

M O D U L E

b

ECOLOGICAL
ASPECTS

Biosafety Resource Book



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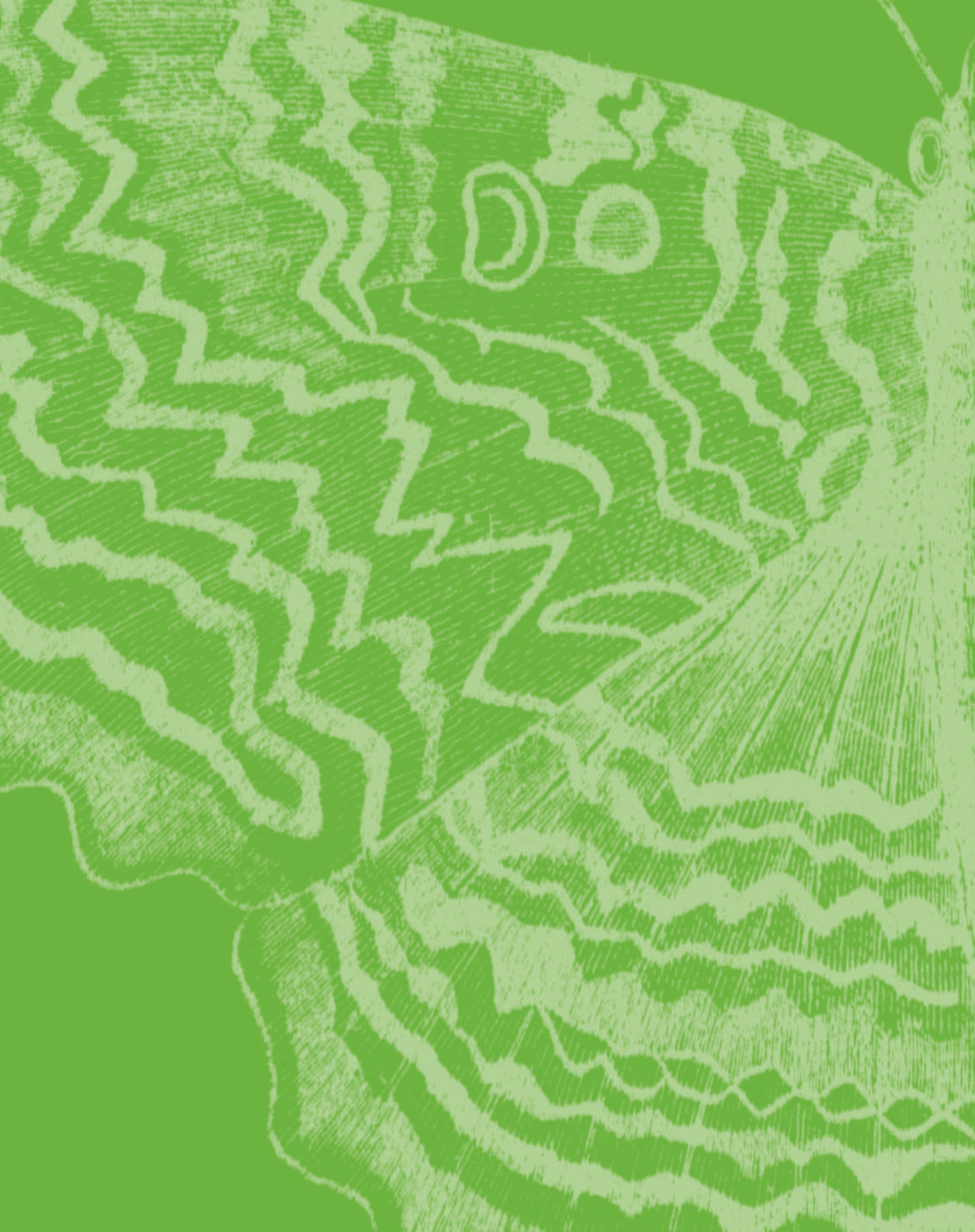
Book **b**

Biosafety Resource

ECOLOGICAL ASPECTS

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LIST OF ABBREVIATIONS

AUIAB & NC	All-Union Institute of Applied Botany and New Crops
Bt	<i>Bacillus thuringiensis</i>
DNA	deoxyribonucleic acid
FAO	Food and Agriculture Organization of the United Nations
GIS	Geographical Information System
GM	genetically modified
GMOs	genetically modified organisms
GURT	genetic use restriction technology
HGT	horizontal gene transfer
IUCN	International Union for Conservation of Nature
MAS	marker assisted selection
NRC-CEI	National Research Council-Committee on Environmental Impacts
PGR	plant genetic resources
QTL	quantitative trait loci
UNCED	United Nations Conference on Environment and Development
VGT	vertical gene transfer

INTRODUCTION TO ECOLOGY: BASIC CONCEPTS AND DEFINITIONS

1.1 WHAT IS ECOLOGY?

The word ecology, coined in 1866 by the German biologist Ernst Haeckel, derives from the Greek word “oikos” meaning “house” or “dwelling”, and *logos* meaning “science” or “study”. Thus, **ecology** is the “study of the household of nature”, namely the systematic study of the distribution and abundance of living organisms - plants, animals, micro-organisms - and their interactions with one another and with their natural environment. The environment consists of both a living component, the **biotic environment** (organisms) and a non-living component, the **abiotic environment**, including physical factors such as temperature, sunlight, soil, rainfall, wind, and marine streams (Begon *et al.*, 2006).

Few fields of study are more relevant to the human society and condition than the field in ecology. The increasing globalization of our economy and the resulting changes in social and political structures have a strong impact on our environment. One example is the both intentional and accidental dispersal of organisms, including pests and diseases, to all corners of the earth – ecological globalization on a grand scale. Generally, all activities of the human population affect the natural systems. Ecology, today, investigates several aspects and concerns:

- » Interactions between organisms and the environment;
- » How to understand, conserve, restore and sustainably use biodiversity;

ECOLOGY

The systematic study of the distribution and abundance of living organisms and their interactions with one another and with their natural environment.

BIOTIC ENVIRONMENT

All living components of the environment.

ABIOTIC ENVIRONMENT

All non-living environmental factors, e.g. temperature, rainfall, wind, insolation etc.

- » Impact of foreign species in ecosystems;
- » Strategies for management, mitigation and reduction of impacts caused by human activity.

Critical considerations for ecological studies are that the natural world is diverse, complex and interconnected; that it is dynamic but at the same time stable and self-replenishing; that it is controlled by physical and biological processes, and that the order of nature is affected by human activity.

Life depends upon the abiotic, physical world, and vice versa affects it. Each organism continually exchanges materials and energy with the physical environment. Organisms interact with one another, directly or indirectly, through feeding relationships or *trophic interactions*. Trophic interactions involve biochemical transformations of energy and the transfer of energy from one individual to the next through the process of consumption. Materials move within ecosystems, and the pathways of such movements are closely associated with the flow of energy (Purves *et al.*, 2004). The flow of energy and its transfer efficiency characterize certain aspects of an ecosystem: the number of trophic levels, the relative importance of detritus, herbivore and predatory feeding, the steady-state values for biomass and accumulated detritus, and the turnover rates of organic matter in the community. Unlike energy, nutrients are retained within the ecosystem and are cycled between its abiotic and biotic components.

BIOGEOCHEMICAL CYCLES

The cycles by which an element or molecule moves through the biotic and abiotic compartments of Earth. Also referred to as nutrient cycles.

Human activities modify or disrupt the **global biogeochemical cycles** and create cycles of synthetic chemicals, such as pesticides. These changes can be large enough to cause serious environmental problems. However, ecosystems have the capacity to recover from many disturbances if the alterations have not been too large and the disturbing forces are reduced or eliminated. Controlling our manipulations of biogeochemical cycles so that ecosystems can continue to provide the goods and services upon which humanity depends is one of the major challenges facing modern societies (Purves *et al.*, 2004).

1.2 ORGANIZATION OF LIFE: HIERARCHY OF INTERACTIONS – LEVELS OF ECOLOGICAL ORGANIZATION

Below, in Table 1, are the most important terms and definitions listed that are employed in ecological sciences:

Table 1.1 | Terms and definitions in Ecology

Individual	An individual is a single organism inhabiting the environment as an isolated entity or as a member of a social group.
Species	Is the basic unit of classification of closely related organisms that have a high level of genetic similarity, are capable of interbreeding producing fertile offspring, and are reproductively isolated from other groups of organisms. This definition works well with animals. However, in some plant species fertile crossings can take place among related species.
Population	A population is a group of individuals of the same species living in a particular area. Populations are characterized by several parameters, such as abundance and distribution of their member organisms. The amount of resources available, diseases, competition for the limited resources, predation, birth and death rates, immigration and emigration affect the size of a population. Populations show characteristic age structures and age distributions. They are also characterized by an intrinsic rate of increase, the biotic potential. Populations do not show unlimited growth, they are limited by the carrying capacity of their habitat. Density-dependent and density-independent factors influence the size and growth of a population.
Community	A community is made up of the interacting, coexisting populations of different species occupying the same geographical area. Communities are characterized by the numbers of species present, their relative abundance, and their feeding and other ecological relationships. Within the community, there is competition for resources, various intra- and inter-species relationships and possibly exchange of genes. Populations and communities include only biotic factors, i.e. living components.
Ecosystem	An ecosystem is the complex of a living community (biotic factors) and abiotic factors (soil, rain, temperatures, etc.) in a given area. Ecosystems are further influenced by global phenomena such as climate patterns and nutrient cycles. The community influences the environment, and the environment influences the community, leading to changes and succession in the ecosystem. Energy flow, biogeochemical, water and nutrient cycles characterize ecosystems. The flow of energy is characterized by clearly defined trophic structures, biotic diversity, and material cycles (i.e. exchange of materials between living and non-living parts) within the ecosystem.

SPECIES

A group of organisms capable of interbreeding producing fertile offspring, and reproductively isolated from other groups of organisms.

POPULATION

A group of individuals of the same species living in a particular area.

ECOSYSTEM

The complex of a living community (biotic factors) and abiotic factors, and the interactions between them, in a given area.

Biosphere	The totality of ecosystems constitutes the biosphere, the portion of the earth that contains living species. It includes the atmosphere, oceans, soils and all the biogeochemical cycles that affect them.
Biome	Is another level of interaction placed between the ecosystem and the biosphere. A biome is a major ecological community or complex of communities, extending over a climatically and geographically defined area. There are two broad categories of biomes: aquatic and terrestrial. Biomes are defined by factors such as plant structures (e.g. trees, shrubs and grasses), leaf types (such as broadleaf and needleleaf), plant spacing (forest, woodland, savannah), and climate. Similar biomes exist on different continents and are often given local names. For example, a temperate grassland or shrubland biome is commonly known as <i>steppe</i> in central Asia, <i>prairie</i> in North America, and <i>pampas</i> in South America.

Attributes of individuals

The ecology of the individual is mainly concerned with the effects of the abiotic and biotic environment on its survival and reproduction rate. Any shortcomings in the phenotype or genotype of an individual will result in a selective pressure being exerted on it, and the individuals mostly affected by the adverse environmental factors will be removed from the population. Conversely, individuals with favourable traits will survive and show a higher rate of reproduction (see also chapter 3). This, of course, can be extended up to the species level, where such selection mechanisms determine the range of species in an ecosystem according to their environmental requirements and susceptibilities.

Attributes of populations

Populations have certain characteristics that define them. They have characteristic distributions over space, and they differ in age structure and size; they can be clumped together, randomly or uniformly distributed in their environment. They show growth rates (including negative growth) which define their abundance. The number of individuals in a population depends on the birth and death rates, and the net result of immigration and emigration. Each population has a tempo-spatial

structure, which includes features such as the density, spacing and movement of individuals, the proportion of individuals in different age classes, genetic variation, and the arrangement and size of areas of suitable habitat, all of which may vary in space and time. Population structure is also affected by the dynamics of parasites and their hosts, including for example, human diseases (Purves *et al.*, 2004). The structure of populations changes continually because demographic events, including births, deaths, immigration (movement of individuals into the area), and emigration (movement of individuals out of the area), are common occurrences. The study of birth, death and movement rates that give rise to population dynamics is known as **demography**. Individuals within a population compete with each other for resources such as space, mating partners and food. A population continues to grow until the habitat carrying capacity is reached. However, density independent factors, i.e. factors that do not depend on the actual number of individuals in a population, such as weather conditions (storms, floods, drought) and natural disasters (earthquakes, volcanic eruptions) may strongly influence population structure.

Genetic differentiation of populations depends far less on the movement of individuals among populations than on the forces of selection, mutation, and random change (genetic drift). Gene flow is the exchange of genetic information among populations resulting from the movement of individuals. The genetic structure of a population describes the distribution of the variation among individuals and among subpopulations, as well as the influence of mating systems on genetic variation. **Genetic variation** is important to a population because it is the basis of the population's capacity to become adapted to environmental change through evolution (Ricklefs and Miller, 1999). Genetic variation is also important to individuals: variation among an individual's progeny may increase the likelihood that at least some of them will be well adapted to particular habitat patches or to changing environmental conditions. Genetic variation is maintained primarily by random mutation and by gene flow from populations in other localities in which different genes have a selective advantage.

DEMOGRAPHY

The statistical study of populations, i.e. of the size, structure and distribution of populations, and spatial and/or temporal changes in them in response to birth, death and migration rates.

GENETIC VARIATION

Differences between individuals attributable to differences in the genotype.

COMMUNITIES

The entirety of interacting organisms/populations sharing the same environment.

Attributes of communities

The same factors that define populations also define communities. **Communities** are usually defined by the interactions among the populations in the community and by the habitat in which the community occurs. Communities are characterized by several interrelated properties, grouped into the categories of *structure* and *function*. Structure refers to the number of species, called species richness, the types of species present and their relative abundances, the physical characteristics of the environment, and the trophic relationships among the interacting populations in the community. Rates of energy flow, properties of community resilience to perturbation, and net productivity are examples of community function. (Ricklefs and Miller, 1999). The species composition of ecological communities changes constantly over time.

Organisms interact with one another in different ways in their community:

- » Two organisms may mutually harm one another. This type of interaction – **competition** - is common when organisms use the same resource. Intraspecific competition is competition among individuals of the same species. Competition among species is referred to as interspecific competition.
- » One organism may benefit itself while harming another, as when individuals of one species eat individuals of another (i.e. herbivores and carnivores). The eater is called a predator or parasite, and the eaten is called prey or host. These interactions are known as predator-prey or parasite-host interactions. Predators act as evolutionary agents by exerting selective pressure on their prey, which may eventually result in adaptation of the prey to protect itself against the predator (e.g. toxic hairs and bristles, tough spines, noxious chemicals and mimicry). This evolutionary mechanism also works in the other direction: once a prey has developed protective measures, selective pressure is exerted on the predator to develop features that allow it to overcome these restrictions and still be able to feed on the prey. It should be noted that these

COMPETITION

A contest between two or more organisms/species for the same resource.

are passive processes that cannot be influenced by the individual species/organism; please refer to Chapter 3 for details of evolution and speciation.

- » Mutualistic interaction takes place when both participants benefit. **Mutualistic interactions** occur between members of different groups of organisms (between plants and prokaryotes, between fungi and protists, between animals and protists, between animals and plants and with other animals). If one participant benefits but the other is unaffected, the interaction is a commensalism. If one participant is harmed but the other is unaffected, the interaction is an amensalism. Mutualism, commensalism and amensalism are all different forms of symbiosis.

Attributes of ecosystems

Ecosystems have **trophic levels**, which can be described as *energy pyramids* or *food pyramids*. The first trophic level is composed of primary producers that utilize light energy to produce high-energy compounds, usually in the form of carbohydrates (sugars). These organisms are referred to as autotrophs and are mostly plants (but include also bacteria and algae). Since only photosynthetic organisms are able to convert light energy to high-energy molecules, they have a key position in the ecosystem. Any factor that affects plants has strong implications on the ecosystem. The second trophic level is made up of primary consumers, which are the herbivores (i.e. plant-feeding organisms). The next level up is composed of secondary consumers, the carnivores (i.e. animal-feeding organisms); followed by top carnivores. Finally, all organisms that decompose dead organic matter are referred to as saprophytes, or detritivores. The feeding relationships ensure transfer of energy from one trophic level to the other. Importantly, only about 10 percent of energy is available for transfer from one trophic level to the next, which is why the possible number of carnivores and top carnivores is low, and hence trophic levels can be depicted as pyramids. The various interactions and feeding relationships between organisms in a community can also be depicted as food web (Box 1.1).

MUTUALISM

The close association of two different kinds of living organisms where there is benefit to both or where both receive an advantage from the association. A prominent example is the colonization of *Rhizobium* spp. inside the roots of leguminous plants.

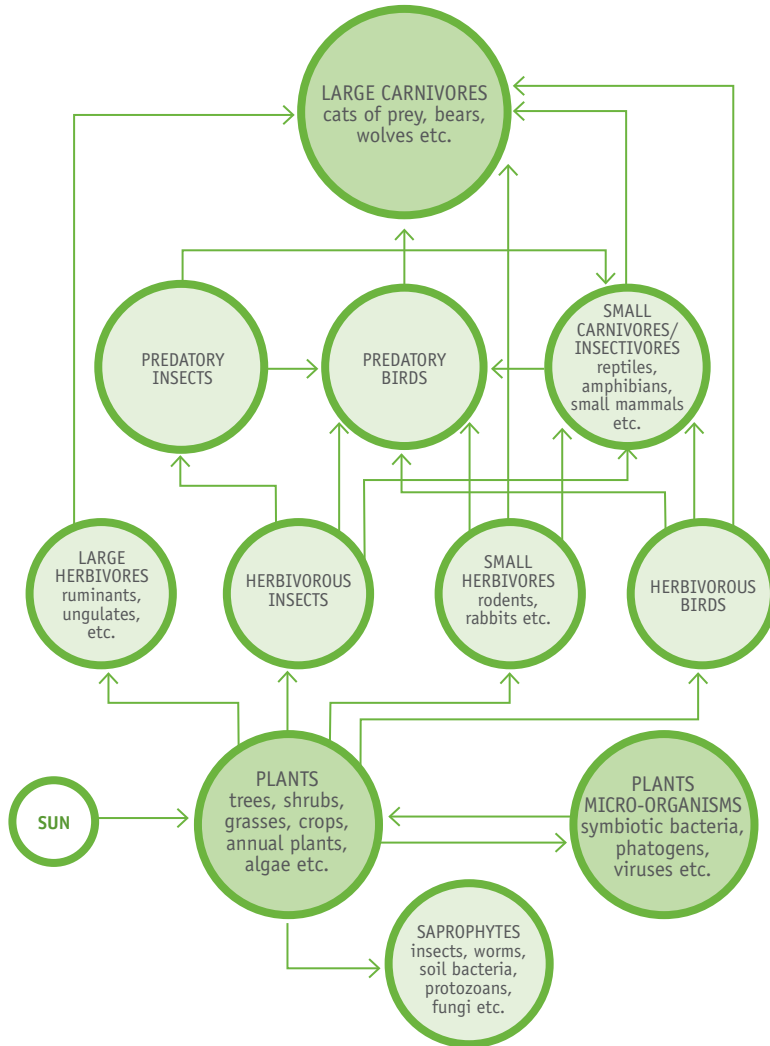
TROPHIC LEVELS

The different positions that an organism/species can occupy in the food chain.

BOX 1.1

TROPHIC LEVELS, FEEDING RELATIONSHIPS AND FOOD WEBS

Below, a highly simplified and generalized depiction of the various feeding relationships in a hypothetical “standard” ecosystem is shown.



As discussed in the text, all energy input in a typical ecosystem is derived from the sun.

Organisms that can directly utilize light energy and convert it into biomass are called autotrophs; this includes all photosynthetic plants. Plants and other autotrophic organisms therefore constitute the first trophic level, and are referred to as primary producers.

The primary producers are consumed by a large variety of primary consumers, the herbivores, constituting the second trophic level. The primary consumers are in turn consumed by secondary consumers (carnivores and insectivores) and so on. As already pointed out in the text, due to energy losses from one trophic level to the next, the number of trophic levels is limited (typically around five) and the maximum number of top carnivores is much lower compared with the number of primary producers. Please note

that all organic matter, if not consumed by other organisms, is ultimately decomposed by the saprophytes (arrows between animals and saprophytes have been omitted for clarity).

In a detailed food web, individual species and their feeding relationships would be depicted, which can result in a highly complex diagram. Plants occupy a central position in food webs, being the primary source of energy and interacting with a large variety of organisms. Therefore, it would be helpful to carefully investigate the ecological relations and establish a detailed food web for a crop species that is subject to genetic modification. This would facilitate the prediction, investigation and assessment of the possible direct and indirect impacts of that genetic modification on the community interacting with and depending on that crop species.

BIODIVERSITY: GENETICS, SPECIES AND ECOSYSTEMS

2.1 BIODIVERSITY

BIODIVERSITY

The variability among living organisms from all sources, including, *inter alia*, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part.

Biodiversity is the variation of life at all levels of biological organization; including genes, species, and ecosystems. At the United Nations Conference on Environment and Development (UNCED) in Rio de Janeiro in 1992, it was defined as: “The variability among living organisms from all sources, including, *inter alia*, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part: this includes diversity within species, between species and of ecosystems”. The three most commonly studied levels of biodiversity are ecosystem diversity, species diversity and genetic diversity. Given that the gene is the fundamental unit of natural selection, the real biodiversity is genetic diversity. For geneticists, biodiversity is the diversity of genes and organisms. They study processes such as mutations, gene exchanges and genome dynamics that occur at the deoxyribonucleic acid (DNA) level and are the driving force for evolution.

In ecological indexes, *Alpha* diversity refers to diversity within a particular area, community or ecosystem, and is measured by counting the number of taxa (usually species) within the ecosystem. *Beta* diversity is species diversity between

ecosystems; this involves comparing the number of taxa that are unique to each of the ecosystems in comparison. *Gamma* diversity is a measure of the overall diversity for different ecosystems within a region. Cultural or anthropological diversity is also involved when studying regional diversity. Biodiversity is not static; it is constantly changing. It is not evenly distributed on earth, and tends to be richer in the tropical regions. It varies with climate, altitude, soil composition and other physical parameters. Hotspots, regions with many endemic species, are usually found in areas with limited human impact, while regions with a high human population tend to have the lowest number of species, and thus a low biodiversity.

2.2 VALUES OF BIODIVERSITY

Biodiversity has paramount importance for the social, cultural and economic development of humankind. Some ecosystem parameters that influence human society are air quality, climate (both global and local), water purification, disease control, biological pest control, pollination and prevention of erosion. Biodiversity plays a part in regulating the chemistry of our atmosphere and water supply; it is directly involved in water purification, recycling nutrients and providing fertile soils. There are a multitude of anthropocentric benefits of biodiversity in the areas of agriculture, science and medicine, industrial materials, ecological services, in leisure, and in cultural, aesthetic and intellectual value. The most direct and important use of biodiversity is as a source of food. Although a large number of plant species are edible, only a small percentage are used intensively in the production of food with significant nutritional value. Likewise, only a few of the numerous animal species are used for food production. Plant biodiversity is the basis of development and sustainability of agricultural production systems. A reduction in the genetic diversity of crops represents an increase in vulnerability to new pests and diseases. The economic value of the reservoir of genetic traits present in wild varieties and traditionally grown landraces is very high for improving crop

VALUES OF BIODIVERSITY

Include, among others, food supply and improvement, climate regulation, water purification, soil fertility, medicine, and aesthetic and cultural values.

performance (The Academies of Sciences, 2007). Important crops, such as potato and coffee, are often derived from only a few genetic strains. Improvements in crop plants over the last 250 years have been largely due to harnessing the genetic diversity present in wild and domestic crop plants.

2.3 ECOSYSTEM, SPECIES, AND GENETIC DIVERSITY

Besides the large diversity of life on earth, our planet also contains a rich variety of habitats and ecosystems. Biodiversity is determined by both its biotic components, represented by living organisms, and its abiotic components, represented by the characteristics of the locations where the organisms live. In a strict sense, diversity is a measure of the heterogeneity of a system. This concept, when applied to biological systems, refers to the *biological heterogeneity that is defined as the amount and proportion of the different biological elements contained in a system.*

ECOSYSTEM DIVERSITY

Comprises the diversity of natural and artificial habitats, plus the species communities they contain.

Ecosystem diversity comprises the diversity of natural and artificial habitats, plus the species communities they contain. A certain species is usually found in a distinct ecological system, such as a tropical forest, a tropical savanna, or a coral reef. However, measuring ecosystem diversity may be difficult because the boundaries among communities and ecosystems are poorly defined. Human influence on natural ecosystems can result in severe consequences, for example, desertification and soil erosion, changes in the climate and the atmospheric composition, pest outbursts, and extinction of species.

SPECIES DIVERSITY

The number of species in an area and their relative abundance.

Species diversity is a result of the relation between the species' richness (number of species) and their relative abundance (number of individuals of each species) in a given area. A more precise concept is taxonomic diversity, which accounts for the diversity of a group of species that are more or less related. One of the major challenges for biologists today is to describe, classify and propose a sustainable

BOX 2.1

MEGADIVERSITY

The term megadiversity refers to areas which account for a high percentage of the world's biodiversity, by virtue of containing the most diverse and the highest number of plant and animal species.

Species diversity in natural habitats is higher in warm and rainy zones and decreases as latitude and altitude increase. The richest zones of the world in terms of biodiversity are undoubtedly the tropical rain forests, which cover 7 percent of the world's surface and contain 90 percent of the insect species of the world. (CBD, 2002; WCMC, 2002). Megadiverse countries are: Brazil, Colombia, Indonesia, China, Mexico, South Africa, Venezuela, Ecuador, United States, Papua New Guinea, India, Australia, Malaysia, Madagascar, Democratic Republic of the Congo, Philippines and Peru.

Concentrating on geographical areas and not on specific countries,

25 hotspots for biodiversity can be identified: Polynesia/Micronesia, Flower Province of California, Central America, Choco/Darien/West Ecuador, central Chile, the Caribbean, Atlantic forest of Brazil, Brazilian Cerrado, forests of West Africa, the Karoo (succulents), the Mediterranean basin, Madagascar, the coastal forests of the eastern arc of Tanzania and Kenya, the Caucasus, Sri Lanka and the Western Ghats, south-central China, Sundaland, the Philippines, Wallacea, South West Australia, New Zealand and New Caledonia. These zones occupy only about 1.4 percent of the earth's surface and contain 44 percent of the known plants and 35 percent of the known animals. Tropical forests and Mediterranean zones predominate. Three of the zones are of special importance; Madagascar, the Philippines and Sundaland, followed by the Atlantic forests of Brazil and the Caribbean. The tropical Andes and Mediterranean basin are also important for their rich plant diversity.

use of organisms living in poorly understood habitats such as those in tropical rain forests, marine ecosystems and soil communities (Ricklefs and Miller, 1999). Species diversity has an important ecological effect on the structure of communities due to the interactions and interdependences among species: the reduction or disappearance of a given species may strongly influence other species that depend on it (WCMC, 2002).

GENETIC DIVERSITY

Refers to the total number of genetic varieties in the gene pool of a population, between populations or within a species, which are created, enhanced or maintained by evolutionary or selective forces.

Genetic diversity refers to the variation of genes within a certain population, among different populations or within a species. This type of diversity can be characterized at the molecular, population, species or ecosystem level. A lot of attention has been paid to genetic diversity due to its practical applications on plant and animal breeding and production, and for evolutionary studies (Purves *et al.*, 2004).

2.4 PROBLEMS AND THREATS TO BIODIVERSITY

Extinction has been a naturally occurring phenomenon over millions of years, without any human involvement. However, due to human activities and their effect on the environment, species and ecosystems have become increasingly threatened in an alarming way (WCMC, 2002), undermining the basis required for sustainable development. Almost all human activities result in a modification of natural environments. These modifications are harmful to the relative abundance of species and may even lead to species extinction. The main causes of environmental modification are: habitat alteration, for example by pollutants; habitat fragmentation, which can divide a big population into small isolated subpopulations and increase their risk of extinction if they are excessively reduced in size; habitat destruction, for example by converting forest to arable land or settlement areas; introduction of exotic or non-native species; overexploitation of plants and animals; soil, water and atmosphere pollution; alteration of the global climate; and agroindustries, including forestry. Although the loss of biodiversity in the form of crop varieties and domestic animal races has little

significance compared with global biodiversity, their **genetic erosion** is of immediate concern as it has profound implications and consequences for food supply and sustainability of local practices of animal and agricultural production (WCMC, 2002). Genetic erosion is difficult to assess quantitatively. It is usually calculated in an indirect way.

After 10 000 years of sedentary agriculture and the discovery of 50 000 varieties of edible plants, only 15 crop species represent today 90 percent of the food of the world. Rice, wheat and maize are the basic food for two thirds of the world's population. The continuous genetic erosion of wild species of cereals and other cultivated plants poses a risk for plant breeding programmes. Unless the loss of genetic diversity is controlled, by 2025 about 60 000 plant species - a quarter of the total world plant capital - might be lost (FNUAP, 2001). Fish stocks are also at risk. The Food and Agriculture Organization of the United Nations (FAO) estimates that 69 percent of marine commercial fish supplies of the world have been depleted. The greatest threats to biodiversity are destruction and deterioration of habitats, particularly in tropical developing countries (where biodiversity is concentrated), and the introduction of exotic species. Many of the factors affecting biodiversity are related to the needs of agricultural production: the increase in population and limited arable land have demanded increased agricultural productivity, and have led to more intensive agricultural practices, which have negative impacts on natural biodiversity. Habitat loss due to the expansion of human activities is identified as a main threat to 85 percent of all species described in the International Union for Conservation of Nature (IUCN) Red List. Main factors are urbanization and the increase in cultivated land surfaces (Amman *et al.*, 2003).

GENETIC EROSION

An already limited gene pool of an endangered species is further reduced when individuals from the endangered population die without breeding with other individuals from their population. Genetic variation, i.e. allelic diversity, is lost.

BOX 2.2

CAUSES OF BIODIVERSITY LOSS**CAUSES OF BIODIVERSITY LOSS**

Include, among others, habitat conversion and fragmentation, genetic erosion, pollution, invasive species, unsuitable land use and management and natural events.

Biodiversity loss has been indicated by the loss in number of genetic resources and species. It has also been inferred from population decline and the degradation of ecosystem functions and processes. Several causes have been suggested; some of them are direct and others are identified as underlying factors.

Among the direct causes are:

- » Habitat conversion/fragmentation
- » Unsuitable land use and management
- » Domestication/genetic erosion
- » Introduction of invasive and exotic species
- » Trade
- » Pollution
- » Natural events

Among the underlying causes of biodiversity loss are:

- » Demographic changes
- » Poverty and inequality
- » Climate change
- » Public policies and markets
- » Economic policies and structures

Climate change is also a factor of biodiversity loss. Excessive burning of fossil fuels is altering the balance of gases in the atmosphere; carbon dioxide (CO₂) is building up to high levels since more CO₂ is released than can be absorbed by the natural ecosystems. The interdependence of ecosystems is amply demonstrated here. For example, deforestation releases CO₂ and methane, which increases global temperatures. It also reduces ground cover, which disrupts water cycles as well as leading to soil erosion. The soil is washed into lakes and rivers, which silt and reduce aquatic biodiversity, among other effects.

Although deforestation can be controlled at a local level, the massive amount of deforestation is due to over-harvesting of trees for economic use, rather than local use. Most of the fossil fuel usage generating the CO₂ in the atmosphere stems from the industrialized nations and transition economies, but the effects are especially apparent throughout the less industrialized world.

2.5 COMMITMENTS AND OPPORTUNITIES

Biodiversity constitutes a part of the national patrimony of each country and represents great environmental, cultural and economic values. Conservation and sustainable use of biodiversity concerns all inhabitants of the world, represents an enormous potential for diverse countries and requires clearly defined strategies and policies for biodiversity management. As the human population grows, the demand for freshwater, food and energy resources puts the **sustainability** of the environment at risk. Developing adequate technologies and changing the way in which we use our resources are a growing challenge, and problems related to governability, social organization and human rights are of increasing importance in achieving sustainable results (FNUAP, 2001). In order to feed 8 000 million people that are expected to live on earth by 2025 and to improve their diets, and avoid malnutrition, the world's societies will have to improve food production and achieve a more equal distribution of food. Given that the available land suitable for agriculture is constantly being reduced, the increase in production will have to be achieved with higher yields instead of more cultivated surface. For example, scientists are working on genes that help plants to efficiently extract nutrients from soil, which would reduce the need for fertilizers; efforts are directed also at the development of drought resistant plants using the genes that allow certain species to survive drought (The Academies of Sciences, 2007). Development strategies that are beginning to materialize in several countries, especially in developing countries, are based mainly on a wide use of natural resources in a sustainable way, maximizing the potential of the plant sciences towards sustainable and environmentally responsible models of production for food, fuel and fibre, and incorporating them steadily into the agricultural sector. Biological resources represent a huge potential, insufficiently exploited, that requires strengthening and applying scientific and technological progress in order to understand, characterize and use these resources for the benefit of local communities. Biotechnology offers valuable tools to use these critical resources (Lemaux, 2008).

SUSTAINABILITY

The term describes how biological systems remain diverse and productive over time; in relation to humans, it refers to the potential for long-term maintenance of wellbeing, which in turn depends on the wellbeing of the environment and the responsible use of natural resources.

**EVOLUTION
AND
SPECIATION****3.1 THE DEVELOPMENT OF EVOLUTIONARY THEORY****EVOLUTION**

The change in the inherited traits (i.e. the genetic material) of a population of organisms from one generation to the next.

The process by which the present diversity of plant and animal life has arisen, and which continues to drive changes in form and mode of existence of all living organisms.

Patterns of reproduction, foraging, social interaction, growth and senescence and all other characteristics of an organism or species are shaped by natural selection through the interactions of organisms with their environment. The behavioral, physiological or developmental responses that allow an organism to accommodate or acclimate to the current conditions are called evolutionary adaptations. In biology, **evolution** is change in the inherited traits of a population of organisms from one generation to the next. These changes are caused by a combination of three processes: variation, reproduction and selection.

In a biosafety context, evolution is one of the most important concepts, considering the possible ecological/evolutionary impacts of escaped genetically modified organisms (GMOs). Some of the principal considerations in this context refer to natural selection pressures and genotype changes (which affect the rate of evolution), phenotypic variance, heritability, response to selection, inbreeding, outcrossing and genetic variation, among others.

Evolutionary biology became a defined science when Charles Darwin published “On the Origin of Species” in 1859. Darwin’s Theory of Evolution is the widely

held notion that all life is related and has descended from a common ancestor. Darwin's general theory presumes that complex creatures evolve from more simplistic ancestors naturally over time. In a nutshell, as random genetic mutations occur within an organism's genetic code, the beneficial mutations are preserved because they aid survival, and ultimately reproduction, of the organism - a process known as "**natural selection**". These beneficial mutations are passed on to the next generation. Over time, beneficial mutations accumulate and the result is an entirely different organism (not just a variation of the original, but a distinct species that, in the case where the ancestor species still exists, is not capable of producing fertile offspring with the ancestor species). Natural selection acts to preserve and accumulate advantageous genetic mutations; natural selection in combination with reproduction is the preservation of a functional advantage that enables a species to compete better in the wild. Natural selection is the naturalistic equivalent to domestic breeding. Over the centuries, human breeders have produced dramatic changes in crop plant and domestic animal populations by selecting superior individuals for breeding; thus breeders eliminate undesirable traits gradually over time. Similarly, natural selection eliminates inferior species gradually over time, while new species constantly arise. However, there is of course no "goal" for evolution, as there is for breeders: instead, species are passively adapted in response to environmental influences.

In Darwin's theory of natural selection, new (genetic) variants arise continually within populations. A small percentage of these variants cause their bearers to produce more offspring than others, because these variants confer some kind of advantage over other members of the population. These variants thrive and supplant their less productive competitors. The effect of numerous instances of such variation in combination with natural selection would lead to a species being modified over time (Purves *et al.*, 2004). Darwin did not know that the actual mode of inheritance was discovered in his lifetime. Gregor Mendel, in his experiments on hybrid peas, showed that genes from a mother and father organism do not blend.

NATURAL SELECTION

The process by which heritable traits that make it more likely for an organism to survive and successfully reproduce accumulate in a population over successive generations.

POPULATION GENETICS

The study of the allele frequency distribution in a population and changes in allele frequency under the influence of natural selection, genetic drift, mutation and gene flow.

An offspring from a short and a tall parent may be medium sized, but it carries genes for shortness and tallness. The genes remain distinct and can be passed on to subsequent generations. It took a long time before Mendel's ideas were accepted. Mendel studied discrete traits; these traits did not vary continuously. The discrete genes Mendel discovered exist at defined frequencies in natural populations. Biologists wondered how and if these frequencies would change over time. Many scientists thought that the more common versions (alleles) of genes would increase in frequency simply because they were already present at high frequency. However, this is not necessarily true; the exact dynamics and frequencies of genes and their alleles, and the influence of environmental factors, are nowadays studied in the field of **population genetics**.

Population genetics investigates the evolutionary mechanisms of selection and genetic variability by developing quantitative predictions of changes in gene frequencies in response to selection. Hardy and Weinberg showed how genetic variation is retained in Mendelian inheritance, and that the frequency of an allele would not change over time simply due to the allele being rare or common. Their model assumed large populations in which there is random mating, no selection, no mutation, and no migration to or from the population. Later, R. A. Fisher showed that Mendel's Laws could explain continuous traits if the expression of these traits were due to the action of many genes (so-called polygenic traits). After this, geneticists accepted Mendel's Laws as the basic rules of genetics.

3.2 GENETIC BASIS OF THE EVOLUTIONARY MECHANISMS

Evolution, the change in the gene pool of a population over time, can occur in different ways. Two mechanisms remove alleles from a population: natural selection and genetic drift. Selection removes deleterious alleles from the gene pool by elimination of the organisms carrying the allele, while genetic drift is a random process that may result in removal of alleles from the gene pool. Three mechanisms

BOX 3.1

DEFINITIONS OF TERMS USED IN EVOLUTION BIOLOGY

Evolution is a change in the gene pool of a population over time. The process of evolution can be summarized in three key steps: genes mutate; individuals are selected; and populations evolve.

Gene is the unit of genetic inheritance that can be passed on from generation to generation. Usually, a gene is defined as a part of the DNA molecule that encodes a given gene product.

Genotype includes all genetic information of an organism and thus determines the structure and functioning of an organism.

Phenotype is the physical expression of the organism, resulting from the interaction of its genotype with the

environment; the outward appearance of the organism.

Gene pool is the set of all genes/alleles in a species or population.

Allele is one of several alternative forms of a gene.

Locus is the location of a particular gene on a chromosome.

Mutation is a permanent change in the genotype (i.e. in DNA sequence) of an organism. Usually the term is applied to changes in genes resulting in new alleles.

Recombination refers to the mixing of genetic material via sexual reproduction.

Gene flow is the transfer of genes/alleles from one population to another.

add new alleles to the gene pool: mutation, recombination and gene flow. The amount of genetic variation found in a population is the balance between the actions of these mechanisms.

MUTATION

Any permanent changes in the DNA sequence that make up an organism's genotype.

Mutation

Mutations, permanent changes in the DNA sequences that make up an organism's genotype, range in size from a single DNA building block (DNA base) to a large segment of a chromosome, or even entire chromosome sets. There are many kinds of mutations. A point mutation is a mutation in which one "letter" (i.e. one base) of the genetic code is changed to another. Furthermore, lengths of DNA sequence can also be deleted from or inserted into a gene, and genes or parts of genes can become inverted or duplicated. Finally, mutations can take place at the level of chromosomes, leading to loss or addition of chromosome parts, entire chromosomes or even chromosome sets (polyploidy). Most mutations are thought to be neutral with regard to fitness of an organism. Mutations that result in amino acid substitutions can change the shape of a protein, potentially changing or eliminating its function. This can lead to inadequacies in biochemical pathways or interfere with the process of development. Only a very small percentage of mutations are beneficial (Purves *et al.*, 2004). A change in environment can cause previously neutral alleles to have selective advantages or disadvantages; in the short term evolution can run on "stored" variation in the gene pool of a population and thus is independent of the mutation rate.

RECOMBINATION

The production of a DNA molecule with segments derived from more than one parent DNA molecule.

In eukaryotes, this is achieved by the reciprocal exchange of DNA between non-sister chromatids within an homologous pair of chromosomes during the first meiotic division.

Recombination

Genetic recombination is the process by which a strand of genetic material (DNA) is broken and then joined to a different DNA molecule in a controlled manner. In eukaryotes, recombination commonly occurs during meiosis as chromosomal crossover between paired chromosomes. Meiosis is a special type of cell division that occurs during formation of sperm and egg cells and gives them the correct number of chromosomes (i.e. a haploid set). Recombination can occur between different genes as well as within genes. Recombination within a gene can form a new allele. Recombination adds new alleles and combinations of alleles to the gene pool.

Gene flow (migration)

New individuals may enter a population by migration from another population. If they mate within the new population, they can introduce new alleles to the local gene pool. This process is called **gene flow**. Immigrants may add new alleles to the gene pool of the population, or may change the frequencies of alleles already present if they come from a population with different allele frequencies. Gene flow operates when there are no or only low spatial barriers that restrict movement of individuals between populations. Gene flow has strong relevance in the context of the introduction of GMOs into the environment, and is therefore the subject of specific attention in this module.

Natural selection

Some individuals within a population produce more offspring than others. Over time, the frequency of the more prolific type will increase. The difference in reproductive capability is called natural selection. Natural selection is the only mechanism of adaptive evolution; it is defined as differential reproductive success of pre-existing classes of genetic variants in the gene pool. The most common action of natural selection is to remove unfit variants as they arise via mutation. This is called reproductive success, and is what is commonly referred to as “**survival of the fittest**”. Fitness is a measure of reproductive success and is due to a number of selection factors:

- » Survival/mortality selection. Any trait that promotes survival increases fitness.
- » Sexual selection. Sexual selection is natural selection operating on factors that contribute to an organism’s mating success. Traits that are a liability to survival can evolve when the reproductive success associated with a trait outweighs the liability incurred for survival. A male who lives a short time, but produces many offspring is much more successful than a long-lived one who produces few.
- » Fecundity selection (size of offspring). High fecundity is due to the production of mature offspring resulting from earlier breeding or a higher number of fertilized eggs produced in species that provide little or no care for their young. The number of offspring gives family size, e.g. in species that take care of their young.

GENE FLOW

The transfer of genes or alleles from one population to another, e.g. by migration, resulting in addition of new alleles to the gene pool or changes in allele frequency.

SURVIVAL OF THE FITTEST

Synonym for natural selection, but not a correct scientific description.

GENETIC DRIFT

Change in allele frequency from one generation to another within a population, due to the sampling of finite numbers of genes that is inevitable in all finite-sized populations. The smaller the population, the greater is the genetic drift, with the result that some alleles are lost, and genetic diversity is reduced.

Genetic drift

Allele frequencies can change randomly in a population. Genetic drift, more precisely termed allelic drift, is the process of change in the gene frequencies of a population due to chance events, which determine which alleles will be carried forward while others disappear. It is distinct from natural selection, a non-random process in which the tendency of alleles to become more or less widespread in a population over time is due to the alleles' effects on adaptive and reproductive success. When sampled from a population, the frequency of alleles differs slightly due only to chance. Alleles can increase or decrease in frequency due to genetic drift. A small percentage of alleles may continually change frequency in a single direction for several generations. A very few new mutant alleles can drift to fixation in this manner (Purves *et al.*, 2004). Both natural selection and genetic drift decrease genetic variation. If they were the only mechanisms of evolution, populations would eventually become homogeneous and further evolution would be impossible. There are, however, the three mechanisms that replace variation depleted by selection and drift, namely mutation, recombination and gene flow.

3.3 SPECIATION

Speciation is the evolutionary process by which new biological species arise. Speciation can take the form of a lineage-splitting event that produces two or more separate species from a common ancestor (cladogenesis), or evolution of a new species from an entire population without lineage split (anagenesis). There are various types of speciation: allopatric, peripatric, parapatric and sympatric speciation, which differ in geographical distribution and the mechanism of speciation of the populations in question. Separate species arise when accumulated genetic changes (mutations) between related populations no longer allow interbreeding, for instance after prolonged geographic separation (Ammann *et al.*, 2003).

The key to speciation is the evolution of genetic differences between the incipient

SPECIATION

The evolutionary process by which new biological species arise.

BOX 3.2

TYPES OF SPECIATION (PURVES ET AL., 2004)

Allopatric (*allo=other, patric=place*) is thought to be the most common form of speciation. It occurs when a population is split into two (or more) geographically isolated subpopulations. In order for a speciation event to be considered allopatric, gene flow between the two subpopulations must be greatly reduced, and eventually the two populations' gene pools change independently until they can no longer interbreed, even if they were brought back together.

Peripatric (*peri=near*); new species are formed in isolated, small, peripheral populations which are prevented from exchanging genes with the main population. Genetic drift, and perhaps strong selective pressure, would cause rapid genetic change in the small population.

Parapatric (*para=beside*); the zones of two diverging populations are separate but overlap; there is no specific extrinsic barrier to gene flow. Individuals mate with their geographic neighbours more than with individuals in a different part of the population's range. In this mode, divergence may occur because of reduced gene flow within the population and varying selection pressure across the population's range.

Sympatric (*sym=same*) speciation occurs when two subpopulations become reproductively isolated without becoming geographically isolated in the first place. Insects that live on a single host plant provide a model for sympatric speciation. If a group of insects switched host plants they would not breed with other members of their species still living on their former host plant. The two subpopulations could diverge and speciate.

species. For a lineage to split once and for all, the two incipient species must have accumulated genetic differences that are expressed in a way that prevents mating between the two species, or causes mating to be unsuccessful (i.e. viable offspring is produced but cannot reproduce). These genetic differences need not be huge. A small change in the timing, location or rituals of mating could be enough. But still, some difference is necessary. This change might evolve by natural selection or genetic drift; reduced gene flow probably also plays a critical role in speciation. Speciation requires that the two incipient species are unable to produce viable/reproductive offspring together or that they avoid mating with members of the other group. Some of the barriers to gene flow (i.e. reproductive isolation) that may contribute to speciation are the evolution of different mating location, mating time or mating rituals; the lack of fit between sexual organs or offspring inviability or sterility. In terms of reproduction, plants have evolved various reproduction methods, in contrast to most animals. Many plants can reproduce sexually, by fertilizing other individuals or themselves, and asexually, by creating clones of themselves through vegetative reproduction, while most animals only reproduce sexually. Similarly, in terms of speciation, plants have more options than animals do. Two modes of speciation are particularly common in plants: speciation by hybridization or speciation by ploidy changes, i.e. changes in the number of chromosome sets per cell (Ricklefs and Miller, 1999).

All species, living and extinct, are believed to be descendants of a single ancestral species that lived more than 3.5 billion years ago (compared with an estimated age of the earth of 4.5 billion years). If speciation were a rare event, the biological world would be very different from what it is today. The result of speciation processes operating over billions of years is a world in which life is organized into millions of species, each adapted to live in a particular environment and to use environmental resources in a particular way (Purves *et al.*, 2004).

3.4 EXTINCTION

Extinction is a natural process in evolution that occurs when every living individual of a species disappears. The history of extinctions on earth includes several mass extinctions during which large numbers of species have disappeared in a rather short period of time (Purves *et al.*, 2004). The main causes of mass extinctions are major ecological disturbances such as volcanic eruptions, impacts of meteorites, fires, floods, species overexploitation, introduction of exotic or non-native species, habitat fragmentation, predation, parasitism, and a reduction of mutualism. Extinction depends on many ecological factors and characteristics of populations. Small populations are in higher danger of extinction than large populations, and **endemic species** - those which are limited to one or very few populations in specific locations and are not found anywhere else in the world - are at higher risk than widespread (cosmopolitan) species (Ricklefs and Miller, 1999). The rate of extinction is affected by population size, geographic range, age structure, and spatial distribution, and may result from a decrease in competitive ability.

Despite mass extinctions, speciation processes (new species arising from preexisting species) have allowed a net increment of species number throughout the history of life on earth. However, current concern arises due to the accelerated rates of extinction. During the past 400 years at least 350 vertebrate and 400 invertebrate species have gone extinct and several hundreds of plants have disappeared as a result of anthropogenic (human-caused) extinction. For the year 2000, the estimated risk of extinction for mammals was 24 percent and for birds, 12 percent. Several national and international conservationist agencies have developed strategies and programmes aimed at the conservation of wild species. For instance, the IUCN has created the Red List of species classifying them into categories according to the level or degree of threat: extinct, extinct in the wild, critical, endangered, vulnerable, susceptible, safe/low risk, insufficiently known and not evaluated. These categories are a guide to conservation activities and the priorities for action to rescue endangered species.

EXTINCTION

The disappearance of every living member of a species.

ENDEMIC SPECIES

A species found only in a specific, unique geographic location.

**AGRICULTURAL
ECOLOGY –
CENTRES OF
ORIGIN/DIVERSITY****AGRO-ECOSYSTEM**

A spatially and functionally coherent unit of agricultural activity, including the biotic and abiotic factors present in that unit and their interactions.

Agricultural activities have become the dominant ecological force over nearly one third of the land areas of the earth. **Agro-ecosystems** incorporate the concepts of ecology into their design and management. After a long history of separation and lack of interaction, ecologists and agronomists are now combining forces to study and help solve the problems confronting our food production systems, and to identify and mitigate the threats to natural resources and the ecological problems in agriculture. Development and application of this knowledge can lead to development of more sustainable agricultural ecosystems in harmony with their larger ecosystem and eco-region (NRCS, 2004). Agro-ecosystems are controlled, by definition, through the management of ecological processes.

For four million years, people procured food by hunting and gathering. Agriculture began in several settings more than 10 000 years ago, and was a necessary factor in the development of civilizations. Crops and farm animals were established by domestication and selection by farmers and breeders took place. Identifying the geographic origin of species is very useful, for example when plant breeders attempt to grow a crop in a zone with environmental conditions different from those of its original zone (Chrispeels and Sadava, 2003). Hybridization has played a major role in the development of new crops, in the modification of existing crops and in

the evolution of some troublesome weeds. One of the consequences of agriculture is the conversion of natural ecosystems into crop fields and pastures by removal of climax vegetation, controlling succession and exposing the soil to erosion.

4.1 DOMESTICATION OF SPECIES

Domestication can be described as accelerated, goal-oriented evolution. Domestication implies changes in the genetic makeup and the morphological appearance and behaviour of plants and animals, so that they fit the needs of the farmer and consumer. For example, in wheat, as in many other grains, a major difference between the wild progenitor and domesticated descendants lies with seed dispersal. Wild plants spontaneously shed their seeds at maturity in order to assure their dispersal. Early farmers, during domestication, selected plants that held on to their seeds to minimize yield losses (Chrispeels and Sadava, 2003). Agriculture began at similar times in different regions of the world. In each of the regions, where the centres of origin of many crops are located, human populations domesticated different crops for similar uses. The evolution of crops is determined by three bottlenecks for genetic diversity: domestication, dispersal from the domestication centres, and crop improvement in the twentieth century. Early agricultural societies domesticated a few plant species, which served as the source of carbohydrates, proteins, fats and fibres. For instance, the emergence of Mediterranean and Middle Eastern civilizations was based on the domestication mainly of wheat, barley, lentils, peas, and linen. Later, the number of domesticated species increased and thus new crops appeared: oat, rye, olives, fruits, and others. Human migrations and exchanges among cultures helped to increase the number of plants cultivated in each region. The discovery of the American continent and all the exchanges by trade that came after led to a high level of genetic diversity within agricultural systems. Unfortunately, at the same time, the new available lands were increasingly used for extensive monocultures, especially of coffee, sugar cane, cotton and tobacco, in the colonies of the New World.

DOMESTICATION
Human selection of plants/animals and subsequent development of a population that fits the needs of the farmer and consumer.

ARTIFICIAL SELECTION

Human selection and breeding of plants/animals for certain traits; opposed to natural selection.

The domestication of plants and animals is based on the use of a reduced fraction of the existing biodiversity in each region and the adaptation of selected species to new environmental conditions suitable for human use. The domestication to new environmental conditions by **artificial selection** is opposed to the evolutionary mechanisms of adaptation by natural selection, as the environments where domestication takes place differ from the natural environments where wild relatives grow, and the selective pressures in each location are different. Domestication results in many morphological and physiological changes in plants or animals that make them, in general, easy to distinguish from their wild relatives. The most noticeable changes in plants are related to seed dispersal, seed dormancy, growth type, harvest index, photoperiod, organ size, presence of toxic compounds, and pest and disease resistance. Due to the fact that almost all crops share the same modified traits that distinguish them from their wild relatives, the whole set of new traits is known as domestication syndrome. Domestication is an artificial selection process directed by farmers. It leads to genetic changes and confers adaptive traits for environmental culture conditions, fitting farmers' and consumers' needs.

4.2 CENTRES OF ORIGIN AND DIVERSIFICATION

Local and global geographic distribution of species depends on ecological conditions, both biotic and abiotic factors, and on evolutionary processes (Purves *et al.*, 2004). The combination of all of these environmental conditions and processes determines the natural flora and fauna found in a given region, as well as the capability of developing certain crops in particular areas. The geographic distribution of wild relatives of a crop provides a general idea of where a crop may have originated. Careful botanic explorations are necessary to determine the precise distribution of wild progenitors. Additional genetic studies involving crosses between the crop and presumptive wild ancestors and a comparison of their genomes can identify in more detail a specific region of domestication.

The **centre of origin** is considered a geographical area where a group of organisms, either domesticated or wild, first developed its distinctive properties. Centres of origin of cultivated plants are identified by the number and diversity of wild species as well as the number of endemic species of the concerned *genus* in a given region, while the **centres of diversity** are recognized by the number and diversity of different varieties, wild and cultivated, of the concerned *species*. Centres of origin may simultaneously be centres of diversity. The centres of origin and centres of diversity of crop plants as known to us are largely based on circumstantial evidence. In the cases of crops that are extensively cultivated over wide geographical ranges, a large number of new varieties were continuously developed, involving a large number of parents, making the issues virtually intangible. For example, IR-64 rice appears to have had more than 100 parents, with consequent extensive genomic rearrangements, some natural and the others induced (Kameswara and Shantharam, 2004).

CENTRE OF ORIGIN

A geographical area where a group of organisms, either domesticated or wild, first developed its distinctive properties.

CENTRE OF DIVERSITY

A geographic area recognized on the basis of the present number and diversity of different varieties, wild and cultivated, of a species.

BOX 4.1

CENTRES OF ORIGIN AND CENTRES OF DIVERSITY

Centres of origin

The geographic locations where a particular domesticated plant species originated. These areas are the likeliest sources of natural genetic variation, and represent ideal targets for *in situ* conservation.

Centres of diversity

The locations recognized on the basis of the number and diversity

of different varieties, wild and cultivated, of a species.

The most important classification of the centres of origin of cultivated plants was established by the Russian geneticist Nikolai Ivanovich Vavilov (1887-1943). Vavilov realized the importance of genetic diversity of crops and their wild relatives for crop improvement.

His most important contribution was the identification of eight major geographic zones, known as “centres of diversity”. There are a limited number of zones where crops originated. They are located in tropical and subtropical zones, at different elevations and a wide variety of topographies, and are characterized by distinct dry and wet seasons. They also correspond in many cases to the places where important human civilizations were established and flourished.

Centres of origin and domestication of cultivated species:

Based on the work of Vavilov in 1940 and Bryant in 2001

» Chinese centre:

soybean (*Glycine max*),
 odder radish (*Raphanus sativus*),
 rapeseed (*Brassica rapa* var. *rapa*),
 pak-choi (*Brassica chinensis*),
 Chinese cabbage
 (*Brassica pekinensis*),
 Japanese shallot
 (*Allium fistulosum*),
 rakkyo (*Allium chinense*),

cucumber (*Cucumis sativus*),
 yam (*Dioscorea batatas*),
 sorghum (*Sorghum* spp.),
 millet (*Panicoideae* subfamily).

» Indo-Malayan centre:

Burma and Assam:
 egg plant (*Solanum melongena*),
 cucumber (*Cucumis sativus*),
 mung bean (*Phaseolus aureus*),
 cowpea (*Vigna sinensis*),
 taro (*Colocasia esculenta*),
 yam (*Dioscorea batatas*),
 rice (*Oryza sativa*).

» Indochina and

Malayan Archipelago:

banana (*Musa paradisiaca*),
 breadfruit (*Artocarpus altilis*),
 coconut (*Cocos nucifera*),
 sugarcane (*Saccharum* spp.).

» Indo-Afghani-

Central Asia centre:

garden pea (*Pisum sativum*),
 broad bean (*Vicia faba*),
 mung bean (*Phaseolus aureus*),
 leaf mustard (*Brassica juncea*),
 onion (*Allium cepa*),
 garlic (*Allium sativum*),
 spinach (*Spinacia oleracea*),
 carrot (*Daucus carota* var. *sativus*),
 apple (*Malus domestica*),
 chickpea (*Cicer arietinum*),
 lentil (*Lens culinaris*).

- » **Near East centre:**
lentil (*Lens culinaris*),
lupin (*Lupinus albus*),
barley (*Hordeum vulgare*),
oat (*Avena sativa*),
wheat (*Triticum* spp.).
- » **Mediterranean centre:**
celery (*Apium graveolens*),
asparagus (*Asparagus officinalis*),
beetroot (*Beta vulgaris* var. *crassa*),
oilseed rape
(*Brassica rapa* var. *rapa*),
cabbage (*Brassica oleracea*
var. *capitata*),
parsnip (*Pastinaca sativa*), pea
(*Pisum sativum*),
rhubarb (*Rheum officinalis*), oat
(*Avena sativa*),
olive (*Olea europea*),
wheat (*Triticum* spp.).
- » **Abyssinian centre:**
okra (*Abelmoschus esculentus*),
watercress (*Lepidium sativum*),
cowpea (*Vigna sinensis*),
barley (*Hordeum vulgare*),
coffee (*Coffea* spp.),
sorghum (*Sorghum* spp.).
- » **Mexico-Central America centre:**
sweet pepper (*Capsicum* spp.),
chili (*Capsicum annuum*),
alcayota (*Cucurbita ficifolia*),
pumpkin (*Cucurbita moschata*),
sweet potato (*Ipomoea batatas*),
lima bean (*Phaseolus lunatus*),
kidney bean (*Phaseolus vulgaris*),
maize (*Zea mays*),
tomato (*Solanum lycopersicum*).
- » **South American centre:**
 - » Peru-Ecuador-Bolivia:
sweet pepper (*Capsicum* spp.),
chili (*Capsicum annuum*),
pumpkin (*Cucurbita* spp.),
tomato (*Solanum lycopersicum*),
kidney bean (*Phaseolus vulgaris*),
potato (*Solanum tuberosum*).
 - » Chile:
potato (*Solanum tuberosum*).
 - » Brazil-Paraguay:
peanut (*Arachis hypogaea*),
cassava (*Manihot esculenta*).
- » **North American centre:**
sunflower (*Helianthus annuus*).
- » **West African centre:**
millet (*Panicoideae* subfamily),
sorghum (*Sorghum* spp.).
- » **North European centre:**
oat (*Avena sativa*),
rye (*Secale cereale*).

4.3 AGRO-ECOSYSTEM CHARACTERISTICS

Agricultural ecosystems - agro-ecosystems - have been described as domesticated ecosystems, in many ways intermediates between natural ecosystems (such as grasslands and forests) and fabricated ecosystems, such as cities (ASAP, 2004).

Just as natural ecosystems, they can be thought of as including the processes of primary production, consumption, and decomposition in interaction with abiotic environmental components and resulting in energy flow and nutrient cycling. Economic, social, and environmental factors must be added to this primary concept due to the human element that is so closely involved with agro-ecosystem creation and maintenance.

Any agro-ecosystem contains some or all of the following factors:

- » Crops – plants cultivated for the benefit of humankind;
- » Weeds – plants that are potential competitors to crops;
- » Pests - animal predators and parasites;
- » Pathogens – micro-organisms causing diseases;
- » Domestic animals;
- » Beneficial micro-organisms - e.g. rhizobia and other nitrogen fixing bacteria, mycorrhizal fungi;
- » Beneficial arthropods - pollinators, natural enemies of pests;
- » Soil.

Definitions of agro-ecosystems often include the entire support base of energy and material subsidies, seeds, chemicals, and even a social-political-economic matrix in which management decisions are made. Agro-ecosystems retain most, if not all, the functional properties of natural ecosystems — nutrient conservation mechanisms, energy storage and use patterns, and regulation of biotic diversity.

4.4 AGRO-ECOSYSTEM PATTERNS AND PROCESSES

Energy and matter flow in agro-ecosystems is altered greatly by human interference. Inputs are derived primarily from human sources and are often not self-sustaining. Agro-ecosystems are open systems where considerable energy is directed out of the system at the time of harvest, rather than stored in biomass that could accumulate within the system. In an agro-ecosystem, recycling of nutrients is minimal, and considerable quantities are lost with the harvest or as a result of leaching or erosion, due to a great reduction in permanent biomass levels held within the system. Because of the loss of niche diversity and a reduction in trophic interactions, populations within such a system are rarely self-regulating.

Agro-ecosystems are solar powered as are natural ecosystems, but differ from natural systems in the following points (ASAP, 2004):

- » There are auxiliary energy sources that are used to enhance productivity; these sources are processed fuels along with animal and human labour as well as fertilizers;
- » Biodiversity is notably reduced by human management in order to maximize yield of specific foodstuffs (plant or animal);
- » Dominant plant and animal species are under artificial rather than natural selection; human inputs determine population sizes - linked to the productivity of the ecosystem.
- » Control is external and goal-oriented rather than internal via subsystem feedback as in natural ecosystems.

Creation and maintenance of agro-ecosystems is necessarily concerned with the economic goals of productivity and conservation of the resource base. They are controlled, by definition, by management of ecological processes and they would not persist but for human intervention. It is for this reason that they are sometimes referred to as artificial systems as opposed to natural systems that do not require

intervention to persist through space and time. Knowledge of the ecological interactions occurring within an agro-ecosystem and the sustainable functioning of the system as a whole allows successful long-term management. Sustainability can be achieved by implementing an agriculture that is ecologically sound, resource-conserving and not environmentally degrading.

4.5 SUSTAINABLE AGRICULTURE

SUSTAINABLE AGRICULTURE

To maximize advantage of existing soil, nutrient and water cycles, energy flows, and soil organisms for food production, while at the same time the natural resource base upon which it depends is maintained.

Sustainable agriculture is both a philosophy and a system of farming. It has its roots in a set of values that reflect an awareness of both ecological and social realities. Sustainable agriculture systems are designed to maximize the advantage of existing soil, nutrient and water cycles, energy flows, and soil organisms for food production.

An ecologically sustainable agriculture maintains the natural resource base upon which it depends, relies on a minimum of artificial inputs from outside the farm system, manages pests through internal regulation mechanisms, and is able to recover from the disturbances caused by cultivation and harvest through successional processes minimizing waste and environmental damage, while maintaining or improving farm profitability (ASAP, 2004). In practice, such systems have tended to avoid the use of synthetic fertilizers, pesticides, growth regulators and livestock feed additives. Biological and cultural controls are used to manage pests, weeds and diseases.

Management of agro-ecosystems for sustainability both influences and is influenced by biodiversity. Sustainable practices leading to increased crop and genetic diversity have resulted in increased agro-ecosystem stability – for example, increasing crop diversity benefits agriculture by reducing insect pests. Conservation tillage increases habitat and wildlife diversity, and raises the numbers of beneficial insect species.

BOX 4.2

SUSTAINABLE AGRICULTURE (ASAP, 2004)

- » is based on the prudent use of renewable and/or recyclable resources. It uses renewable energy sources such as biological, geothermal, hydroelectric, solar, or wind energy.
- » protects the integrity of natural systems so that natural resources are continually regenerated. Sustainable agricultural systems should maintain or improve groundwater and surface water quality and regenerate healthy agricultural soils.
- » improves the quality of life of individuals and communities. In order to stem the rural to urban migration, rural communities must offer people a good standard of living including diverse employment opportunities, health care, education, social services and cultural activities.
- » is profitable. Transition to new ways of knowing, doing and being require incentives for all participants.
- » is guided by a land ethic that considers the long-term well-being of all members of the land community. An agro-ecosystem should be viewed as a dynamic, interdependent community composed of soil, water, air and biotic species, with capacity for self-renewal.

Many of the approaches in conventional agriculture (minimum tillage, chemical banding) already indicate the way towards sustainable, efficient agriculture. Efforts to introduce safe products and practices (botanical pesticides, bio-control agents, imported manures, rock powders and mechanical weed control) are being pursued. Despite the reduced negative environmental damage associated with them, they remain problematic. Botanical pesticides also kill beneficial organisms, the release of bio-controls does not address the question of why pest outbreaks occur,

dependence on imported fertilizer materials makes the system vulnerable to supply disruptions, and excessive cultivation to control weeds is detrimental to the soil. As in conventional agricultural systems, the success of sustainable approaches is highly dependent on the skills and attitudes of the conductors (ASAP, 2004). What has become increasingly clear in the last few years is that good agronomy is based on an understanding of ecology. An agro-ecological approach is used increasingly by agricultural professionals to analyse the success of sustainable farming systems, and to identify ways of improving the productivity, profitability, and resource efficiency of these systems.

4.6 AGRICULTURAL BIODIVERSITY

AGRICULTURAL BIODIVERSITY

Includes all components of biological diversity of relevance to food and agriculture, and all components of biological diversity that constitute the agricultural ecosystems.

GENETIC RESOURCES FOR FOOD AND AGRICULTURE

Include the genetic resources of plants, animals and micro-organisms with relevance for food and agriculture.

Agricultural biodiversity is a broad term that includes all components of biological diversity of relevance to food and agriculture, and all components of biological diversity that constitute the agricultural ecosystems, also named agro-ecosystems: the variety and variability of animals, plants and micro-organisms, at the genetic, species and ecosystem levels, which are necessary to sustain key functions of the agro-ecosystem, its structure and processes (CBD, COP decision V/5, Appendix). It includes crops and livestock and their wild relatives, but also many other organisms such as soil fauna, weeds, pests and predators. Agricultural biodiversity is the outcome of the interactions among genetic resources, the environment and the management systems and practices used by farmers. It is the result of both natural selection and human intervention developed over millennia.

Dimensions of agricultural biodiversity

- 1) **Genetic resources for food and agriculture**, which constitute the units of production in agriculture, and include cultivated and domesticated species, managed wild plants and animals, as well as wild relatives of cultivated and domesticated species:

- » Plant genetic resources (PGR), including crops, wild plants harvested and managed for food, trees on farms, pasture and rangeland species;
 - » Animal genetic resources, including domesticated animals, wild animals hunted for food, wild and farmed fish and other aquatic organisms;
 - » Microbial and fungal genetic resources.
- 2) **Components of biodiversity that support ecosystem services** upon which agriculture is based. These include a diverse range of organisms that contribute, in varying degrees to, *inter alia*, nutrient cycling, pest and disease regulation, pollination, pollution and sediment regulation, maintenance of the hydrological cycle, erosion control, climate regulation and carbon sequestration.
 - 3) **Abiotic factors**, such as local climatic and chemical factors and the physical structure and functioning of ecosystems, which have a determining effect on agricultural biodiversity.
 - 4) **Socio-economic and cultural dimensions**. Agricultural biodiversity is largely shaped and maintained by human activities and management practices, and a large number of people depend on agricultural biodiversity for sustainable livelihoods. These dimensions include traditional and local knowledge of agricultural biodiversity, cultural factors and participatory processes, as well as tourism associated with agricultural landscapes.

Biodiversity and agriculture are strongly interrelated: while biodiversity is critical for agriculture, agriculture can also contribute to conservation and sustainable use of biodiversity. Indeed, sustainable agriculture both promotes and is enhanced by biodiversity. Maintenance of this biodiversity is essential for the sustainable production of food and other agricultural products and the benefits these provide to humanity, including food security, nutrition and livelihoods.

CONSERVATION OF GENETIC RESOURCES

5.1 GENETIC RESOURCES FOR FOOD AND AGRICULTURE

GENETIC RESOURCES

The genetic material, in its overall diversity, of an agriculturally valuable plant or animal species.

Genetic resources for food and agriculture are the biological basis of world food security and, directly or indirectly, support the livelihoods of every person on earth. Considering their importance for both traditional farming and breeding as well as genetic engineering, they constitute a world patrimony of invaluable usefulness for human existence. PGR comprise diversity of genetic material contained in traditional varieties, modern cultivars, crop wild relatives and other wild species (Fraleigh, 2006). Genetic diversity provides farmers and plant breeders with options to develop, through selection and breeding, new and more productive crops, resistant to virulent pests and diseases and adapted to changing environments.

Genetic diversity of the majority of modern crops is very limited in comparison with their wild ancestors. This reduction in diversity during crop evolution is not recent, as it began with crop domestication. The development of improved “*elite*” varieties during the twentieth century accelerated the pace of genetic erosion. The better performance and higher yield obtained with new varieties led farmers to stop using their local varieties and instead switch to high-yielding hybrids and new varieties preferred by consumers (Chrispeels and Sadava, 2003). Domestication,

artificial selection and constant manipulation of biological diversity by humankind over the past 10 000 years in conjunction with overall human activities impacting on the environment have resulted in a constant decline in genetic resources as well as the conversion of vast forest extensions, savannahs and prairies into cultivated land. Human societies, at present, are mostly applying monocultures, the worst condition with regard to diversity; two well known examples illustrating this are the devastating consequences of the Irish famine (caused by a potato disease) and the desertification of Sumer in ancient Mesopotamia due to soil salinization. Genetic erosion reduces considerably the possibilities for crop improvement for the world community and in particular the small farmers, who depend in many cases on wild species and natural habitats to subsist (Pullin, 2002).

FAO estimates that since 1900, 75 percent of crop genetic diversity has been lost. Without a constant contribution of new, “wild” genes, plant geneticists and breeders cannot continue improving basic crops. Plants obtained by means of crop selection must be invigorated every 5 to 15 years in order to provide them with new or better traits such as pest and disease resistance, higher yields, or higher tolerance to droughts and saline soils. The most effective way to achieve this is by mixing commercial varieties with wild ones. Many of the local varieties and wild species that are being lost may contain genes with potential utility to plant breeders and biotechnologists for crop improvement (FAO, 2001; WCMC, 2002).

The growing deterioration of natural and agricultural environments, and concerns for the loss of biodiversity, have resulted in rapid development of the discipline of conservation biology. The origins of genetic resource conservation and the interest of agriculturalists in the origin of domesticated crops and in the use of wild relatives for breeding programmes can be traced to the 1910s. By 1924 the Russian botanist Vavilov founded the All-Union Institute of Applied Botany and New Crops (AUIAB & NC) in Leningrad and established a large seed bank. The number and size of crop gene banks have continued to grow dramatically ever since.

5.2 CONSERVATION AND RESTORATION

CONSERVATION BIOLOGY

deals with the use and management of the biodiversity present in natural and cultivated ecosystems in order to guarantee their renewal, conservation and productivity.

RESTORATION ECOLOGY

investigates how to recover and rehabilitate an ecosystem when degradation and decline are extreme.

Conservation biology studies the use and management of the biodiversity present in natural and cultivated ecosystems in order to guarantee their renewal, conservation and productivity, thus providing benefits and opportunities for present and future generations. The main approaches used today in conservation biology include conservation strategies for undisturbed natural ecosystems, restoration strategies for disturbed ecosystems and sustainable use strategies for transformed ecosystems, which include agro-ecosystems, urban ecosystems, dams, gardens and recreation areas, among others. (WCMC, 2002).

When degradation and decline are extreme, and no preservation is possible, **restoration ecology** investigates how to recover and rehabilitate an ecosystem. Restoration involves species reintroduction, i.e. the total or partial replacement of extinct populations with the same or similar species having an ecological, social, cultural or economic value. The most effective way to conserve viable populations is to conserve zones which are large enough to allow species and their habitats to exist. An important concept in wildlife conservation is that of biological corridors, which are strips of land connecting fragmented habitats through which species can move from and to different fragments of their natural habitats. Corridors allow the recolonization of habitat fragments where populations have disappeared and help to avoid inbreeding or endogamy in small subpopulations (Pullin, 2002; Ricklefs and Miller, 1999). There is no global consensus on what constitutes an important species, but species may be singled out for conservation if they fall into one or more of the following categories:

- i) threatened species,
- ii) ecologically important species,
- iii) species useful to humans, and
- iv) species with non-use value.

5.3 *IN SITU* AND *EX SITU* CONSERVATION OF PLANT GENETIC RESOURCES

As already mentioned, agro-biodiversity is currently threatened by the progressive loss of plant genetic diversity. This problem has increased agriculture vulnerability and has also impoverished food provision for humans (Fraleigh, 2006). The growing concern on genetic erosion has led to the establishment of **germplasm** conservation programmes worldwide. The effort to save biodiversity is directed at both crops and wild relatives. Wild relatives of crops are critical for increasing and improving agricultural production by providing useful genes for resistance against disease and pests, abiotic stress tolerance (drought, salinity, water logging), as well as for improving nutritional qualities. They also provide ecosystem services such as pollination, nutrient recycling and water flow management. The effort to conserve crop wild relatives is taking place at national and global levels, as it is believed to be one of the most important ways to improve food security. Countries that are richest in genetic diversity are, generally, the poorest in economic terms, so that international efforts might be required to help them secure and conserve their genetic resources.

There are two complementary approaches for conservation of PGR, namely *in situ* and *ex situ*. *In situ* conservation involves maintaining genetic resources in the natural habitats where they occur, whether as wild and uncultivated plant communities or crop cultivars in farmers' fields as components of traditional agricultural systems. *Ex situ* conservation involves conservation outside the native habitat and is generally used to safeguard populations in danger of destruction, replacement or deterioration. Samples from such species are stored in centralized banks away from the origin. Approaches to *ex situ* conservation include methods such as seed storage banks, field gene banks, botanical gardens, world heritage sites, research centres and laboratories. DNA and pollen storage also contribute indirectly to *ex situ* conservation of PGR (Rao, 2004). Bioversity International and

GERMPLASM

Can be defined as the sum of genetic resources for a given species. Germplasm can be conserved either by protecting organisms in their natural habitat (*in situ*), or by storing and preserving them in designated facilities (*ex situ*).

the Svalbard Global Seed Vault efforts are directed at genetic resources conservation. As a part of the worldwide work, about 6 million accessions are being conserved by 1 300 seed banks around the world, although there has been limited success when using wild seeds in crop improvement crosses (Bryant, 2001).

5.3.1 *In situ* conservation of plant genetic resources

IN SITU CONSERVATION
Maintaining genetic resources in the natural habitats where they occur, whether as wild and uncultivated plant communities or crop cultivars in farmers' fields.

LANDRACES
Traditional crop varieties, generally composed of a heterogeneous mixture of genotypes, adapted to local conditions and often providing valuable genes for crop improvement.

The aim of *in situ* conservation is to protect habitats of target species so that a population of that species can stably persist and evolution processes are assured. It includes establishing protected areas such as national parks, caring for peasant plots containing local varieties, and preserving forests to protect medicinal or wild species used by indigenous communities. The vision is for the protected areas to allow for multiple uses, and to allow the systems to preserve rare, endangered and threatened species. In these systems, there is a need to increase the geographic distribution of target species, improve population structure, and influence the dynamics and genetic variability within and between populations. Further, identification of threats to target species in the wild and suitable mitigation actions are required, and effective management plans for ecosystems, genetic resources, ecological restoration and species recovery programmes need to be implemented. The *in situ* conservation strategies for natural ecosystems include national natural parks, forests, protected areas, reserves and sanctuaries, and, especially for agro-biodiversity, community and domestic parcels including landraces and folk varieties. *In situ* conservation of cultivated species is primarily concerned with the on-farm maintenance of traditional crop varieties (**landraces**) and with forage and agroforestry species (Rao, 2004). Active participation by farmers and other users of genetic resources is an important part of *in situ* conservation of cultivated species. Crop resources in landraces are passed from generation to generation of farmers and are subject to different selection pressures to fit specific farming situations.

5.3.2 *Ex situ* conservation of plant genetic resources

Among the various *ex situ* conservation methods (germplasm banks), **seed storage** is the most convenient for long-term conservation of PGR. Seeds are dried to low moisture content and stored at subzero temperatures in cold stores or deep freezers. According to FAO, this technique accounts for 90 percent of the six million accessions conserved *ex situ* globally. One of the most important examples is the Svalbard Global Seed Vault, which is a secure seed bank located on the Norwegian island of Spitsbergen in the remote Arctic. The facility was established to preserve a wide variety of plant seeds from locations worldwide in an underground cavern, and holds duplicate samples, or “spare” copies, of seeds held in gene banks worldwide. The Seed Vault provides insurance against the loss of seeds in gene banks, as well as a refuge for seeds in the case of large-scale regional or global crises. However, there are a large number of important tropical and subtropical plant species which produce recalcitrant seeds that quickly lose viability and do not survive desiccation, hence conventional seed storage strategies are not possible. There are also a number of other important crop species that are sterile or do not easily produce seeds, or seed is highly heterozygous and clonal propagation is preferred to conserve elite genotypes.

***Ex situ* conservation** requires skills in management of resources, development of infrastructure and facilities to accommodate the collections. It should be considered as a tool to ensure survival of wild populations and other diversity, and should be integrated into *in situ* conservation. The collections include:

- » Whole plant/animal collections;
- » Zoological parks and botanic gardens where species can be kept safe from threat;
- » Wildlife research facilities;
- » Germplasm collections of wild and domesticated taxa in any form including zygotes, gametes and somatic tissue.

SEED STORAGE

One of the most convenient methods for long-term conservation of plant genetic resources.

EX SITU CONSERVATION

Conservation of genetic resources outside the native habitat, generally used to safeguard populations in danger of destruction, replacement or deterioration.

Strategies used in *ex situ* conservation include: seed banks and germplasm banks, reproduction propagation (as in clonal orchards) and reintroduction of endangered species into the wild.

5.4 BIOTECHNOLOGY FOR CHARACTERIZATION, CONSERVATION AND SUSTAINABLE USE OF BIODIVERSITY

Humans have manipulated the genetic make-up of plants and animals since agriculture began more than 10 000 years ago. This exploitation of the natural variation in biological organisms has given us the crops, plantation trees, farm animals and farmed fish of today, which often differ radically from their early ancestors. Increasing the efficiency of agricultural production can reduce these impacts; biotechnologies can have an important role in this respect. Biotechnology is an important tool for biodiversity conservation and utilization, and is a complement – not a substitute – for many areas of conventional agricultural research. It offers a range of tools to improve our understanding and management of genetic resources for food and agriculture. Modern biotechnologies can help to counteract trends of genetic erosion in all food and agriculture sectors (FAO, 2004). Molecular markers are one of the most valuable molecular biology techniques; they are used in identification and characterization of species, populations and genotypes, and are very useful for quantifying the genetic diversity within populations. Molecular **marker assisted selection** (MAS) is a powerful tool in conventional plant breeding and crop improvement programmes, because it facilitates the identification of genes with agronomic importance (pest and disease resistance genes), hybridization ratios, to distinguish variety lines, and enables the purity control and certification of varieties (Henry, 2000; FAO, 2007). Molecular techniques are also useful tools when studying the influence of plant genetic diversity on ecosystem sustainability, due to the fact that diversity within species may contribute in a significant way to the productivity of an agro-ecosystem. Modern agricultural biotechnology

MARKER-ASSISTED SELECTION (MAS)

A molecular biology technique used in breeding programmes to facilitate the identification and selection of genes with agronomic importance.

includes a range of tools that scientists employ to understand and manipulate the genetic make-up of organisms for use in the production or processing of agricultural products. Problems that are addressed include diseases and pests, abiotic stresses (drought, salinity), improving nutritional quality, creation of new diagnosis tools, measurement, conservation and study of genetic resources, and production of vaccines (FAO, 2004).

BOX 5.1

GERMPLASM CHARACTERIZATION**Germplasm characterization**

requires observation, measurement and documentation of heritable plant traits. There is need for identification, classification and confirmation of plant sample collections by using descriptors for the stored species:

- » *Morphological descriptors*, which describe the morphology of the plant, which are easy and reliable to use and cheap, but are limited because of limited polymorphisms that can be visualized. They are also affected by the environment, which affects phenotypic

expression. These descriptors can also be highly subjective.

- » *Agronomic descriptors/traits*, which are useful for crops, but require large-scale field experiments, and are labour-intensive.
- » *Molecular descriptors*, which use molecular marker technology to identify polymorphisms. These descriptors have proved to be very useful in identifying and tracing genes of interest for use in plant breeding and genetic engineering. There is a high throughput of information and most techniques yield highly reproducible results.

GERMPLASM CHARACTERIZATION

Germplasm stored in seed banks needs to be characterized, e.g. according to morphological, agronomic and molecular descriptors.

Biotechnology is being utilized for collecting and storing genetic information through seed and tissue culture. It is also being used for detection and elimination of diseases in gene bank collections. Identification of desired genes using molecular techniques ensures that the genotypes of choice are used for downstream operations. Long-term storage using cryopreservation of tissue culture results in safer and more efficient storage and distribution of germplasm. Molecular techniques are used to confirm identities of germplasm when it is taken out of the banks for regeneration of plants, in addition to screening the accessions for identification of genes of interest.

The aim of modern breeders is the same as that of early farmers – to produce superior crops or animals. Conventional breeding, relying on the application of classic genetic principles based on the selection of phenotype or physical characteristics of the organism concerned, has been very successful in introducing desirable traits into crop cultivars or livestock breeds from domesticated or wild relatives or mutants. Biotechnology can make the application of conventional breeding methods more efficient (FAO, 2004). Progress in molecular techniques and *in vitro* culture of plant organs, tissues and cells has been increasing over the past 50 years. Traditional plant breeding combined with improved agricultural practices and modern biotechnology techniques have resulted in higher crop yields (Henry, 2000). Recombinant DNA technology has also been an important tool in crop improvement.

5.5 BIOTECHNOLOGY, BIODIVERSITY AND SUSTAINABLE AGRICULTURE

Biotechnology has the potential to improve sustainability in several ways and is expected, thereby, to help maintain natural as well as agricultural biodiversity. Agriculture has to respond, in addition to the traditional focus on higher yields, by addressing the protection of environmental goods as well as consumer concerns for food safety and quality. Biotechnology can overcome some production constraints

which are difficult or intractable to tackle by conventional methods. It can speed up conventional breeding programmes, create crops resistant to diseases and pests, reduce the use of toxic chemicals that harm the environment and human health, and it can provide diagnostic tools and vaccines that help control devastating human or animal diseases. It can improve the nutritional quality of staple foods such as rice and cassava and create new products for health and industrial uses (FAO, 2004).

Developing sustainable agricultural systems with minimal impact on biodiversity will require utilizing all available technologies while simultaneously encouraging appropriate farming practices. Biotechnology should be part of integrated and comprehensive agricultural research and development programmes that give priority to the problems of the poor. Biotechnology is not a substitute for research in other areas such as plant breeding, integrated pest and nutrient management and livestock breeding, and feeding and management systems (FAO, 2004). A great deal needs to be done so that developing country producers are empowered to make their own decisions regarding these technologies for their own benefit. Identifying small farmers' constraints to technology access and use continues to be an issue that the international community must address. Investments in biotechnology research capacity for the public sector will only be worthwhile if the current difficulties in delivering conventional technologies to subsistence farmers can be reversed (FAO, 2004). We need a better understanding of the sustainability of crop and animal production systems, as well as to promote the development of integrated crop management systems linked to biotechnology progress, in order to establish production systems more friendly to the environment and thus to guarantee resources to future generations.

BIOTECHNOLOGY, BIODIVERSITY AND SUSTAINABLE AGRICULTURE

Biotechnology has the potential to improve sustainability in several ways and is expected, thereby, to help maintain natural as well as agricultural biodiversity. Biotechnology should be part of integrated and comprehensive agricultural research and development programmes that give priority to the problems of the poor.

GENE FLOW

The movement or exchange of genes between different species or between different populations of the same species.

Gene flow, also known as gene transfer, is the movement or exchange of genes between different species or between different populations of the same species. Genes may flow (transfer) from one organism to its offspring via reproduction with sexually compatible relatives, in which case it is called vertical gene transfer (VGT), or by other means – i.e. by infection - to totally unrelated species and families of organisms, generally referred to as horizontal gene transfer (HGT). Gene flow is a natural process, with importance for the maintenance of genetic variation in populations, as well as for the spread of new traits among populations and across species boundaries. It can add new alleles to the gene pool of populations or change the frequencies of alleles present (Ammann *et al.*, 2003). Gene transfer within species is almost essential to preserve the fitness of most species of plants and animals, naturally including many species of crop plants, and is the basis for evolution. In crops (and other flowering plants), gene flow typically involves movement of pollen and is dependent upon wind or animal vectors (pollinators). Gene flow occurs with all species, and thus with all crop species, but the amount of gene flow is a function of species biology. Given its importance, the processes that affect gene flow have been widely studied and generally are well understood.

6.1 VERTICAL GENE TRANSFER

Vertical gene flow occurs naturally between crops and weeds and from crop-to-crop. It occurs between sexually compatible plants and wild relatives if the appropriate conditions are met. Gene transfer between crops and sexually compatible relatives has occurred since the domestication of plants began more than 10 000 years ago. Over the centuries farmers kept seed from the best plants in their crops that had been formed by mutation or had arisen from natural crosses. Gradually, major differences arose between the domesticated and wild species, so that farmers were keeping plants that contained combinations of genes that improved the domestic attributes of the crops (Ammann *et al.*, 2003). Most ecological scientists agree that vertical gene flow between crops and wild species is not an environmental problem unless it leads to undesirable consequences. In nature, vertical gene flow takes place through pollen transfer to the ovaries. For plants, gene flow may occur by pollen spreading from one population to another. The pollen may be spread in a variety of ways, e.g. by wind, water or insects and other animals. In self-pollinating plants, pollen transfer can be simply by gravity. Genes from the resulting offspring can be spread further by pollen or by seeds.

VGT from GM crops to non-GM crops or wild relatives of the crop in question is regarded as one of the major problems associated with the cultivation and release of GM crops. The minimum requirements for gene flow from a GM plant to a non-GM plant to occur are the presence of a sexually-compatible non-GM population in close proximity to the GM population, the possibility of **outcrossing** between the two populations and the production of fertile hybrids. The degree of outcrossing varies amongst species: maize and millet, for example, are typically cross-pollinated while rice, wheat and barley are primarily self-pollinated. An important aspect is that gene flow refers to the exchange of genes among populations and not simply to the dispersal of pollen or seeds. **Introgression** is what defines the stable incorporation of genes from one pool to another, and determines the actual gene flow between

VERTICAL GENE TRANSFER

Gene flow from a parent organism to offspring, during sexual or asexual reproduction.

OUTCROSSING

The occurrence of crosses, and thus transfer of genetic material, between two distinct species/populations.

INTROGRESSION

Movement of gene(s) between the gene pools of different species, typically by production of interspecific hybrids that backcross with one of the parent species.

populations. Introgression takes place by creation of a hybrid plant (i.e. a cross between a GMO variant and a wild relative) and subsequent backcrossing of that hybrid with the parent species, resulting in the introduction of foreign genes to the parent species gene pool.

Since vertical gene transfer can potentially happen between crops/wild relatives and GM crops as soon as the latter are introduced to an environment, it is important to know the crop progenitors as well as their wild relatives in order to assess the likelihood of gene transfer. The answer to the question “Does gene transfer occur?” now seems clear: gene flow is inevitable from those crops that naturally outcross both to conventional varieties of the same crop and to a small number of wild relatives, although this latter phenomenon is usually a rare event. However, for ecologists and agronomists the key question is “Does it matter?” More specifically, does outcrossing of transgenes affect fitness of recipient offspring in both natural and agricultural ecosystems? The inherent characteristics of a crop and its proximity to closely related plants are some of the factors that determine the likelihood of gene transfer to other plants. The key to understanding vertical gene flow is knowledge of the sexual compatibility of the crop with other species growing in the same habitat.

Factors affecting VGT

Gene flow depends on many ecological and agronomical factors: the reproductive biology of the plant species, whether or not the crop is allowed to flower, how far its pollen travels, success of fertilization, extent of seed dispersal and seed survival, among others. Even if a gene does “escape”, its future may be bleak if it handicaps its new host. The probability of successful pollination depends on a great number of interrelated factors, including level of pollen production, rate of self- and cross-fertilization of receptor plants, rate of pollen dispersion, pollinating agents, spatial distance between donor and recipient population, local density of recipient population, and differences in phenology between crop

and wild population. There is, therefore, a need to evaluate crop and recipient populations' overlap in space and time, hybridization between different crops, the stable incorporation of the transgene into the population (introgression) depending on the fertility of the hybrid produced, and use of landraces. In Kenya, for example, farmers frequently cross landraces with the improved varieties, thus crop-to-crop gene flow is already widespread.

A trait with a selective advantage and improved fitness has a chance of accumulating in a population. If the trait is outcrossed with wild relatives, it has a good chance of accumulating in the wild population, and that trait may be preferentially attained. There must be a benefit associated with the given gene in order for it to persist. If there is such a benefit, for example by increasing survival or reproduction, it is likely to spread more rapidly through the population. Conversely, if it has a detrimental impact on the fitness of individuals, the rate of gene flow is likely to be reduced and the gene may eventually be lost.

BOX 6.1

KEY ISSUES TO CONSIDER FOR VERTICAL GENE FLOW IN CROPS

- » Sexual compatibility between plant species, presence of wild or domesticated relatives
- » Pollen production rate
- » Outcrossing rate and auto-pollination
- » Pollen dispersal rate
- » Pollen viability and competitive ability
- » Characteristics of the pollinating agents
- » Spatial distances between GMOs and recipients
- » Environmental factors
- » Local density of the population
- » Temporal differences in flowering (phenologic isolation). Synchrony of flowering (timing for pollen shed, anthesis) and receptivity must coincide for the crop and nearby relatives
- » The resulting offspring must be viable and fertile

HORIZONTAL GENE TRANSFER

An organism incorporates genetic material from another organism without being the offspring of that organism.

6.2 HORIZONTAL GENE TRANSFER

HGT refers to non-sexual gene transfer between totally unrelated species and families of organisms. HGT is not a new phenomenon: it has regularly occurred during the history of life on earth. It has been a very important feature in the evolution of species and will continue to be important, but there is no obvious reason why its rate should be enhanced or altered by biotechnology and GMOs. HGT is very common for bacteria, where DNA may move easily between unrelated bacterial species, but not so common between other groups of organisms. HGT is frequently an essential component of the pathogenic relationship between a host and a pathogenic micro-organism. For example, gene transfer from bacteria to plants is a well-known natural phenomenon and forms the basis for one method of plant genetic manipulation. The bacteria concerned, *Agrobacterium* species, have evolved a series of plasmid-borne genes that enable them to attach to exposed cells in wounded plants, transferring genes from the plasmid to apparently random sites within the plant genome (Chrispeels and Sadava, 2003). *Agrobacterium* genes are thus introduced into plant genomes and this process constitutes the basis for *Agrobacterium*-mediated plant genetic transformation. There is no evidence to date that other bacteria have evolved specific methods to transfer genes to plants or animals (Ammann *et al.*, 2003).

6.3 MECHANISMS AND EFFECTS OF HORIZONTAL AND VERTICAL GENE TRANSFER

As discussed, HGT between species is a common natural process, especially among micro-organisms. There is an absolute need for the incoming DNA to be integrated and replicated with the host genome if the genes carried are to be stably maintained in the new host. If foreign DNA that has entered a new host is to be maintained, there is a need for it to confer a selective advantage on the host. If it does not, the frequency at which these genes are present in a population will remain at

BOX 6.2

**DIFFERENCES AND SIMILARITIES BETWEEN
TRANSGENE INSERTION AND TRANSPOSITION**

It has been argued that transgene insertion is not different from transposition, a natural process that involves genes moving from one locus to another in a genome. These so-called jumping genes, or mobile genetic elements, that are also used as vectors in genetic engineering, were first discovered in maize.

There are similarities between the two processes, but there are also major and fundamental differences. *Transposons occur endogenously in plants, whereas transgenes are artificially introduced.* Transposition is a rare event that seldom gives rise to new plant characteristics, while transgenic plants are common today and may display significantly altered characteristics compared with the parent organism. Both transgenes and transposons can silence genes and activate dormant genes. Both are capable of causing mutations. Activation of the transposase gene in plants is not a foreign process, and normally transposons do not provide new information in a plant.

The integration and movement of the transposons are regulated by the plant. There is conflicting evidence about the insertion of transposons: some studies show site-specific insertions, while others show no site preferences. In maize, the frequency of transposition depends on the developmental stage of the plant. Activation and deactivation of transposon genes are controlled by the plant. Transgenes, on the other hand, are present throughout the development of the plant. Transposons are also known to insert in sequences that have been duplicated before, although it is not clear whether this is a consequence of the jump or a presupposition of insertion.

The integration of transgenes is irreversible, while transposon insertion is reversible, although this reversibility might imply higher risks associated with transposition in terms of side effects because of the mutations they cause.

the frequency at which these genes are taken up. Thus, although some species are very effective in taking up DNA from the environment, they remain defined species because integration of foreign DNA is very infrequent and seldom does such integrated DNA confer a selective advantage on the new host. Other factors that are likely to reduce the frequency with which foreign DNA can be maintained in populations are differences in regulatory signals controlling the expression of genes between the parent and the host species, or different levels of gene expression depending on different preferences for codon usage (Ammann *et al.*, 2003).

In crops, the homology of the genomes between related species leads to a wide range of possibilities for the introgression of a transgene, or any other gene after the first hybrid generation. Meiotic abnormalities caused by the distant relationship between parental genomes decrease rates of introgression into new genotypes, thus the production of initial hybrids does not ensure that transgenes will move into weeds or wild relatives. Meiotic abnormalities of hybrid plants may result in higher rates of infertility and decreased rates of seed production. Recombination – an important process in the incorporation of foreign DNA - is reduced by the unstable chromosome configuration of hybrids produced by distant relatives (Chrispeels and Sadava, 2003). When crosses between plants result in a stable incorporation of genes from one pool to another, differently composed gene pool, the process is called introgression or introgressive hybridization. Introgression is often difficult to prove with certainty because shared traits may also be the result of common ancestors or convergent evolution. The most powerful way to detect introgression is by tracking linked molecular markers.

The **consequences of the transfer of transgenes** to weeds or wild relatives depend on the nature of the novel gene and the biology and ecology of the recipient plant. Gene flow from GM plants to wild relatives has two potentially harmful consequences: the evolution of weeds with increased invasiveness and persistence, and the likelihood of extinction of wild relatives. The transfer of herbicide tolerance genes,

CONSEQUENCES OF TRANSGENE TRANSFER

Possible consequences include the evolution of weeds with increased invasiveness and persistence, extinction of wild relatives, and transgene establishment in wild species with subsequent ecological impacts and disturbances.

for example, is unlikely to confer any competitive advantage to hybrids outside agricultural areas. On the other hand, the transfer of traits such as resistance to particular pests and diseases or stress tolerance could potentially give selective advantages to a given plant (increased fitness). Transgenes related to agricultural practices (herbicide tolerance) will likely not affect non-agricultural environments. In the case of herbicide tolerance, wild weed species may become superweeds. Transgenes that provide fitness-enhancing characteristics under natural conditions have the potential to disrupt the balance of established ecosystems. For insect resistance, wild species may become unpalatable and this would affect non-target invertebrates if their host plants take up the resistance gene. Crops that are being engineered for attributes such as modified starch content, reduced pod shatter, virus resistance, etc. may affect wild relatives and cause ecological imbalances.

6.4 EVALUATION OF GENE TRANSFER

Studies in risk evaluation for gene flow must consider primarily, for each crop in each location, the distinctive characteristics of pollen production, as well as the pollen dispersal and the potential for outcrossing. There are three main types of crops:

- » Crops with no sexually compatible wild relatives;
- » Crops with wild relatives but with poor compatibility, although spontaneous hybridization could still occur, e.g. oilseed rape and wild turnip;
- » Crops with fully compatible wild relatives, e.g. sugar beet, which hybridizes readily with wild sea beet.

The possible implications of hybridization and introgression between crops and wild plant species are so far unclear because it is difficult to predict how the transgenes will be expressed in a related wild species. The fitness of wild plant species containing introgressed genes from a GM crop will depend on many factors involving both the genes introgressed and the recipient ecosystems. While it

EVALUATION OF GENE TRANSFER

To assess the potential for gene transfer, studies should focus on the distinctive characteristics of pollen production, the pollen dispersal and the potential for outcrossing for each GM crop in each location.

BOX 6.3

MEASURES TO LIMIT GENE FLOW IN PLANTS: BIOLOGICAL AND PHYSICAL BARRIERS

MEASURES TO LIMIT GENE FLOW IN PLANTS

This includes a variety of biological and physical barriers; details are provided in Module D.

- » **Separating distance:** Especially important when the purity of a crop is paramount, e.g. organic crops grown in the vicinity of transgenic crops.
 - » **Barrier crops** planted around the transgenic crop and intended to capture any pollen drift. Thus, border rows act as buffers to pollen dispersal.
 - » **Crop isolation zones** between the GM crop and non-GM crop neighbour, creating a geographic barrier to ensure purity of non-GM crops.
 - » Manipulation of **flowering time** or blocking flowering.
 - » Prevent access of **pollinators** to the flowers of the transgenic plants.
 - » **Bag flowering structures** to prevent pollen spread by insect vectors, wind, or mechanical transfer, or cover female flowers after pollination to prevent loss or dissemination of GM seed.
 - » If seed production is not required, **remove flower heads** before pollen and seed production.
 - » **Harvest** plant material of experimental interest before sexual maturity;
 - » **Locate test plots** surrounded by roads or buildings to ensure isolation.
 - » **Cleistogamy** incorporated into the crop so that flowers remain closed during pollination (as happens, for example, in wheat and soybeans).
 - » **Hybrid barriers:** Pre-fertilization interspecific incompatibility at the stigma surface or within the style, or post-fertilization barriers that cause seed abortion.
 - » Genetically engineered **male sterility** so that plant produces infertile anthers.
 - » **Seed sterility** so that the GM plant produces seed that cannot germinate.
 - » **Apomixes**, the production of seed without fertilization.
- For a detailed discussion of GMO containment measures, please refer to Module D.

is important to determine frequencies of hybridization between crops and wild relatives, it is more important to determine whether genes will be introgressed into wild populations and establish at levels which will have a significant ecological impact (Eastham and Sweet, 2002). The information needed to assess potential environmental risks associated with outcrossing from transgenic plants include: biogeographical information on the species involved, reproductive biology of the plant and distribution of sexually compatible relatives, and the impact of the introduced trait, if introgressed into other plant species. Currently there are several useful tools available for evaluation, such as the Geographical Information System (GIS), modelling, and data related to geographical origin, and region of cultivation. Considerable information is already available on the biology of all major crops, making it relatively straightforward to characterize the likelihood of gene flow for any given crop using published literature and simple field surveys. Overall, the potential impacts of gene flow from GM crops are assessed in two steps:

BOX 6.4

KEY QUESTIONS ABOUT GM CROP - WILD SPECIES GENE FLOW

- » Is the crop cultivated in vicinity to its wild relative and do they flower at the same time? How far can pollen from the crop travel?
- » How easily can crop alleles introgress into wild/weedy populations? Do some crop alleles persist indefinitely?
- » What is the baseline fitness of crop-wild hybrids compared with the wild relative?
Are there strong interactions?
Are later generations more fit than early ones?
- » Are transgenic traits associated with fitness benefits and/or fitness costs? Could fitness-enhancing traits exacerbate weed problems (spread of herbicide resistance) or harm non-target organisms (pollinators)?
- » Considerations related with viability and fertility of the hybrid progeny:
Are the seeds produced viable?
Will the plants be fertile and produce viable seeds?

(1) the potential for gene flow to occur (likelihood) between the GM crop and any wild relatives is estimated (the exposure component), and (2) the potential environmental impact of gene flow (the hazard component), if it were to occur, is assessed. Gene flow will be higher from crops possessing characteristics that include high pollen production, an ability to disperse pollen over long distances, pollen production over a long period of time, and/or abundant, outcrossing wild relatives.

The development of effective strategies for the safe use of GM crops will depend on adequate biological and ecological characterization of the systems of interest that can only be achieved through a combination of appropriate field tests conducted in relevant environments and development of appropriate models and monitoring methods (Ammann *et al.*, 1999). The Committee on Environmental Impacts Associated with Commercialization of Transgenic Plants of the National Research Council (NRC-CEI, 2002) found that ...“the transgenic process presents no new categories of risk compared to conventional methods of crop improvement but that specific traits introduced by both approaches can pose unique risks”.

ECOLOGY OF GM CROPS – ENVIRONMENTAL EFFECTS

Prior to the advent of genetic engineering, plant breeding was not subjected to a great deal of regulation. Seed certification standards ensured the purity and quality of seeds, but little attention was paid to the possible food safety or environmental impacts of new plant varieties derived from conventional breeding. Conventional plant breeding differs considerably from natural selection. Artificial selection and conventional plant breeding break down the resilience in agro-ecosystems, thereby creating gene combinations that would rarely survive in nature. Conventional breeding has been responsible for a few cases of negative effects on human health. The concerns associated with genetically transformed crops are equally applicable to conventional crops. Most of the world's major food crops are not native to their major production zones; rather, they originated in a few distinct "centres of origin" and were transferred to new production areas through migration and trade. Highly domesticated plants are grown all over the world and migration outside cultivated areas has only rarely caused a serious problem (FAO, 2004; NRC-CEI, 2002). While there are risks associated with the introduction of any novel organisms into a habitat, the ecology of genetically engineered organisms is exactly the same as the ecology of any other living thing (FAO, 2004). The ecological rules are precisely the same, no matter how the genotype is put together. Nevertheless, the ecological risks associated

with a GMO, associated either with the GMO itself or a possible introgression of transgenes from the GMO to related species, need to be assessed and evaluated on a case-by-case basis.

ECOLOGICAL RISKS OF GM CROPS

These include persistence, invasion, gene flow, reduction of biodiversity, development of pests resistant to GM crops, development of superweeds and effects in non-target organisms, amongst others.

Ecological risks of GM crops that need to be considered are:

- » persistence: the transgenic plants become serious arable weeds;
- » invasion: the transgenic crops become invasive of natural habitats;
- » gene flow: transfer of introduced genes via pollen (or some other process) to other plant species (so that these then become persistent or invasive);
- » reduction of *in situ* biodiversity;
- » development of pests resistant to GM crops;
- » effects on non-target organisms.

The risks are currently not perceived as being high; transfer of genes resulting from conventional crop breeding into non-crop plants has not created conspicuous problems, nor have traditional crop plants themselves become invasive of natural habitats (FAO, 2004). To date, none of the potential risks has been manifest to any significant extent. Of course, this does not imply that these risks do not exist and that thorough investigations and safety measures need not be taken before releasing a GMO into the environment.

The foremost environmental issue is the presence of sexually cross-compatible relatives, whether domesticated or wild. The wild types may be directly related to a crop as progenitors, or they may be indirectly related as neighbouring taxa. Domesticated relatives are local, farmer selected cultivars, also called landraces. Both wild and domesticated relatives fulfill important roles as reflections of socio-cultural identities, production capital of farmers, and repositories of genetic diversity for plant breeders and farmers alike. An important feature of these domesticated or wild relatives is that they generally cross readily with introduced cultivars. This feature sets the stage for potentially extensive gene flow in domestication centres

between transgenic cultivars and their relatives. On the other hand, crops have evolved to increase self-pollination, which reduces gene flow among crop varieties.

The concerns related to GMOs can also be classified by **type of impact**:

» **Impact on the environment.**

- » Persistence of the transgene (better adaptation, invasiveness) or the products of the transgene (cumulative effects);
- » Susceptibility of non-target organisms;
- » Increased use of agro-chemicals;
- » Unpredictable expression of the transgene or transgene instability.

» **Impact on agriculture and agricultural production.**

- » Development of resistance or tolerance in target and non-target organisms;
- » Development of weeds and superweeds;
- » Reduction in nutritive value;
- » Reduction in number of varieties (increase in susceptibility to pest and diseases) and loss of biodiversity (for preference of GM crops over conventional crops);
- » Increased costs of agricultural production;
- » Lack of capacity for risk evaluation and management;
- » Ethical aspects, dependence on seeds, labelling (rights to information).

» **Impact due to interactions**

- » Genetic contamination through pollen and seed dispersal and horizontal transfer of genes;
- » Transfer of the transgene to micro-organisms or generation of new viruses;
- » Interaction among different GMOs.

To assess and evaluate these potential impacts and the likelihood with which they will occur, a detailed ecological risk assessment needs to be conducted for each newly developed GMO that is considered for commercial release.

TYPES OF IMPACT

of GMOs include impact on the environment, impact on agricultural practices, and impact due to interactions.

BOX 7.1

AIMS OF ECOLOGICAL RISK ASSESSMENT**ECOLOGICAL RISK ASSESSMENT**

To investigate and assess the ecological risks associated with the release of a GMO; for details please refer to Module C.

- » to determine the potential for persistence and spread of transgenic crops in a variety of habitats;
 - » to determine the range of plant species that can cross-pollinate with transgenic crops;
 - » to investigate the ecological performance of hybrid plants produced by such pollination;
 - » to develop protocols that would allow crop breeders to carry out their own ecological risk assessments on new transgenic plants in the future.
- The risk assessment studies need to consider the fate of the genetically engineered plants (and their pollen) and the effects of the introduction on the environment (i.e. on subsequent crops in the same fields, on adjacent crops, and in nearby natural habitats), considering:
- » problems concerned with the persistence of the vegetative plant and its propagules in different kinds of environments;
 - » problems related to the spread of the plant by vegetative growth and by seed in both arable fields and natural habitats;
 - » problems involving the risks of lateral spread of the engineered genes, either by pollination of different plant species or by other means.

Certain principles guide the risk assessment. First, the risk assessment must be specific to the crop and trait involved and the region where introduction is going to occur on a case-by-case basis. Because the environmental impact of the product will depend upon local conditions and practices, the ecological risk assessment must consider the nature of local agro-ecosystems and farming practices within these systems. Differences in cropping practices and native flora and fauna must

be taken into consideration when identifying potential hazards and prioritizing research needs. Second, it is not possible to demonstrate absolute safety for any technology or activity, as all technologies and activities carry some risk. Instead, relative safety compared with alternative technologies is what must be assessed. A regulator must consider whether the product involves greater risks than comparable technologies. Alternatively, the regulator may compare the net benefit (benefit-risk balance) for the product. Note that this risk-benefit balance will reflect local views on the importance of risk and uncertainty, and thus regulators in different regions may make different decisions based on the same data. The assessment then should consider the relative risks and benefits of the new product relative to current practices, and should include the potentially important ecological impacts of these technologies. For an insect-control product like Bt cotton, current practices typically involve the use of conventional insecticides. For herbicide-tolerant crops, there would be other herbicide regimes. These comparisons must be carried out based on local conditions.

7.1 CONCERNS AND POTENTIAL RISKS OF GMOs TO THE ENVIRONMENT

7.1.1 Persistence of the crop/transgene

In the evaluation of possible impacts of a transgenic plant, one of the fundamental issues is to establish whether the introduced genes (traits) can result in the crop becoming more persistent (weedy) in an agro-ecosystem or more invasive in natural habitats. It is known that the characteristics of a weed are the sum of many different traits and that the addition of a single gene is unlikely to turn a plant into a weed. Special attention should be paid, however, to those crops that already have some weed traits or those in which addition of a gene might increase competitiveness in agro-ecosystems or their invasiveness in natural ecosystems. For example, crops that have a short history of domestication are closest to this situation as they still have many “wild” genes and traits, conferring

PERSISTENCE
Potential of a GM crop to grow outside of an agricultural setting and thus become a potential weed.

competitiveness, that are usually eliminated during selection processes to improve a crop. Those GM crops used to date do not show evidence of having increased in persistence or invasiveness. It is important to consider whether a crop is sown in its centre of origin or domestication, and the type of environment that it is introduced into. For this reason risk must be studied and evaluated on a case-by-case and step-by-step basis.

7.1.2 Gene flow and gene dispersal from transgenic crops

Gene flow and gene dispersal are two separate phenomena and their potential consequences are different. Gene flow refers to exchange of genes (transgenes) among species, usually mediated in the case of plants by hybridization, whereas **gene dispersal** refers solely to movement of pollen. Concerns for gene flow are that there will be genetic pollution of species through creation of “unnatural” hybrids and that new superweed species could be created that would have direct consequences for the environment and agriculture. If gene dispersal has any effect, it is likely to be short-term, but effects of gene flow could be long-lasting and persistent. Introduced genes could potentially spread in adjacent populations creating new phenotypes. Investigating and evaluating this process requires insight into ecological impacts of such events, including studies of population sizes, dynamics, and spread and development to quantify and predict possible scenarios.

An additional factor in the need to restrict inadvertent gene flow is the possibility of generating feral populations of the crop. Many crops do not survive long periods off-farm, but under semi-natural conditions seed may remain dormant but viable for long periods and feral populations of the crop might eventually establish. This represents a potential problem especially among members of the cabbage family, where species such as rape have become serious weeds. If weedy species contain herbicide resistance genes, for example, they could pose a particularly serious management problem. If these genes were passed

**GENE
DISPERSAL**
The movement
of (transgenic)
pollen.

among different species within a genus, or among related genera, hybrid weeds could be created. Similar concerns as those that have been voiced for herbicide tolerance genes will likely be heard should **genetic use restriction technology (GURT)** genes be deployed in crop plants. The major fear, again, in this case is that these genes could be transferred to non-genetically modified crops of the same or related species. The spread of resistance or tolerance genes to pests and diseases has to be considered in a double sense. There are possibilities for those genes to render related weed species more resistant, but depending on the case, they could represent possibilities for better survival of wild species. In general terms, it is likely that they represent an environmental impact only when a new transgene confers enhanced fitness to a crop or its wild relatives with which it is sexually compatible.

In general, assessing the impacts of introducing new technologies into centres of diversity requires a special degree of care for several reasons. There is widespread consensus among scientists and policy-makers that the biological and genetic diversity of these regions needs to be preserved, and may be vulnerable to ecological disturbances. Centres of diversity, and centres of origin for crop species, represent areas where many potentially-impacted wild species may exist, including wild relatives of crop species that may be recipients of gene flow, as well as many non-target species that could be directly or indirectly impacted by changes in agro-ecosystems (Lemaux, 2008).

7.1.3 Susceptibility of non-target organisms

Toxicity to living organisms refers to inadvertent effects caused by GMOs to benign organisms in the environment. This can be the case if a GM crop carries resistances to pests and diseases. The ideal situation in GM development is to identify a resistance gene to a pest or disease and introduce it so that it is expressed solely in the tissues where needed. Only then is it likely to have an effect only on the

GENETIC USE RESTRICTION TECHNOLOGY (GURT)

A proposed technology applying transgenesis to genetically compromise the fertility or the performance of saved seed of a cultivar or of second generation animals. The intention is to protect the market for the seed producer or to prevent undesired escape of genes. Two types of GURTs have been patented: variety-level GURT (V-GURT), which produces sterile progeny, and trait-specific GURT (T-GURT), in which only the added value transgenic trait is genetically protected.

SUSCEPTIBILITY OF NON-TARGET ORGANISMS

Constitutes a major concern regarding the introduction of pest or disease-resistant GM crops. Any effects of such a crop on non-target, possibly beneficial organisms must be carefully assessed and evaluated.

target organism and not on non-target organisms; although non-target organisms feeding on the tissue might still be affected. To achieve this, however, is not easy. There are current advances in this area and there are commercial cultivars that show tissue-specific gene expression. For example, there are numerous maize lines that express toxins from *Bacillus thuringiensis* (Bt) specifically to combat insect infestation, others with increased expression of genes for lysine production in the grain, canola that expresses genes leading to male sterility in the pollen, maize with higher oil content in the grain and others with a changed fatty acid profile and starch structure.

The most studied examples of genetically manipulated resistance in crops are those employing the Bt delta endotoxins. The Bt soil bacterium is abundant under natural conditions and produces a toxin that is lethal to certain insect pests with specific characteristics. One of the most discussed experiments involved Bt toxins and the monarch butterfly (a non-target organism) in the United States. The results of a laboratory study published in 1999 suggested that Bt maize represented a danger to the monarch larvae that consumed *Asclepias* spp. that were covered with transgenic maize pollen. The study did not determine the ecological consequences of the results and the tests were done under laboratory conditions that did not equate with natural conditions (Losey *et al.*, 1999). The publication based on the results of the experiments generated global interest and stimulated the set-up of a cooperative research programme in the same year. The research centred on the effects of the supposedly toxic transgenic maize pollen on monarch larvae feeding on pollen-dusted leaves of their food plant. The authors concluded that although the Bt pollen could be toxic at certain high concentrations, under field conditions there was little risk to the monarch larvae as such high concentrations of pollen would be unlikely to occur in nature (Stanley-Horn *et al.*, 2001). The ideal resistance mechanism for pest control would be one with no unwanted adverse effects on other organisms or the ecosystem.

A second example: ladybirds are generally considered to be beneficial organisms; many eat aphids that are capable of damaging crops through direct feeding and vectoring viruses. Recent studies on the effect of the Bt toxin Cry1Ab from transgenic maize on the biology of the ladybird *Stethorus punctillum* indicated that the toxin had no effect on its fitness. It was shown that the ladybird lacked the midgut receptors for the active toxin to bind to (Alvarez-Alfageme *et al.*, 2008). This research indicates that there is a long way to go before the effects of transgenic crops on non-target organisms are well understood.

A further area that must not be overlooked is the effect of dead transgenic plant material on soil organisms (detritivores) feeding on it. The expression of a transgene in plant tissue might have effects on the small animals and micro-organisms decomposing it, with possible secondary effects for the entire soil community. Therefore, the effect of a GMO on the soil community needs to be carefully assessed and evaluated.

7.1.4 Unforeseen gene expression and instability of transgenes

This potential risk relates to concern over wide crosses in conventional crop breeding. In conventional breeding techniques it is not possible to determine *a priori* which genes will be introduced by a cross. This implies a long process of targeted selection after crossing to remove unwanted genes and traits. With GM crops, however, it is known with almost certainty which genes are introduced and it is the subsequent laboratory work that determines which will be expressed and will be stable. In general terms, given that there is ample knowledge of the genes and DNA sequences used in genetic transformation, the number of genes introduced into a GM plant is smaller than in a conventional cross. Technical developments mean that a transgene insertion can be specifically located and its

UNFORESEEN GENE EXPRESSION AND INSTABILITY OF TRANSGENES

After producing a GMO, it needs to be verified that the transgene is expressed in the desired temporal and spatial manner, and that it is stably integrated in the genome and passed on from one generation to the next.

expression quite accurately controlled. What distinguishes this technology from the conventional technology is the improved precision in introduction of a small number of well-known genes to make for a much better controlled process. To date there appears to be no evidence of phenomena like uncontrolled gene expression or transgene instability in the GM crops studied and evaluated. Nevertheless, each GM crop needs to be carefully evaluated to verify the expression pattern of the introduced genes and the stability of the transgene.

7.1.5 Weeds

WEEDS

Concerning weed management, biotechnology so far has been mainly applied to create herbicide-resistant crops.

Future goals include improved resistance to parasitic weeds.

Weeds fall into two major classes, parasitic and non-parasitic. Weed control is a major component of crop management programmes. Biotechnology has been less successfully applied to weed management than to management of other biotic stresses. For non-parasitic weeds, biotechnology has been applied to develop herbicide resistance, an indirect control strategy where the crop is the target of the transgene and not the weed. Species of two parasitic weed genera, *Striga* and *Orobanche*, represent important weeds of the tropics and Mediterranean areas. They are currently managed through various strategies including manual weeding, crop rotations, chemical control and biocontrol. Biotechnology has the potential to transform crops to allow herbicide application for weed control and to alter gene action controlling the stimuli that trigger germination and development of parasitic weed seed. More knowledge of the host-parasite relationship at the molecular level will allow more environmentally sound management methods to be developed.

Parasitic weeds represent a very specific management challenge. Each plant of *Striga hermontheca*, a major problem of cereal crops in the tropics, is able to release 100 000 seeds into the soil, each of which can remain viable for up to fifteen years. There is variation in resistance of some crops, including sorghum, which appears to be under genetic control. This can be selected for using traditional plant

breeding methods, but can probably be enhanced in the future using methods from molecular biology such as MAS. For crops, including maize, there is no naturally occurring host-plant resistance and the only possibilities of obtaining any, though this has not been done yet, would be to induce it or transfer non-host resistance, which occurs in many grass species. Unfortunately, very little is known about the mechanisms of non-host resistance.

Transforming crops to tolerate contact herbicides would not be effective in managing parasitic weeds as they have already done their damage before they appear above the soil surface. Transforming the crop for application of systemic herbicides, as has been done for non-parasitic weed management, is unlikely to be effective as the crop breaks down the herbicide into harmless chemicals that do not consequently reach the parasite, which is intimately linked with the crop via its roots. Enzymes in the crop that are associated with herbicide uptake could be modified to prevent herbicide binding and promote build-up of the herbicide in the parasite. Glyphosate resistance works in this way, which is termed target-site resistance. This represents the most feasible form of control and has been effective in controlling *Striga* and *Orobanche* infestations in various crops sprayed with several herbicide formulations. Seed dressings that rely on this mechanism can also be used.

One issue constantly being raised is that of the development of a **superweed** which, created through flow of herbicide tolerance transgenes, would become impossible to control using standard herbicides. To date such a weed has not developed, but serious weed problems have arisen through deliberate introduction of new ornamental plants and inadvertent introduction of exotics. Some of these have literally become some of the world's worst weeds and yet have been relatively unnoticed by environmental lobby groups. They represent introductions of entire new genomes, and are not merely the result of (trans)gene flow. Perhaps, in the future, there will generally be a better understanding of the relative level of risk posed by the flow of ethically contentious genes.

SUPERWEED

The development of a herbicide-resistant weed through flow of herbicide tolerance genes from a GM crop to a weedy relative.

BOX 7.2

FIELD TESTING

Realistic, small-scale field tests are necessary to evaluate potential risks as well as benefits for commercial-scale uses of GMOs.

QUESTIONS ADDRESSED BY FIELD TESTING

Some questions related to the release of genetically engineered organisms can be answered only with practical experience. Realistic, small-scale field tests are the way to evaluate potential risks from commercial-scale uses of genetically engineered organisms. However, these short-term studies are only appropriate to risk assessments on annual crop plants.

At the end of a three-year study of the population biology of transgenic and non-transgenic annual crop plants, one should be in a position to:

- » Provide data on persistence and invasion in natural and arable habitats.
- » Show how (and if) genetic engineering alters these parameters.
- » Describe pollen spread by insect vectors and by other means.
- » Show how (and if) genetic engineering alters the production, spread, or compatibility of pollen.
- » Catalogue the wild plants that share insect pollinators with the crop.
- » Provide quantitative data on successful cross-pollination between the crop and its wild relatives.
- » Provide data on the persistence and invasiveness of any transgenic hybrid plants produced by crossing experiments.

7.2 POTENTIAL BENEFITS OF GMOs

The use of industrial agrochemicals has a substantial bearing on the sustainability of agro-ecological systems. Pesticides have not only had direct negative impacts on the quality of the environment, but have also adversely affected biodiversity through removing beneficial and inoffensive organisms. Interestingly, glyphosate, which several crops have been transformed to tolerate, is much less toxic than

some of the herbicides (e.g. atrazine) it replaced. There is concern that GMO use in the field of herbicide resistance will result in increased use of herbicides. Evidence suggests that this has not been the case, but that herbicide use has been reduced at the commercial level. Reduction in pesticides can be obtained by identifying, developing and deploying durable host-plant resistance to pests and diseases. Insect pests (9 000 species), plant pathogens (50 000 species) and weeds (8 000 species) account for the greatest crop losses, and their control requires the greatest use of agro-chemical crop protection. The advantages of host-plant resistance are numerous and include: it is relatively inexpensive for the farmer in comparison with chemical control; it is always present; it has no effect on organisms other than the target ones; it can be extremely durable; it can employ a diversity of resistance genes; it does not interfere negatively with other forms of control; and it has no negative effects on yield. There are also many possibilities to improve crop production through breeding for adaptation to a range of abiotic stresses, including drought, salt and heat, and more efficient use of nitrogen and water.

Biotechnology applications to date have focused on engineering traits such as herbicide resistance for some of the major commodity crops, but there is considerable potential for expanding the methods to include a broader range of crops and genetically more complex traits. Many disease resistances are governed by few genes and represent relatively easy targets for the molecular breeder. Resistance to some diseases is controlled by many genes, each to little effect. Using modern methods, including quantitative trait loci (QTL) analysis, important areas of the genome in resistant lines can be identified, located and ultimately cloned for inclusion into susceptible, but otherwise adapted, germplasm.

Table 7.1 | Potential direct and indirect effects of GM crops on the environment¹

ENVIRONMENTAL EFFECTS OF GMOs				
Direct Effects				
Invasiveness of GM crops ↓	Gene flow ↓	Environmental fate of transgenic products ↓	Effects on non-target organisms ↓	Effects on target organisms ↓
Survival outside the cultivated area	Pollen transfer to wild relatives and hybrid formation	Persistence, degradation and spread of transgenic pollen	Direct or indirect uptake of transgenic products through feeding	Resistance development in target organisms
Reproduction outside the cultivated area	Survival and reproduction of hybrids	Accumulation of transgenic products in soil	Effects on non-target organisms	Effects on population dynamics
Transgenic population (hybrids/crops) with enhanced fitness compared to wild population		Eluviation of transgenic products from soil	Effects on population dynamics	
Spread and persistence of transgenic plants (hybrids/crops) outside the cultivated area		Immission of transgenic products into water	Effects on ecosystems	
Outside the cultivated area (substitution of natural population)	In the cultivated area (super weeds)			
Environmental damage	Economic damage	Environmental damage	Environmental damage	Economic damage

¹ Adapted from Sanvido O., M. Stark, J. Romeis and F. Bigler (2006) Ecological impact of genetically modified crops – experiences from ten years of experimental field research and commercial cultivation. ART Schiftenreihe 1, Agroscope Reckenholz-Tänikon Research Station ART, Zurich, Switzerland.

ENVIRONMENTAL EFFECTS OF GMOs				
Indirect Effects				
Resistance development		Effects on agricultural methods and cropping systems		
↓	↓	↓	↓	↓
Resistance development on target pest/disease	Selection of herbicide tolerant wild plants	Changes in cultivation practice/tillage	Changes in cropping intervals/cultivation area	Excess of agronomic competitiveness of GMOs
Loss of effectiveness of transgenic products	Reduced effectiveness of specific herbicide	Changes in spectrum of pests, diseases and beneficial organisms	Changes in physical, chemical and biological soil characteristics	Substitution of cultivations which have no GMO available
Need to change pest/disease control strategies			Decrease in soil quality	Substitution of traditional varieties
		Effects on biodiversity		
Economic damage		Environmental damage		

REFERENCES

- Alvarez-Alfageme F., Ferry, N., Castañera, P., Ortego, F., & Gatehouse, A.M.** 2008. Prey mediated effects of Bt maize on fitness and digestive physiology of the red spider mite predator *Stethorus punctillum* Weise (Coleoptera: Coccinellidae). *Transgenic Res.* 17(5): 943-54.
- Ammann, K.** 2003. *Biodiversity and agricultural biotechnology: a review of the impact of agricultural biotechnology on biodiversity*. Botanischer Garten Bern, Switzerland. 54 p.
- ASAP (Agroecology/Sustainable Agriculture Program).** 2004. Principles of sustainable agriculture (available at: <http://www.aces.uiuc.edu/~asap/index.html>).
- Begon, M., Townsend, C.A. & Harper, J.L.** 2006. *Ecology: from Individuals to ecosystems*. 4th Edition. Wiley-Blackwell.
- CBD (Secretariat of the Convention on Biological Diversity).** *Biodiversity and Agriculture: Safeguarding Biodiversity and Securing Food for the World*. Montreal, 2008.
- CBD (Secretariat of the Convention on Biological Diversity).** Texts and documents (available at: www.cbd.int).
- Chrispeels, M. J. & Sadava, D.E.** 2003. *Plants, genes and crop biotechnology*. Second Edition. American Society of Plant Biologists and the ASPB Education Foundation. Salisbury, Massachusetts, USA, Jones and Bartlett Publishers.
- Eastham, K. & Sweet, J.** 2002. *Genetically Modified Organisms (GMOs): The significance of gene flow through pollen transfer*. European Environment Agency EEA's Corner Series Environmental Issue Report N° 28. 75 p.
- FAO.** 2001. *Genetically modified organisms, consumers, food safety and the environment* (available at: www.fao.org).
- FAO.** 2004. *The state of food and agriculture 2003-2004 (SoFA)*. Agricultural biotechnology: meeting the needs of the poor?
- FAO,** 2007. *Marker-assisted selection. Current status and future perspectives in crops, livestock, forestry and fish*.
- Fraleigh, B.** 2006. Global overview of crop genetic resources, as part of FAO publication *The role of biotechnology in exploring and protecting agricultural genetic resources*.
- Henry, R. J.** 2000. *Practical applications of plant molecular biology*. London, Chapman & Hall. 258 p.
- Kameswara Rao, C. & Shantharam, S.** 2004. *Can GM crops be introduced into crop centres of origin and diversity?* Special to AgBioView, 13 April 2004.
- Lemaux, P.G.** 2008. Genetically engineered plants and foods: a scientist's analysis of the issues (Part I). *Annu. Rev. Plant. Biol.* 59: 771-812.
- Losey, J.E., Ravor, L.S. & Carter M.E.** 1999. Transgenic pollen harms monarch larvae. *Nature* 399(6733): 214.

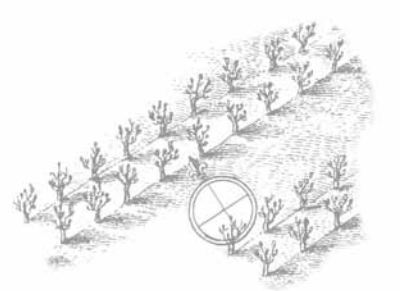
- NRC-CEI (National Research Council Committee on Environmental Impacts).** 2002. *Environmental effects of transgenic plants*. Washington, DC, National Academy Press. 320 p.
- NRCS (Natural Resources Conservation Service – USDA).** 2004. *Agricultural ecosystems and agricultural ecology* (available at: www.nrcs.usda.gov).
- Purves, W.K., Sadava, D., Orians, G.H. & Heller, H.G.** 2004. *Life: the science of biology*. Sunderland, Massachusetts, USA, Sinauer Associates, Inc. 7th Edition. 1121 p.
- Rao, N.K.** 2004. Plant genetic resources: advancing conservation and use through biotechnology. *African Journal of Biotechnology* 3(2): 136-145.
- Ricklefs, R.E. & Miller, G.L.** 1999. *Ecology*. New York, USA, W. H. Freeman & Co. 4th Edition. 822 p.
- Stanley-Horn, D.E., Dively, G.P., Hellmich, R.L., Mattila, H.R., Sears, M.K., Rose, R., Jesse, L.C., Losey, J.E., Obrycki, J.J., & Lewis, L.** 2001. Assessing the impact of Cry1Ab-expressing corn pollen on monarch butterfly larvae in field studies. *Proc. Natl. Acad. Sci. U S A* 98(21): 11931-6.
- The National Academies.** USA. 2007. *New horizons in plant sciences for human health and the environment* (available at: http://www.nationalacademies.org/plant_genome).
- WCMC (World Conservation Monitoring Centre).** 2002. Biodiversity: an overview. (available at: www.wcmc.org.uk/infoserv/biogen/biogen.html).

USEFUL READINGS

- ACRE (Advisory Committee on Releases to the Environment UK).** 2007. *Managing the footprint of agriculture: towards a comparative assessment of risks and benefits for novel agricultural systems*. Report of the ACRE Sub-Group on Wider Issues raised by the Farm-Scale Evaluations of Herbicide Tolerant GM Crops (available at www.defra.gov.uk/environment/acre).
- AGBIOS (Agriculture & Biotechnology Strategies, Inc.).** 2002. Essential Biosafety™. A comprehensive source of scientific and regulatory information. CD-ROM^{2nd} Edition.
- AgriFood Awareness.** 2004. New co-existence study on GM and non-Gm crops in the EU (available at: http://www.pgeconomics.co.uk/pdf/Co-existencestudyEU_PG_Economicsmay2004.pdf).
- Ammann K., Jacot, Y., Simonsen, V. & Kjellsson, G. (Eds.).** 1999. *Methods for risk assessment of transgenic plants*. III. Ecological risks and prospects of transgenic plants, where do we go from here? A dialogue between biotech industry and science. Basel, Switzerland, Birkhäuser-Verlag. 260 p.
- Ammann, K.** 2007. Reconciling Traditional Knowledge with Modern Agriculture: A Guide for Building Bridges. In *Intellectual Property Management in Health and Agricultural Innovation: A Handbook of Best Practices* (eds. A Krattiger, RT Mahoney, L Nelsen, et al.). Oxford, U.K., MIHR, and Davis, USA, PIPRA (available at www.ipHandbook.org).
- Ammann, K., Jacot, Y. & Braun, R. (Eds.)** 2003. *Methods for risk assessment of transgenic plants*. IV. Biodiversity and biotechnology. Basel, Switzerland, Birkhäuser-Verlag. 177 p.
- Benbrook, C.M.** 2002. A perspective on actual versus potential environmental benefits of agricultural biotechnology. In: *Environmental Savior or Saboteur? Debating the Impacts of Genetic Engineering*. 4 February, San Francisco, California (available at: <http://www.biotech-info.net>).
- Bradford, K.J., Van Deynze, A., Gutterson, N., Parrot, W. & Strauss, S.H.** 2005. Regulating transgenic crops sensibly: lessons from plant breeding, biotechnology and genomics. *Nature Biotechnology* 23: 439- 444.
- Brookes, G. & Barfoot, P.** 2006. Global impact of biotech crops: socio-economic and environmental effects in the first ten years of commercial use. *AgBioForum* 9(3): 139-151.
- Brookes, G. & Barfoot, P.** 2008. *GM crops: global socio-economic and environmental impacts 1996-2006*. UK, PG Economics Ltd.
- CIAT-UN-BIODIVERSITY-REDCAPA-CTA.** 2007. Multi-Institutional Distance Learning Course on the Ex-situ Conservation of Plant Genetic Resources (available at: www.ciat.org).
- Cohen, J.I.** 2005. Poorer nations turn to publicly developed GM crops. *Nature Biotechnology* 23: 27-33.

- Conner, A.J., Glare, T.R. & Nap, J.P.** 2003. The release of genetically modified crops into the environment, Part II. Overview of ecological risk assessment. *The Plant Journal* 33: 19-46.
- Dale, P.J., Clarke, B. & Fontes, E.M.G.** 2002. Potential for the environmental impact of transgenic crops. *Nature Biotechnology* 20: 567-574.
- Daniell, H.** 2002. Molecular strategies for gene containment in transgenic crops. *Nature Biotechnology* 20: 581-586.
- DEFRA (Department for Environment, Food & Rural Affairs UK).** 2002a. *Guidance on best practice in the design of Genetically Modified Crops* (available at: www.defra.gov.uk/environment/acre/bestprac/consult/guidance/).
- DEFRA (Department for Environment, Food & Rural Affairs UK).** 2002b. *Guidance on the assessment of risk to wider biodiversity from proposed cultivation of GM crops* (available at: www.defra.gov.uk/environment/consult/biodiversity/risk/index.htm)
- DEFRA (Department for Environment, Food & Rural Affairs UK).** 2002c. *Farm-scale evaluations of genetically modified crops. Answers to some frequently asked questions* (available at: www.defra.gov.uk/environment/fse/raq/index.htm).
- Edmeades, S. & Smale, M.** 2006. A trait-based model of the potential demand for a genetically engineered food crop in a developing economy. *Agricultural Economics* 35(3): 351-361.
- Halpin, C.** 2005. Gene stacking in transgenic plants – the challenge for 21st century plant biotechnology *Plant Biotechnology Journal* 3: 141-155.
- Hota, M.** 2007. *Crop biotech & biosafety*. International Service for the Acquisition of Agri-biotech Applications (ISAAA), New Delhi.
- ICSU (International Council for Science - Nuffield Council on Bioethics).** 2003. GM Science Review Panel. 298 p.
- IFPRI (International Food Policy Research Institute).** 2008. *Insecticide use on vegetables in Ghana. Would GM seed benefit farmers?* IFPRI Discussion Paper 00785. Environment and Production Technology Division (available at: www.ifpri.org).
- James, C.** 2007. *Global status of commercialized biotech/GM crops*. ISAAA Brief No. 37, Ithaca, NY, ISAAA.
- Kolady, D.E. & Lesser, W.** 2008. Is genetically engineered technology a good alternative to pesticide use? The case of GE eggplant in India. *International Journal of Biotechnology* 10(2/3): 132-147.
- Lemaux, P.G.** 2001. *Nudging mother nature: the promise and reality of AgBiotech for farmers* (available at: <http://ucbiotech.org/resources/biotech/talks/>).
- Miller, H., Morandini, P. & Ammann, K.** 2008. Is biotechnology a victim of anti-science bias in scientific journals? Trends in biotechnology. 122-125 pp (available at <http://www.botanischergarten.ch/Peer-Review/Miller-Morandini-Ammann-Peer-Review-2008.pdf>).

- Nap, J.P., Atanassov, A. & Stiekema, W.J.** (Eds.) 2004. *Genomics for biosafety in plant biotechnology*. NATO Science Series. Amsterdam, IOS Press. 247 p.
- Pidgeon, J.D., May, M.J. & Dewar, A.M.** 2003. GM crop management for environmental benefit. In: 7th ICABR International Conference: Public Goods and Public Policy for Agricultural Biotechnology. Ravello, Italy, 29 June – 3 July.
- Potrykus, I.** 2004. Experience from the humanitarian Golden Rice project: extreme precautionary regulation prevents use of green biotechnology in public projects. BioVision Alexandria, 3-6 April 2004.
- Pullin, A.S.** 2002. *Conservation Biology*. Cambridge, U.K., Cambridge University Press. 345 p.
- Rull, V.** 2008. Speciation timing and neotropical biodiversity: the tertiary–quaternary debate in the light of molecular phylogenetic evidence. *Molecular Ecology* 17: 2722–2729.
- The World Bank.** 2007. *World Development Report 2008*. Agriculture for Development (available at: www.worldbank.org)
- Traynor, P.L., Frederick R. & Koch M.** 2002. *Biosafety and risk assessment in agricultural biotechnology (A workbook for technical training)*. The Agricultural Biotechnology Support Project, Institute of International Agriculture, Michigan State University, USA. 142 p.
- UN Millennium Project.** 2005. *Investing in development: a practical plan to achieve the Millennium Development Goals. Overview*.
- Vavilov, N.I.** 1997. Five Continents. (Rodin LE,Ed.) International Plant Genetic Resources Institute, Rome, Italy. 198 p.



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Biosafety Resource Book

MODULE B

ECOLOGICAL ASPECTS

provides the necessary background information on ecology and evolution needed to analyse and understand the consequences of introducing GMOs into the environment.

For additional information
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