Poster 63. A genomic study of homoeologous recombinants of the Lr19 (T4) translocation in wheat.

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Wheat is an important global food crop and is of major importance for international food security. Wheat leaf rust, caused by *Puccinia triticina*, can result in significant yield losses. The use of resistance genes is the most economical and environmentally friendly way to combat the cereal rusts. These genes have had great impact on stabilizing wheat production globally. Numerous genes have been identified in the hexaploid wheat gene pool and used in breeding for new resistant cultivars. However, the constant evolution of pathogens to overcome new sources of resistance is a major threat to sustained wheat production. Overuse of the primary gene pool of wheat, coupled with the narrow genetic base of common wheat has left the crop vulnerable to diseases, pests, and changes in the environment. The wild relatives possess numerous resistance genes that can be exploited in wheat breeding. Various wheat–*Thinopyrum ponticum* (*Lr19*) translocations involving wheat chromosome 7DL were produced in the 1960s and 70s. Unfortunately, these translocations could not be used for breeding in many countries, due to the presence of a linked gene (*Y*) for yellow endosperm pigmentation. As a result, lines with white endosperm have been derived through homoeologous recombination or mutation. One such attempt involved the T4 translocation and produced several 7BL recombinants that lacked both the *Y* and *Sr25* genes. The latter modified translocations have not been thoroughly characterized and mapped to determine the actual alien chromatin amounts. This study employed fluorescent genomic in situ hybridization (FGISH) and mapped simple sequence repeat markers to confirm the earlier conclusions and to determine the physical sizes of the remaining alien chromosome fragments in the shortest recombinants. An integrated cytogenetic and linkage map has been constructed for the recombinant chromosomes through FGISH and marker analyses. The recombinants with smallest alien fragments are being characterized for their agronomic usefulness and are simultaneously being backcrossed into the NDSU winter wheat breeding populations.

Poster 64. Enhancement of Lr34 function by its over-expression in transgenic wheat.

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Lr34 is a resistance gene that is mainly used against leaf rust caused by *Puccinia triticina* Eriks and stripe rust caused by P*uccinia striiformis* Westend. f. sp. *tritici* Eriks. A susceptible, *Lr34* allele is caused by a single nucleotide polymorphism in exon 11 or exon 12 that resulted in an alteration of an amino acid residual in the *Lr34* protein or a point mutation in exon 22, which produced a nonfunctional form of the *Lr34* protein due to the presence of a premature stop codon. A resistant *Lr34* allele should be transcribed into initial pre-mRNA transcript in the transcription, during which an interrupted intron between two neighboring exons is removed, and retained exons are concomitantly joined to make up a matured mRNA. In a recent study, however, we have found that even though a wheat cultivar carries a resistant *Lr34* allele, the majority of *Lr34* transcripts in this cultivar were mis-spliced due to intron retention (a complete or partial intron was not spliced out) or exon skipping (a complete or partial exon was mistakenly spliced out). These mis-splicing or alternative splicing events have resulted in nonfunctional forms of the *Lr34* protein. We are testing to determine if the plant resistance to leaf rust and stripe rust could be significantly enhanced when a complete and functional *Lr34* cDNA is over-expressed in transgenic wheat using a cultivar carrying the resistant *Lr34* allele.