SPEEDING UP THE DISCOVERY OF NOVEL SOURCES OF LEAF RUST RESISTANCE IN WHEAT

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Abstract

Leaf rust (LR) caused by Puccinia triticina, is among the most important diseases of wheat (Triticum aestivum L.) crops globally. Deployment of cultivars incorporating genetic resistance, such as adult plant resistance (APR) or all-stage resistance (ASR), is considered the most sustainable control method. APR is preferred, which places lower selection pressure on the pathogen and is often polygenic, thus considered more durable. In the search for new sources of APR, here we explored a diversity panel sourced from the N. I. Vavilov Institute of Plant Genetic Resources (VIR). Based on DNA marker screening, 83 of the 300 accessions were deemed to carry known APR genes, namely Lr34, Lr46, and Lr67. Interestingly, accessions carrying Lr67 were mostly landraces from India and Pakistan, reconfirming the likely origin of the gene. Rapid phenotypic screening using a method that integrates assessment at both seedling and adult growth stages under accelerated growth conditions (i.e. constant light and controlled temperature) identified 50 accessions carrying APR. Levels of APR corresponded well with phenotypes obtained in a field nursery inoculated using the same pathotype ($R^2 = 0.82$). The second year of field testing using a mixture of pathotypes with additional virulence for racespecific APR genes (Lr13 and Lr37), identified a subset of 13 accessions that consistently displayed high levels of APR across years and pathotypes. Thus, providing useful sources of resistance for future research. A strategy combining rapid generation advance coupled with phenotyping under controlled conditions could accelerate introgression of these potentially novel alleles into adapted genetic backgrounds.

Key words

Triticum aestivum L., *Puccinia triticina*, Adult plant resistance, Landraces, Accelerated growth conditions, *Lr67*