Syntenic relationship of the wheat greenbug-resistance gene Gb3 region with rice and Brachypodium distachyon.

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The greenbug, *Schizaphis graminum* (Rondani), is an important aphid pest of small-grain crops in many parts of the world. A single dominant gene, *Gb3* that originated from *Ae. tauschii*, has been deployed in the hard winter wheat cultivars TAM 110 and TAM 112 and has provided consistent and durable resistance against prevailing greenbug biotypes. Previously, we mapped *Gb3* in the recombination-rich, telemetric bin of wheat chromosome arm 7DL. In the present study, high-resolution, subgenome mapping was carried out using an F_2 segregating population of *Ae. tauschii* and two hexaploid populations. Molecular markers were developed by exploring the Triticeae ESTs and the syntenic relationships among wheat, rice, and *B. distachyon* in the *Gb3* region. The *Brachypodium* sequences in super contig_0 aligned with Triticeae ESTs were thoroughly examined. A high degree of colinearity between the wheat 7DL distal bin and the *Brachypodium* super contig_0 was observed. Total of 70 *Gb3*-linked markers were mapped in the *Ae. tauschii* population, of which 21 were based on wheat–*Brachypodium* colinearity. Markers closely linked with *Gb3* were used to screen *Ae. tauschii* and wheat 7DL-specific BAC libraries. BAC contigs were constructed with markers flanking *Gb3*. Fifteen *Ae. tauschii* BAC-end sequence-based markers were fine mapped in a *Gb3* window of 3.0 cM. This research demonstrates the value of publicly available resources such as the wheat D-genome mapping database ((http://wheat.pw.usda.gov/PhysicalMapping/), the rice database (http://wheat.tigr.org/tdb/e2k1/tae1/index.shtml), and the *B. distachyon* database (http://www.brachypodium.org).