



Ecology, Breeding and Integrated Management of Fungal Diseases in Wheat

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Abstract

Approximately 50% more food would need to be produced by agriculture in 2050 as a result of the world population growth and dietary changes (FAO, 2017). Given that wheat is one of the most important staple crops in the world and contributes 20% of the calories and proteins in human nutrition, wheat production should increase. This growth will primarily be based on yield improvements due to the fierce competition for the limited amount of productive arable land from other societal sectors (FAOSTAT, 2020). Future demand must be met by sustainable expansion that combines integrated disease and pest control, climate adaptation for more frequent abiotic pressures, and sparing use of water and other resources.

Integrated Wheat Disease Management

When the danger is high before the season begins, epidemic prediction is a useful tool for creating effective integrated management measures. According to Simón et al. (2011), cultural methods such as proper fertilisation, management of crop rotation, timing of planting, and tillage that speeds up residue decomposition are crucial in minimising disease intensity. Additionally important techniques to lessen the disease's severity and minimise production losses are biological and chemical controls.

In this special issue, Kim and Choi

conducted a retrospective research based on a wheat blast epidemic in Bangladesh and calibrated a model to ascertain if seasonal wheat blast risk forecasts for epidemic reduction actions are viable.

Wheat Disease Resistance Mechanisms

To completely comprehend how pathogens and crops interact, it is important to investigate disease resistance mechanisms. In this special issue, Mohammadi et al. demonstrated the important biological role of the ZtR1m1 gene, encoding a MADS-box

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transcription factor, in the final stage of infection of *Zymoseptoria tritici* P. Crous, the causative agent of Septoria leaf blotch. This indicates that ZtR1m1 affects penetration, colonisation, fungal biomass production, pycnidial formation, differentiation, and melanisation.

This disease must be induced by particular crop processes and gene expression. When spikelets were infected with *Fusarium graminearum*, Nilsen et al. observed cell wall thickening in the rachis node and visible hyphae, but only at the inoculation site in a resistant cultivar. Chromosomes with high nucleotide diversity, such as 5AL, have genes that impact processes involved in infection and the formation of DON and can distinguish across cultivars.

Resistance to Wheat Pathogens Determined by QTL and Genes

Resistance that ranges from moderate to high levels can be implemented. Quantitative resistance is imperfect, polygenic, isolate-non-specific, and more resilient than qualitative resistance, which is essentially full, isolate specific, and follows a gene for gene interaction (Brading et al., 2002).

Traditional breeding methods as well as molecular techniques to select plants based on the presence of certain genes and/or QTL are essential for producing resistant cultivars. Initially, low genomic resolution, limited allelic variation, and biparental populations were used to map the QTL. The genome-wide association studies (GWAS), which analyse the genetic basis of complex traits while taking

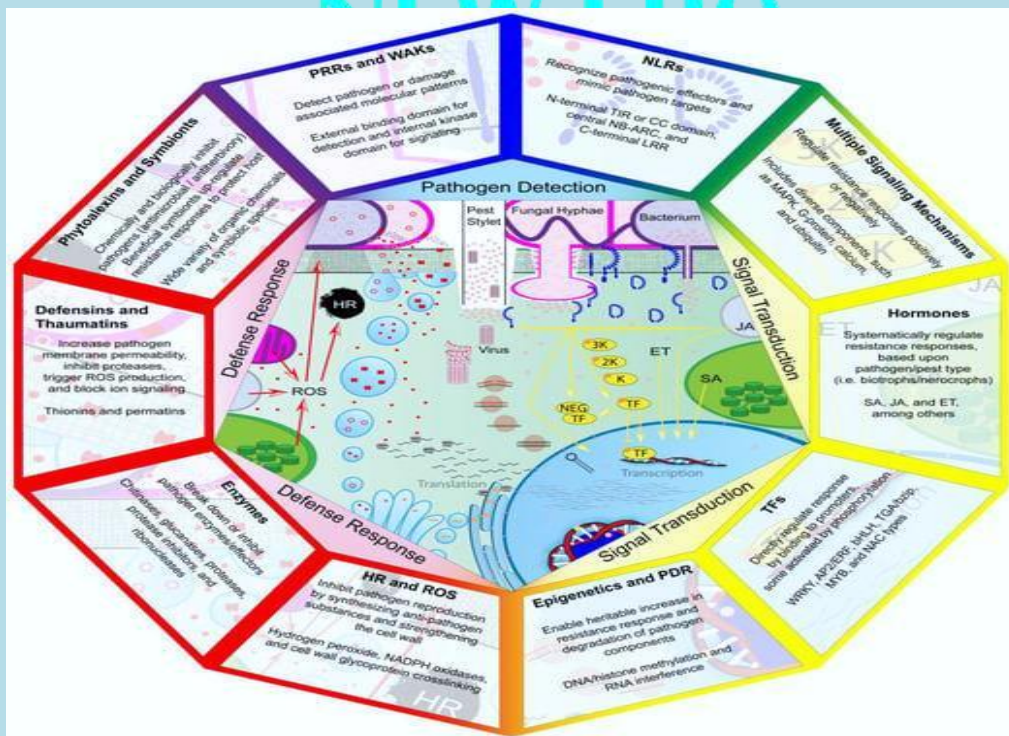


Figure 1: Defense of Plants Relies on Detection and Reaction

into account naturally existing genetic variation and offering greater mapping resolution, have recently helped to overcome some of the limitations of this traditional mapping (Korte and Farlow, 2013; Liu et al., 2016).

adult stage. There were no copies of the genes Yr5 and Yr15, which are resistant to all races in the USA, or Yr46, which is resistant to many races.

Resistance Adaptation in Wheat Cultivars through Genomic Selection

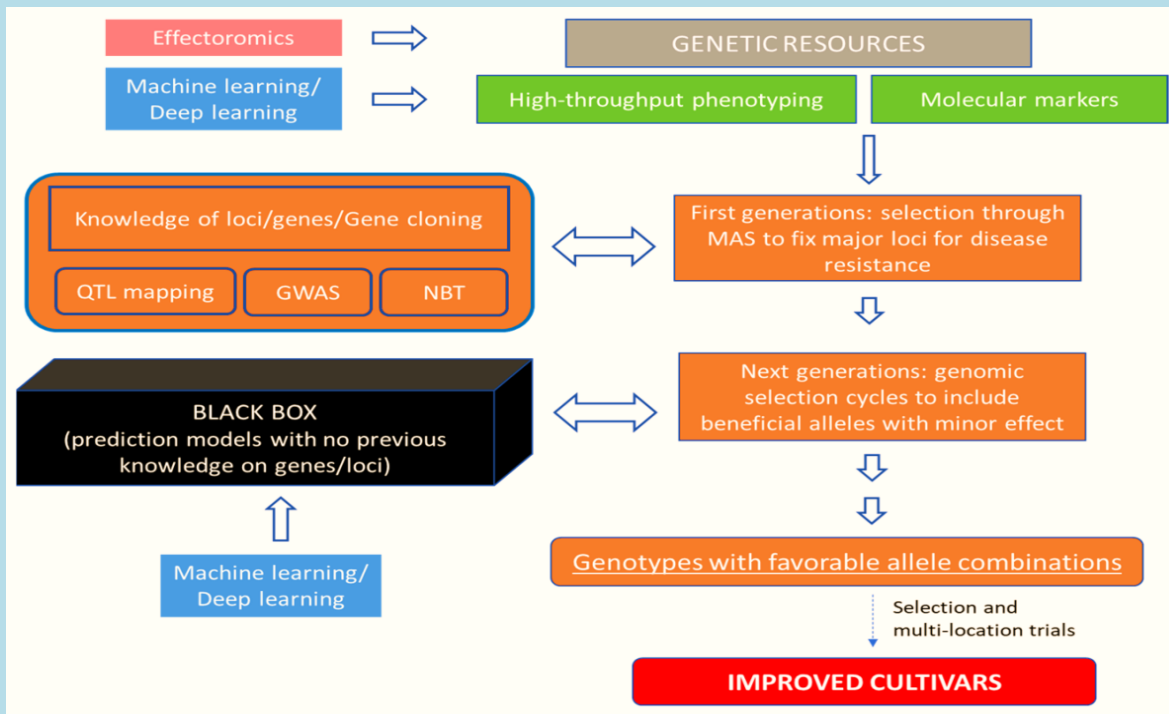


Fig 2: Workflow for developing better cultivars of disease-resistant crops by combining several molecular methods

In recent years, epidemics in warmer parts of the world were brought on by new, aggressive strains of *Puccinia striiformis* Westend (Liu et al., 2017). A panel of 857 USA genotypes were genotyped with genetic markers for 18 resistance genes or QTL using a GWAS by Mu et al. They identified 51 loci linked with resistance by phenotyping the accessions in seedlings with the six most prevalent or virulent races of *Puccinia striiformis* and by spontaneous infection in the

Genomic selection (GS) is a sort of marker-assisted selection used to accelerate genetic progress by estimating the genetic values of untested populations using genome-wide markers and phenotypic data from observed populations (Wang et al., 2018). Verges et al. verified that local breeding programmes may employ area nurseries as a source of lines to forecast genomic predicted breeding values for Fusarium head blight. They also created an index to locate lines

resistant to Fusarium head blight and low in DON levels.

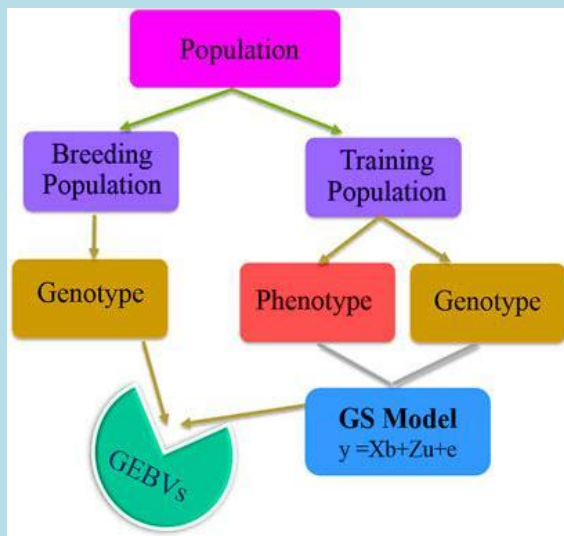


Fig 3: A Method for Increasing the Effectiveness of Molecular Breeding to Create Crops Resistant to Climate Change

Wheat Diseases: Biological and Chemical Control

According to Chakraborty et al., some secondary metabolites derived from a marine *Bacillus subtilis* strain suppress the wheat blast disease by altering the morphology of germinated *Magnaporthe oryzae* Triticum pathotype conidia and by inhibiting mycelial growth, conidiogenesis, and conidial germination. According to Castro Tapia et al., while spike size and the number of grains per spike increased, some strains of *Pseudomonas protegens* reduced by 16.8% the severity of the wheat crown and root rot pathogens *Gaeumannomyces graminis* var. *tritici* (Sacc.) Arx D. L. Olivier, *Rhizoctonia cerealis* van der Hoeven, and *Fusarium culmorum*.

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