

RFLP-based genetic maps of the homoeologous group 5 chromosomes of bread wheat (*Triticum aestivum* L.)

D. X. Xie, K. M. Devos, G. Moore, M. D. Gale

Cambridge Laboratory, Colney Lane, Norwich NR4 7UJ, UK

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Markers

Thirty-eight anonymous cDNA and gDNA clone sequences from the libraries described in Devos et al. (1992) were shown to be located on the homoeologous group 5 chromosomes of wheat by nullisomic-tetrasomic analysis, and 26 of these were mapped. Two further anonymous cDNA markers, *Xksu8* and *Xksu26* (Kam-Morgan et al. 1989) and the cDNA clones containing the coding regions for ADP-glucose-pyrophosphorylase (Olive et al. 1989), α -amylase-3 (Baulcombe et al. 1987), β -amylase-1 (Kreis et al. 1987), acyl carrier proteins I and III (Hansen 1987) and II (Hansen and Kauppinen 1991), a ubiquitin activating enzyme (Hatfield et al. 1990), a catalase (Bethards et al. 1987) and a bZIP protein (Guiltinan et al. 1990) also detected sequences on the wheat group 5 chromosomes. The genetic map position of the 18S.26S rDNA locus on the short arm of chromosome 5DS was determined using the clone pTa71 (Gerlach and Bedbrook 1979). The genetic location of a39 (PSR1201), a clone isolated using the *ph1b* mutant of Sears (1977) and mapping within the deletion on 5BL, was also determined. All DNA markers are presented with their chromosome arm location, copy number and relative hybridization strength in Table 1.

Maps

The genetic maps were developed using a population of 120 individual F₂ plants from the wide cross 'Chinese Spring' \times 'Synthetic' (Devos et al. 1992). Eight loci were mapped in one linkage group on the long arm of chromosome 5A, and 21 and 20 loci were mapped in linkage

blocks spanning both arms on chromosomes 5B and 5D, respectively (Fig. 1A). *Xpsr170-5A*, expected from the ditelosomic analysis to map on the short arm, was independent from all other 5A markers. Thus, the long arm linkage block could not be positioned relative to the centromere. The overall arrangement of the genetic maps of the homoeologous group 5 chromosomes, i.e. clustering of sequences around the centromere on 5D and conservation of gene order between the maps, was similar to that of the previously published wheat maps (Chao et al. 1989; Devos et al. 1992, 1993b). The co-linearity of the three wheat maps (Fig. 1A) and the rye maps (Devos et al. 1993a; Plaschke et al. 1993) allowed the construction of a consensus map (Fig. 1B) and the placement, by extrapolation, of a further 53 homoeoloci in addition to the 50 points mapped. Probes which detect homoeoloci on the wheat, rye and barley chromosomes are presented on the right-hand side of Fig. 1B, while non-homoeologous markers are depicted on the left-hand side. The presence of a non-homoeologous translocation between the long arms of chromosomes 4A and 5A is well established (Naranjo and Fernández-Rueda 1991; Liu et al. 1992). With the development of the linkage map of chromosome 5A, however, the position of the 5AL.4AL breakpoint could be narrowed to the interval between *Xpsr370* and *Xpsr164*. Interestingly, there is no evidence to suggest that this translocation is different to the 5RL.4RL breakpoint in rye (Devos et al. 1993a), which raises the possibility that they may represent the same evolutionary event prior to the divergence of the A and R genomes.

The *XNor-3* locus

In bread wheat, nucleolus organizing regions (*Nor*) containing the 18S.26S ribosomal DNA multigene families

Table 1. Chromosomal location in wheat, copy number in wheat (W), barley (B), and rye (R), and relative hybridization in rye and barley for group 5 probes

Probe	Wheat group 5 locations			Copy number ^e			Signal strength ^g		Other wheat locations
	A	B	D	W	B	R	B	R	
Known function clones ^a									
pTA71 (<i>XNor</i>)	5AS	–	5DS	H	H	H	+++	+++	1AS, 1BS, 6BS
pACP11 ^b (<i>XAcl1</i>)	5AS	5BS	5DS	1	1	1	+++	+++	
pcβC51 (<i>Xβ-Amy-1</i>)	5AL	4BL	4DL	2	2	2	+++	+++	2AS, 2BS, 2DS
pCat2.1c (<i>XCat</i>)	5AL	4BL	4DL	2	2	2	+++	++	
p33 (<i>Xα-Amy-3</i>)	5AL	5BL	5DL	1	1	2	+++	+++	
WL:agal (<i>XAdpg1</i>)	5AL	5BL	5DL	1	2	1	+++	+++	
pACPII (<i>XAcl2</i>), pUBA1 (<i>XUba</i>)	5AL	5BL	5DL	1	1	1	+++	+++	
pGC19 (<i>XEmbp</i>)	5AL	5BL	5DL	5	1	4	+++	+++	3BL, 6AL, 6BS, 7DS
pACP1 (<i>XAcl3</i>)	–	5BL	–	2	1	1	+++	++	7AS, 7BS, 7DS
Anonymous clones ^c									
PSR118, <u>PSR1204</u>	5AS	5BS	5DS	1	1	1	+++	+++	
PSR170	5AS	5BS	5DS	3	2	2	+++	+++	3AL, 3BL, 3DL
<u>PSR326</u>	5AS	5BS	5DS	2	–	–	+	+	
PSR618	–	5BS	–	4	–	–	+	+	
PSR628	5AS	5BS	5DS	1	1	1	++	+++	
PSR903	–	–	5DS	3	–	–	+	+	2DS, 3AS, 3BS, 3DS
PSR929	5AS	5BS	5DS	1	M	1	++	+++	
PSR940	5AS	5BS	5DS	1	1	nd ^f	++	nd	
<u>PSR945</u>	5AS	5BS	5DS	1	1	nd	+++	nd	
PSR946	–	–	5DS ^d	5	1	1	++	+++	2DS, 7AL, 7DS, 7DL
PSR115	4AL	5BL	5DL	1	1	1	+++	+++	
PSR580	4AL	5BL	5DL	1	1	1	++	++	
<u>PSR1206</u>	4AL	5BL	–	2	2	2	++	++	
PSR1316	4AL	5BL	–	2	–	–	–	–	
PSR79, <u>PSR128</u> , PSR360	5AL	5BL	5DL	1	1	1	+++	+++	
PSR100	5AL	5BL	5DL	2	2	2	+++	+++	2AS, 2BS, 2DS
<u>PSR109</u>	5AL	5BL	5DL	5	5	5	+++	+++	2AS, 2BS, 2DS
PSR120, PSR145	5AL	5BL	5DL	3	3	3	+++	+++	
PSR150	5AL	5BL	5DL	3	3	3	+++	+++	2AS, 2BS, 2DS, 7AS, 7BS, 7DS
<u>PSR426</u> , <u>PSR370</u>	5AL	5BL	5DL	1	1	1	++	+++	
PSR574, PSR637, PSR906, PSR911, PSR1194	5AL	5BL	5DL	1	1	1	++	++	
PSR912	5AL	–	5DL	2	2	1	+++	+++	2AS, 2BS, 2DS
PSR918	–	–	5DL	1	–	–	–	+	
<u>PSR1094</u>	5AL	5BL	5DL	1	1	1	+	++	
<u>PSR1101</u>	5AL	5BL	5DL	1	–	1	–	++	
PSR1201	5AL	–	4DL ^d	3	–	–	–	–	1AS
	–	5BL	–						
PSR1202	5AL	–	–	M	–	–	–	–	
PSR164	5AL	4BL	4DL	1	1	1	+++	+++	
PSR567	7BS	5BL	5DL	4	3	3	++	++	4BL, 4DL

Note: For PSR probes, which are available for research purposes, more detailed descriptions of characteristics, including charts of the CS fragment sizes in different restriction digests, are available

^a Sources of the known function clones: pTA71, M. O'Dell; pACP1, pACP11, and pACPII, L. Hansen; pcβC51, M. Kreis; pCat2.1c, J. G. Scandellios; p33, D. C. Baulcombe; WL:agal, W. W. Schuch; pGC19, R. S. Quatrano; pUBA1, P. M. Hatfield

^b Anonymous clones are isolated from wheat cDNA (PSR50-PSR200) and gDNA (PSR numbers > 300) libraries as described in Devos et al. (1992)

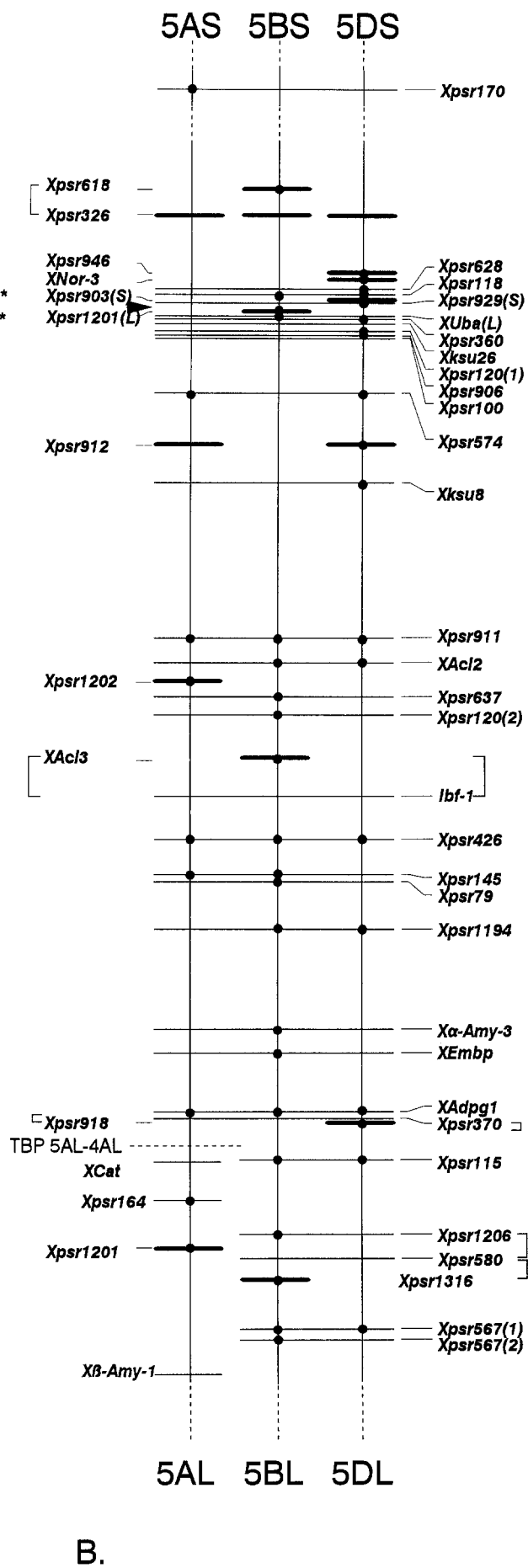
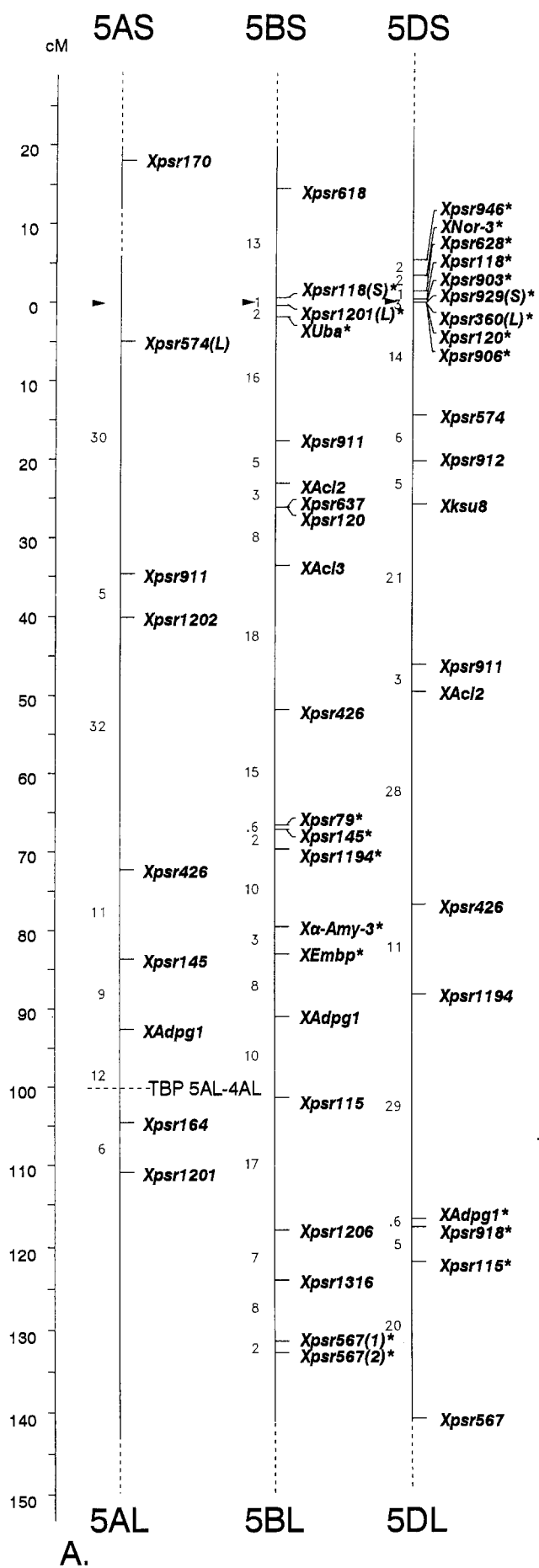
^c Underlined probes have not been mapped

^d Location obtained by linkage in varieties other than CS, which is null at these loci

^e The copy number is determined from the minimum number of hybridizing bands per genome over four restriction digests; M, Moderately repeated; H, highly repeated

^f nd, No data available

^g The relative strength of the hybridization signal in comparison to wheat: + + +, signal comparable in strength to wheat; + +, weaker, but adequate signal; +, weak signal; –, no detectable hybridization



have been detected by *in situ* hybridization on chromosome arms 1AS, 1BS, 5DS, 6BS and 7DL (Mukai et al. 1991). The physical position of the *Nor-D3* locus, the 18S.26S rDNA site on chromosome 5DS, was at the distal end of that chromosome arm. Genetically, however, *XNor-D3* is no more than 3 cM from the centromere. Quantitatively similar results, where the relative genetic distance is shorter than the physical distance in centromeric regions, have been obtained for the *XNor-B1* and *XNor-B2* loci on chromosomes 1B (Snape et al. 1985) and 6B (Dvořák and Chen 1984) in wheat, and for the *XNor-R1* locus on rye (Wang et al. 1991).

The *ph1b* deletion

Chromosome pairing in allohexaploid wheat is limited to homologues at metaphase I by the action of the *Ph1* gene on chromosome 5B. Two independent deletion lines are available, both of which lack the segment of 5BL carrying *Ph1* and in which homoeologous pairing occurs. These mutant lines are *ph1b* in the hexaploid wheat cv 'Chinese Spring' (Sears 1977) and *ph1c* in the tetraploid wheat cv 'Cappelle' (Giorgi 1978).

Recently, Clarke et al. (1992) described the isolation of a clone, a39 (PSR1201), from a library produced by PERT driven by *ph1b* genomic DNA. PSR1201 detects sequences on 5AL, 4DL, 5BL and 1AL, and the *Xpsr1201-5B* locus is deleted in both the *ph1b* and *ph1c* mutants. The probe has been mapped on both group 5 chromosomes (Fig. 1). *Xpsr1201-5A* is located in the distal region of 5AL within the segment translocated from 4A and is therefore likely to be homoeologous to the *Xpsr1201-4D* locus. *Xpsr1201-5B*, however, is located close to the centromere on 5BL. These locations, the presence of an additional copy on 1AL and the absence of a significant hybridization signal in rye or barley are consistent with the behaviour of PSR1201 as a 'non-homoeologous' clone. The location of *Xpsr1201-5B* indicates that, genetically, the *Ph1* locus lies close to the centromere on 5BL, which is consistent with the finding of Jampates and Dvořák (1986). The discrepancy between the genetic location of the deletion in the *ph1b* mutant near the centromere and its physical location near the middle of the long arm of 5BL (Dvořák et al. 1984) is again attributable to the distal localization of recombination.

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References

- Baulcombe DC, Huttly AK, Martienssen RA, Barker RF, Jarvis MG (1987) A novel wheat α -amylase gene (α -Amy3). *Mol Gen Genet* 209:33–40
- Bethards LA, Skadsen RW, Scandalios JG (1987) Isolation and characterization of a cDNA clone for the *Cat2* gene in maize and its homology with other catalases. *Proc Natl Acad Sci USA* 84:6830–6834
- Chao S, Sharp PJ, Worland AJ, Warham EJ, Koebner RMD, Gale MD (1989) RFLP-based genetic maps of wheat homoeologous group 7 chromosomes. *Theor Appl Genet* 78:495–504
- Clarke BC, Stancombe P, Money T, Foote T, Moore G (1992) Targeting deletion (homoeologous chromosome pairing locus) or addition line single-copy sequences from cereal genomes. *Nucleic Acids Res* 20:1289–1292
- Devos KM, Atkinson MD, Chinoy CN, Liu C, Gale MD (1992) RFLP-based genetic map of the homoeologous group 3 chromosomes of wheat and rye. *Theor Appl Genet* 83:931–939
- Devos KM, Atkinson MD, Chinoy CN, Harcourt RL, Koebner RMD, Liu CJ, Masojc P, Xie DX, Gale MD (1993a) Chromosome rearrangements in the rye genome relative to that of wheat. *Theor Appl Genet* 85:673–680
- Devos KM, Millan T, Gale MD (1993b) Comparative RFLP maps of the homoeologous group 2 chromosomes of wheat, rye and barley. *Theor Appl Genet* 85:784–792
- Dvořák J, Chen K-C (1984) Distribution of non-structural variation between wheat cultivars along chromosome arm 6Bp: evidence from the linkage and physical map of the arm. *Genetics* 106:325–333
- Dvořák J, Chen K-C, Giorgi B (1984) The C-band pattern of a *Ph*⁻ mutant of durum wheat. *Can J Genet Cytol* 26:360–363
- Gerlach WL, Bedbrook JR (1979) Cloning and characterization of ribosomal RNA genes from wheat and barley. *Nucleic Acids Res* 7:1869–1885
- Giorgi B (1978) A homoeologous pairing mutant isolated in *Triticum durum* cv 'Cappelle'. *Mutat Breed News* 11:4–5
- Guilinan MJ, Marcotte WR, Jr, Quatrano RS (1990) A plant leucine zipper protein that recognizes an abscisic acid response element. *Science* 250:267–271
- Hansen L (1987) Three cDNA clones for barley leaf acyl carrier proteins I and III. *Carlsberg Res Commun* 52:381–392
- Hansen L, Kauppinen S (1991) Barley acyl carrier protein II: nucleotide sequence of cDNA clones and chromosomal location of the *Acl2* gene. *Plant Mol Biol* 97:472–474
- Hatfield PM, Callis J, Vierstra RD (1990) Cloning of ubiquitin activating enzyme from wheat and expression of a functional protein in *Escherichia coli*. *J Biol Chem* 265:15813–15817

Fig. 1A,B. RFLP maps of the homoeologous group 5 chromosomes of wheat. **A** Linkage maps. For the marked loci (*) the map position could not be determined precisely (LOD <2.5) and only a preferred location could be given. *TBP*, Translocation breakpoint. **B** Consensus map. ● Mapped loci, *full lines over the A, B and D genome chromosomes* indicate homoeoloci (conserved over the wheat, barley and rye genomes), *bold line fragments* indicate map positions of non-homoeologous loci, *Drackets linking markers* indicate adjacent loci for which the order could be based only on relative map distances in the A, B, D and R genomes

- Jampates R, Dvořák J (1986) Location of the *Ph1* locus in the metaphase chromosome map and the linkage map of the 5Bq arm of wheat. *Can J Genet Cytol* 28:511–519
- Kam-Morgan LNW, Gill BS, Murthukrishnan S (1989) DNA restriction fragment length polymorphisms: a strategy for genetic mapping of D genome of wheat. *Genome* 32:724–732
- Kreis M, Williamson MS, Buxton B, Pywell J, Hejgaard J, Svendsen I (1987) Primary structure and differential expression of β -amylase in normal and mutant barleys. *Eur J Biochem* 169:517–525
- Liu CJ, Devos KM, Chinoy CN, Atkinson MD, Gale MD (1992) Non-homoeologous translocations between group 4, 5 and 7 chromosomes in wheat and rye. *Theor Appl Genet* 83:305–312
- Mukai Y, Endo TR, Gill BS (1991) Physical mapping of the 18S.26S rRNA multigene family in common wheat: Identification of a new locus. *Chromosoma* 100:71–78
- Naranjo T, Fernández-Rueda P (1991) Homoeology of rye chromosome arms to wheat. *Theor Appl Genet* 82:577–586
- Olive MR, Ellis RJ, Schuch WW (1989) Isolation and nucleotide sequences of cDNA clones encoding ADP-glucose pyrophosphorylase polypeptides from wheat leaf and endosperm. *Plant Mol Biol* 12:525–538
- Plaschke J, Börner A, Xie DX, Schlegel R, Koeber RMD, Gale MD (1993) RFLP mapping of genes affecting plant height and growth habit in rye. *Theor Appl Genet* 85:1049–1054
- Sears ER (1977) An induced mutant with homoeologous pairing in common wheat. *Can J Genet Cytol* 19:585–593
- Snape JW, Flavell RB, O'Dell M, Hughes WG, Payne PI (1985) Intrachromosomal mapping of the nucleolus organiser region relative to three marker loci on chromosome 1B of wheat (*Triticum aestivum*). *Theor Appl Genet* 69:263–270
- Wang ML, Atkinson MD, Chinoy CN, Devos KM, Harcourt RL, Liu CJ, Rogers WJ, Gale MD (1991) RFLP-based genetic map of rye (*Secale cereale* L.) chromosome 1R. *Theor Appl Genet* 82:174–178