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EDITORIAL

Durable Genetic Plant Resistance: A Key to Sustainable Pathogen Management

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Article History

Received: October 20, 2022

Revised: February 08, 2023

Accepted: February 16, 2023

Plants are forced to keep constant control *versus* pathogens for their survival. The hosts and their pathogens are participated in a fighting without ending with a view to maximal adaptation in a particular habitat [1]. Between the years 2005 and 2050, it has been predicted that the human demand for agricultural products will grow by 60-110% [2]. Plants defense against pathogens that create infestation diseases, and is a main asset for worldwide nutrition safety and potential plant output [3]. The most environmentally friendly and trustworthy schema to save production is the growing of lines with genetic resistance *versus* their pathogens [4]. Genes for resistance to diseases are classified into two classes [5]. Qualitative resistance is mostly composed of gene-for-gene recognition mechanisms and confers near-complete protection against disease [6]. Generally, this single dominant *R* gene resistance is not durable because of quick modifications in the pathogen [1]. By contrast, quantitative resistance is commonly governed by various genetic features (quantitative trait loci, QTLs) and leads to a reduction in epidemic progress over time compared to producing a plant without diseased symptoms, which occasionally leads to elevated levels of control [7]. More and more breeders are realizing the employment of quantitative resistance as a useful strategy to protect agricultural production. Nevertheless, it is generally less efficient when plant tissue or environmental conditions are suitable for disease. More importantly, QTLs can be overcome by a swift pathogen population like a qualitative resistance [4, 8].

Since the biological function of gene-for-gene relationships in forming the phenotypic and genetic layout of pathogens in host frameworks is fully recognized, the effect of quantitative resistance on the evolution of life-history features of the pathogen is less reported [1, 3, 4]. Quantitative resistance may be more durable than high levels of qualitative resistance [4] since it exerts less selective pressure on the pathogen [6].

However, the evolutionary possibility of host pathogens to adapt to plant resistance [1] creates perfect surveillance fundamental to achieving sustainable utilization of this valuable resource [3].

Durable resistance is a prolonged research objective of plant breeding and crop production programs [7, 8]. Durable resistance is described retrospectively and empirically as resistance that has been efficient over a relatively large zone for a relatively prolonged duration where factors are mostly suitable to the disease [9]. Resistance durability is beneficial due to decreasing the threat that genotypes with maximum production, quality, or agronomy will become vulnerable to a serious pathogen [3]. It minimizes the danger of plant defeats in subsistence farming, reduces unplanned expenses on host defense, and assists to preserve the persistence of food supplies [4]. Durable resistance requires not to be complete; moderate but credible resistance is generally helpful to farmers and breeders [8]. The domain of durable resistance was mostly prevailed by research on powdery mildews and rusts of small grain crops and potato late blight for many years [3]. Progressively, the scope has extended to a variety of perennial and annual plants, to the ecological community, and to a broad range of bacteria, nematodes, fungi, oomycetes, and viruses [3]. McDonald and Linde [1] distinguished pathogens with high and pathogens with low evolutionary possibility. Pathogens with elevated evolutionary possibility and hence a greater danger of eroding and/or breaking down resistance genes have high mutation rates, large effective population sizes, a high possibility for genotype flow, and a mixed reproduction system. Restricted durability of the resistance, nevertheless, remains a main problem in the use of resistant genotypes [7 - 9]. Therefore, enhancing resistance durability to plant pathogens has become central in maintaining the human demand for agricultural production quartering both, the quality and quantity.

These challenges and approaches to maintain an acceptable and durable level of genetic plant resistance in main crops to a wide range of the most noticeable and harmful pathogens were discussed and reported in a special issue of The Open

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Agriculture Journal entitled “Durable genetic plant resistance: A Key to Sustainable Pathogen Management”. These review articles were focused on several topics in the host-pathogen interactions for improving durable plant resistance: (1) using of molecular approaches to improve the resistance in staple food crops (*i.e.*, wheat, barley, rice, and potato), (2) developing of gene pyramided varieties that increase resistance in rice and wheat to major and emerging rice diseases and Fusarium head blight (FHB), and (3) combining novel *in vitro* data linked with quick screening approaches to assess quantitative resistance in various plant-fungal relationships.

This edition is started with a review, prepared by Kozub *et al.* [10], of the major progression in the production of durable-resistant cultivars in the worldwide principal nutrition crops, rice, barley, and wheat, as well as potato. The authors believe that key developments in the release of host plants with durable resistance are established on research of molecular functions of host immunity and its particular traits for pathogens with several habitats through the employment of biotechnological techniques such as marker-assisted selection for pyramiding of qualitative *R* genes or monogenic quantitative resistance genes, the introduction of transgenes, genome and mutagenesis editing aimed at silencing susceptibility genes, and alternations in the expression of specific genes linked with resistance.

Two review articles [11, 12] have been devoted to the development of a gene pyramiding approach to enhance durable plant resistance to diseases. In particular, Bag *et al.* [11] article arranges findings linked with resistance in rice *versus* different main and emerging diseases as well as their usage to develop gene pyramided cultivars that augment resistance to those pathogens to attain durable resistance. It has been shown that an arrangement of genetic map and strong molecular markers of the host has made application of marker-assisted selection potential for the characteristics governed by resistant QTLs or genes to stimulate durable resistance in the plant. A global evaluation on the identification, sources, and use of resistance QTLs/genes of main and emerging diseases of rice will assist in the development of rice cultivars with durable resistance to important and emerging disease-causing pathogens.

Sakr [12] reviewed new findings linked to the potential capacity of FHB fungi to evolve pathogenicity, erosion of quantitative FHB resistance in barley and wheat as well as applying gene pyramiding which increases crop resistance to FHB invasion to attain durable FHB resistance. The author found that if a pyramiding of several resistances enhancing QTL linked with selection *versus* suspected susceptibility components is achieved in new genotypes, the evolution of *Fusarium* fungi might be slowed due to decreased exposure to the pathogen, disruptive selection on *Fusarium* populations and consequently decreased fitness of FHB pathogens. This would stabilize the *Fusarium* population and participate in the durability of head blight resistance.

Ternovska *et al.* [13] showed data about resistance types in wheat *versus* powdery mildew and the molecular nature of *Pm* genes' products. They are tandem kinase proteins, nucleotide-binding, leucine-rich repeat proteins-immune receptors,

transporters, receptor-like kinases, mitogen-activated kinases, and plant-specific proteins. They demonstrated an obvious comprehension of the molecular nature of the plant protein governing resistance and its function in the development of the molecular schema of plant defense against the pathogen is required to evaluate the probabilities of any resistance gene for transfer to the genetic pool of wheat in relation to its capacity to exhibit long-lasting and effective powdery mildew resistance.

In another review article prepared by Sakr [14] about the *in vitro* approach to estimate quantitative resistance in fungus-host interactions, an *in vitro* method was found to be successful and efficient in terms of plant samples, inoculum volume, and working space. The major usefulness of this technique is its predictive capacity of mature plant disease resistance. Also, it presents reproducible data and was found to be a reliable and simple approach. The *in vitro* trial permits early and quick determination of susceptibility/resistance to fungal pathogens, which can be combined into a breeding program for distinguishing resistant plants.

The review articles presented in the special issue will be of interest to plant-pathogen researchers dealing with durable resistance in major crops worldwide to main destructive plant pathogens, and more particularly to present some special review articles to achieve durable genetic plant resistance which express a key to sustainable pathogen management.

ACKNOWLEDGEMENTS

The author would like to thank the Atomic Energy Commission of Syria for providing assistance for this research.

REFERENCES

- [1] McDonald B, Linde C. Pathogen population genetics, evolutionary potential, and durable resistance. *Annu Rev Phytopathol* 2002; 40: 349-79.
- [2] Alexandratos N, Bruinsma J. World Agriculture Towards 2030/2050: The 2012 Revision. ESA Working paper at Rome. FAO 2012; 12-03.
- [3] Mundt CC. Durable resistance: a key to sustainable management of pathogens and pests. *Infect Genet Evol* 2014; 27: 446-55.
- [4] Parlevliet JE. Durability of resistance against fungal, bacterial and viral pathogens; present situation. *Euphytica* 2002; 124: 147-56.
- [5] Van der Plank JE. Disease Resistance in Plants 1st ed. New York, USA: Academic Press 1968; p. 208.
- [6] Dangl JL, Jones JG. Plant pathogens and integrated defence responses to infection. *Nature* 2001; 411: 826-33.
- [7] Cowger C, Brown JKM. Durability of quantitative resistance in crops: greater than we know? *Annu Rev Phytopathol* 2019; 57: 253-77.
- [8] Brown JKM. Durable resistance of crops: a Darwinian perspective. *Annu Rev Phytopathol* 2015; 53: 513-39.
- [9] Johnson R. A critical analysis of durable resistance. *Annu Rev Phytopathol* 1984; 22: 309-30.
- [10] Kozub N, Sozinova O, Sozinov I, *et al.* Advances in durable resistance to diseases in staple food crops: a review. *Open Agric J* 2022; 16e187431292208240
- [11] Bag MK, Raghu S, Banerjee A, Prabhukarthikeyan SR, Baite MS, Yadav M. Durable resistance of rice to major and emerging diseases: present status. *Open Agric J* 2023; 17e187433152212301
- [12] Sakr N. Erosion of quantitative resistance in wheat and barley to Fusarium head blight: gene pyramiding achieves and durability study. *Open Agric J* 2022; 16e187433152211150
- [13] Ternovska TK, Iefimenko TS, Antonyuk MZ. Improvement of wheat genetic resistance to powdery mildew. retrospects and prospects. *Open Agric J* 2022; 17e187433152210310
- [14] Sakr N. *In vitro* methodology to assess quantitative resistance in plant-fungus pathosystems. *Open Agric J* 2022; 17e187433152210120