

## Extensive Genetic Variation at the *Sr22* Wheat Stem Rust Resistance Gene Locus in the Grasses Revealed through Evolutionary Genomics and Functional Analyses

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**Current Position:** Senior lecturer at the Universiti Putra Malaysia

**Education:** Ph.D. degree in biological sciences at the University of East Anglia (John Innes Centre), Norwich, UK; M.S. degree in plant biotechnology at Wageningen University and Research Centre, The Netherlands; and B.S. degree in biotechnology at the International Islamic University of Malaysia.

**Non-scientific Interests:** Playing football, traveling, and cooking.

**Brief-bio:** I am a senior lecturer at the Faculty of Agriculture, Universiti Putra Malaysia. I teach agricultural biotechnology and agricultural biochemistry courses for undergraduate students. The focus of my research is on investigating the genetic basis of resistance to two major diseases of rice—bacterial leaf blight and bacterial panicle blight. I am attempting to identify genes responsible for resistance, as well as susceptibility, in rice to develop resistant varieties against the diseases. The research work published in *MPMI* was one of my Ph.D. projects under the supervision of **Dr. Brande Wulff** at the John Innes Centre in collaboration with other colleagues on site, and also from the Commonwealth Scientific and Industrial Research Organization, Canberra, Australia, and the University of Minnesota, USA. Our project focused on the functional and evolutionary characterization of a wheat gene, *Sr22*, which confers broad-spectrum resistance to one of the most damaging fungal disease of wheat—stem rust. We showed that *Sr22* exists as a simple, single-copy locus across the Triticeae, except in barley, which has undergone complex expansion and rearrangements. We also functionally characterized three distinct alleles of *Sr22* and showed that the gene is sufficient for resistance to the wheat stem rust Ug99 isolate, which is virulent to most stem rust resistance genes currently deployed in wheat and poses a major threat to global wheat production. The results reported in this article will contribute additional knowledge toward understanding the molecular evolution and function of plant disease resistance genes to facilitate the improvement of crops against agriculturally important diseases.

