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Editorial

Special Issue: Plant Genetics and Biotechnology in Biodiversity

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Abstract: The rapid progress and increasing affordability of novel investigation tools in plant genetics and biotechnology offer previously inaccessible opportunities for the exploitation of plant genetic diversity in agriculture. The Special Issue was lunched to highlight how new technologies are improving both genotyping and phenotyping methods, thus allowing us to uncover crop diversity and use genetic variability for plant breeding with remarkable precision and speed. Three thematic reviews report on scientific, technological, and legal advances in plant diversity and agriculture. Three contributions provide specific examples of the exploitation of different kinds of genetic resources, ranging from landraces to mutant populations. Six research articles are illustrative examples of the study of molecular and/or phenotypic diversity to address basic or applied questions in different plant species. Finally, this SI was also launched to honor the memory of Prof. Gian Tommaso Scarascia Mugnozza and a dedicated Editorial acknowledges his work in plant breeding and biodiversity protection.

Keywords: genetic diversity; agro-biodiversity; landraces; crop; breeding; agriculture

The worldwide loss of biodiversity is a concern of increasing importance, and the field of agriculture is no exception. If we only take into account the number of cultivated plant varieties, it is evident that we are witnessing an unprecedented loss of agricultural genetic resources: more than 90 percent of crop varieties have disappeared from farmers' fields in less than a century [1]. The rise of intensive farming is arguably the major driver of agro-diversity loss. This system of cultivation is virtually a "technological standard" in many industrialized economies and also essential to support a rapidly increasing world population. Input-intensive agricultural systems benefit from uniformity and, in every setting, they associated with a rapid displacement of "traditional" crops and livestock. Industrial agriculture proved to be effective in supplying a large variety of affordable and abundant food, yet its multiple negative consequences (e.g. biotic and abiotic stress vulnerability, dependence on chemicals, yield stagnation, habitat degradation, decreasing profits for small farm-based communities, etc.) have largely remained unaddressed. In addition, the loss of agricultural diversity irredeemably reduces the options and resources for long-term sustainability and prosperity.

Agriculture is an indispensable element in the food production of any economy, and therefore should contribute to both conservation and the sustainable use of biodiversity. If necessary, this goal should be pursued beyond the constraints imposed by the profit motive. There is a growing consensus that whenever a reliable and safe food supply is guaranteed, intensive agricultural systems should move towards more diversified agro-ecological production systems. Reducing the use of off-farm chemical inputs, safeguarding biodiversity, and stimulating beneficial interactions between different species are all part of an integrated strategy that includes a more profitable exploitation of plant genetic diversity, and, in the narrower sense, the use of already existing or improved landraces.

For instance, landraces can compete with modern cultivars in terms of output, especially under durable environmental stress and with reduced chemical input. Moreover, landraces may contribute to improved health thanks to their higher content of beneficial bioactive compounds (e.g. antioxidants, glycosides, flavonoids, etc.).

This Special Issue (SI) was lunched to highlight how the rapid advances and increasing affordability of novel investigation tools in plant genetics and biotechnology offer previously inaccessible opportunities. New technologies are improving both genotyping and phenotyping methods, allowing us to uncover crop diversity and exploit genetic variability for plant breeding with remarkable precision and speed.

The SI includes three thematic reviews that guide readers through the main recent scientific [2], technological [3], and legal [4] developments for the characterization, conservation, and use of plant genetic resources. The source of diversity as well as the approaches to its use can be different. Three more specific contributions present the possibilities, limitations, and achievements related to improving crops by exploiting different kinds of genetic resources, landraces in the case of tomatoes [5], wild gene pools for wheat [6], and mutants for barley [7]. Research articles also offer varied examples of the study of molecular and/or phenotypic diversity in trees (olive and grape) [8,9] as well as herbaceous crops (maize, rice, and wheat) [10–12] and wild species [13]. These papers illustrate how recent knowledge about DNA-based analytical tools is converted into useful applications for the description, understanding, and utilization of the genetic diversity.

This SI was also launched to honor the memory of Prof. Gian Tommaso Scarascia Mugnozza. We were pleased to include an Editorial that acknowledges not only his work in plant breeding and diversity, but also his incessant activities "to protect, conserve and utilize biodiversity properly, and in particular genetic resources" [14,15]. Prof. Scarascia Mugnozza was an active promoter of international collaborations, and we would like to pay tribute to him, remembering especially his memorable quote: "as the importance of plant genetic resources will be more acknowledged, partnership will not be any easier, it will be more necessary." Our closing wish is that this SI and its content would also serve to strengthen partnerships and promote a future alliance of ideas and goals in order to study, protect, and exploit biodiversity for the agricultural challenges that lie ahead [16].

Finally, we thank all the authors for their important contribution to this SI. We would also like to acknowledge the various submissions that could not be published. Regrettably, part of the editors' work is to make a decision based on the reviewers' comments—for which we are deeply grateful—and their own opinion. We also wish to thank the staff members at the MDPI editorial office (in particular Ms. Wei Zhang) for their support.

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