





**Fig. 1.** ClustalW alignments of nucleotide binding site-leucine-rich repeat (A) and kinase (B) containing resistance genes. Arrows identify the conserved motifs used to design primers. Positional identities of amino acids are highlighted in gray and dashes indicate computer generated gaps needed for alignments.





Fig. 2. ClustalW alignments of amino acid (aa) sequences from the nucleotide binding site (NBS) RGAs cloned from Jagger and TA2460. These clones were compared with three NBS sequences from wheat *Yr10*, *Cre3*, and *KSUD14*, *Xa1*



lack of intergenomic polymorphism or the comigration of fragments.

The greatest number of fragments were assigned to the B genome (48%), followed by the D genome (28%) and the A genome (24%). Group 1 chromosomes contained the largest number of RGL loci with chromosomes 1B e











