An exploration of monitoring and modelling agrobiodiversity

From indicator development towards modelling biodiversity in agricultural systems on the sub-specific level

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Preface

This report summarizes the main results of a study on ‘Genetic indicators for the GLOBIO model’. This research was part of the project ‘Widening the analytical scope of GLOBIO3 – Modelling Global Biodiversity’ (BO-10-003-01). The study was carried out by the Centre of Genetic Resources, the Netherlands (CGN) in close cooperation with the Netherlands Environmental Assessment Agency (PBL) and was funded by the Research Programme International Cooperation and International Agreements of the Ministry of Agriculture, Food Quality and Nature Management of the Netherlands.

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Executive summary

On a global level both for crop and livestock species there has been a general tendency towards uniformity in the culture of crops and livestock production systems. Local varieties are replaced by a small number of highly productive – non native – ones, dominating the world's agriculture. The loss of diversity in cultivated varieties and livestock breeds also has been referred to as genetic erosion and may form a hazard for sustainable agricultural production or food security, agricultural products and income. It is for these threats that it is important to have an idea on the status of genetic biodiversity (agrobiodiversity) within a particular agricultural production system in the past, present and future.

Consequently, the CBD (Convention on Biological Diversity) aims at establishing indicators that monitor status and trends in agrobiodiversity. The FAO Commission on Genetic Resources for Food and Agriculture (CGRFA) also included development of indicators in its Multi Year Program of Work. After their development and (international) acceptance they can be used to assess the state, trends, causes and possible consequences of changes. Also, they can be applied to examine or model effects of different policy measures.

The aim of this project is to contribute to the development of a few key agrobiodiversity indicators drawing on and coherent with the work under the CBD, FAO and in the European program Streamlining European Biodiversity Indicators (SEBI). Analysis and modelling of the relationships between pressure factors and agrobiodiversity will enable assessments of past, present and future trends and their consequences on various human functions such as food security, poverty, environmental quality, landscape and wild biodiversity. The project was carried out by the Centre of Genetic Resources, the Netherlands (CGN) in close cooperation with the Netherlands Environmental Assessment Agency (PBL) and was funded by the Research Programme International Cooperation and International Agreements of the Ministry of Agriculture, Food Quality and Nature Management of the Netherlands.

First a review of potential indicators for monitoring agrobiodiversity from literature has been made. CBD, OECD, FAO, etc. proposed various indicators. More recently, Eaton, *et al.* (2006) evaluated these indicators and proposed new ones. Based on these studies a shortlist was selected in the context of our research.

A few indicators were tested with data to facilitate the choice. Within the framework of GLOBIO, it is important that the indicators are widely acceptable and are coherent with work already carried out by international fora, that they are *in situ* measures and that they are measurable, clearly understandable, sound, and applicable for modelling on a global scale. In two case studies the 'Share of breeding female population between introduced and native livestock breeds' (EEA, 2007a,b) and the 'Share of major varieties in total production' (FAO, 2002) were applied with available data from the Netherlands and Germany. The chosen species -cattle, wheat and potato- represent major agricultural species. In addition, the suggested Mean Variety Abundance (MVA) indicator (Hiemstra, 2007), analogous to the Mean Species Abundance (MSA) indicator for wild biodiversity, was included in the calculations and compared with the other indicators.

The case studies showed that the 'Share of breeding female population between introduced and native livestock breeds' (EEA, 2007a,b) and the 'Share of major crop varieties in total production' (FAO, 2002) suit the topic of research of GLOBIO. Although they are slightly different, they both describe the loss of agrobiodiversity at the intraspecific level. For pragmatic reasons (low data availability) the 'Share of major crop varieties in total production' should be used in combination with the 'Number of crop varieties available' indicator. Additionally, this richness indicator shows the balance between landraces and registered varieties in a country and in this way also reflects the stage of agricultural intensification in that country. Together they give a first insight in the process of genetic diversity loss and can be used as an 'early warning system'.

The 'Share of breeding female population between introduced and native livestock breeds' (SEBI) is a suitable indicator for GLOBIO as it clearly indicates the replacement of local by non-native (introduced) breeds, by which

global diversity is likely to decrease. Compared to the MVA indicator, it scores better regarding data gathering, broad acceptance and analytical soundness.

A conceptual framework for intra specific agrobiodiversity was drawn up, also describing the causal factors. Subsequently a literature search was undertaken to investigate the relevance of the causal factors suggested. Both global factors and processes, related to demographic, socio-economic and technological development, environmental impact and factors playing a role at the microeconomic level were discussed. It became clear that market integration is a key factor. It is expected that with an increased market integration the diversity will decrease. Agrobiodiversity will be high in traditional farming systems, less integrated in the market, and lowest in the commercial farming systems. A little integration in the market, may lead to higher diversity at the farm compared to subsistence farming. This was in particular demonstrated in literature for crop farmers. A number of internal factors such as larger farms, higher diversity in soils/environments, age, better education, experience may give farmers the possibility to cultivate a combination of varieties suitable for self-consumption and market production.

The study so far should be seen as a first feasibility study regarding the development of a ‘genetic module’ in GLOBIO. The relationship between drivers and genetic resources is a complex one. The first step would be to better understand this relationship. As starting point for modelling, we think that agrobiodiversity is a function of: environmental and climatic heterogeneity, diversity of farmer types/production systems including extent of market integration, trade intensity, infrastructure and a number of societal and political factors.

1. Introduction

1.1 Background

Agrobiodiversity results from the interaction between the abiotic and biotic environment, genetic resources and the land and water resource management practices applied by culturally diverse people in agriculture. These systems produce food, fodder, fibre, fuel, ornamentals and other goods.

On a global level the last 5-6 decennia there has been a general tendency towards uniformity in crops and livestock. This uniformity not only concerns the holding of a single crop or livestock species on a farm but also loss of diversity of the breeds and varieties. This loss at the intraspecific level also has been referred to as genetic erosion and was the reason to start several activities on the conservation of genetic resources (both *in situ* and *ex situ*) since the 1960s.

Sufficient agrobiodiversity (*i.e.* intraspecific) is a main condition for obtaining agricultural goods and thus for sustainable agriculture. Furthermore, agrobiodiversity is important to be able to adapt to future changes in production systems, climate or market conditions. Agricultural production is not only important for food for the farmer's own household and income. On a wider scale it applies on countries and also on the world community. Both goods for own consumption and income contribute to the improvement of human well-being for the household, local communities and national economies. Therefore, it is important to have an idea on the status of agrobiodiversity in the past, present and future.

1.2 Definition of agrobiodiversity

In the Convention on Biological Diversity (CBD, 1992), three levels of biodiversity have been defined:

- Ecosystem diversity (of ecosystems)
- Species diversity (between species)
- Genetic diversity (within species)

Agrobiodiversity, sometimes also called agricultural biodiversity, 'encompasses the variety and variability of animals, plants and micro-organisms which are necessary to sustain key functions of the agro ecosystem, its structure and processes for, and in support of, food production and food security' (FAO, 1999).

Agrobiodiversity comprises biodiversity both at the inter- and intraspecific level of crops, livestock, forests, fish and micro-organisms that are used in production systems for food and agriculture. Also, wild biodiversity can be found in agro ecosystems and therefore makes part of agrobiodiversity. These different levels (ecosystem, interspecific and intraspecific) that are important in agrobiodiversity are illustrated in Figure 1.

In agro ecosystems part of the wild biodiversity is native to the area where the agricultural activities have been started, but another part of this wild biodiversity has been induced by the agricultural activities (*e.g.* meadow birds) and should be considered culture dependent. Yet another level of agrobiodiversity is the presence of pests, pathogens and invasive species. Often, these species make part of the native or culture dependent wild biodiversity, or they may have been introduced by man to control e.g. pests and thereby themselves became pests. Increase in the abundance of these undesired species may result in loss of income for the farmer, hazards on health for animals or people or disturbance of wild biodiversity and landscape.

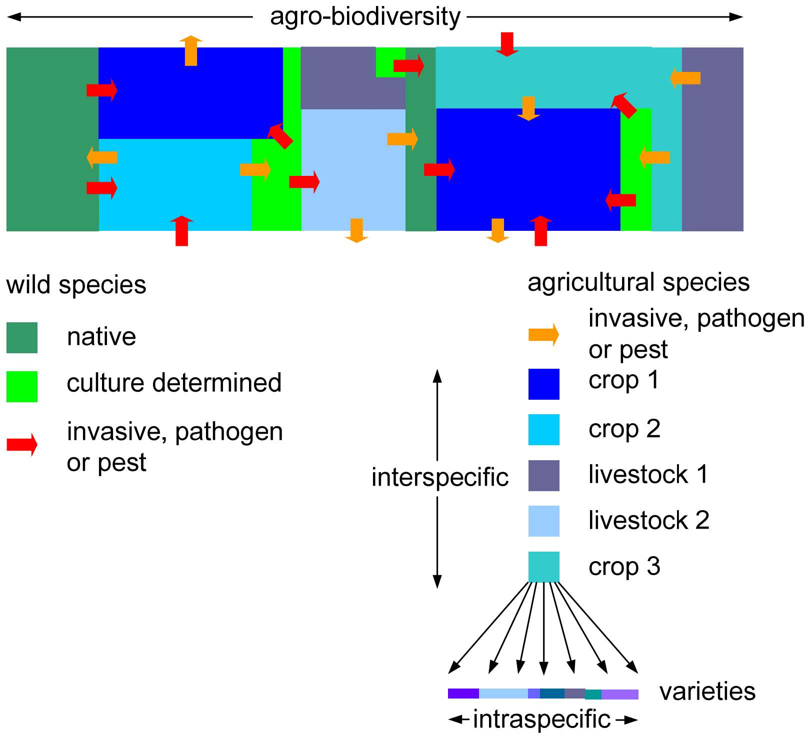


Figure 1. Different levels of agrobiodiversity.

With respect to biodiversity in agricultural species two levels can be distinguished. At the interspecific level, different farming systems exist with different combinations of crop, livestock, forest, fish or micro-organism species. Diversity within these farming systems may be low (*e.g.* monoculture cropping systems or intensive animal husbandry) to high (*e.g.* multi-cropping systems, herding of multiple livestock species or mixed livestock-crop farming systems). At the intraspecific level different numbers of varieties or breeds may be cultivated per crop or livestock species, resulting (dependent on the diversity within and between the varieties or breeds) in low to high (genetic) diversity.

This study focusses on agrobiodiversity, especially the diversity at the intraspecific level.

1.3 Impacts by agrobiodiversity

Agrobiodiversity has various impacts on the safety and security of food and agricultural production, (micro) climate, water and soil management, culture and several sociological and economic conditions of people. In a sustainable agricultural production system all of these impacts have been optimized with a minimum amount of negative side effects.

Food safety highly depends on the production conditions. Besides these also the quality of food is important. Quality depends on how food is processed and stored and whether the products themselves are not very perishable. The latter property relates to breeds and varieties.

Food security has various aspects, such as yield and the vulnerability of the agricultural production system for disturbance by (a)biotic factors. Varieties or breeds can differ considerably in productivity or resistance/tolerance towards *e.g.* diseases, pests and drought or fodder shortage. Holding of different varieties and breeds can be important for responding to environmental variation that might affect the production. Thus a higher degree of agrobiodiversity on the farm, may ensure a more robust production and better economic position (subsistence) for the farmer. (Thrupp, 2000).

Agrobiodiversity affects the (micro) climate and environment. Farming systems differ in intensity and composition of crops or livestock. The same holds for the disturbance of wild biodiversity and landscape by different farming systems. At first sight, these impacts relate to the interspecific level of agrobiodiversity. However, varieties and breeds may require, to a different extent, management and inputs affecting climate, water, soil, landscape and wild biodiversity differently.

With respect to wild biodiversity two different kinds of impact can be distinguished. Farming practices affect wild biodiversity and vice versa. Wild species may compete with cultivated species or cultivated species may invade wild habitat.

Agrobiodiversity also provides other ecosystem services on farm, such as pollination, pest and disease management and water retention (Hajjar, *et al.*, 2008).

Socio-economic impacts of agrobiodiversity can be very broad and can differ from culture-specific farming systems that disappear due to intensification of agriculture to dependence of farmers on seeds, fertilizer, fodder and other inputs. Especially, the application of hybrid varieties (*e.g.* in the cultivation of corn) and inclusion of killer genes in recent breeding programs for new varieties has largely increased the dependency of farmers on seed supplying companies, making them economically more vulnerable.

1.4 Aim of project

From the CBD (Convention on Biological Diversity) there is a need for indicators that monitor status and trends in agrobiodiversity at the genetic level. The FAO Commission on Genetic Resources for Food and Agriculture (CGRFA) also included development of indicators in its Multi Year Program of Work. After development and (international) acceptance on these biodiversity indicators they can be used to assess causes of changes in the cultivation of varieties and husbandry of livestock breeds.

The objective of this project is to contribute to the development of a number of key biodiversity indicators for crops and livestock in agriculture drawing on and coherent with the work under the CBD, FAO and in the European program Streamlining European Biodiversity Indicators (SEBI), with the ultimate aim to use these indicators in modelling global trends and possible changes in agrobiodiversity. Thereby, the anticipated indicators should measure the status of agrobiodiversity on the genetic level (*i.e.* at the intra-specific level, see also Figure 1) and should reflect the trend towards uniformity and associated genetic erosion process in both crops and livestock on a regional or global scale. Such indicators should further play a central role in modelling agrobiodiversity. Therefore, the selected indicators need to be incorporated in a model, *e.g*. the IMAGE/GLOBIO model developed by the Netherlands Environmental Assessment Agency (PBL). Within the GLOBIO model changes in wild biodiversity in the past, present and future are assessed on a global scale. By incorporating selected agrobiodiversity indicators in a ‘genetic module’ within GLOBIO past, present and future trends in agrobiodiversity can be assessed and the effects of different policy measurements can be modelled. Furthermore, it will allow us to analyze the impact of agrobiodiversity on various human functions and values such as food security, poverty, environmental quality, water availability, landscape and wild biodiversity.

Modelling agrobiodiversity requires insight in relationships between pressures/drivers and agrobiodiversity. In this first feasibility study, these relationships are further explored.

1.5 Outline of this report

Following the introduction, chapter two of this report gives a review of potential indicators that are described in literature and which are proposed to be used for monitoring genetic diversity in crops and livestock species. The chapter also discusses which aspects of diversity an ideal indicator should measure in relation to the research focus. For evaluation of the potential indicators criteria are needed. An overview of criteria is given, which are used by different organizations for selecting suitable (sets) of indicators. In the third chapter a number of indicators out of the shortlist mentioned in chapter 2 are further explored and tested with data. In two case studies the various indicators are applied for a livestock species and two crop species with available data from the Netherlands and Germany. The chosen species (cattle, wheat and potato) represent the main species used in agriculture in the Netherlands. In addition, the suggested Mean Variety Abundance (MVA) indicator (Hiemstra, 2007), analogous to the Mean Species Abundance (MSA) for wild biodiversity, was included in the calculations and compared with the other indicators. In Chapter 4 a conceptual framework for intraspecific agrobiodiversity is presented, describing the factors driving the genetic diversity. The fifth chapter describes the results of a literature search undertaken to see if the level of genetic diversity can be understood as the resultant of the main pressure factors that are described in the conceptual frame work. In more detail it focuses on the major global drivers of change for agrobiodiversity and shows us which factors determine the level of diversity managed on the farm. The final chapter (6) is concerned with suggestions on further research on modelling agrobiodiversity.

2. Indicators of intraspecific agrobiodiversity

In this chapter regular used criteria for selecting indicators are mentioned. A review is given of agrobiodiversity indicators from literature. Out of this long list a short list is selected, which best suits our topic of research. The focus is agrobiodiversity at the intraspecific level.

2.1 Criteria for selection of agrobiodiversity indicators

Monitoring of biodiversity is possible by the measurement of one or more suitable indicators over time. If well chosen, these suitable indicators can serve four basic functions(CBD, 2003a):

- Simplification
  Not a set of various different parameters needs to be measured, but a single indicator
- Quantification
  The value of the chosen indicator represents a value for biodiversity that can be compared with other values for the same indicator.
- Standardization
  With indicators which have been agreed upon, the status of biodiversity can be represented in a standardized way.
- Communication
  Indicators can be used in the communication between policy makers, researchers or other people when working on the monitoring of the status of biodiversity.

For the selection of suitable indicators several criteria have been identified by participants of the ninth meeting of the Subsidiary Body on Scientific, Technical and Technological Advice of the CBD (CBD, 2003a):

- Policy relevance and meaningfulness
  Indicators should send a clear message and provide information at a level appropriate for policy and management decision-making by assessing changes in the status of biodiversity (or pressures, responses, use or capacity), related to baselines and agreed policy targets if possible.
- Biodiversity relevance
  Indicators should address key properties of biodiversity or related issues as pressures, state, impacts and responses.
- Scientifically soundness
  Indicators must be based on clearly defined, verifiable and scientifically acceptable data, which are collected using standard methods with known accuracy and precision, or based on traditional knowledge that has been validated in an appropriate way.
- Broad acceptance
  The power of an indicator depends on its broad acceptance. Involvement of the policy makers, and major stakeholders and experts in the development of an indicator is therefore crucial.
- Affordable monitoring
  Indicators should be, measurable in an accurate and affordable way and part of a sustainable monitoring system, using determinable baselines and targets for the assessment of improvements and declines.
- Affordable modeling
  Information on cause-effect relationships should be achievable and quantifiable, in order to link pressure, state and response indicators. These relation models enable scenario analyses and are the basis of an ecosystem approach.
- Sensitiveness to trends
  Indicators should be sensitive to show trends, and where possible, permit distinction between human-induced and natural changes. Indicators should thus be able to detect changes in systems in time frames and on the scales that are relevant to the decisions, but also be robust so that measuring errors does not affect the interpretation. It is important to detect changes before it is too late to correct the problems being detected.

Often, not a single indicator is sufficient for the measurement of a policy relevant issue, but rather a set of indicators need to be developed for monitoring. For the selection of indicators in these sets, besides the criteria listed above, also the following additional criteria are recognized (CBD, 2003a):

- Representativeness
  The set of indicators should provide a representative picture of the pressures, biodiversity state, responses, uses and capacity (coverage).
- Small number of indicators in the set
  The smaller the total number of indicators in a set, the more communicable they are to policy makers and the public. Also, for a smaller number of indicators in a set, the costs are lower. The same holds for the sensitiveness of indicators to errors (robustness).
- Aggregation and flexibility
  Indicators should be designed in a manner that facilitates aggregation at a range of scales for different purposes.

Recently, Eaton, *et al.* (2006a) evaluated (sets of) agrobiodiversity indicators according to four main criteria which have been identified by the OECD Joint working Party on Agriculture and Environment in 2003 (OECD, 2003):

- Policy relevance
  The indicators need to deal with issues across states or relevant to the CBD and other agreements.
- Analytical soundness
  The indicators must be well founded based on international consensus, scientifically valid and also comparable across states.
- Measurability
  Data to compose the indicators need to be available now, but also in the near future.
- Interpretation
  The indicators should be clearly understandable by policy decision makers, stakeholders as well as the general public.

What follows from the conclusions in Eaton, *et al.* (2006a) is that not a single set of indicators scores better than the others according to all four criteria.

2.2 Agrobiodiversity at the intraspecific level

Typically, agrobiodiversity is measured on the sub-species (intraspecific) level. Crops can consist of a single (*e.g. Solanum tuberosum* in case of potato) or a few (*e.g. Triticum aestivum* and *T. durum* in case of wheat) species for which several varieties are cultivated for the production of food or other agricultural products. The same principle holds for livestock, where several breeds of one species are held for labour, land management or the production of meat, dairy, fibre/textiles, fertilizer or other animal products.

For sustainable agricultural production several aspects are of importance:

- Diversity within the varieties or breeds. Whereas some varieties are propagated clonally (*e.g.* potato) and therefore represent a small spectrum of genetic diversity, others represent a much wider spectrum of genetic diversity (*e.g.* highly variable varieties of Rhodes grass, a perennial forage grass; Ubi, *et al.*, 2003). Land varieties or landraces are the result of selection by local farmers and are adapted to the local circumstances. In general, the diversity within land varieties is larger than the within diversity of more formally bred cultivars (the latter being the result of breeding activities by companies, institutes or non-governmental organizations). Livestock breeds are only propagated sexually. The within-breed diversity is mostly larger in animal breeds compared to plant varieties and (maintaining opportunities for) within-breed selection is relatively more important in livestock compared to crops.
- Diversity between the varieties or breeds. The general trend since the industrial revolution in agriculture is that the diversity between varieties or breeds in crops and animals becomes smaller. Crops or breeds with a smaller genetic basis become more vulnerable to diseases, inbreeding depression or other hazards. For this reason, in the second half of last century several (gene bank) collections for the conservation of (threatened)

varieties and breeds have been started.
Information on diversity between crop varieties or livestock breeds can be obtained from parental information. Varieties lists for crops may give information on the crosses that have been made to obtain the varieties. (see Table 1 in Appendix A for wheat example). Comparing this parental information for the wheat varieties on the lists of 1950, 1980 and 2004 shows that in the more recent years some varieties are based upon the same parents. As a result, it can be expected that the diversity between wheat varieties in recent years is smaller than around 1950.

- Genetic resources collections (*i.e.* gene banks and *in situ* collections). Several varieties and breeds are being conserved in collections outside the agricultural production systems (*ex situ*). These are available as a source for desired properties for new varieties or breeds. Also, the collections may function as a safeguarding of older varieties or breeds in case they have become extinct. Especially for crops old varieties are replaced by new varieties within a few years. In Figure 2 this has been illustrated for wheat. The figure shows that most wheat varieties are deleted from the variety list within five years.

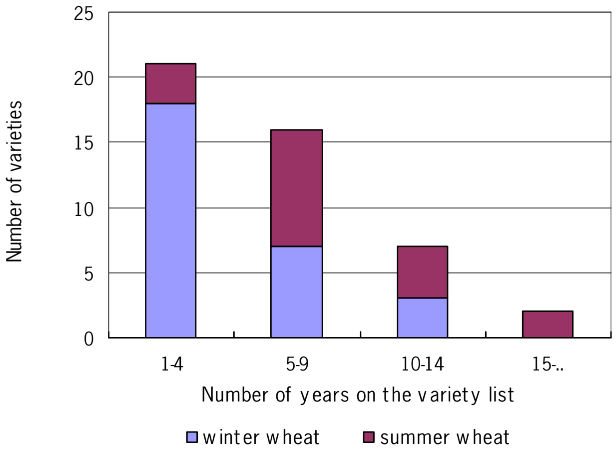


Figure 2. Number of years that wheat varieties are on the variety list.

- Besides gene bank collections also wild relatives of crop or livestock species may function as a source for desired properties. Especially crop wild relatives are frequently used by plant breeders in their programs in order to acquire resistance against pathogens and pests in new cultivars. Although the cross ability over species borders makes application of related wild species in animal breeding more complex, new techniques (*e.g.* genetic modification) more and more overcome these barriers.
- Abundance of varieties or breeds. Ideally, equal amounts of genetically mutually distinct varieties or breeds are held in a particular area. However, this is seldom the case. Most farms hold only one or a few varieties, making them vulnerable for diseases and other hazards.
- Access to genetic diversity. Access to genetic resources for new varieties and breeds may be hampered due to various reasons. Multilateral agreements on genetic resources within the framework of (*e.g.*) the CBD, the International Treaty on Plant Genetic Resources for Food and Agriculture (IT PGRFA) and CITES may lead to equal sharing of benefits, but may also block the access. Further, breeder's rights as well as intellectual property rights and patents can function as a limiting factor on the access.
- Generation time. Besides access also time is needed for developing new varieties and breeds. New varieties and breeds need to be propagated to obtain sufficient starting material. Development time as well as propagation time are important in case of recovery of an agricultural production system after a hazard.

For assessment of agrobiodiversity at the intraspecific level, in general, three main aspects are relevant:

- Richness in varieties or breeds
- Abundance of varieties or breeds
- Similarities between varieties or breeds

Ideally, an indicator measures agrobiodiversity with respect to all of these three aspects. The number of varieties or breeds gives an idea on the richness of varieties or breeds in a region or production system.
The number of varieties or breeds depends on breeding activities, the number of varieties or breeds that are held and the existence of collections.
Equal shares of different varieties or breeds in the total production contribute to the heterogeneity. However, in most cases, often the production is determined by only one or a few dominant varieties or breeds. Uniformity may be alarming if the dominance of a few varieties or breeds applies globally.

Besides richness and dominant share (abundance) also the similarity (genetic overlap) between varieties or breeds is relevant. In case several varieties are used agrobiodiversity seems okay, but if they are very similar, diversity at the genetic level may still be quite low. Although important, this aspect is difficult to use in an indicator as, generally, studies on (genetic) similarities between varieties or breeds are lacking. Breeding companies are very reluctant in making parental information publically available. For these reasons of measurability, it seems recommendable to exclude indicators on similarity. Consequently, indicators based upon the first two aspects rather measure the potential than the actual intraspecific diversity.

2.3 Proposed sets of agrobiodiversity indicators in literature

For the monitoring of biodiversity in crops and livestock on the intraspecific (*i.e.* genetic) level, various indicators have been proposed in different concerted actions. Appendix II gives a listing of indicators that have been proposed earlier (by CBD, OECD, FAO, etc.). Also, in a recent study by Eaton, *et al.* (2006a) agrobiodiversity diversity have been evaluated including existing indicators (Wetterich, 2003; CBD, 2003b; OEDC, 2003, see also Appendix II) and newly proposed indicators. In their study they proposed two sets of indicators: an 'extended' set and a 'restricted' set. However, their conclusion was that no single set of indicators scores better than others taking into account policy relevance, soundness, measurability and interpretation. The extended set builds on contributions of Wetterich (2003) and OECD (2003) and particular scores better in terms of policy relevance and analytical soundness, but lower for measurability. A restricted set was selected (as a subset of the extended set) as an attempt to offer a set of indicators that scores better for data availability and interpretation by a broader audience than the extended set (Table 1).

Table 1. 'Restricted' set of indicators (Eaton, et al. 2006,a,b; Hiemstra, 2007).

Livestock	Crops
• Number of breeding males of breeds characteristic for landscape/production environments important for biodiversity and characteristic for a region or country	• Area of varieties characteristic for landscapes/production environments important for biodiversity and characteristic for a region or country
• Share of high input/output breeds in total production	• Area of low production/high biodiversity agriculture
• Number of breeding organizations of high production breeds	• Percentage of seeds originating on farm of three major (high production) varieties
• Number of breeding males in gene bank(s) of characteristic (low production) breeds	• Number of characteristic (low production) varieties stored in gene bank

3. Options for appropriate agrobiodiversity indicators for GLOBIO

In this chapter a few indicators are further explored with data to facilitate the choice of agrobiodiversity indicators for monitoring and modelling within GLOBIO. As starting point for livestock the ‘restricted’ set of indicators (Eaton, *et al.*, 2006a, b; Hiemstra, 2007) is taken, which includes:

a. Number of breeding males/individuals of breeds characteristic for landscapes/production environments important for biodiversity and characteristic for a region or country
b. Share of high input/output breeds in total production
c. Number of breeding organizations of high production breeds
d. Number of breeding males of characteristic (low production) breed in gene banks

This set of indicators suits the topic of research, but they should also meet the CBD criteria. As a set it meets the requirement towards representativeness: indicator a. and b. reflect the state of genetic diversity in livestock and the trend towards homogenization (or genetic uniformity in production systems); indicator c. can be used as a pressure indicator, while indicator d. is related to responses as it covers conservation measures. Also the criterium ‘a low number of indicators in the set’ is fulfilled.

For monitoring and modelling the state of agrobiodiversity indicators a. and b. are considered both relevant. However, indicator a. needs to be further elaborated and questions such as should all breeds on a global scale be covered or should only a sample of representative breeds in each country be included still need to be answered. Moreover, the application of this indicator may be hindered by data availability.

Indicator b. within this ‘restricted’ set, reflects the homogenization and associated genetic erosion process and is relevant for our modelling purposes, but is not widely accepted. Therefore we propose to substitute this indicator for the more or less similar indicator ‘Share of breeding female population between introduced and native livestock breeds’ (EEA, 2007a,b). It is developed within the European program Streamlining European Biodiversity Indicators (SEBI) with the aim to have insight in the status of genetic diversity of European livestock breeds.

Similar to the one’s described above for livestock, a set of indicators can be given for diversity in crops :

a. Area of varieties characteristic for landscapes/production environments important for biodiversity and characteristic for a region or country (Eaton, *et al.*, 2006a).
b. Share of major varieties (top 5 or top 10) in total area for production (CBD, 2003b, FAO, 2002).
c. Number of breeding companies/institutes per crop (Wetterich, 2003).
d. Number of characteristic (low production) varieties stored in *ex situ* collections (Eaton, *et al.*, 2006a).

Here the same arguments apply. Indicator a. and b. are both relevant for monitoring and modelling the state of genetic diversity in crops. Indicator a. needs to be further elaborated, e.g. the term ‘characteristic’ needs to be defined. For crops also preference is given to indicators that are widely accepted. For plant genetic resources an indicator like the one for livestock is not yet further developed by the SEBI workgroup, but this will probably follow indicators suggested by the CBD, FAO. Therefore the ‘Share of major varieties in total area for production’ has been selected.

Besides the above mentioned indicators, an alternative indicator for agrobiodiversity (not mentioned in the appendix) is the Mean Variety/Breed Abundance (MVA) as suggested by Hiemstra (2007) and ten Brink (personal communication). MVA could be developed analogous to the Mean Species Abundance (MSA) for wild biodiversity which has been developed at the Netherlands Environmental Assessment Agency within the framework of monitoring and modelling wild biodiversity (Alkemade, *et al.*, 2006). A MVA measures both richness in the number of crop varieties or livestock breeds and the abundance of them in the total agricultural production. For example, a MVA for breeds shows the value of the average native breeds’ abundance relative to the original abundance of the breed ('baseline situation'). As a baseline 1950 or 'pre-industrial' has been suggested. Such a MVA relates very much to the indicators mentioned above under a. for crops and livestock.

In the following section (3.1) the indicators b. are further explored with data. In addition, the MVA is further explored with data to test it's suitability as an alternative for these 'Share' indicators. For crops, the 'Number of varieties' is also added, as we know that data on acreages might be difficult to gather (Table 2.). Calculations are performed with cattle data from the Netherlands and Germany and wheat and potato data from the Netherlands.

Table 2. Agrobiodiversity indicators used in the case studies.

	Indicator	Description
Livestock	I. Share of livestock breeds	Share of breeding females population between introduced and native breeds (EEA, 2007a,b)
	II. MVA	Mean variety/breed abundance (Hiemstra, 2007)
Crops	I. Number of crop varieties	Total number of crop varieties per crop that are available to farmers in the locality/country/world (FAO, 2002)
	II. Share of major varieties in total production	% of total acreage of top 5 varieties (FAO, 2002)
	III. MVA	Mean variety/breed abundance (Hiemstra, 2007)

Indicators based upon number (richness) and share (abundance) rather measure the potential than the actual (here referred to as the diversity at DNA level) genetic diversity. The indicators in Table 2 measure the potential genetic diversity, but they might over- or underestimate the actual genetic diversity. It is possible that loss of genetic diversity occurs within breeds even if the number of breeds and their shares remain the same. The same applies to varieties, even if the number or shares may be the same in the course of time, the actual genetic diversity may be less if varieties become more related to each other. In many crop species the within-variety diversity can be neglected nowadays. Modern registered varieties are homogeneous and uniform, because they have to fulfil the 'DUS' (Distinct, Uniform and Stable) criteria for Plant Breeder's Rights (PBR) registration. Only landraces or non-hybrid varieties of allogamous species are expected to be genetically heterogeneous populations. A literature research has been undertaken to have insight in any change in actual genetic diversity over time of in the three species: cattle, wheat and potato. The actual genetic diversity can be measured by pedigree analysis or direct measures using molecular data. Subsequently, it can be evaluated if the trend given by the indicators coincides with the trend for changes in the actual genetic diversity in the three species.

GLOBIO

The GLOBIO (Global Methodology for Mapping Human Impacts on the Biosphere) consortium aims to develop a global model for exploring the impact of environmental change on biodiversity. It is designed to support United Nations Environment Programme (UNEP) activities relating to environmental assessment and early warning. The model is designed to produce policy relevant indicators for use in assessments, scenario exercises and exploration of the impact of policy options. The main indicator produced is the mean abundance of the original species belonging to an ecosystem (MSA): that is, the abundance of native wildlife. The latest GLOBIO3 model has been developed to assess human-induced changes in biodiversity, in the past, present, and future at regional and global scales. Drivers considered are land cover change, land-use intensity, fragmentation, climate change, atmospheric nitrogen deposition and infrastructure development. (See also www.globio.info, Alkemade, *et al.*, 2009)

3.1 Case studies

Below the indicators in Table 2 are illustrated with data. The calculations will in particular give us insight in the measurability and sensitivity to trends. Within the SEBI project (EEA, 2007b) the 'Share of livestock breeds' was already calculated for different years (1995, 2000, 2005) for three countries. However, it would be interesting to investigate whether they are able to detect changes over a longer time scale or larger geographic scale. Here we have chosen to calculate the indicators over a longer time period for the Netherlands, because given the time frame of the project it was easiest to get data from this country. Three species were chosen for the case studies: cattle, wheat and potato. For cattle also an additional data set from Germany was used. Wheat and potato were chosen because they are the two most important agricultural crops in the Netherlands and cattle as it is a representative livestock species for land-based agriculture in the Netherlands.

3.1.1 Cattle

I. Share of livestock breeds (EEA, 2007a,b)

This indicator shows the share of breeding females population between introduced (i.e. non-native) and native breeds. It is developed by the SEBI 2010 expert group of EEA to have insight in the status of genetic diversity of European livestock breeds and is based on a number of sub-indicators:

- Total number of breeding females per breed
- Total number of breeding females of native breeds
- Total number of breeds

It addresses the individual country responsibility to maintain the local genetic diversity, as a contribution to the global genetic diversity. As a result, it does not give insight in the total amount of diversity present in a country. Neither, this indicator gives insight in the population sizes of the individual native breeds and the trends in changes in population's sizes. For the development of population sizes of individual native breeds based on their status of endangerment an extra indicator is needed, for instance a 'red list-like' index.

Whether a breed is considered native or not has been defined by the country in this study. In general a breed is considered native to the country when it has been bred for many generations within a country and when a country recognizes a particular responsibility for the protection/conservation of the breed.

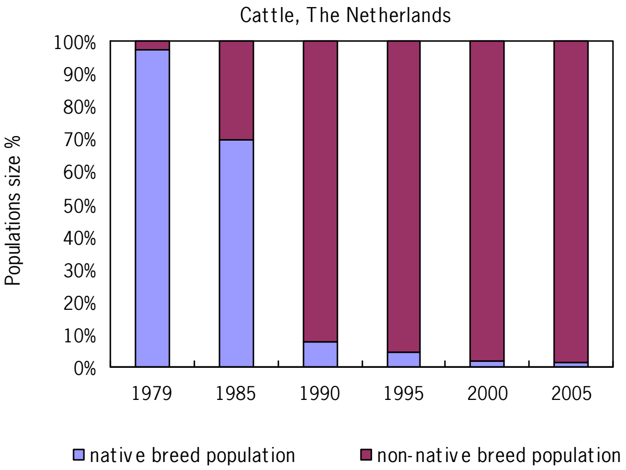


Figure 3. *Share of breeding females population between introduced and native breeds in the Netherlands (Data source: NRS/ASG).*

The indicator was calculated for the Netherlands and Germany (Figure 3 and 4a). Data on the Dutch cattle breeds was derived from the Dutch Cattle Syndicate (NRS). An estimation of the number of breeding females was made, based on data of herd book-registered female calves (pure-bred) born per year. The number of breeding females was estimated roughly twice the number of born female calves. Calculations for the German cattle diversity were based on 'herd book-registered breeding female animals' (Data source TGRDEU/ADR, data before 1997 not complete).

Figure 3 shows us that the proportion of introduced breeds is high in the Netherlands since 1990 and has hardly changed since 2000. The introduced breeding females population is dominated by mainly one breed, Holstein Friesian, which makes up about 70% of the total breeding populations in 2005. Since the past 30 years hardly any new breeds have been introduced. Also in Germany the Holstein Friesian is dominating the breeding females population (64% in 2005), however this is not shown in the indicator. In Germany the Holstein Friesian breed is recognized as a 'native' breed. If it is categorized as an 'introduced' breed, the proportion of introduced breeds increases enormously (Figure 4b) and consequently the indicator shows the same trend to homogenization as in the Netherlands. However, absolute figures for proportion of introduced breeds between the Netherlands and Germany differ considerably.

Figure 4. Share of breeding females population between introduced and native breeds in Germany: a) Holstein Friesian categorized as native breed, b) Holstein Friesian categorized as an 'introduced' breed (Data source: TGRDEU/ADR).

II. Mean Variety/Breed Abundance (MVA)

Analogous to MSA for wild biodiversity within GLOBIO (Alkemade, *et al.*, 2006), a MVA for agrobiodiversity can be calculated. The MSA represents the average remaining abundance of native species relative to the natural 'undisturbed' situation. Comparable with MSA, a MVA for breeds shows the value of the average native breeds' abundance relative to the original abundance of the breed ('baseline situation'). It shows the trend in native genetic diversity for breeds, but does not capture the diversity of high production breeds. A baseline could be 1950 ('pre-intensification times') or pre-industrial times. After 1950 a period started in which an increase in production and intensification occurred in combination with commercial breeding and technological innovations (artificial insemination). Before this date it is assumed that only local breeds were used. A baseline set in pre-industrial times (1850) as proposed by the CBD would be the traditional agricultural state before industrialization of agricultural practices started (CBD, 2003a).

In Figure 5 the MVA is calculated for four representative cattle breeds for the Netherlands: Blaarkop (G); Fries Hollands roodbont (FrRb), Fries Hollands zwartbont (FH), Meuse-Rhine-Yssel (MRY including Brandrood (BRR)). The MVA has declined considerably since 1985 and shows the same trend of declining native genetic diversity as the SEBI indicator. The MVA was calculated with 1950 as baseline. For female breeding populations of cattle breeds in the Netherlands the first available data point is 1979 (estimated on herd book-registered female calves, data source NRS). For 1950 a historical reference value of the population sizes was reconstructed. Therefore an estimation of the population sizes of the four native breeds in 1950 had to be made. The size of the total cattle population in 1950 was estimated by extrapolating the data of the population size between 1979 and 2005. Subsequently the sizes of populations of the individual breeds were estimated based on their ratios in 1979. This is a very rough estimate. Actually, for estimating these population sizes in the past also historical data and expert judgments should be taken into account as several factors (e.g. some breeds declined rapidly around 1950 due to cattle regulations) may have influenced the breed's demography's and ratio's between them. In this illustration a breed is considered representative for the Netherlands if it had a substantial population size in the past (in 1979). For this reason, the native breeds Lakenvelder and Witrik, which were already marginal in 1979, have not been taken into account. Because of lack of reliable data no MVA was calculated for cattle breeds in Germany.

Apart from calculating a MVA for all native breeds, it can also be calculated for a particular production environment. In Figure 5b the MVA is calculated for native cattle breeds specific for extensive farming systems (in terms of input/output). Here the native breed MRY is excluded as it is not specific for extensive farming but also used in intensive systems.

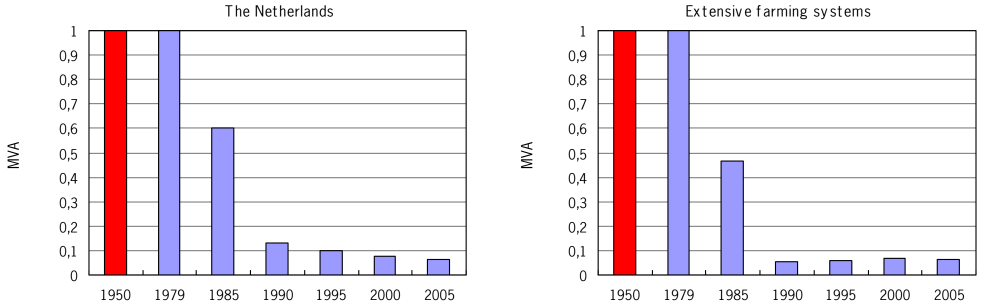


Figure 5. *MVA for cattle in the Netherlands: a) for all native breeds, b) for native breeds specific for extensive farming systems. (Data source: NRS/ASG).*

3.1.2 Wheat and potato

Here 'Number of varieties' and 'Share of major varieties in total production' are calculated for wheat and potato in the Netherlands. The 'Number of varieties' was added, as we know that data on shares (the area cultivated) might be difficult to gather.

I. Total number of varieties per crop that are available to farmers (FAO, 2002)

This indicator describes the richness of available diversity, *i.e.* 1) registered varieties; and 2) named varieties/farmer managed-units of diversity e.g. landraces, morphotypes. Available means grown in the field or available on the market. The balance between registered varieties and named varieties also indicates the type of system (traditional or modern agriculture). The number of registered varieties gives insight in the potential diversity in the field.

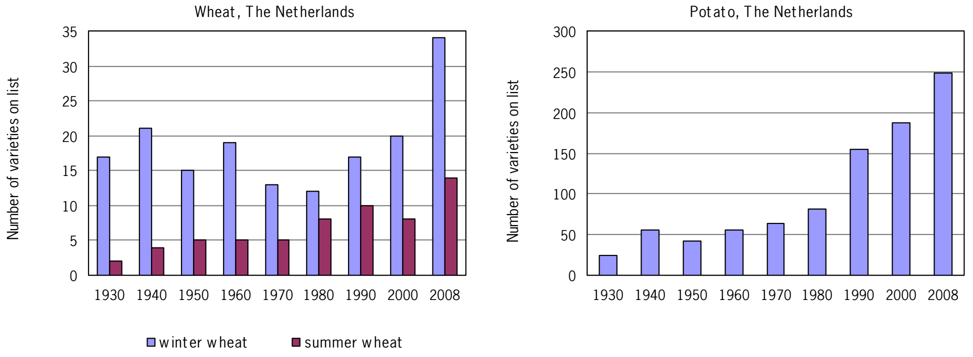


Figure 6. *Number of varieties on variety lists/national lists in the Netherlands between 1930 and 2008 for: a) wheat and b) potato (excluding potato varieties used for starch production) (Data source Dutch Variety lists/National lists).*

Figure 6 presents the indicator for available varieties, calculated for wheat and potato in the Netherlands between 1930 and 2008. The number of varieties available on the market is obtained from the Variety List/National List. According to EU regulations only varieties included in this National List are permitted to be marketed. Actually, the total number of varieties available for Dutch farmers is higher than the number of varieties placed on the National lists due to the following reasons. Although, no landraces of wheat are present on the Variety List since 1930, they were still grown around 1930, but the exact number is unknown. Wheat landraces were displaced by breeder's varieties rapidly between 1931 and 1934, with some regional exceptions. After 1940 hardly any wheat landraces were cultivated (Jongerden & Ruivenkamp, 1996). A low number of old varieties (landraces) is still maintained today without commercial use, but data on this is difficult to get. Another reason is the Common Catalogue of agricultural crops created by the EU since 1966, which is a collection of all National catalogues within the EU. Varieties listed on this catalogue are also free to be commercialized throughout the EU and with that also available for Dutch agriculture.

For both potato and summer wheat the number of available varieties has increased steadily since 1930. For winter wheat no large differences in number of varieties are shown between 1930 and 2000, except for 2008.

II. Share of major varieties in total production (FAO, 2002)

This indicator describes the evenness of diversity in use and is here calculated as 'the share in production of the top 5 varieties of a crop'.

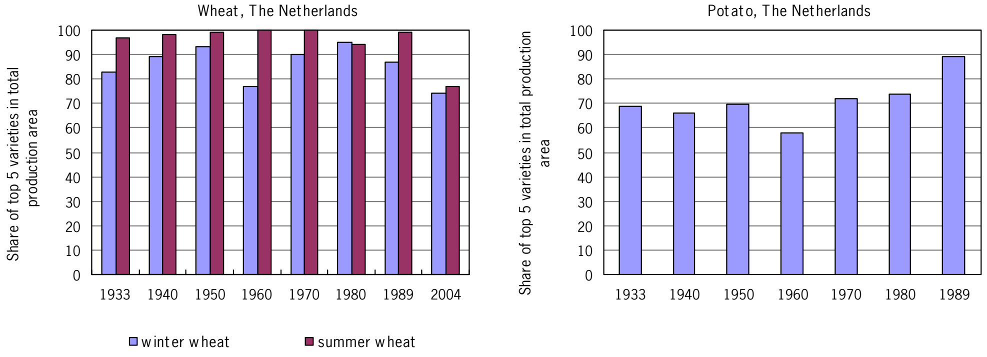


Figure 7. *Share of five major varieties in total production area in the Netherlands between 1933 – 2004 for a) wheat and b) potato (excluding starch potato varieties). Share of major varieties of wheat in 2004 is estimated based on data on certification areas for seed production (Data source Dutch Inspection Service, NAK).*

Figure 7 shows the indicator calculated for wheat and potato in the Netherlands between 1933 – 2004. For wheat the share of the leading varieties is high, but has not changed much over the past decades, except for 2004. In 2004 it decreased substantially compared to the previous periods, however it should be noted that for this year it was estimated on the percentage of certified multiplication area. This should be a reasonable estimation if no farmer-saved seeds are used. For both winter and summer wheat the production area is mainly dominated by one or two varieties. This same trend has been described for other wheat-producing countries in Europe such as France, the United Kingdom and Italy (Lupton, 1992).

For potato the share of the five major varieties has fluctuated around 70% with a substantial increase to 89% in 1989. This is due to an increase of the share of Bintje in that year. No data are available after 1989 for varietal shares in production areas. Estimations based on certification area for seed potatoes is not reliable as a large part of the certified seed potatoes is exported abroad.

The turnover of the varieties is much lower in potato than in wheat. While in wheat the five major varieties have been replaced by new varieties in each period, in potato varieties are dominant for several decades. For example, two of the five dominant varieties (Bintje and Eigenheimer) in 1933 are still dominant in use in 1989.

Comparison of both indicators I. and II. shows that an increase in number is not directly correlated with a decrease in share of the top 5 varieties in the field. The number of available varieties, represented here by varieties placed on the Variety List only gives insight in the potential diversity in the field. The top 5 varieties of wheat dominating in the field are mainly the ones that are selected as 'of special interest for Dutch agriculture'. In the specific years they were included in the Recommended List of Varieties and noted as 'recommended for general or fairly general use'.

III. Mean Variety/Breed Abundance (MVA)

In case of crops a MVA could show the trend in crop area of characteristic local varieties (or landraces) used within a region or country. Such a MVA for crops has similarities with the indicator a. 'Crop area of varieties characteristic for landscapes/production environments important for biodiversity and characteristic for a region or country', proposed by Eaton, *et al.* (2006a). A starting point for measuring change in crops could be the period in which institutionalization of breeding started. In the Netherlands the development of breeder's varieties started at the end of the 19th century and beginning of the 20th century. For wheat the percentage of landraces in the total area diminished already rapidly in the 1930's. After 1940 hardly any landraces were grown in the Netherlands. Potato varieties have been introduced in the nineteenth century and the old local varieties have all originated from these first accessions (around 30). So for potato it is arguable what can be considered as original varieties. A few of these old local varieties are still grown today (e.g. Bintje, Eigenheimer, Eersteling), but most of them are replaced by others. The varietal turnover (related to the length of time it takes for farmers to abandon their varieties and replace it with others) can be high (e.g. in wheat). This is especially true for breeder's varieties but also for the (old) local varieties.

Therefore, the short longevity and high turnover of (old) crop varieties in general makes a MVA for crops, calculated in analogy with MSA, less appropriate.

3.1.3 Actual genetic diversity

The indicators mentioned above do not directly measure the actual genetic diversity. If molecular studies or pedigree studies are available for cattle, wheat and potato in the Netherlands they can give us insight in changes in the actual genetic diversity within the given period. A literature research was undertaken to evaluate the relationship between the trend given by the indicators and the trend in actual genetic diversity based on molecular studies or pedigree data within the species.

Dutch cattle breeds

Genetic diversity between breeds is mostly studied using genetic distances, while the genetic diversity within breeds is usually estimated based on parameters related to inbreeding such as heterozygosity, effective population size, and effective number of alleles. To know the genetic diversity of a breed, both should be taken into account. Eding (2002) described a method for assessing genetic diversity based on marker estimated kinships (MEK), which describes the average (estimated) kinships between (and within) populations using genetic markers. Lenstra, *et al.* (2006) used this method to estimate the diversity within 69 European cattle breeds, including four native Dutch breeds, for conservation purposes. Unfortunately, no literature is available describing temporal trends in genetic diversity of the Dutch native cattle breeds with this method or other methods measuring the diversity at DNA level.

The share of the introduced breeds in the SEBI indicator calculated for the Netherlands is mainly represented by Holstein-Friesian, which is a high producing dairy breed worldwide. The uniformity within this breed has increased, due to the incorporation of high productivity traits, that happened at the cost of declining genetic diversity within the breed.

The native breeds in the SEBI and MVA indicator calculated for the Netherlands are mainly represented by two breeds: Meuse-Rhine-Yssel (MRY) and Dutch Frisian (FH). Their population sizes have decreased dramatically during the past three decades (> 99%), but especially in the period before 1985 (See also Figure 8). A decrease in population size increases the chance of inbreeding and loss of diversity within a breed. One study (Van Eijndhoven, 2007) was available that describes the level of genetic diversity in these two breeds over the past three decades. Based on pedigree data the diversity was analyzed by estimating a number of diversity parameters (rate of inbreeding, inbreeding coefficient and average mean kinship). The study showed that both breeds have strongly decreased in genetic diversity in the period 1970 - 2005. Although the population size of MRY is higher than that of FH, the overall genetic diversity for MRY seemed to be lower than for FH. Apparently, the population size is not the only factor determining the genetic diversity in these breeds. Evaluation of the variance in sire contributions suggested that the utilization of only a few MRY bulls has decreased the diversity in MRY. From this study it appears that the diversity in the native breeds MRY and FH has declined even more in the period 1970 till 2005 than the SEBI and MVA indicators reveal us.

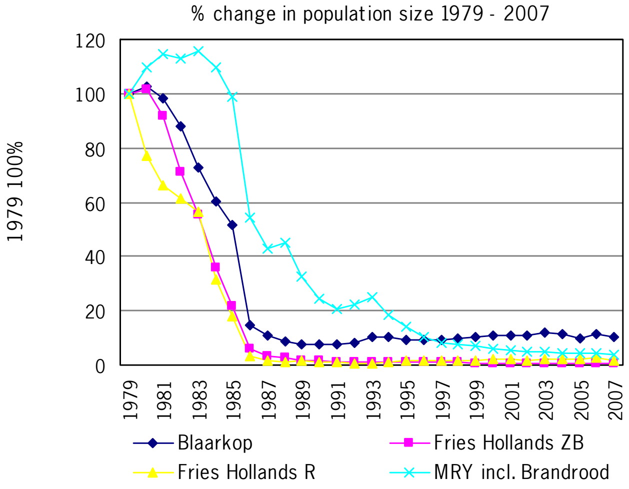


Figure 8. *Percentage change in population size of native Dutch cattle breeds between 1979 – 2007 (Data source: ASG/NRS).*

Dutch wheat varieties

No literature was available examining the actual genetic diversity in the Dutch wheat varieties using molecular data. There are only two recent studies on changes in genetic diversity in European wheat varieties including Dutch cultivars. Roussel, *et al.* (2005) examined 480 bread wheat varieties from 15 West-European countries released between 1840 – 2000. The study showed a clear separation between groups of varieties released before and after 1970. Moreover varieties from West-European countries (France, the Netherlands, Great Britain, and Belgium) displayed a lower diversity than the other European countries. The results suggest that diversity is not randomly distributed but can be explained by both temporal and geographical variation trends linked to breeding practices and agricultural policies in the different countries. The other study (Huang, *et al.*, 2007) assessed whether modern plant breeding has led to loss of genetic diversity in European wheat varieties. In their study 282 varieties (including Dutch) representing the Recommended Lists in eight North-Western European countries in the period 1945 – 2000 were examined, but no indication for genetic erosion was found in this varietal set during this period.

In general there is neither evidence from literature that the genetic diversity in European wheat varieties has dramatically changed over time nor that modern plant breeding has significantly reduced diversity, except that some studies report a bottleneck at the end of the 1960s (Donini, *et al.*, 2000; Christiansen, *et al.*, 2002; Roussel, *et al.*, 2004). However, no conclusions can be drawn on the level of diversity that may have existed among landraces grown in the previous period compared to the breeder's varieties.

Because no studies were found that reveal changes in the actual genetic diversity in the Dutch varieties grown during the past decades, no direct conclusions can be drawn in relation to the indicators.

There is no reason to assume that temporal changes in actual genetic diversity in the Dutch cultivars will be very different from the other North-Western European varieties. If temporal changes in diversity were reported by authors, these were explained by changes in breeding strategies, such as use of new, exotic germplasm or interspecific crosses, exchange of germplasm between breeders, change in number of breeders or integration of breeding programs at an EU level. The latter is not likely to be an issue except for the impact of Green revolution (e.g. introduction of short-straw varieties). Analysis of the origin of the germplasm used by (Dutch) breeders would give better insight in this.

Dutch potato varieties

The majority of European potato varieties are derived from a small number of founding varieties (probably around 30 varieties), introduced in the 19th century (Wang, 2007). Since then breeding has been practiced in the Netherlands, but in the early period mainly by amateur breeders. Some of the major varieties still cultivated today are bred by them, such as Bintje. Modern breeding of potato is mainly focused on disease resistance, through introgression with wild relatives, yield and quality traits. This modern breeding might even have broadened the genetic diversity in the modern potato varieties grown today compared to the early introductions.

There are two recent reports examining changes in the genetic diversity in the European potato varieties using molecular data, in which also Dutch cultivars are included (Reeves, *et al.*, 2004, Wang, 2007). In these studies 546 potato varieties from the UK, the Netherlands and Germany from three different time periods 1945 – 1950, 1971 – 1975 and 1996 – 2000 were characterized for genetic diversity at neutral (SSRs, SNPs) and resistance gene loci (NBS profiling). Both studies concluded that the genetic diversity in these cultivated varieties has not substantially changed during the last 70 – 80 years.

Besides molecular studies, pedigree data are available from the potato pedigree database (Van Berloo, *et al.*, 2007), which contains pedigree details of over 7500 potato accessions for up to eight generations. Based on this pedigree information the relatedness between varieties can be determined (e.g. coefficient of parentage analysis). However, no such studies for Dutch potato cultivars in literature were found.

Similar to wheat, no direct conclusions can be drawn in relation to the indicators as no studies were found that give direct insight in changes in actual genetic diversity, based on pedigree or molecular data for the Dutch potato cultivars.

3.2 Evaluation of indicators

This report section describes the review of the indicators with regard to criteria provided by CBD (2003a). The MVA for crops is not an appropriate indicator and is left out of the evaluation. The results of this evaluation are summarized in Table 3.

Policy relevance and meaningfulness

All four indicators score well for relevance and meaningfulness. They all provide direct information on the process of genetic diversity loss and show the homogenization process. Both livestock indicators are highly relevant by addressing the country responsibility to maintain native breeds, as a contribution to global genetic diversity.

The ‘Number of crop varieties’ describes the richness of available diversity. For pragmatic reasons it can provide a proxy for evenness described by the ‘Share of major varieties’ indicator. The ‘Share of major varieties’ also relates to genetic vulnerability.

Biodiversity relevance

All four indicators refer to the genetic (within species) component of biodiversity.

Scientific soundness

The ‘Number of crop varieties’ is not sufficient as a single indicator to assess trends in genetic diversity. The potato and wheat data for the Netherlands illustrate that the number of available varieties has increased since 1930, while the share of varieties grown in the field remained more or less the same. In this respect the ‘number of varieties grown in the field’ is a better indicator, but for practical reasons (data availability) one might choose for the ‘number of available varieties’. This indicator should be presented together with the ‘Share of top 5 varieties’, which represents the dominance and evenness of varieties in the field. For traditional varieties the richness and evenness of varieties grown on farms seems to be highly correlated as shown by a recent study in 27 crop species (Jarvis, *et al.*, 2008). They found that if appropriately transformed, one can be used for an approximation of the other.

Both indicators do not capture all genetic diversity, but serve as a proxy indicator for actual genetic diversity. As illustrated for wheat and potato in the Netherlands the share of the five major varieties has not changed much over the past decades. However, the varieties used in the early periods are different ones than the ones used today, with probably different genetic differences among them. No studies were found that give direct insight in changes in actual genetic diversity in this period. Based on ‘Share of the top 5 varieties’ solely it is difficult to say whether genetic erosion occurred in these crops as long as no information on the genetic differences (pedigree data, molecular data) among the major varieties is known.

The ‘Share of livestock breeds’ clearly addresses the native genetic diversity of a country. It may not give the actual trend in genetic erosion as the diversity within the breed is not captured. The study on actual genetic diversity in the two Dutch native cattle breeds illustrated this also. Moreover, the indicator may show inconsistent trends, depending on the definition of ‘native’.

A MVA is partly based on direct measurements as it also includes expert knowledge or historical information to obtain data in the baseline situation. When establishing a baseline, one should weigh the reliability and accuracy of the data. Often no data are available in the baseline situation and estimations have to be made. For example for calculating the MVA for cattle breeds, an appropriate baseline is the state of diversity in ‘pre-intensification times’.

Accurate data back in time could only be obtained for 1979, while a more appropriate baseline would be 1950. Therefore an estimation of the population sizes in 1950 had to be made.

The concept 'breed' complicates calculating a MVA for which comparisons in abundance of a breed at different points in time have to be made. A breed is not a fixed entity as it is (e.g.) heterogeneous, dynamic and not completely genetically isolated. Comparisons of population sizes over longer time periods may be misleading and may misrepresent the analytical soundness of the indicator. A MVA might still be of interest for livestock breeds with a high longevity (such as cattle and sheep breeds), but not for others.

Broad acceptance

The 'Share of livestock breeds' and both crop diversity indicators are broadly accepted in international fora. The MVA does not fulfill this requirement.

Data availability

The 'Number of available crop varieties' scores reasonable well for data availability. The data availability should be reasonable high for registered varieties and for certain conservation varieties (e.g. the EU directive 2008/62/EC allows derogations from DUS requirements to enable conservation varieties to be placed on the national and common lists). Data availability for landraces might be medium to low, depending on the crop.

Preferably data for the 'Share of the top 5 varieties acreage' should be obtained from area production data, which should be reasonable available for high potential areas in most developed countries. In other countries data availability will probably be low or only on a case-study base. In the Netherlands the Recommended list of Varieties provided these data for most crops, based on surveys compiled by the Netherlands Inspection Service (NAK). However since 1990 data on production areas separated by variety are only available for maize, starch potato and sugar beet. If there is no variety specific information available on the productions areas, seed multiplication area's can serve as a proxy. Alternatively, estimates could also be based on seed sales. The seed multiplication areas should be highly correlated with the production areas, provided that the crops are multiplied in their own country, harvest is not (partly) exported or stockpiled and farmers don't use their own harvest for sowing the next year. In the Netherlands this data source is reasonable reliable for wheat as nothing is exported, however no insight in the amount of farm-saved seed is available. For potato multiplication areas are not a reliable estimate, because a part of the seed potatoes grown in the Netherlands is exported.

Data to implement the 'Share of livestock breeds' should be reasonable available, at least within the EU. Data can be directly derived from national databases if existing or from the European database EFABIS (www.efabis.tzv.fal.de, data for 38 European countries). At a global level the FAO database DAD-IS (www.dad.fao.org) can provide data, however the quality is variable. Recently the DAD-IS and EFABIS database are linked. Both databases provide reliable data after 1997, but before this date the database shows gaps for population's sizes of breeds, so time series might only be available on an occasional basis.

According to data quality, information on the origin of the breeds should be available as well. Currently the definition of what is a 'native' breed is set by the country. Harmonization of these national definitions is needed to obtain higher quality of the data. The EFABIS data base defines a 'native' breeds as follow: 'A native (syn. indigenous or autochthonous) breed - originating from, adapted to and utilized in a particular geographical region - forms a subset of the locally adapted breeds, which have been in the country for a sufficient time to be genetically adapted to one or more traditional production systems or environments in the country'. The FAO database (DAD-IS) also gives information on the origin of the breed, but no definitions are proposed.

For calculating the MVA for livestock species data availability is low. The existing national and international databases (e.g. DAD-IS) are incomplete and do not provide the necessary data on populations sizes of breeds in the baseline. Historical data on time series will only be available on an occasional basis and will generally rely on expert estimations.

Sensitiveness to trends

It is expected that the indicators reflect changes in a relatively short time period. At a national level the sensitiveness of the 'Share of livestock breeds' to external factors (e.g. conservation policies) is probably not very high as small changes in the shares of the native breeds are not revealed in this indicator. For this a more refined indicator is needed.

Modelling

Some of the causal links between the pressure/driving force indicators (described within the conceptual framework, presented in chapter four) and the changes in diversity as reflected by the indicators are probably qualitative. Better insight in data availability and quality of data of the driving force indicators is needed.

Aggregation to different scales

In principle the indicators are applicable to all scales (country, region, and world). For aggregation of richness and share problems can be expected in double counting because different names are used for the same variety in different places.

For making comparisons between countries the 'Share of livestock breeds' will score well, but for modelling within GLOBIO downscaling at the level of (agro) production systems might be preferable. For instance this indicator could be calculated per livestock production system, based on the 11 world livestock production systems described by the FAO (FAO, 1995). However, currently no data are available that link the characteristics of livestock production systems to breeds. Data on number and abundance of breeds are yet only available per country/region.

A MVA needs a common baseline as far back in time as possible. Yet, data availability back in time is not the same for all countries. Therefore, harmonization of baselines over countries may complicate aggregation of data on a supranational level.

Table 3. Scores for evaluation of the indicators.

Criteria	Share of livestock breeds	MVA livestock	Number of varieties available	Share of varieties in total production
Policy relevance	++	++	++	++
Biodiversity relevance	++	++	++	++
Soundness	±	-	-	±
Broad acceptance	++	-	+	+
Data availability	+	-	++	+
Sensitiveness	±	+	+	+
Modelling	±	±	±	±
Aggregation	+	±	+	+

3.3 Conclusion

According to the focus of GLOBIO, modelling agrobiodiversity on a global scale, the two 'share' indicators for livestock and crops seem to be suitable indicators. Although they are slightly different, they both describe the loss of agrobiodiversity at the intraspecific level and are related to the intensification or homogenization process.

For crops the ‘Share of major varieties’ should be used in combination with ‘Number of crop varieties’. It shows the trend in evenness in use, but for pragmatic reasons (data availability) the richness indicator should be used as a proxy for evenness. The richness indicator also shows the balance between landraces and registered varieties in a country and in this way also reflects the stage of agricultural intensification in that country. Together they give a first insight in the process of genetic diversity loss and can be used as an ‘early warning system’.

The ‘Share of livestock breeds’ indicates clearly that if local breeds are replaced by non-native (introduced) breeds, diversity at a global scale is likely to decrease. Compared to this indicator, the MVA seems to be less useful mainly due to difficulties in data gathering and analytical soundness. The ‘Share in livestock breeds’ is especially relevant for monitoring at a global scale. In countries where local breeds almost have disappeared, it is insignificant. Therefore at a country-level in such industrialized situations a more refined indicator, that monitors the status of these individual native breeds in more detail, is preferable.

The ‘Share of livestock breeds’ and the ‘Share of crop varieties’ both provide a picture of the diversity at the intraspecific level. They do not necessarily capture the actual genetic diversity (variation at gene loci).
As shown for the case of cattle breeds in the Netherlands the indicator may underestimate the loss of genetic diversity, as also the genetic diversity within (some of) the native breeds, estimated with pedigree data, has decreased. For the crop cases, the shares of the major varieties has not changed much in the past decades. So, based on this indicator it is plausible to conclude that there is no loss of genetic diversity in wheat and potato within this period. However, as long as we have no insight in the genetic differences among the five major varieties based on pedigree data or molecular data conclusions regarding loss of genetic diversity should be made with reservation. Different other factors may be involved that can amplify or mitigate the loss of the actual genetic diversity, for instance change in breeding strategies, use of new, exotic germplasm.

4. Causal framework for modelling intraspecific agrobiodiversity

Monitoring of the status of agrobiodiversity over time makes it possible to assess the dependency of agricultural production systems on agrobiodiversity as well as it's impacts (*e.g.* food safety, food security, socio-economical effects, quality of landscape and wild biodiversity). Moreover, it may help the evaluation of policy decisions in regulating agricultural or environmental issues. Where monitoring informs on the earlier and current state of agrobiodiversity, modelling can be applied to predict the status of agrobiodiversity in the future. Also, via modelling the effect of different policy decisions on agrobiodiversity can be simulated.

Therefore, it is important to have an idea on the causal framework which describes interactions between society, environment and agrobiodiversity. A commonly used causal framework is the driver, pressure, state, impact and response (DPSIR) model which is based on the PSR framework model proposed by OECD in 1993 (see EEA, 1999). The DPSIR categories are represented in Figure 9.

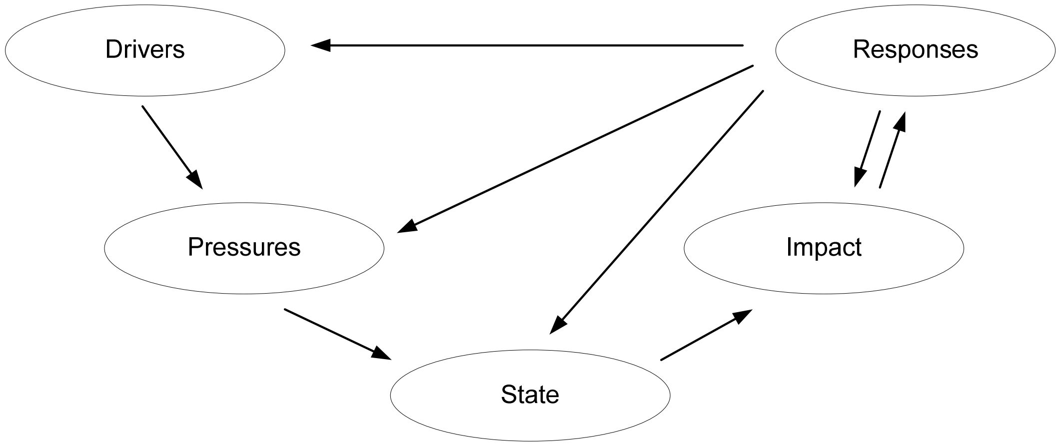
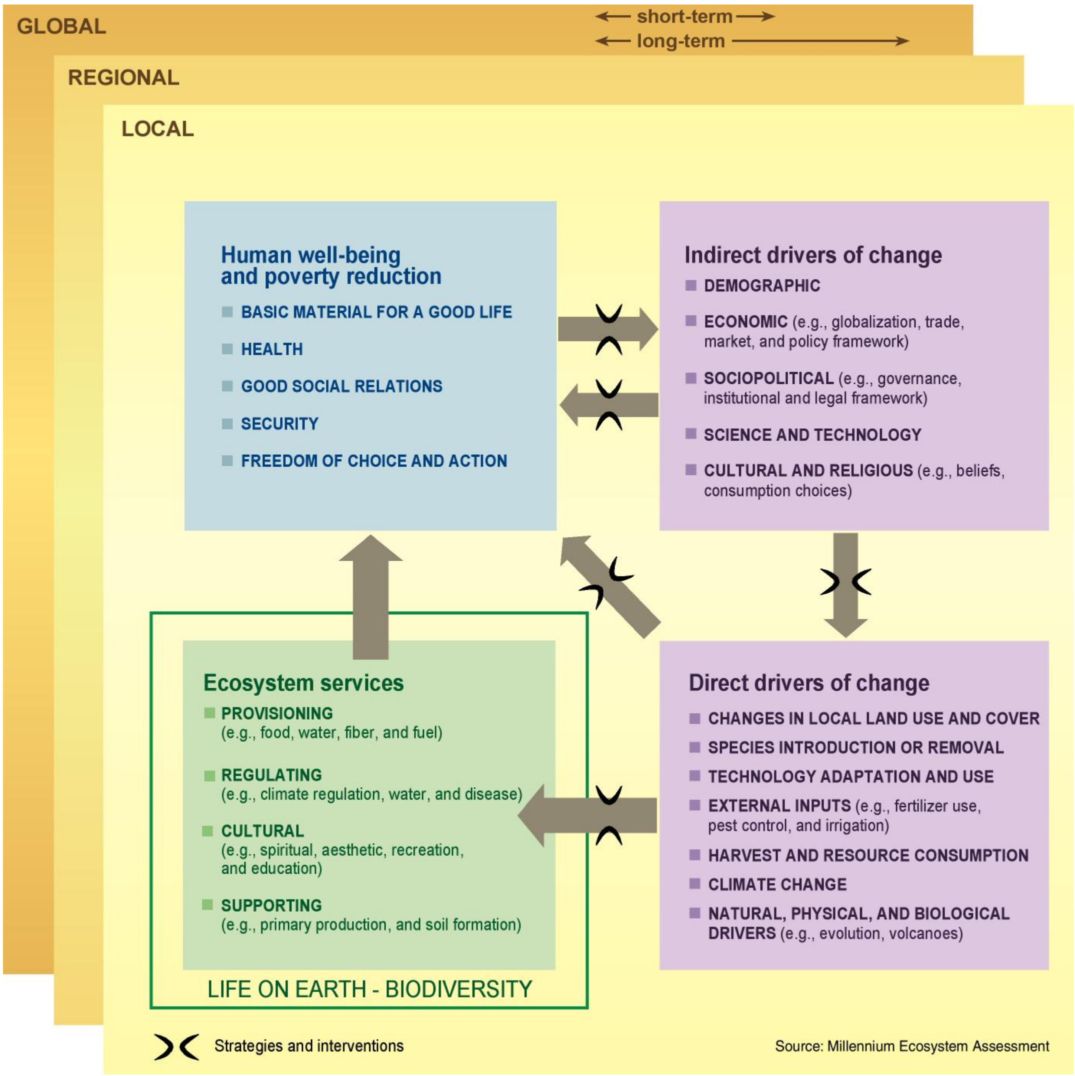


Figure 9. The five categories of the DPSIR model with their relationships (from EEA, 2007a).

Driving forces can be social, demographic and economic developments in societies and the corresponding changes in lifestyles, overall levels of consumption and production patterns. They may result in different pressures. These pressures include the release of substances (emissions), physical and biological agents, the use of resources and the use of land. Pressures have a direct or indirect effect on the state of (a)biotic environment. For the abiotic environment the state refers to the condition of soil, air and water; for the biotic environment the state refers to biodiversity at ecosystem/habitat, species/community and genetic level. Adverse (a)biotic environments which may result from pressures have different impacts on human and ecosystem health, resource availability and biodiversity. In order to overcome or prevent adverse (a)biotic environments different measures are taken that can address drivers, pressures, states or impacts.

When well chosen, indicators each measure a particular aspect of the DPSIR model and can be categorized according to their measurement on drivers, pressures, states, impacts and responses.



Source: Millennium Ecosystem Assessment

Figure 10. The Millennium Ecosystem Assessment conceptual framework (Millennium Ecosystem Assessment, 2003).

The DPSIR model has been used as a basis for the Millennium Ecosystem Assessment (MA) approach (Millennium Ecosystem Assessment, 2003) which has been developed as a general framework to highlight the role of ecosystem services for human well-being and poverty reduction. The MA approach is illustrated in Figure 10. Responses are not included in this figure, because they differ depending on the context-specific analysis. Examples of such responses can be altered policies and measures for the mitigation of unwanted changes.

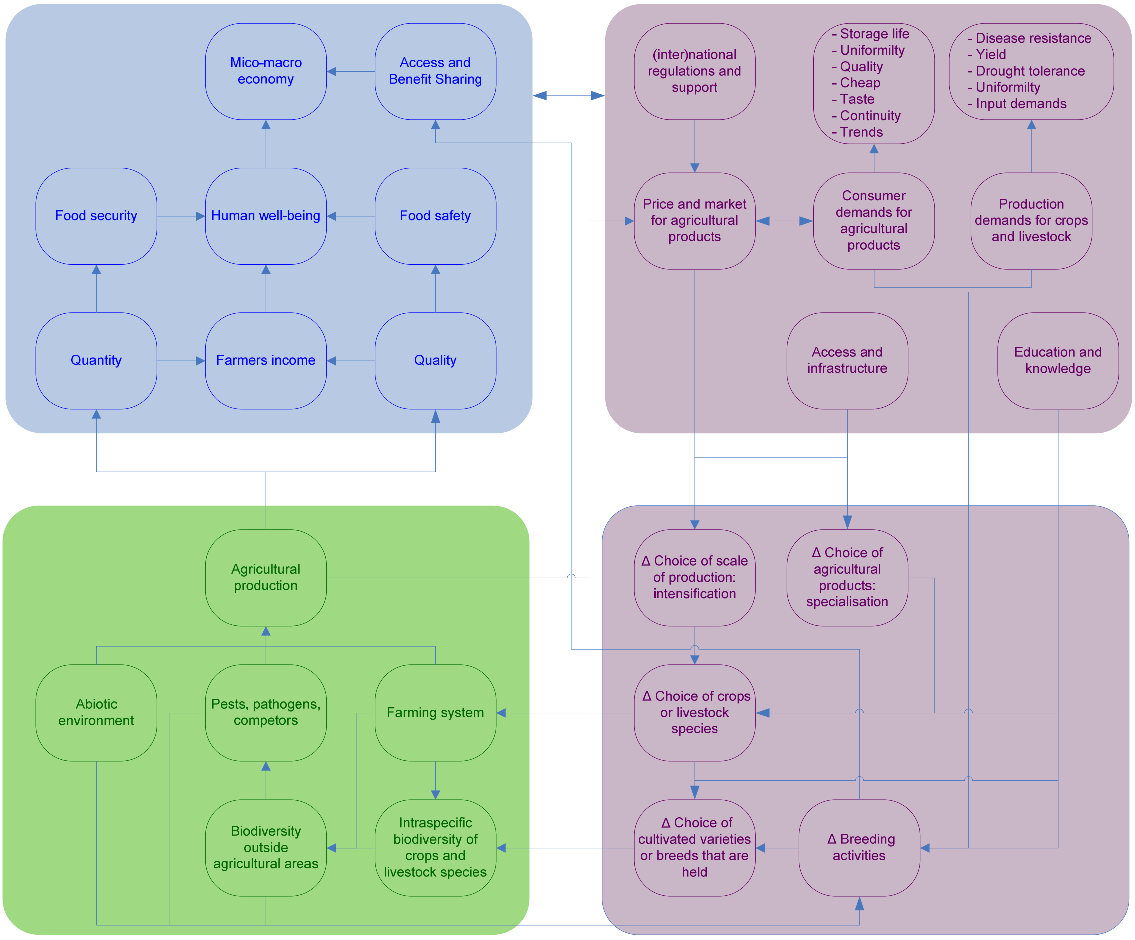


Figure 11. *The MA framework filled in for intraspecific agrobiodiversity. (Arrows represent the influence of one factor on another).*

More specifically, the MA framework can be filled in for intraspecific agrobiodiversity (Figure 11). In this figure, factors are given that we think have an indirect or direct relationship with the status of intraspecific agrobiodiversity. According to Figure 11 intraspecific biodiversity may change due to shifts to other farming systems including other crops or livestock species. Also, farmers may decide to hold other varieties or breeds. Input for making these decisions can be sought in factors like intensification of production and specialization for particular products, depending on changes in market demand (free market processes) and the infrastructure that is available for (*e.g.*) getting access to resources or transport of agricultural products. Input for changing towards other varieties or breeds is also provided by changing breeding activities. New varieties and breeds are produced as a response to changing farming conditions, pests and pathogens challenges and demands for agricultural products, crops and livestock by consumers and farmers. Education and knowledge of farmers is important for making choices on crops and livestock as well as on varieties or and breeds. Also, education and knowledge have an effect on the breeding activities that provide new varieties and breeds.

The relationships between agrobiodiversity and impacts such as food security, food quality, landscape, wild biodiversity, environment, social-economic effects are complex, although most relevant. For the time being they are not further described here.

The following chapter goes more deeply into the driving forces that have a direct of indirect effect on the state of agrobiodiversity.

5. Identifying drivers of change

For development of a ‘genetic module’ in GLOBIO, further exploration of the relationship between use of agrobiodiversity, the characteristics of production systems and the drivers of change is needed. This relationship is a complex one as it is part of the social system. As seen from the conceptual framework (Figure 11), agrobiodiversity is determined by a number of human, economic, technical, socio-political and environment-based factors. These factors have different effects at global, regional level and farm level. Some might even have a negative effect at one level, but a positive effect at the other level.

A literature search was undertaken to investigate the relevance of the factors suggested in the earlier described conceptual framework. Here the main global drivers and factors at the farm level, that are described in literature, are further discussed.

5.1 Global factors

This section gives an overview of the global factors and processes, that contribute to changes (mainly loss) in agrobiodiversity. They are related to demographic, economic and technological developments, environmental changes and socio-political developments at national or international level, including policies, legal or institutional structures.

Demographic development

- Population growth and related urbanization have a negative impact on the genetic diversity. They are one of the drivers for change in agricultural systems (mainly in developing countries) and indirectly impact the accompanying genetic diversity used in the systems. (FAO, 1996, Trupp, 2000, Sere, *et al.*, 2007).

Economic development

- Changing agricultural systems or intensification (FAO, 1996, Sere, *et al.*, 2007)
  Intensification of agriculture refers to the increase in output per unit of land used in production. Intensification of agricultural systems is driven by population growth, urbanization, globalization, change in market demand. This change in agricultural systems from more traditional (extensive) to industrial intensive systems has an important effect on the crop and livestock genetic diversity. In more industrial systems, there is no need to adapt to the local environment, but the environment can be adapted to the varieties or breeds. In these systems modern, high yielding varieties or commercial breeds and hybrids are used, resulting in loss of genetic diversity. In the less intensive systems under heterogeneous environments still different varieties and breeds are required.
  Intensification of agricultural systems may also result in habitat destruction, when drainage, large-scale irrigation is introduced or fertilizers and pesticides are used.
- Globalization (Sere, *et al.*, 2007, Tisdell, 2003)
  Integration of the world economy has led to increase of agricultural markets (both for inputs and outputs). Globalization and economics of scale ask for uniformity in production systems, specialization in one uniform product which means loss of genetic diversity as fewer varieties or breeds are kept on the farm.
  In case of increased international trade, due to globalization, the choice of varieties may be more influenced by market trends in importing countries. On the other hand, in case of trade restrictions, that hinder the international trade, local, regional and national markets trends become more important.
- Change in market demands (FAO, 2007, Sere, *et al.*, 2007, Tisdell, 2003)
  Changes in market demands can also influence the genetic diversity in farming systems. A growing demand for agricultural products may lead to loss of genetic diversity. In general a growing demand for agricultural products is driven by population growth, purchasing power (income rise), consumer/ processor preferences and relative prices of the agricultural products. For example, industrial processing and higher market standards ask for homogenous and high consistent quality goods (e.g. milling suitability and baking performance of wheat), which results in a small number of specific varieties.

In livestock the growing demand for animal products ('livestock revolution') has led to the replacement of multipurpose local breeds by crossbreeds or exotic breeds with higher milk, meat and egg production and with this to a lower genetic diversity. This change in animal product consumption is mainly influenced by purchasing power (income rise) and urbanization. As a third factor influencing consumption trends consumer taste and preference is mentioned, which are far more of local importance.
If relative prices for agricultural products are changing this can lead to a shift in the demand and as described above leads to a change in genetic diversity.
Moreover, a growing niche market can lead to diversification. In areas with good market access there might be opportunities for producing relative small quantities for a niche market. The genetic material involved here is probably not produced by large private breeding companies. It is therefore expected that the genetic diversity used by farming systems producing for a niche market is higher.

Science and technology development (FAO, 1996, 2007, Tisdell, 2003)

- Impact of international & national breeding programs as well as other trends in breeding. The impact of the breeding sector on the genetic diversity depends to a large extent to the breeding objectives and whether *ex-situ* conserved material is used to broaden the genetic base of the material. In general it seems that breeding objectives are correlated with economic growth and are determined by productivity (yield or growth performance), agro industrial cultivation/husbandry and processing and to a minor extent consumer choice. For instance, in crops the replacement of landraces by modern high-yielding varieties is seen as a main cause of loss of diversity. This impact of breeding of high-yielding varieties differs per region and crop (Evenson (2003). It might have a less negative impact if the aim is to breed for specific environments (development of several different varieties each adapted to the local environment).
  In industrialized countries livestock breeding has led to more productive animals and the change from multipurpose breeds (mostly loss of local genetic diversity) to highly specialized breeds, which are needed in the more industrial production systems. In the industrial livestock systems (e.g. poultry, pigs) disease resistance and local adaptation is of minor concern. In some regions of developing countries the impact of breeding has mainly been in these systems. Breeding for the more traditional, extensive systems is more challenging and therefore it's impact so far has been less (less loss of the local genetic diversity).
- Investments in agricultural research (public/private) in general or in breeding research. In commercial systems the supply of varieties (that is the available genetic diversity) is determined by lagged investments in research. The level of investment in private and public breeding and their ratio is related to socio-political developments. In the last three decades of the 20th century the privatization of plant breeding in industrialized countries has accelerated. An important underlying force for this was the change in intellectual property protection for plant varieties (Heisey, *et al.*, 2001).
- Technology development
  Modern technology (*e.g.* artificial insemination, multiple ovulation, embryo transfer, sexed semen) may speed up the breeding process and if adapted and used at the farming system may contribute to the homogenization process. These technologies are mainly used in developed countries.

Socio-political development (FAO, 1996, 2007, Wolf, 2004, Thrupp, 2000).

- Institutional (seed market, seed supply system) structures. Local seed systems and formal seed systems will have a different effect on genetic diversity. Higher diversity can be expected if local seed sources are used by farmers. These local seed systems are mainly used in the traditional agricultural systems. Modern agricultural systems are more linked to the formal seed system. Formal seed systems, that take advantage of breeding, modern seed technology (see also science and technology development) and legal structures (Plant Variety Protection, registration and certification schemes) are expected to lead to a lower genetic diversity.
- Policy/legal framework
  - Policies and legal instruments that regulate access to and control over genetic resources influence the availability of varieties/breeds to farmers and indirectly affect the choice of the material. Examples of policy and legal instruments are Intellectual property rights (IPR), Sovereignty regimes (CBD) or Seed and breeding regulations. Two major IPR regimes that may have impact on agrobiodiversity are Plant Variety Protection (PVP) and patents. The plant variety protection system of the UPOV may be negative for agrobiodiversity. The criteria for variety protection, the so-called DUS criteria, have an impact on the plant

variability. Moreover, it precludes the protection of landraces which have higher within-variety diversity. However, it is also argued that introduction of PVP regimes enhance genetic diversity as they have positively effected the number of new, registered varieties. An example of seed and breeding regulations, is the compulsory variety registration system within the EU (Common catalogue of registered varieties). In order to market seeds commercially within the EU, varieties need to fulfil specific criteria, including DUS criteria. This EU regulation discourages the cultivation of variable landraces.

  - Regulations to eradicate diseases (EU) or that effect ownership, land and water resources access (in particular for livestock).
  - Economic policy interventions may have both negative and positive impacts on the availability and use of varieties and breeds. For instance policies that promote unsustainable technologies and agricultural practices by supporting use of modern high-yielding varieties and chemicals (e.g. through credit policies, subsidies, market standards) may lead to uniform productions systems and use of uniform varieties and breeds and subsequent loss of genetic diversity.

Changing environment and climate change (FAO, 1996, 2007)

- Habitat destruction or loss, land clearance, abandonment of marginal land, overgrazing may lead to loss of local genetic diversity. Most of them also relate to urbanization.
- Climate change (increased temperatures, changes in precipitation) may have severe consequences for genetic diversity held in agricultural systems. In the future more climate variability can be expected. Predictions show that precipitation is likely to increase in high latitudes, while more tropical or sub-tropical areas are likely to get less precipitation (IPCC, 2007). This change in climate may effect the production and distribution and characteristics of the agricultural systems and consequently the related diversity. Moreover, climate change may increase the weather-related disasters (more and more severe events), that have a negative impact on genetic diversity. Indirectly, climate change will affect diseases in crops and livestock or water availability. So even if breeds/varieties are well-adapted today, extreme climate events may lead to losses and threaten the genetic diversity. It is likely to assume that climate change will have the greatest impact in the traditional systems.

Diseases and disasters (FAO, 1996, Tisdell, 2003)

- Natural disasters such as floods, droughts, heath stress and impact of disease epidemics can lead to loss of crop varieties or dying out of breeds. These factors may have a greater impact on animal diversity than crop diversity. Actually these factors should be seen more as ‘disturbers’ of the expected agrobiodiversity than as drivers of change. For instance, the real agrobiodiversity may be different from the expected agrobiodiversity if due to diseases breeds/sowing-seed is lost, but is replaced with foreign material in stead of local.

Wars and civil strife (FAO, 1996; Richards & Ruivenkamp, 1997; Tisdell, 2003)

- War, civil strife and conflicts can have a disastrous impact on genetic diversity if they lead to loss of crop varieties or dying out of breeds. They also probably have impact on the flow and distribution of genetic diversity as they have impact on the formal sector of resource management facilities as well on the informal seed system, through changes in the social relations. They will especially affect the small-scale farmers. These factors should, similar to disasters, be seen as ‘disturbers’.

Socio-cultural and religious factors

- Consumption choices or tastes (e.g. consumer preference for leaner meat) could lead to changes in genetic diversity, if these preferences are related to specific breeds or varieties.

5.2 Factors on the farm level

The above mentioned generic factors are outside the control of farmers, and vary at a regional level or country-level. In the conceptual framework we assume that there are other factors explaining the intraspecific agrobiodiversity, which are relevant for their effect on farmer’s choices (which, how many and area/population size). To understand these factors it is essential to keep the type of agricultural system in mind as they are not all of the same importance in the different systems. According to their characteristics a variety of agricultural systems can be distinguished, varying from more traditional to modern agricultural systems. An example of distinguishing crop farmers/systems according to their concerns and decisions in maintaining diversity is given by Bellon (1996). Given the environment and the degree of market integration he distinguished three types of farmers: commercial farmers, surplus farmers and subsistence farmers. It is hypothesized that the degree of diversity maintained by each type of farmer is different. The different groups of farmers are described below (adapted from Bellon, 1996):

Commercial oriented farmers

Commercially oriented farmers produce exclusively for the market. Their choice of varieties is mainly determined by market prices (price premia) and farm technology. They have large farms with good environmental conditions (homogenized, irrigated, high quality soils) and hired labor. They focus on maximizing production rather than avoiding risk. Important variety characteristics for the farmer are yield (mean yield, stability, better resistance), response to high rates of inputs, homogeneous, adapted to mechanical processing. They purchase certified seeds of modern varieties. The availability of these varieties is mainly determined by the performance of public research institutions and seed industry.

Surplus farmers

These farmers produce both for self-consumption as well as surplus for the market. Their farms are medium sized, with a mixture of good and marginal environments. They are not fully integrated in the market, and their variety choices are therefore not only influenced by market prices and farm technology, but also by farm and house hold characteristics, market isolation and seed supply. They use family labour in combination with hired labour. Important variety characteristics may be yield but also storage (management), sub products (e.g. fodders) and different uses (consumption). The availability of seed may be determined by official as well unofficial (local) seed markets.

Subsistence farmers

These farmers produce a crop for self-consumption. They farm small areas, in marginal environments and use family labour. The varieties are well adapted to marginal environments, which require low management and input, may generate sub products and fulfil different uses (diet, tastes). Yield is considered a less important variety characteristic compared to other concerns. For poor farmers, for which the crop is the main component of their diet, consumption characteristics are important.

A literature search was undertaken to investigate the factors that in particular play a role in the level of genetic diversity managed (or varieties choices made) at the micro-economic level. A clear bias in the number of studies found in literature related to this topic was found. Most studies concerned crop species compared to livestock. Furthermore, most studies were related to the more traditional agricultural systems (group of subsistence/surplus farmers) and were focusing on on-farm conservation of genetic diversity or adoption of modern varieties. So less attention is here paid to the commercial situation.

For the group of crop subsistence/surplus farmers (here also referred to as traditional agricultural systems), a variety of case studies, based on farmer's decision-making models, were found. In these studies in particular the influence of farm physical characteristics (structural, environmental, agro ecological), household characteristics (social, human or financial), market-related characteristics (distance or physical impediments to participate in markets) and seed supply factors are described. In Table 4 an overview of studied determinants and their general association with intraspecific diversity at the farm level for subsistence/surplus farmers is given based on case studies mentioned in Smale (2006).

Although, it is difficult to make generalizations based on these different case studies, some general conclusions can be made for these traditional systems. In general larger farms, higher number of plots or more fragmented plots, variation in soil types on the farm, relative market isolation are associated with higher genetic diversity at the farm. Also higher education, age and experience of the household head and use of family labour are significant for higher genetic diversity. On the other hand the effect of wealth and off-farm income differs in direction depending on the country. The effect of participation and access to markets also differs in direction, depending on how this factor is described. Extension programs, including introduction of modern varieties do not have a negative effect on the diversity. Apparently, farmers do not always substitute modern varieties for landraces but continue to cultivate both simultaneously. Reasons for this can be the complementary traits of the varieties, mitigating risk by diversifying sources of income and the fact that modern variety input packages are 'lumpy' (Smale, pers. comm.).

No thorough literature search was done for commercial farmers. In high-potential environments where farmers are entirely producing for the market and specialized in a particular crop or livestock species, they are motivated by profit. It can be assumed that diversity at these farms is mainly driven by market prices and farm technology.

Table 4. Determinants of intraspecific diversity (i.e. genetic diversity) at the farm level of subsistence/surplus crop farmers (adapted from Smale, 2006).

Determinant		Association with genetic diversity	Remark
Farm characteristics	Farm size (also indicator of wealth)	+	For all income levels and crops
	Number of plots/fragments	+	
	Good quality land, soil, moisture etc.	+,-	Different effects reflect different farming systems, effect consistent with population genetics and biogeography of species
	Elevation, slope	+,-	
Household characteristics	Education	+	In lower and middle-income countries
	Women's education	+	Location and crop dependent
	Age	+	In higher-income countries the effect of age diminishes
	Experience	+	Also positively related to age
	Family labour (quantity and quality)	+	In labour-intensive farming systems
	Off-farm income, migration	+, -	Differs by country or crop
	Wealth (land, livestock, durable consumables)	+	In lower-income countries
		+, -	In higher-income countries, also specialization
Market	Isolation (from physical infrastructure, road density)	+	
	Participation	+,-	
	Access to different types of markets	+,-	
	Cooperative marketing	+	In economically marginalized area
Seed supply	Markets (official, unofficial)	0,+	
	Interventions (disaster relief, extension programs including introduction of modern varieties)	0	

(+) positive, (-) negative, (0) no effect.

5.3 Conclusion

In the previous sections both generic factors acting at the macroeconomic level and factors determining agrobiodiversity at the microeconomic level are outlined. It became clear that for understanding the underlying driving forces it is necessary to distinguish the different farmer types/agricultural systems, because they manage diversity differently. It seems most logical to do this in relation to market integration. In Figure 12 a simplified and generalized picture of the hypothetical relation between agrobiodiversity and the level of market integration is visualized. For both crops and livestock it is expected that with increased market integration agrobiodiversity will decrease. In the commercial systems, fully integrated in the market, market-related drivers as described in section 5.1 determine the diversity at the farm. The degree of agrobiodiversity at these systems is the lowest. Within this group of commercial farmers, individual farmers, cooperative farmers and farmers focusing on a niche market can be distinguished. One can hypothesize that farming for a niche market leads to more diversification and might lead to an increased agrobiodiversity at the farm compared to the others.

Agrobiodiversity maintained by subsistence farmers is expected to be high compared to commercial farming. In general, these farmers, producing only for self-consumption, are poor small farmers/livestock keepers in marginal environments. They keep a high level of diversity, mainly locally adapted material. When farmers become a little integrated in the market (surplus farmers) they might maintain some more diversity than subsistence farmers. As shown for crop farmers, a number of factors such as larger farms, higher diversity in soils/environments, age, better education, experience, may give them the possibility to have a combination of varieties suitable for self-consumption and market production, which lead to a higher agrobiodiversity on the farm.

For livestock keepers, it is expected that partly integration in the market mainly leads to loss of local diversity as a result of cross-breeding and breed substitution.

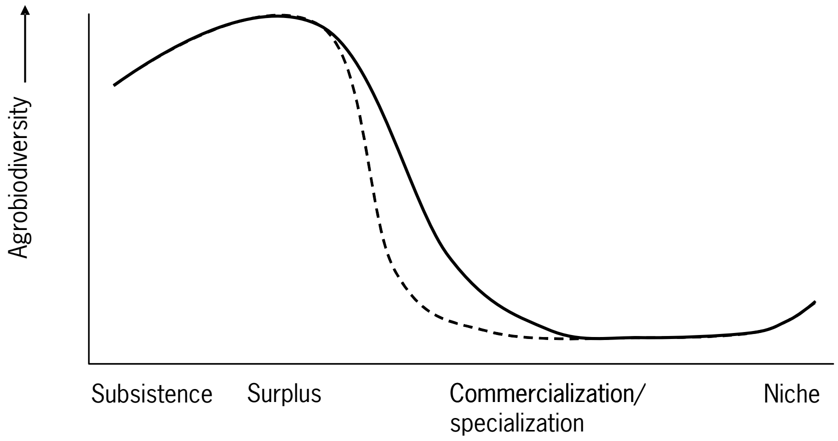


Figure 12. Hypothetical relationship between agrobiodiversity and the level of market integration of the agricultural system.

6. Outlook on modelling

Our aim is to model global trends in agrobiodiversity and their consequences on various human functions such as food security, poverty, environmental quality, landscape and wild biodiversity. In the previous chapters some suggestions are done for indicators (chapter 3) and factors driving agrobiodiversity are described (chapter 4 and 5). Further research should focus on understanding the relationships between these drivers (and related pressures) and agrobiodiversity better and to (semi)quantify them for input for modelling. For the time being less attention was paid to the direct and indirect relationship with impacts, but in subsequent steps these links could be investigated.

The first step in further research is to investigate whether a global agrobiodiversity map can be produced based on the suggested indicators in chapter 3. If such an agrobiodiversity map is available the following step is examining the relationship between (loss of) biodiversity and driving forces. A correlation analyze between drivers and genetic diversity indicators based on country-level data should tell us which drivers are important. In a subsequent analyze the so-called archetype approach could be followed to get insight in hotspots of agrobiodiversity based on these underlying driving forces/determinants. The archetype approach was developed by UNEP (2007) for identifying and mapping patterns of vulnerability of people in relation to environmental and socio-economic changes. They are called archetypical as the same patterns occur on different places in the world. A similar approach could be followed for agrobiodiversity in order to create 'archetypes of agrobiodiversity'. However for doing this, data (both for driving force and genetic diversity indicators) are needed on a sub national level (grid level). Then, an 'archetype agrobiodiversity' map can be produced by doing a cluster analysis of these indicators, which would allow us to find similar patterns of the archetype agrobiodiversity around the world.

Below we give some considerations for choosing species for calculating the genetic diversity indicators and producing an agrobiodiversity map. Subsequently, we attempt to give a description of determinants from which agrobiodiversity result and that we think are relevant for modelling according to our knowledge. These determinants are based on the information from the previous chapters. For some of these determinants, indicators are suggested that we think could feed such an archetype analysis.

6.1 Selecting species for monitoring

A first step in further research on modelling is producing a global agrobiodiversity map by calculating the agrobiodiversity indicators based on country-level data. This could be done for both livestock and crops. For livestock species data can be obtained from national databases, DAD-IS (FAO) or EFABIS (EU countries). For crop species data might be obtained from national databases or case-studies. Knowing that it is impossible to monitor the state of genetic diversity in all species, a representative selection should be made. Here some considerations are given for choosing species to be included in an agrobiodiversity map for crops and livestock.

- Socio-economic importance/importance for food security
  For assessment and modelling of diversity loss it is obvious to focus on socio-economically important species or species important for food security as there is also an interest to link the consequences of agrobiodiversity with wealth, food security and poverty alleviation. About 30.000 plant species are edible of which 7.000 species are used in agriculture and contribute to food security. However only a few crops, the so-called major crops, are important for food security. At a global scale there are only 30 major crops, as these provide 95% of the energy intake. The top 10 crops for the world food production, accounting for 75% of the energy uptake, are wheat, rice, maize, sorghum, millet, potato, yam, soybean, sugarcane and sugar beet. On a national scale 103 crops are important (Prescott-Allen & Prescott-Allen, 1990). Besides major crops there are a large number of minor crops or underutilized crops which are important to people at a local level. These include staple crops for specific regions such as teff, quinoa, but also vegetables, fruits gathered for food or multipurpose trees and wild species that can be harvested. For monitoring on a country basis a selection of species that represent both major and minor crops can be made. However, for minor and underutilized species

it is expected that data will be difficult to get (FAO, 1996).
For livestock species similar groups can be made according to their socio-economic importance. About 40 of the 50.000 known avian and mammalian species are domesticated. On a global scale only five of them are of major importance: cattle, sheep, chicken, goats and pigs. Besides these five species there are many other livestock species, such as yak, camels, horses, water buffalo, which are of socio-economic importance at a local level. For instance, for poor livestock keepers in developing countries or for the utilization of marginal areas. Within the DAD-IS database breed-related information is reported for 36 species (FAO, 2007).

- Types of crops/livestock species
  For crops the set of species might be selected according to use: staple crops, other food crops and feed, fibre, cash crops. For livestock a distinction could be made between ruminants and monogastrics or between species important for landless systems or land-based systems. If the focus is modelling livestock diversity and its consequences for landscape and environment, grazing animals such as cattle, horses and small ruminants should be represented.

- Breeding system of the species
  The genetic diversity within and between crop varieties and the spatial distribution of diversity in the field all depend on the mating system of the species and breeding methods applied. For instance Jarvis, *et al.* (2008) showed that at the farm level crops with different breeding systems did not differ for diversity. However, at the community level significant differences were found in diversity between clonal crops and other systems. The clonal crops showed higher variety richness than the others at the community level. Ideally all main reproduction/mating systems should be represented in the set of species. Therefore the indicator should be based on a representative species out of the group of in breeders, out breeders, partial out breeders and vegetatively propagated crops.
  Also for selecting livestock species differences in breeding methods (pure bred, cross or hybrid breeding) should be taken into account.

6.2 Description of agrobiodiversity

We assume that agrobiodiversity within an area is a function of environment, farmer type diversity, trade intensity, infrastructure and several societal and political factors:

$A = f\,(E, F, T, I, S)$

Where :
A = the level of agrobiodiversity within an area
E = the environmental and climatic heterogeneity
F = the diversity of farmer types within the area
T = trade intensity
I = infrastructure
S = a number of societal and political factors.

Based on the effect of these components we can hypothesize whether agrobiodiversity will be high or low. Basically, we think that when a considerable environmental variation exists within an area and this area is mainly dominated by the more traditional farmers (subsistence/surplus farmers) and pressures of trade intensity, infrastructure and other societal/political factors are low, the highest agrobiodiversity can be found. Below each of the components is further discussed:

- Environmental and climatic heterogeneity
  First, agrobiodiversity within an area is determined by the agro-ecological environment. When the agro-ecological environment (including soil, climate, rainfall, elevation, moisture, land quality, slope) is heterogeneous a high agrobiodiversity can be found. Farmers may use different varieties/breeds, each

adapted to their local conditions. In marginal areas under uncertain environmental conditions farmers also tend to avoid risks, resulting in a higher diversity on the farm. On the other hand, if less environmental or climatic variation is found within the area, or when the agricultural land can be easily homogenized lower agrobiodiversity is expected.

- Diversity of farmer types

  The second component is the diversity of farmer types within an area. To understand the influence of heterogeneity of farmer types within an area an analysis of the different farmer types in relation to agrobiodiversity should be done. Given the environmental conditions (determined by the farm biophysical characteristics) it can be assumed that farmer types differ for agrobiodiversity managed at the farm according to the following components:

  1. Market integration
  2. Internal factors, such as farm technology, household characteristics (age, education, skills) and farm structural characteristics
  3. Remoteness (seen as isolation from physical infrastructure)

  Following the hypothetical relationship between agrobiodiversity and extent of market integration (Figure 12) agrobiodiversity will be high at farms that are characterized as being not integrated in the market. A little increase can be expected when farmers produce partly for the market, while a decrease can be expected when market integration is high. Each farmer type is expected to use different varieties/breeds, each adapted to their own needs and constraints (capital, human, social). When a particular area is mainly occupied by subsistence/surplus farmers it can be expected that the agrobiodiversity is highest. On the contrary, when a large part of the area is occupied with commercial farmers, diversity is expected to be low. However, we should not assume that only subsistence or surplus farmers exist in low-potential agricultural or marginal areas. Sometimes a mixture of farmer types can be expected, together they determine the agrobiodiversity.

- Trade intensity

  The impact of trade intensity is determined by the density and diversity of the market infrastructure within an area. A high trade intensity implies that farmers have better access to markets for input (e.g. seed supply), output or labour and are producing for different type of markets including national and global markets. In such typical agro-industrialized areas a lower agrobiodiversity can be expected. Alternatively, agrobiodiversity will be high in areas where the market infrastructure is mainly lacking and farmers are producing for a local or regional market.

- Infrastructure

  Another important component is infrastructure. Hard infrastructure such as roads, railways, airports, determines the access to resources and transport of the agricultural products. Commercial farmers can only sustain if the supporting infrastructure is present. If infrastructure is lacking in the area, a high agrobiodiversity can be expected as fewer replacements of local varieties/breeds occur. When areas become more accessible loss of agrobiodiversity is observed.

- Societal and political factors

  There are a number of societal and political factors. Together they determine the farmer's access to diversity or substitutes for natural resources. They can affect agrobiodiversity in a positive or a negative way. Here we include at least:

  S_1 = Diversity of stakeholders

  The influence of a wide range of stakeholders on agrobiodiversity within an area is not so clear. In this respect it might also be useful to analyze the stakeholders in an area or country. The most important stakeholder groups affecting the availability of varieties/breeds are: the seed supply sector, scientists, breeders and gene banks. The formal seed supply sector, scientists and breeders will mainly have their impact on diversity in the more commercial agriculture. It is expected that they have a negative effect if this means replacement of local diversity by modern varieties, unless breeders aim at developing material for different environments or farmer's preferences. In these cases agrobiodiversity may be maintained. If more breeders are involved in a particular crop with more and different breeding goals, one might expect a higher agrobiodiversity. Gene banks have

their influence through facilitating access and exchange of genetic resources that may broaden the gene pools to be used in breeding. Other stakeholders that importantly affect the demand of diversity are processors and retailers and to a minor extent consumers (only in niche markets), NGO's and national governments.
S_2 = governance
There are a number of political factors, such as good/bad governance, corruption, political instabilities, (lack of) policies, laws that determine the extent of socialization in an area or country. However, it is difficult to predict how they will affect agrobiodiversity. Moreover, insight in political factors is probably hard to come by. Here we consider governance. If good governance involves initiatives to promote productivity, better access to inputs and integration in the market for farmers, this can indirectly have a negative effect on maintaining agrobiodiversity.

A number of the earlier described drivers are not taken into account in the above conceptual function. Social-cultural and religious factors, e.g. consumer choices are not included, they are mainly of local importance. For giving a global picture of agrobiodiversity they are less relevant. War and conflicts, diseases, and environmental stresses, induced by climate change, are seen as 'disturbers' and are also left out for the time being.

For further research a better qualitative description of agrobiodiversity in relation to these components is needed. Moreover, the subsequent identification of a set of indicators (of proxies) for the most important components needs much more thinking. Here, some suggestions are given for potential driving force indicators that cover the above mentioned aspects (see also Table 5):

- Insight in the agricultural potential of an area related to the environmental and climatic heterogeneity is needed. As a basis the FAO agro-ecological zone maps (AEZ) can be used, to which other relevant environmental and climatic information can be added such as irrigation, soil quality, cultivated area.

- The type of agricultural system (more traditional or industrial system) should be kept in mind. If an analysis of the assemblage of the different farmer types within an area is not feasible, as an alternative, farming systems following the classification of Dixon, *et al.* (2001), the livestock production systems of FAO (1995) or a modification of these could be used. These farming systems could be refined by adding extra information such as technology adoption (including income, knowledge, education, farm size). This would give a better differentiation between the farmers' skills to manage diversity.

- Trade intensity at a national level is mainly determined by purchasing power and urbanization. Furthermore, it is determined by the extent of integration in the global market. Insight in trade intensity may be obtained from indicators on size of trade in commodities, regional or national labour markets and macro economic development indicators.

- Access to hard infrastructure can be represented by road density.

- An analysis of the stakeholders that support farmers and natural resource users is needed to further investigate the importance of this group in affecting agrobiodiversity. Scientists, seed industry and breeders are seen as important stakeholders as development in science and breeding is an important driver of change in the homogenization process. Data on investment in breeding research are probably difficult to get, even for the public sector. As an alternative, aggregated data for the whole agricultural research area can be used, which are better available (agricultural science & technology indicators (ASTI) for developing countries (IFPRI/ISNAR). As a proxy for investment in breeding research also the number of breeding entities active in a crop/livestock species could be used. Additionally for crops, insight in the structure of the seed industry can be given by the number of applications for Plant Variety Protection (PVP) per breeding entity.

- A governance index could be included.

Table 5. Potential driving force indicators to be used for further analysis.

Type	Indicator	Description	Data source
Environmental-based	Agro potential	Agro ecological zones	FAO
Economic-based	Purchasing power		World Bank
	Urbanization	People in the pixel (PHOENIX model)	PBL
	Value added in agriculture (% of GDP)	Agricultural GDP	World Bank
	Foreign direct investment (FDI)	Integration in global market	OECD/ World Bank
	Share of (agricultural) imports plus exports in GDP		
	(In- and out) migration		
	Infrastructure	Road density (GLOBIO model)	PBL
Science and technological-based	Number of breeding entities per crop/species (individual, domestic or international companies, governmental institutes)		
	Technology development	Land and labor productivity (IMAGE model?)	PBL
	Agricultural R& D indicators for developing countries	Investments in agricultural research (public/private) for developing countries	ASTI
	S&T indicators	Science and Technology investments for developed countries	OECD
Socio-political-based	Number of applications for PVP total or per breeding entity (domestic public, universities, domestic seed companies, domestic individual breeders, foreign entities	Structure of seed industry/ Impact of plant variety protection	UPOV
	Governance	UNDP, transparency or governance index	UNDP/ World Bank

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Appendix I.
Varieties of summer and winter wheat

Table 1. Varieties of summer and winter wheat that are placed on the variety list of 2004. From the information on the parents it can be found that the varieties 'Ilias' and 'Kampa' are derived from the same parents. The same holds for the varieties 'Residence' and 'Semper'.

Variety	Type	Parents
Baldus	Summer wheat	Sicco x sel (Sicco x (N66 x MGH 653)) x Kolibri
Bristol	Winter wheat	Wilde Emmer Composite Cross x Estica
Drifter	Winter wheat	Ronos x Estica
Globus	Winter wheat	onbekend
Harlem	Winter wheat	Heven x (Moulin x Hereward)
Ilias	Winter wheat	Estica x Urban
Kampa	Winter wheat	Urban x Estica
Lavett	Summer wheat	(WW 118466 x Kadett) x Dragon
Limes	Winter wheat	Line C 16 x Rialto
Melon	Summer wheat	(Walter x stam uit (Famos x Solo x Kolibri)) x Minaret
Napier	Winter wheat	Hussar x Lynx
Pasteur	Summer wheat	Cadenza x (Palermo x KS WGRC 11-1)
Residence	Winter wheat	Obelisk x (Cebeco 8451 x Arminda)
Semper	Winter wheat	Obelisk x (Cebeco 8451 x Arminda)
SW Tataros	Winter wheat	(Tambor x Rendezvous) x Tambor
Thasos	Summer wheat	(Max x ZE 73.1331) x Minaret
Tulsa	Winter wheat	EC 351366 x Toronto
Tybalt	Summer wheat	ZE 2355 x Chablis
Vivant	Winter wheat	Boxer x Gawain

Appendix II.
Proposed indicators for agrobiodiversity

Table 2. Proposed indicators for agrobiodiversity within crop or livestock species on the intraspecific level.

Nr.	Name	Description	Reference
1.	Number of livestock breeds	Number of breeds of livestock species per region.	CBD (2003b)
		For the main livestock categories the total number of livestock breeds that have been registered and certified for marketing.	OECD (2001)
		Number of key livestock breeds (native endangered, native not endangered, non-native).	Wetterich (2003)
		Total number of cattle sheep/breeds.	EEA (2007a,b)
2.	Number of crop varieties	Number of varieties per crop by region.	CBD (2003b)
		For the main crop categories the total number of crop varieties that have been registered and certified for marketing.	OECD (2001)
		Total number of crop varieties per crop that are available to farmers in the locality/country/world; *i.e.*: registered varieties and named varieties/farmer-managed-units of diversity.	FAO (2002)
		Number of key crop varieties (domestic, non-domestic).	Wetterich (2003)
3.	Share of livestock breeds	Share of key livestock breeds in respective categories of livestock numbers (*i.e.* in total livestock population per species).	OECD (2001)
		Share of the three major livestock breeds (native, non-native breeds).	Wetterich (2003)
		Total number of breeding females of cattle/sheep breeds.	EEA (2007a,b)
		Total number of breeding females of native cattle/sheep breeds.	EEA (2007a,b)
4.	Share of crop varieties	Share of major varieties in total production for individual crops.	CBD (2003b)
		Share of key crop varieties in total marketed production for individual crops.	OECD (2001)
		Number of major varieties accounting for 50% of the total acreage or production for individual crops.	FAO (2002
		Percentage of total acreage or production of the top 5 and top 10 varieties.	FAO (2002)
		Share of the three major crop varieties in seed production area or diversity index.	Wetterich (2003)
		Area of varieties characteristic for landscapes/ production environments important for biodiversity and characteristic for a region or country.	Eaton, *et al.* (2006a)

Nr.	Name	Description	Reference
5.	Number of endangered livestock breeds	The number of national livestock breeds that are endangered.	OECD (2001)
		Native breeds'population size and status of endangerment	Wetterich (2003)
		Total number of cattle/sheep breeds which population is endangered (*i.e.* below a threshold defined by each country).	EEA (2007a,b)
		Population size native breeds – number of breeds conserved *in situ*	Eaton, *et al.* (2006a)
6.	Number of endangered crop varieties	The number of national crop varieties that are endangered.	OECD (2001)
		Number (and names) of endangered varieties.	FAO (2002)
		Number of endangered national crop varieties.	Wetterich (2003)
		Distribution of risk status of national livestock breeds in agriculture.	EEA (2005)
7.	Share of endangered crop varieties	Indication of population size of endangered varieties.	FAO (2002)
8.	Genetic differences among crop varieties	Estimation of genetic differences among major varieties, determined from pedigree data or direct measures.	FAO (2002)
		Number of founder lines.	FAO (2002)
		Number of landraces and crop wild relatives employed per breeding target environment.	FAO (2002)
9.	Potential genetic erosion for crops	Percentage of major varieties exceeding 50% of the total acreage or production for individual crops.	FAO (2002)
		Increase rate of spread of major varieties for individual crops.	FAO (2002)
10.	Crop breeding activities	Number of independent breeding programs per crop.	FAO (2002)
		Number of fulltime plant breeders per crop.	FAO (2002)
		Number of full-time employees involved in genetic enhancement per crop.	FAO (2002)
		Consolidation of seed/breeding companies.	FAO (2002)
		Entry of multinational companies in developing countries.	FAO (2002)
		Size of breeders working collections.	FAO (2002)
		Number of breeders per crop.	Wetterich (2003)
		Intensification and use of modern plant breeding strategies.	Eaton, *et al.* (2006a)
		Number of different crop breeding goals.	Eaton, *et al.* (2006a)
11.	Livestock breeding activities	Number of livestock breeder's associations.	Wetterich (2003)
		Application of high-selective livestock breeding methods.	Wetterich (2003)
		Intensification and use of modern animal breeding strategies.	Eaton, *et al.* (2006a)
		Number of different livestock breeding goals.	Eaton, *et al.* (2006a)
		Number of breeding organizations of high production breeds	Eaton, *et al.* (2006a)

Nr.	Name	Description	Reference
12.	Relation with crop farmer management	Percentage of new seed per season.	FAO (2002)
		Percentage seed originating on farm of three major (high production) breeds.	Eaton, *et al.* (2006a)
		Ratio of changed varieties to total varieties per farmer or community for a certain number of years.	FAO (2002)
		Degree of specialization of genetic resources related knowledge and activities of farmers.	FAO (2002)
		Selection and conservation activities of nodal farmers; farmer-breeders.	FAO (2002)
		Presence or absence of geneflow with wild relatives.	FAO (2002)
		Share of genetically heterogeneous and homogeneous varieties.	Wetterich (2003)
		Share of varieties with and without evolutionary potential.	Wetterich (2003)
		Share of crop varieties and species adapted to landscapes/production environments important for biodiversity and/or characteristic for a region or country.	Eaton, *et al.* (2006a)
		Area of low production/high biodiversity.	Eaton, *et al.* (2006a)
13.	Relation with animal farmer management	Number of breeding males of breeds characteristic for landscapes/production environments important for biodiversity and/or characteristic for a region or country.	Eaton, *et al.* (2006a)
14.	Conservation of plant genetic resources	Landraces or wild relatives in areas that have not been well-collected.	FAO (2002)
		Number of accessions of plant genetic resources conserved *ex situ*.	FAO (2002)
		Number of crop varieties and wild relatives per crop conserved *ex situ*.	FAO (2002)
		Conservation conditions, facility, safety duplication of the collection and regeneration status.	FAO (2002)
		Completeness of data in the documentation of the *ex situ* collection.	FAO (2002)
		Number of plant genetic resources accessions characterized.	Eaton, *et al.* (2006a)
		Accessions in the *ex situ* collection whether or not in the Multilateral system and/or international network, and/or otherwise freely available.	FAO (2002)
		Number of characteristic (low production) varieties stored in gene bank.	Eaton, *et al.* (2006a)
15.	Conservation of animal genetic resources	Number of breeds conserved *ex situ*.	Eaton, *et al.* (2006a)
		Number of animal genetic resources accessions characterized.	Eaton, *et al.* (2006a)
		Number of breeding males in gene bank(s) of characteristic (low production) breeds.	Eaton, *et al.* (2006a)