

Poster 13. Unraveling a meiotic gene complex on wheat chromosome arm 5BL.

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The *Ph1* (pairing homoeologous 1) locus has been at the heart of wheat research since its discovery in early 1950s. From that time, much speculation and hypotheses have been proposed to explain its mode of action but the identify of the underlying gene(s) remained illusive. Building upon its localization to chromosome arm 5BL, we first localized the locus to a ~3-Mb segment bracketed by the deletion breakpoints of 5BL-1 (FL 0.55) and *ph1c* on chromosome 5B (*Ph1* gene region). Additional mapping of 238 wheat group-5 specific markers assigned nine loci to the *Ph1* gene region. A consensus genetic-linkage map of the whole region also was constructed to determine the order of markers within the region. Extensive blastn/tblastn comparisons of the *Ph1* gene region marker sequences with the rice genomic DNA sequences allowed identification of a 450-kb orthologous region on the rice chromosome 9. This wheat–rice comparison not only allowed alignment of the *Ph1* gene region to the BAC scaffold of rice R9 but also with the BAC scaffold of wheat chromosome 5B. To determine the location of the deletion break points of 5BL-1 and *ph1c* (delimiting the *Ph1* gene regions) on the BAC scaffold of bread wheat, we designed primers from six selected genes and used additional deletions spanning the region. The analysis allowed demarcation of the *Ph1* gene region to a very small fraction of the 2.5-Mb wheat BAC scaffold, carrying only 12 genes. To identify gene responsible for the *Ph*-like phenotype, we undertook virus-induced gene silencing (VIGS) of three candidate genes and nine other genes flanking the region of interest (including *TaDMC1*, *TaASY1*, and *TaCDC2-4*). The candidate genes were short-listed on the basis of domain/motif searches. Silencing of the *TaDMC1* via VIGS showed univalents, whereas *TaASY1* showed multivalents. When VIGS was performed on the *Ph1* gene candidates mapping in the *Ph1* gene region, one of the candidates (*TaWSU-1*) showed formation of quadrivalents/higher order pairing upon silencing, which is a characteristic phenotype of the *ph1* gene mutants. Another candidate (*TaH51L*) showed an average of four univalents and 19 bivalents. These findings suggest that one of the candidate genes, *TaWSU-1*, represents a novel meiotic gene that influences diploid like pairing behavior of hexaploid wheat and also suggests the role of other genes in chromosome just apposition and synapsis at meiotic prophase I.

Poster 14. Virus-induced gene silencing for durable Russian wheat aphid resistance in wheat.

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Russian wheat aphid (RWA), *Diuraphis noxia* (Kurdjumov), is an important insect pest of wheat (*Triticum aestivum* L.) and barley (*Hordeum vulgare* L.) in the western United States. The most effective control strategy is the development of resistant cultivars, but a gene-for-gene relationship between RWA virulence effectors and R genes results in biotype-specific resistance. Therefore, identifying more durable resistance, effective against all RWA biotypes, would be a significant advantage. Our objective was to test whether silencing a candidate gene, with suspected involvement in compatible interactions between the aphid and wheat, would confer resistance to a susceptible wheat cultivar. Several genes have been identified as being up-regulated in the susceptible cultivar Gamtoos-S (GS) or down-regulated in the near-isogenic resistant line Gamtoos-R (GR; carrying *Dn7*), in a transcript profiling study. Virus-induced gene silencing (VIGS), using the barley stripe mosaic virus, was used to test whether a candidate gene identified from the microarray experiment is involved in the susceptible reaction of GS. Controlled infestation with RWA2, the most virulent biotype to date, was used to estimate aphid fecundity and aphid prenympophositional period (PNP) and to assess symptom development. No variation in PNP was observed among the treatments. However, silenced plants did show significantly lower aphid fecundity compared to GS and the viral control and similar fecundity to GR. At 14 days-post-infestation, chlorosis scores for the silenced treatment were not significantly different from GR. There also was a significant correlation between the average aphid counts and expression of the candidate gene across treatments. These results indicate that this gene may play an important role in susceptibility and could be exploited for breeding broad-spectrum resistance.