

WAGENINGEN **UR**
For quality of life



Training course at the Centre for Genetic Resources, the Netherlands.



Characterisation of part of the CGN's radish collection

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Acknowledgements

Before starting this report, I would like to sincerely thank Ms Noortje Bas who accepted me like a spontaneous trainer during these two months at CGN. I have to thank her for her availability and for her sweetness to prepare my coming with administrative steps. She also spent a large part of her work time to explain me different things related to CGN's work. I also want to thank all the CGN staff who allowed me to do my trainee course in this structure and who make me a great welcome. A special thank to Frank Manting for his hospitality, his humour and his availability for extra work. To finish about the CGN's characters, I want to thank Theo van Hintum who spent a long time with me to explain about Genetic Resources and his work.

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Thank at all...

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LIST OF ABBREVIATIONS

AHC : Automatic Hierarchical Classification
CBD: the Convention on Biological Diversity
CGIAR: the Consultative Group on International Agricultural Research
CGN: the Centre for Genetic Resources, the Netherlands
CGRFA: the Commission on Genetic Resources for Food and Agriculture
CIMMYT: The International Maize and Wheat Improvement Center
ECPGR: the European cooperative Programme for Plant Genetic Resources
FAO: the Food and Agriculture Organization of the United Nations
GENIS: GENetic resources Information management System
GPA: the Global Plan Action
INIBAP: the International Network for Improvement of BANana and Plantain
IPGRI: the International Plant Genetic Resources Institute
IPNI: the International Plant Names Index
IRRI: the International Rice Research Institute
ITPGRFA: the International Treaty on Plant Genetic Resources for Food and Agriculture
IUPGRFA: International Undertaking on Plant Genetic Resources for Food and Agriculture
MCA : Multiple Component Analysis
PGR: Plant Genetic Resources
SMTA: the Standard Material Transfer Agreement
TRIPS: the Agreement on Trade-Related Aspects of Intellectual Property Rights
UPOV: The International Union for the Protection of New Varieties of Plants
WTO: the World Trade Organization

INTRODUCTION

During the 2007 summer, I performed a 2-months-training course in the Centre for Genetic Resources, The Netherlands (CGN). I looked for working in this kind of organisation in order to learn how the conservation of genetic resources is generally organized, and specifically in Europe. In this training, I worked under the responsibility of Mrs Noortje Bas, curator at the CGN. She is in charge of the Crucifers and some Agricultural crops collections. Within the context of my training period, she decided I would work on *Raphanus sativus* species. The work mainly involved selecting plant descriptors and characterising part of CGN's *Raphanus* collection.

But at first, I would like to go into Genetic Resources, the International Genetic Resources Network and the structure, mandate and staff of CGN. Then, I will present my work and I will underline the skills I have acquired during this training period.

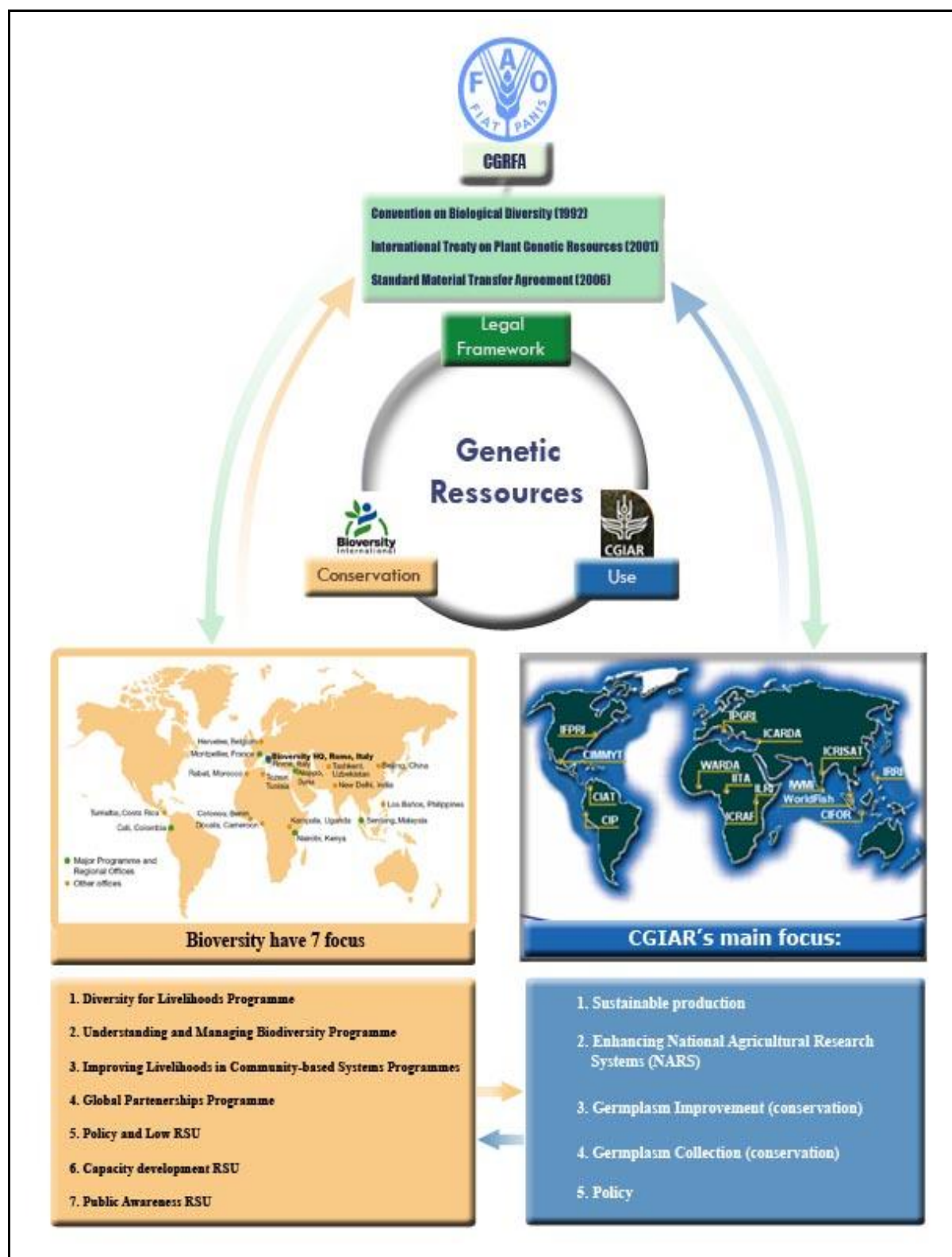


Figure 1: Genetic Resources, a quick overview

1.GENETIC RESOURCES

1.1.Definition

The Convention on Biological Diversity (CBD) defines “genetic resources” as “genetic material of actual or potential value”, while “genetic material” means “any material of plant, animal, microbial or other origin containing functional units of heredity”.

Around this definition three main fields have been developed at the global scale (fig.:1):

- Establishment of a legal framework of Genetic Resources
- Conservation of Genetic Resources
- Use of Genetic Resources

1.2.A historical point of Genetic Resources framework and International Agreements

Use of genetic resources is defined by a strict legal framework: intellectual property rights. The United States were the first to adopt a specific legal framework for the protection of plant varieties, with the Plant Variety Act, which is patent-based. In Europe, policy in this area diverges from the patent model. It materialized in 1961 via the establishment of UPOV, an international agreement that comprised, at the time, about 20 countries. Today, these agreements are covered by a highly binding legal document: the Agreement on Trade-Related Aspects of Intellectual Property Rights (TRIPS). Signed in 1994, at the same time as the World Trade Organization was established, the TRIPS agreements regulate the use of patents.

In parallel to this, the growing focus worldwide on the conservation of genetic diversity has prompted several organizational and legal developments within international bodies:

- 1983: the FAO established the Commission on Genetic Resources for Food and Agriculture (CGRFA), which adopted, also in 1983, the International Undertaking on Plant Genetic Resources for Food and Agriculture;
- 1992: at the Earth Summit in Rio, a set of general principles, known as Agenda 21, were adopted, as well as several legal agreements, in particular the **Convention on Biological Diversity (CBD)**. The main idea of this convention is to give countries ownership of Genetic Resources ;
- 1996: the CGRFA developed a **Global System** where **Global Plan Action (GPA)** for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture is a key element (See attachment 1: Global System managed by CGRFA and the Global Plan Action).

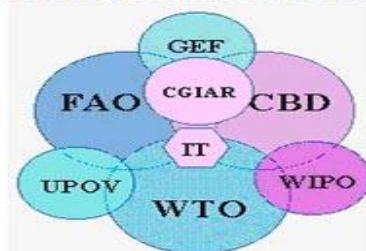
- 2001: the members of the Food and Agriculture Organisation of the United Nations (FAO) adopted the **International Treaty on Plant Genetic Resources for Food and Agriculture** (ITPGRFA). It entered into force 29 June 2004. The objectives of the ITPGRFA are the conservation and sustainable use of plant genetic resources for food and agriculture and the fair and equitable sharing of the benefits arising out of their use. The core of the Treaty is a multilateral system for the facilitation of access and benefit sharing pertaining to 35 central food crops and 29 forage crops, so called Annex I crops. For a better overview of this complex system, fig. 2 tries to position different structures involved with their goal. Details of the main structures will be described above.
- 2006: adoption of the Standard Material Transfer Agreement by the Governing Body of the ITPGRFA for Annex I crops.
- 2007: the Governing Body of the Treaty will amend an interim MTA for use by the Centres for the remaining crops.

At present a legal framework is developed by FAO in order to apply different international treaties like the International Treaty on Plant Genetic Resources for Foods and Agriculture (ITPGRFA) and the Convention on Biological Diversity (CBD). CGRFA facilitates and oversees co-operation between FAO and other relevant intergovernmental and non-governmental bodies, including countries also involved in the Consultative Group on International Agricultural Research (CGIAR).

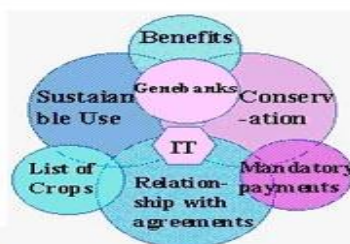
INTERNATIONAL SEED TREATY at "crossroads of agriculture, trade and the environment"



Complex Intergovernmental Governance



...shall not claim any intellectual property...
on PGRFA



According to P. Mulvany (ITDG) and A. Wijeratna (ActionAid),
IPRs and the FAO Seed Treaty (ITPGRFA) (2002)

Figure 2: International Seed treaty organization

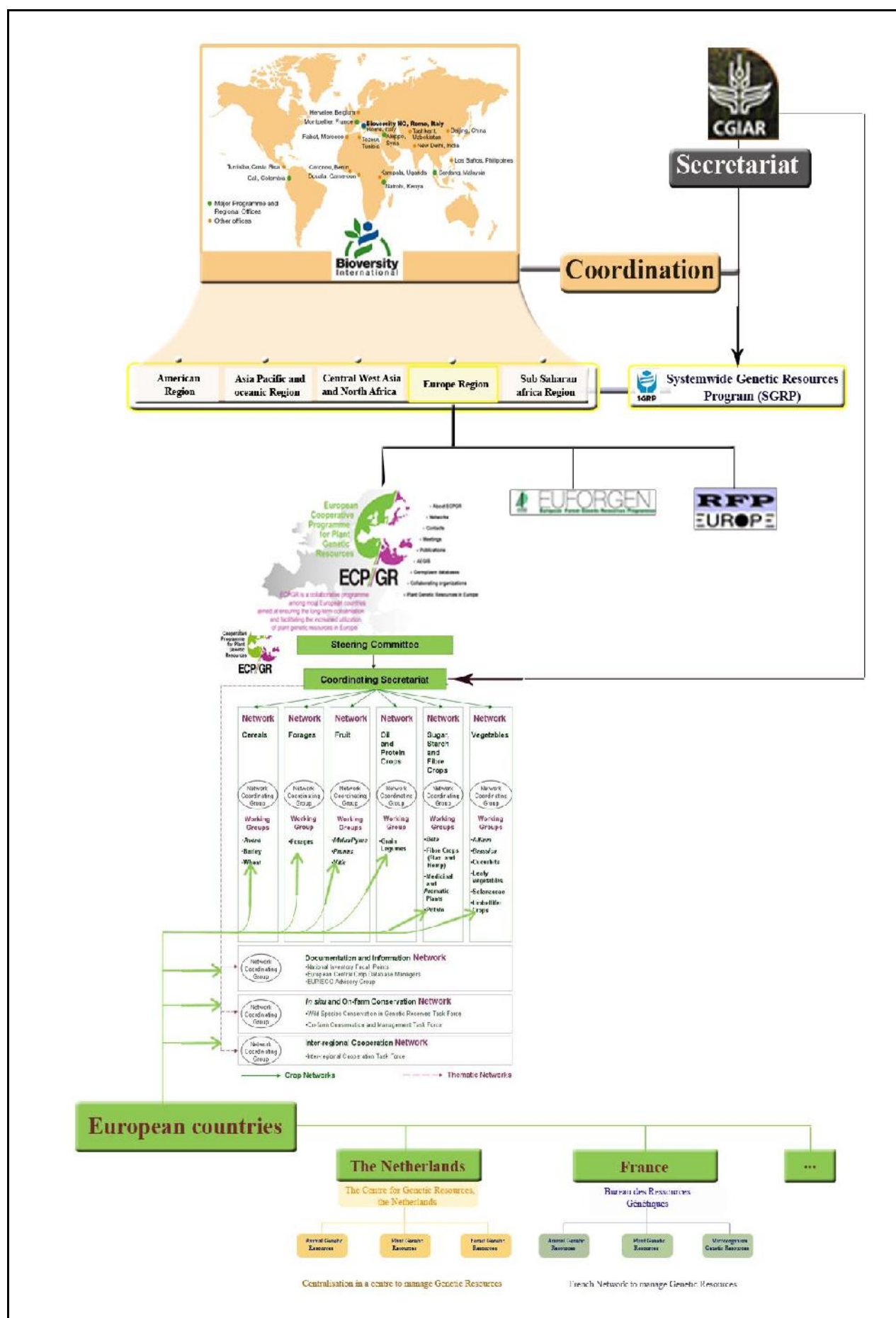


Figure 3: Bioversity International: structure and function

1.3.Genetic Resources conservation

1.3.1.Definition

According to the Convention on Biological Diversity (Article 2, UNEP 1992), two principal kinds of conservation occur:

- **In situ conservation:** The conservation of ecosystems and natural habitats and the maintenance and recovery of viable populations of species in their natural surroundings and, in the case of domesticated or cultivated species, in the surroundings where they have developed their distinctive properties.
- **Ex situ conservation:** The conservation of components of biological diversity outside their natural habitats.

The conservation of plant genetic resources, both "in situ" and "ex situ" is essential for food security and environmental sustainability.

1.3.2.Organisation of Genetic Resources conservation

To avoid a complex view of the Genetic Resources conservation organisation, it is quite right to present Bioversity International like the most important international research organisation dedicated into managing conservation (but also involved in the use of biodiversity). Bioversity International is a merging between the International Plant Genetic Resources Institute (IPGRI) and the International Network for Improvement of BANana and Plantain (INIBAP) in 2006. Many research programmes and networks are coordinated by this organisation. Bioversity International covers a world wide area with 51 governments who have signed and ratified the Bioversity Establishment Agreement. Each part of the world is represented and for the European region, the European cooperative Programme for Plant Genetic Resources (ECPGR) coordinates cooperation in conservation (and use) of PGR. The main goal of European Genetic Resources Network and programmes is to increase homogeneous information available in term of database format and content, seeds transfer facility (For more details on Bioversity International see fig.:3).

It is important to note that Bioversity coordinates an important CGIAR Programme: The CGIAR System-wide Genetic resources Programme (SGRP). SGRP is a mechanism for collective action impacts on the work of individual Centres (genebank), on CGIAR System as a whole, and beyond. Its outputs can be classified as below into five thematic areas:

- policy
- public awareness and representation
- knowledge and information
- strategies and methodologies
- capacity building and institutional support

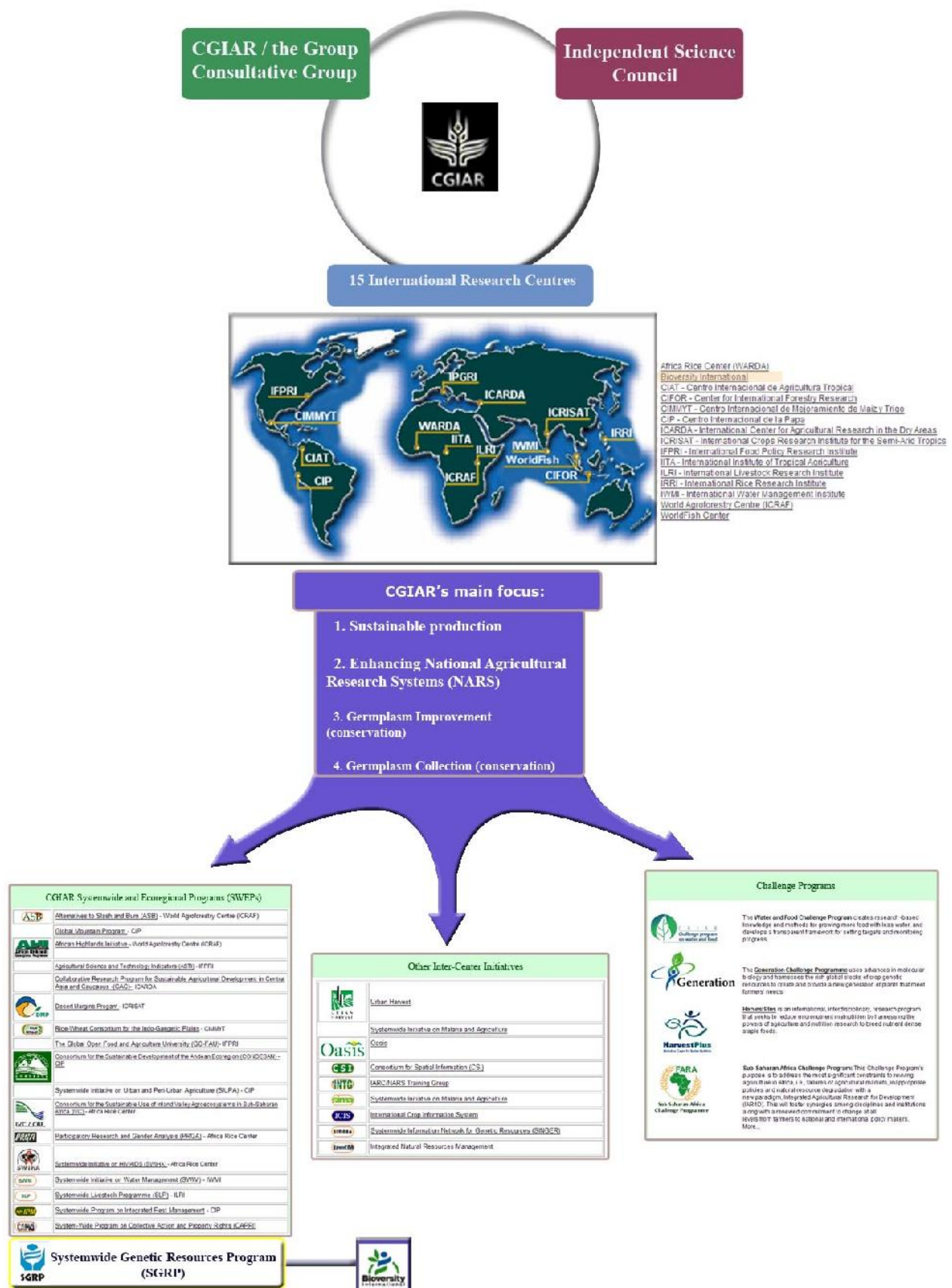


Figure 4: CGIAR: Structure and Function

1.4.Genetic Resources use

Since the Green Revolution in the 40-70, people started to think that Plant Genetic Resources (PGR) should be conserved. Indeed, people accorded that PGR with its huge diversity constitute the main source of interesting traits (tolerance or resistance of pathogens, dry-tolerance, and quantity of other agronomic traits...). For that it seems important to conserve this potential to improve new varieties by introgression.

The CGIAR system, as mentioned in the name, is composed of a Consultative Group working on International Agricultural Research (CGIAR/the Group) but it is also composed of an Independent Science Council. It supports 15 International Agricultural Research Centres (including the International Maize and Wheat Improvement Centre (CIMMYT) and the International Rice Research Institute (IRRI)). It was established in 1971. We have to note that FAO is represented during CGIAR's meetings and councils. The three components of the CGIAR system are interdependent and work for the same goal: to achieve sustainable food security and reduce poverty in developing countries through scientific research and research-related activities in the fields of agriculture, forestry, fisheries, policy and environment. The CGIAR system initiates, coordinates and participates to different programmes quickly presented in the fig.:4: CGIAR: Structure and Function

Now we have a better overview of the genetic resources at the international scale, we could look how the genetic resources are managed and organized in the Netherlands.

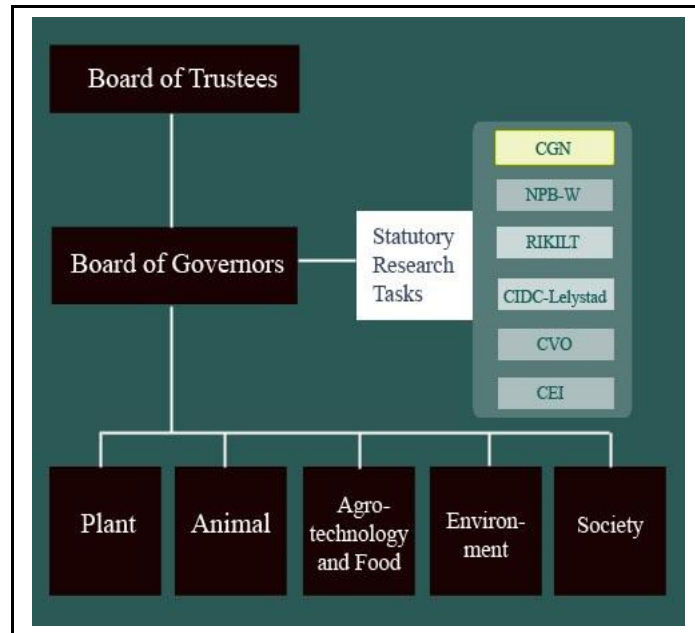


Figure 5: A particular statutory for the CGN and Genetic Resources in the Netherlands
(Scheme from the Wageningen UR publication)



Figure 6: CGN's Environment

1.5.CGN, Netherlands authority mandated to manage Dutch Genetic Resources

1.5.1.CGN place in the Dutch landscape – A particular status

The Wageningen University accommodates the CGN. The Wageningen University and Research Centre (UR) is the umbrella organisation of Wageningen University and DLO Foundation and therefore has access to a wide range of scientific experts and facilities. Part of Wageningen UR supports the Dutch government and the EU in the implementation of rules and regulations to guarantee safe food, healthy animals and a sustainable environment. So, a special status was created: The Statutory Research Task. The Statutory Research Tasks are conducted under the legal responsibility of DLO Foundation. This agreement safeguards the independence, reliability and transparency of the support provided. The reliability of the research results is guaranteed through ISO quality control systems with alternatively internal and external audits. The statutory research tasks are carried out by two institutes and four programme units, among them (see fig.:5: A particular statutory for the CGN and Genetic Resources in the Netherlands)

1.5.2.CGN's Mission

The Centre for Genetic Resources, the Netherlands (CGN) plays a key role between different organizations in the Dutch Genetic Resources landscape but also at the international level (See Fig : 6: CGN's Environment and Fig.: 7: CGN staff and work organisation). CGN conducts, on behalf of the Dutch government, statutory research tasks concerning the genetic diversity and identity of species that are important for agriculture and forestry. Its activities are aimed at the *ex situ* conservation, support for *in situ* conservation, and promotion of the use of genetic resources in support of breeding and research, and as part of our bio-cultural heritage.

Policy support of the Dutch government and international organizations is provided as a complementary activities (we can find the same aims in international research institutes' focus Fig.7: Genetic Resources, a quick overview).

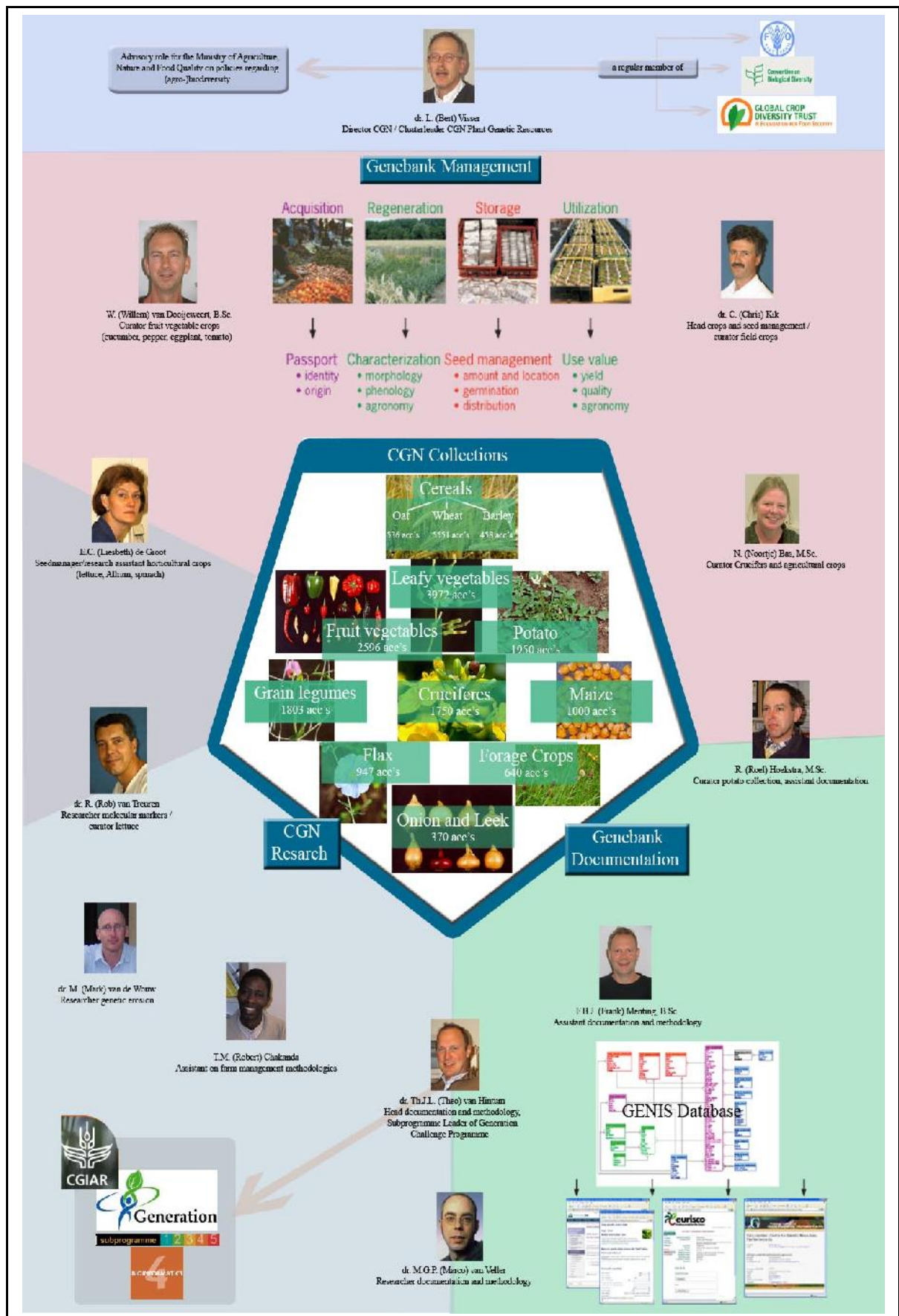


Figure 7: CGN's characters and work organisation

1.5.3. **Three main areas in CGN**

The CGN's programme concerns crops and forest species as well as domestic animals. Dr Bert Visser is the director of CGN and he is also the Cluster leader of Plant Genetic Resources (his other functions are present on the fig.: 7: CGN's characters and work organisation). Sipke Joost Hiemstra and Sven de Vries are the two other persons respectively in charge of Animal Genetic Resources and Forest Genetic Resources.

As I did my trainee in CGN PGR, I will only describe in detail this part of CGN.

A priority for CGN is to improve the quality of the collections but also accessibility to the data (See fig.) . So, the CGN work is organized around three main topics:

1. The first one is interested in collection management (acquisition, regeneration, characterisation, seedstorage)
2. The second one works on documentation (creation and updating of databases for a better utilization of Dutch Genetic Resources Data)
3. The third one brings up theoretical aspects with a research approach (research on methodology of agrobiodiversity management and research also on molecular markers as characterisation tools of genetic diversity).

The different characters involved in each topic are showed on the fig.: 7: CGN's characters and work organisation.

Note:

Probably because of a difference in country size (16 times smaller than France) and a lower diverse agricultural activity, we can observe that the Dutch Genetic Resources System is more simple than in France. To give an order of idea, around 20 000 accessions are included in the Dutch collection versus 160 000 accessions in France. In fact, looking at the French organisation, we can see that in France a supplementary level of network exists : a national level. The French equivalent of the CGN is the Bureau des Ressources Génétiques. But in France, each crop is conserved by a specific INRA centre and BRG only coordinates the network.

The main inconvenience for the French system is to centralize all the data in a same database. Today, different French collections are connected to different international programmes and networks but there is not a French database yet. Consequently there are difficulties of data access.

2. PRACTICAL ACTIVITIES AT CGN

As we have just seen, several tasks are realised at CGN. During my trainee I have had the opportunity to overview a large part of them. So, I already want to thank Mrs Noortje Bas for that.

It is that why I would like to start this part with these different overviews and my different “small jobs”. After this brief part, I will talk you about the main part of the trainee, the work on characterisation of part of CGN’s *Raphanus* collection.

2.1.Different minor tasks performed at CGN during my trainee: a possibility to understand how CGN’s staff works

First, thanks to Ms Noor Bas and Mr Frank Menting, I have understood the organisation and the different functions of GENIS, the relational database developed by CGN under Oracle. They showed me how to use the different tasks facilitated by the software and how to make basic inquiries with SQL language. We discussed different problems concerning the database and more generally genebank management. For instance, the existence of duplication within and between germplasm collections but also matters of communication and information transfers between CGN and users. In fact, when users work on an important number of accessions they could bring rich information to the CGN database but they generally do not transmit this information.

I also have seen wild lettuce, pepper, asparagus, wheat and barley greenhouse regenerations and I have harvested a small part of them. At last, I participated in potato regeneration by helping using a spoon Mr. Roel Hoekstra to pollinate some accessions which have not produced fruit yet.

2.2.My main task: Characterisation of part of CGN’s Radish collection

Among the different tasks of CGN in management of Genetic Resources, during my trainee, I contributed to characterize morphologically a part of the CGN *Raphanus sativus* collection (132 accessions out of 298). This work is a preliminary work to the completed description of the CGN *Raphanus* collection in the next years.

I will introduce my work with a presentation of the radish (*Raphanus sativus*) knowledge. Then, I am going to explain the organisation of the work and will conclude with some results and a discussion.

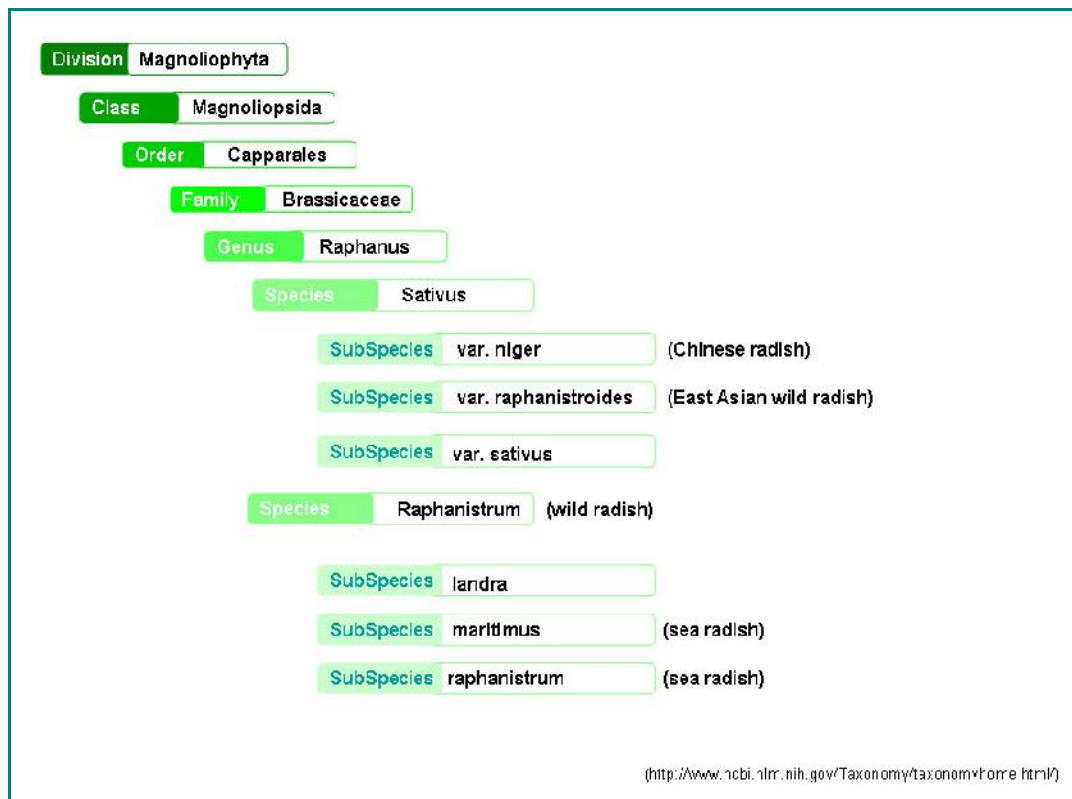


Figure 8: *Raphanus Sp.* Higher taxonomy

2.2.1. The *Raphanus sativus*

Taxonomy: *Raphanus* are dicotyledonous and the Genus *Raphanus* belongs to the *Brassicaceae*'s family. *Raphanus* taxonomy has not settled yet. Today, only 2 species are accepted in Taxonomy Nomenclature: the *Raphanus raphanistrum* L. which is a wild Radish and the *Raphanus sativus* in which is included a wild radish but also contains the cultivated radish (Looks Fig.: 8: *Raphanus Sp.* Higher taxonomy). Other species like *R. aucheri*, *R. boissieri*, *R. caudatus* L. , *R. ericoides*, *R. landra* Mor., *R. maritimus*, *R. microcarpus* (Lange) Willk., *R. niger* ILL., *R. raphanistroides* (Makino) Sinsk., *R. rostratus*, *R. silvestris* Lam., Etc... are described but have not been integrated in taxonomy according to The International Plant Names Index (IPNI) yet. Cultivated Radish is a diploid species with a chromosome number $2n=18$ and small genome size C-Value=0,55pg (The Royal Botanic Gardens Kew 2003). Radish system mating is a strict allogamy (Kaneko and Matsuzawa 1993).

Origin: Origin of *Raphanus sativus* is not yet clear. A thesis supposes it is originated east of the Mediterranean and the Middle East (Simmonds, 1976). An other says, it could come from the Chinese Centre (Rubatzky and Yamaguchi 1997).

Botany: The botanical name *Raphanus* is a Latin form of the Greek for radish. It is said to derive from a phrase meaning 'easily reared'. This is appropriate considering the plant's wide adaptability and its short period from sowing to maturity. The radish has been cultivated for a long time. Inscriptions on the inner walls of pyramids tell us that the niger type was important food in Egypt about 2000 BC.

Use: Radish (*R. sativus cutivar*) in Europe is mainly used as a vegetable but also as an oil or fodder crop. Daikon which is more an Asian Radish is used for roots as vegetable, for leaves in salad or for seeds after sprouting and in soup.

Climatic and soil requirements : The radish is essentially a cool-season crop. It grows best in the spring and autumn and will tolerate light winter frosts. The high temperatures of summer cause the plant to develop small tops, and roots rapidly become pithy and strongly pungent after reaching maturity. For this reason producing quality radishes during midsummer can be difficult. Radishes do best on the lighter, sandy, well-drained soils. This allows for even root development and ease of washing after harvest.

Varieties: There are several types of radish that can be grown. At first, there are outside and greenhouse Radishes. Then, the main differences between them are size, shape and colour of the root. Type denomination is generally given by the breeders and it is quite specific for each country. At CGN, they make the choice to use Dutch types. So, as they use Dutch words, I do not make the full description.

Land preparation: A fine, well-prepared seed bed is important for growing radishes. The application of animal manure or compost, approximately 6 weeks before sowing helps to build up the water-holding capacity of the soil and balance the nutrient supply (Doug Hocking, 1997).

Plant spacing: Seed is sown 10–20 mm deep in rows about 20 cm apart. Plants germinate 4–8 days after sowing. A density of 40–55 plants per metre of row is desirable and early thinning may be required to achieve this. Excessive plant densities will produce irregular-sized, misshapen roots.

Irrigation: To produce a high quality radish, plants must make continuous growth. One way to ensure this is to maintain satisfactory soil moisture throughout the growth of the plant. This will often mean irrigating every day in the warmer months of the year (Doug Hocking, 1997)

Weed control: Because radishes have such a short growing period and are grown only in small areas, weed control is generally not a serious problem. If weeds are a problem, encourage the weed seeds to germinate and control them with a knockdown herbicide prior to planting radishes. It may also be necessary to use inter-row cultivation and hand-weeding during the growth of the crop (Doug Hocking, 1997).

Pests: As a member of the crucifer family, radishes are attacked by the same pests which attack cabbages and cauliflowers. Major pests include cabbage white butterfly, aphids and diamondback moth. Other pests of crucifers will cause damage from time to time. (Doug Hocking, 1997)

Diseases: Because of the short growing period, only a few diseases cause economic losses in radishes. The most important are mildew and black rot. Black rot is a disease caused by a soil-borne fungus. Dark irregular patches develop on the radish root and eventually give the entire root a black colour. Long-rooted cultivars can be severely attacked. The round types may escape infection in infested soil but are not resistant. Radishes are also attacked by white rust. This disease causes raised white pustules on the leaves, stems and flowers. (Doug Hocking, 1997)

Harvesting and marketing: Under normal conditions, harvest commences 6 weeks after planting. (Doug Hocking, 1997)

Breeding: Radish breeding was practiced for centuries, by means of mass or pedigree selection. Since two decades, the production of F1 hybrids using cytoplasmic male sterility has widely replaced fairly simple breeding methods based on morphological traits (Yamane *et al.*, 2005) to generate genetically uniform varieties. The uniformity of a variety is becoming a high priority goal in radish breeding. Most breeding work is aimed at further adaptation to different growing conditions, improved resistance to *Peronospora parasitica* and *Albugo candida* (Muminović, 2005), specific market preferences, and improved marketing conditions.

Genetic Resources Management: The CGN *Raphanus* Collection consists of 299 accessions; radish cultivars come namely from Europe (*R. sativus*) (123 acc's) and giant radish cultivars come from Asia and Germany (70 acc's) but also 43 accessions of Fodder radish. Of 63 accessions the group is unknown (See fig.:9: CGN's Radish collection). Then, a large part of the radish collection is of unknown type. Consequently, the main objective was to identify what kind of material exists in CGN's collection. That is why we make a characterisation's work on a part of the collection.

So, to response to this query, we identified 3 main goals of the work I contributed to do:

- To describe a part of *Raphanus* collection in order to file the CGN GENIS Database.
- To select minimum descriptors necessary to distinguish the different types
- To find information on Internet and with experts (researchers, public and private breeders, retired people with knowledge of old varieties...) in order to document accession's characteristics if possible.

At last, I would like to try to add information on the collection exploiting the accession description data, particularly using statistical approach.

I participated in this work during a period of 2 months from the beginning of the descriptors' selection to the harvesting of a large part of the sowing accessions.

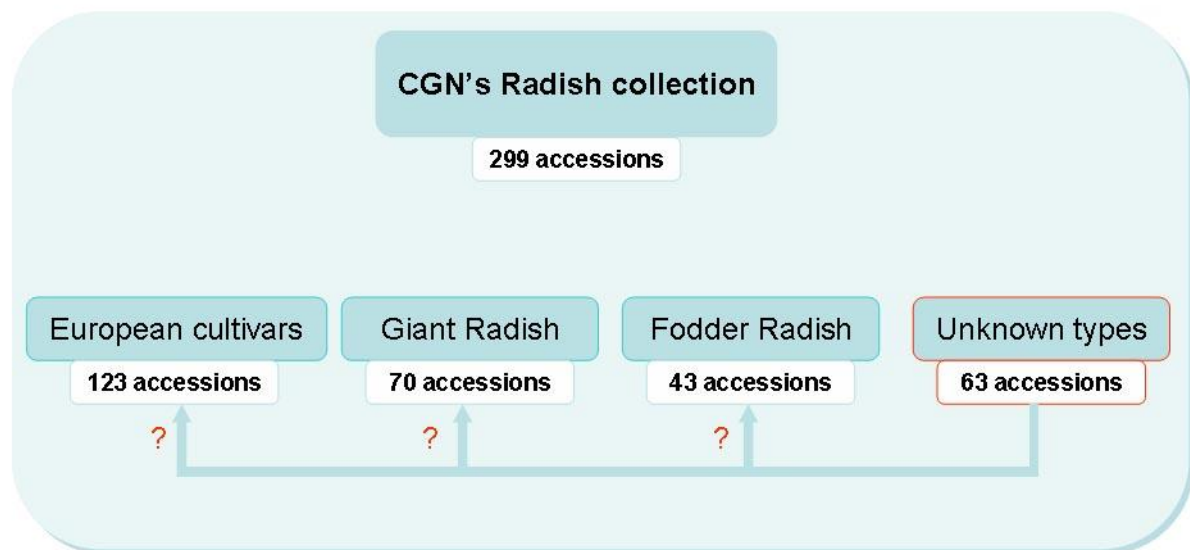


Figure 9: CGN's Radish collection

Radish's morphological characterization : The Process

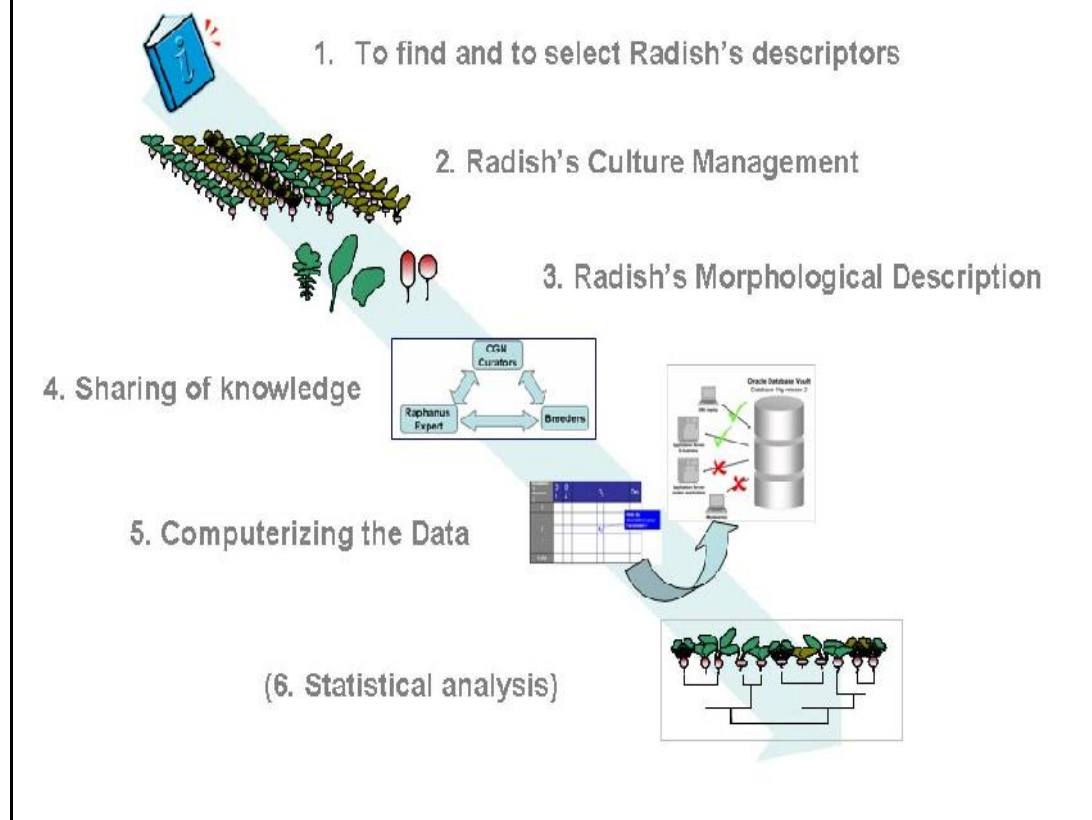


Figure 10: Process of the Radish's morphological characterization

2.2.2. How work was organized? (fig.:10: Process of the Radish's morphological characterization)

Initial material and data:

As it was explain in genetic resource part about CGN's Radish collection, a large amount of group is yet unknown. 132 accessions were studied. 13 of them are standards used to facilitate the description. About the 119 others, 49 were group Radish, 4 were group Giant Radish and 2 were group Mougri. So, 64 accessions were unkown group. The main work of this study was to the majority of unknown group.

1. *Raphanus* Descriptors

At first, we had to choose which descriptors we were going to use. For that, we mainly used the "Guidelines for the conduct of tests for distinctness, uniformity and stability" published by the International Union for the Protection of New Varieties of Plants (UPOV – 1999), and a publication by the International Board for Plant Genetic Resources (IPBPGR – 1990) called "Descriptors for *Brassica* and *Raphanus*". Minor information was extracted from research articles about Radish and other websites. All of this information was collected in an Excel file with traits and methods we intended to use. Concerning methods, nomenclature used in CGN is a discrete numerical scoring (for instance to the leaf's trait, methods could be: 1=small leaf, 2=intermediate leaf, 3=large leaf). The number and the different methods and traits were not defined before starting the experiment. According to the facility of description, if the descriptor is relevant or not, methods could be changed or certain traits could be added or deleted.

2. *Raphanus* Culture Management

When I came early in July, N. Bas had already selected accessions to be characterised.

A sowing scheme was made:

Normal radish

- length of one lea: 1,50m
- inter-plant distance: 3 cm
- inter-lea distance: 12,5cm

Giant radish:

- length of one lea: 1,50m
- inter-plant distance: 5 cm
- Inter-lea distance: 25cm

Because the characterisation was qualitative no replication was done to limit experimentation's cost. Standards were grown on the border to avoid border-effect. Seeds were sown with anti-slug to avoid damage to young plant eating. One week and half after the sowing, we thinned out extra plants. Then, gardeners took care of weed control and provided water if necessary. Mildew treatment was carried out once.

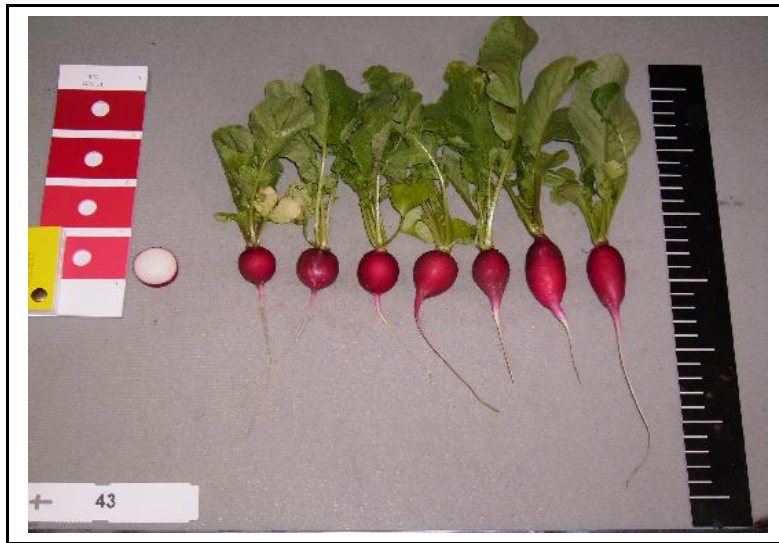


Figure 11 : Example of photo setup

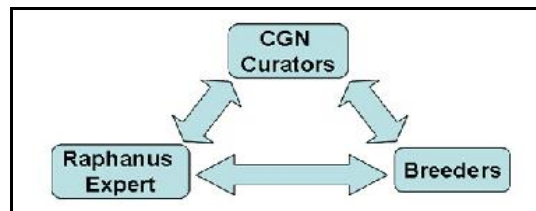


Figure 12: CGN's network to optimize knowledge about radish

3. *Raphanus* Description

Characterisation started when the majority of accessions was ripe for harvesting. The principal difficulty met during this work was the heterogeneity. Two different sources of heterogeneity are possible:

- the first one can be due to a soil heterogeneity
- the second one can be due to genetic heterogeneity intra-accession

In fact, with this kind of material, it is possible that more variability can be expected between two plants of one accession than two plants of two different accessions. Actually, in a same accession, you can observe several scores for a same trait. So, it is not really useful to give a global score. In order to consider this fact, CGN uses a system for scoring heterogeneous population based on proportion of each score. But as it was quite long and hard to define a score with this system, we decided to give a mark by accession corresponding to the main character. In the same way, when we found that some descriptors were not easy to use we decided to skip them. On the other hand, if we observed other distinctions between accessions we tried to find a new suitable descriptor.

To describe hypocotyls we pulled out 5 to 10 plants for accession during harvest time. Then we put them down in a special place where there always was the same light. We also used a ruler and a standardised colour palette (using the Royal Horticultural Society colour chart) in order to be able to compare different photos (accessions). We organized a setup to try to always take photos in same conditions (see an example fig.: 11). So, we could describe roots *a posteriori*.

4. Sharing of knowledge (Fig.:12: CGN's network to optimize knowledge about radish)

Like in other genetic resources centres, N. Bas works with Dutch breeders and related persons for several reasons:

- to contribute to increase the number of regeneration of crops per year
- also to learn more information about specific crops
- to make CGN material known to the breeders for future utilizations

Several breeders and researchers were invited and came to see the characterisation plot:

- Marianne de Leeuw and Joop Koenes, involved in Plant Variety Research (NAK tuinbouw)
- Rene Deneer, Breeder (Rijkzwaan)
- Joep van Balen and Marco Binnendijk, Senior Breeders (Enza zaden)
- Oene Dolstra, Researcher, who developed Xbrassicaraphanus accessions and had other material in working collection; part of this is now in CGN collection (Plant Research Institute)
- Hans Bongers, Breeder (BEJO seeds)
- Edwin Wilkes, Breeder interested in fodder radish (Joorden's Zaden)
- Nico van Marrewijk, he was involved in plant variety research for several horticultural crops, before he retired

Much information rises up from these meetings, particularly about the different types of radish (based on type of culture (outside or forced), period of culture (Winter, Spring Raddish...), and more information on the different types used by the Dutch Breeders.

5. Computerizing the Data

As the results are to be entered into GENIS database, we had to computerise our data in Excel files in format to be easily included by the CGN's documentation staff. In order to avoid making too many mistakes when we are recopying data from a field sheet to an Excel sheet, we used a palmtop. Then we updated the data after each scoring time. Finally, we generated a small Access Database with these different tables:

- Passport data: containing all the data known by accession (donor, origin, year, taxonomy data as it is possible...). Specialists' information collected was filed in this table.
- Description: containing all the descriptors used with the scores for each accession
- Photos: containing all the hypertext links of the photos taken per accession

The main goal of this database is to join all the data concerning this experiment together to have a better overview of the data and to allow statistical analysis. Secondly, in this way photos for characterisation could be used making a query which joins the description table with the photo table to make scoring more easily.

6. Statistic analysis

Question: Could we determine the group of unknown radish only with early morphological traits?

Among the 132 accessions sown, 76 were European radish, growing in approximately four weeks. 20 descriptors were used to describe them. The other accessions had not made large root yet in this period or never and produced more leaves. For the statistic analysis only 12 descriptors were used communally on the 132 accessions.

The kind of data obtained with this experiment, allowed to do Factorial Analysis because we work on multidimensional data. In fact, each accession is a statistical individual characterized by the description pattern. With our set of data, we decided to use the different descriptors as discreet variables and we made a Multiple Component Analysis (MCA) connected to an Automatic Hierarchical Classification (AHC). The software used was Spad. Groups were used as illustrated data. This work permits to order the different accessions on the base of morphological traits. Then, we could observe if the different groups are joined together or mixed. We could also conclude if there were contradictions between breeders' information and statistic results. More details and analysis can be found in the result part.

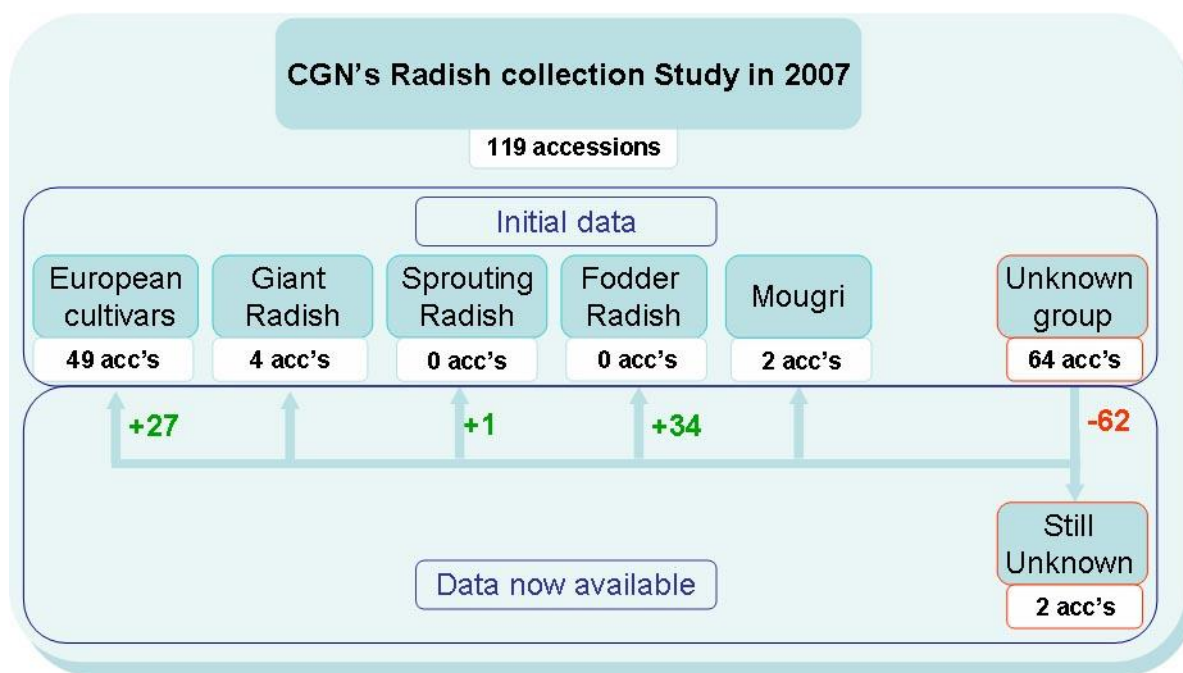


Figure 13: Evolution of available data of part of CGN's Radish collection studied

2.3.Results - Discussion

2.3.1.Main results

Matrix of results is proposed in attachment 2. The two first columns identified accessions on the base of the field number and the accession number. Then, 23 next columns represent different traits scored. Details of the method used are located in attachment 3: Traits and Methods selected for this experiment and selection for a next experiment. The two last columns are updated groups and updated types. That corresponds to the new information soon available in GENIS database concerning radish collection. Detail is presented in fig. 13: Evolution of available data about part of CGN's Radish collection studied

At the end of this work it is important to go into three main points:

- a heterogeneous material and uncontrolled environmental conditions
- non-appropriated guidelines to describe the material studied
- increasing of knowledge about part of CGN's radish collection

At the end of this work, we easily can understand the different problems met by curators. Basically, the global heterogeneity observed per accession is a result of genotypes heterogeneity inside accessions but also soil heterogeneity. The heterogeneity is a real limiting factor in the description but the lack of initial knowledge (documentation) on the seeds material received by other centres or collections is also a limiting fact. With this experiment, because genetic approach with molecular markers is too expensive, I could observe that the main information source of the curator is based on morphological observations and on relation with her network of breeders.

To characterise morphologically the material we finally used 20 traits for the Small Radish and between 15 and 20 traits for the Fodder and Black Radish. Ms Bas might use smaller number of traits the next time than we used for this experiment. But as the description of all the accessions has not been completed, we could not decide what will be traits she will use in the future for characterise the rest of the collection.

Unfortunately for this experiment, only one guidebook for the conduct of tests for distinctness, uniformity and stability dedicated to the Small Radish was used. Specific guidebook for the Fodder Radish and for the Black Radish was found to late to be used for this description. Table I shows which traits and methods were used, and which could be removed or added according the two new guidebooks.

Nevertheless, thanks to Breeders, the majority of the sown radishes are known in term of group. Especially concerning the European Radishes, the type is also known in many cases (see attachment 2).

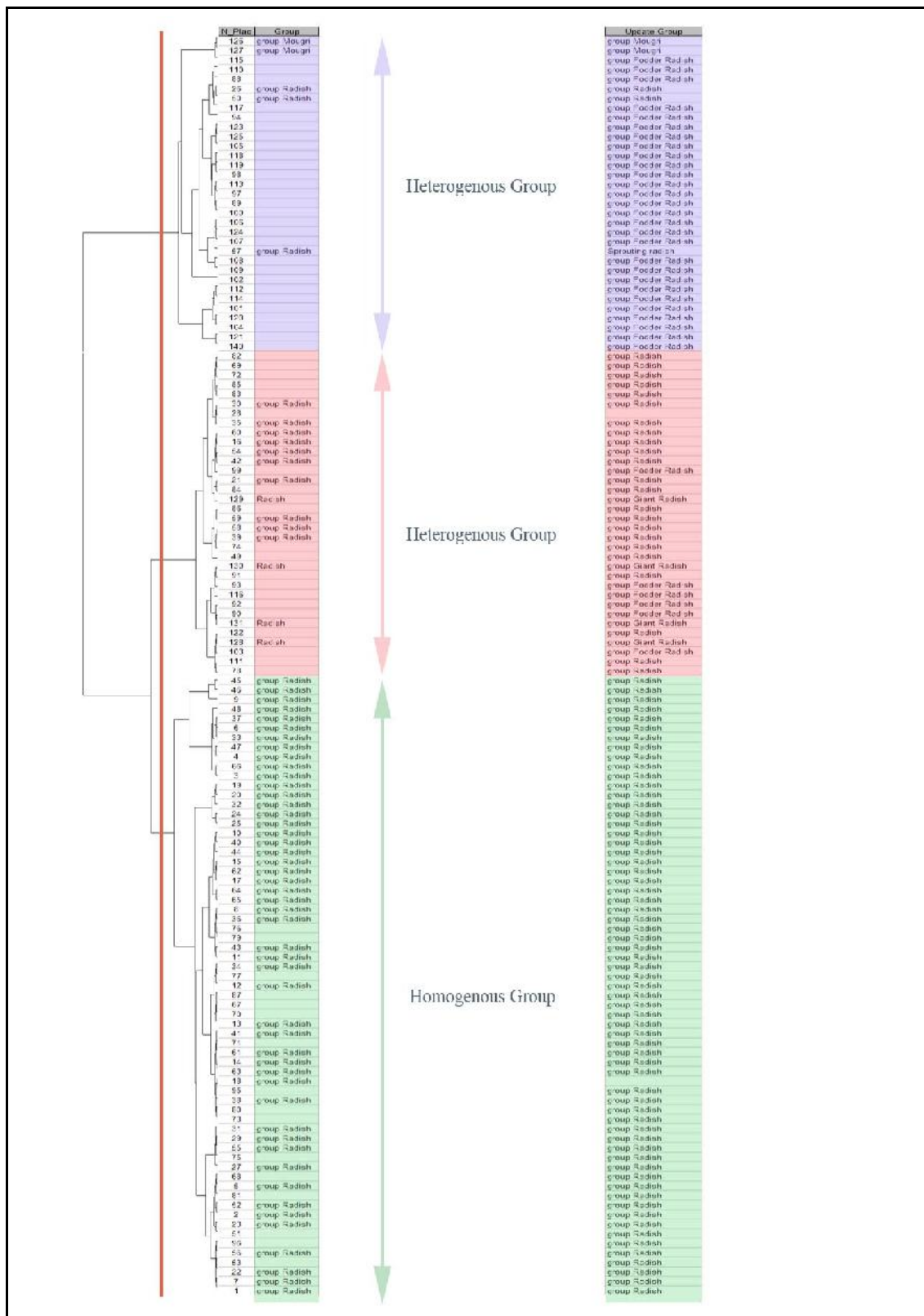


Figure 14: Radish Dendrogramme based on morphological description (12 descriptors). Confrontation between initial knowledge about radish group and the last update

2.3.2. Statistical results

The 132 accessions were classified according to the Automatic Hierarchical Classification based on the 10 first Principal Components (Fig.:14: Radish Dendrogramme based on morphological description). A cutting was done to define three main classes (red line). Comparing to the initial data available about groups and the new data now available (sharing of knowledge), we can note that the two of the three classes are heterogeneous because they contain different groups (for instance, group Radish and group Fodder Radish in class 1). Even though the third class contain only group Radish (European cultivar).

Consequently, this method can not be used in the future to predict during the early step when groups are present. An explanation of this phenomenon could be a not enough strong analysis due to not enough descriptors to make discrimination between different groups. An other hypothesis could be that we need more information about the different traits studied. Actually, discussing with T. van Hintum about this problem of group characterisation, he explained me that biometric data could help to weight some descriptors and could modify dendrogramme pattern.

CONCLUSION - PERSPECTIVES

To conclude this report, I could say many things have been seen during this trainee. I could touch on the International Genetic Resources Network organisation mainly thanks to Mr. Theo van Hintum with his explanations and a consistent bibliographical work. It was really important for me to understand this because I am really interested in it and it was a really good opportunity for me to meet this person there.

Then, I could approach one side of *Ex-situ* Conservation of Genetic Resources. Actually, I could participate to the characterisation of part of CGN's Radish collection. This work upraises different problems of heterogeneity but also permits to upraise questions about the content of the description. Indeed, the content of the database should correspond to the users expectation. Curators need to be aware of the type of users targeted (researchers, NGO, National/International Breeder?) and what decisions do they have to take. For instance, during the trainee Mrs. Noor Bas decided to describe the accessions on the base of root type in Dutch because it is used more in Dutch breeding companies. So, that would be useful for them but is it a best way?

Of course it is a relevant question in genebank management. Quality of genetic resources depends of germplasm quality in genebanks but also of quality of documentation in databases. I think it is one of the main considerations in Genetic Resources Management.

The biggest international programmes are developing international databases but it is just the beginning. 6 000 000 accessions are being stored worldwide in a total of 1 308 genebanks (FAO Report on State of the conservation of Genetic Resources (1996)). Today, only around 600 000 accessions are held by CGIAR genebank network (available in SINGER database). We can expect this number of accessions to increase in the future. Moreover, many of international programmes also use plant genetic resources, especially in the developing countries. So for the future, we can expect a better coordination with the time between the different characters of Genetic Resources to increase the efficiency of the PGR conservation at the international scale.

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FAO - CGRFA -The Commission on Genetic Resources: FAO Commission on Genetic Resources for Food and Agriculture (Last look : 01/08/07):

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IPGRI-ICRA Project: ICRA provides professional training in interdisciplinary team research in agriculture (Last look : 01/08/07):

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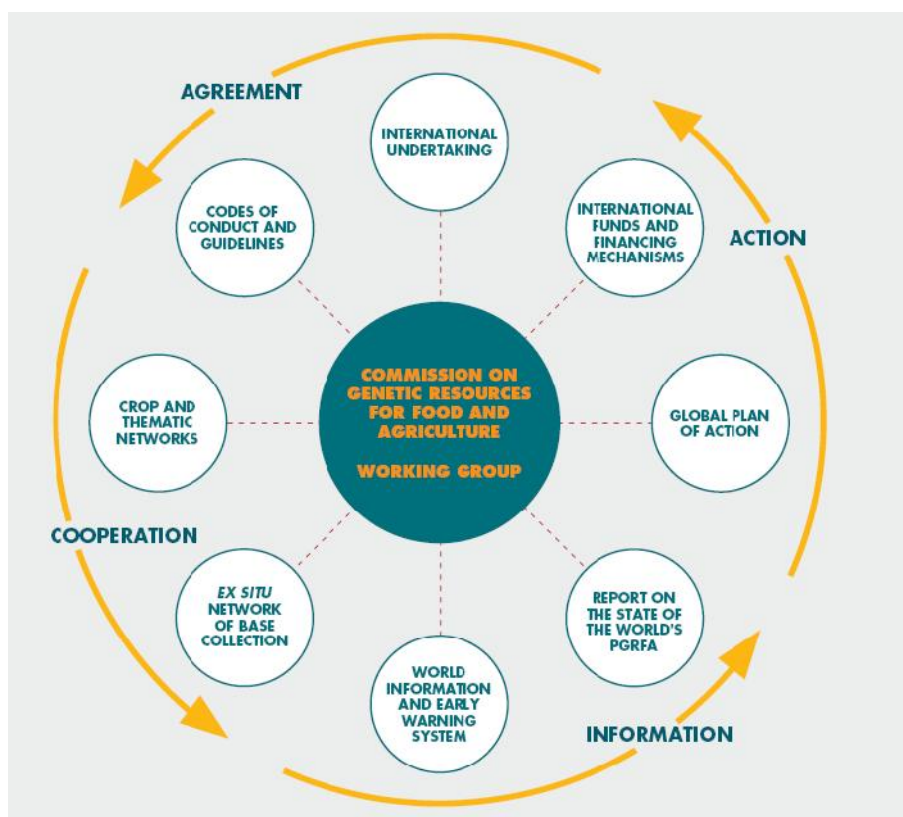
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ATTACHMENTS

Attachment 1: Global System managed by CGRFA and the Global Plan Action



<p><i>In Situ</i> Conservation and Development</p> <ol style="list-style-type: none"> 1. Surveying and inventorying plant genetic resources for food and agriculture 2. Supporting on-farm management and improvement of plant genetic resources for food and agriculture 3. Assisting farmers in disaster situations to restore agricultural systems 4. Promoting <i>in situ</i> conservation of wild crop relatives and wild plants for food production 	<p>Utilization of Plant Genetic Resources</p> <ol style="list-style-type: none"> 9. Expanding the characterization, evaluation and number of core collections to facilitate the use of genetic resources 10. Increasing genetic enhancement and base-broadening efforts 11. Promoting sustainable agriculture through diversification of crop production and broader diversity in crops 12. Promoting development and commercialization of under-utilised crops and species 13. Supporting seed production and distribution 14. Developing new markets for local varieties and "diversity-rich" products
<p><i>Ex Situ</i> Conservation</p> <ol style="list-style-type: none"> 5. Sustaining existing <i>ex situ</i> collections 6. Regenerating threatened <i>ex situ</i> accessions 7. Supporting planned and targeted collecting of plant genetic resources for food and agriculture 8. Expanding <i>ex situ</i> conservation activities 	<p>Institutions and Capacity Building</p> <ol style="list-style-type: none"> 15. Building strong national programmes 16. Promoting networks for plant genetic resources for food and agriculture 17. Constructing comprehensive information systems for plant genetic resources for food and agriculture 18. Developing monitoring and early warning systems for loss of plant genetic resources for food and agriculture 19. Expanding and improving education and training 20. Promoting public awareness of the value of plant genetic resources for food and agriculture conservation and use

Attachment 2: Matrix of results

[illegible]

Attachment 3: Traits and Methods selected for this experiment and selection for a next experiment

[illegible]

Conserved trait/method at the next experiment

New trait/method at the next experiment

Deleted trait/method at the next experiment