

## B8 Genetic resources for food and agriculture



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## Overview

This module describes the nature of genetic resources for food and agriculture and outlines why these are essential for climate-smart agriculture. [Chapter B8.2](#) provides a brief description of genetic resources for food and agriculture, considers how they may be affected by climate change and highlights their role in climate-smart agriculture. The next four chapters look specifically at the genetic resources used in four major agricultural sectors: crop production; livestock production; forestry; and fisheries and aquaculture. [Chapter B8-7](#) deals with micro-organisms and invertebrate genetic resources. Each chapter describes how the sustainable use and development of the genetic resources can support climate change adaptation and mitigation, by referring to the main components of genetic resource management: characterization,<sup>i</sup> evaluation,<sup>ii</sup> inventory,<sup>iii</sup> monitoring,<sup>iv</sup> sustainable use and conservation. The module concludes with a summary of a set of cross-sectoral actions that could be undertaken to improve the sustainable management of genetic resources to support climate-smart agriculture, which were laid out in the *Voluntary Guidelines to Support the Integration of Genetic Diversity into National Climate Change Adaptation Planning* (FAO, 2015a).

## Key messages

- Genetic resources for food and agriculture are the basis for sustainable, climate-smart agriculture and food security.
- A better understanding of genetic resources and their role in agriculture and food production is a prerequisite for developing climate change adaptation and mitigation strategies. More attention needs to be given to

invertebrates and micro-organisms that sustain ecosystem functions.

- The diversity of genetic resources, which provides options for adapting agricultural production to the impacts of climate change, needs to be conserved and used for the well-being of present and future generations.
- Genetic diversity plays a key role in carbon sequestration, particularly in aquatic ecosystems, natural and planted forests, and soils.
- Many genetic resources can be conserved in genebanks (*ex situ*). Others need to be conserved in agricultural production systems or in natural or semi-natural habitats (*in situ*). Where possible, a combined approach involving complementary *in situ* and *ex situ* conservation measures is recommended.
- Access to genetic resources with relevant traits for climate change adaptation and mitigation is crucial. It is important to recognize that individual countries rely for a significant part upon genetic resources originally collected from other countries.

## Genetic resources for food and agriculture

Genetic resources for food and agriculture (referred to in this module as genetic resources) are the basis for sustainable agriculture and food security. These resources are essential for food, nutrition, energy and shelter. They also sustain ecosystem services in all agricultural production systems, and support critical functions, such as pollination, soil formation and pest and disease control.

Genetic diversity determines the range of characteristics that enable plants, animals and micro-organisms to fulfil different roles in agricultural production systems and adapt to changing environmental conditions, such as extreme temperatures, drought, flooding and outbreaks of pests and diseases. This diversity also shapes the way in which plants and animals make use of inputs and resources, such as fertilizer, water and feed.

Centuries of selection and domestication by farmers, pastoralists and breeders, combined with natural selection, have led to the development of many diverse varieties, breeds, stocks and strains. Over the generations, this rich diversity has allowed people to obtain food and sustain their livelihoods in difficult environments and under extreme climatic conditions. This diversity also provides materials that can be used by breeding programmes to ensure plant and animal populations can adapt to future conditions – conditions that will be influenced by the impacts of climate change and by the shifting demands of human societies.

However, genetic diversity is being lost. The main causes of genetic erosion are intensive agricultural production systems that uses fewer and more genetically uniform crop varieties and animal breeds (see [Chapter B1 - 1.1](#)), changing consumer demands, changes in land use, excessive use of pesticides and fertilizers, invasive alien species and climate change.

Climate change poses risks to genetic resources and creates obstacles to their sustainable management (FAO, 2016a). These threats and challenges can be associated with gradual changes, such as increasing temperatures, and with the increasing incidence of abrupt and catastrophic events, such as extreme weather events and outbreaks of pests and diseases. Climate change is expected to alter the distribution of species, population sizes, the composition of ecological communities, the timing of biological events, and the behaviours of different species and their interactions. Extreme events may lead to the sudden extinction of small, spatially limited populations.

Genetic resources and their diversity are essential to climate change adaptation and mitigation efforts. For example, genetic resources play a key role in carbon sequestration, particularly in aquatic ecosystems, natural and planted forests (see [module B3](#) on climate-smart forestry and [module B5](#) on agroforestry) and soils (see [Box B7.3](#)).

Specifically adapted genetic resources may offer unique opportunities to adapt to environmental and climatic changes. To contribute to climate-smart agriculture, these resources must be managed in a sustainable way. The

main components of genetic resource management are characterization,<sup>v</sup> evaluation,<sup>vi</sup> inventory,<sup>vii</sup> monitoring,<sup>viii</sup> sustainable use and conservation<sup>ix</sup>.

A strong political and institutional framework enables relevant stakeholders at local, national and international levels to address the challenges posed by climate change. The FAO [Commission on Genetic Resources for Food and Agriculture](#) promotes the conservation of genetic resources and their sustainable use for climate change adaptation and mitigation (Box B8.1).

### **Box B8.1 The Commission on Genetic Resources for Food and Agriculture**

The FAO Commission on Genetic Resources for Food and Agriculture is the only permanent intergovernmental forum for the discussion and negotiation of matters relevant to all components of biological diversity for food and agriculture. One of its outputs, the *Voluntary Guidelines to Support the Integration of Genetic Diversity into National Climate Change Adaptation Planning* (FAO, 2015a), promotes the use of genetic resources for food and agriculture in climate change adaptation, and supports their integration into national climate change adaptation planning. The Commission also oversees the development of global plans of actions for the conservation and sustainable use of genetic resources (FAO, 2007, 2011a, 2014).

## **Climate-smart management of plant genetic resources**

Plant genetic resources are defined by the [International Treaty on Plant Genetic Resources for Food and Agriculture](#) as “any material of plant origin, including reproductive and vegetative propagating material, containing functional units of heredity of plant origin of actual or potential value for food and agriculture”. These resources are used, or have the potential to be used, for food and other agricultural purposes. They include crop wild relatives ; other species that could interbreed with crops; wild plants that are harvested for food; landraces and farmer varieties; and formally registered crop varieties. The diversity of plant genetic resources underpins global food security and nutrition. Plant genetic resources consist of a vast diversity of heritable traits that have enable crops to adapt to physical and biological stresses (e.g. drought, heat, cold, pests and diseases). This diversity needs to be harnessed to help crop production systems adapt to the consequences of climate change. However, despite the existence of diverse crops and their varieties, only 17 crops provide about 80 percent of human food energy needs met by plants out of the over 50,000 edible plant species (figures for 2013 as recorded in FAO’s statistical database FAOSTAT (FAO, 2017a). (see also chapter B1 - 1.1 on the need for sustainable production intensification and diversification). In fact, just seven of these (rice, wheat, sugarcane, maize, soyabean, potatoes and sugarbeet) account for about 55 percent of the energy intake of the world’s population (figures for 2013 as recorded in FAO’s statistical database FAOSTAT (FAO, 2017a).

### **B8 - 3.1 Impact of climate change on plant genetic resources**

Climate change affects the concentration of carbon dioxide in the atmosphere, temperatures, precipitation patterns and the distribution of land suitable for cultivating many crops. See [chapter B1 - 1.2](#) for the most universally accepted effects of climate change on crop production. It is predicted that in sub-Saharan Africa, the Caribbean, India and northern Australia, the amount of land suitable for crop production will decline. Without measures to adapt to these new conditions, production of the world’s major staple crops (wheat, rice and maize) will be negatively affected in these areas (FAO, 2015b). There is evidence that climate change has already reduced wheat

and maize yields in many regions (Lobell, Schlenker and Costa-Roberts, 2011). Crop management practices and technologies for adaptation to climate change are presented in chapter B1 - 2, and these management practices in the context of specific farming systems are presented in [chapter B1 - 3](#).

Genetic vulnerability<sup>xi</sup> results when a widely planted crop is uniformly susceptible to a pest, pathogen or environmental hazard as a result of its genetic constitution. This creates the potential for widespread crop losses. Genetic vulnerability threatens agricultural production in 60 countries (FAO, 2010). For example, of the 120 cultivars included in the Russian Official List of 2002, 96 percent of all the varieties of winter wheat in Russia were descendants of either one or both of two cultivars, Bezostaya 1 and Mironovskaya 808 (Martynov and Dobrotvorskaya, 2006). A new type of a particularly virulent pest or disease, which could emerge as a consequence of climate change, could conceivably cause considerable crop losses, as all the plants would be uniformly susceptible. An example of the dangers of genetic vulnerability is the infamous potato blight, which caused significant yield losses and contributed to unprecedented famine in Ireland in the mid-19th century. More recently, in the summer of 1970, corn fields in the middle and south central parts of the United States were devastated by a strain of *Helminthosporium maydis*.

Climate change will also affect the ability of many crop wild relatives, which are potential gene donors for crop improvement programmes, to survive in their current locations. Species without alternative habitats will be vulnerable to extinction (Jarvis, Lane and Hijmans, 2008). Thomas *et al.* (2004) have predicted that by 2050, 15 to 37 percent of wild plant biodiversity, including the wild relatives of many crop species, will be threatened with extinction due to climate change. Of the 50 000 to 60 000 known species of crop wild relatives, it has been estimated that between 16 and 22 percent of these may be in danger of extinction by 2055 (Jarvis, Lane and Hijmans, 2008).

## **B8 - 3.2 Characterization, evaluation, inventory and monitoring of plant genetic resources**

Characterization is the description of plant germplasm<sup>xii</sup>. It defines the expression of highly heritable characters including morphological, physiological or biochemical features, and entails the description of a minimum set of standard phenotypic, physiological and seed qualitative traits (FAO, 2014d). Some of the activities involved in characterization include true-to-type identification, gene flow studies and reference profiling. These activities can also assist in the detection of duplicates stored in genebanks (FAO, 2014d).

Evaluation is the study of environmental response traits and their function in diverse ecosystems. The evaluation of plant genetic resources, which is used to assess the agronomic performance of a crop, requires an analysis of agronomic data obtained through appropriately designed experimental trials.

Characterizing and evaluating the variation of plants along environmental gradients is crucial for estimating their vulnerability to climate change. Having access to this information facilitates effective planning of how these resources could best be used and developed to harness production systems to climate change.

Both characterization and evaluation are carried out using crop descriptor lists, such as those developed by [FAO/Bioversity International](#), by [International Union for the Protection of New Varieties of Plants](#) and by [United States Department of Agriculture's National Plant Germplasm System](#).

Documentation plays an important role in the management of germplasm. The success or failure of a programme for the conservation and sustainable use of plant genetic resources depend to a large extent on the amount and quality of information that is available about these resources and the environments to which they are adapted, as well as on the effectiveness of the systems used to manage this information. This information is critical for making decisions about how to harness genetic resources to address the impacts of climate change.

*In situ* national inventories of crop wild relatives and wild food plants, and knowledge and information systems

based on their genetic and eco-geographical analyses, can provide a solid foundation for establishing conservation priorities and monitoring the *in situ* diversity of these vulnerable plant groups (FAO, in press).

In *ex situ* collections, passport data<sup>xiii</sup> represent the first basic information that helps document and characterize the plant diversity conserved. FAO and Bioversity International have recently published a revised set of passport descriptors widely used for documenting and exchanging germplasm (Alercia, Diulgheroff and Mackay, 2015). Descriptors associated with the location and date of collection are of particular relevance for crop wild relatives, wild food plants and, to a certain extent, landraces. Accurate data on these descriptors allow for the association of a conserved accession<sup>xiv</sup> with its eco-geographical data of the area and habitat in which the population has evolved. A number of tools are freely available for eco-geographical analysis including [CAPFITOGEN](#) and [DIVA-GIS](#).

Characterization and evaluation data are very important for the targeted use of germplasm. Information about germplasm allows for greater precision in the identification of sources of heritable traits for use in breeding programmes. Germplasm management systems, such as [GRIN-Global](#), are increasingly being used for documenting not only passport but also characterization and evaluation data in genebanks. A number of national, regional and global specialized web portals currently publish information on *ex situ* collections, among these the [United States Department of Agriculture Germplasm Resources Information Network \(GRIN\)](#), [EURISCO](#), [SESTO \(NordGen\)](#) and [GENESYS](#). [USDA-GRIN](#) and [GENESYS](#) provides access to passport data as well as characterization and evaluation data.

The [World Information and Early-Warning System on Plant Genetic Resources for Food and Agriculture \(WIEWS\)](#) is the information system used by FAO for the preparation of periodic, country-driven global assessments of the status of conservation and use of plant genetic resources for food and agriculture. WIEWS also monitors indicators on the implementation of the [Second Global Plan of Action for Plant Genetic Resources for Food and Agriculture](#) (FAO, 2011a) and contributes to the elaboration of the plant component of [Sustainable Development Goal indicator 2.5.1](#).

### **B8 - 3.3 Sustainable use and development of plant genetic resources for climate change adaptation**

The sustainable use of plant genetic resources encompasses trait evaluation; pre-breeding; plant breeding, including genetic enhancement and base-broadening<sup>xv</sup>; diversification of crop production; development and commercialization of varieties; support to seed production and distribution; and development of new markets for local varieties and products. These activities can contribute to addressing the impacts of climate change on sustainable crop production.

Farmer varieties and landraces are generally well adapted to current conditions in their local production environments and have been a successful source for adaptive genes in crop improvement (Mba, Guimaraes and Ghosh, 2012; Lopes *et al.*, 2015). However, changing climatic conditions will mean that they may lose this adaptation (Bellon, Hodson and Hellin, 2011). The introduction of varieties of more suitable crops from elsewhere may not always be a practical solution (Bellon and van Etten, 2014). The breeding of new varieties may be the only viable option.

An unintended consequence of the successes of genetic improvement is the increasingly narrow genetic base of cultivars, especially for the major crops (Tester and Langridge, 2010; Martynov and Dobrotvorskaya, 2006; Mba, 2013; Mba, Guimaraes and Ghosh, 2012; Nass and Paterniani, 2000). The increased homogeneity and uniformity (i.e. genetic vulnerability) render crops potentially more susceptible to the impact of climate change (see [module B1 - 1.1](#) on the impacts of climate change on crop production). This genetic vulnerability may be reduced by incorporating into cultivars the novel traits (e.g. resistance to biotic and abiotic stresses) that are often found in crop wild relatives (Lane and Jarvis, 2007; Dwivedi *et al.*, 2008; Maxted *et al.*, 2008), and landraces and farmer

varieties. Pre-breeding (i.e. the generation of intermediate materials that are used as parents in plant breeding) is a means to introgress novel alleles from non-adapted materials into crop varieties (Nass and Paterniani, 2000). The FAO e-learning course on pre-breeding (FAO, 2011b) is a useful capacity-building tool for this new crop improvement discipline.

Some examples of the successful introduction of novel stress-tolerant traits into cultivars from crop wild relatives are presented in Table B8.1.

**Table B8.1.**

Examples of traits obtained from crop wild relatives and the cultivated species to which they contributed resilience (Brozynska, Furtado and Henry, 2015; Maxted and Kell, 2008)

TRAIT	WILD RELATIVE	CULTIVATED SPECIES
Water stress tolerance	Slender wild oats ( <i>Avena barbata</i> )	Oat ( <i>Avena sativa</i> )
Leaf tolerance to cold stress	Wild grapevine species ( <i>Vitis amurensis</i> )	Grape ( <i>Vitis vivifera</i> )
Adaptation to high salinity and tolerance to submergence in saline water	Wild relative of rice ( <i>Oryza coarctata</i> )	Rice ( <i>Oryza sativa</i> )
Stress tolerance, nutritional and grain quality improvement	Wild rice ( <i>Oryza glaberrima</i> )	Rice ( <i>Oryza sativa</i> )
Early leaf spot resistance	Wild peanuts ( <i>Arachis appressipila</i> , <i>A. paraguariensis</i> )	Peanut ( <i>Arachis hypogaea</i> )
Resistance to nematods, Rust, early and late leaf spot	Wild peanuts ( <i>Arachis cardenasii</i> )	Peanut ( <i>Arachis hypogaea</i> )
Grain size		
Drought resistance	Wild plantain ( <i>Musa balbisiana</i> , <i>M. nagensium</i> )	Banana and plantain ( <i>Musa acuminata</i> , <i>M. balbisiana</i> )
Adaptation to high altitudes and cool temperatures	Wild cassava ( <i>Manihot rubricaulis</i> )	Cassava ( <i>Manihot esculenta</i> )

It is possible to use predictive characterization tools based on eco-geographic and climate data to determine remotely the diversity and geographical locations of crop wild relatives and landraces (Glaszmann *et al.*, 2010; Redden, 2013). This approach is known as the Focused Identification of Germplasm Strategy. A useful tool for carrying out this strategy is the technical guideline developed by Bioversity International (Thormann *et al.*, 2016).

Increasing the yields of major food crops – or even maintaining them – in the face of climate change will depend to a large extent on the ability of plant breeders and geneticists to introduce adaptive traits found in plant genetic resources to breed locally adapted varieties (Jarvis *et al.*, 2008). The active participation of farmers in crop varietal development significantly increases the adoption rates of new varieties (Sperling *et al.*, 2001; Ashby, 2009; Efishue *et al.*, 2008; Witcombe *et al.*, 1996; TAC Secretariat, 2001).

The development of crop varieties that tolerate the stressors brought about by climate change (Foresight, 2011; World Economic Forum, 2010) requires the use of a range of methodologies, such as induced mutations (Maluszynski *et al.*, 2000; Ahloowahlia, Maluszynski and Nichterlein, 2004; Shu, 2009; [Joint FAO/IAEA Mutant Varieties and Genetic Stocks Database](#)); biotechnological applications, including cell and tissue biology, marker-assisted selection and genetic engineering; and novel plant breeding techniques, including genome editing procedures. The development of Scuba Rice, a flood-tolerant variety of rice, and its wide dissemination in flood-prone areas, such as those found in Bangladesh, India and the Philippines is an example of the successful breeding of a crop variety that supports climate-smart agriculture (Singh *et al.*, 2010). The adoption of climate-ready

varieties in locations where extreme events, such as flooding, are expected to increase as a result of climate change, can be a key component of climate-smart agriculture strategies.

Many edible plant species are neglected and underutilized but are resilient and adapted to marginal areas (Ebert, 2014; Kahane *et al.*, 2013; Padulosi, Bergamini and Lawrence, eds., 2011; FAO, 2010). Examples include Bambara groundnut (*Vigna subterranea*), the jicama or yam bean (*Pachyrhizus erosus*) and Moringa (*Moringa oleifera*). In drought-prone regions, replacing staples, such as maize, with drought-resistant crops, such as cassava and millets, would make agronomic sense. However, this shift in production would become a viable climate-smart agricultural adaptation strategy only if farmers are willing to adopt these new crops (Burns *et al.*, 2010; Rezaei *et al.*, 2015).

Farmers can only benefit from suitably adapted crop varieties if they can access the seeds and planting materials in a timely manner, in the right quantity and quality, and at an acceptable cost. For these diverse crops and crop varieties to contribute to climate change adaptation and sustain rural livelihoods, it is important to put in place effective seed delivery systems that cater to these new crops and can reach the remotest regions (Rubyogo *et al.*, 2010; McGuire and Sperling, 2013; Sperling, Boettiger and Barker, 2014; Westengen and Brysting, 2014). Seed delivery systems involve variety release procedures, seed production, quality control, and marketing (Tripp, 2001; Louwaars and de Boef, 2012). As discussed in [chapter B1 - 2](#), these systems are usually subject to national and international policies and regulations (FAO, 2015c), and involve diverse actors, such as government authorities, private firms, community-level cooperatives, input dealers, and contracted out-growers.

### **B8 - 3.4 Sustainable use and development of plant genetic resources for climate change mitigation**

Overall, plant genetic resources contribute more significantly to climate adaptation than to climate change mitigation. A number of strategies, however, can improve the sequestration of greenhouse gases and contribute to mitigating climate change. One approach is to maintain or increase carbon content in plants, through the increased cultivation of crops that produce a four-carbon compound during photosynthesis (known as C4 plants), such as maize, sorghum, sugarcane and millets (Lara and Andreo, 2011). Studies have shown that increased carbon sequestration capacity, which is realized through improved photosynthesis, is a heritable trait that can be enhanced through conventional breeding (El-Sharkawy, 2016). Breeding activities in this area have led to varieties that are more productive and sequester more carbon.

There is also significant diversity in the nitrogen-fixing capacity of legume crops, including pulses, such as garden pea, lentil, groundnut, mung bean, cowpea, pigeon pea and chickpea (Abi-Ghanem *et al.*, 2013; Cernay, Pelzer and Makowski, 2016; Cook, 2014; Gresshoff *et al.*, 2015). The cultivation of pulses and other legumes would provide additional support climate change mitigation, as increased nitrogen fixation is also correlated with increased carbon sequestration (see Box B1.7) (Jensen *et al.*, 2012; Mapope *et al.*, 2016).

### **B8 - 3.5 Conservation of plant genetic resources**

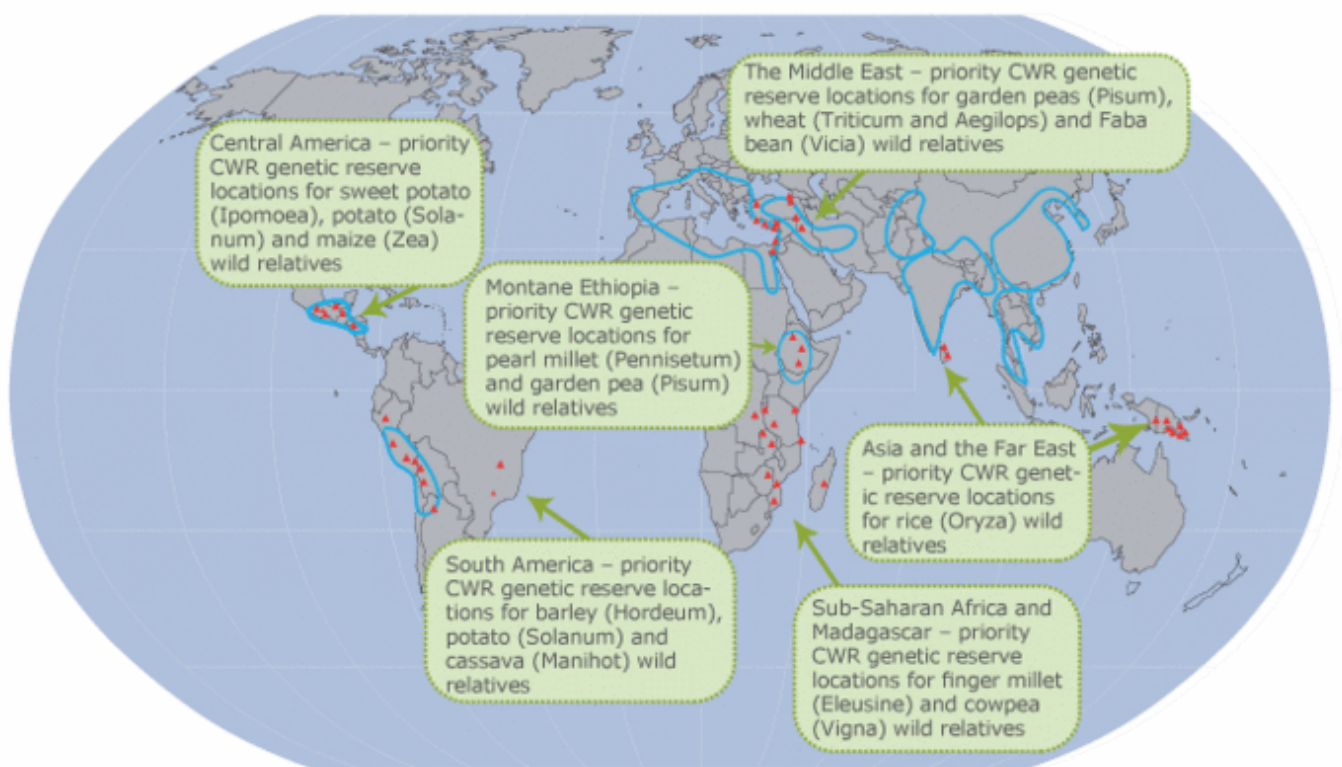
The conservation of plant genetic resources serves to maintain genetic diversity among and within plant species. Conservation strategies include safeguarding these resources in their natural habitats (*in situ* conservation), especially for crop wild relatives; managing these resources on farms (i.e. cultivating a diversity of crops and their varieties, especially farmer varieties and landraces); and storing accessions or samples in genebanks (*ex situ* conservation). Genetic studies provide tools for population monitoring and assessment that can be utilized for conservation planning (Govindaraj, Vetriventhan and Srinivasan, 2015). An efficient collaboration between genebank curators, breeders, and national programmes can help ensure the sustainable conservation of these resources.

*In situ* conservation<sup>xvi</sup> involves locating, describing the conservation status, and actively managing and monitoring targeted wild plant populations in their natural habitats. Many crop wild relatives are at risk of extinction from habitat loss, habitat fragmentation, changes in land use and land management practices, and introgression back from agricultural relatives. Climate change has become another threat to their survival. Species in some habitats, such as those found in montane environments and island or coastal areas, are especially vulnerable, as they tend to be highly specialized and/or isolated. These populations are likely to be the first casualties of climate change.

Much of existing plant diversity, particularly of crop wild relatives and underutilized species, still needs to be secured. These species are fast disappearing due to the standardization of agricultural practices and changes in food habits (Rojas *et al.*, 2009; FAO, 2010). There has been an overall increase in the awareness for conservation. However, significant issues still need to be resolved with regard to surveying, carrying out inventories and conserving plant genetic resources both *in situ* and on farms. Crop wild relatives remain a relatively low priority in germplasm collection, and significant gaps remain in their collection and conservation (Figure B8.1; Maxted and Kell, 2009).

**Figure B8.1.**

Global priority areas for conservation of crop wild relatives (CWR) of 12 food crops.



Source: Maxted and Kell (2009)

The on-farm conservation and management of landraces and farmers' varieties contribute to the continued evolution and adaptation of diversity. Activities in this area lead to the development of variants that are better suited to specific environments and are essential for future crop improvements. Farmers and indigenous and local communities play a critical role in the conservation and management of plant genetic diversity *in situ* and on farms.

*Ex situ* conservation<sup>xvii</sup> of plant genetic resources in genebanks safeguards a large and important amount of resources that are vital to global food security. Germplasm of crops and crop wild relatives is conserved in more



than 600 genebanks worldwide and adds up to a total of about 4.7 million accessions maintained under medium- and long-term conditions globally (United Nations, 2017). Much of this plant diversity is important for breeding crop varieties that are adapted to climate change. The 11 genebanks of the Consultative Group for International Agricultural Research and the World Vegetable Centre maintain over 770 000 accessions comprising over 650 different genera. Since 1996, almost 2 million accessions have been added to *ex situ* genebanks with medium- and long-term collections, though gaps still exist (WIEWS, 2017).

Securing adequate storage conditions for the genetic materials already collected and providing for their regeneration and safety duplication are essential. Yet many of these collections are still vulnerable, exposed to natural disasters, including those caused by climate change, and man-made calamities such as civil unrest. Plant genetic resources are similarly vulnerable due to avoidable adversities resulting from lack of funding and/or poor management. To address these on-going issues, the [Svalbard Seed Vault](#) was created to provide backup (black box) storage for the global collections. The Seed Vault has the capacity to store 4.5 million varieties of crops, providing safeguarding for some 2.5 billion seeds. Currently, the Vault holds more than 930,000 samples, originating from almost every country in the world.

## Climate-smart management of animal genetic resources

This module uses the definition of animal genetic resources that was used in the Second Report on the State of the World's Animal Genetic Resources for Food and Agriculture:

*“animal genetic resources are here taken to include those animal species that are used, or may be used, for food production and agriculture, and the populations within each. Distinct populations within species are usually referred to as breeds.”* (FAO, 2015d, p.3)

Food production from livestock is heavily concentrated in a small group of species. While more than 30 mammalian and bird species have been domesticated, three species (cattle, chickens and pigs) account for about 88 percent of the world's annual meat production from livestock; two species (cattle and buffaloes) for about 96 percent of milk production; and just one species (chickens) for about 92 percent of egg production (FAO, 2017a). Animal genetic resources include more than 8 800 livestock breeds. In the Executive Brief for the Global Strategy for the Management of Farm Animal Genetic Resources, a breed is defined as:

*“either a subspecific group of domestic livestock with definable and identifiable external characteristics that enable it to be separated by visual appraisal from other similarly defined groups within the same species or a group for which geographical and/or cultural separation from phenotypically similar groups has led to acceptance of its separate identity”* (FAO, 1999, p.5).

Single breeds, such as the Holstein dairy cattle and the commercial Leghorn chicken reported in 132 and 52 countries, respectively, account for a large proportion of the production of particular commodities, particularly in highly commercialized production systems.

### B8 - 4.1 Impact of climate change on animal genetic resources

For breeds that are raised in extensive conditions, climate is a key element of the production environment. If climatic conditions change rapidly, the adaptive link between a livestock population and its local production

environment may be broken. This rupture, which will contribute to a loss of adaptedness, productivity and fitness in local breeds, may cause livestock keepers to change their breed or species, migrate to other areas, or cease livestock production entirely (Box B8.2). In Mauritania for instance, a change in species can be observed between 1994 and 2014, the number of cattle has decreased from 2.3 to 1.9 million heads, while the number of camels has increased from 0.6 to 1.5 million heads (FAOSTAT, 2016), presumably due in part to changes in climate.

### **Box B8.2 The potential impact of climate change on breed distribution**

As climate change is expected to threaten the adaptedness of some animal breeds to their environment, FAO has developed a tool, the [breed distribution model](#), to predict the potential impacts of climate change on different breeds. The current geographic distributions, which are available at the national level and in some cases at a subnational level, of about 8 800 livestock breeds, as recorded in the Domestic Animal Diversity Information System ([DAD-IS](#)), have been used to model suitable areas for breeds under current and expected future conditions. The tool takes several temperature and humidity parameters into account: maximum temperature of warmest month, minimum temperature of coldest month, annual precipitation, precipitation seasonality measured as coefficient of variation, mean temperature of wettest month and driest month. It then incorporates this data into different models and scenarios. Analyses of this kind can contribute to more informed decision-making on breed management under changing climatic conditions and strengthen the capacity of national governments, livestock keepers and farmers to protect and enhance food security and manage their animal genetic resources sustainably. The model is most useful for local breeds that at present are found in only one country and that are known to be mainly kept under relatively extensive conditions. The potential distribution of transboundary breeds kept under intensive production systems is not expected to be as directly influenced by climate change.

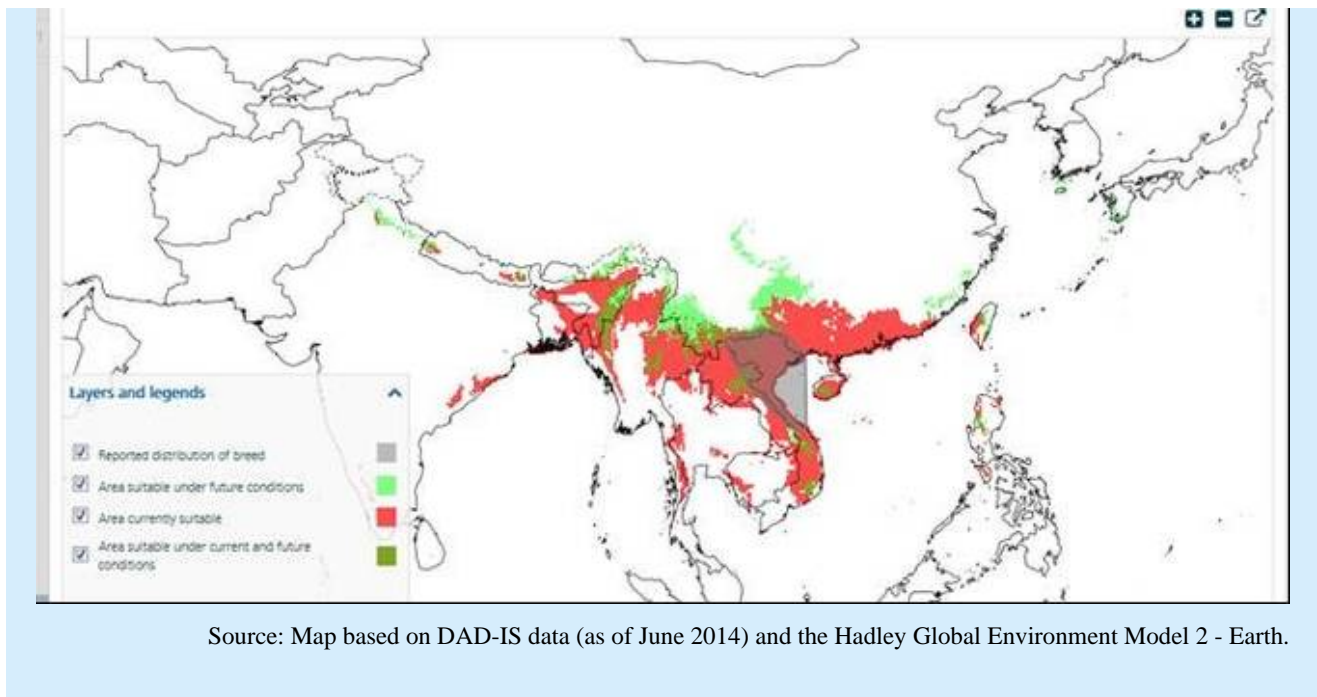
#### **Figure B8.2 The Mong Cai Pig (Viet Nam)**



Photo credit: Kerstin Schöll.

For example, as illustrated in Figure B8.3 climate change will shift the suitable area for Vietnamese Mong Cai pigs (see Figure B8.2). Areas where these animals are reported to live now may not be suitable from them in the future. The map shows modelled areas of projected habitat loss (red), areas of no expected change (dark green) and areas of habitat gain (light green).

#### **Figure B8.3 Influence of climate change on the habitat suitable for the Vietnamese Mong Cai pig**



Heat stress affects animals in a number of ways. It increases their water requirements, reduces their feed intake and physical activity, and increases their expenditure of metabolic energy to regulate body temperature. All of the effects of heat stress lead to declines in production and fertility, and increases in mortality. In the tropics and subtropics, in particular, rising temperatures will create significant problems for livestock production. Death of animals during extreme heat waves is already a serious risk in feedlots (Hatfield *et al.*, 2008) and confined production environments in countries, such as the United States of America.

In general, high-output breeds from temperate regions are not well adapted to the effects of high temperatures, high humidity and poor feeding. Increased temperatures associated with climate change are likely to exacerbate the problem of heat stress in these animals unless their management is modified to protect them. Under favourable circumstances, this is technically feasible, for example, by adjusting the animals' diets to easily digestible feed that generates less heat, and introducing cooling technologies, such as ventilation fans, water sprays or misters. However, for many producers, the costs of these measures may be prohibitive.

Extreme climatic events, such as droughts, floods and hurricanes, have the potential to kill large numbers of animals. If a breed population is concentrated within a limited geographical area, it may be devastated, or even completely wiped out, by a climatic disaster. Climate change is predicted to increase the frequency and severity of climatic disasters, heightening the risk to vulnerable breed populations.

As discussed in [chapter B2 - 2.2](#), the spread of pathogens or even small spatial or seasonal changes in disease distribution may expose livestock populations that lack resistance or acquired immunity to new animal diseases. A major outbreak of a serious animal disease can pose a catastrophic threat to the livelihoods of livestock producers, particularly if large numbers of animals have to be slaughtered to prevent the further spread of the disease. The extent to which climate change will increase the threat that epidemics pose to livestock diversity is uncertain. However, it is likely that the distribution of diseases spread by vectors, such as insects and ticks, will be influenced by climate. Some worrying recent developments, such as the spread of bluetongue virus in Europe, may be linked to climate change.

Outcomes in terms of disease epidemiology are difficult to predict because of the complexities of interactions between pathogens, vectors and host animals, and other components within an ecosystem, and the influence of a broad range of external factors and management measures. The expected increase in outbreaks of livestock

diseases, some of them novel, will favour genotypes that are resistant or tolerant to the diseases in question (Hoffmann, 2010a).

Livestock are major consumers of crops. Any negative impacts of climate change on plant genetic resources used for feed, such as reduced availability, altered nutritional content and increased costs, will also affect livestock production (see [chapter B8 - 3](#)). Climatic conditions will also have an impact on the growth of pastures, which can be expected to influence the productivity of grazing livestock and contribute to changes in the geographical areas to which specific breeds of livestock are adapted.

## **B8 - 4.2 Characterization, evaluation, inventory and monitoring of animal genetic resources**

Substantial additional efforts are required to characterize the phenotypic characteristics of livestock breeds, especially in relation to survival, fecundity and performance in specific production environments and their degree of adaptedness to specific diseases and tolerance or resistance to particular diseases (FAO, 2015d). The Domestic Animal Diversity Information System ([DAD-IS](#)), which contributes to monitoring livestock breeds nationally and globally, includes a database of information on national breed populations from all around the world (FAO, 2015d). Genetic characterization, using DNA information to discern the relationships among adaptive phenotypes and diversity at the molecular level, may also help improve the management of animal genetic resources with respect to climate change.

Characterization of animal genetic resources has been carried out for many years, both on the phenotypic and genetic levels. Initial studies concentrated on phenotypes related to appearance, morphology and production, and simple genotypes involving a small number of markers sufficient to characterize basic aspects of genetic diversity (for a review, see Groeneveld *et al.*, 2010). However, recent advances in molecular biotechnologies that have allowed for the genotyping of individual animals have created greater opportunities to study functional characteristics of animal populations. Concurrent developments in geographic information systems have permitted the assignment of biological samples (and thus animals and populations) to geographic positions, facilitating the association of breeds and their genotypes with environmental and climatic variables. The application of these technologies has already yielded insights into the genetic basis for adaptations of specific breeds to their environments (e.g. Benjelloun *et al.*, 2015; Gorkhali *et al.*, 2016). The newest genomic technologies also provide results that are more robust and consistent across laboratories, allowing for a meta-analysis of studies undertaken in different geographic regions, and enhancing the understanding of adaptation to climatic conditions in common across continents. For example, the international [ADAPTmap project](#) (Stella, 2014) has gathered genomic and geographical data from studies for 144 breeds of goats from 37 countries and six continents and combined them with regular agricultural activities to create a unique resource for studying livestock adaptation.

## **B8 - 4.3 Sustainable use and development of animal genetic resources for climate change adaptation**

Many livestock-keeping communities have considerable experience in managing their livestock in harsh and fluctuating environments. They may do this, for example, by raising several types of species or breeds and/or migrating with their animals to areas with the most favourable conditions (see [chapter B2 - 3.2](#) on risk management and system changes for climate-smart livestock production). Nonetheless, rapid and substantial changes to local climates may outstrip the capacity of animal populations to adapt through natural or human selection. Also, livestock keepers may not be able to adapt their husbandry practices or find a suitable production environment quickly enough to keep pace with these changes. This situation may create the need to find replacements for current livestock breeds and or species. Substitutions of this kind present a significant challenge. Great care must be taken to ensure that introduced species and breeds are well adapted to local conditions and that the original species and breeds do not become extinct.

In different animal breeds, there are many populations, particularly in mountainous and arid areas, that are good walkers and well adapted to extreme ranges in temperature. These breeds, which can deal with coarse vegetation, have low water requirements and can survive on poor quality fodder, may merit further research. The genetic strategy for adaptation includes the development of breed improvement programmes, which involves potentially crossbreeding different breeds, and the substitution of different breed or species for less well-adapted animals. Among the key influential factors for the success of adaptation strategies are the expected rate of climate change and the speed with which genetic change can realistically occur. Substitution and cross-breeding can expedite genetic change, but their implementation may be more complex than pure-breeding and require additional research (e.g. on genotype and environment interaction) (Boettcher *et al.*, 2014). Genomic selection has the potential to accelerate both pure- and cross-breeding programmes for adaptation, if phenotypic data based on performance recording are available. In the longer term, highly advanced technologies, such as genome editing and cloning, may complement traditional methods of breeding to enhance the development of adapted livestock populations.

Local livestock breeds and populations may possess specific phenotypes related to adaptedness that could be used to cope with environment change. Between 2000 and 2015, the inheritance mode of a growing number of those traits was identified, as illustrated in Table B8.2.

**Table B8.2. Examples of specific phenotypes related to adaptedness in livestock**

Trait	Category	Expression/Inheritance	Population scale
Salt tolerance	Physiology	Threshold/complex (some genes identified)	Species (bactrian camel)
Altitude adaptation	Physiology	Threshold/complex (some genes identified)	Breeds (Tibetan pig and goat breeds, Ethiopian cattle breeds)
Resistance to gastro intestinal parasites	Physiology	Threshold/complex (some Quantitative Trait Loci identified)	Breeds (Red Massai sheep)
Heat resistance/Slick hair coat	Morphology	Qualitative/monogenic (slick locus <sup>xviii</sup> )	Breeds (Senepol and some criollo cattle breeds)

(adapted from Leroy *et al.*, 2015)

## **B8 - 4.4 Sustainable use and development of animal genetic resources for climate change mitigation**

Globally, cattle are the major source for enteric methane emissions (Smith *et al.*, 2014). Dietary manipulation and improved feeding systems can reduce methane emissions and nitrogenous emissions and contribute to climate change mitigation. A better understanding of the micro-organisms involved in the digestive processes in the rumen will provide a basis for interventions that improve the efficiency of digestion and reduce the amount of pollutants produced by ruminant livestock (McSweeney and Mackie, 2012).

In addition to selecting traits for increased production, any selection that reduces mortality and increases early maturity, fertility and longevity tends to contribute to increasing the animal's input conversion efficiency (i.e. less greenhouse gases are emitted per unit of food production) (Hoffmann, 2010b). Since the 1940s, improved nutrition, breeding for high performance and improved feed-conversion ratio, and better hygienic management to decrease illness and mortality, have significantly reduced the amount of feed (and land needed to produce this feed) per unit of product. This reduction was greater in monogastrics and dairy cattle than in beef cattle or sheep. Based on data from the United States of America, the carbon footprint for producing a given quantity of milk decreased by 63 percent between 1944 and 2007 owing to improvements in genetics and animal husbandry (Capper *et al.*, 2009). See [module B2](#) for a comprehensive overview of the mitigation possibilities in the livestock sector.

Given the impact of livestock on climate, the inclusion of environmental impacts in breeding goals could be considered. However, trade-offs between the breeding goals and the traits selected need to be taken into account. Negative correlations exist between several traits, for example, production, environmental load, robustness. Generally, the more productive breeds show better input conversion efficiency, but these animals require more inputs in absolute terms and often show limited robustness. Reduced robustness may require management actions to avoid losses tied to poor survival and fertility. Highly productive breeds also tend to yield only a single product, such as meat, milk or eggs, whereas local breeds often provide multiple products and a range of other benefits, including landscape maintenance, wealth protection and cultural preservation. The definition of 'more productive' must be sufficiently inclusive, and take into account not only the value of provisioning services, such as food and fibre, but also the value of other ecosystem services (see [module B7](#) for climate change impacts on soil and land resources, and [chapter B2 - 4.1](#) for the management practices for grazing and pasture management). Moreover, any kind of genetic selection, be it within or across breeds, decreases genetic diversity. The improvements in mitigation described by Capper, Cady and Bauman (2009) were accompanied by a similarly large decrease in the range of breeds commonly used for dairy production, with the Holstein cow being more favoured. There were also large decreases of variation within breeds. This loss of diversity comes with a corresponding loss of adaptive capacity, as discussed in [chapter B8 - 2](#).

When considering greenhouse gas emissions from enteric fermentation, attention should be paid not only of differences within and across breeds in the gross efficiency of converting feed inputs to produce animal-based foods for humans, but also of differences among species in their ability to use forage plants that cannot otherwise be used by humans.

## **B8 - 4.5 Conservation of animal genetic resources**

For animal genetic resources, the combination of both *in situ* and *ex situ* conservation measures is viewed as the optimal way to protect endangered breeds from extinction and ensuring they continue to deliver ecosystem services. This involves a wide range of measures, including incentives to maintain breeds at risk, conservation breeding, awareness raising activities, the promotion of agrotourism and niche marketing of livestock products. The cryoconservation of semen or embryos, which is described in the Global Plan of Action for Animal Genetic Resources (FAO, 2007), is another possible conservation pathway. Recent assessments (FAO, 2015d) have underlined the fact that there are still major gaps in the breeds that are covered by conservation programmes, especially in developing regions, and particularly for *ex situ in vitro* conservation programmes.

Climate change, which is expected to test the resilience of livestock systems, may constitute a major threat to the most vulnerable breeds and require the strengthening of conservation measures. Cryopreservation of semen and embryos from vulnerable breeds would allow for the reconstitution of breeds that may suffer severe declines in numbers from catastrophic events. It would also increase the availability of germplasm that could be used to facilitate the introduction of traits associated with improved adaptation to new environmental conditions. However, to realize these potential benefits would require the storage of sufficient amounts of material, the adequate characterization of phenotypes relative to environmental features, and significant improvements in breed coverage for *ex situ* conservation. In addition to the usual goals of maintaining or increasing population sizes, controlling inbreeding and improving profitability, *in situ* conservation programmes would have to consider climate change adaptation among their objectives.

## **Climate-smart management of forest genetic resources**

Forest genetic resources refers to the heritable materials maintained within and among tree and other woody plant species that are of actual or potential economic, environmental, scientific or societal value (FAO, 2014b). As

mentioned in the Millenium Ecosystem Assessment (MEA), forests are home to the vast majority of the Earth's terrestrial biodiversity (MEA, 2005), and trees are the keystone species of forest ecosystems. Forest trees differ from other plant species in their capacity to maintain high levels of genetic diversity within populations rather than among populations (Hamrick, 2004). This results from their outcrossed mating system, extensive gene flow and large population sizes (Petit and Hampe, 2006). Forest trees and other woody plant species provide wood, fibre, fuel and many non-wood forest products. They also contribute to a broad range of ecosystem services and fulfil environmental functions. According to Botanic Gardens Conservation International (BGCI), there are approximately 60 000 tree species (BGCI, 2017), but only very few have been studied in any depth for their present and future potential. Globally, around 2 400 species of trees, shrubs, palms and bamboo are actively managed for products and/or services, and approximately 700 tree species are subject to tree improvement programmes (FAO, 2014b).

## **B8 - 5.1 Impact of climate change on forest genetic resources**

Tree populations can respond to climate change in three different ways: exhibiting phenotypic plasticity<sup>xix</sup>; adapting to new climatic conditions; or migrating to new areas with more suitable climates (e.g. Aitken *et al.*, 2008). Most tree species have a high degree of phenotypic plasticity (e.g. Rehfeldt *et al.*, 2002). This means that tree populations can grow well under a range of climatic conditions around their climatic optimum. When tree populations adapt to local conditions, they generally maintain high genetic variation in their adaptive traits (Savolainen, Pyhäjä and Knurr, 2007). For this reason, some scientists (e.g. Hamrick, 2004) consider that many tree populations have sufficient phenotypic plasticity and genetic diversity to enable them to adapt reasonably well to climate change. However, others foresee significant problems (e.g. Mátyás, 2007; Rehfeldt *et al.*, 2002).

The migration rate of forest trees is often over-estimated. This is due to the fact that many species have extensive gene flow, especially through pollen. In wind-pollinated forest trees, gene flow can be 100 kilometres or more. Climate and species distribution models indicate that migration rates should be more than 1 kilometre per year to allow plants to follow the predicted shifts in their current climatic niches (Malcolm *et al.*, 2002). However, it has been estimated that the post-glacial migration rates of temperate forest trees were less than 100 metres per year (McLachlan, Clark and Manos, 2005). Therefore, it is unlikely that forest trees would be able to cope with the current rate of climate change through natural migration. Most scientists agree that measures, such as modified silvicultural practices and assisted migration, are necessary to facilitate the survival, adaptation and migration of forest trees under changing climatic conditions, and that selection and breeding strategies need to be redesigned (Alfaro *et al.*, 2014).

In addition to affecting physiological and genetic processes in forest tree species, climate change is expected to affect forest genetic resources through its impact on ecological processes. Changes in temperature and precipitation may inhibit the capacity of trees to regenerate and alter the composition of tree species in forests. Climate change may also break the synchronism between the flowering periods of trees and the active periods of pollinator species. A decline in the availability of pollinators limits gene flow and reduces the effective size of tree populations, impeding their capacity to adapt to climate change. Invasions of problematic species may also become more common, with native trees being outcompeted by species that can migrate and reproduce rapidly.

As the climate changes, the distribution range for some tree species are expected to expand, while for others it may shrink. In temperate regions, the ranges of tree species are likely to shift towards the poles and towards higher elevations. The retreat at the receding edge of species' distributions is likely to be more rapid than the advance into new areas. In tropical regions, changes in rainfall regimes may be the most important climatic factor influencing tree distribution. Research has indicated that a dry climate is a particular barrier to migration for tropical tree species (e.g. Muchugi *et al.*, 2006, 2008). As in temperate regions, natural migration rates in the tropics will not be sufficient to keep pace with the predicted rate of climate change.

Some invasive species may be exceptional in this regard, as they may have a greater capacity to respond rapidly to changing conditions, either because their seeds are dispersed over very long distances or because they reach maturity very quickly.

In the future, extreme weather events that kill large numbers of trees may become more common. In some places, pest and disease attacks may become more severe as climatic conditions become more favourable for pests or because climate-induced stress makes trees more susceptible to attack. Climate change is also likely to have a significant effect on the distribution of insect pests of trees.

## **B8 - 5.2 Characterization, evaluation, inventory and monitoring of forest genetic resources**

For forest genetic resources, it is important to characterize genetic diversity both at a broad scale that includes the entire distribution range of a species, and on a finer scale within the species itself. This is needed to increase the understanding of the adaptation of forest trees to different climatic conditions. Characterizing genetic diversity is done for two main purposes: to support conservation planning and forest management; and support tree breeding and improvement. In the first case, the activities may include identifying tree populations with high genetic diversity for *in situ* or *ex situ* conservation, and describing the relationships between genetic variation and environmental variables to define seed zones within which transfer of genetic material is recommended. In the second case, activities include the identification of individual trees with desirable characteristics for breeding and the selection of tree stands for production of forest reproductive material (i.e. seeds, cuttings and other propagating parts of the tree).

In addition to characterizing morphological differences within tree species, provenance and progeny trials have long been used in forestry for analysing genetic variation in quantitative traits related to growth (e.g. diameter increment), physiology (e.g. nutrient or water use efficiency) and phenology (e.g. bud burst). Laboratory-based techniques based on molecular markers have also been applied for studying genetic variation among tree populations. However, as many of these techniques use neutral markers, they mostly reveal historical and demographic processes. New genomics tools offer possibilities to link genetic diversity at the molecular level, or even individual genes, to adaptive traits (Neale and Kremer, 2011). Progress is being made in whole genome sequencing and marker-assisted selection in several tree species. The next challenge is to link the increasing amounts of gene-level data to phenotypic data from tree populations.

Genetic monitoring of tree populations is needed to verify how well genetic diversity is maintained over time, and how this diversity is shaped by forest management practices and climate change. However, considering the number of tree species, it is impossible to implement genetic monitoring in all or even most tree species. A genetic monitoring system should be based on a sample of tree populations, such as permanent forest monitoring plots (Konnert *et al.*, 2011) or conservation units (Aravanopoulos *et al.*, 2015).

## **B8 - 5.3 Sustainable use and development of forest genetic resources for climate change adaptation**

Forest genetic resources are used by people to grow trees for many purposes from obtaining wood and non-wood products to providing a range of other ecosystem services. The utilization of forest genetic resources started millennia ago. However, the use and international transfer of forest genetic resources have been more extensive during the past 200 years (Koskela *et al.*, 2014). The oldest form of research and development is testing of tree species and their provenances for different purposes and under different environmental conditions. The main purpose of provenance research is the identification of well-growing and sufficiently adapted tree populations to be used as seed sources for tree planting (König, 2005). The results of provenance research have also been used for initiating tree breeding programmes (FAO, 2014b) and, since the 1990s, for studying the impacts of climate change



on tree growth.

Tree breeding typically aims at a gradual improvement of breeding populations rather than development of new varieties. It is a slow process, as one cycle of testing and selection may take decades. Traditional tree breeding is based on the phenotypic selection of individual trees in wild populations (referred to as 'plus trees'), testing their progeny and then reselecting the best individuals for the establishment of seed orchards and further breeding. The testing is focused on growth, wood properties, resistance or tolerance to pests and diseases, and other traits of commercial interest. Traits related to climate change adaptation, such as plasticity and drought tolerance, are also increasingly being considered by tree breeding programmes (FAO, 2014b). New breeding approaches, such as molecular marker-assisted selection, have raised hopes for reducing the long breeding cycles. However, the fact that a trait is typically influenced by a large group of genes in forest trees and the variable expression of quantitative trait loci across environments have slowed down progress in applying this new approach to forest trees (Neale and Kremer, 2011).

In response to climate change, many countries have pledged to restore millions of hectares of forests. These forest restoration efforts will further increase the demand for forest reproductive material. Unfortunately, there are not enough seed orchards for many tree species to meet the current demand for reproductive material. Seed collection from wild tree populations (seed stands) remains a common and much needed practice. For trees species in which the germination capacity of seeds starts declining right after their maturation (recalcitrant seed behaviour), naturally regenerated seedlings (wildings) can be collected for tree planting elsewhere. Forest reproductive material is also produced through vegetative propagation, with multiplication from rooted cuttings being the most frequently used method (Wilhelm, 2005). Micropropagation methods, such as microcuttings and somatic embryogenesis, are increasingly being applied in forestry (FAO, 2004).

Key approaches for using forest genetic resources to promote the adaptation of forests to climate change are presented in box B8.3.

### **Box B8.3 Options for using forest genetic resources to promote the adaptation of forests to climate change**

There are three approaches for using forest genetic resources to promote the adaptation of forests to climate change (e.g. Hubert and Cottrell, 2007). Firstly, forest management practices should maintain genetic variation in tree populations and promote natural regeneration, when possible. Secondly, forest managers could adopt a 'portfolio approach' in which a mix of different provenances are planted in a given site alongside the existing tree population. This approach can be considered as an insurance policy against a complete failure of tree planting efforts carried out in response to climate change. Thirdly, migration of tree species and populations could be assisted by planting different provenances and species in new areas where climatic conditions are favourable, or are expected to become favourable, in the near future.

## **B8 - 5.4 Sustainable use and development of forest genetic resources for climate change mitigation**

As discussed in [module B3](#) on climate-smart forestry and in [chapter B5 - 3.1](#) on the contribution of agroforestry to climate change mitigation, conserving and enhancing existing carbon stocks in forests, establishing new forests, integrating forestry into crop and livestock production systems, and planting trees on agricultural lands offer considerable opportunities for mitigating climate change (Alfaro *et al.*, 2014).

Genetically diverse tree populations are crucial for long-term mitigation of climate change and for maintaining the

capacity of forests to adapt to changing climatic conditions (Alfaro *et al.*, 2014). However, the important role of forest genetic resources is often poorly understood by policy makers and forest managers. For example, as mentioned above, as part of global efforts aimed at restoring forests and reducing deforestation and forest degradation, countries around the world have expressed their commitment to massive tree planting efforts targeting millions of hectares. However, many countries still have problems related to the quantity and quality of forest reproductive material (FAO, 2014b). This is often due to lack of well-functioning national tree seed systems capable of supplying adequate amounts of reproductive material for producing seedlings for tree planting efforts. The establishment and maintenance of national tree seed systems have proven challenging for many countries. These systems are still struggling to reach various users of tree germplasm, in particular smallholder producers (Graudal and Lillesø, 2007).

Between 2010-2015, the global area of planted forests increased by 3.2 million hectares per year and reached 7 percent of the world's forest area (FAO, 2016b). Considering the current and planned tree planting efforts to mitigate climate change, as well as a growing demand for forest products and environmental services, the area of planted forests can be expected to continue increasing in coming years or even decades (Box B8.4). Presently, the global supply of reproductive material for boreal and temperate trees, as well as for fast-growing tropical and subtropical trees, seems to meet or exceed demand, while for tropical hardwoods, demand is often higher than supply (Koskela *et al.*, 2014). For agroforestry tree species, a lack of high-quality tree germplasm prevents smallholders from increasing the productivity of their agroforestry systems (e.g. Nyoka *et al.*, 2011). As tropical hardwoods and agroforestry tree species are increasingly favoured in climate change mitigation and forest restoration, research and development efforts should focus on increasing the supply of tested and improved germplasm of these species, and developing novel genomic approaches for identifying and selecting trees with required traits for propagating planting stock and tree breeding. For practical forest management, genetic considerations, such as maintaining genetic diversity and selecting an appropriate provenance for a given site, should be given more attention in both tree planting efforts (e.g. Bozzano *et al.*, 2014) and the management of existing forests (e.g. Ratnam *et al.*, 2014), as this can significantly increase the long-term success and sustainability of these actions.

#### **Box B8.4 Using local woody species for land restoration in Africa**

In Africa's Great Green Wall programme, an initiative to combat the effects of climate change and desertification, community needs and preferences were taken into account to select suitable native species for large-scale natural capital restoration. To increase plant diversity and restore degraded land, 120 dryland village communities in cross-border regions of Burkina Faso, Mali and Niger assisted in the selection of 193 plant species, most of which were mainly used for food, medicine, fodder, and fuel. Of these, 170 were native and considered suitable for enriching and restoring degraded lands. Fifty-five woody and herbaceous species of economic value and well adapted to the environment were given priority. Quality seeds for these species were collected, and nursery seedlings were planted to restore 2 235 hectares of degraded land (Sacande and Berrhamouni, 2016).

### **B8 - 5.5 Conservation of forest genetic resources**

The preferred approach for conserving forest genetic resources is *in situ* conservation because it is a dynamic process that allows for forest genetic diversity to change over time and by location. *Ex situ* conservation, on the other hand, is mostly static, maintaining the genetic diversity of the sampled species in a fixed state. The main goal of *in situ* conservation is maintaining the evolutionary processes (i.e. natural selection, genetic drift, gene flow and mutation) within tree populations, rather than simply preserving their present day genetic diversity (e.g. Lande and Barrowclough, 1987; Eriksson, Namkoong and Roberds, 1993; FAO, FLD and IPGRI, 2004a). Given that present

day conditions will change along with the climate, this dynamic approach is crucial for the long-term conservation of forest genetic resources. It is also often easier and cheaper to conserve tree populations in their natural habitat than under *ex situ* conditions.

*In situ* conservation of forest genetic resources is typically carried out in protected areas or managed natural forests by designating specific conservation stands or units for this purpose (FAO, DFSC and IPGRI, 2001). These units may harbour conservation populations for one or more tree species. Silvicultural treatments are applied, if necessary, to maintain or enhance genetic processes within tree populations. Ideally, the network of these conservation units should cover the whole distribution range of a tree species.

Forest genetic resources are also conserved *ex situ* in seed banks, seed orchards, field collections, provenance trials, planted conservation stands and botanical gardens to complement *in situ* conservation, especially when the population size is critically low in the wild. In forest trees species that have orthodox seeds (i.e. seeds that maintain their viability when dried and stored at low temperature), *ex situ* conservation is relatively easy. However, many tree species produce recalcitrant or intermediate seed, which lack dormancy and are sensitive to both desiccation and low temperatures. This presents a major difficulty for conservation, especially in humid tropics, where more than 70 percent of tree species have recalcitrant or intermediate seed behaviour (Sacande *et al.*, 2004). *Ex situ* conservation of these species is carried out in field collections, *ex situ* conservation stands and breeding populations. More technically sophisticated approaches, such as cryopreservation, seedling conservation, *in vitro* conservation, pollen storage and DNA storage, are also used (FAO, FLD and IPGRI, 2004b).

Climate change is expected to alter or increase biotic threats (e.g. pests, diseases and species competition) and abiotic threats (e.g. fire and land-use changes) to tree populations. The climatic niches of tree species are also predicted to shift as a result of climate change. It is important to assess the vulnerability to climate change of individual genetic conservation units, as well as the networks of these units and their distribution range, and identify high-risk units for further monitoring and complementary or enhanced conservation measures. In Europe, for example, it has been predicted that the genetic conservation units located in lowlands and in the southern edges of distribution ranges of tree species will be the most vulnerable to climate change (Schueler *et al.*, 2014). It is necessary to incorporate climate change considerations into the development and implementation of both *in situ* and *ex situ* conservation strategies (e.g. Kelleher *et al.*, 2015).

## **Climate-smart management of aquatic genetic resources**

Aquatic genetic resources are the genetic material (populations, individuals, gametes, DNA and alleles) of all aquatic plants and fish that provide food and related goods and services to humans, or that have potential to do so (Pullin and White, 2011). The world's aquatic ecosystems contain over 150 000 species of fish, molluscs, crustaceans and aquatic plants (Bartley and Halwart, 2017). The world's fisheries harvest over 2 000 species including fish, crustaceans, molluscs, coelenterates (e.g. jellyfish), echinoderms (e.g. sea urchins and sea cucumbers) and aquatic plants (FAO, 2014c). The number of farmed aquatic species is smaller, but still extremely high. FAO aquaculture production statistics have registered close to 600 species of fish and aquatic invertebrates and plants farmed around the world. However, only ten species (shellfish, crustaceans, plants and fin fish) account for half of the total aquaculture production (FAO, 2013a). Unlike terrestrial agriculture in which farmers have been using thousands of breeds and varieties for thousands of years, the domestication of aquatic species in aquaculture became more widely practiced only during the twentieth century (Nash, 2011). An exception is the common carp, which was domesticated centuries ago (Balon, 1995). Nonetheless, aquaculture is the fastest growing food production sector (8 percent average growth per year between 2006-2016) and is expected to play a major role in providing aquatic food in the future, as production from capture fisheries has plateaued (FAO, 2014c). As of 2014, about 50 percent of the aquatic food consumed comes from aquaculture (FAO, 2016c).

## **B8 - 6.1 Impact of climate change on aquatic genetic resources**

Climate affects many aspects of aquatic environments, including water temperature; oxygenation; the acidity, salinity and turbidity of seas, lakes and rivers; the depth and flow of inland waters; the circulation of ocean currents; and the prevalence of aquatic diseases, parasites and toxic algal blooms. The impacts of climate change on fisheries and aquaculture are addressed in detail in [chapter B4 -3.1](#). This chapter addresses the specific impacts of climate change on aquatic genetic resources.

Acidification of seawater, caused by increasing levels of carbon dioxide in the atmosphere (Nellemann, Hain and Alder, 2008) may compromise the role calcifying organisms play in sequestering carbon, especially in shore areas. This will slow the growth rate of many aquatic species of molluscs and certain crustaceans, including zooplankton, and will have implications for the whole structure and functions of aquatic ecosystems. Over the long term, climate change is also expected to change some ocean currents, affecting the migration routes of some aquatic species and the dispersal of eggs and larvae (FAO, 2015b).

Rising temperatures affect the distribution and abundance of marine organisms. Some warm-water aquatic species are shifting towards the poles, and driving some native cold-water species towards extinction. In most environments, higher temperatures promote an increase in the productivity and growth rates of aquatic organisms. However, higher temperatures may also disrupt the timing of reproduction, negatively affect life cycles, limit the availability of food supplies or increase the prevalence of diseases, parasites and predators. Many aquatic organisms depend on having stable biological communities around them (FAO, 2015b). They are therefore vulnerable not only to direct effects on their own physiology, but also to disruptions that may occur because of the impacts climate change has on other organisms (Guinotte and Fabry, 2008). Some aquatic communities are reliant on particular species, such as corals, kelp, mangroves and sea grass. If these species are unable to adapt, whole communities will be disrupted and may disappear completely. Extreme weather events may lead to escapes from fish farms, with adverse effects on the genetic diversity of wild populations (FAO, 2015b).

Estuaries, lagoons and other coastal brackish waters are likely to be affected in several ways by climate change (Bates *et al.*, 2008; Andrews, 1973; Smock *et al.*, 1994). These environments are particularly vulnerable to hurricanes and storms, which are predicted to become more frequent under climate change. Rising sea levels will also be a threat. Heavy rainfall over the land may increase the runoff of freshwater, nutrients, sediments and pollutants into coastal waters (FAO, 2015b).

Many rivers will be affected by changing patterns in precipitation and evaporation (Ficke, 2007; MEA, 2005). More frequent droughts increase the risk that small lakes and rivers will dry out completely, creating barriers to waterbody connectivity and fish migration, major disruptions of local fisheries and threats to biodiversity. Unusually heavy rains may result in extreme flooding, temporarily merging previously separated water bodies and facilitating the introduction and spread of invasive species (FAO, 2015b). Runoff increases turbidity and siltation, which can lead to the elimination of aquatic species that require very clear water (e.g. giant clams and corals feeding through symbiotic zooxanthellae<sup>xxi</sup>). Turbidity also lowers light penetration and reduces the abundance and activity of the phytoplankton that form the basis of most aquatic food webs. For other species, it also hampers vision making it harder to feed, reproduce and avoid predators. Siltation can lead to the physical burial of sessile organisms, such as corals and bivalves (FAO, 2015b). Greater availability of nutrients can also cause rapid increases in the abundance of some invertebrates (Flint, 1985). Runoff can also generate harmful algal blooms or pollute the water (De Casablanca *et al.*, 1997). Harmful algal blooms are also likely to increase as waters become warmer, threatening coastal aquaculture and fisheries. Climate change may also favour some microbial pathogens and promote the spread of diseases among aquatic populations. Where the direct effects of climate change are combined with increasing water abstraction and other anthropogenic pressures, the loss of significant numbers of aquatic species may occur.

Climate change will increase physiological stress in some farmed aquatic species populations, affecting

productivity and susceptibility to certain diseases. However, in some areas, higher temperatures may also increase the ranges of some fisheries and allow the farming of some aquatic species in new areas and with increases in growth rates and productivity (FAO, 2015b).

## **B8 - 6.2 Characterization, evaluation, inventory and monitoring of aquatic genetic resources**

More than 150 000 species of finfish, molluscs, crustaceans and aquatic plants have been described and recorded in various databases. FAO production statistics show that almost 600 species are being used in aquaculture (Bartley and Halwart, 2017). Information is largely at the species level (FAO, 2017b). Despite a much shorter history of domestication and genetic improvement compared to agriculture, the processes of domestication and selection have created significant inter- and intra-specific diversity, in the form of specific strains<sup>xxii</sup>, varieties<sup>xxiii</sup>, stocks<sup>xxiv</sup>, hybrids<sup>xxv</sup>, polyploids<sup>xxvi</sup> and other genetic types (see also [module B4](#) on climate-smart fisheries and aquaculture). Many identification tools are readily available (FAO, 2013b) and are becoming increasingly refined with the advance of molecular technologies.

Genetic information and technologies, which are useful for coping with and mitigating climate change, are not commonly used in fisheries and aquaculture. In aquaculture, the switching from one species to another has been a successful strategy for coping with disease outbreaks or other problems. This may also be an option for the sector for responding to the impacts related to climate change. Although genetic information has been used for the development and management of some aquatic species, examples are usually limited to a few commercially important species in developed countries.

## **B8 - 6.3 Sustainable use and development of aquatic genetic resources for climate change adaptation**

Climate change will have impacts on availability of freshwater resources and ambient temperatures, which will have consequences for the survival, spawning and migration of aquatic species. Different species will have varying abilities to tolerate changes to the changing environmental conditions. Indirect impacts on aquatic organisms will result from changes in ecosystem functions. The impacts of climate change are expected to be greater in equatorial and tropical regions, where aquatic species live at the upper end of their thermal tolerance.

From the perspective of genetic resources development, there is little that can be done to promote adaptation to climate change among the target species of wild capture fisheries production systems. As discussed in [module B4](#) on climate-smart fisheries, adaptation actions are linked mainly to environmental management, which typically involve the maintenance of water quality, flow and connectivity, and the protection of habitat. In some instances, it is possible to restock aquatic ecosystems with wild or hatchery-reared fish that have the appropriate environmental adaptations. This can be used to restore production in irreversibly damaged systems. However, restocking can also have large and irreversible genetic effects on surviving wild populations. When maladapted farmed species are introduced into open waters, they can breed with wild relatives and threaten their viability or simply displace them. One typical maladaptation in farmed fish is the trait of precocious breeding or out-of-season breeding. This is due to on-farm selection for early spawning or later migration, which is preferred in aquaculture systems. However, this trait causes fish to respond inappropriately to environmental cues for breeding and migration.

Aquaculture as a managed food production system has greater potential for adaptation to climate change than capture fisheries. It is potentially a climate-smart production system, particularly for the opportunities it offers for raising low trophic level species that have a lower carbon footprint than many intensive livestock systems.

There is a considerable diversity of aquaculture species across a wide range of taxa (Table B8.3) with the greatest diversity in the Asia. More species are used in marine and coastal aquaculture (526) than in inland aquaculture

(441).

**Table B8.3. Diversity of aquaculture species by region.**

All aquaculture	Africa	Americas	Asia	Europe	Oceania
Finfish	81	119	194	122	30
Molluscs	16	41	31	35	21
Crustaceans	14	19	39	20	17
Other animals	3	4	11	7	1
Plants	8	11	23	14	3
<b>Total - all aquaculture taxa</b>	<b>122</b>	<b>194</b>	<b>298</b>	<b>198</b>	<b>72</b>

Environment/Region	Africa	Americas	Asia	Europe	Oceania	Total by environment
Marine and coastal	59	102	187	126	52	<b>526</b>
Inland aquaculture	69	105	145	95	27	<b>441</b>

This genetic diversity in aquaculture food production shows the tremendous potential that exists to use genetic information and technologies for reducing risk, responding to external shocks and climate change, and accommodating changes in consumer demands or government policies (Singh, Boukerrou and Miller, 2010; Harvey *et al.*, 2017). Some of these species can be used not only to produce food but other products, such as pharmaceuticals and biofuels. Aquaculture is a new and rapidly diversifying production sector, so there have been relatively little improvements made in the genetic resources that are used. However, where efforts have been made to systematically improve the breeds used in aquaculture, the results indicate that selective breeding can increase aquatic food production by 5 to 12 percent per year (Gjedrem, Robinson and Rye, 2012). There are financial and management challenges to overcome for improving genetic resources used in aquaculture, which is why significant progress has been made with only a handful of species so far. The focus has largely been on typical domestication objectives, such as increasing production, improving feed conversion, accelerating growth rates and strengthening disease resistance.

## **B8 - 6.4 Sustainable use and development of aquatic genetic resources for climate change mitigation**

With over 70 percent of the planet covered by water, marine and freshwater ecosystems and their biota account for the largest carbon and nitrogen fluxes on the planet and also serve as its largest carbon sinks (Pullin and White, 2011). Terrestrial aquatic ecosystems include wetlands, rice fields, peatlands, mangroves, rivers, streams, ponds and lakes. In marine ecosystems, there are many coastal and oceanic processes that cycle and sequester nitrogen and carbon. Aquatic ecosystems and their associated biodiversity have immense importance and offer future potential for mitigating climate change.

As is the case with all agricultural sectors, food production from aquaculture and fisheries depends on ecosystem goods and services. The extent to which ecosystem habitats and processes deliver these goods and services is linked to the integrity of the ecosystem. Aquatic genetic diversity is an important component of ecosystem integrity. Environmental changes, both anthropogenic and climate driven, can disturb the integrity of the ecosystem and disrupt its functions, including those that contribute to climate change mitigation. For example, the sequestration of carbon in coral is affected by bleaching, which in turn is linked to sea temperature and nutrients. Likewise, wetlands and peatlands (see [Box B7.2](#)) can sequester carbon and organic matter, but will only do so when maintained in permanently wet conditions. Disturbances on peatlands, especially drainage, result in rapid

mineralization of stored carbon – a process that releases carbon dioxide emissions. Managed wetland landscapes, such as rice farming systems (see [chapter B1 - 3.1](#)), also release greenhouse gases, primarily methane.

Food production is one of the principle human activities that drive change in aquatic ecosystems. Other drivers of change include pollution and water use for other economic sectors. Efforts need to be made to minimize the impacts of these diverse forces on aquatic ecosystem functions. There are a range of cross-sectoral interventions that can serve to mitigate these impacts. In the terrestrial domain, most of these interventions revolve around the reduction of the impacts of climate change on hydrological regimes. This is done through better watershed management, particularly erosion and pollution control, which can be partly accomplished through the sustainable soil and land management practices, which are dealt with in [module B7](#). The maintenance of freshwater connectivity is critical as it allows aquatic species to migrate and breed. Conserving and restoring damaged and threatened coastal areas, for example, by replanting mangroves, is also important. Other cross-sectoral forms of land and water management linked to food production that could contribute significantly to climate change mitigation include the integrated crop-aquaculture production systems (e.g. fish raised in flooded rice fields) and multitrophic mariculture. Potential approaches that need further research and trial development include the redesign of reservoirs and management of natural lakes to minimize their greenhouse gas emissions.

There is a need to appraise the practical application of aquaculture and fisheries systems that extract and capture nutrients, particularly carbon, and the mass production and harvesting of micro-and/or macroalgae as feedstocks for clean biofuels.

## **B8 - 6.5 Conservation of aquatic genetic resources**

*In situ* and *ex situ* conservation are both important for the conservation of aquatic genetic diversity, the development of commercial applications for this diversity, and its application to support climate change adaptation and make improvements in aquaculture species and breeds.

Intraspecific genetic characterization in terms of local populations, stocks and strains of aquatic genetic resources is an essential first step in the conservation of these resources (see chapter B8 - 6.2). Within a given species, distinct populations can tolerate different ranges of ecological conditions and they will have different levels of susceptibility to climate change. This aspect deserves particular attention in the *in situ* conservation of fish stocks in fisheries management. The traditional definition of a fish stock is usually geographically based and does not always consider that a given stock can be made up of distinct locally adapted populations requiring different management approaches (Bonanomi *et al.*, 2015). Aquatic species tend to track closely their temperature boundaries of tolerance over generations, shifting their geographical range as the water warms. On a global scale, climate change is contributing to redefining aquatic species spatial distributions and the composition of biological communities at an increasing rate. To best adjust to these shifts in the ranges of species and populations, a traditional *in situ* conservation approach that mainly relies upon the retention of historical conditions in designated protected areas in marine, brackish and freshwaters may no longer be applicable in many cases. For this reason, there is a need for a critical reconsideration of conservation laws and programmes (Pecl *et al.*, 2017).

Combined with *in situ* management, the *ex situ* conservation of aquatic genetic resources of farmed species and their wild relatives in aquaculture facilities, culture collections, gene banks, research facilities, zoos and aquaria is essential to preserve the different stages of an organism's life cycle. For example, the cryopreservation of sperm, embryos and tissue DNA allows for the maintenance of genetic diversity that may be useful or potentially useful for coping with the impacts of climate change.

According to preliminary data submitted by countries for the State of the World on Aquatic Genetic Resources for Food and Agriculture (FAO, 2016d), 600 species are actively conserved *in situ* through protected and managed areas. Some countries consider that protected areas are effective for conserving aquatic genetic resources. Seventy percent of surveyed countries have current *ex situ* conservation programmes. The genetic resources of more than

344 aquatic species are the subject of *ex situ* conservation programmes in 112 facilities in 47 surveyed countries. The potential of these species for climate change adaptation is seen as the lowest priority for *ex situ* conservation programmes. It is important to raise awareness about the value of adaptation and the need to establish *ex situ* aquaculture facilities to maintain fish germplasm of threatened species used in aquaculture operation and restocking programmes. Aquatic plants and micro-algae collections are easier to maintain. Many species and strains of aquatic microalgae are kept as *ex situ* tissue culture collections.

Living on-farm gene banks of some species do exist, which would qualify as *in situ* on-farm conservation. However on-farm *in situ* conservation and on-farm *ex situ* conservation are often difficult to distinguish. For on-farm *in situ* conservation, the farm would need to maintain the desired species in a stable production environment, with no further genetic alteration or manipulation to occur. Most of these conditions do not exist in commercial farming operations because adaptive management to maintain profitability is the first priority. As a result, the desired species would adapt to the production environment over time, and this could not be considered the genetic conservation of the original strain (Lorenzen *et al.*, 2013).

## Climate-smart management of micro-organisms and invertebrates

Micro-organisms (e.g. bacteria, fungi and yeasts) and invertebrates (e.g. insects, arachnids and earthworms) are invaluable contributors to terrestrial and aquatic ecosystems on which food production and agriculture depend. They pollinate plants including crops and cultured trees, recycle nutrients in soils, ferment bread and cheese, help animals digest otherwise indigestible forage and, with proper management, and can provide natural protection against plant pests in farmers' fields. Micro-organisms and invertebrates also include pathogens and vectors, parasites and pests that attack plants and animals, and spread diseases. Agriculture and food production would not exist without this 'hidden' but critically important biodiversity (Beed *et al.*, 2011).

### B8 - 7.1 Impact of climate change on micro-organisms and invertebrates

It is very difficult to predict how climate change will affect micro-organisms and invertebrates, their interactions with the other components of the ecosystem, and their capacities to provide ecosystem services or act as pests. Only a few studies have attempted to investigate these issues. Nevertheless, there is a growing consensus that climate change could lead to an overall increase in the abundance and diversity of pests, as habitats become more favourable for their establishment and development; new ecological niches appear; stabilizing interactions are disrupted; and the distribution range of invasive species expands (e.g. Cannon, 1998; Patterson *et al.*, 1999; Rosenzweig *et al.*, 2001; Fuhrer, 2003; Luedeling *et al.*, 2011; Grace *et al.*, 2015).

#### Soil biodiversity

The impacts of climate change on soil biodiversity and the services it provides are to a large extent mediated through plants. For example, shifting rainfall patterns and changes in temperature are expected to affect the nutritional composition of plant leaves and grazing patterns of animals, which will in turn have an impact on the diets of soil invertebrates. Modifications in diet will influence the capacity of these organisms to decompose plant litter, which could affect the turnover of soil organic matter and the rate at which nutrients are released and made available to plants (FAO, 2015b).

Both elevated temperatures and elevated carbon dioxide levels are known to affect the abundance and composition of soil communities (e.g. Jones *et al.*, 1998; Briones *et al.*, 2009). They also influence many of the processes that micro-organisms and invertebrates are involved in, including the retention and loss of soil nutrients, nitrogen



mineralization and denitrification, litter decomposition and soil respiration. However, the impact of changes in these processes is expected to be stronger in soils in intensive farming systems, where a limited range of crops are grown, than in soils in natural ecosystems, where the diversity of the soil micro-organism community may allow for more rapid adaptation to change (Mocali *et al.*, 2008).

## **Plant pathogens and biological control**

As explained in [chapter B1 - 1.2](#), climate change is expected to affect the distribution of crop species and varieties. Some pathogens will migrate with these crops and establish themselves in areas where they have not previously caused problems and where there may be no natural enemies to keep them under control. The newly established crops will also be exposed to potentially harmful indigenous micro-organisms.

Climate change is also likely to affect the behaviour, distribution, development, survival and reproduction of invertebrates. For instance, warmer temperatures could influence the ability of insects to act as disease vectors. Warmer temperatures are also expected to alter the hunting behaviour of predators and the feeding habits of herbivores. With a 2 °C rise in temperature, it is estimated that many insects will be able to complete one to five extra life cycles per season (Yamamura and Kiritani, 1998). Increasing humidity and temperatures may also boost the growth of food-spoiling micro-organisms on plants (e.g. moulds), which could in turn affect the dynamic equilibrium between these organisms and natural biological control agents. This disrupted equilibrium could necessitate increases in pesticide use. See also [chapter B3-1.2](#) and [Box B3.2](#) for the interactions between climate change and forest insect pests.

Climate change is expected to cause significant changes in the degree of synchrony between the life cycles of different species, which could substantially influence the efficacy of biological control agents on a local scale. Moreover, according to some climate change models, the level of ultraviolet-B radiation is set to increase due to depletion of the ozone layer. This could have a particularly significant impact on biological control by micro-organisms, as fungi and bacteria are generally more sensitive to damage by ultraviolet-B radiation than weeds and insects.

## **Invertebrates**

Aided in some cases by human activities, the majority of invertebrate pollinators and pests, along with their natural enemies, can be expected to move with their host plants, as the distribution ranges of crops and forages change (Cock *et al.*, 2011). Many pollinators are able to move over long distances without assistance from humans. However, it is likely that climate change will increase demand for assisted movement of pollinators between countries.

Invertebrate species differ in their sensitivity to temperature and other climatic factors. As the climate changes, the species composition of invertebrate communities and the synchrony between the life cycles of individual pollinating species and those of flowering plants will also change. Not all species may be able follow their associated crop or livestock production systems. What the consequences of these changes will be are unknown (FAO, 2015b). Many pollinators are sensitive to high temperatures and drought. For example, increases in temperature may enhance the performance of insect species living at higher latitudes, as they have broader thermal tolerance and are living in climates cooler than their optimal thermal range. In contrast, warming could have negative impacts in tropical climate zones, where most pollinators already live close to their optimal range of temperature tolerance (Deutsch *et al.*, 2008).

## **B8 - 7.2 Characterization, evaluation, inventory and monitoring of micro-organisms and invertebrates**

While micro-organisms and invertebrates make up an immense and diverse population of living organisms, very little is known about their composition and dynamics. The 'invisible' nature of micro-organisms means that changes are particularly difficult to observe (FAO, 2015b). In most soil ecosystems, the resident micro-organism and invertebrate species have even not been counted, let alone identified and described. The intricate ecological relationships within soil communities, and between them and above-ground biodiversity, also remain very poorly understood (FAO, 2015b).

Some predator species are considered 'specialists' because they may attack and reproduce on only a single pest species. Other species are 'generalists', attacking a range of pest species. Likewise, specialist bees forage for pollen that can only be found on a few or only just one plant species, while generalist bees often visit a wide range of flower types and species when seeking out pollen. To 'select' useful species from the diversity of micro-organisms and invertebrates that could be conserved and used for food and agricultural purposes, it is crucial to understand the specificity and functionality of these organisms, and the complex and dynamic relationships they have with other components of their environment (e.g. natural enemy-pest and plant-pollinator relationships). This requires extensive ecological research, taxonomical identification and related expertise (Waage, 2007; CBD, 2017). As reference collections, living *ex situ* culture collections are of enormous value in supporting research and taxonomy of micro-organisms. In the same way, collections of dead invertebrate material in natural history museums and botanical gardens help identify insects, spiders and mites that have the potential to be used in new biological control programmes. Culture collections will be important for gaining a better understanding of the identity of any new organisms discovered, and these organisms may then be added to these collections as future taxonomic resources (Waage, 2007).

Generally speaking, taxonomy and genetic characterization of micro-organisms and invertebrates, including soil organisms, biological control agents and pollinators, found in agricultural ecosystems need to be improved. Systematic monitoring programmes that are able to identify trends in micro-organism and invertebrate genetic resources are also required. Some monitoring initiatives for soil organisms and pathogens have been established in technologically advanced countries, but similar programmes need to be set up in developing countries. Techniques for characterizing micro-organism and invertebrate species, communities and functions must also be improved, and studies are required on the effects of climate on micro-organisms and invertebrates and the services they provide. This will involve a combination of field and laboratory-based work. Techniques need to be standardized to allow a comparison of data from different locations (FAO, 2015b).

## **B8 - 7.3 Sustainable use and development of micro-organisms and invertebrates for climate change adaptation**

When it comes to responding to climate change, invertebrates and micro-organisms seem to have several advantages over other larger species. For example, their unparalleled rate of reproduction, which they achieve thanks to their short reproductive cycles, enables them to adapt extremely rapidly to changes in their environment or evolve in response to changing climatic conditions (FAO, 2015b). Micro-organisms also benefit from 'horizontal gene transfer', whereby DNA is able to move from one micro-organism cell to another. This means that micro-organisms do not have to wait for the next generation in order to change their genetic characteristics.

Micro-organisms can play a key role in global efforts to adapt to the impacts of climate change. For example, plant-associated micro-organisms that contribute to plant traits, such as drought tolerance, may help crops to adapt to some of these impacts. However, much work needs to be done to better understand how micro-organisms can contribute to traits that increase adaptation to climate change in crops and the extent to which micro-organisms

from one plant species may be adapted for use with other plant species (Beed *et al.*, 2011).

Micro-organism communities in the soil can change the soil environment to make it less favourable or suppressive to fungal, bacterial or nematode pathogens. The potential of the soil micro-organism community to create these so-called suppressive soils represents a form of naturally occurring biological control that can reduce losses from plant disease (Beed *et al.*, 2011). Management practices promoting the preservation and increase of micro-organism and invertebrate diversity, such as no-tillage farming in combination with a sound crop rotation-system and the retention of crop residue to keep the soil covered (conservation agriculture) also contribute to the effects of naturally occurring biological control (see [chapter B1 - 2](#) on sustainable soil and land management). These practices can help keep the population of damaging pest and diseases at levels that do not cause economic losses. It is also possible that many other, currently unknown, roles of biological control micro-organisms exist, which will be able to be utilized in adapting to climate change (Beed *et al.*, 2011). For example, research has shown that rice can cope with elevated carbon dioxide levels when combined with the right strains of mycorrhizal fungi (Tang *et al.*, 2009).

Most invertebrates are expected to change their geographical distribution in response to climate change, so that they remain in areas to which they are well adapted. Many of the challenges associated with the management of invertebrate genetic resources in agriculture in response to climate change adaptation will relate to climate-driven or human-assisted movement of these organisms. In this respect, it will be important to maintain predator and parasite species that could be deliberately introduced as biological control agents to assist crop production systems in adapting to new pest problems that arise because of climate change (Cock *et al.*, 2011).

## **B8 - 7.4 Sustainable use and development of micro-organisms and invertebrates for climate change mitigation**

Micro-organisms and invertebrates can contribute to mitigation of climate change in agriculture and food production systems in multiple ways. Soil micro-organisms play an important role in the sequestration of carbon in soil organic matter and the release of carbon in the form of carbon dioxide when soil organic matter decomposes. Given the enormous amount of carbon stored in the world's soils, micro-organisms are extremely significant in global efforts to mitigate climate change. Their contribution to carbon sequestration can be promoted by practices such as amending soil with organic fertilizers, proper management of crop residues, no-tillage agriculture, maintaining cover crops on the soil surface, avoiding flood irrigation and carefully managing the use of fertilizers.

Many beneficial micro-organisms provide their services at a relatively low cost in terms of greenhouse gas emissions. For example, mycorrhizal fungi and rhizobia contribute to plant nutrition and increase plant productivity without the greenhouse gas emissions associated with production, transport and application of mineral fertilizers. The use of micro-organisms to increase shelf-life has potential to reduce the amount of energy expended on freezing or refrigerating food (Di Cagno *et al.*, 2009). In ruminants, certain modifications to the composition of micro-organism populations in the rumen are believed to have a positive effect on methane emissions (methanogenesis). Current and future research on the role of these populations could provide a greater understanding of rumen function, feed conversion efficiency, methanogenesis and plant cell wall degradation, which would help find an optimal balance between food production and greenhouse gas emissions.

Sustainable use and domestication of edible insects may represent a climate-smart alternative to the production of food from other animals. Insects produce much smaller quantities of greenhouse gases per kilogram of product than conventional livestock species (Oonincx *et al.*, 2010). See [chapter B5 - 3](#) and [Box B2.2](#) for more information on insect-based systems.

By helping to maintain soil structure and retain water throughout the soil profile, earthworms can contribute to alleviating the effects of drought on crop production (e.g. Johnson *et al.*, 2011). Studies have also revealed the

remarkable ability of diverse soil invertebrate communities to restore the structure of degraded soils (e.g. Barros *et al.*, 2004). Soil restoration or protection of soils against erosion can contribute both to retaining and increasing soil carbon stocks.

Few if any deliberate attempts have been made to introduce soil invertebrates into new countries or ecosystems to enhance their beneficial roles. Given the potential for these species to become invasive, it is inadvisable to attempt any such introductions until soil ecology is much better understood.

## **B8 - 7.5 Conservation of micro-organisms and invertebrates**

### **Conservation of micro-organisms**

Living *ex situ* microbial collections are of enormous value in the collection, authentication, maintenance and distribution of cultures of microorganisms and cultured cells. They also contribute to understanding the identity of newly discovered organisms, which may then be added to these collections as taxonomic references. Of the many existing microbial collections, several are of global significance, such as the [Agriculture Research Service Culture Collection of the United States Department of Agriculture](#) and the [Centre for Agriculture and Bioscience International \(CABI\) Genetic Resources Collection](#), which provide microbial cultures freely to researchers. There are also important specialist collections, for example for species used in biological control, which are in effect an *ex situ* repository of microbial biological control agents (Waage, 2007).

*In situ* conservation also has an important role to play. For example, the *in situ* conservation of wild crop relatives depends on the maintenance of the micro-organism communities to which they are associated under field conditions. This allows co-evolution among plants and micro-organisms to continue. Determining what micro-organism communities need to be maintained is challenging because of the limited knowledge of the dynamic interactions among the environment, plants and micro-organisms. Because micro-organisms are highly adaptive to new scenarios, such as those likely to be induced by climate change, *ex situ* collections of micro-organisms may become out-dated. Efforts are required to advance *in situ* conservation methods for micro-organisms.

Developing a more complete understanding of many micro-organisms is important for determining how to prioritize micro-organism conservation. For example, micro-organisms that have the potential to support crop adaptation to new environments could be prioritized for conservation.

Most of the foods currently eaten are partly the products of from different types of micro-organism processes that give food its specificity and unique taste. *Ex situ* conservation of cultures of food-borne micro-organisms is instrumental in maintaining specific food production systems and making them more adaptable to climate change. Conservation of food-borne micro-organisms also has a cultural function in that it helps maintain traditional food production systems.

### **Conservation of invertebrates**

While micro-organisms are essentially conserved *ex situ*, the preferred approach for conserving invertebrates remains *in situ* conservation. The most important reservoirs for biological control agent species are agricultural ecosystems where management practices do not hinder their survival (e.g. those with little pesticide use). Most biological control agents are also likely to have reservoir populations in natural ecosystems (i.e. those not used for agriculture). Such habitats tend to harbour additional genetic diversity within known biological control agent species. They may also be home to unknown species with future potential to act as biological control agents. Conservation of both natural ecosystems and diversity-rich farming systems is essential to ensure that sufficient biological control agents remain available for the future. More research is needed before it will be possible to know which ecosystems are particularly important for maintaining biological control agents, and which biological control

agents are particularly important to maintain.

Maintaining insect species that can provide pollination services for a wide range of crops is also vital to the future of agriculture. Pollinator populations not only need to be able to cope with changing climatic conditions, they must also be able to provide the pollination services needed to meet increasing demands for food and retain the capacity to adapt to potential changes in the types of crops grown. For this reason, the natural habitats of wild pollinator species need to be identified and preserved. As land use changes, it may be necessary to protect or develop corridors of suitable habitats that ensure food and nesting resources are available for pollinators.

## Conclusion

Genetic resources, including aquatic and terrestrial plants, animals and micro-organisms, must be viewed as a vital component in strategies to develop and implement climate-smart agricultural technologies and practices. The *Voluntary Guidelines to Support the Integration of Genetic Diversity into National Climate Change Adaptation Planning* (FAO, 2015a) outlines the cross-sectoral actions that could be undertaken to improve the sustainable management of genetic resources to support climate-smart agriculture. These actions are summarized in Box B8.5).

### **Box B8.5 Possible actions to improve the sustainable management of genetic resources to cope with climate change**

#### **a) Characterization, evaluation, inventory and monitoring of genetic resources**

- Develop standard methods to identify and select potentially valuable species, varieties, breeds and populations.
- Make inventories of agricultural and forest ecosystems and identify genetic variants related to specific environmental features that are of potential interest for climate change adaptation.
- Collect information on distribution of species, varieties, breeds and populations that have been prioritized on the basis of their socio-economic importance and provision of ecosystem services.
- Collect scientific and traditional knowledge relevant to adaptation and use of species, varieties, breeds and populations.
- Establish monitoring programmes at national, subnational and community levels to assess the risks and vulnerability of prioritized species, varieties, breeds and populations, and evaluate the effectiveness of conservation measures.

#### **b) Sustainable use and development of genetic resources**

- Develop and implement crop, animal, tree or fish species improvement programmes to provide materials that can be used to adapt agricultural production systems to climate change, and give long-term support for the evaluation and use of wild relatives.
- Support community programmes for the reintroduction, maintenance and improvement of traditional crop varieties, locally adapted breeds, agroforestry and traditional forestry areas, and traditional fisheries management practices.
- Identify and put in place measures to support, protect and restore diversity within production systems at the landscape, community and farm levels.
- Support the adoption of improved soil management practices (e.g. no-till practices and conservation agriculture).

- Monitor and evaluate pollinators and the services they provide; identify their risks and vulnerabilities with respect to climate change; and implement measures to maintain or improve pollination.
- Strengthen water management in terms of quality and quantity at the landscape and seascape, community and farm levels through the sustainable management of aquatic resources.

### c) Conservation of genetic resources

- Prioritize species, varieties, breeds and populations, including wild relatives, for conservation on the basis of their socio-economic importance and the provision of ecosystem services.
- Develop and implement *ex situ* conservation plans for prioritized species, varieties, breeds and populations and strengthen information systems to improve access to genetic resources that can be used as potential options for climate change adaptation.
- Develop and implement *in situ* conservation plans for prioritized species, varieties, breeds and populations.

Many of the genetic resources needed may need to come from other parts of the world. In addition to improving the availability of traditional breeds and varieties, provenances of forest trees likely to be more adapted to changed conditions and to populations of fish species with desirable adaptive characteristics, actions should also aim at facilitating movement of materials and supporting regional and international collaboration.

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## References

**Abi-Ghanem, R., Bodah, E.T., Wood, M. & Braunwart, K.** 2013. Potential breeding for high nitrogen fixation in *Pisum sativum* L.: germplasm phenotypic characterization and genetic investigation. *American Journal of Plant Sciences*, 4(8): 1597-1600.

**Ahloowalia B.S., Maluszynski M. & Nichterlein, K.** 2004. Global impact of mutation derived varieties. *Euphytica*, 135(2): 187-204.

**Aitken, S.N., Yeaman, S., Holliday, J.A, Wang, T. & Curtis-McLane, S.** 2008. Adaptation, migration or extirpation: climate change outcomes for tree populations. *Evolutionary Applications*, 1(1): 95-111.

**Alercia, A., Diulgheroff, S. & Mackay, M.** 2015. [FAO/Bioversity Multi-Crop Passport Descriptors \(MCPD V.2.1\)](#). Rome, FAO and Bioversity International.

**Alfaro, R.I., Fady, B., Vendramin, G.G., Dawson, I.D., Fleming, R.A., Sáenz-Romero, C., Lindig-Cisneros, R.A., Murdock, T., Vinceti, B., Navarro, C.M., Skråppa, T., Baldinelli, G., El-Kassaby, Y. & Loo, J.** 2014. The role of forest genetic resources in responding to biotic and abiotic factors in the context of anthropogenic climate change. *Forest Ecology and Management*, 333: 76-87.

**Andrews, J.D.** 1973. Effects of tropical storm Agnes on epifaunal invertebrates in Virginia estuaries. *Chesapeake Science*, 14: 223–234.

**AQUALEX.** 1998. *Multilingual glossary of aquaculture terms / Glossaire multilingue relatif aux termes utilisés en aquaculture*. CD ROM, John Wiley & Sons Ltd. & Praxis Publ., UK.

**Aravanopoulos, F.A., Tollefsrud, M.M., Graudal, L., Koskela, J., Kätzel, R., Soto, A., Nagy, L., Pilipovic, A., Zhelev, P., Bozic, G. & Bozzano, M.** 2015. *Development of genetic monitoring methods for genetic conservation units of forest trees in Europe*. Rome, Bioversity International.

**Art, H.W. (eds.)** 1993. *The dictionary of ecology and environmental science*. New York, Henry Holt & Co. 632p.

**Ashby, J.A.** 2009. The impact of participatory plant breeding. In S. Ceccarelli, E.P. Guimaraes, E. Weltzien, eds. *Plant breeding and farmer participation*, pp. 649-671. Rome, FAO.

**Balon, E.K.** 1995. Origin and domestication of the wild carp, *Cyprinus carpio*: from Roman gourmets to the swimming flowers. *Aquaculture*, 129: 3-48.

- Barros, E., Grimaldi, M., Sarrazin, M., Chauvel, M., Mitja, D., Desjardins, T. & Lavelle, P.** 2004. Soil physical degradation and changes in macrofaunal communities in Central Amazon. *Applied Soil Ecology*, 26(2): 157-168.
- Bartley, D. & M. Halwart.** 2017. Aquatic genetic resources in aquaculture. In: D. Hunter, L. Guarino, C. Spillane and P. McKeown (eds.) *Routledge Handbook of Agricultural Biodiversity*, pp. 86-98. Routledge.
- Bates, B.C., Kundzewicz, Z.W., Wu, S. & Palutikof, J.P. (eds.)**. 2008. *Climate change and water*. Technical Paper of the Intergovernmental Panel on Climate Change, IPCC Secretariat, Geneva.
- Beed, F., Benedetti, A., Cardinali, G., Chakraborty, S., Dubois, T., Garrett, K. & Halewood, M.** 2011. [Climate change and micro-organism genetic resources for food and agriculture: state of knowledge, risks and opportunities](#). CGRFA Background Study Paper No. 57. Commission on Genetic Resources for Food and Agriculture. Rome, FAO
- Bellon, M. R., Hodson, D., & Hellin, J.** 2011. Assessing the vulnerability of traditional maize seed systems in Mexico to climate change. *Proceedings of the National Academy of Sciences of the United States of America*, 108(33): 13432-13437.
- Bellon M.R. & van Etten, J.** 2014. Climate change and on-farm conservation of crop landraces in centres of diversity In M. Jackson, B. Ford-Lloyd & M. Parry, eds. *Plant genetic resources and climate change*, pp. 137-150.
- Benjelloun B., Streeter I., Boyer F., Coissac E., Stucki S., BenBati M., Ibelbachyr M., Chentouf M., Bechchari A. & Leempoel K.** 2015. Characterizing neutral genomic diversity and selection signatures in indigenous populations of Moroccan goats (*Capra hircus*) using WGS data. *Frontiers in Genetics*, 6:107.
- Botanical Gardens Conservation International (BGCI).** 2017. [Global Tree Search database](#). Accessed 24 Apr 2017. Kew, UK.
- Boettcher, P.J., Hoffmann, I., Baumung, R., Drucker, A.G., McManus, C., Berg, P., Stella, A., Nilsen, L.B., Moran, D., Naves, M. & Thompson, M.C.** 2014. Genetic resources and genomics for adaptation of livestock to climate change. *Frontiers in Genetics*, 5:461.
- Bozzano, M., Jalonen, R., Thomas, E., Boshier, D., Gallo, L., Cavers, S., Bordács, S., Smith, P. & Loo, J. (Eds).** 2014. *Genetic considerations in ecosystem restoration using native tree species*. State of the World's Forest Genetic Resources - Thematic Study. FAO and Bioversity International, Rome.
- Briones, M.J.I., Ostle, N.J., McNamara, N.P. & Poskitt, J.** 2009. Functional shifts of grassland soil communities in response to soil warming. *Soil Biology & Biochemistry*, 41(2): 315-322.
- Brozynska, M., Furtado, A., & Henry, R.J.** 2015. Genomics of crop wild relatives: expanding the gene pool for crop improvement. *Plant Biotechnology Journal*, 14(4): 1070-1085.
- Burns, A., Gleadow, R., Cliff, J., Zacarias, A., & Cavagnaro, T.** 2010. Cassava: the drought, war and famine



crop in a changing world. *Sustainability*, 2(11): 3572-3607.

**Cannon, R.J.C.** 1998. The implications of predicted climate change for insect pests in the UK, with emphasis on non-indigenous species. *Global Change Biology*, 4(7): 785-796.

**Capper, J.L., Cady, R.A. & Bauman, D.E.** 2009. The environmental impact of dairy production: 1944 compared with 2007. *Journal of Animal Science*, 87(6): 2160-2167.

**Convention on Biological Diversity (CBD).** 2017. [Why is Taxonomy Important?](#) [Online]. Accessed on 7 June 2017.

**Cernay, C., Pelzer, E. & Makowski, D.** 2016. A global experimental dataset for assessing grain legume production. *Scientific Data*, 3: 160084.

**Cock, M.J.W., Biesmeijer, J.C., Cannon, R.J.C., Gerard, P.J., Gillespie, D., Jiménez, J.J., Lavelle, P.M. & Raina, S.K.** 2011. *Climate change and invertebrate genetic resources for food and agriculture: state of knowledge, risks and opportunities*. CGRFA Background Study Paper No. 54. Commission on Genetic Resources for Food and Agriculture. Rome, FAO.

**Cook, D.R.** 2014. Ecological Genomics at Chickpea's Center of Origin: Mining Wild Crop Relatives for Climate Resilience and Nitrogen Fixation for Crop Improvement in the Developing World. Plant and Animal Genome XXII Conference, 11-15 January 2014, San Diego, USA.

**De Casablanca, M.-L., Laugier, T. & Marinho-Soriano, E.** 1997. Seasonal changes of nutrients in water and sediment in a Mediterranean lagoon with shellfish farming activity (Thua Lagoon, France). *ICES Journal of Marine Science*, 54: 905–916.

**De Jong, G.** 2005. Evolution of phenotypic plasticity: patterns of plasticity and the emergence of ecotypes. *New Phytologist*, 166(1): 101-118.

**Di Cagno, R., Surico, R.F., Minervini, G., De Angelis, M., Rizzello, C.G. & Gobbetti, M.** 2009. Use of autochthonous starters to ferment red and yellow peppers (*Capsicum annum* L.) to be stored at room temperature. *International Journal of Food Microbiology*, 130(2): 108-116.

**Dwivedi, S.L., Stalker, H.T., Blair, M.W., Bertoli, D.J., Upadhyaya, H., Nielen, S. & Ortiz, R.** 2008. Enhancing crop gene pools with beneficial traits using wild relatives. *Plant Breeding Reviews*, 30: 179-230.

**Ebert, A.W.** 2014. Potential of underutilized traditional vegetables and legume crops to contribute to food and nutritional security, income and more sustainable production systems. *Sustainability*, 6(1): 319-335.

**Efissue, A., Tongoona, P., Derera, J., Langyintuo, A., Laing, M. & Ubi, B.** 2008. Farmers' perceptions on rice varieties in Sikasso region of Mali and their implications for rice breeding. *Journal of Agronomy and Crop Science*,

194(5): 393-400.

**El-Sharkawy, M.A.** 2016. Prospects of photosynthetic research for increasing agricultural productivity, with emphasis on the tropical C4 Amaranthus and the cassava C3-C4 crops. *Photosynthetica*, 54(2): 161-184.

**Eriksson, G., Namkoong, G. & Roberds, J.H.** 1993. Dynamic gene conservation for uncertain futures. *Forest Ecology and Management*, 62(1-4): 15-37.

**FAO.** 1999. [\*The global strategy for the management of farm animal genetic resources\*](#). Executive Brief. Rome.

**FAO.** 2004. *Preliminary review of biotechnology in forestry, including genetic modification*. Forest Genetic Resources Working Paper FGR/59E. Rome.

**FAO.** 2007. [\*Global Plan of Action for Animal Genetic Resources and the Interlaken Declaration\*](#). Adopted by the International Technical Conference on Animal Genetic Resources for Food and Agriculture, Interlaken, Switzerland, 3-7 September 2007. Commission on Genetic Resources for Food and Agriculture. Rome.

**FAO.** 2010. [\*The Second Report on The State of the World's Plant Genetic Resources For Food And Agriculture\*](#). Rome, FAO.

**FAO.** 2011a. [\*Second Global Plan of Action for Plant Genetic Resources for Food and Agriculture\*](#). Adopted by the FAO Council, Rome, Italy, 29 November 2011. Rome.

**FAO.** 2011b. [\*Pre-breeding for Effective Use of Plant Genetic Resources: E-learning course\*](#).

**FAO.** 2013a. [\*Climate-Smart Agriculture Sourcebook\*](#). Rome.

**FAO.** 2013b. *Fish identification tools for biodiversity and fisheries assessments: review and guidance for decision-makers*. Edited by Fischer, J. FAO Fisheries and Aquaculture Technical Paper No. 585. Rome, FAO. 2013. 107 pp.

**FAO.** 2014a. [\*Genebank Standards for Plant Genetic Resources for Food and Agriculture\*](#). Rev. ed. Rome.

**FAO.** 2014b. [\*The State of the World's Forest Genetic Resources\*](#). Rome.

**FAO.** 2014c. [\*The State of World Fisheries and Aquaculture 2014\*](#). Opportunities and challenges. Rome.

**FAO.** 2015a. [\*Voluntary Guidelines to Support the Integration of Genetic Diversity into National Climate Change Adaptation Planning\*](#). Rome.

**FAO.** 2015b. [\*Coping with climate change - the roles of genetic resources for food and agriculture\*](#). Rome.

- FAO. 2015c. [\*Voluntary Guide for National Seed Policy Formulation\*](#). Rome.
- FAO. 2015d. [\*The Second Report on the State of the World's Animal Genetic Resources for Food and Agriculture\*](#). Rome.
- FAO. 2016a. [\*Climate change and food security: risks and responses\*](#). Rome.
- FAO. 2016b. [\*Global Forest Resources Assessment 2015\*](#). How are the world's forests changing? Second edition. Rome.
- FAO. 2016c. [\*The State of World Fisheries and Aquaculture 2016\*](#). Contributing to food security and nutrition for all. Rome.
- FAO. 2016d. [\*The State of the World's Aquatic Genetic Resources For Food And Agriculture - Draft Report\*](#). Rome.
- FAO. 2017a. [\*FAOSTAT Database on Agriculture\*](#).
- FAO. 2017b. [\*FAO Databases\*](#).
- FAO. (in press). [\*Voluntary Guidelines for the National Level Conservation of Crop Wild Relatives and Wild Food Plants \[endorsed by the Commission on Genetic Resources at its Sixteenth Regular Session\]\*](#).
- FAO, DFSC & IPGRI. 2001. *Forest genetic resources conservation and management*. Vol. 2: In managed natural forests and protected areas (in situ). Rome, International Plant Genetic Resources Institute.
- FAO, FLD & IPGRI. 2004a. *Forest genetic resources conservation and management*. Vol. 1: Overview, concepts and some systematic approaches. Rome, International Plant Genetic Resources Institute.
- FAO, FLD & IPGRI. 2004b. *Forest genetic resources conservation and management*. Vol. 3: In plantations and genebanks (ex situ). Rome, International Plant Genetic Resources Institute.
- FAOSTAT. 2016. [\*FAOSTAT\*](#) [online]. Rome. [cited 10 July 2017].
- Ficke, A., Myrick, C.A. & Hansen, L.J. 2007. Potential impacts of global climate change on freshwater fisheries. *Reviews in Fish Biology and Fisheries*, 17: 581-613.
- Flint, R.W. 1985. Coastal ecosystem dynamics: relevance of benthic processes. *Mar. Chem.*, 16: 351-367.

- Foresight.** 2011. *The Future of Food and Farming*. Final Project Report. London, The Government Office for Science.
- Fuhrer, J.** 2003. Agroecosystem responses to combinations of elevated CO<sub>2</sub>, ozone, and global climate change. *Agriculture, Ecosystems & Environment*, 97(1-3): 1-20.
- Gjedrem T., Robinson, N. & Rye, M.** 2012. The importance of selective breeding in aquaculture to meet future demands for animal protein: A review. *Aquaculture*, 350: 117-129.
- Glaszmann, J.C., Kilian, B., Upadhyaya, H.D. & Varshney, R.K.** 2010. Accessing genetic diversity for crop improvement. *Current Opinion in Plant Biology*, 13(2): 167-173.
- Gorkhali, N.A., Dong, K., Yang, M., Song, S., Kader, A., Shrestha, B.S., He, X., Zhao, Q., Pu, Y., Li, X., Kijas, J., Guan, W., Han, J., Jiang, L. & Ma, Y.** 2016. Genomic analysis identified a potential novel molecular mechanism for high-altitude adaptation in sheep at the Himalayas. *Scientific Reports*, 6: 29963.
- Govindaraj, M., Vetriventhan, M. & Srinivasan, M.** 2015. Importance of genetic diversity assessment in crop plants and its recent advances: an overview of its analytical perspectives. *Genetics research international*, 2015: 431487.
- Graudal, L. & Lillesø, J.-P.B.** 2007. *Experiences and future prospects for tree seed supply in agricultural development support: based on lessons learnt in Danida supported programmes 1965-2005*. Copenhagen, Ministry of Foreign Affairs of Denmark. Danida.
- Grace, D., Bett, B., Lindahl, J. & Robinson T.** 2015. *Climate and livestock disease: assessing the vulnerability of agricultural systems to livestock pests under climate change scenarios*. CCAFS Working Paper no. 116. Copenhagen, Denmark: CGIAR Research Program on Climate Change, Agriculture and Food Security (CCAFS).
- Gresshoff, P.M., Hayashi, S., Biswas, B., Mirzaei, S., Indrasumunar, A., Reid, D., Samuel, S., Tollenaere, A., van Hameren, B., Hastwell, A. & Scott, P.** 2015. The value of biodiversity in legume symbiotic nitrogen fixation and nodulation for biofuel and food production. *Journal of Plant Physiology*, 172: 128-136.
- Groeneveld, L.F., Lenstra, J.A., Eding, H., Toro, M.A., Scherf, B., Pilling, D., Negrini, R., Finlay, E.K., Jianlin, H., Groeneveld, E., Weigend, S. & The GLOBALDIV Consortium.** 2010. Genetic diversity in farm animals—a review. *Animal Genetics*, 41(s1): 6-31.
- Guinotte, J.M & Fabry, V.** 2008. Ocean acidification and its potential effects on marine ecosystems. *The Year in Ecology and Conservation Biology*, 1134: 320-342.
- Hamrick, J.L.** 2004. Response of forest trees to global environmental changes. *Forest Ecology and Management*, 197(1-3): 323-335.
- Harvey, B., Soto, D., Carolsfeld, J., Beveridge, M. & Bartley, D.M. (eds).** 2017. *Planning for aquaculture*

*diversification: the importance of climate change and other drivers*. FAO Technical Workshop, 23-25 June 2016, FAO Rome. FAO Fisheries and Aquaculture Proceedings No. 47. Rome, FAO. 154 pp.

**Hatfield, J., Boote, K., Fay, P., Hahn, L., Izaurrealde, C., Kimball, B.A., Mader, T., Morgan, J., Ort, D., Polley, W., Thomson, A., & Wolfe, D.** 2008. Agriculture. In CCSP, ed. *The Effects of Climate Change on Agriculture, Land Resources, Water Resources, and Biodiversity in the United States*. A Report by the U.S. Climate Change Science Program (CCSP) and the Subcommittee on Global Change Research. Washington, DC.

**Hoffmann, I.** 2010a. *Climate Change in Context: Implications for Livestock Production and Diversity*. In N.E. Odongo, M. Garcia & G.J. Viljoen, eds. Sustainable improvement of animal production and health, pp. 33-44. Vienna, FAO/IAEA.

**Hoffmann, I.** 2010b. Climate change and the characterization, breeding and conservation of animal genetic resources. *Animal Genetics*, 41(s1): 32-46.

**Hubert, J. & Cottrell, J.** 2007. [\*The role of forest genetic resources in helping British forests respond to climate change\*](#). Forestry Commission Information Note FCIN086. Edinburgh, Forestry Commission.

**Jarvis, A., Lane, A. & Hijmans, R.** 2008. *The effect of climate change on crop wild relatives*. *Agriculture, Ecosystems & Environment*, 126(1-2): 13-23.

**Jarvis, A., Upadhyaya, H.D., Gowda, C.L.L., Agrawal, P.K., Fujisaka, S. & Anderson, B.** 2008. [\*Climate change and its effect on conservation and use of plant genetic resources for food and agriculture and associated biodiversity for food security\*](#). Thematic Background Study. Rome, FAO.

**Jensen, E.S., Peoples, M.B., Boddey, R.M., Gresshoff, P.M., Hauggaard-Nielsen, H., Alves, B.J.R. & Morrison, M.J.** 2012. Legumes for mitigation of climate change and the provision of feedstock for biofuels and biorefineries. A review. *Agronomy for Sustainable Development*, 32(2): 329-364.

**Johnson, S.N., Staley, J.T., McLeod, F.A.L. & Hartley, S.E.** 2011. Plant-mediated effects of soil invertebrates and summer drought on above-ground multitrophic interactions. *Journal of Ecology*, 99(1): 57-65.

**Jones, T.H., Thompson, L.J., Lawton, J.H., Bezemer, T.M., Bardgett, R.D., Blackburn, T.M., Bruce, K.D., Cannon, P.F., Hall, G.S., Hartley, S.E., Howson, G., Jones, C.G., Kampichler, C., Kandler, E. & Ritchie, D.A.** 1998. Impacts of rising atmospheric carbon dioxide on model terrestrial ecosystems. *Science*, 280(5362): 441-443.

**Kahane, R., Hodgkin, T., Jaenicke, H., Hoogendoorn, C., Hermann, M., Hughes, J.D.A., Padulosi, S. & Looney, N.** 2013. Agrobiodiversity for food security, health and income. *Agronomy for Sustainable Development*, 33(4): 671-693.

**Kelleher, C. T., de Vries, S.M.G., Baliuckas, V., Bozzano, M., Frydl, J., Gonzalez Goicoechea, P., Ivankovic, M., Kandemir, G., Koskela, J., Koziol, C., Liesebach, M., Rudow, A., Vietto, L. & Zhelev Stoyanov P.** 2015.

*Approaches to the Conservation of Forest Genetic Resources in Europe in the Context of Climate Change*. European Forest Genetic Resources Programme (EUFORGEN). Rome, Bioversity International.

**König, A.O.** 2005. Provenance research: evaluating the spatial pattern of genetic variation. In T. Geburek, J. Turok, eds. *Conservation and Management of Forest Genetic Resources in Europe*, pp. 275-333. Zvolen, Slovakia, Arbora Publishers.

**Konnert, M., Maurer, W., Degen, B. & Kätzel, R.** 2011. [Genetic monitoring in forests - early warning and controlling system for ecosystemic changes](#). *iForest*, 4:77-81.

**Koskela, J., Vinceti, B., Dvorak, W., Bush, D., Dawson, I., Loo, J., Kjær, E.D., Navarro, C., Padolina, C., Bordács, S., Jamnadass, R., Graudal, L. & Ramamonjisoa, L.** 2014. Use and transfer of forest genetic resources: A global review. *Forest Ecology and Management*, 333: 22-34.

**Lande, R. & Barrowclough, G.** 1987. Effective population size, genetic variation, and their use in population management. In M.E. Soulé, ed. *Viable Populations for Conservation*, pp. 87-123. Cambridge, UK, Cambridge University Press.

**Lane, A. & Jarvis, A.** 2007. [Changes in climate will modify the geography of crop suitability: agricultural biodiversity can help with adaptation](#). Paper presented at ICRISAT/CGIAR 35th Anniversary Symposium "Climate-Proofing Innovation for Poverty Reduction and Food Security", 22-24 November 2007, ICRISAT, Patancheru, India. Accessed 8 March 2010. 12 pp.

**Lara, M.V. & Andreo, C.S.** 2011. [C4 plants adaptation to high levels of CO2 and to drought environments](#). In A. Shanker & B. Venkateswarlu, eds. *Abiotic Stress in Plants-Mechanisms and Adaptations*, pp.415-428. Rijeka, Croatia, InTech.

**Lawrence, E.** 1995. *Henderson's dictionary of biological terms*. New York, John Wiley & Sons Inc. 693p. 11th ed.

**Leroy, G., Besbes, B., Boettcher, P., Hoffmann, I., Capitan, A., & Baumung, R.** 2015. Rare phenotypes in domestic animals: unique resources for multiple applications. *Animal Genetics*, 47(2): 141-153.

**Lobell, D.B., Schlenker, W. & Costa-Roberts, J.** 2011. Climate trends and global crop production since 1980. *Science*, 333(6042): 616–620.

**Lopes, M.S., El-Basyoni, I., Baenziger, P.S., Singh, S., Royo, C., Ozbek, K., Aktas, H., Ozer, E., Ozdemir, F., Manickavelu, A., Ban, T., & Vikram, P.** 2015. Exploiting genetic diversity from landraces in wheat breeding for adaptation to climate change. *Journal of Experimental Botany*, 66(12): 3477-3486.

**Lorenzen, K, Beveridge, M.C.M. & Mangel, M.** 2012. [Cultured fish: integrative biology and management of domestication and interactions with wild fish](#). *Biological Reviews*, 87: 639-660.

- Louwaars, N.P.L., & de Boef, W.S.** 2012. Integrated seed sector development in Africa: a conceptual framework for creating coherence between practices, programs and policies. *Journal of Crop Improvement*, 26(1): 39-59.
- Luedeling, E., Steinmann, K.P., Zhang, M., Brown, P.H., Grant, J. & Girvetz, E.H.** 2011. Climate change effects on walnut pests in California. *Global Change Biology*, 17(1): 228-238.
- Malcolm, J.R., Markham, A., Neilson, R.P. & Garaci, M.** 2002. Estimated migration rates under scenarios of global climate change. *Journal of Biogeography*, 29(7): 835-849.
- Maluszynski, M., Nichterlein, K., Van Zanten, L. & Ahloowalia, B.S.** 2000. [Officially Released Mutant Varieties - The FAO/IAEA Database](#). Plant Breeding and Genetics Section, Joint FAO-IAEA Division. Vienna, International Atomic Energy Agency.
- Mapope, N. & Dakora, F.D.** 2016. N<sub>2</sub> fixation, carbon accumulation, and plant water relations in soybean (*Glycine max* L. Merrill) varieties sampled from farmers' fields in South Africa, measured using <sup>15</sup>N and <sup>13</sup>C natural abundance. *Agriculture, Ecosystems & Environment*, 221: 174-186.
- Martynov, S.P. & Dobrotvorskaya, T.V.** 2006. Genealogical analysis of diversity of Russian winter wheat cultivars (*Triticum aestivum* L.). *Genetic Resources and Crop Evolution*, 53(2): 386-386.
- Mátyás, C.** 2007. What do field trials tell us about the future use of forest reproductive material? In Koskela, J., Buck, A. and Teissier du Cros, E. (Eds), *Climate change and forest genetic diversity: implications for sustainable forest management in Europe*, pp. 53-69. Bioversity International, Rome.
- Maxted, N., Ford-Lloyd, B.V., Kell, S.P., Iriondo, J.M., Dulloo, M.E. & Turok, J., (eds).** 2008. *Crop Wild Relative Conservation and Use*. Wallingford, UK, CABI Publishing.
- Maxted, N. & Kell, S.** 2009. [Establishment of a Global Network for the In Situ Conservation of Crop Wild Relatives: Status and Needs](#). CGRFA Background Study Paper No. 39. Commission on Genetic Resources for Food and Agriculture. Rome, FAO.
- Mba, C.** 2013. Induced mutations unleash the potentials of plant genetic resources for food and agriculture. *Agronomy*, 3(1): 200-231.
- Mba, C., Guimaraes, E.P., & Ghosh, K.** 2012. Re-orienting crop improvement for the changing climatic conditions of the 21st century. *Agriculture & Food Security*, 1:7.
- McGuire, S. & Sperling, L.** 2013. Making seed systems more resilient to stress. *Global Environmental Change*, 23(3): 644-653.
- McLachlan, J.S., Clark, J.S. & Manos, P.S.** 2005. Molecular indicators of tree migration capacity under rapid climate change. *Ecology*, 86(8): 2088-2098.

**McSweeney, C.S., & Mackie, R.** 2012. *Micro-organisms and ruminant digestion: State of knowledge, trends and future prospects*. Commission on Genetic Resources for Food and Agriculture. CGRFA Background Study Paper No. 61. Rome, FAO.

**MEA.** 2005. [\*Ecosystems and Human Well-being: Biodiversity Synthesis\*](#). A Report of the Millennium Ecosystem Assessment. Washington, DC, World Resources Institute.

**Mocali, S., Paffetti, D., Emiliani, G., Benedetti, A. & Fani, R.** 2008. Diversity of heterotrophic aerobic cultivable microbial communities of soils treated with fumigants and dynamics of metabolic, microbial and mineralization quotients. *Biology and Fertility of Soils*, 44(4): 557-569.

**Muchugi, A., Lengkeek, A., Kadu, C., Muluvi, G., Njagi, E. & Dawson, I.** 2006. Genetic variation in the threatened medical tree *Prunus africana* in Cameroon and Kenya: implications for current management and evolutionary history. *South African Journal of Botany*, 72(4): 498-506.

**Muchugi, A., Muluvi, G.M., Kindt, R., Kadu, C.A.C., Simons, A.J., & Jamnadass, R.H.** 2008. Genetic structuring of important medicinal species of genus *Warburgia* as revealed by AFLP analysis. *Tree Genetics & Genomes*, 4(4): 787-795.

**Nash, C.E.** 2011. *The History of Aquaculture*. Hoboken, USA, Wiley-Blackwell.

**Nass, L.L. & Paterniani, E.** 2000. Pre-breeding: a link between genetic resources and maize breeding. *Scientia Agricola*, 57(3): 581-587.

**Neale, D.B. & Kremer, A.** 2011. Forest tree genomics: growing resources and applications. *Nature Reviews Genetics*, 12(2): 111-122.

**Nellemann, C., Hain, S. & Alder, J. (eds).** 2008. *In dead water, merging of climate change with pollution, overharvest and infestations in the world's fishing grounds*. Arendal, Norway, UNEP Rapid Response Assessment.

**Nyoka, B.I., Ajayi, O.C., Akinnifesi, F.K., Chanyenga, T., Mngómba, S.A., Sileshi, G., Jamnadass, R. & Madhibha, T.** 2011. Certification of agroforestry tree species in Southern Africa: opportunities and challenges. *Agroforestry Systems*, 83: 75-87.

**Ooninx, D.G.A.B., van Itterbeek, J., Heetkamp, M.J.W., van den Brand, H., van Loon, J.J.A. & van Huis, A.** 2010. An exploration on greenhouse gas and ammonia production by insect species suitable for animal or human consumption. *PLoS ONE*, 5(12): e14445.

**Padulosi, S., Bergamini, N. & Lawrence, T., eds.** 2012. [\*On farm conservation of neglected and underutilized species: status, trends and novel approaches to cope with climate change\*](#). Proceedings of an International Conference, Frankfurt, 14-16 June, 2011. Rome, Bioversity International.



- Patterson, D.T., Westbrook, J.K., Joyce, R.J.V., Lingren, P.D. & Rogasik, J.** 1999. Weeds, insects, and diseases. *Climatic Change*, 43(4): 711-727.
- Pecl, G.T., Araújo, M.B., Bell, J.D., Blanchard, J., Bonebrake, T.C., Chen, I.C., Clark, T.D., Colwell, R.K., Danielsen, F., Evengård, B. & Falconi, L.** 2017. Biodiversity redistribution under climate change: Impacts on ecosystems and human well-being. *Science*, 355:6332.
- Petit, R.J. & Hampe, A.** 2006. Some evolutionary consequences of being a tree. *Annual Review of Ecology, Evolution, and Systematics*, 37: 187-214.
- Pullin, R. & White, P.** 2011. *Climate change and aquatic genetic resources for food and agriculture: state of knowledge, risks and opportunities*. CGRFA Background Study Paper No. 55. Commission on Genetic Resources for Food and Agriculture. Rome, FAO.
- Ramirez-Villegas, J., Khouri, C., Jarvis, A., Debouck, D.G., Guarino, L.** 2010. A gap analysis methodology for collecting crop gene pools: a case study with *phaseolus* beans. *PLoS ONE*, 5(10): 13497.
- Ratnam, W., Rajora, O.P., Finkeldey, R., Aravanopoulos, F., Bouvet, J.-M., Vaillancourt, R.E., Kanashiro, M., Fady, B., Tomita, M. & Vinson, C.** 2014. Genetic effects of forest management practices: Global synthesis and perspectives. *Forest Ecology and Management*, 333: 52-65.
- Redden, R.** 2013. New approaches for crop genetic adaptation to the abiotic stresses predicted with climate change. *Agronomy*, 3(2): 419-432.
- Rehfeldt, G.E., Tchebakova, N.M., Parfenova, Y.I., Wykoff, W.R., Kuzmina, N.A. & Milyutin, L.I.** 2002. Intraspecific responses to climate in *Pinus sylvestris*. *Global Change Biology*, 8: 912-929.
- Rezaei, E.E., Gaiser, T., Siebert, S., & Ewert, F.** 2015. Adaptation of crop production to climate change by crop substitution. *Mitigation and Adaptation Strategies for Global Change*, 20(7): 1155-1174.
- Rojas, W., Valdivia, R., Padulosi, S., Pinto, M., Soto, J.L., Alcocer, E., Guzman, L., Estrada, R., Apaza, V. & Bravo, R.** 2009. From neglect to limelight: issues, methods and approaches in enhancing sustainable conservation and use of Andean grains in Bolivia and Peru. pp. 87-117, in: A. Buerkert and J. Gebauer (editors). *Agrobiodiversity and Genetic Erosion*. Contributions in Honor of Prof. Dr Karl Hammer. Supplement 92 to the *Journal of Agricultural and Rural Development in the Tropics and Subtropics*. Kassel University Press GmbH.
- Rosegrant, M.W., Koo, J., Cenacchi, N., Ringler, C., Robertson, R.D., Fisher, M., Cox, C.M., Garrett, K.; Perez, N.D. & Sabbagh, P.** 2014. *Food security in a world of natural resource scarcity: The role of agricultural technologies*. Washington, D.C.: International Food Policy Research Institute (IFPRI).
- Rosenzweig, C., Iglesias, A., Yang, X.B., Epstein, P.R. & Chivian, E.** 2001. Climate change and extreme weather events: implications for food production, plant diseases, and pests. *Global Change and Human Health*, 2(2): 90-104.

- Rubyogo, J.C., Sperling, L., Muthoni, R. & Buruchara, R.** 2010. Bean seed delivery for small farmers in Sub-Saharan Africa: the power of partnerships. *Society and Natural Resources*, 23(4): 285-302.
- Sacande, M. & Berrahmouni, N.** 2016. Community participation and ecological criteria for selecting species and restoring natural capital with native species in the Sahel. *Restoration Ecology*, 24(4): 479-488.
- Sacande, M., Jøker, D., Dulloo, M.E. & Thomsen, K.A. (eds).** 2004. [\*Comparative storage biology of tropical tree seeds\*](#). Rome, International Plant Genetic Resources Institute.
- Savolainen, O., Pyhäjä, T. & Knurr, T.** 2007. Gene flow and local adaptation in trees. *Annual Review of Ecology, Evolution and Systematics*, 38: 595-619.
- Schueler, S., Falk, W., Koskela, J., Lefèvre, F., Bozzano, M., Hubert, J., Kraigher, H., Longauer, R. & Olrik, D.C.** 2014. Vulnerability of dynamic genetic conservation units of forest trees in Europe to climate change. *Global Change Biology*, 20: 1498-1511.
- Shu, Q.Y.** 2009. [\*Induced Plant Mutations in the Genomics Era\*](#). Proceedings of an International Symposium on Induced Mutations in Plants, 11-15 August 2008. Plant Breeding and Genetics Section, Joint FAO-IAEA Division. Vienna, International Atomic Energy Agency. Rome, FAO.
- Singh, Aradhana** (Lead Author); **Lakhdar Boukerrou and Michelle Miller** (Topic Editors). Diversification in agriculture. In: Encyclopedia of Earth. Eds. Cutler J. Cleveland (Washington, D.C.: Environmental Information Coalition, National Council for Science and the Environment). (Published in the Encyclopedia of Earth November 17, 2009; Retrieved (February 22, 2010).
- Singh, U.S., Bari, M.A., Kumar, A., Ismail, A. & Mackill, D.J.** 2010. [\*Status of Stress Tolerant Rice in South Asia\*](#). Proceedings of the Workshop on Public and Private Participation in the Development and Adoption of Stress Tolerant Rice Varieties in the coastal region of Bangladesh. Organised by the International Finance Corporation and South Asia Enterprise Development Facility, Dhaka, 19 August 2009.
- Smith, P., Bustamante, M., Ahammad, H., Clark, H., Dong, H., Elsiddig, E.A., Haberl, H., Harper, R., House, J., Jafari, M., Masera, O., Mbow, C., Ravindranath, N.H., Rice, C.W., Robledo Abad, C., Romanovskaya, A., Sperling, F., & Tubiello, F.** 2014. [\*Agriculture, Forestry and Other Land Use \(AFOLU\)\*](#). In O. Edenhofer, R. Pichs-Madruga, Y. Sokona, E. Farahani, S. Kadner, K. Seyboth, A. Adler, I. Baum, S. Brunner, P. Eickemeier, B. Kriemann, J. Savolainen, S. Schlömer, C. von Stechow, T. Zwickel & J.C. Minx, eds. *Climate Change 2014: Mitigation of Climate Change. Contribution of Working Group III to the Fifth Assessment Report of the Intergovernmental Panel on Climate Change*. Cambridge, UK, and New York, USA, Cambridge University Press.
- Smock, L.A., Smith, L.C., Jones, J.B. Jr. & Hopper, S.M.** 1994. Effects of drought and a hurricane on a coastal headwater stream. *Archiv für Hydrobiologie*, 131: 25-38.
- Snook, L., Dulloo, M. E., Jarvis, A., Scheldeman, X. & Kneller, M.** 2011. Crop germplasm diversity: the role of

gene bank collections in facilitating adaptation to climate change. Chapter 25. In S.S Yadav, R. Redden, J.L. Hatfield, H. Lotze-Campen and A. Hall, eds. *Crop Adaptation to Climate Change*. John Wiley & Sons, Inc.

**Sperling, L., Ashby, J.A., Smith, M.E., Weltzien, E. & McGuire, S.** 2001. A framework for analyzing participatory plant breeding approaches and results. *Euphytica*, 122(3): 439-450.

**Sperling, L., Boettiger, S. & Barker, I.** 2014. [Integrating seed systems](#). *Planning for Scale Brief*, 3.

**Stella, A. (on behalf of the NEXTGEN and ADAPTmap consortia).** 2010. [Insights into the interactions of goat breeds and their environments](#). Proceedings of the 10th World Congress of Genetics Applied to Livestock Production. Vancouver, Canada.

**TAC Secretariat.** 2001. [Systemwide review of breeding methodologies in the CGIAR](#). Technical Advisory Committee (TAC) of the Consultative Group on International Agricultural Research (CGIAR).

**Tang, J., Xu, L., Chen, X. & Hu, S.** 2009. Interaction between C4 barnyard grass and C3 upland rice under elevated CO<sub>2</sub>: impact of mycorrhizae. *Acta Oecologica*, 35(2): 227-235.

**Tester, M. & Langridge, P.** 2010. Breeding technologies to increase crop production in a changing world. *Science*, 327(5967): 818-822.

**Thomas, C.D., Cameron, A., Green, R.E., Bakkenes, M., Beaumont, L.J., Collingham, Y.C., Erasmus, B.F.N., Ferreira De Siqueira, M., Grainger, A., Hannah, L., Hughes, L., Huntley, B., Van Jaarsveld, A.S., Midgley, G.F., Miles, L., Ortega-Huertas, M.A., Peterson, A.T., Phillips, O.L. & Williams, S.E.** 2004. Extinction risk from climate change. *Nature*, 427: 145-148.

**Thormann, I., Parra-Quijano, M., Rubio-Teso, M.L., Endersen, D.T.F., Dias, S., Iriondo, J.M. & Maxted, N.** 2016. Predictive characterization methods for accessing and using CWR diversity. In N. Maxted. *et al* (eds). *Enhancing Crop Genepool Use: Capturing Wild Relative and Landrace Diversity for Crop Improvement*. CABI p. 64-77.

**Tripp, R.** 2001. *Seed provision & agricultural development: the institutions of rural change*. London, Overseas Development Institute (ODI). 182 pp.

**Waage, J.** 2007. [The sustainable management of biodiversity for biological control in food and agriculture: status and needs](#). Commission on Genetic Resources for Food and Agriculture. CGRFA Background Study Paper No. 38. Rome, FAO.

**Westengen, O.T. & Brysting, A.K.** 2014. Crop adaptation to climate change in the semi-arid zone in Tanzania: the role of genetic resources and seed systems. *Agriculture & Food Security*, 3:3.

**Westengen, O.T., Jeppson, S. & Guarino, L.** 2013. Global ex-situ crop diversity conservation and the Svalbard

Global Seed Vault: assessing the current status. *PLoS ONE*, 8(5): e64146.

**Wilhelm, E.** 2005. Micro- and macropropagation of forest trees. In T. Geburek, & J. Turok, eds. *Conservation and Management of Forest Genetic Resources in Europe*, pp. 623-650. Zvolen, Slovakia, Arbora Publishers.

**Witcombe, J.R., Joshi, A., Joshi, K.D. & Sthapit, B.R.** 1996. Farmer participatory crop improvement. I. Varietal selection and breeding methods and their impact on biodiversity. *Experimental Agriculture*, 32(4):445-460.

**World Economic Forum.** 2010. [\*Realizing a New Vision for Agriculture: A roadmap for stakeholders\*](#). Geneva, Switzerland.

**Yamamura, K. & Kiritani K.** 1998. A simple method to estimate the potential increase in the number of generations under global warming in temperate zones. *Applied Entomology and Zoology*, 33(2): 289-98.