Durable but complex: stem rust resistance from emmer wheat

Wolfgang Spielmeyer\(^1\), R. Mago\(^1\), L. Tabe\(^1\), C. Hiebert\(^2\), J. Briggs\(^3\), J. Kolmer\(^4\), C. McCartney\(^2\), M. Rouse\(^4\) & J. Ellis\(^1\)

\(^1\)CSIRO Agriculture GPO Box 1600, Canberra 2601 Australia
\(^2\)AAFC-Cereal Research Centre, 101 Route 100, Morden, MB, Canada R6M 1Y5
\(^3\)University of Minnesota, Department of Plant Pathology, 1991 Upper Buford Circle, 495 Borlaug Hall St. Paul, MN 55108, USA
\(^4\)USDA-ARS Cereal Disease Laboratory, 1551 Lindig St, Saint Paul, MN 55108, USA

Two emmer wheats are the source of durable stem rust resistance in bread wheat. Ilumillo emmer was crossed with Marquis in Minnesota in 1914 that later gave rise to the cultivar Thatcher (Tc) while a Yaroslav emmer x Marquis cross in South Dakota in 1916 produced the resistant bread wheat cultivar Hope. One-hundred years later, both Thatcher and Hope still carry moderate levels of stem rust resistance. The most important gene transferred from emmer into Hope was \(Sr2\) which confers race non-specific, partial resistance. We identified several candidate genes at the \(Sr2\) locus and it is possible that more than one gene is required for \(Sr2\) resistance. Resistance in Thatcher sourced from emmer is also complex consisting of several known race-specific genes and unknown genes that are only effective in adult plants. \(Sr12\) is one of the race-specific genes that originated from emmer. In several mapping studies strong field resistance in Tc was associated with the \(Sr12\) locus, although field races used in these experiments had virulence to this gene at the seedling stage. These results suggest that some major genes that are considered “defeated” as determined by seedling assays may still contribute to adult plant resistance. We have fine mapped \(Sr12\) to the centromeric region on chromosome 3BL and developed mutants that will assist in gene cloning and in dissecting complex Tc stem rust resistance at the molecular level. A KASP assay for a tightly linked SNP-based marker was developed that will facilitate selection for this gene in breeding programs.