridata=’CGRD’
Count
* 609
count for coll_lat<>CGRD_lat
* 527
count for coll_long<>CGRD_long
* 526
count for coll_long<>CGRD_long or coll_lat<>CGRD_lat
*528
count for coll_long<>CGRD_long and coll_lat<>CGRD_lat
```

All data with datapublisher=CGRD are well found in CGRD when using the accession number as index key.

The files contain 609 data from CGRD of which 527 with modified latitude (modicgrd=’a’), 526 with modified longitude (modicgrd=’o’), 528 with latitude or longitude modified, 525 with latitude and longitude modified (field modicgrd=2), 81 not modified (modicgrd=’s’)[2]. Internship has localised 13 accessions which were not or partially referenced in CGRD:

BRA GBR04 ; CRI SLBD ; CRI SLT43 ; CRI SLT44 ; CRI SLT45 ; CRI SLT46 ; CRI SLT47 ; CRI SLT48 ; CRI SLT49 ; CRI SLT62 ; MHP-SBRM-1 ; ZRC GAT ; ZRC PD19

30 records have a difference in latitude superior to 1, and 42 have a difference in longitude superior to 1, and both for 22[3].

---

[2]
```
Set filter to oridata=’CGRD’
Count
* 609
count for coll_lat<>CGRD_lat
* 527
count for coll_long<>CGRD_long
* 526
count for coll_long<>CGRD_long or coll_lat<>CGRD_lat
*528
count for coll_long<>CGRD_long and coll_lat<>CGRD_lat
```

[3]
```
Set filter to oridata=’CGRD’
repla all diflat with coll_lat-cgrd_lat
repla all diflong with coll_long-cgrd_long
count for diflat>1 or diflat<-1
*30
count for diflong>1 or diflong<-1
* 42
```

Data available in CGRD and not used by internship

In CGRD, They are 1005 accessions collected in farmers fields (field rejuv=’F), of which 708 have latitude or longitude, and 705 both latitude and longitude<>0. The differences of 3 are the accession: ZRC GAT, ZRC PD19, and MHP-SBRM-1 with longitude=0. In the files GISNEW file, only MHP-SBRM-1 is present and was corrected.

```
count for (coll_lat<>0 or coll_long<>0) and rejuv='F'
* 708
count for (coll_lat<>0 and coll_long<>0) and rejuv='F'
* 705
count for (coll_lat<>0 and coll_long=0) or (coll_lat=0 and coll_long<>0)
*3
```

We need to have all the 708 accessions from CGRD with geographical data in the same file, the 609 data used by the internship, and the 111 not used by the internship. The files GISNEW2.dbf and GISNEW2.xls contains the 111 georeferenced data from CGRD not used by the internship.
We created a file GISNEW2.xls which contains the georeferenced data from farmer’s fields available in CGRD which are not in GISNEW.XLS (not used by the internship).

```
*programme temp.prg
Close all
Use Access
Dele file temp.dbf
Copy to temp.dbf for rejuv=’F’ and (coll_lat<>0 or coll_long<>0)
* temp.dbf contains the 705 accessions from farmers field with geographical data
Sele 2
Use GISNEW
Dele file GISNEW2.DBF
Copy stru to gisnew2.dbf
Sele 1
Use GISNEW2
Appe from temp.dbf
Go top
Do while not eof()
Store Access_nb to maccess
Sele 2
Locate for Access_nb=maccess
If found()
Sele 1
Repla Incgrd with ‘Y’
Endif
Sele 1
Skip
Enddo
Dele all for incgrd=’Y’
pack
go top
Repla all CGRD_lat with coll_lat
Repla all CGRD_long with coll_long
Repla all coll_lat with 0
Repla all coll_long with 0
Brow
Dele file GISNEW2.XLS
Copy to GISNEW2.XLS type XL5
```

```
count for (diflong>1 or diflong<-1) and (diflat>1 or diflat<-1)
*22
list all cnt,'$', alltrim(oridata),'$', access_nb,'$', coll_lat,'$', coll_long,'$', cgrd_lat,'$', cgrd_long,'$', Diflat,'$', Diflong,'$', modicgrd,'$', alltrim(cult_name),'$', alltrim(population) off to temp.doc
```

4. Latitudes and longitudes of ex situ genebanks

The following field are describing the place where the accession is planted: RI_COUNTRY, RI_NB, RI_LAT_OLD, RI_LAT, RI_LON_OLD, RI_LONG, RI_ELEVAT, RI_FARM

In the file Access.dbf, as of 16/03/2012, 23 values of Ri_country, so 23 countries were the germplasm is conserved ex-situ. We find initially 90 unique combinations of country, latitudes and longitudes as calculated under:

```
use access
Set unique on
Dele file temp.idx
Index on ri_country+str(RI_LAT)+str(RI_LONG) to temp
Brow fields site, cult_name, RI_COUNTRY, RI_NB, RI_LAT_OLD, RI_LAT, RI_LON_OLD, RI_LONG, RI_ELEVAT, RI_FARM, EVALUATOR, EVAL_NOTES
```

Many of these 90 combinations are mistaken. We did the following:

2013-20-03 Accessions from Brazil, Vanuatu, Fiji

```
Use access
*Brazil
repla all Ri_lat with -10.419259, RI_long with -36.568550 for site='BRA' and RI_farm=’Campo Exper. de Betume’
repla all Ri_lat with -11.102193, RI_long with -37.185911 for site='BRA' and RI_farm=’Campo Exp. Itaporanga’
*Fiji
repla all Ri_lat with -16.703291, RI_long with -179.907703, ri_farm with 'Taveuni Coconut Centre' for site='TCC' and RI_farm=’Taveuni’
*Vanuatu
repla all Ri_lat with -15.449136, RI_long with 167.206885, ri_farm with 'VARTC Saraoutou' for site='VT '
```

2013-20-03 Accessions from Côte d’Ivoire

In Côte d’Ivoire, the old genebank (5.239339°; -3.896493° to 5.243264°; -3.883309°) was invaded by people and destroyed. We take an average value of 5.241056°; -3.891410°. The Assinie-Canal plantation (5.188150 -3.642330) had some old accessions. For the new genebank, we take an average value of 5.274716; -3.842083.

For Côte d’Ivoire the field Other_nb2 contains the plot number where are planted the accessions. If the plot number begans by S, this is the old station; if it begans by A, this is the Assinie Canal plantation; in other case, this is the new research station.

```
repla all Ri_lat with 5.241056, RI_long with -3.891410, ri_farm with 'Marc Delorme Old Station' for site='SMD' and other_nb2=’S’
repla all Ri_lat with 5.188150, RI_long with -3.642330, ri_farm with 'Assinie Canal Plantation' for site='SMD' and other_nb2=’A’
repla all Ri_lat with 5.274716, RI_long with -3.842083, ri_farm with 'Marc Delorme Res. Station' for site='SMD' and other_nb2<>’A’ and other_nb2<>’S’
```

At this stage the 90 unique combinations of country, latitudes and longitudes were reduced to 80, there is a lot of work remaining.

2013-28-03 Accessions from Tanzania

```
*Homogeneization of the data
Repla all RI_LAT with -6.06670, RI_LONG with 39.33330 for ri_farm=’Bambi seed garden’ and site =’NCDP’
Repla all RI_LAT with -6.33330, RI_LONG with 37.63330 for ri_farm=’Chambezi Agr. Res. Stat.’ and site =’NCDP’
Repla all RI_LAT with -6.08330, RI_LONG with 39.23330 for ri_farm=’Kidichi improv. block’ and site =’NCDP’
Repla all RI_LAT with -7.55000, RI_LONG with 39.28330 for ri_farm=’Kifumangao trial site’ and site =’NCDP’
Repla all RI_LAT with - 7.86670, RI_LONG with 39.81670 for ri_farm=’Mafia Kilombero seed gar.’ and site =’NCDP’
Repla all RI_LAT with -7.88330, RI_LONG with 39.66670 for ri_farm=’Mafia Tereni seed garden’ and site =’NCDP’
```

```
Repla all RI_LAT with - 6.03330, RI_LONG with 39.23330 for ri_farm='Selem seed garden' and site ='NCDP'
```

2013-28-03 – work on global data

Sele distinct ri_country, ri_farm, ri_lat, ri_long, count (*) group by ri_country, ri_farm, ri_lat, ri_long from access.dbf

5. Improving the field "Country".

15/03/2013

This is the country where are located the parent palm of the accession. For example, if a Dwarf variety coming initially from Thailand is planted in Tanzania but from parent planted in Côte d'Ivoire, the country will be Côte d'Ivoire. For more details, see the book "coconut genetic resources" p. 32, chapter "Georeferencing coconut accessions".

In the CGRD software, all country codes are in the table country.dbf. We modified this table by adding a field CGRD (C,1). Then we wrote a small procedure to fill the field CGRD:

```
close all
sele 2
use access
sele 1
use country
do while .not. eof()
store code to mcode
sele 2
locate for alltrim(country)=mcode
if found()
sele 1
repla cgrd with '*'
endif
sele 1
skip
enddo
*dele file temp.doc
*copy to temp.doc delim
*modi comm temp.doc
```

They are 221 countries in the table Country.dbf, of which 44 are represented in the CGRD database.

In the file Access.dbf, as of 16/03/2012, 1680 accessions of which 56 are empty for field country. The field "country" takes 46 values, calculated as follow:

```
use access
Set unique on
Dele file temp.idx
Index on country to temp
Count
```

6. Number of palms in the female and male parent populations

As an example, for the accession SMD GPY2 R1, Field 22 (EX_FEM_POP) et 25(EX_MAL_POP) does not appears in the software when the value is 1 in the table Access.dbf. Value 1 is not planned as an option and was given by mistake. 58 data corrected the 1st february 2013 (Value 2 for « exact » instead of 1).

Table 5. Number of palms in the female and male parent populations

21	NB_FEM_POP	NUMBER OF PALMS IN THE FEMALE PARENT POPULATION
22	EX_FEM_POP	Exact or estimated for descriptor 1.9
24	NB_MAL_POP	NUMBER OF PALMS IN THE MALE PARENT POPULATION
25	EX_MAL_POP	Exact or estimated for descriptor 1.11

Set filter to NB_MAL_POP>0 and EX_MAL_POP=1

Le comptage donne 30 enregistrement tous sur SMD

Repla all EX_MAL_POP with 2 for NB_MAL_POP>0 and EX_MAL_POP=1

Set filter to NB_FEM_POP>0 and EX_FEM_POP=1

Le comptage donne 28 enregistrement tous sur SMD

Repla all EX_FEM_POP with 2 for NB_FEM_POP>0 and EX_FEM_POP=1

7. Size and inventory/counting of accessions

An update was conducted the 2nd February 2012, 1831 data added or transferred.

Table 6. Size and inventory/counting of accessions

		Fields in CGRD6		Value on Internet 15/01/2013	Value on CGRD6 15/02/2013	Changes
30	ORIGINAL SIZE OF THE ACCESSION	ORI_SIZE	Numeric	0	105	105
31	ACCESSION SIZE	LAST_SIZE	Numeric	0	1374	1374
32	DATE OF LAST INVENTORY	AC_SIZE_DT	Character	1137	1137	0
33	PRESENT ACCESSION STATUS	PRES_STAT	Character	4	356	352
	Total	1680		1141	1680	1831

Brow field access_nb, cult_name, Population, abbrev, ORI_SIZE, LAST_SIZE, AC_SIZE_DT, PRES_STAT

Use access

Count for ORI_SIZE>0 to mORI_SI

Count for LAST_SIZE>0 to mLAST_SI

Count for val(substr(AC_SIZE_DT,5,4))>0 to mAC_SI

Count for PRES_STAT<>' ' to mPRES_ST

?mORI_SI, mLAST_SI, mAC_SI, mPRES_ST

F. Analysing the Passport data

1. Ageing accessions

Accessions of tall varieties must be regenerated when they reach 25 years old, otherwise the palms become too tall (tall varieties) or unproductive (Dwarfs). This could be refined later (first approach).

Method based on the age of the palms in CGRD. There are five fields that give indications on dates.

Table 7. Dates on CGRD6 (1680 data)

	Name CGRD5	Explanation	Name CGRD6	Type CGRD5	Length CGRD5	Initial Number of data 15/03/13	Actual Number of data
27	**ACQ_DATE**	ACQUISITION DATE	ACQ_DATE	Character	8	1566	
39	**COLL_DATE**	COLLECTION DATE OF ORIGINAL SAMPLE	COLL_DATE	Character	8	1073	
105	**FIE_EST_DT**	Date of field establishment	FIE_EST_DT	Character	8	1568	
96	HARVEST_DT	Date of harvest	HARVEST_DT	Character	8	348	
97	SOWING_DT	Date of sowing	SOWING_DT	Character	8	277	

The collection date must be the date when the sample was initially collected from farmer’s fields, it was mistaken at the beginning of the database.

```
Brow fields site, access_nb, abbrev, ACQ_DATE, COLL_DATE, FIE_EST_DT, HARVEST_DT,
SOWING_DT
Count for ACQ_DATE<>’ ‘
Count for COLL_DATE<>’ ‘
Count for HARVEST_DT<>’ ‘
Count for SOWING_DT<>’ ‘
Count for FIE_EST_DT<>’ ‘
```

For selecting the ageing accessions, witch where planted before 1988, we used the Date of field establishment :

```
Set filter to val(Substr(FIE_EST_DT,5,4))<1988
Count
* 832 enregistrements
```

For going further, we needed to add a field ‘OLD’ to access.dbf. Value of the OLD field:

O (letter): planted before 1988
R: planted before 1988 but the accession was regenerated
A; planted before 1988 but the accession was regenerated and is still alive

We have to write a foxpro procedure OLD.PRG to fill the field OLD

```
Close all
Use access
Dele file temp.idx
Index on site+abbrev+Substr(FIE_EST_DT,5,4) to temp
Repla all old with ‘O’ for val(Substr(FIE_EST_DT,5,4))<1988
Brow fields site, site, abbrev, FIE_EST_DT, rejuv, old, PRES_STAT, access_nb, fem_acc_nb, mal_acc_nb
Go top
```

```
Do while not eof()
 If OLD=’O’
 Store site to msite
 Store abbrev to mabbrev
 Skip
 If


 Endif
Skip
Enddo
```

G. Analysing of characterisation/evaluation data

1. Request from Mike Foale

Following a request from Mike Foale, we began to analyse the fruit composition data. We first extracted the related data from the file ACCESS.dbf[4]: In the standard descriptors, and in the CGRD database, there is no data regarding the size of the nut, and this should be improved. Polar and equatorial diameter of fruit and the husked coconut, both for Fresh and mature coconut, should be added to the list of descriptors, as it is important for stakeholders of the industry. Among the 1680 accessions recorded in the Database, they are 470 records with fruit weight superior to 0. Fruit weighs ranges from 240.5 g (Tahitian Red Dwarf) to 2578.6 g (Ta tall in Vietnam). Among the 1680 accessions recorded in the Database, they are 470 records with Husked nut weight superior to 0. Nut weighs ranges from 142.6 g (Tahitian red Dwarf) to 1659.0 g (Thailand Tall Kalok).

2. Analysis of fruit data in CGRD database 6.1

Data about fruit composition, available in the CGRD database, is organized in the following way:

- The number of trees sampled for fruit analysis
- The fruit, nut, shell, endosperm weights [g]
- The Endosperm thickness (mm)
- The solid endosperm dry matter content (%)
- The standard deviations for these six characteristics
- Categories describing fruit polar and equatorial sections

Fruit weight is available for 470 accessions (42% of the total). The number of accessions having complete data for fruit, nut, shell and endosperm weighs is 430. Only 302 of these 430 accessions have a recorded number of trees sampled for fruit analysis with in average 42 trees analyzed (from 2 to 151 palms[5]).

Endosperm thichness and solid endosperm dry matter content are available for respectively 295 (18%) and 98 (6%) data. In average, 13% (212) of the value of standard deviation are given for the six concerned descriptors[6].

---

[4] Brow field site, access_nb, cult_name, population, FR_POL_SEC, FR_EQU_SEC, NB_TREES, FR_WEI, SD26, NUT_WEI, SD27, S_AN_M_WEI, SD28, SHELL_WEI, SD29, MEAT_WEI, SD42, ENDO_THIC, SD30

[5] aver NB_TREES for FR_WEI* NUT_WEI* SHELL_WEI* MEAT_WEI>0 and NB_TREES>0

[6] Count for SD27>0 to mSD27

Count for SD28>0 to mSD28

Count for SD29>0 to mSD29

Count for SD42>0 to mSD42

Count for SD30>0 to mSD30

Count for SD31>0 to mSD31

?(mSD27+ mSD28+ mSD29+ mSD42+ mSD30+ mSD31)/6

Table 8: Fruit descriptors in CGRD

172	Fruit polar section	FR_POL_SEC	Numeric	1	
173	Fruit equatorial section	FR_EQU_SEC	Numeric	1	
174	Number of trees analysed	NB_TREES	Numeric	3	
175	Fruit weight [g]	FR_WEI	Numeric	6	1
176	Standard deviation of fruit weight [g]	SD26	Numeric	6	1
177	Nut weight [g]	NUT_WEI	Numeric	6	1
178	Standard deviation of nut weight [g]	SD27	Numeric	6	1
179	Shell and meat weight [g]	S_AN_M_WEI	Numeric	6	1
180	Standard deviation of shell and meat weight [g]	SD28	Numeric	6	1
181	Shell weight [g]	SHELL_WEI	Numeric	5	1
182	Standard deviation of shell weight [g]	SD29	Numeric	5	1
183	Meat weight [g]	MEAT_WEI	Numeric	6	1
184	Standard deviation of meat weight [g]	SD42	Numeric	6	1
185	Endosperm thickness [mm]	ENDO_THIC	Numeric	4	1
186	Standard deviation of endosperm thickness [mm]	SD30	Numeric	4	1
187	Solid endosperm dry matter content	S_E_DR_MAT	Numeric	4	1
188	Standard deviation of solid endosperm dry matter content	SD31	Numeric	4	1

There is also, hidden in the database, a field called “Shell and meat weight”, but this field does not appear when using CGRD software, so it is not possible for users to fill it. Nevertheless, there are data in this field for 348 accessions[7]. For 113 accessions, the “Shell and meat weight” is greater than 0 and different from the sum of the shell and meat weighs[8], but this difference is more than 3g for only 18 data among the 113.

In order to conduct a global analysis, we choose the 430 data having fruit, nut, shell, endosperm weights. The data comes from 16 genebanks in these countries: BRA, CHN, THA, JAM, LKA, VNM, MYS, IND, IDN, MYS, TZA, PHL, CIV, FJI, VUT. Table 9 gives the minimum, maximum and average value for these characteristics.

---

[7] Count for S_AN_M_WEI>0

[8] Count for S_AN_M_WEI>0 and S_AN_M_WEI<>SHELL_WEI+ MEAT_WEI

Dele file temp.idx

Index on S_AN_M_WEI- (SHELL_WEI+ MEAT_WEI) to temp

Set filter to S_AN_M_WEI>0 and S_AN_M_WEI<>SHELL_WEI+ MEAT_WEI

Disp all S_AN_M_WEI, (SHELL_WEI+ MEAT_WEI)

Table 9. Analysis of the 430 data having fruit, nut, shell, endosperm weights.

Parameter	Min	Max	Average	Remarks
Fruit weight [g]	240.5	2578.6	1267.03	Data looks consistent
Nut weight [g]	142.6	1659.0	838.05	One fake data DGEC/L015 with value 112.2; another fake data NCDP-D5 with value 6433.9; in red, and excluded from the average.
Meat weight [g]	81.2	725.6	388.7	One fake data MHP-PLKI-1 with value 65.9; in red, and excluded from the average.
Shell weight [g]	45.6	379.8	193.94	Data looks consistent
Endosperm thickness [mm]	Na (7)	Na (18)	Na (12.7)	116 values are incorrect, because in cm when other in mm – should be corrected
Solid endosperm dry matter content	7.8	61.8	47.8	The 18 values under 38.5 to be further studied, not sure probably immature fruits – in orange color

Note: 0 values excluded for Endosperm thickness and Solid endosperm dry matter content

Among the 430 data, 318 are Tall-types, 110 Dwarf types, and 2 are King Coconut of Sri Lanka. A field was added as an attempt to classify the cultivars into groups. The classification given by Luc Baudouin in the Draft paper was taken into account. A field containing the q value (Weight of meat on the weight of fruit without free water was also added to help for this classification). For the 318 data on Tall cultivars, the present classification gives the following table.

Table 10. Classification of the cultivars into groups of origins.

Groupe	Sigle	Number of analysis
Indo-atlantic	A	52
Pacific	P	52
South East Asia	S	176
Introgressed	I	18
Unknown	U	20
Total		318

Data should be improved and checked by other researchers. We also added to the file the available latitude and longitudes, taking into account that the data held by Dr Geo Coppens are better and should be intregrated to the next version of CGRD.

Finally an Excel file (CGRDfrui.xls) was generated for further improvement and discussion with Luc and Geo.

3. Analysis of fruit data in CDM database of CIV and Vanuatu?

This section gathers analysis conducted on the CGRD database and on CDM database (Côte d'Ivoire and Vanuatu).

Using CGRD for selecting 4 cultivars to conduct a comparative analysis

First step: to find on CGRD the cultivars which have the more fruits analysis. On the 1680 existing records, 433 have characterization both for fruit, nut and meat weigh.

Table 11: cultivars with the most complete fruit characterization data in CGRD

Cultivar name	Number of fruit characterization
Cameroon Red Dwarf	10
Malayan Yellow Dwarf	**8**
Malayan Red Dwarf	7
West African Tall	**7**

Aromatic Green Dwarf	6
Rennell Island Tall	**6**
Equatorial Guinea Green Dwarf	5
Niu Leka Dwarf	5
Sri Lanka Green Dwarf	**5**
Baybay Tall	**4**

The analysis by cultivars[9] and populations and the field knowledge conducted to select the following 5 cultivars for conducting a first analysis:

- West African Tall (populations akabo and mensah, similar for fruits)
- Malayan Yellow Dwarf (and Ghana yellow dwarf, same genotype)
- Rennell Island Tall
- Sri Lanka Green Dwarf
- Baybay Tall

Analysis of data available in Côte d'ivoire from CDM database

We used a file FRUIT.dbf[10] from the database CDM-PB containing 178485 fruit characterizations observed from February 1977 to June 2011. We merged FRUIT.dbf with the file TREES.dbf[11] which contains the identity of the palms into a file TEMPFRUI.DBF; then we calculated the weighs of fruit, husk, shell, albumen and water for all data.

We selected the 37280 records corresponding to the five cultivars[12] where fruit analysis was conducted on a palm by palm basis. Then, separately for each cultivar, we eliminated 2 % (749 data) of the

---

[9] Sele distinct cult_name, population, count(*) from access.dbf group by cult_name, population where fr_wei*nut_wei*meat_wei>0 into table tempfrui.dbf

[10] Location: C:\roland2011\Cocotier\Cogent\Databases\CDM\Calcul2013\PB

[11]
```
* Creation of the file tempfrui.dbf
Close all
Select trees.field as Elim, trees.field, trees.row, trees.tree, trees.yplant, trees.mother, trees.father, trees.exper, trees.plot, trees.sp_pec, ;
fruit.YEAR, fruit.MONTH, fruit.NB_SAMFR, fruit.FR_TOTW, fruit.NUT_TOTW, fruit.SPNUT_TOTW, fruit.NB_ABSPNUT, fruit.SH_TOTW, fruit.EN_THICK, fruit.FMSAM_W, fruit.DMSAM_W, ;
(fruit.FR_TOTW/fruit.NB_SAMFR) as fruit, ;
((fruit.FR_TOTW-fruit.NUT_TOTW)/fruit.NB_SAMFR) as husk, ;
(fruit.SH_TOTW/fruit.NB_SAMFR) as shell, ;
((fruit.SPNUT_TOTW-fruit.SH_TOTW)/fruit.NB_SAMFR) as albumen, ;
((fruit.NUT_TOTW-fruit.SPNUT_TOTW)/fruit.NB_SAMFR) as water ;
from trees,fruit where trees.field+str(trees.row)+str(trees.tree)+str(trees.yplant) = fruit.field+str(fruit.row)+str(fruit.tree)+str(fruit.yplant) into table tempfrui.dbf
repla all elim with ' '
go top
brow
```

[12]
```
*Filter for selecting the 5 cultivars
Set filter to ;
((mother='NJM' or mother='NJG') and (father='FL' or father='FA' or father='AF' or father='NJM  ' or father='NJG  ')) or ;
(mother='GOA3' or mother='GOA4' and (father='GOA03' or father='GOA04' or father='FL')) or ;
(mother='GRL' and (father='GRL' or father='FL')) or ;
(mother='NVS  ' and (father='NVS  ' or father='FL')) or;
(mother='GBB' and father='FL')
```

records, considered as abnormal taking in account the weight of fruits components and looking at the file data per data.

From the file TEMPFRUI.DBF, we created a file INDIFRUI.DBF, containing average values by palms[13]. We calculated a value of fruit components for each palm and then group the palms according to the year and field of planting in a file INDIFRUI.dbf. The data obtained correspond to a total of 7757 palms.

we retained only the 6135 palms (79%) on which at least 10 separate analysis of fruits where conducted.

Then from this last file, we calculated average by location, year of planting and cultivars in a file CULTFRUI.dbf[14]. Then we applied the filter to restrict the analysis to the 5 studied cultivars[15], in order to get the data presented in table ZZ which correspond to 1191 palms, 36250 distinct fruit analysis made on a total of 112131 fruits.

In order to get a view of seasonal variation, it will be possible to calculate averages by cultivar, year of planting, year and month of harvest.

---

[13]
```
* Creation of the file INDIFRUI.dbf
close all
Dele file indifrui.dbf
Sele distinct field, row, tree, yplant, mother, father, sp_pec, Count(*) as nbanal, ;
Sum(NB_SAMFR) as nb_samfr, Avg(husk) as husk, Avg(shell) as shell, ;
Avg(albumen) as Albumen, Avg(water) as water ;
Group by field, row, tree, yplant ;
where elim=' ' from tempfrui.dbf Into table indifrui.dbf
Close all
Use indifrui
```

[14]
```
* Creation of the file CULTFRUI.dbf
close all
dele file Cultfrui.dbf
Sele distinct ;
Field, yplant, mother, father, Count(*) as nbpalm, Sum(nbanal) as nbanal,;
Sum(NB_SAMFR) as nb_samfr, ;
Avg(husk) as husk, Avg(shell) as shell, Avg(albumen) as Albumen, ;
Avg(water) as water ;
Group by field, yplant,mother,father ;
Where nbanal>9 ;
From indifrui.dbf Into table cultfrui.dbf
brow nomod
```

[15]
```
* Edition of data for the 5 cultivars - agerage by cultivar, field and year of planting
use cultfrui.dbf
Set filter to ;
((mother='NJM' or mother='NJG') and (father='FL' or father='FA' or father='AF' or father='NJM   ' or
father='NJG  ')) or ;
(mother='GOA3' or mother='GOA4' and (father='GOA03' or father='GOA04' or father='FL')) or ;
(mother='GRL' and (father='GRL' or father='FL')) or ;
(mother='NVS  ' and (father='NVS  ' or father='FL')) or;
(mother='GBB' and father='FL')
Dele file temp.idx
index on mother+str(husk+shell+albumen+water) to temp
```

Table 12: result of fruit analysis according to location and year of planting for five cultivars in the International Genebank for Africa and Indian Ocean, Côte d’Ivoire

Variety	Field	Planting year	Number of palms	Number of analysis	Number of fruit analysed	**Fruit (g)**	Husk	Shell	Meat	Water
GBBFL	142	1982	50	1620	5858	**1291**	351	200	462	279
GOA3FL	S12	1956	59	2168	8185	**929**	420	149	277	82
GOA3GOA3	M63	1982	50	1558	5743	**999**	391	160	335	113
GOA3FL	S13	1956	43	1274	4733	**1147**	533	173	333	108
GOA4FL	S12	1956	69	2492	9173	**917**	407	150	285	75
GOA4FL	S20	1956	50	660	2588	**954**	416	158	303	77
GOA4FL	S20	1955	66	819	3225	**971**	421	159	307	84
GOA4FL	S13	1956	101	3134	11753	**1064**	478	164	316	106
GRLGRL	043	1994	79	2941	10973	**1395**	357	198	494	346
GRLGRL	091	1988	10	185	624	**1594**	422	243	550	380
GRLFL	070	1968	41	1406	5441	**1651**	475	249	556	371
GRLFL	081	1968	93	1935	7082	**1666**	459	247	572	387
GRLFL	060	1968	64	2324	9039	**1689**	479	257	565	389
GRLGRL	091	1989	19	303	972	**1693**	468	248	570	407
NJMNJM	081	2002	1	12	39	**604**	206	80	219	99
NJMNJM	092	1979	10	350	664	**609**	197	89	221	103
NJMNJM	092	1978	19	696	1343	**618**	195	90	226	108
NJMFL	132	1985	50	1747	3304	**641**	195	92	239	115
NJMFL	142	1982	39	1203	2355	**648**	189	94	243	121
NJMAF	132	1982	40	1339	2601	**650**	193	95	243	119
NJMFL	142	1983	10	260	510	**650**	201	93	241	115
NJMNJM	132	1982	39	1302	2515	**662**	196	98	246	122
NJMNJM	115	1993	22	398	759	**665**	201	95	246	123
NJMNJM	051	2002	2	23	80	**716**	216	99	243	158
NJMFL	S20	1955	50	2237	4017	**738**	259	103	246	130
NJMNJM	112	1973	31	843	2630	**881**	295	125	313	147
NVSFL	092	1978	49	1732	3379	**377**	205	50	101	22
NVSFL	112	1972	35	1289	2546	**463**	210	67	147	40
Total			1191	36250	112131					

Analysis of data available in Vanuatu from CDM database

We applyied the same procedure to the data from Vanuatu. We used a file FRUIT.dbf[16] from the database CDM-VT containing 13139 fruit characterizations observed from June 1989 to May 1995.

We had to adapt the filter to the nomenclature of Vanuatu:

```
Set filter to ;
mother='NJM' or mother='NJG' or ;
mother='GOA' or mother='GRL' or ;
mother='NVS' or mother='GBB'
```

H. Preparation of Data for GIS analysis

28/05/2013 – with Geo Coppens and Prune Komba, we prepared a Foxpro procedure to extract the Data from CGRD6.0 and transform it in the appropriate format for checking GIS Data (inspired from GBIF format). Only the data of accessions coming from farmers fields (REJUV=’F’ or the uncertain data (REJUV=’C’) were included. The accessions coming from transfer from a genebank to another, or regeneration in the same genebank were removed. The file was ranked by country abbreviation.

The field BASIREC of CGRD6TRF.XLS was temporary filled with the values of the field REJUV of ACCESS.DBF from CGRD6.

```
* procedure geotrf.prg
* transfer of data from CGRD6.0 to an Excell file on GBIF Format
* R. Bourdeix, 29/05/2013
close all
dele file temp.dbf
dele file CGRD6TRF.XLS
Select;
 'CGRD' as Datapub, 'CGRD' as Dataset,;
 Site as collname,;
 COLL_NB as collnumb, COLL_DATE as datecoll,;
 RI_NB as instcode, RI_NB as collcode,;
 access_nb as catalnb,;
 rejuv as basisrec,;
 'xxxx' as imgurl,;
 AC_SIZE_DT as lastinde,;
 COLL_NB as identif,;
 FIE_EST_DT as iddate,;
 'Cocos nucifera' as Sciename,;
 COUNTRY,;
 COLL_SITE as localit1, ;
 ' ' as locality,;
 DEPT as county, ;
 PROVINCE,;
 'xxx' as region, ;
 COLL_LAT as latitude, COLL_LONG as longitud, ;
 STAT_SAMP as coordina,;
 'xxx' as cellid, 'xxx' as minalti, 'xxx' as maxalti,;
 CATEGORY, CULT_NAME, POPULATION ;
 from access.dbf into table temp.dbf
set unique off
dele file temp.idx
repla all locality with alltrim(localit1)
index on country to temp
```

---

[16] Location: C:\roland2011\Cocotier\Pbdata\base CDM\vt

```
set filter to basisrec='F' or basisrec='C'
go top
brow
copy to CGRD6TRF type XL5
* fin procedure
```

Le fichier CGRD6TRF.xls contient 1031 données. Integer à un fichier comprenant toutes les données GIS Coco global.xls

Ce qui est traité: latitutde longitude elevation

- en Rouge (OK vu sur google earth), localié en bleu qui contient “CGRD” plus indications localisation (exact. Numéro d’accession dans le champ catalogue.

- en violet: données incertaines non supprimées.

Il y a un champ qui contient l’origine des données; dataset ou data publisher

Poubelle?

Données modifiées et des données peu sures.

Un exemple Bangladesh: BG0028 – en noir dans la poubelle – en noir dans le fichier global, il s’agit d’une donnée incertaine.

Dans le fichier initial: 23.23330 89.86670

40 données du Bangladesh

I. Calculation for the strategy

1. Number of accessions with latitude and longitude

Done

2. Gaps in collecting

To create a list of countries where germplasm was collected

```
sele distinct country, rejuv, count(*) group by country, rejuv into table tempgap.dbf from access.dbf where rejuv='F'
```

```
* 45 countries were germplasm was collected
* create a layer with these 45 countries
* data transferred in the file coundiva.dbf obtained from Diva[17]
* dans coundiva, sum de cocoF vaut 1003, 44 pays ; dans tempfgap 1005 point, 45 pays on en perd 2!
* on regarde ceux dans tempgap qui on cnt=2
*MAD F  2
*MDG F  2
*NGA F  2
*PAN F  2
*SUR F  2
*TTO F  2
```

3. Localization of Genebanks

RAS

4. Exchanges via embryos

Type of material received 1 is embryos TYPE_MAT

```
set filter to country<>ri_country
*accessions transferred from a country to another country: 408
set filter to country<>ri_country and type_mat=1
*accessions transferred via embryo from a country to another country: 68
brow field site, EMBR_CULT, type_mat, fie_est_dt, site, cult_name, population, country, ri_country,last_size
```

---

[17] Close all

```
Sele 2
Use tempgap
Sele 1
Use coundiva
Do while .not. eof()
Store substr(ISO3,1,3) to mISO3
Sele 2
Locate for country=miso3
If found()
Store cnt to mcnt
Sele 1
Repla cocof with mcnt
endif
sele 1
Skip
enddo
Brow
```

```
set filter to country<>ri_country and val(substr(fie_est_dt,5,4))>1980
*accessions transferred from a country to another country after 1908: 212
* aver last_size
set filter to country<>ri_country and val(substr(fie_est_dt,5,4))>1980 and type_mat=1
*accessions transferred via embryo from a country to another country after 1981: 68

*update field type_mat
set filter to type_mat=1
*88
set filter to type_mat=1 and country<>ri_country
*68
set filter to type_mat<>1 and country<>ri_country
*340
set filter to country<>ri_country
*408
aver effi_size for effi_size>0 and type_mat=1 and country<>ri_country
* 68 average 26
aver effi_size for effi_size>0 and type_mat<>1 and country<>ri_country
* 293 average 45
```

5. Exchanges at international levels

```
Brow field rejuv, site, access_nb, fem_acc_nb, country, ri_country, fie_est_dt
Index on substr(fie_est_dt,5,4) to temp
set filter to rejuv='T' and val(substr(fie_est_dt,5,4))>1982
count
145
Count for country=RI_country
17
Close all
use access
set filter to rejuv='T' and val(substr(fie_est_dt,5,4))>1982 and country<>RI_country
Index on substr(fie_est_dt,5,4) to temp
Copy to temp
sele distinct country, count(*) group by country from temp
```

Table 13. International exchanges

COUNTRY "	" CNT
Côte d'Ivoire	57
Philippines	15
Papua new Guinea	12
Bangladesh	8
Sri Lanka	8
Mauritius	5
Fiji	4
Indonesia	4
India	4
Thailand	4
Solomon Islands	3
Madagascar	2

Malaysia	2

6. Total number of “efficient” accessions and palms in ex situ genebanks

Twenty-four COGENT genebanks are referenced in CGRD. Some of the conserved cultivars, such as for instance Boyolali Tall in Indonesia, are conserved only in one genebank; some other cultivars are conserved in many countries, such as for instance Malayan Yellow Dwarf (19) or West African Tall (10). Indeed, for breeding purposes, genebanks must have a core collection with a set of well-know referenced varieties. Nevertheless, for conservation purpose, we conducted an analysis aiming to assess the efficiency of the present system at the species level.

Table 14 summarize the result of this analysis. It shows that, if accurate standards are applied, only a third of the palms existing in ex situ collection are really useful to the conservation of the species at global level. This represents 857 accessions with an average size of 56 palms per accessions (37 for Dwarf-types and 60 for other kind of varieties), equivalent to 321 ha of coconut plantations.

```
close all
use access
set unique on
index on site+cult_name+population to temp
copy to temp
use temp
sele distinct cult_name, population, count(*) group by cult_name, population from temp.dbf
index on -cnt to temp
brow.
```

At the first level of analysis, there are 1680 coconut accessions registered in the CGRD, totalling 144559 palms referenced as alive and covering about 900 ha. There are 153 old accessions removed from the fields with 0 as accession size; more 153 accessions do not have a recorded size (data not sent by curators). So, the 1374 remaining accessions count in average 105 living palms.

```
count for last_size<>0 and !isnull(last_size)
*1374
aver last_size for last_size<>0 and !isnull(last_size)
105.2
```

Some accessions registered in the CGRD have a number of living palms which is too large for conservation purposes only. For instance, the highest accession size was recorded on an accession of Malayan Yellow Dwarf in Tanzania with 6400 palms[18]; this relies to a full seed garden for producing hybrids and not only to an accession designed for conservation. So it is important to make the difference between the numbers of palms presently registered in the database, and the numbers of palms really useful for conservation purposes. The recommended sample size for an accession ranges from 72 to 96[19] palms for heterogeneous allogamous Tall populations, and 45 palms for autogamous homogeneous dwarfs. **At the second level of analysis,** we calculated an “efficient size” limited to 45 palms for accession of Dwarf-types and to 96 palms for accessions of all other varieties.

```
Close all
use access
dele file tempcoun.dbf
Copy to tempcoun for !isnull(last_size) and last_size<>0
use tempcoun
brow field site, cult_name, population, last_size
Repla all last_size with 96 for last_size>96 and category<>2
Repla all last_size with 45 for last_size>45 and category=2
sum last_size
```

---

[18] Use Access.dbf; index on -last_size to temp; brow field site, cult_name, population, last_size

[19] We took 96 palms per accession of Tall-types for calculation

Some of the genebanks are conserving more than one accession per variety or population, because they are still maintaining both old accessions and their recent progenies. For Instance, Indonesia genebank recorded 9 accessions of Salak Green Dwarf of which 6 are still alive with 374 palms. **At the third level of analysis**, we merged duplicates within genebanks considering that each genebank should conserve no more than one accession per variety or population. For instance, in the case reported in previous paragraph, only one accession of Salak Green Dwarf with 45 palms should be taken in account for Indonesia.

```
Select distinct site, category, cult_name, population, count(*), sum(last_size) as last_size, 0000 as ha group by site, cult_name, population from tempcoun.dbf into table tempcou2.dbf
Use tempcou2
Repla all last_size with 96 for last_size>96 and category<>2
Repla all last_size with 45 for last_size>45 and category=2
Count
*987
sum last_size
* 53647
```

For safety duplication, each cultivar or population should be conserved by only three accessions in three genebanks located in three different countries. **At the fourth level of analysis**, we limited conservation of cultivars/population at only 3 replications worldwide. For instance, the cultivar Catigan Green Dwarf (CATD) is conserved in 9 countries with accessions sizes ranging from 4 to 1118 palms; six countries conserve accessions with more palms than the standard. So we considered only 3 accessions of CATD each with 45 palms as sufficient for accurate conservation.

```
Close all
Sele 2
Use tempcou2
Set unique on
Dele file tempuni.dbf
dele file temp.idx
index on cult_name+population to temp
copy to tempuni
close index
sele 1
use tempuni
Do while not eof()
Store cult_name+population to mcult
Sele 2
Count for cult_name+population=mcult to mcoun
Repla ha with mcoun for cult_name+population=mcult
Sele 1
Skip
Enddo
Sele 2
dele file temp.idx
set unique off
index on cult_name+population+site to temp
set filter to ha>3
repla all rien with '2' for last_size>44 and category=2
repla all rien with '1' for last_size>95 and category<>2
Brow
* After we finished by correcting the data by hand one by one.
```

A **fifth level of analysis** will deals with accessions conserved under different names but which are genetically similar. For instance, in Sri Lanka, 95 accessions of the local Tall have been collected, for a total of more than 6000 palms. Some of these populations are probably closely related. Only the systematic observations of standard descriptors and complementary DNA analysis will allow identifying and merging these duplicates.

Table 14. Analysis of accessions for global efficiency of conservation

Level of analysis	Description	Number of accessions	Number of palms	Palms per accessions
(1)	All living palms	1374	144559	105
(2)	Excluding over representation due to excessive accession sizes: - over 96 palms for tall-types - over 45 palms for Dwarf-types	1374	65460	48
(3)	Excluding (2) and accessions duplicated in the same genebank	987	53647	54
(4)	Excluding (2),(3) and limiting the conservation of cultivars/population at only 3 replications worldwide	857	47816	56

**** The file tempcou2.dbf was renamed as effiacc.dbf***

```
Use tempcou2
Copy to effiacc
use effiacc
index on site+cult_name to temp
copy to efficult
use efficult
brow
sele distinct cult_name, count(*) from efficult group by cult_name
count
count for cnt=1
count for cnt=2
count for cnt>2

680
29
*337 37
aver effi_size for effi_size>0 and rien<>D
*1037 53
```

```
Select distinct site, cult_name, population, count(*), sum(last_size) as last_size, 0000 as effi_size, group by site, cult_name, population from access.dnf into table tempcoun.dbf
```

```
brow field site, EMBR_CULT, type_mat, fie_est_dt, site, cult_name, population, country, ri_country,last_size, effi_size, category, poll_group, rien
```

This is needed to check and correct the fields poll_group and category.

```
brow field site, EMBR_CULT, type_mat, fie_est_dt, site, cult_name, population, country, ri_country,last_size, effi_size, category, poll_group, rien
repla all rien with 'T ' for (poll_group=2 or poll_group=3) and category=1
 * allogamous tall: rien=’T’ - 999 replacements
repla all rien with 'D ' for (poll_group=1 or poll_group=2) and category=2
* autogamous dwarfs: ’ 392 replacements
*data were corrected
```

```
repla all rien with 'T ' for (poll_group=2 or poll_group=3) and category=1
 * allogamous tall: rien=’T’ – 1238 replacements
repla all rien with 'D ' for (poll_group=1 or poll_group=2) and category=2
* autogamous dwarfs: ’ 409 replacements
*total 1647 on 1680, 33 remaining are intermediate forms

* mise a jour du champ effi_size
Repla all effi_size with 100 for rien<>’D’ and effi_size>100
Repla all effi_size with 50  for rien=’D’ and effi_size>50
* calcul des moyennes
Sum last_size
*144559
Sum effi_size
*67530
* 53% of the palms recorded in CGRD belongs to over-represented accession.
aver effi_size for effi_size>0 and rien=D
*337 37
aver effi_size for effi_size>0 and rien<>D
*1037 53

Sum l

* one accession per variety per genebank – remove duplicates within genebanks
Select distinct site, cult_name, population, category, poll_group; rien, count(*), sum(last_size) as last_size, 0000 as effi_size group by site, cult_name, population from access.dbf into table tempcoun.dbf
brow
index on -cnt to temp
brow
* the case of PAKI DOAS et CHIN has to be addressed
Use access
Set filter to site=”PAKI” or site=”DOAS” or site=”CHIN”
Index on site+cult_name+population+substr(fie_est_dt,5,4) to temp
Brow field site, cult_name, population, fie_est_dt freeze population
* corrigé
repla all rien with 'T ' for (poll_group=2 or poll_group=3) and category=1
 * allogamous tall: rien=’T’ – 935 replacements
repla all rien with 'D ' for (poll_group=1 or poll_group=2) and category=2
* autogamous dwarfs: ’ 227 replacements
*total 1182, ZZ remaining are intermediate forms
Repla all effi_size with 100 for rien<>’D’ and effi_size>100
Repla all effi_size with 50  for rien=’D’ and effi_size>50
* calcul des moyennes
Sum last_size
*144559
Sum effi_size
*57707
Aver effi-size
*Duplicates between genebanks
Select distinct cult_name, population, category, poll_group, rien, count(*), sum(last_size) as last_size, sum (effi_size) as effi_sire group by cult_name, population from tempcoun.dbf into table tempdupli.dbf
index on -cnt to temp
brow
```

91 accessions have an accession size of more than 200 palms, with an average of 800 palms. These high numbers cannot be considered for conservation purposes. It was decided not to count the palms exceeding 200 per accessions to have an estimate of the total number of palms conserved in ex situ collection.

Table 15: estimation of the number of palms in ex situ genebanks

Size of accessions	Number of accessions	Total number of palms	Corrected Total number of palms
>200	91	72837	18200
100-199	194	26752	26752
50-99	375	27607	27607
20-49	384	14157	14157
1-19	330	3146	3146
0	153	0	0
Null	153	0	0
Total[20]	1680	142979	89862

The null values are mainly from Bangladesh, Mexico, Pakistan and Vanuatu.

So the total number of palms conserved ex situ is 89862; palms are generally planted at 144 palms/ha for Talls and 200 palms for Dwarf. Taking in account an average planting density of 170, it gives about 529 hectares of coconut plantations.

---

[20] *programme cnt.prg

```
close all
use access.dbf
Sum last_size for last_size>200                  to m200
Sum last_size for last_size>99 and last_size<201  to m100_200
Sum last_size for last_size>49  and last_size<100   to m50_99
Sum last_size for last_size>20  and last_size<50    to m20_49
Sum last_size for last_size>0   and last_size<20    to m1_19
Sum last_size for last_size=0                     to m0
Sum last_size for isnul(last_size)                to misnul
count for last_size>200                   to c200
count for last_size>99 and last_size<201   to c100_200
count for last_size>49  and last_size<100   to c50_99
count for last_size>19  and last_size<50    to c20_49
count for last_size>0   and last_size<20    to c1_19
count for last_size=0                     to c0
count for isnul(last_size)                to cisnul
dele file temp.doc
set alter to temp.doc
set alter on

?c200,"$",m200
?c100_200,"$",m100_200
?c50_99,"$",m50_99
?c20_49,"$",m20_49
?c1_19,"$",m1_19
?c0,"$",m0
?cisnul,"$",misnul

set alter on
set alter to
modi comm temp.doc
```

7. Estimation of the number of living accessions

We considered as living accessions those accessions having an accession size superior to 0, plus some where the accession size is not available (Null value). We choose this option because we know that, among the 153 accessions with Null value, at least those 32 from Pakistan (32), Bangladesh (24) and Vanuatu (22). So the total number of living accession is 1527 of which 730 are conserved in international genebanks.

```
Sele distinct site, ri_country, count(*) group by site where isnull(last_size) from access.dbf
set unique off
dele file temp.idx
index on -cnt to temp
list all site,”$”,ri_country, ”$”,cnt to temp.doc off
Modi comm temp.doc
```

Table 16. number of living accessions.

Site	Country	Number of accession with unavailable accession size2
PAKI	PAK	32
BARI	BGD	24
VT	VUT	22
CICY	MEX	20
CIB	JAM	13
DOAS	MYS	8
NCDP	TZA	7
SRS	PNG	7
TON	TON	7
SP	BEN	4
WS	WSM	3
IND	IND	2
CHRC	THA	1
OPRI	GHA	1
TCC	FJI	1
YSI	SLB	1

8. Percentage of accession of Autogamous dwarf types

```
Use access
Count
*1680
Count for category=2
* 427
* The percentage of dwarf accession is 427/1680=25%
```

9. Date of planting of accessions at global level

A table giving the date of planting of accessions in ex situ genebank was needed. May be one for farmer’s fields and second for regeneration. Thats means that we need to well make differences between kinds of accessions:

The field ’fie_est_dt’ was used as reference.

```
* programme Tempnb.prg
Close all
Dele file temp.doc
Set alter to temp.doc
Set talk off
Set alter on
Sele 1
Use access
Dele file temp.idx
Set unique on
```

```
Index on substr(fie_est_dt,5,4)to temp
Dele file tempnb.dbf
Copy to tempnb.dbf
Close index
Sele 2
Use tempnb
Go top
Do while .not. eof()
Store substr(fie_est_dt,5,4) to myear
Sele 1
Count for substr(fie_est_dt,5,4)=myear and rejuv='F' to Fmyear
Count for substr(fie_est_dt,5,4)=myear and rejuv='T' to Tmyear
Count for substr(fie_est_dt,5,4)=myear and rejuv='R' to Rmyear
Sele 2
?substr(fie_est_dt,5,4)+'*',Fmyear,'*',Tmyear,'*',Rmyear
Skip
Enddo
Set alter off
Set alter to
Modi comm Temp.doc
```

This procedure generates the following table

Table ZZ. Transfers between genebanks

Years	Introduced from farmers fields	Transfers between genebanks	Regeneration within genebanks
1912	1	0	0
1927	1	0	0
1935	2	1	0
1939	1	0	0
1940	13	0	0
1941	3	0	0
1946	1	0	0
1947	2	0	0
1949	1	0	0
1952	4	0	0
1954	1	0	0
1955	14	2	0
1956	6	2	1
1957	1	0	1
1958	2	0	0
1959	5	3	0
1960	13	3	0
1961	7	1	0
1962	6	9	0
1963	5	4	1
1964	12	8	1
1965	11	4	0
1966	14	8	2
1967	7	3	0
1968	10	8	0
1969	3	1	0
1970	8	1	1
1971	1	0	0
1972	6	5	8
1973	6	1	0
1974	6	1	0

Years	Introduced from farmers fields	Transfers between genebanks	Regeneration within genebanks
1975	5	3	0
1976	9	6	0
1977	14	3	2
1978	28	11	1
1979	9	6	0
1980	11	5	1
1981	16	18	12
1982	23	11	11
1983	50	27	7
1984	44	11	4
1985	43	11	5
1986	34	2	0
1987	23	13	1
1988	32	2	15
1989	32	5	10
1990	10	6	19
1991	9	3	12
1992	22	2	10
1993	10	2	48
1994	43	12	27
1995	15	2	40
1996	10	5	3
1997	56	4	5
1998	71	1	26
1999	65	3	8
2000	25	0	9
2001	5	2	24
2002	15	0	23
2003	3	0	0
2004	20	12	6
2005	22	5	1
2006	22	15	10
2007	13	0	8
2008	20	0	36
2009	0	0	2
2010	1	0	1
2011	1	0	0
2012	1	0	0
Total	1005	273	402

J. Annexes

1. Table A. 1. List of fields in the CGRD database

List of fields in the CGRD database and their classification for evaluation of the genebanks
as of CGRD6 (Internet, 1st February 2011), and precious version CGRD5

Note: in Blue, fields modified from CGRD6 to CGRD5

	Name CGRD5 (Old)	Explanation	Name CGRD6 (New)	Type CGRD5	Length CGRD5		Null	Class RB	Value?	Remarks
1	SITE	SITE OF CONSERVATION	SITE	Character	4		No	P0	0,1	
2	ACCESS_NB	ACCESSION NUMBER	ACCESS_NB	Character	12		No	P0	1	
3	DONOR_NAME	DONOR NAME	DONOR_NAME	Character	25		No	P1	0,1	
4	DONOR_NB	DONOR NUMBER	DONOR_NB	Character	15		No	P0	0,1	
5	FEM_ACC_NB	FEMALE PARENT ACCESSION NUMBER	FEM_ACC_NB	Character	12		No	P1	0.5	
6	MAL_ACC_NB	MALE PARENT ACCESSION NUMBER	MAL_ACC_NB	Character	12		No	P1	0.5	
7	OTHER_NB1	Other number 1	OTHER_NB1	Character	12		No	P0	0,1	
8	OTHER_NB2	Other number 2	OTHER_NB2	Character	12		No	P0	0,1	
9	OTHER_NB3	Other number 3	OTHER_NB3	Character	12		No	P0	0,1	
10	CATEGORY	Category (= 'Type')	CATEGORY	Numeric	1		Yes	P1	0,3	
11	COLOUR1	Colour 1	COLOUR1	Numeric	2		Yes	P1	0,1	
12	COLOUR2	Colour 2	COLOUR2	Numeric	2		Yes	P0	0,1	
13	COLOUR3	Colour 3	COLOUR3	Numeric	2		Yes	P0	0,1	
14		**Old cultivar name with population**	**CULT_OLD**	**Character**	**30**		**Asc**		**0**	**New (1) Do not appear in the software**
15	**CULT_NAME**	**Translation/transliteration**	**CULT_NAME**	**Character**	**30**		**Asc**	**P1**	**1**	**Mofidied in the new**

										format – cultivar names and population names are now in 2 separate fields
16		**Population Name**	**POPULATION**	**Character**	**30**		**No**		**1**	**New (2) Appears in the software**
17	SYNONYM1	Synonym1	SYNONYM1	Character	30		No	P1	0,1	
18	SYNONYM2	Synonym2	SYNONYM2	Character	30		No	P0	0	
19	SYNONYM3	Synonym3	SYNONYM3	Character	30		No	P0	0	
20	ABBREV	Accepted abbreviation	ABBREV	Character	6		No	P1	1	
21	NB_FEM_POP	NUMBER OF PALMS IN THE FEMALE PARENT POPULATION	NB_FEM_POP	Numeric	5		Yes	P1	0,3	
22	EX_FEM_POP	Exact or estimated for descriptor 1.9	EX_FEM_POP	Numeric	1		Yes	P0	0,1	
23	NB_FEM_SAM	NUMBER OF PALMS FROM THE FEMALE PARENT POPULATION REPRESENTED BY THE SAMPLE	NB_FEM_SAM	Numeric	3		Yes	P1	0,3	
24	NB_MAL_POP	NUMBER OF PALMS IN THE MALE PARENT POPULATION	NB_MAL_POP	Numeric	5		Yes	P1	0,1	
25	EX_MAL_POP	Exact or estimated for descriptor 1.11	EX_MAL_POP	Numeric	1		Yes	P0	0,1	
26	NB_MAL_SAM	NUMBER OF PALMS FROM THE MALE PARENT POPULATION REPRESENTED BY THE	NB_MAL_SAM	Numeric	3		Yes	P1	0,3	

		SAMPLE								
27	ACQ_DATE	ACQUISITION DATE	ACQ_DATE	Character	8		No	P1	0,3	
28	POLL_GROUP	POLLINATION GROUP	POLL_GROUP	Numeric	1		Yes	P1	0,3	
29	TYPE_MAT	TYPE OF MATERIAL RECEIVED	TYPE_MAT	Numeric	1		Yes	P1	0,1	
30		ORIGINAL SIZE OF THE ACCESSION	ORI_SIZE	Numeric	5		Yes		0,3	New (3). Appears in the software
31	ACC_SIZE	ACCESSION SIZE	LAST_SIZE	Numeric	5		Yes	P1	0,3	
32	AC_SIZE_DT	DATE OF LAST INVENTORY	AC_SIZE_DT	Character	8		No	P1	0,3	
33		**PRESENT ACCESSION STATUS**	**PRES_STAT**	**Character**	**10**		**No**		**0,1**	**New. Appears in the new software. 3 possible values: Alive, Cut or Lost. Unknown to be added.**
34	TYPE_MAIN	TYPE OF MAINTENANCE	TYPE_MAIN	Numeric	1		Yes	P1	0,1	
35	ACC_NOTES	NOTES	ACC_NOTES	Memo	4		No	P1	0,3	
36	COLL_INST	COLLECTING INSTITUTE(S)	COLL_INST	Character	25		No	P1	0,1	
37	SITE_NB	SITE NUMBER	SITE_NB	Character	8		No	P0	0,1	
38	COLL_NB	COLLECTOR'S NUMBER	COLL_NB	Character	12		No	P0	0,1	
39	COLL_DATE	COLLECTION DATE OF ORIGINAL SAMPLE	COLL_DATE	Character	8		No	P1	0,3	
40	COUNTRY	COUNTRY OF COLLECTION	COUNTRY	Character	3		No	P1	0,1	
41	PROVINCE	PROVINCE/STATE	PROVINCE	Character	20		No	P1	0,3	

42	DEPT	DEPARTMENT/COUNTY	DEPT	Character	20		No	P1	0,3	
43	COLL_SITE	COLLECTION SITE	COLL_SITE	Memo	4		No	P1	0,3	
44		**LATITUDE OF COLLECTION SITE in hexadecimal minute and degrees**	**CO_LAT_OLD**	**Character**	**8**		**No**	**P1**	**1**	**New (5). Do not appear in the software. Old longitude format in minutes and seconds**
45	**COLL_LAT**	**LATITUDE OF COLLECTION SITE now in hexadecimal format**	**COLL_LAT**	**Numeric**	**9**	**5**	**No**		**0**	**Old but change format from minutes and degrees to hexadecimal**
46		**LONGITUDE OF COLLECTION SITE in hexadecimal minute and degrees**	**CO_LON_OLD in minutes and seconds**	**Character**	**8**		**No**		**1**	**New (6). Do not appear in the software. Old longitude format.**
47	**COLL_LONG**	**LONGITUDE OF COLLECTION SITE**	**COLL_LONG**	**Numeric**	**9**	**5**	**No**	**P1**	**0**	**Old but change format – now in hexadecimal minute and degrees instead of minutes and seconds**
48	ORIGINE	Origin of population to be sampled	ORIGINE	Numeric	1		Yes	P1	0,3	
49	GENERATION	Generation structure	GENERATION	Numeric	1		Yes	P1	0,1	
50	AGE	Age estimate of parent material	AGE	Numeric	3		Yes	P1	0,3	
51	COLL_SRCE	Collection source	COLL_SRCE	Numeric	2		Yes	P1	0,1	
52	ADJ_ISOL	ADJACENT PALM STATUS (Isolation)	ADJ_ISOL	Numeric	1		Yes	P1	0,1	
53	ADJ_TYPE	ADJACENT PALM STATUS (Type (Same/Different) if not	ADJ_TYPE	Numeric	1		Yes	P1	0,1	

		isolated)								
54	COLL_PRO	COLLECTION PROCEDURE	COLL_PRO	Numeric	1		Yes	P1	0,3	
55	SAMP_PRO	SAMPLING PROCEDURE	SAMP_PRO	Numeric	1		Yes	P1	0,3	
56	STAT_SAMP	STATUS OF SAMPLE	STAT_SAMP	Numeric	1		Yes	P1	0,5	
57	APPEARANCE	GENERAL APPEARANCE OF POPULATION	APPEARANCE	Numeric	1		Yes	P1	0,3	
58	POLLEN_SRC	POLLEN SOURCE	POLLEN_SRC	Numeric	1		Yes	P1	0,1	
59	EMBR_CULT	EMBRYO CULTURE STATUS	EMBR_CULT	Numeric	1		Yes	P0	0,1	
60	TISS_CULT	TISSUE CULTURE STATUS	TISS_CULT	Numeric	1		Yes	P0	0,1	
61	SIZE_POP	SIZE OF THE POPULATION	SIZE_POP	Numeric	5		Yes	P1	0,3	
62	EX_SIZ_POP	Exact or estimated size of the population	EX_SIZ_POP	Numeric	1		Yes	P1	0,1	
63	UN_SIZ_POP	Unit of descriptor size of the population	UN_SIZ_POP	Numeric	1		Yes	P1	0,3	
64	DENSITY	PLANT POPULATION DENSITY	DENSITY	Numeric	3		Yes	P1	0,3	
65	EX_SAMPLE	Exact or estimated number of number of palms sampled	EX_SAMPLE	Numeric	1		Yes	P0	0,1	
66	NB_SAMPLE	NUMBER OF PALMS SAMPLED IN THE POPULATION	NB_SAMPLE	Numeric	3		Yes	P1	0,3	
67	ME_SAMPLE	Method used for estimation of descriptor 2.22	ME_SAMPLE	Numeric	1		Yes	P0	0,1	

68	NB_SEEDNUT	TOTAL NUMBER OF SEEDNUTS, PLANTLETS OR EMBRYOS COLLECTED	NB_SEEDNUT	Numeric	4		Yes	P1	0,3	
69	POLLEN_WEI	TOTAL WEIGHT OF POLLEN COLLECTED [g]	POLLEN_WEI	Numeric	3		Yes	P0	0,1	
70	CROP_SYST	CROPPING SYSTEM AND ASSOCIATED FLORA	CROP_SYST	Numeric	1		Yes	P1	0,3	
71	CULT_STAT	CULTIVATION STATUS	CULT_STAT	Numeric	1		Yes	P1	0,3	
72	LOC_NAME	LOCAL/VERNACULAR NAME	LOC_NAME	Character	15		No	P1	0,3	
73	LANGUAGE	Language or ethnic group	LANGUAGE	Character	15		No	P1	0,1	
74	USE1	USES OF THE SOURCE POPULATION (1)	USE1	Numeric	1		Yes	P1	0,3	
75	USE2	USES OF THE SOURCE POPULATION (2)	USE2	Numeric	1		Yes	P0	0,1	
76	USE3	USES OF THE SOURCE POPULATION (3)	USE3	Numeric	1		Yes	P0	0,1	
77	OTHER_USE	Other use of the source population	OTHER_USE	Character	12		No	P0	0,1	
78	SPICATA	Frequency of spicata type	SPICATA	Numeric	1		Yes	P0	0,1	
79	PLICATA	Frequency of plicata type	PLICATA	Numeric	1		Yes	P0	0,1	
80	ANDROGENA	Frequency of androgena type	ANDROGENA	Numeric	1		Yes	P0	0,1	
81	MAKAPUNO	Frequency of makapuno type	MAKAPUNO	Numeric	1		Yes	P0	0,1	
82	OTHER_CAR	Other special character	OTHER_CAR	Character	12		No	P0	0,1	

83	OTHER_FREQ	Frequency of other special character	OTHER_FREQ	Numeric	1		Yes	P0	0,1	
84	CROWN	OVERALL APPEARANCE/SHAPE OF CROWN OF PARENT TREE	CROWN	Numeric	1		Yes	P1	0,1	
85	COLL_NOTES	COLLECTOR'S NOTES	COLL_NOTES	Memo	4		No	P1	0,3	
86	RI_COUNTRY	COUNTRY	RI_COUNTRY	Character	3		No	C1	0,1	
87	RI_NB	Site number	RI_NB	Character	8		No	C0	0,1	
88	**RI_LAT**	**Latitude in hexadecimal format**	**RI_LAT_OLD**	**Character**	**8**		**No**	**C1**	**1**	**New (7) , do not appears in the software. Old Format, Minutes and seconds**
89		**Latitude in decimal format**	**RI_LAT**	**Numeric**	**9**	**5**	**No**		**0**	**Modified format. Now: in hexadecimal format instead of minutes and seconds**
90	**RI_LONG**	**Longitude in hexadecimal format**	**RI_LON_OLD**	**Character**	**8**		**No**		**1**	**New (8) , do not appears in the software. Old Format, Minutes and seconds**
91		**Longitude in decimal format**	**RI_LONG**	**Numeric**	**9**	**5**	**No**	**C1**	**0**	**Modified format. Now: in hexadecimal format instead of minutes and seconds**
92	RI_ELEVAT	Elevation [m]	RI_ELEVAT	Numeric	4		Yes	C1	0,1	
93	RI_FARM	Name of farm or institute	RI_FARM	Character	25		No	C1	0,1	
94	EVALUATOR	EVALUATOR'S NAME AND ADDRESSE	EVALUATOR	Memo	4		No	C1	0,3	

95	EVAL_NOTES	Evaluator's notes	EVAL_NOTES	Memo	4		No	C0	0,3	
96	HARVEST_DT	Date of harvest	HARVEST_DT	Character	8		No	CG	0,3	
97	SOWING_DT	Date of sowing	SOWING_DT	Character	8		No	CG	0,3	
98	GER_SET_NB	Number of nuts set to germinate	GER_SET_NB	Numeric	4		Yes	CG	0,3	
99	GER_NUT_NB	Number of germinated nuts	GER_NUT_NB	Numeric	3		Yes	CG	0,3	
100	GERM_25	Number of days to 25% germination	GERM_25	Numeric	3		Yes	CG	0,3	
101	GERM_50	Number of days to 50% germination	GERM_50	Numeric	3		Yes	CG	0,5	
102	GERM_75	Number of days to 75% germination	GERM_75	Numeric	3		Yes	CG	0,3	
103	GERM_MAX	Number of days to maximum germination	GERM_MAX	Numeric	3		Yes	CG	0,5	
104	MAX_PERC	Maximum germination rate	MAX_PERC	Numeric	3		Yes	CG	0,3	
105	FIE_EST_DT	Date of field establishment	FIE_EST_DT	Character	8		No	C1	0,5	
106	PL_DENSITY	Planting density	PL_DENSITY	Numeric	3		Yes	C1	0,3	
107	TIM_MEA_AG	Age at the time of measurement [years]	TIM_MEA_AG	Numeric	2		Yes	C1	0,3	
108	GIR_20	Girth at 20cm above soil level [cm]	GIR_20	Numeric	5	1	Yes	CS	0,3	
109	SD38	Standard deviation for girth at 20 cm above soil level [cm]	SD38	Numeric	5	1	Yes	CS	0,1	
110	GIR_150	Girth of stem at 1.5m height [cm]	GIR_150	Numeric	5	1	Yes	CS	0,3	
111	SD39	Standard deviation of girth	SD39	Numeric	5	1	Yes	CS	0,1	

		at 1.5 m height [cm]								
112	DATE1	Date 1	DATE1	Character	8		No	CS	0,1	
113	HEIGHT1	Height 1 [cm]	HEIGHT1	Numeric	5		Yes	CS	0,5	
114	SD40	Standard deviation of height 1 [cm)	SD40	Numeric	5	1	Yes	CS	0,1	
115	DATE2	Date 2	DATE2	Character	8		No	CS	0,1	
116	HEIGHT2	Height 2 [cm]	HEIGHT2	Numeric	5		Yes	CS	0,5	
117	SD41	Standard deviation of height 2 [cm)	SD41	Numeric	5	1	Yes	CS	0,1	
118	BOLE_CAT	Bole category	BOLE_CAT	Numeric	1		Yes	CS	0,3	
119	LEA_SC_HEI	Height of 10 internodes	LEA_SC_HEI	Numeric	5	1	Yes	CS	0,5	
120	SD43	Standard deviation of height of 10 internodes	SD43	Numeric	5	1	Yes	CS	0,1	
121	PETIO_LEN	Petiole length [cm]	PETIO_LEN	Numeric	5	2	Yes	CL	0,5	
122	SD2	Standard deviation of petiole length [cm]	SD2	Numeric	5	1	Yes	CL	0,1	
123	PETIO_WID	Petiole width [cm]	PETIO_WID	Numeric	5	2	Yes	CL	0,3	
124	SD3	Standard deviation of petiole width [cm]	SD3	Numeric	5	2	Yes	CL	0,1	
125	PETIO_THIC	Petiole thickness [cm]	PETIO_THIC	Numeric	5	2	Yes	CL	0,3	
126	SD4	Standard deviation of petiole thickness [cm]	SD4	Numeric	5	2	Yes	CL	0,1	
127	RACHIS_LEN	Rachis length [cm]	RACHIS_LEN	Numeric	5	1	Yes	CL	0,5	
128	SD5	Standard deviation of rachis length [cm)	SD5	Numeric	5	1	Yes	CL	0,1	
129	LEALT_NB	Number of leaflets	LEALT_NB	Numeric	5	1	Yes	CL	0,3	

130	SD6	Standard deviation of leaflets number	SD6	Numeric	5	1	Yes	CL	0,1	
131	LEALT_LEN	Leaflet length [cm]	LEALT_LEN	Numeric	5	1	Yes	CL	0,3	
132	SD7	Standard deviation of leaflet length [cm]	SD7	Numeric	5	1	Yes	CL	0,1	
133	LEALT_WID	Leaflet width [cm]	LEALT_WID	Numeric	5	2	Yes	CL	0,3	
134	SD8	Standard deviation of leaflet width [cm]	SD8	Numeric	5	2	Yes	CL	0,1	
135	Y_LEA_NB	Rate of leaf production	Y_LEA_NB	Numeric	4	1	Yes	CL	0,3	
136	SD9	Standard deviation of rate of leaf production	SD9	Numeric	4	1	Yes	CL	0,1	
137	SAMPL_SIZE	Sample size	SAMPL_SIZE	Numeric	2		Yes	C1	0,5	
138	CEN_AX_LEN	Length of central axis [cm]	CEN_AX_LEN	Numeric	5	1	Yes	CI	0,3	
139	SD10	Standard deviation of length of central axis [cm]	SD10	Numeric	5	1	Yes	CI	0,1	
140	STALK_LEN	Length of stalk [cm]	STALK_LEN	Numeric	5	1	Yes	CI	0,5	
141	SD11	Standard deviation of stalk length [cm]	SD11	Numeric	5	1	Yes	CI	0,1	
142	STALK_GIR	Stalk girth [cm]	STALK_GIR	Numeric	5	2	Yes	CI	0,3	
143	SD12	Standard deviation of stalk girth (cm)	SD12	Numeric	5	2	Yes	CI	0,1	
144	STALK_WIDT	Stalk width [cm]	STALK_WIDT	Numeric	5	2	Yes	CI	0,3	
145	SD44	Standard deviation of stalk width [cm]	SD44	Numeric	5	2	Yes	CI	0,1	
146	Stalk_thic	Stalk thickness [cm]	STALK_THIC	Numeric	5	2	Yes	CI	0,3	
147	SD45	Standard deviation of stalk	SD45	Numeric	5	2	Yes	CI	0,1	

		thickness [cm]								
148	F_FL_SP_NB	Number of spikelets with female flowers	F_FL_SP_NB	Numeric	4	1	Yes	CI	0,3	
149	SD13	Standard deviation of number of spikelets with female flowers	SD13	Numeric	4	1	Yes	CI	0,1	
150	N_FL_SP_NB	Number of spikelets without female flowers	N_FL_SP_NB	Numeric	4	1	Yes	CI	0,3	
151	SD14	Standard deviation of number of spikelets without female flowers	SD14	Numeric	4	1	Yes	CI	0,1	
152	SPIKLT_LEN	Length of spikelet [cm]	SPIKLT_LEN	Numeric	4	1	Yes	CI	0,3	
153	SD15	Standard deviation of spikelet length [cm]	SD15	Numeric	4	1	Yes	CI	0,1	
154	FEM_FL_NB	Number of female flowers	FEM_FL_NB	Numeric	5	1	Yes	CI	0,5	
155	SD16	Standard deviation of number of female flowers	SD16	Numeric	5	1	Yes	CI	0,1	
156	Y_INF_NB	Number of inflorescences/year	Y_INF_NB	Numeric	4	1	Yes	CI	0,3	
157	SD17	Standard deviation of number of inflorescences/year	SD17	Numeric	4	1	Yes	CI	0,1	
158	PHASE_CONC	Concordance of phases	PHASE_CONC	Numeric	3	Yes	Yes	CI	0,3	
159	SD18	Standard deviation of concordance of phase	SD18	Numeric	3	1	Yes	CI	0,1	
160	MAL_PH_LEN	Length of male phase [days]	MAL_PH_LEN	Numeric	4	1	Yes	CI	0,3	
161	SD19	Standard deviation of length of male phase [days]	SD19	Numeric	4	1	Yes	CI	0,1	

162	FEM_PH_LEN	Length of female phase [days]	FEM_PH_LEN	Numeric	4	1	Yes	CI	0,3	
163	SD20	Standard deviation of length of female phase [days]	SD20	Numeric	4	2	Yes	CI	0,1	
164	INT_PH_PER	Period between phases [+ days]	INT_PH_PER	Numeric	5	1	Yes	CI	0,3	
165	SD21	Standard deviation of period between phases [days]	SD21	Numeric	4	1	Yes	CI	0,1	
166	SU_INF_PER	Period between successive inflorescences [+ days]	SU_INF_PER	Numeric	5	1	Yes	CI	0,3	
167	SD22	Standard deviation of period between successive inflorescences [days]	SD22	Numeric	4	1	Yes	CI	0,1	
168	NOP_INF_AG	Age when 50% palms bear their first (unopened) spathe [months]	NOP_INF_AG	Numeric	4	1	Yes	CI	0,3	
169	OP_INF_AG	Age when 50% palms with open inflorescences [months]	OP_INF_AG	Numeric	5	1	Yes	CI	0,3	
170	B_IN_LE_NB	Number of leaves emitted until the leaf bearing the first inflorescences	B_IN_LE_NB	Numeric	5	1	Yes	CL	0,3	
171	SD25	Standard deviation of nb. of leaves until the leaf bearing the first infl.	SD25	Numeric	5	1	Yes	CL	0,1	
172	FR_POL_SEC	Fruit polar section	FR_POL_SEC	Numeric	1		Yes	CF	0,3	
173	FR_EQU_SEC	Fruit equatorial section	FR_EQU_SEC	Numeric	1		Yes	CF	0,3	
174	NB_TREES	Number of trees analysed	NB_TREES	Numeric	3		Yes	CF	0,3	

175	FR_WEI	Fruit weight [g]	FR_WEI	Numeric	6	1	Yes	CF	0,3	
176	SD26	Standard deviation of fruit weight [g]	SD26	Numeric	6	1	Yes	CF	0,1	
177	NUT_WEI	Nut weight [g]	NUT_WEI	Numeric	6	1	Yes	CF	0,3	
178	SD27	Standard deviation of nut weight [g]	SD27	Numeric	6	1	Yes	CF	0,1	
179	S_AN_M_WEI	Shell and meat weight [g]	S_AN_M_WEI	Numeric	6	1	Yes	C0	0,3	
180	SD28	Standard deviation of shell and meat weight [g]	SD28	Numeric	6	1	Yes	C0	0,1	
181	SHELL_WEI	Shell weight [g]	SHELL_WEI	Numeric	5	1	Yes	CF	0,3	
182	SD29	Standard deviation of shell weight [g]	SD29	Numeric	5	1	Yes	CF	0,1	
183	MEAT_WEI	Meat weight [g]	MEAT_WEI	Numeric	6	1	Yes	C0	0,3	
184	SD42	Standard deviation of meat weight [g]	SD42	Numeric	6	1	Yes	C0	0,1	
185	ENDO_THIC	Endosperm thickness [mm]	ENDO_THIC	Numeric	4	1	Yes	CF	0,3	
186	SD30	Standard deviation of endosperm thickness [mm]	SD30	Numeric	4	1	Yes	CF	0,1	
187	S_E_DR_MAT	Solid endosperm dry matter content	S_E_DR_MAT	Numeric	4	1	Yes	CF	0,3	
188	SD31	Standard deviation of solid endosperm dry matter content	SD31	Numeric	4	1	Yes	CF	0,1	
189	OBS_BEG_DT	Date observations began	OBS_BEG_DT	Character	8		No	CY	0,5	
190	OBS_END_DT	Date observations ended	OBS_END_DT	Character	8		No	CY	0,5	
191	MORTALITY	Percentage of mortality	MORTALITY	Numeric	4	1	Yes	CY	0,3	

192	OBS_P_NB	Number of palms observed	OBS_P_NB	Numeric	4		Yes	CY	0,3	
193	BUN_P_Y_NB	Number of bunches/palm/year	BUN_P_Y_NB	Numeric	4	1	Yes	CY	0,5	
194	SD32	Standard deviation of number of bunches/palm/year	SD32	Numeric	4	1	Yes	CY	0,1	
195	RN_P_Y_NB	Number of ripe nuts/palm/year	RN_P_Y_NB	Numeric	5	1	Yes	CY	0,5	
196	SD33	Standard deviation of ripe nuts/palm/year	SD33	Numeric	5	1	Yes	CY	0,1	
197	CO_NUT_WEI	Copra weight per nut [kg]	CO_NUT_WEI	Numeric	5	1	Yes	CY	0,5	
198	SD34	Standard deviation of copra weight per nut [kg]	SD34	Numeric	5	1	Yes	CY	0,1	
199	CO_P_Y_YIE	Copra yield/palm/year	CO_P_Y_YIE	Numeric	4	1	Yes	CY	0,5	
200	SD35	Standard deviation of copra yield/palm/year	SD35	Numeric	4	1	Yes	CY	0,1	
201	DR_ME_OIL	Dry matter content oil [%]	DR_ME_OIL	Numeric	5	2	Yes	CY	0,3	
202	SD36	Standard deviation of dry matter content oil [%]	SD36	Numeric	5	2	Yes	CY	0,1	
203	FR_ME_OIL	Fresh meat oil content [%]	FR_ME_OIL	Numeric	5	2	Yes	CY	0,5	
204	SD37	Standard deviation of fresh meat oil content [%]	SD37	Numeric	5	2	Yes	CY	0,1	
205	HUSK_WEI	HUSK WEIGHT	HUSK_WEI	Numeric	6	1	Yes	CF	0,5	
206	SD46	STANDARD DEVIATION FOR HUSK WEIGHT	SD46	Numeric	6	1	Yes	CF	0,1	
207	WATER_WEI	WATER WEIGHT	WATER_WEI	Numeric	6	1	Yes	CF	0,3	
208	SD47	STANDARD DEVIATION	SD47	Numeric	6	1	Yes	CF	0,1	

		FOR WATER WEIGHT								
209	ENDO_WEI	ENDOSPERM KERNEL WEIGTH	ENDO_WEI	Numeric	6	1	Yes	CF	0,3	
210	SD48	STANDARD DEVIATION FOR ENDOSPERM KERNEL WEIGTH	SD48	Numeric	6	1	Yes	CF	0,1	
Total									50	

2. Procedure for correcting the values of decimal latitudes and longitudes

```
*geo.prg
close all
Use access
dele file temp.idx
index on substr(fie_est_dt,5,4)+substr(acq_date,5,4)+substr(coll_date,5,4)to temp
copy field site, access_nb, acq_date, fie_est_dt, cult_name, population, abbrev, country, province,
dept, coll_lat, coll_long, co_lat_old, co_lon_old to tempgeo.dbf
close index
*Brow fields site, abbrev, fie_est_dt,acq_date,coll_date
use tempgeo
*Brow fields site, abbrev, fie_est_dt,acq_date
set unique on
dele file temp.idx
index on str(coll_lat)+str(coll_long) to temp
copy to temp
zap
appe from temp
repla all coll_lat with -coll_lat for substr(co_lat_old,6,1)='S'
repla all coll_long with -coll_long for substr(co_lon_old,6,1)='W'
*brow field site, access_nb, acq_date, cult_name, population, abbrev, country, province, dept, coll_lat,
coll_long, co_lat_old, co_lon_old
copy to tempgeo.xls type xl5
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3. Table of countries from Country.dbf

As of 15th March 2013, from the file Country.dbf

Table A.2. Codes for countries

Code région	Code	Name	Full Name	CGRD	Coconut can grow Easily (E) Difficult (D)	Tag for country	Url Tag for country
	AGO	ANGOLA	People's Republic of Angola		E		
	AND	ANDORA	Andora				
	ANT	ANTILLES	Netherlands Antilles				
	ARE	U A EMIRATES	United Arab Emirates				
	ARG	ARGENTINA	Argentine Republic				
	ATA	ANTARCTICA	Antarctica				
	ATG	ANTIGUA	Antigua		E		
	ATN	DRONNING MAUD LA	Dronning Maud Land				
	AUS	AUSTRALIA	Commonwealth of Australia		E		
	BDI	BURUNDI	Republic of Burundi				
	BEL	BELGIUM	Kingdom of Belgium				
	BGR	BULGARIA	People's Republic of Bulgaria				
	BHR	BAHRAIN	State of Bahrain				
	BHS	BAHAMAS	Commonwealth of the Bahamas		D		
	BLZ	BELIZE	Belize				
	BMU	BERMUDA	Bermuda				
	BOL	BOLIVIA	Republic of Bolivia				
	BRB	BARBADOS	Barbados				
	BRN	BRUNEI	Brunei				
	BTN	BHUTAN	Kingdom of Bhutan				
	BVT	BOUVET IS	Bouvet Island				
	BWA	BOTSWANA	Republic of Botswana				
	BYS	BYELORUSSIAN SSR	Byelorussian Soviet Socialist Republic				

	CAF	CENTRAL AFRICA	Central African Republic				
	CAN	CANADA	Canada				
	CCK	COCOS IS	Cocos (Keeling) Islands				
	CHE	SWITZERLAND	Swiss Confederation				
	CHL	CHILE	Republic of Chile				
	CPV	CAP VERDE	Republic of Cape Verde				
	CSK	CZECHOSLOVAKIA	Czechoslovak Socialist Republic				
	CTE	CANTON-END IS	Canton and Enderbury Islands				
	CXR	CHRISTMAS IS	Christmas Island				
	CYM	CAYMAN IS	Cayman Islands				
	CYP	CYPRUS	Republic of Cyprus				
	DDR	EAST GERMANY	German Democratic Republic				
	DEU	WEST GERMANY	German Federal Republic				
	DJI	DJIBOUTI	Republic of Djibouti				
	DMA	DOMINICA	Commonwealth of Dominica				
	DNK	DENMARK	Kingdom of Denmark				
	DOM	DOMINICAN RP	Dominican Republic				
	DZA	ALGERIA	People's Democratic Republic of Algeria				
	ESP	SPAIN	Spanish State				
	FIN	FINLAND	Republic of Finland				
	FLK	FALKLAND IS	Falkland Islands (Malvinas)				
	FRA	FRANCE	France Republic				
	FRO	FAEROE IS	Faeroe Islands				
	GAB	GABON	Gabonese Republic				
	GBR	UNITED KINGDOM	United Kingdom of Great Britain & N Irla				
	GIN	GUINEA	Revolutionary People's Republic of Guine				
	GMB	GAMBIA	Republic of the Gambia				
	GNB	GUINEA-BISSAU	Republic of Guinea-Bissau				
	GRC	GREECE	Greece Hellenic Republic				
	GRD	GRENADA	Grenada				
	GRL	GREENLAND	Greenland				
	GUF	FRENCH GUIANA	French Guiana				
	GUY	GUYANA	Republic of Guyana				

	HKG	HONG KONG	Hong Kong				
	HNM	H-MCD IS	Heard and Mc Donald Islands				
	HUN	HUNGARY	Hungarian People's Republic				
	IOT	BR-IN-OC-TR	Brithish Indian Ocean Territory				
	IRL	IRELAND	Ireland				
	IRN	IRAN	Islamic Republic Iran				
	IRQ	IRAQ	RepubliC of Iraq				
	ISL	ICELAND	Republic if Iceland				
	ISR	ISRAEL	State of Israel				
	ITA	ITALY	Italian Republic				
	JOR	JORDAN	Hashemite Kingdom of Jordan				
	JPN	JAPAN	Japan				
	JTN	JOHNSTON IS	Johnston Island				
	KNA	ST KITTS	St. Kitts-Nevis-Anguilla				
	KOR	KOREA REP	Republic of Korea				
	KWT	KUWAIT	State of Kuwait				
	LAO	LAOS	Lao People's Democratic Republic				
	LBN	LEBANON	Lebanese Republic				
	LBR	LIBERIA	Republic of Liberia				
	LBY	LIBYA	Socialist People's Libyan Arab Jamahiriy				
	LIE	LIECHTENSTEIN	Principality of Liechtenstein				
	LSO	LESOTHO	Kingdom of Lesotho				
	LUX	LUXEMBOURG	Grand Duchy of Luxembourg				
	MAC	MACAU	Macau				
	MAR	MOROCCO	Kingdom of Morocco				
	MCO	MONACO	Principality of Monaco				
	MDV	MALDIVES	Republic of Maldives				
	MID	MIDWAY IS	Midway Islands				
	MLI	MALI	Republic of Mali				
	MLT	MALTA	Republic of Malta				
	MNG	MONGOLIA	Mongolian People's Republic				
	MRT	MAURITANIA	Islamic Republic of Mauritania				
	MSR	MONTSERRAT	Montserrat				
	MWI	MALAWI	Republic of Malawi				
	NAM	NAMIBIA	Namibia				

	NER	NIGER	Republic of the Niger				
	NFK	NORFOLK IS	Norfolk Island				
LAC	NIC	NICARAGUA	Republic of Nicaragua				
	NIU	NIUE	Niue				
	NLD	NETHERLANDS	Kingdom of the Netherlands				
	NOR	NORWAY	Kingdom of Norway				
	NPL	NEPAL	Kingdom of Nepal				
	NRU	NAURU	Republic of Nauru				
	NTZ	NEUTRAL ZONE	Neutral Zone				
PAC	NZL	NEW ZEALAND	New Zealand				
	OCN	PITCAIRN IS	Pitcairn Island				
SAME	OMN	OMAN	Sultanate of Oman				
	PCI	PACIFIC IS	Pacific Islands				
	POL	POLAND	Polish People's Republic				
	PRI	PUERTO RICO	Puerto Rico				
	PRK	KOREA DPR	Democratic People's Repulbic of Korea				
	PRT	PORTUGAL	Portuguese Republic				
	PRY	PARAGUAY	Republic of Paraguay				
	QAT	QATAR	State of Qatar				
	REU	REUNION	Reunion				
	ROM	ROMANIA	Socialist Republic of Romania				
	RWA	RWANDA	Rwandese Republic				
	SAU	SAUDI ARABIA	Kingdom of Saudi Arabia				
	SDN	SUDAN	Democratic Republic of the Sudan				
	SEN	SENEGAL	Republic of Senegal				
	SGP	SINGAPORE	Republic of Singapore				
	SHN	ST HELENA	St. Helena				
	SJM	SVALBARD IS	Svalbard and Jan Mayan Islands				
	SLE	SIERRA LEONE	Republic of Sierra Leone				
	SMR	SAN MARINO	Republic of San Marino				
	SOM	SOMALIA	Somali Democratic Republic				
	SPM	ST PIERRE	St. Pierre and Miquelon				
	STP	SAO TOME	Democratic Republic of Sao Tome and Prin				
	SUN	USSR	Union of Soviet Socialist Republic				

	SWE	SWEDEN	Kingdom of Sweden				
	SWZ	SWAZILAND	Kingdom of Swaziland				
	SYR	SYRIA	Syrian arab Republic				
	TCA	TURKS CAICOS IS	Turks and Caicos Islands				
	TCD	CHAD	Republic of Chad				
	TGO	TOGO	Togolese Republic				
	TKL	TOKELAU	Tokelau				
	TMP	EAST TIMOR	East Timor				
	TRA	TRANSKEI	Transkei				
	TUN	TUNISIA	Republic of Tunisia				
	TUR	TURKEY	Republic of Turkey				
	TUV	TUVALU	Tuvalu				
	TWN	TAIWAN	Taiwan Province of China				
	UGA	UGANDA	Republic of Uganda				
	UKR	UKRAINIAN SSR	Ukrainian Soviet Socialist Republic				
	USA	UNITED STATES	United States of America				
	VCT	ST VINCENT	Saint Vincent and the Grenadines				
	VGB	UK VIRGIN IS	British Virgin Islands				
	VIR	US VIRGIN IS	United States Virgin Islands				
	WAK	WAKE IS	Wake Island				
	ZAF	SOUTH AFRICA	Republic of South Africa				
AIO	COG	CONGO	People's Republic of the Congo				
AIO	EGY	EGYPT	Arab Republic of Egypt				
AIO	ESH	WESTERN SAHARA	Western Sahara				
AIO	ETH	ETHIOPIA	Ethiopia				
AIO	GIB	GIBRALTAR	Gibraltar				
AIO	HVO	BURKINA FASO	Burkina Faso				
AIO	ZAR	ZAIRE	Republic of Zaire				
AIO	ZMB	ZAMBIA	Republic of Zambia				
AIO	ZWE	ZIMBABWE	Zimbabwe				
EUR	ALB	ALBANIA	People's Socialist Republic of Albania				
EUR	VAT	VATICAN	Vatican City State (Holy See)				
EUR	YUG	YUGOSLAVIA	Socialist Federal Republic of Yugoslavia				
LAC	COL	COLOMBIA	Republic of Colombia				
LAC	CRI	COSTA RICA	Republic of Costa Rica				

LAC	ECU	ECUADOR	Republic of Ecuador				
LAC	GLP	GUADELOUPE	Guadeloupe				
LAC	GTM	GUATEMALA	Republic of Guatemala				
LAC	HND	HONDURAS	Republic of Honduras				
LAC	HTI	HAITI	Republic of Haiti				
LAC	MTQ	MARTINIQUE	Martinique				
LAC	SLV	EL SALVADOR	Republic of El Salvador				
LAC	URY	URUGUAY	Eastern Republic of Uruguay				
LAC	VEN	VENEZUELA	Republic of Venezuela				
PAC	AUT	AUSTRIA	Republic of Austria				
PAC	COK	COOK IS	Cook Islands				
PAC	PUS	US PACIFIC IS	United States Miscellaneous Pacific Isla				
PAC	WLF	WALLIS IS	Wallis and Futuna Islands				
SAME	AFG	AFGHANISTAN	Democratic Republic of Afghanistan		E		
SAME	YEM	YEMEN	Yemen Arab Republic				
SAME	YMD	YEMEN DEMOCRATIC	People's Democratic Republic of Yemen				
SEA	BUR	BURMA	Socialist Republic of the Union of Burma				
AIO	BEN	BENIN	People's Republic of Benin	*		1	http://maps.google.com/mapfiles/kml/paddle/1.png
AIO	CIV	IVORY COAST	Republic of Ivory Coast	*		2	http://maps.google.com/mapfiles/kml/paddle/2.png
AIO	CMR	CAMEROON	United Republic of Cameroon	*			
AIO	COM	COMOROS	Federal and Islamic Republic of Comoros	*			
AIO	GHA	GHANA	Republic of Ghana	*			
AIO	GNQ	EQUATORIAL GUINE	Republic of Equatorial Guinea	*			
AIO	KEN	KENYA	republic of Kenya	*			
AIO	MDG	MADAGASCAR	Democratic Republic of Madagascar	*			
AIO	MOZ	MOZAMBIQUE	People's Republic of Mozambique	*			
AIO	MUS	MAURITIUS	Mauritius	*			
AIO	NGA	NIGERIA	Federal Republic of Nigeria	*			
AIO	SYC	SEYCHELLES	Republic of Seychelles	*			
AIO	TZA	TANZANIA	United Republic of Tanzania	*			

LAC	BRA	BRAZIL	Federative Republic of Brazil	*			
LAC	CUB	CUBA	Republic of Cuba	*			
LAC	JAM	JAMAICA	Jamaica	*			
LAC	LCA	SAINT LUCIA	Saint Lucia	*			
LAC	MEX	MEXICO	United Mexican States	*			
LAC	PAN	PANAMA	Republic of Panama	*			
LAC	PER	PERU	Republic of Peru	*			
LAC	SUR	SURINAME	Republic of Suriname	*			
LAC	TTO	TRINIDAD TOBAGO	Republic of Trinidad and Tobago	*			
PAC	ASM	AMERICAN SAMOA	American Samoa	*	E		
PAC	FJI	FIJI	Fiji	*			
PAC	GUM	GUAM	Guam	*			
PAC	KIR	KIRIBATI	Kiribati	*			
PAC	NCL	NEW CALEDONIA	New Caledonia	*			
PAC	PNG	PAPUA NEW GUINEA	Papua New Guinea	*			
PAC	PYF	FRENCH POLYNESIA	French Polynesia	*			
PAC	SLB	SOLOMON ISLANDS	Solomon Islands	*			
PAC	TON	TONGA	Kingdom of Tonga	*			
PAC	VUT	VANUATU	Vanuatu	*			
PAC	WSM	SAMOA	Independent State of Western Samoa	*			
SAME	BGD	BANGLADESH	People's Republic of Bangladesh	*			
SAME	IND	INDIA	Republic of India	*			
SAME	LKA	SRI LANKA	Democratic Socialist Republic of Sri Lan	*			
SAME	PAK	PAKISTAN	Islamic Repulbic of Pakistan	*			
SEA	CHN	CHINA	People's Republic of China (Inc. Taiwan)	*			
SEA	IDN	INDONESIA	Repulbic of Indonesia	*			
SEA	KHM	KAMPUCHEA	Kampuchea Democratic	*			
SEA	MYS	MALAYSIA	Malaysia	*			
SEA	PHL	PHILIPPINES	Republic of the Philippines	*			
SEA	THA	THAILAND	Kingdom of Thailand	*			
SEA	VNM	VIET NAM	Socialist Republic of Vietnam	*			

Localisations of Genebank Sites

36*-11.10219*-37.18591 BRA*Campo Exp. Itaporanga*13
37*-10.41926*-36.56855 BRA*Campo Exper. de Betume*16
38*19.55000*110.78330 CHN*Coconut Res. Institute*17
39*5.18815*-3.64233 CIV*Assinie Canal Plantation*7
40*5.24106*-3.89141 CIV*Marc Delorme Old Station*17
41*5.27472*-3.84208 CIV*Marc Delorme Res. Station*125
42*-16.70329*-179.90770 FJI*Taveuni Coconut Centre*11
43*0.00000*0.00000 GHA*12
44*4.83330*1.93330 GHA*Agona Junction (OPRI)*1
45*5.03330*2.46670 GHA*Anyinasi (MOFA)*1
46*5.05000*2.16670 GHA*Bamiankor (OPRI)*1
47*0.00000*0.00000 GHA*Oil Palm Research Inst.*1
48*-2.63330*120.70000 IDN*Bone-Bone Res. Centre*22
49*2.63330*120.70000 IDN*Bone-Bone Res. Centre*14
50*1.55000*124.91670 IDN*KIma Atas Exp. Garden*1
51*1.50000*124.91670 IDN*Kayuwatu Exp. Garden*1
52*-1.55000*124.91670 IDN*Kima Atas Exp. Garden*3
53*1.55000*124.91670 IDN*Kima Atas Exp. Garden*11
54*-1.51670*124.93330 IDN*Mapanget Exp. Garden*11
55*-1.51670*124.96670 IDN*Mapanget Exp. Garden*3
56*1.51670*124.93330 IDN*Mapanget Exp. Garden*24
57*1.51670*124.96670 IDN*Mapanget Exp. Garden*20
58*-6.93330*106.93330 IDN*Pakuwon Exp. Garden*13

59*6.93330*106.93330 IDN*Pakuwon Exp. Garden*12

60*0.00000*0.00000 IDN*Pandu Exp Garden.*1

61*0.00000*0.00000 IDN*Pandu Exp. Garden*16

62*-1.51670*124.96670 IDN*Paniki Exp. Garden*1

63*1.51670*124.93330 IDN*Paniki Exp. Garden*10

64*1.51670*124.96670 IDN*Paniki Exp. Garden*10

65*-0.43330*101.50000 IDN*Sikijang Exp. Garden*12

66*0.43330*101.50000 IDN*Sikijang Exp. Garden*18

67*-12.50000*75.00000 IND*CPCRI Kasaragod Kerala*15

68*12.50000*-75.00000 IND*CPCRI Kasaragod Kerala*2

69*12.50000*75.00000 IND*CPCRI Kasaragod Kerala*164

70*12.50000*75.00000 IND*CPCRI Kidu Res. Centre*90

71*-12.50000*-75.00000 IND*WCGC, Sipighat, Andamans*5

72*12.50000*75.00000 IND*WCGC, Sipighat, Andamans*25

73*18.21670*76.68330 JAM*Agualta Vale*2

74*-18.21670*76.68330 JAM*Coconut Industry Board*1

75*18.21670*-76.68330 JAM*Coconut Industry Board*3

76*18.21670*76.68330 JAM*Coconut Industry Board*53

77*18.21670*76.68330 JAM*Torkington Estate*1

78*7.68330*79.88330 LKA*Ambakelle Seed Garden*3

79*-7.33330*79.86670 LKA*Bandirippuwa Estate*2

80*7.31670*79.86670 LKA*Bandirippuwa Estate*1

81*7.33330*-79.86670 LKA*Bandirippuwa Estate*2

82*7.33330*79.86670 LKA*Bandirippuwa Estate*36

83*7.63330*80.46670 LKA*Lenawa Estate*14

84*7.63330*80.50000 LKA*Lenawa Estate*2

85*7.68330*79.91670 LKA*Pallama field genebank*6

86*7.70000*79.86670 LKA*Pallama field genebank*2

87*7.70000*79.93330 LKA*Pallama field genebank*42

88*7.68330*79.91670 LKA*Pothukulama Research St.*24

89*7.68330*79.91670 LKA*Pothukulama Research Sta.*2

90*7.68330*79.91670 LKA*Pottukulama Estate*2

91*7.55000*80.48330 LKA*Raddegoda Estate*19

92*21.50000*-89.00000 MEX*San Crisanto*20

93*0.90000*100.85000 MYS*MARDI*1

94*3.83330*100.86670 MYS*MARDI*1

95*3.88330*100.85000 MYS*MARDI*1

96*3.88330*100.86670 MYS*MARDI*19

97*3.90000*100.85000 MYS*MARDI*13

98*0.00000*0.00000 MYS*SKAES*1

99*0.00000*0.00000 MYS*UDARS*44

100*3.88330*100.86670 MYS*mardi*9

101*0.00000*0.00000 PAK*32

102*13.20000*123.61670 PHL*Albay Research Center*11

103*11.43330*122.56670 PHL*Panay State Poly. College*82

104*-6.98330*121.91670 PHL*Zamboanga Research Center*3

105*6.91670*121.91670 PHL*Zamboanga Research Center*1

106*6.98330*-121.91670 PHL*Zamboanga Research Center*13

107*6.98330*121.91670 PHL*Zamboanga Research Center*76
108*7.00000*-121.91670 PHL*Zamboanga Research Center*1
109*7.00000*121.91670 PHL*Zamboanga Research Center*37
110*-4.31670*152.01670 PNG*Cocoa and Coconut Res Ins*3
111*-5.11670*145.80000 PNG*Stewart Research Station*47
112*5.11670*145.80000 PNG*Stewart Research Station*6
113*51.00000*162.00000 PNG*Stewart Research Station*1
114*-9.00000*159.16670 SLB*RIPEL*9
115*9.00000*-159.16670 SLB*RIPEL*1
116*9.00000*159.16670 SLB*RIPEL*11
117*-10.23330*99.11670 THA*Chumphon Hort Res Centre*1
118*10.23330*-99.11670 THA*Chumphon Hort Res Centre*5
119*10.23330*99.11670 THA*Chumphon Hort Res Centre*22
120*0.00000*0.00000 THA*Kanthuli Seed garden*24
121*21.15000*175.23330 TON*Vaini Experimental Stat..*7
122*0.00000*0.00000 TZA*1
123*-6.06670*39.33330 TZA*Bambi seed garden*7
124*-6.33330*37.63330 TZA*Chambezi Agr. Res. Stat.*49
125*-6.08330*39.23330 TZA*Kidichi improv. block*3
126*-7.55000*39.28330 TZA*Kifumangao trial site*1
127*-7.86670*39.81670 TZA*Mafia Kilombero seed gar.*2
128*-7.88330*39.66670 TZA*Mafia Tereni seed garden*7
129*-6.03330*39.23330 TZA*Selem seed garden*2
130*10.20000*-106.56670 VNM*OPI VietNam/ Dong Go*1

131*10.20000*-106.40000 VNM*OPI VietNam/ Dong Go*4

132*10.20000*106.40000 VNM*OPI VietNam/ Dong Go*25

133*10.20000*106.40000 VNM*OPI Vietnam / Dong Go*1

134*-15.44914*167.20689 VUT*VARTC Saraoutou*79

135*13.83330*171.96670 WSM*Olomanu Seed Garden*9