## Fine structure mapping of a gene-rich region of wheat carrying *Ph1*, a suppressor of crossing over between homoeologous chromosomes

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The wheat gene-rich region (GRR) '5L0.5' contains many important genes including *Ph1*, the principal regulator of chromosome pairing. Comparative marker analysis identified 32 genes for the GRR controlling important agronomic traits. Detailed characterization of this region was accomplished by first physically localizing 213 wheat group 5L-specific markers using group 5 nulli-tetrasomics, three *Ph1* gene deletion/insertion mutants, and nine terminal deletion lines with their breakpoints around the '5L0.5' region. The Ph1 gene was localized to a much smaller region within the GRR (*Ph1* gene region). Of the 61 markers that mapped in the four sub-regions of the GRR, nine mapped in the 'Ph1 gene region'. High stringency sequence comparison (e <1e<sup>-25</sup>) of 157 group 5L-specific wheat ESTs identified orthologs for 80% sequences in rice and 71% in Arabidopsis. Rice orthologs were present on all rice chromosomes although maximum (34%) were on rice chromosome 9 (R9). No single collinear region was identified in Arabidopsis even for a smaller region such as 'Ph1 gene region'. Seven of the nine *Ph1* gene region' markers mapped within a 450kb region on R9 with the same gene order. Detailed domain/motif analysis of the 91 putative genes present in the 450kb region identified 26 candidates for the Ph1 gene, including genes involved in chromatin reorganization, microtubule attachment, acetyltransferases, methyltransferases, DNA binding, and meiosis/anther specific proteins. Five of these genes shared common domains/motifs with the meiosis specific genes Zip1, Scp1, Cor1, RAD50, RAD51 and RAD57. Wheat and Arabidopsis homologs for these rice genes were identified.