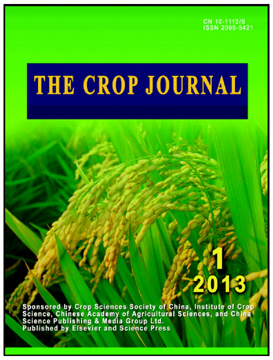

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Review

Wheat stripe rust resistance gene *Yr24/Yr26*: A retrospective review

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Abstract: The objective of this review is to describe events in China and elsewhere that are related to the discovery, genetic identification, use, and ultimate break-down of a single wheat gene for resistance to stripe rust, namely *Yr24/Yr26*. In our retrospective analysis there was an early assumption of at least three genes at or near the locus, which caused an erroneous presumption of genetic diversity for resistance. It is an example of another boom and bust cycle in plant breeding with races virulent to *Yr26* (V26 races) now being the majority race group in the Chinese *Pst* population. We have attempted to present our story in a historical and personal context demonstrating research inputs from different national and international groups, as well as some significant contemporary side issues. It covers the period from the late 1980s to 2017, during which significant rapid advances in the molecular biology of host : pathogen genetics occurred. We attempt to describe both successes and drawbacks in our work.

Keywords: *Puccinia striiformis*; Resistance genes; *Triticum aestivum*; Virulence; Yellow rust

1 Introduction

Stripe or yellow rust (caused by *Puccinia striiformis* Westend. f. sp. *tritici*) is a significant wheat disease worldwide. Although many genes for resistance have been documented and a number given permanent designations, there are many more that have been documented and given temporary names because they require either further validation, suitable germplasm to represent a permanent designation, or the stocks carrying them are not internationally accessible. In other cases, resistances have been named as quantitative trait loci (QTL) that span considerable genetic length and again need further work for validation and Mendelization. Nevertheless, resistances in the last two groups can be given temporary names or QTL designations according to the rules of genetic nomenclature for wheat.

Stripe rust, along with Fusarium head blight, are currently the two most important diseases of wheat worldwide. Major stripe rust epidemics in China are infrequent, but can be spectacular in scope and consequence. These well described epidemics, were consequences of the introduction and widespread use of initially effective resistance genes, either in widely grown varieties, or suites of derivatives with the same resistance genes, followed by the emergence of virulent races. This pattern of resistance breeding and subsequent disease epidemics clearly follows the predictable boom-and-bust cycle.

Since the 1950s there have been five documented boom and bust stripe rust episodes in China [1]. The first occurred in the 1950s with the use of variety Bima 1 that carries gene *Yr1* [2]. The second was in 1964, but in this

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