LIST OF FIGURES

physical mapping of a brachypodium EST-SSR bde55 (192 bp), which is mapped on chromosome arm 6BS in proximal bin; Lanes M 100-bp ladder, 1 Bd21, 2 Chinese Spring (CS), 3 N6BT6A, 4 N6BT6D, 5 Dt6BS, 6 Dt6BL, 7 6BS-1, 8 6BS-4, 9 6BS-5, 10 6BS-9, 11 6BS- 6, 12 6BS-2, 13 6BS-7. **(d)** PCR amplification profiles used for physical mapping of a brachypodium EST-SSR bde16 (205 bp), which is mapped on chromosome arm 1BS in centromeric bin; Lanes M 100-bp ladder, 1 Bd21, 2 Chinese Spring (CS), 3 N1BT1A, 4 N1BT1D, 5 Dt1BS, 6 Dt1BL, 7 1BS-21, 8 1BS-15, 9 1BS-20, 10 1BS-2, 11 1BS- 5, 12 1BS-19

Figure 7a-u. Integrated physical maps of SSRs for all the 21 wheat chromosomes (right side) and its comparison with available genetic maps (left side). Arrows and description on the right side of integrated physical map are deletion break points, deletion designations and fraction lengths; boxes on the left contain mapped markers within bins covered by a vertical line; corresponding SSR loci in physical and genetic maps are connected by dotted lines

Figure 8a-g. Graph plots showing physical distribution of recombination frequencies (cM/Mb) along individual wheat chromosomes. The frequency of recombination was calculated by dividing the length of a genetic sub-region in cM by the length of the corresponding physical sub-region (bin) in Mb and was plotted at the midpoint of each physical sub-region or bin. The oval shaped black dot indicates physical position of the centromere, which is also represented by 'C'. Vertical lines on the chromosome ideogram indicate break points that divide the chromosome into sub-regions or bins. Name and fraction length of each bin is given below the break point and along the chromosome

Figure 9. Distribution of orthologous bEST contigs (BdC) on wheat chromosomes belonging to homoeologous groups 1 to 7 (21 chromosomes). bEST contigs are shown on the right and arm fraction lengths are given on the left. Vertical lines on the right, covering an arm, means that the corresponding bEST contig (shown in bold) could not be assigned to a specific bin and was assigned to the arm; vertical lines covering more than one bins means that corresponding wEST was earlier mapped to a 'combined bin', rather than to an individual bin. The bEST contigs, which could not be assigned to bins and were assigned to individual chromosomes (with no information about arm), are listed at the bottom of each such individual chromosome

Figure 10. Distribution of orthologous bEST contigs (BdC; shown on the right side) on 12 rice chromosomes

Figure 11. A pie-chart showing relative frequencies (%) of ESTs among 183 conserved bEST orthologous sequences based on different biological functions and molecular activities

Figure 12. A representative pattern of brachypodium SSR marker PCR products showing conservation in the genomes of wheat and rice. Lane M, 100 bp DNA ladder; lane 1, brachypodium DNA (Bd 21); lane 2, wheat DNA (Chinese Spring); lane 3, rice DNA (IR-1). The primers (L/R) used were (A) BDEST01P1_Contig9; (B) BDEST01P1_Contig1223; (C) BDEST01P1_Contig2416; (D) BDEST01P1_Contig3247; (E) BDEST01P1_Contig3747

Figure 13. Syntenic relationships between wheat and brachypodium genomes. The seven consensus chromosomes of wheat are shown in pink colour. The deletion break points and

fraction length values are shown on the left of each chromosome. The boxes are colour coded according to the syntenic relationships with brachypodium chromosomes. The number of wESTs showing significant matches with brachypodium sequences is shown inside the coloured boxes, while the number of wESTs showing significant matches with more than one brachypodium chromosomes is shown outside the coloured boxes. 'C' represents position of centromere

Figure 14. Histogram showing Ka/Ks distribution among 153 homolog pairs of wheat and brachypodium

Figure 15. Evolution of the wheat (*n*=7) and brachypodium (*n*=5) chromosomes from a common intermediate ancestral genome with *n*=12