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Editorial

Genetic Diversity as a Key to Understanding Physiological and Biochemical Mechanisms

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1. Introduction

Modern agriculture is at the heart of economic and societal functioning for feeding a galloping world population, but also for ensuring a profit for producers, processors, and traders [1]. However, this “balancing act” has reached its limits, not only because of its own objectives (to produce more and more), but also because of current global climatic and geostrategic changes. Indeed, 2022 was the hottest year on record, with such a strong impact on agricultural production that it led, in part, to economic inflation affecting all countries. The heatwaves that occurred in 2022 will recur in the years to come. Therefore, it seems important to rethink our agriculture. As well as reviewing our production systems to reduce greenhouse gas emissions and make better use of essential natural resources, particularly water and soil, in order to achieve the sustainable development goals, set by the United Nations (UN-SDGs), we will need to rethink the way we exploit biodiversity and genetic variability. The genetic breeding of new varieties that has been underway for decades is largely based on “remodelling” elite cultivars. These choices have led to an impoverishment of the genetic bases of these cultivated species. For these reasons, it is vital to put genetic resources and diversity back at the heart of the way knowledge is acquired and used, in a concerted way at the national, regional, and global levels. Consequently, it is becoming clear that the study of genetic variability will not only make it possible to observe genetic, physiological, and biochemical polymorphisms, but also to rethink their rational use for the sustainable management of agrosystems in order to achieve the UN-SDGs (Figure 1). This editorial highlights a collection of scientific work focusing on genetic variability for the examination of complex morphological, physiological, and biochemical traits.



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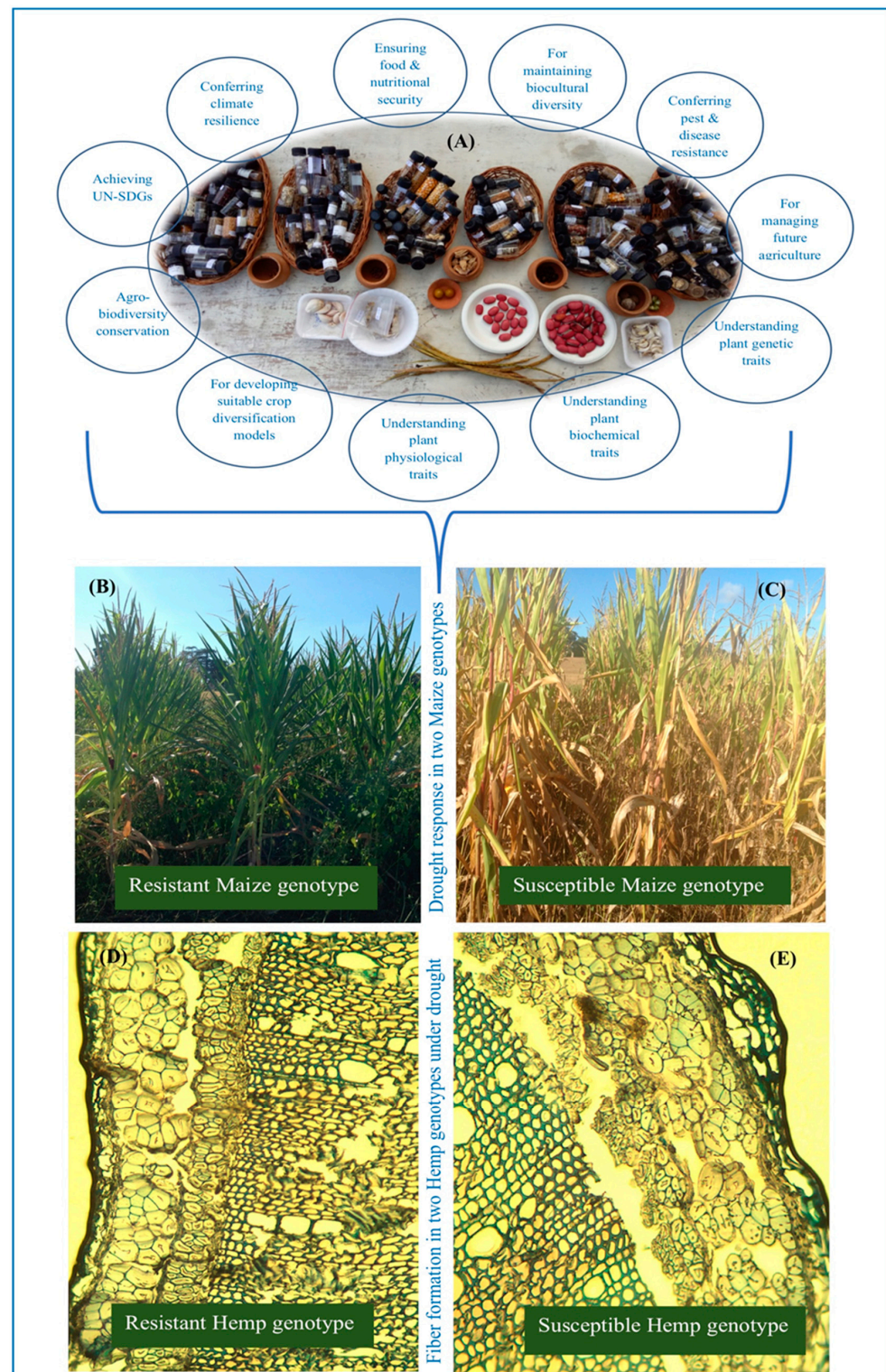


Figure 1. Maintaining plant genetic diversity is not only essential for food production and thereby achieving the associated UN-SDGs, but also imperative to maintaining the biocultural diversity of local people and also for conferring improved traits in crop plants under futuristic climatic conditions. (A) Some of the indicative benefits of maintaining plant genetic diversity such as agrobiodiversity conservation, developing sustainable crop diversification models, and also for understanding the biochemical as well as physiological responses in plants. (B) Drought response in a resistant maize genotype and (C) the response in a susceptible Maize genotype. (D) The fibre formation in a hemp genotype (resistant) in response to drought and (E) the fibre formation in susceptible hemp genotype.

2. To Be or Never to Be

There would have been no findings for the comparison of the inter-species diversity of *Eucalyptus* if these had not been discovered in the study by Andrade et al. [2]. In this work, 15 *Eucalyptus* species were studied for their behaviour in the face of phosphorus (P) deficiency. It appeared that P deficiency increased root exudation. However, the composition profile of the root exudates remained similar between the species in the absence of phosphorus, regardless of its concentration in the soil. These exudates were mainly composed of organic acids, amino acids, and phenols. It emerged that this genetic response mechanism is conserved in *Eucalyptus* genera.

The exploitation of agricultural land has reached a peak. We need to look for new land to cultivate. In some parts of the world, abiotic stresses such as salinity, due to proximity to the sea or anthropisation, or drought considerably limit agricultural cultivation. However, the food needs of populations must be met. The need to understand the mechanisms by which species and/or genotypes adapt is essential.

This study of Ibrahimova et al. [3] assessed the physiological and biochemical responses to salt stress, as well as the regulation of the expression of the K^+/Na^+ -*TaHKT1;5* transporter gene, in two bread wheat genotypes with contrasting tolerances to salinity. The results showed that excess salt led to lipid peroxidation, an accumulation of soluble sugars and proline, an overall decrease in all physiological, biochemical, and enzymatic traits, and an increase in antioxidant enzyme activity in both genotypes. However, there was a contrasting response between the two wheat genotypes. The salinity-tolerant genotype showed higher enzyme activity, soluble sugar, and proline content, and lower osmotic potential and lipid peroxidation than the sensitive genotype [3]. This suggests that the tolerant genotype has a greater osmotic adjustment capacity [4], which enables it to absorb more water [5,6] while maintaining its enzymatic activity [7,8]. This is confirmed by the differences in the expression of the *TaHKT1;5* gene (which codes for selective Na^+ transport) in its leaves in favour of the salinity-sensitive genotype [3] and has been confirmed in recent studies [9,10].

Radzikowska et al. [11] examined the response to drought in six varieties of spelt (*Triticum aestivum* ssp. *spelta*) from different European countries and one variety (Bogatka) of common wheat (*Triticum aestivum* ssp. *vulgare*) in terms of photosynthetic activity, chlorophyll fluorescence, relative water content, and proline and anthocyanin content under well-watered and dry conditions. The results showed that two spelt cultivars showed a greater resistance to water deficit than the common wheat, thanks to a slight drop in CO_2 assimilation, probably due to a drop in their rubisco activity [12], without any reduction in transpiration and a high accumulation of proline and anthocyanins, which could be explained by a significant osmotic adjustment capacity. This capacity, coupled with the activity of the antioxidant defence system and action of the photosynthetic apparatus, could contribute to variations in tolerance to water deficit between spelt wheat cultivars.

Tartary buckwheat (*Fagopyrum tataricum* (L.) Gaertn), a polygonaceae grown in Asia, Europe, and North America, is an important pseudocereal crop used for human nutrition. Despite its importance as a foodstuff, little is known about this species. The aim of the study by Lv et al. [13] was to examine the genotypic diversity of a collection of 31 Tartary buckwheat accessions, analyse the accumulation patterns of ten fatty acids during its seed development, and identify its fatty acid biosynthesis genes. As a result, the oil content varied twice. The fatty acids present were mainly saturated and unsaturated C16 and C18. An examination of the genes in the fatty acid biosynthesis pathway revealed the importance of the *Fatty Acid Desaturase-5* (*FAD5*) enzyme, which is involved in desaturation, in the fatty acid composition of this species, and the differences between accessions as found in two tea varieties [14]. Two excellent accessions of Tartarian buckwheat were identified for their high levels of total flavonoids and fatty acids, and therefore their greater health-promoting value.

Cereals are the most widely produced and consumed food species in the world. They are also the most subject to environmental stresses, which have a major impact on their

production. In order to select the most suitable varieties, we need to know how the morphophysiology of their genotypes' functions under difficult conditions [15]. Seed production and filling are the main purposes of these crops for the production of food flour [16,17]. The study by Islam et al. [18] was in line with this approach. The authors examined the performance of wheat plant height and spike characteristics under late sowing conditions in 327 wheat accessions from various regions of the world. As expected, all morphological characteristics decreased with later sowing dates. Ten varieties showed stable performances at different sowing dates, indicating a good resistance to late sowing (which can be assimilated to water-stressed conditions). The better varieties maintained their physiological functioning in the upper parts of the seed fill, in line with what has already been found in other cereals [19–22], and yielded more [23,24]. The results of this study have laid the foundations for breeding high-yielding wheat varieties resistant to late sowing.

Environmental protection also requires the use of genotypes capable of making better use of mineral resources, particularly nitrogen. For example, the study by Deng et al. [25] examined nine quinoa genotypes with different nitrogen use efficiencies (low, intermediate, and high). To assess their responses, these genotypes were exposed to different doses of nitrogen (0, 0.4, and 0.8 mM). As expected, the absence of nitrogen altered their morphophysiological traits (roots, biomass, chlorophyll, protein content, and sugar content). In addition, the enzymes involved in nitrogen metabolism (nitrate reductase, glutamine synthetase, and glutamate synthetase) were inhibited. The most nitrogen-tolerant genotypes showed a maximum photosystem II efficiency (Fv/Fm), higher root vitality, and higher nitrogen content in comparison to the sensitive genotype. This study also showed that the parameters studied (shoot and root dry biomass, chlorophyll content, nitrogen-metabolising enzymes, and nitrogen content) can be reliable indicators of tolerance to low nitrogen during the first phase of quinoa growth.

3. From Diversity Springs Richness

Lifestyle and stress in society are factors in the deterioration of health. The search for a healthy diet, rich in beneficial natural compounds that are present in food, for better health is important. This is in line with the UN-SDGs (3 and 12). For example, the genus *Cucurbita* is known to be a good source of carotenoids, including β -carotene, which is a precursor of vitamin A.

Barboza et al. [26] evaluated a collection of 23 accessions and 2 commercial varieties of *Cucurbita maxima* for their carotenoid content, β -carotene, and the pulp colour of the accessions. This examination revealed four groups where the total carotenoid content had the greatest influence on their formation. A wide variability was observed for the total carotenoids in the genotypes studied. Some accessions (notably CMAX-10 and CMAX-13) showed the highest levels of total carotenoids and β -carotene, higher than those of the commercial varieties. These accessions from UFERSA's cucurbit germplasm collection could thus be used in selection programmes for biofortification.

Safflower is an oilseed species of economic interest that is adapted to drought [27,28]. It is used for its oil, but also for its flowers as a food-colouring agent (false saffron) [29,30]. However, little is known about the latter interest and this deserved to be examined in the study by Erbaş and Mutlucan [31]. The authors studied 10 genotypes from different geographical origins with different flower colours. The flower and dye yields varied between the genotypes. The results highlighted significant differences in terms of total phenol composition. Yellow flowers had the highest phenol content, while white flowers had the lowest. Gallic, rosmarinic, and chlorogenic acids were present in greater quantities in the genotypes with orange flowers. Red flowers contained more kaempferol. One genotype stood out for all these characteristics: Askon-42.

Díaz-Fernández et al. [32] examined the aromatic profiles of 20 white grape varieties from the Iberian Peninsula over three consecutive vintages. Volatile compounds were obtained using solid-phase microextraction and gas chromatography with mass spectrometry

(SPME-GC-MS). Significant varietal differences were found for the terpenes in the free fraction and for the acids, aldehydes, terpenes, and norisoprenoids in the glycosidically bound fraction. These differences made it possible to distinguish between the grape varieties and make certain groupings of varieties belonging to the same reconstituted genetic populations (RPP). Varietal aromatic profiling appears to be a good chemotaxonomic tool. A more detailed analysis showed that the aromatic profile made it possible to differentiate the varieties more with the free profile than with the glycosidic profile. But what is most interesting is that this aromatic profile method made it possible to bring together certain varieties that belonged to the same genetic–geographical group or the same reconstituted population (RPP) on the basis of their molecular characterisation, thus opening up the prospect of a promising chemotaxonomic approach. It also emerged that, in some cases, there were minor varieties (Branco Lexítimo and Albilla do Avia) included in some of the community’s wine-growing DOMs, or even varieties not included (Fernão Pires) in the community register, used to make quality white wines in Portugal, which could be exploited for their great aromatic potential, richness, and diversity in the geographical area studied, even more so than some other varieties already included in the community’s DOMs.

4. Conclusions

Genetic diversity is the key to unravelling the morphological, physiological, biochemical, and genetic, as well as molecular, traits in plants, thereby enabling the adoption of suitable crop improvement programs for refining the positive traits of existing crop plants and also for breeding climate-smart crops under futuristic climatic conditions. Unfortunately, modern agricultural practices largely based on monocropping practices have resulted in the erosion of genetic diversity from our agricultural landscapes. Therefore, inventive measures are essential for bringing back both genetic and species diversity to our agricultural systems, and various policy measures are urgently needed to conserve genetic diversity for managing agrobiodiversity and also for attaining the food, nutritional, fodder, fuel, and medicinal requirements of the current and future generations. In addition, it is high time to exploit indigenous and local knowledge for conserving plant genetic diversity for the wellbeing of both people and the planet.

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