



Agrobiodiversity and Plant Genetic Resources

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Abstract

The science of agrobiodiversity has emerged during the last 10 years. Here we review the most important aspects related to plant genetic resources. The term plant genetic resources (PGR) was coined in 1959, and since then it developed very fast and was one of the most successful programmes for collecting, maintaining, evaluating and use of landraces of cultivated plants ("plant genetic resources movement", Pistorius 1997) which have been threatened by genetic erosion.

To enlarge the basis of agricultural and horticultural resources for human nutrition and other uses including animal nutrition, a sustainable use of these native resources is necessary. With the emergence of agrobiodiversity, new elements come into consideration especially concerning species diversity and ecosystem diversity, whereas genetic diversity was traditionally considered by crop specialists. The total number of species cultivated as agricultural and horticultural crops is estimated at almost 7000. However, only 30 major crops "feed the world". Six million plant accessions are conserved in genebanks worldwide and all these accessions belong to a very limited number of species. About half of them are cultivated cultivars or breeders' lines. Minor and underutilized species are underrepresented in these collections.

Emerging issues in agrobiodiversity led to changes in the plant genetic resources approach, thus resulting in a paradigm shift. The new practical issues coming out of the Convention of Biological Diversity (CBD, 1992) resulted in a "harmonization" process, which modified the former Undertaking on Plant Genetic Resources (1984) into the International Treaty of Plant Genetic Resources" (ITPGR, 2001).

Keywords: Agrobiodiversity, genetic resources, cultivated plants, species diversity, ecosystem diversity.

تنوع زیستی کشاورزی و ذخایر ژنتیکی گیاهی

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چکیده

علم تنوع زیستی کشاورزی در دهه گذشته شکل گرفته است. این مقاله مروری است بر مهم‌ترین جنبه‌های این علم که به ذخایر ژنتیکی گیاهی مربوط می‌شود. اصطلاح ذخایر ژنتیکی گیاهی برای نخستین بار در سال ۱۳۳۸ به کار رفت. این علم از آن زمان به سرعت توسعه یافت و به یکی از موفق‌ترین برنامه‌ها برای جمع‌آوری، حفاظت، ارزیابی و استفاده از ارقام محلی گیاهان کشاورزی که در معرض خطر فرسایش ژنتیکی قرار داشت، میل شد. به منظور توسعه پایه‌های ذخایر کشاورزی و باغبانی برای تغذیه بشر و دیگر کاربردها نظیر تغذیه حیوانات، لازم است تا از این ذخایر اصلی استفاده پایدار به عمل آید. در حالی که تنوع زیستی ژنتیکی به صورت سنتی مورد توجه متخصصان علوم گیاهی بوده، با پدید آمدن تنوع زیستی کشاورزی افق‌های نوینی به ویژه در مورد تنوع گونه‌ای و اکوسیستم به وجود آمده است. اگر چه تعداد کل گونه‌های مورد استفاده در کشاورزی و باغبانی حدود ۷۰۰۰ گونه برآورد شده است، اما فقط ۳۰ گونه گیاهی بیشترین کاربرد را در تغذیه جامعه بشری دارند. حدود ۶ میلیون گونه گیاهی در بانک‌های ژن دنیا نگهداری می‌شوند که اغلب آن‌ها به معنوی از گیاهان زراعی محدود می‌شوند. در حدود نیمی از آن‌ها را وارته‌های کشاورزی یا لاین‌های اصلاح شده تشکیل می‌دهند. گیاهان کمتر استفاده شده، ارقام و وارته‌های محلی به‌ویژه از مراکز پیدایش، درصد بسیاری از نمونه‌های موجود در بانک ژن را تشکیل می‌دهند. امروز فقط یک سوم از نمونه‌های موجود در بانک ژن‌ها به صورت کامل مورد ارزیابی قرار گرفته‌اند.

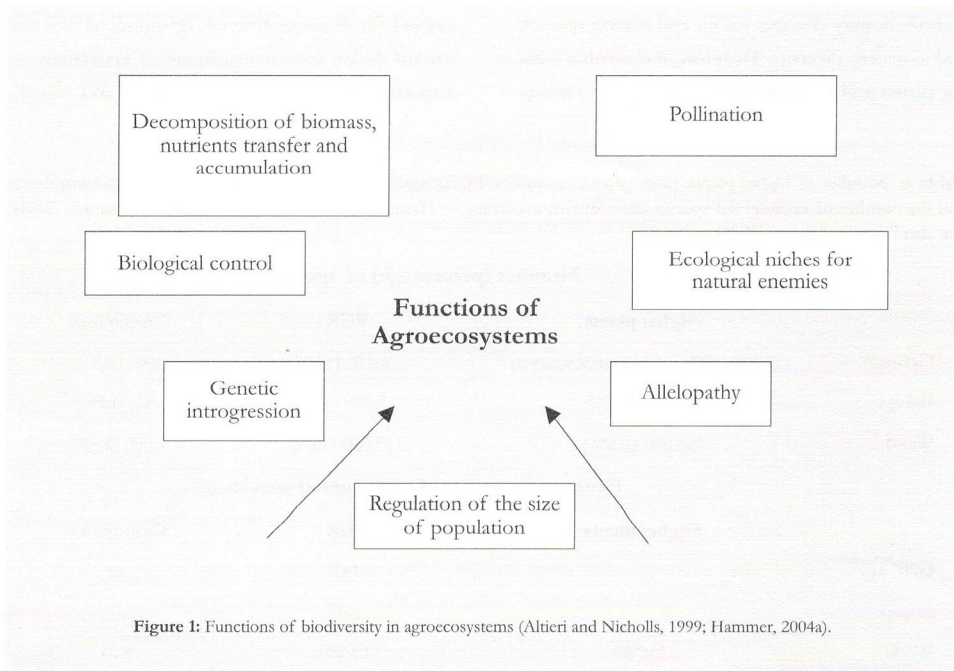
کلیدواژه‌ها: تنوع زیستی کشاورزی، ذخایر ژنتیکی، گیاهان زراعی، تنوع گونه‌ای، تنوع اکوسیستم.

Introduction

Agrobiodiversity includes all crops and livestock, wild relatives, interacting species-pollinators, symbionts, pests, parasites, predators, and competitors (Qualset *et al.*, 1995). It is a new discipline that has recently developed from a synthesis of biodiversity research and the genetic resources approach.

Whereas the term biodiversity was coined at a symposium (National Academy of Sciences, National Forum on BioDiversity) held in the USA in 1986 (Barthlott *et al.*, 1999), the earliest publication mentioning the term agrobiodiversity was not published until 8 years later (Brookfield and Padoch, 1994) following the Convention on Biological Diversity (CBD, 1992). Later on, the term was used by many others from 1995 onwards (e.g. Almekinders *et al.*, 1995; Anon. 1995; Qualset *et al.*, 1995; Hardon 1996; Swaminathan Research Foundation, 1996).

Soon after this, the first large-scale research was reported (Hammer, 1998; Thrupp, 1998; Collins and Qualset, 1999; Wood and Lenné, 1997, 1999). As with the literature on biodiversity (Abe *et al.*, 1997), a strong input for agrobiodiversity came from ecology (e.g. Altieri, 1987). Since biodiversity deals mainly with "numbers and difference" (Gaston, 1996), in this review we try to stress the aspects of agrobiodiversity which are most important for conservation issues (Frankel *et al.*, 1995; Qualset *et al.*, 1995; Altieri, 1989; Brown *et al.*, 1989; Fiedler and Jain, 1992; Frankel and Soulé, 1981; Maxted *et al.*, 1997). Furthermore, the main emphasis is on the diversity of plants, and other components are only referred to peripherally. The relevance of animal genetic resources and differences to the plant sector has been discussed in detail recently (Barker, 2000. See also, Oetmann, 1996). The functions of agrobiodiversity are shown in Figure 1.



There has been a significant loss of diversity during the last 100 years. Unfortunately, the process of extinction and advanced gene erosion continues unabated. Crops, cultivated plants, and their wild relatives (now named plant genetic resources for food and agriculture, PGR, or PGRFA) include all those species that provide food, medicine, fodder for domestic animals, fiber, clothing, shelter, energy, and other uses. Forest plants and ornamentals are not part of this group and are therefore not mentioned in the following tables due to the lack of relevant recent Figures. PGRs comprise 42.5% of the total number of higher species. Crop plants only represent 2.5% of the higher plants (Table 1).

The irreversible loss of cultivated and wild species, the loss of subspecies, landraces, former varieties, "single" genes, and combinations of characteristics during the past 100–150 years is of major concern to gene banks and plant professionals. Polymorphism is the primary source of variation in the morphological and physiological appearance of plants. This leads to evolutionary changes within and among species, and to genetic diversity. Therefore, it presents a basis for plants and animals to adapt actively to varying

environmental conditions. Diversity allows them to respond to future challenges.

External factors have rarely been the basis for economic decisions in the past. The further development of agriculture must include more awareness of ecological and environmental concerns. New approaches to the research and management of biodiversity are now required, and new marketing systems should be developed to take them into account. These changes constitute some of the most substantial changes in the biological sciences and can be described as a paradigm shift (Kuhn, 1970; see also Hammer, 2003). In the future, we must come to understand the threats to biodiversity better than we do today, including the consequences of introducing new species and genetically modified organisms (GMOs) into native and cultivated environments. Changes in agricultural practices and land use, disturbance, fragmentation, isolation and pollution of ecosystems also have to be seriously taken into future considerations. A substantial shift toward the conservation of agrobiodiversity, and toward the on-farm management of ecosystems as a special form of *in situ* conservation (FAO, 1996b),

Table 1: Number of higher plants, plant genetic resources (PGR), and crop plants in Germany, Europe, and worldwide and the number of endangered species (assessments according to Hammer, 1998; Hammer *et al.*, 2001, Hammer, 2004a; See also Lucas and Synge, 1996).

Number (percentage) of species of			
	Higher plants	PGR	Crop plants
Germany	3.200 (100% of botanical species)	1.150 (35.9%)	400 (12.5%)
Europe	11.500 (100%)	5.290 (46%)	700 (6.1%)
World	250.000 (100%)	115.000 (46%)	7.000 (2.8%)
Estimated number of endangered species of			
	Higher plants	PGR	Crop plants
Germany	-	142	20
Europe	-	640	67
World	33.730	13.500	940

additionally towards *ex situ* conservation, has to take place, be developed on a larger scale, and become stabilized beyond the experimental stage (Zeven, 1996; Brush, 1989). A similar change can already be observed with regard to the strategies for the most effective study and utilization of *ex situ* plant genetic resource collections (Tanksley and McCouch, 1997). The impact of modern biotechnology on agriculture, breeding, and agroecosystems should not be underestimated (Callow *et al*, 1997).

PGR and PGRFA

The term PGR (Plant Genetic Resources) and PGRFA (Plant Genetic Resources Food and Agriculture) mirror a breeder's view of plant diversity. Specialized scientific plant breeders have been plying their trade for about 200 years. They took over the most important role and became important donors of new plant varieties. Sometimes they have been considered as the only improvers of the "primitive" farmer's material. This simplistic view overlooks the fact that farmers have grown and carefully selected their "primitive" plants over many generations, for over 10,000 years. The progress made with regard to yield, homogeneity, nutritional value, and other crop characteristics was slow. Because of this slow pace, adaptation to climatic and soil conditions and specific uses was sustainable. Of course, the introduction of new plant material also happened, even from other continents. Many of the local landraces were low-input varieties, and the harvest was relatively stable, even under extreme conditions. Because of the variability between and within the plant populations, the annual harvest was poor compared with that of modern varieties. However, in contrast to modern homogeneous crop varieties, space between the individual plants was well-utilized by companion plants, weeds, and animals. The soil tended to remain fertile, for example, through fallow farming or the simple input of manure as fertilizer. Synthetic chemicals were not utilized for plant

protection. Watering was often limited to kitchen gardens, where vegetables, herbs, and spices were raised. Most field crops, on the other hand, had to be drought-resistant to survive without irrigation. At that time, salinity, soil erosion and allergies were not the major problems that they are today. The combination of these different factors led to an amazing diversity of cultivated plants and domestic animals. In turn, this diversity often protected people from complete loss of the harvest.

One of the primary losses is the diversity of landraces once grown on-farm. This, in turn, has led to an increased establishment of gene banks, so-called *ex situ* collections, which have existed for about 100 years. Their origins are seen in botanical gardens, often associated with colonial development, and later plant breeders considered the specialized collections as a resource for introduced crops and varieties either for direct use by farmers or for indirect use. Genetic erosion was thought to be a more recent concern (Harlan and Martini, 1938; Harlan, 1950). But already E. Baur (1916) discussed the problem of disappearing landraces in view of their use for future plant breeding (see Flitner, 1995). The definition of genetic erosion has been provided by Frankel (1970), see also Brush (1999). Whereas for wild species "extinction" (more information about endangered crop plants is provided by Hammer and Khoshbakht, in print) is the correct technical term (this term has been also used by Baur for crop plants), "genetic erosion" has been chosen as a new term for plants especially for crop plants. Genetic erosion is defined as the loss of traditional landraces caused by the introduction of modern cultivars. It is difficult to measure genetic erosion (Guarino, 1999). Only a few techniques are available for measuring genetic erosion on the basis of morphological characters (Ahn *et al*, 1996, Hammer *et al*, 1996). Molecular methods are used increasingly to solve this problem. The comparison between morphological and molecular results is still under discussion (see Figure 2).

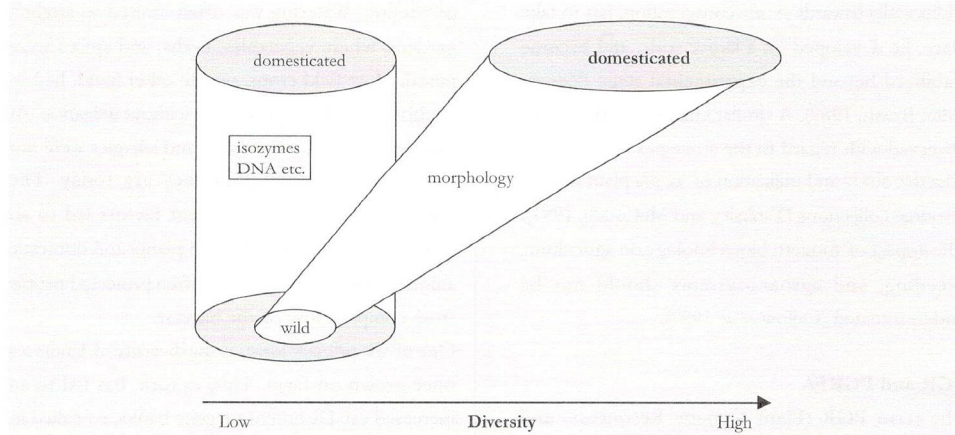


Figure 2: Diagram showing that in morphology a domesticated species is different from its wild ancestor and displays much greater diversity, whereas in isozymes, DNA or other molecular markers the diversity remains much the same. This is also of relevance for measuring of genetic erosion - disappearing of old landraces, which are displaced by modern varieties (after Lester and Daunay, 2003).

Nowadays we have also lost the close relationship between plants and culture (see also Szabó, 1996 on ethnobiodiversity). The value of plants in commercial farming is now automatically reduced to the market value of a current-season crop. There is no space allowed in the fields for weeds, and there is no recognized use for fallow land. Seed is not saved from each harvest, and the evolution and development of plant varieties has been turned over to specialists, to plant breeders. But even they have been subject to a dramatic decrease in their numbers in recent years. Will modern techniques compensate for the loss of evolutionary options?

From the viewpoint of a cultivated plant species or a plant population, the lower its market value, the better chances it has of being maintained and used by farmers instead of breeders. Farmers sometimes maintain dominant crops, and underutilized or neglected crops are in danger of being lost forever (Hammer *et al.*, 2001). If breeders work with one species and its relatives, then the space left over for all other species decreases dramatically. Before genome research and genetic engineering were established, PGRs belonged, according to Harlan and de Wet

(1971), to the primary or to the secondary gene pool of the species in question. Living beings and viruses might be included in a tertiary gene pool. This pool is now being enlarged almost infinitely with new developments and application of new techniques. This third gene pool is generally used as source for establishing "new", i.e., transgenic crops. The existence of a fourth gene pool should also be considered, composed of organisms or organismoids. These are combinations of organisms, or parts of organisms, with components of artificial origin, not occurring in nature, or at least not in that concrete combination: for example, synthetic proteins, nucleic acids, incorporated instruments from the IT branch or other developing technologies, up to complete organisms like constructed machines (see Gladis and Hammer (2000) for a more in-depth discussion). These organismoids have cells or celloids containing partly or completely synthetic strains, with nucleic acids, i.e., DNA or RNA, at frequencies that do not occur in nature. These are incorporated into chromosomes or organelles of living animals and plants for future animal and crop design (see Figures 3 and 4).

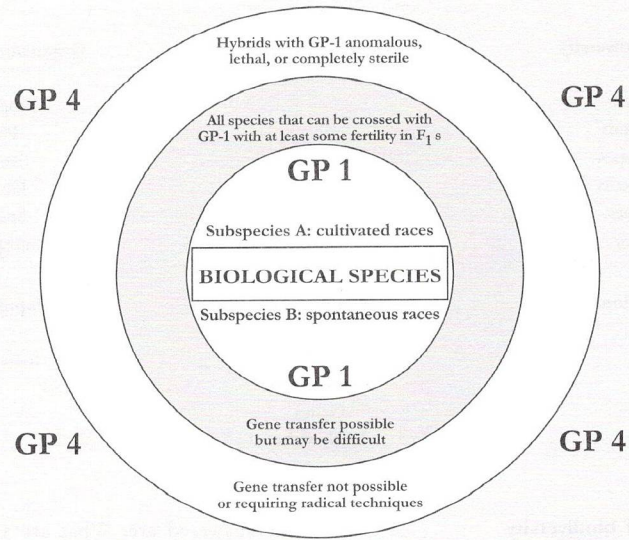


Figure 3: The gene pool concept, established by Harlan and de Wet (1971), modified. *GP 1* The biological species, including wild, weedy and cultivated races. *GP 2* All species that can be crossed with GP 1, with some fertility in individuals of the F_1 generation; gene transfer is possible but may be difficult. *GP 3* Hybrids with GP 1 do not occur in nature; they are anomalous, lethal, or completely sterile; gene transfer is not possible without applying radical techniques. *GP 4* Any synthetic strains with nucleic acid, i.e., DNA or RNA, frequencies that do not occur in nature (after Hammer *et al.*, 2003).

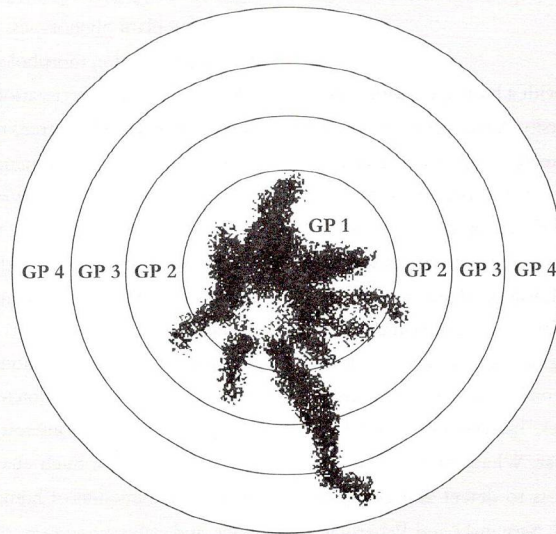


Figure 4: Example of an organismoid or a hypothetically designed crop with a genome composed of different gene pools and synthetic genes [for the explanation of this complicated matter, see Gladis and Hammer (2000)] (after Hammer *et al.*, 2003).

Table 2: The three levels of biological diversity (after Heywood and Watson, 1995; Hammer, 2004a).

Ecological diversity	Genetic diversity	Organismic diversity
Biomes		Kingdoms
Bioregions		Phyla
Landscapes		Families
Ecosystems		Genera
Habitats		Species
Niches		Subspecies
Populations	Populations	Populations
	Individuals	Individuals
	Chromosomes	
	Genes	
	Nucleotides	

The three levels of biodiversity

The three main levels of biodiversity are considered to be genetic (intraspecific) diversity, organismic (species) diversity, and ecosystem diversity (Heywood, 1995; Wilson, 1988). Using these levels, we can present an analytical approach for agrobiodiversity. They meet at the level of populations (see Table 2).

Genetic diversity

It seems logical to start with a basic level within the scientific field of biodiversity. A number of methods are available to us for analysing genetic diversity. Since each of these provides different types of information, the choice of the appropriate method depends upon the information required, as well as the resources and technological infrastructure available. Diversity can be studied, measured, and quantified at different organizational levels and these, in turn, can be researched on several levels: ecosystem, plant sociology, species, intraspecific, cellular, subcellular, or molecular. Whatever the level of analysis is, the purpose is to detect and quantify diversity (Hawkes, 1983; Serwinski and Faberová, 1999; Ahokas and Manninen, 2000; Diederichsen and Hammer, 2003). Some of the basic questions to

be answered are: What are suitable units for quantifying diversity at the respective levels? What kind of variation should be investigated? For research on cultivated plants and for the utilization of the diversity of plant genetic resources for food and agriculture, measurements of the extent of variation (i.e. polymorphism,) can easily be made by observing plant phenotypes. If clear-cut qualitative traits such as color, morphology, or enzyme variants are used for characterization, genetic diversity is reflected to a high degree, relatively independent from environmental influences. A more technical approach is needed to analyze genetically complex, quantitative traits that vary widely. These include agronomic traits, such as yield or plant height, which are more typical for evaluation data in the PGR context.

Morphological and agronomic characteristics are often used for basic characterization, because this information is of high interest to users of the genetic diversity of PGR. Such characterization requires considerable amounts of human labor, organizational skills, and elaborate systems for data documentation although it can be carried out by using simple techniques and can reach a high sample throughput.

This data is not only interesting for users of PGR collections, but also allows for interpretation of relationships between the genotype and environmental conditions. Conclusions can be reached on the evolutionary response of the given species to selection pressures. This is essential for understanding the evolutionary pathways of cultivated plants. Taxonomical treatments of infraspecific variation tend to favor qualitative traits in their analysis of diversity. The species is usually considered as the basic unit of taxonomy. Breeders, however, focus on the infraspecific level and on quantitative traits in order to reach their breeding goals. Quantitative agronomic traits can be used to measure the differences between individuals and populations with regard to genetically complex issues such as yield potential and stress tolerance. The diversity of a population, considering such complex issues, can be described by using its mean value and genetic variance in statistical terms. The traits detected are of great interest, but are frequently subject to strong environmental influence, which makes their use as defining units for the measurement of genetic diversity problematic. Formal taxonomical classifications are not based on such characteristics, while informal classifications used in agriculture are frequently based on such traits.

The major advantage of using molecular methods for characterization is their direct investigation of the genotypic situation, which allows them to detect variation at the DNA level, thereby excluding all environmental influences. They can also be employed at very early growth stages. The advantages and disadvantages of some commonly used molecular techniques for characterization of PGR are summarized in Hammer (2004a). Taking the chosen method into account, they are very sensitive to any genetic differences and therefore detect much more genetic diversity than the classical morphological methods. Molecular marker techniques have become powerful and accurate tools for the analysis of genetic diversity.

If molecular markers can be correlated to interesting characteristics in breeding programs, they are invaluable, helping to accelerate breeding progress considerably. In some cases, molecular markers (quantitative trait *loci*) have been found for quantitatively interesting traits in plant breeding. Tanksley and McCouch (1997) state: "New findings from genome research indicate that there is tremendous genetic potential locked up in seed banks that can be released only by shifting the paradigm from searching for phenotypes to searching for superior genes with the aid of molecular linkage maps."

The tendency to use molecular marker techniques exclusively to assess diversity has already marginalized other methods used for this purpose. Nevertheless, markers are useful tools in characterizing plant genetic diversity, and in particular PGR, not only on a molecular level. They help to develop scientifically enhanced units for the measurement of genetic diversity. The classical infraspecific taxa have traditionally been the first step for establishing a comprehensive system (see Table 3). Further information from molecular research can then be added to these systems. A broad approach is required in order to analyse diversity and to support the conservation, management, and development of plant genetic resources. Better methods for the quantification of biological diversity are essential in order to describe diversity and to get a clear picture of ongoing gene erosion.

Organismic diversity

We have abundant (although not sufficient) knowledge about the most important world crops (see Table 4). These species provide more than 90% of human nutrition, including calories, protein, vitamins, and other essential components of our food and that of our domestic animals. Therefore, modern plant breeding and molecular biology attempt to guarantee food security, for example in the field of plant

Table 3: Matrix of the signs of infraspecific variability of einkorn, *Triticum monococcum* convar. *monococcum* (according to Szabó and Hammer, 1996. See also Filatenko *et al*, 1999).

1	2	3	4	5	6	7	8	9	
X				X		X			<i>var. monococcum</i>
					X	X			<i>var. tauricum</i>
	X			X		X			<i>var. flavescens</i>
	X				X	X			<i>var. pseudoflavescens</i>
			X		X	X			<i>var. sofiarum</i>
X				X			X		<i>var. macedonicum</i>
X					X		X		<i>var. pseudomacedonicum</i>
	X			X			X		<i>var. vulgare</i>
	X				X		X		<i>var. atriaristatum</i>
		X			X		X		<i>var. symphaeropolitanum</i>
			X		X		X		<i>var. nigricultum</i>
X				X				X	<i>var. bobensteinii</i>
	X			X				X	<i>var. bornemanii</i>
	X				X			X	<i>var. pseudobornemanii</i>

Table 4: Thirty crops with the highest number of accessions in *ex situ* collections (according to FAO, 1996a. See also Harlan, 1995).

Crop	Total accessions world-wide	Crop	Total accessions world-wide
Wheat (<i>Triticum</i>)	784,500	Chickpea (<i>Cicer</i>)	67,500
Barley (<i>Hordeum</i>)	485,000	<i>Prunus</i>	64,500
Rice (<i>Oryza</i>)	420,500	Clover (<i>Trifolium</i>)	61,500
Maize (<i>Zea</i>)	277,000	<i>Capsicum</i>	53,500
Garden bean (<i>Phaseolus</i>)	268,500	Cotton (<i>Gossypium</i>)	49,000
Oat (<i>Avena</i>)	222,500	Grape (<i>Vitis</i>)	47,000
Soybean (<i>Glycine</i>)	174,500	<i>Triticale</i>	40,000
<i>Sorghum</i>	168,500	Alfalfa (<i>Medicago</i>)	33,000
<i>Brassica</i>	109,000	Sweet potato (<i>Ipomoea</i>)	32,000
Apple (<i>Malus</i>)	97,500	Potato (<i>Solanum tuberosum</i>)	31,000
Millet (<i>Eleusine, Panicum</i>)	90,500	Fava bean (<i>Vicia faba</i>)	29,500
Cowpea (<i>Vigna</i>)	85,500	Sunflower (<i>Helianthus</i>)	29,500
Groundnut (<i>Arachis</i>)	81,000	Lupin (<i>Lupinus</i>)	28,500
Tomato (<i>Lycopersicon</i>)	78,000	Cassava (<i>Manihot</i>)	28,000
Pea (<i>Pisum</i>)	72,000	Rye (<i>Secale</i>)	27,000

Table 5: Number of plant species cultivated for food and agriculture according to different inventories published in the 20th century (see Hammer, 1995).

Source	Year	Number of species	
		Reported number	Estimated total number
Mansfeld, 1st edn	1959	1,430	1,700–1,800
Vul'f (before 1941)	publ 1987	2,288	–
Vul'f and Malceva	1969	2,540	–
Mansfeld, 2nd edn ^a	1986	4,800	–
Mansfeld, 3rd edn ^b	2001	–	>6,000
General estimation	2001	–	7,000

^a Schultze-Motel, 1986

^b Hanelt and IPK, 2001

breeding, by the development of better resistance against disease in higher yielding varieties. They also try to compensate for shortfalls in the nutrition of a rapidly growing human population. Conservation of diversity has always received attention because it contributes to food quality and to the diversification of food products. However, the total number of species employed by humans is much larger than just 30: estimates suggest that there are almost 7,000 botanical species (Table 5).

The number of PGR accessions in *ex situ* collections worldwide is estimated at 6.1 million accessions (FAO, 1996a; see Table 6).

The 30 species listed in Table 4 represent 4,036,000 of these 6 million accessions. We cannot attempt to make an accurate estimate of the number of accessions maintained on farms and in gardens. Above and beyond this, there are almost no methods of monitoring the process of evolution within cultivated plants, and their migration with migrating

Table 6. Number of *ex situ* collections and conserved accessions by region (FAO, 1996a).

Region	Gene banks		Accessions	
	Number	%	Number	%
Africa	124	10	353,523	6
Asia	293	22	1,533,979	28
Europe	496	38	1,934,574	35
Near East	67	5	327,963	6
North America	101	8	762,061	14
Latin America and Caribbean	227	17	642,405	12
Total	1,308	100	5,554,505	100
CGIAR			593,191	
Total			6,147,696	

peoples. Because of this, several crop species have been completely ignored by agricultural scientists, as well as by breeders. There is also an unknown rate of duplication within and between these collections. The total number of unique accessions in the collections established to preserve diversity is estimated at only one or two million. Around 40% of all accessions in gene banks belong to the cereal group. More than 1 million accessions are divided among the three main crops: wheat, corn (maize), and rice. Food legumes comprise about 15%. Vegetables, roots, and tubers; fruits; and forage plants each account for less than 10% of global collections (Chang, 1989). Spices, medicinal, aromatic, and ornamental species are generally underrepresented in gene banks, though there have been several welcome proposals to expand their number. One of the main reasons is a general problem with maintaining a number of accessions from these groups. Weeds, wild relatives of cultivated plants, crops which run wild, and introgressions between wild and cultivated material are not sufficiently taken into consideration or collected, despite the fact that they are of the

utmost interest for studying evolutionary processes and plant domestication (Hoyt, 1988; Hammer, 1999). This is demonstrated in Figure 5.

Weeds that have been subjected to coevolution or codomestication with cultivated plants in agroecosystems have also developed a wide range of diversity. Occasionally, they possess potential value for cultivation. They are rarely collected systematically (Hammer, 1985; Hammer *et al*, 1997). There is a significant lack of knowledge about the diversity and geographical distribution of less utilized agricultural species and a real need for more attention to such crops and crop-weed complexes in conservation and utilization programs. Knowledge about the varied species cultivated worldwide for food and agriculture is still increasing. Because of this, the estimated number of species of cultivated plants has also increased considerably. This is revealed in the figures presented in Table 5. Rudolf Mansfeld (1901–1960), the first Director of the Gatersleben gene bank, compiled a dictionary of all the cultivated plants of the world (excluding forest plants and ornamentals because of a lack in time) in 1959, and the manual

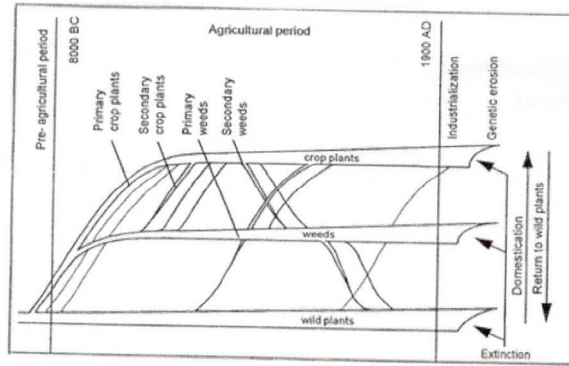


Fig. 5: Plants under human influence. Sources: Gladis (1996a), Hammer *et al*, (1997), Spahillari *et al*, (1999).

has been continuously revised since then. The third edition is now available in book and electronic form, and contains extensive bibliographic notes (Hanelt and IPK, 2001). Schultze-Motel (1966) published a comparable dictionary of forest plants. Ornamental plants still lack a comprehensive treatment (Begemann *et al*, 2001).

It has already been pointed out that taxonomists often neglect utilized and domesticated species. The same has held true for the time of Darwin (1879, cited by Schultze-Motel, 1986). Cultivated plants that have never been documented or described by taxonomists may still be found in developed countries (Gladiš, 1996b, 2002; Hoang *et al*, 1997; Arrowsmith *et al*, 1998). Monographs have been published on neglected and underutilized crop species (see Table 7).

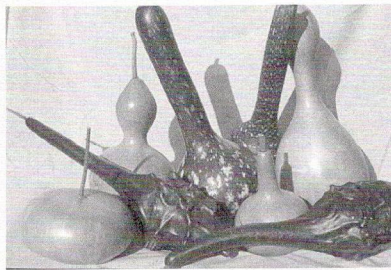


Figure 6a, Photo: Michael Weitz, 2001.



Figure 6b, Photo: Michael Weitz, 2001.

Figure 6: The genetic diversity of different bottle gourds (a) and the species diversity of the squash family (b).

Botanical gardens, apart from their job of keeping and displaying rare and exotic plants over the centuries, and playing an important role in the distribution of important crop species, have only recently begun to recognize plant genetic resources (PGR) as a major concern and have started to develop concepts about how to maintain these resources (Raurer *et al*, 2000). The literature dealing with long-term experience of the management of large *ex situ* collections of cultivated plants has also been widely ignored up until now (see Hammer and Hondelmann, 1997). Not only the limited species diversity of our most important crop plants, but also the genetic diversity indicated by the gene bank accessions per crop can be estimated with the help of Table 5. This is mainly a result of breeding activities.

Figure 6 illustrates the genetic (intraspecific) diversity of different bottle gourds [*Lagenaria siceraria* (Molina) Standl.] (part a) and the species diversity using the example of the squash family (Cucurbitaceae) (part b).

Ecological diversity

"Primitive" agroecosystems are quite similar to natural systems. They are rich in wild species and contain highly variable crops. Farmers try to design optimal growing and reproduction conditions for animals and plants. In Europe, beds for watercress (*Nasturtium officinale*) and cranberries (*Oxycoccus* spp.) or extensively used heaths and moors are good examples of the encouragement of endangered or lost agroecosystems. Nowadays, endangered agroecosystems are managed like endangered nature reserves and are merely protected and extensive grazing with adapted local breeds has occurred there for centuries. This is the best, cheapest, and most sustainable way to maintain or to bring back the former diversity to these areas. In contrast, conditions in modern, industrial farming systems are nearly as homogeneous as the plant varieties and the animal races found at this level. Scientific animal and plant breeding adapts the

Table 7: Monographs published to date on neglected and underutilized cultivated plants in the framework of a IPK/ IPGRI project (according to Hammer *et al*, 2001).

Species	Botanical name	Authors	Year	Pages
Physic nut	<i>Jatropha curcas</i>	J. Heller	1996	66
Yam bean	<i>Pachyrhizus spp.</i>	M. Sorensen	1996	141
Coriander	<i>Coriandrum sativum</i>	A. Diedrichsen	1996	83
Hulled wheats	<i>Triticum spp.</i>	S. Padulosi, K. Hammer and J. Heller, ed.	1996	262
Niger	<i>Guizotia abyssinica</i>	A. Getinet and S. Sharma	1996	59
Pili nut	<i>Canarium ovatum</i>	R. E. Coronel	1996	57
Safflower	<i>Carthamus tinctorius</i>	Li. Dajue and H.-H. Mündel	1996	83
Chayote	<i>Sechium edule</i>	R. Lira Saade	1996	58
Bambara ground	<i>Vigna subterranea</i>	J. Heller, F. Begemann and J. Mushonga, ed.	1997	166
Bread fruit	<i>Artocarpus altilis</i>	D. Ragone	1997	77
Cat's whiskers	<i>Cleome gynandra</i>	J.A. Chweya and N.A. Mnzava	1997	54
Tef	<i>Eragrostis tef</i>	Seyfu Ketema	1997	50
Sago palm	<i>Metrazylon sago</i>	M. Flach	1997	76
Oregano	<i>Origanum spp.</i>	S. Padulosi, ed.	1997	176
Black nightshades	<i>Origanum nigrum</i>	J.M. Edmonds and J.A. Chweya	1997	113
Traditional vegetables	Various species	L. Guarino, ed.	1997	171
Carob tree	<i>Ceratonia siliqua</i>	I. Batlle and J. Tous	1997	92
grasspea	<i>Lathyrus sativus</i>	C. Campbell	1997	92
Buckwheat	<i>Fagopyrum esculentum</i>	C. Campbell	1997	93
Peach palm	<i>Bactris gasipaes</i>	J. Mora-uurpi, J.C. Weber and C.R. Clement	1997	83
Andean root crops:	<i>Arracacia scanthorrbiza</i>	M. Herman and J. Heller, ed.	1997	256
Arracacha, yacon,	<i>Polymnia sonchifolia</i>			
maca and ahipa	<i>Lepidium meyenii</i> and <i>Pachyrhizus ahipa</i>			
Chenopods Asia	<i>Chenopodium album</i>	Tejpartap, B.D. Joshi and N. Galwey	1998	67
Lupines	<i>Lupinus spp.</i>	W. Cowling, B. Buirchell and M. Tapia	1998	105
Aibika	<i>Abelmoschus manibot</i>	S. Preston	1998	97

organisms perfectly to human preferences and requirements. The species develop domesticated characteristics to the highest degree, and they are no longer able to survive under natural conditions. Genetic erosion and erosion in agricultural landscapes are highly intertwined (Hammer *et al.*, 1996; Brush, 1999; Guarino, 1999).

There are still many landraces in areas of agricultural diversity the so called centers of diversity or gene centers according to Vavilov (1926-1997). For these, an on-farm management is urgently necessary (Brush, 1995). The evolutionary power of these and other similar areas has to be maintained.

In Italy specific exploration and monitoring has been carried out over the last 20 years, starting in south Italy with the use of checklists (Hammer, 1991). They allowed the compilation of catalogues summarizing the available information on South, Central and Northern Italy (Hammer *et al.*, 1992 and 1994). In the second phase of this project the small agricultural islands have been also considered and a protection of selected areas was proposed (Hammer *et al.*, 1997). Similar work has been conducted in Albania (Hammer *et al.*, 1994) where the quickly disappearing landraces required emergency action. Such action is also necessary in case of wars endangering large ecosystems and destroying agrobiodiversity (Blom *et al.*, 2000). Often the ecosystems themselves can not be maintained but a collection of the plant genetic resources and their long-term storage in genebanks can provide the basis for a later reconstruction of valuable farms and gardens.

Homegardens as specific local ecosystems turned out to be especially rich in plant genetic resources (Hammer *et al.*, 1992-94; Knüpffer and Hammer, 1999; Watson and Eyzaguirre, 2002). This is true not only for tropical and subtropical areas. A project for examining the role of homegardens is also under way in Iran. In this project relationships between the agroecological and socioeconomic aspects of

homegardens in the north of Iran (Savadkouh area) are studied. Plant diversity was highest for fruits (33 species), followed by vegetables (26 species), pulses (8 species) and finally other crops with 6 species (Khoshbakht *et al.*, in preparation).

Conclusions and outlook

Two important separate issues, i.e., finding and studying minor and underutilized species for germplasm collections and assessing the genetic diversity of landraces, should be given top priority in the field of crop plant research. Though there have been efforts for centuries to increase the study and use of minor and underutilized crops by different players, so far, success has been limited. Will this situation improve in the light of agrobiodiversity? Are the living fields our agricultural heritage (Harlan, 1995)? The discovery, collection, conservation, and identification of potentially valuable but endangered plant genetic resources for food and sustainable agriculture (as well as other plant genetic resources that have potential value for future development) are the primary obligations of all countries and institutions adhering to the FAO International Undertaking on plant genetic resources (Ford- Lloyd and Jackson, 1986; Plucknett *et al.*, 1997). The Global Plan of Action (GPA) for the conservation and sustainable utilization of plant genetic resources for food and agriculture (FAO, 1996b) emphasizes not only *in situ* and on-farm conservation (Esquivel and Hammer, 1988 and 1992; Hammer *et al.*, 1992-94; Hammer, 1994; Chweya, 1994; Brush, 1995; Jarvis and Hodgkin, 1998; Maxted *et al.*, 2002), but also the importance of *ex situ* conservation. The total number of accessions in worldwide collections is very large. However, beyond the problem of duplication among accessions, the security of *ex situ* conservation as a whole is also endangered. About half of all gene bank accessions urgently require rejuvenation, and in several countries the percentage is even higher. Political instability and lack of funds further threaten these collections.

Table 8: Conservation methods for different categories of diversity rated by their importance for specific groups of diversity (based on Hammer, 1998 and 2004a).

Category of diversity	Method of conservation			
	<i>Ex situ</i>	On-farm (agro-ecosystems)		<i>In situ</i>
	(gene banks)	Developing countries	Developed countries	(other ecosystems)
Intraspecific diversity	C**	C***	C**	C ⁰
	R*	R***	R*	R***
	W**	W***	W*	W*
Diversity of species	C*	C***	C**	C ⁰
	R*	R***	R*	R**
	W**	W***	W**	W*
Diversity of ecosystems	C ⁰	C***	C*	C ⁰
	R ⁰	R***	R**	R**
	W ⁰	W***	W***	W*

The number of stars indicates the relative importance of the methods for the various diversity groups: C = crop species, R = wild relatives of crop species, W = weeds.

⁰ = no importance ; * = low importance ; ** = important ; *** = very important

Despite of the numerous accessions of important crop species, it is difficult to identify what proportion of all diversity is actually present in the collections. Diversity is always subject to evolutionary adaptations and changing conditions. Gene banks usually try to exclude these factors as much as possible, avoiding genetic shift and drift during the rejuvenation and long-term conservation of germplasm. Defining three different categories of biological diversity should not result in neglecting the existing marked interactions between these categories. From the viewpoint of plant genetic diversity for food and agriculture, the diversity of (1) cultivated plants, (2) wild relatives of cultivated plants, (3) introgressions between cultivated plants and their relatives, and (4) weeds should be differentiated.

For each of these categories and for each specific

group within these categories, a different strategy for the conservation of biodiversity may be the most appropriate *modus operandi*. Table 8 rates the advantages of each conservation strategy for each category of biological diversity and the specific groups. Complementary action between these strategies is necessary for the work to be effective. This means increased cooperation between departments or institutions. At a time when budgets are generally being cut, it is difficult to argue for such an approach, but the results speak for themselves if the relative superiority of the different conservation methods is taken into consideration (Diederichsen, 1998; see Table 8). A scheme demonstrating the different conservation methods is presented in Figure 7. Table 9 shows the advantages and disadvantages of the different conservation strategies.

Table 9: Strategies for the maintenance of agrobiodiversity (after Frank *et al*, 2000; Hammer, 2004a).

Maintenance method	Advantages	Disadvantages
<i>In situ</i>	<ul style="list-style-type: none"> • Interactions with other species and organisms are possible • Interspecific and infraspecific variations can be combined can also used for vegetative reproducible species or those with recalcitrant seeds (Characterization, Property rights) 	<ul style="list-style-type: none"> • Large area necessary for maintenance • Only a small number of genotypes can be managed this way. Does not protect against epidemics, diseases, etc., possible losses. • Access to the material is difficult
<i>In situ</i> or <i>on farm</i>	<ul style="list-style-type: none"> • Further evolution through natural evolution and choice of varieties is possible 	<ul style="list-style-type: none"> • No conservation of the status quo, selection • Gene erosion is possible
<i>Ex situ</i> Seed banks	<ul style="list-style-type: none"> • Seed (accession) is always available • Catalog • Little space necessary (small seeds) • Genetic status quo of the stored seeds can be maintained with appropriate reproduction strategy 	<ul style="list-style-type: none"> • No further evolutionary development on the surrounding environment • Problems with the maintenance of recalcitrant and vegetatively reproducible species • Large amount of space necessary for storage (large seeds) • The original surrounding flora is not conserved as well • Regeneration needs space and is money and labor intensive • Only a limited portion of the variability is collected and maintained • Change of population structure through reproduction that are too small
Tissue culture	<ul style="list-style-type: none"> • Little space needed • Good for vegetative material and recalcitrant species • Disease minimized 	<ul style="list-style-type: none"> • High technical outlay • Somaclonal variation • Related species are not maintained as well
DNA	<ul style="list-style-type: none"> • Little space needed • Can be used anywhere • Future method of last resort in isolated cases 	<ul style="list-style-type: none"> • Is not a germplasm conservation <i>per se</i>

Ecogeographic surveys of the range of distribution of a species were first implemented by N.I. Vavilov (1926). They are still the basic tool for developing adequate strategies for monitoring and collecting the relevant diversity of a plant species in the context of PGR (Guarino *et al*, 1995). Such studies deliver basic information about (1) the geographic distribution of a particular species, (2) patterns of intraspecific diversity, and (3) the relationship between survival and frequency of variants under specific (agro)ecological conditions. Such studies are essential for understanding the process of domestication and diversification on the intraspecific level of cultivated plant species. The identification of primary and secondary centers of diversity is based on these studies (Sauer, 1993; Harlan, 1971; Davis *et al*, 1994; Myers *et al*, 2000). The number of cultivated plants and domestic animals comprises only a small portion of all known animal and plant species. Within each species, domestication has limited the genetic diversity to useful genotypes, adapted to local conditions.

After the onset of industrialization, the diversity of domestic crops and animals decreased dramatically at the levels of species and intraspecific categories such as subspecies, varieties, and races. At the same time, the need for genetic resources in order to develop new and improved varieties or races increased (and is expected to increase even more in future). *Ex situ* reserve collections are presently limited in their diversity. More attention needs to be given to plant and animal genetic resources (PGR and AGR) in future conservation and utilization programs. Therefore we suggest the establishment of a manual for domesticated animals as a complement to Mansfeld's encyclopedia of agricultural and horticultural crops – excluding ornamentals (Hanelt and IPK, 2001) and to the dictionary of forest plants of the world (Schultze-Motel, 1966).

A review of the strategies for the characterization of existing collections is also necessary. At the same time, various strategies for the most effective conservation of the different categories of diversity

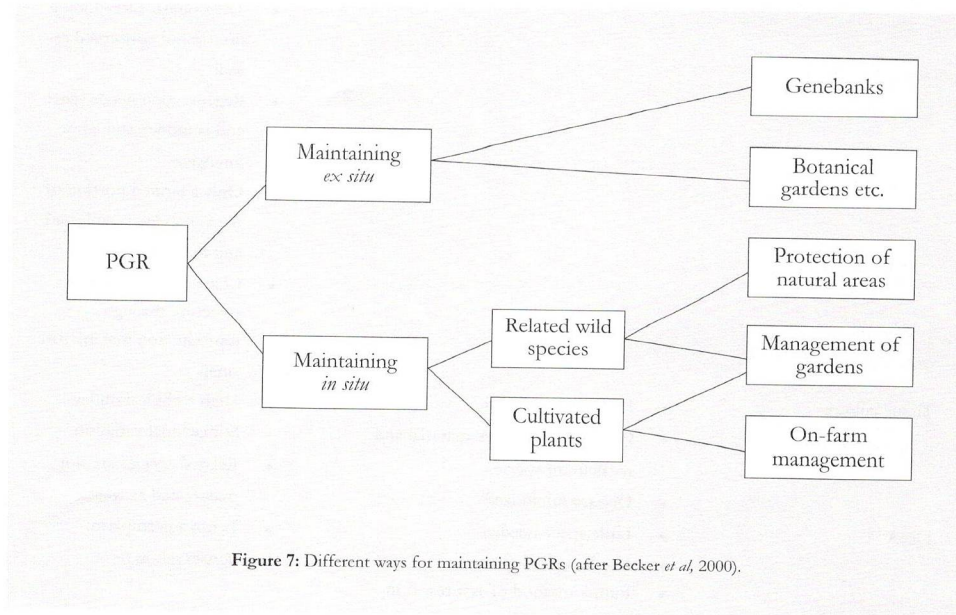


Figure 7: Different ways for maintaining PGRs (after Becker *et al*, 2000).

have to be developed and strengthened. Their relative superiority for the different levels and categories of PGR and AGR have to be recognized in order to allocate better limited financial resources for conservation. Breeders and breeding companies are currently not very interested in using gene bank material in breeding work. It is more time-consuming to make long-distance crosses than to include exotic and well-defined genes into optimised crop genomes. As a result of this, access to, as well as knowledge about, the biodiversity of cultivated plants and domestic animals is decreasing in the developed and developing countries. On the other hand, nongovernmental organizations (NGOs), agricultural institutions, museums, and schools are becoming more interested in this material, interpreting it as living human heritage. With animal and plant genetic resources, the CBD approach of national sovereignty contradicts farmers' and consumers' rights to the living beings providing them with food and clothing (Meyer *et al.*, 1998). The more aware the public becomes about biodiversity losses, the more demand will grow for a broad spectrum of utilized biodiversity. The diversity conserved in the *ex situ* collections of gene banks, botanical and zoological gardens etc., has always been easily accessible to the worldwide community of researchers, breeders, and all other users. Further research into morphological and molecular markers and their application will contribute to the quantification of genetic diversity and gene erosion. Taxonomy has to become more involved in these activities and pays more attention to changing needs in the field of domesticated animals and cultivated plants. There is a pressing need for further study and effort to fill the gaps in present *ex situ* holdings (see Hammer, 1997). This may lead, together with the necessary evolutionary studies (Hammer and Perrino, 1995; Hammer and Schlosser, 1995; Ladizinsky, 1998) to a renaissance of human knowledge in this fascinating field of research and to a new flowering of genetic diversity.

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