

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.

NES NES AA VI I G I H G V S G S G K S T N K SU90 NBS aa C V G K T T NS U90 NBS aa C G V G K T T NS U90 NBS aa C G V G K T T NS U90 NBS aa C G V G K T T NS U90 NBS aa C G V G K T T NS U94 Ne S aa C G V G K T T SU944 Ne S aa A L E G V I G S FS K S T NSU944 Ne S aa A L E G V S G R G K T T NSU944 Ne S aa A L E G V S G R G K T T	I L A QIF (Y Y) A H E (KN D) K Q D N KE D H P D L Y M W H VS Q D F S VI M QIF (Y Y) A H E (KN D) K Q D N KE D H P D L Y M W H VS Q D F S VI M QIF (Y Y) A H E (KN D) K Q D N KE D H P D L Y M W H VS Q D F S VI M QIF (Y Y) A H E (KN D) K Q D N KE D H P D L Y M W H VS Q D F S VI M QIF (Y Y) A H E (KN D) K Q D N KE D H P D L Y M W H VS C D F S VI M QIF (Y Y) A H E (KN D) K Q D N KE D H P D L Y M W H VS K E [Y D V] I Y Y D R F [KU N] K M Q C Y S K E [Y D V] Y Y D R F [KU N] K M Q C Y S K E [Y D V] Y Y D R F [KU N] Y Y A H E K KI R [K H F D L] [M Q I H Y S [Q H F S H]] Y A H E K KI R [K H F D L] [M Q I H Y S [Q H F S H]] Y A H E K KI R [K H F D L] [M Q I H Y S [Q H F S H]] Y A H E K KI R [K H F D L] [M Y Y Y S [X H F S H]] Y A H E K Y [K H Y] [K K H H Y S [Q H F S Y]] Y A H E K Y [K H Y] [K K H Y] [Y Y Y] [K K H Y] [Y Y] [X] [K H Y] [Y Y] [X] [X] [X] [X] [X] [X
2 KSU014 ID IFHEN (LIK \$1 T = 3 D IP G T L L T K IQ H R C KSU940 NBS aa D L P G T L L T K IQ H R C KSU941 NBS aa D L L G T L I T K I Q H R C KSU942 NBS aa D L M R C M L G T L I T K I Q H R C M R R C M R R C M R R R R R R R R R R R R R R R R	S S S S S S S S S S S S S S S S S S S
KSUP14 KSUP14 KSUP358 aa KSUP35NBS aa LILDDIWVR A KNDA KSUP35NBS aa LILDDIWVR NKNDA KSUP35NBS aa LILDDIWVR KKNDA KSUP35NBS aa LILLDDIWVR KKNDA KSUP35NBS AA KSUP35NBS AA KS	N Q E L P & L L S F L K K. G K K G S K I L V T A B T K O H L E E L I S F L N E G L K G S K I L V T A B T K O M C N A FO G L K G S K V N Y T T T N K O M C N A FO G I H G S R V M Y T T T N K O M C N A FO G I H G S R V M Y T T N K O M C N A FO G I H G S R V M Y T T N K O M C N A FO G I H G S R V M Y T T N K O M C N A FO G I H G S R V M Y T T N K H G I H G S R V M Y T T N K G K G S K L V T S R K M I K T T N K G K G S K L V T S R K M I K T T N K G M K G S K L L V T S R K M N N K I K T T N K G M K G S K L L V T S R K M N N K K L L K L S F L N V G M K G S K K L L V T A R T K M N K K L L A F L R P N O V N S Q E A S G N M I I L T T T I Q E T F W E L F L A F L V S -
$\begin{array}{c c} Y_{1}TPN_{D3} \\ Cre3 NBS ATi \\ X_{5}U544^{0}MbN9S \\ KSU941 NBS ati \\ KSU941 NBS at$	VYQLKPLSTSDSGQLFYQ%]FGIGDKRPPIQL TAMPITEVDDF
$\begin{array}{c c} Yr10 \cdot NBS & A & E \vee S & E \times T & G & K \subset G \\ Cre3 \cdot NBS AA & & & & & & & & & & & & & & & & & &$	

 Xal NBS
 Q V L G K Q I AS E L K G N P L A A K T Y

 Rp1-D NBS-LRR
 E D T A V I A K R L G Q C P L A A K V L G

 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 con-tained the largest number of RGL loci with chromosomes 1B e

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MALEKI ET AL.: RGA CLONE MAPPING IN WHEAT