Cloning stem rust resistance from bread wheat progenitors

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The diploid grass species *Triticum monococcum* (sub sp *monococcum* and *boeoticum*) and *Aegilops tauschii*, represent the A and D genome relatives respectively of common wheat (*T. aestivum*), and they harbour diverse resistance genes which includes *Sr22*, *Sr33* and *Sr45* that are effective against stem rust races prevalent in Africa, USA, Australia and Asian continents. Through inter-specific hybridisation, these resistance genes have been successfully transferred into bread wheat and used in commercial production. As part of the objectives towards dissecting the biology and immune recognition of these genes to different stem rust races, my past and the on-going research are focused on isolating these important genes using a combination of conventional positional cloning and mutagenesis approaches.

Despite the complexity of the genomes of wheat and its wild relatives, due in part to multiple gene copies and highly repetitive DNA sequences, positional or map-based gene cloning techniques have been successful in isolating traits of agronomic importance, albeit at a relatively slow rate. This approach was used in identifying, the chromosomal region of *Ae. tauschii* harbouring *Sr33* which contained a mixed cluster of resistance gene analogs (RGAs). Mutational and complementation analysis enabled confirmation of the *Sr33* gene member. With the rapid advances of next generation sequencing combined with mutational genomics, *Sr33* mutants could be detected, and this approach has been extended to the cloning of *Sr22* (from *T. monococcum*) and *Sr45* (from *Ae. tauschii*).