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INTERVAL MAPPING OF GENES CONTROLLING GROWTH OF RYE PLANTS

ABSTRACT

The F_2–type population derived from the cross between DS2 and RXL1O inbred lines was used for interval mapping of five growth related traits i.e. plant height, spike length, thousand grain weight, kernel length and kernel thickness. Scanning of the whole 1,140 cM length of rye genetic map consist–ing of 286 marker loci revealed the existence of 6 regions containing QTL5 on chromosomes 1R–5R. Plant height was strongly affected by 1–3 linked dwarfing genes from a distal region of the chromo–some 5RL and by 1 gene on the chromosome 3RL, tightly linked to a marker loci *Xpsr4 75.* These same genes regulated also thousand grain weight and kernel length and thickness. Spike length was deter–mined only by the QTL from chromosome 5RL. In addition a single QTL from chromosome 2R affecting thousand grain weight and kernel thickness was identified, near the molecular marker locus *Xrsq8OS. 1.* Kernel length and kernel thickness were additionally controlled by QTL5 on chromosomes 2R and 1R and 4R, respectively.

Key words: QTLs, growth, genetic map, molecular markers, *Secale cereale* L.

INTRODUCTION

Genetic maps of rye genome developed using molecular markers (Devos *et al.* 1993, Korzun et at. 2001, Ma *et al.* 2001, Masojć et at. 2001) constitute a powerful tool for identification of loci underlying agronomically important traits. Quantitative trait loci (QTLs) can be located on chromosomes by the method of interval mapping (IM) performed with the help of a MAPMAKER\QTL computer programme (Paterson *et al.* 1988, Lincoln *et al.*1993). The main preconditions for successful interval mapping are:

1) individuals included in a mapping population as well as parental lines vary significantly in respect to a given trait,
2) this variation shows normal distribution and
3) individuals are scored in respect to genotype in a mapped molecular marker loci and a trait is measured in a fairly uniform environmental conditions.

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First QTLs identified on rye map were those controlling sprouting resis–tance and alpha–amylase activity, located by Masojë et at. (1998) on chro–mosomes 1–3R and 5R. Two other loci strongly affecting heading time were mapped on chromosomes 4R and 5R (Masojó, Milczarski 1999). Börner et at. 1999 and Korzun et at. (2001) using individually developed mapping population have shown positions of several QTL5 affecting traits related to plant growth. They detected a cluster of QTL5 on the distal region of chro–mosome 5RL, controlling, among others, plant height, thousand grain weight and peduncle length.

DS2 × RXL1O mapping population shows genetic diversity in respect to traits connected with plant growth. It is not surprising, because parental line RXL1O originated from cv. Zeeland is a recessive dwarf, having short, compact spike and round grain. On the other hand maternal line DS2 de–rived from the CtO ss between S. *dighoricum* and S. *cereale* is moderately high, with longer spikes and kernels. The actual map of molecular markers built on DS2 × RXL1O mapping population consists of 286 molecular markers including 201 RFLP, 73 RAPD and 12 isozyme loci and spans the distance 1140 cM (Masojć *et al.* 2001).

The aim of this study was identification and mapping of QTL5 underlying plant growth in the DS2 × RXL1O mapping population.

MATERIAL AND METHODS

99 F_5 families, each derived from individual F_2 plant of the original DS2 × RXL1O cross, were sown in "nests", containing 10–15 plants. Prior to flowering time, F_5 families were bagged to prevent inter–crossings. Ten plants from each family were measured in respect to plant height and spike length at the stage of full ripeness. After harvest, whole grain of each family was bulked and thousand grain weight was determined. Kernel length and thickness were measured on samples consisting of 30 kernels. Mean values of the analysed traits were used for computation in a com–puter programme MAPMAKER\QTL, kindly provided by E.S. Lander (Lincoln *et al.* 1993). Interval mapping was performed using LOD value exceeding 2.0 as a default criterion for discerning QTLs.

RESULTS

The range between parental lines in respect to growth related traits was generally less wide than the range found among F_5 families (Table 1). Also the mean values found within the mapping population was close to the highest parental value. This can be explained by a strong inbreeding effect imposed on lines during selfmg. The sib–crossed plants from each F_5 fam–ily were less affected. Evaluated traits exhibited normal or close to normal distribution within the mapping population and thus could be analysed by a MAPMAKER\QTL.

Table 1

Growth related characters evaluated in parental lines and among F_5 families of DS2 × RXL10 mapping population

Trait name	Trait symbol	Measured values of the trait			
		DS2	RXL10	Mapping population	
				Range	Mean
Plant height	Ht	89 cm	55 cm	40.00 – 137.00	90 cm
Spike length	Sl	6.5 cm	4.5 cm	4.40 – 9.30	6.7 cm
Thousand grain weight	Tgw	19.6 g	20.6 g	10.90 – 27.90	20.9 g
Kernel length	Kl	7.3 g	6.6 mm	6.60 – 9.43	8.2 mm
Kernel thickness	Kt	2.00 mm	2.20 mm	2.41 – 3.22	2.9 mm

Table 2

Characterisation of the QTLs affecting plant growth in DS2 × RXL10 rye mapping population*

Locus	LOD	VE [%]	Additive effect of the RXL10 allele	Nearest marker	Linkage with the nearest marker [cM]
Q Ht uas–3R.1	4.7	25.2	11.9	Xpsr475	0.0–2.0
Q Ht uas–5R.1	15.7	63.1	–24.7	?– Amy3	2.6–3.4
Q Ht uas–5R.2	14.3	49.2	–23.6	Xpsr164	0.0
Q Ht uas–5R.3	25.7	75.1	–27.5	Dw1	0.0
Total Q Ht	24.3	77.2			
Q Sl uas–5R.3	9.5	40.7	–9.5	Dw1	4.4
Q Tgw uas–2R.1	2.2	10.9	–2.0	Xrsq805.1	0.0
Q Tgw uas–3R.`	3.1	16.7	–1.5	Xpsr475	2.0
Q Tgw uas–5R.1	3.3	18.1	–3.5	Dw1	6.0
Total Q Tgw	7.7	36.9			
Q Kl uas 2R.1	3.4	23.1	0.5	Apr2.7	2.0
Q Kl uas 3R.1	3.6	17.8	0.4	Xpsr475	0.0
Q Kl uas 5R.1	10.1	38.3	–0.6	Xpsr164	0.0
Q Kl uas 5R.2	11.4	49.8	–0.7	Dw1	4.0
Total Q Kl	18.1	67.3			
Q Kt uas 1R.1	2.5	17.2	–0.008	Xcdo99	12.0
Q Kt uas 2R.1	2.6	12.6	–0.03	Xrsq805.1	0.0
Q Kt uas 3R.1	2.5	12.3	0.05	Xpsr475	0.0
Q Kt uas 4R.1	3.3	15.5	0.04	Xphp1005	0.0
Q Kt uas 5R.1	2.4	10.7	–0.07	Dw1	4.0
Total Q Kt	12.4	54.3			

Four QTL5 related to plant height were identified on the map (Fig. 1). Three tightly linked QTLs were mapped between *Amy3* and *APR5.2* markers in a SRI distal region containing recessive dwarfing gene *Dwl,* earlier detected by qualitative scoring. Fourth QTL was discerned on

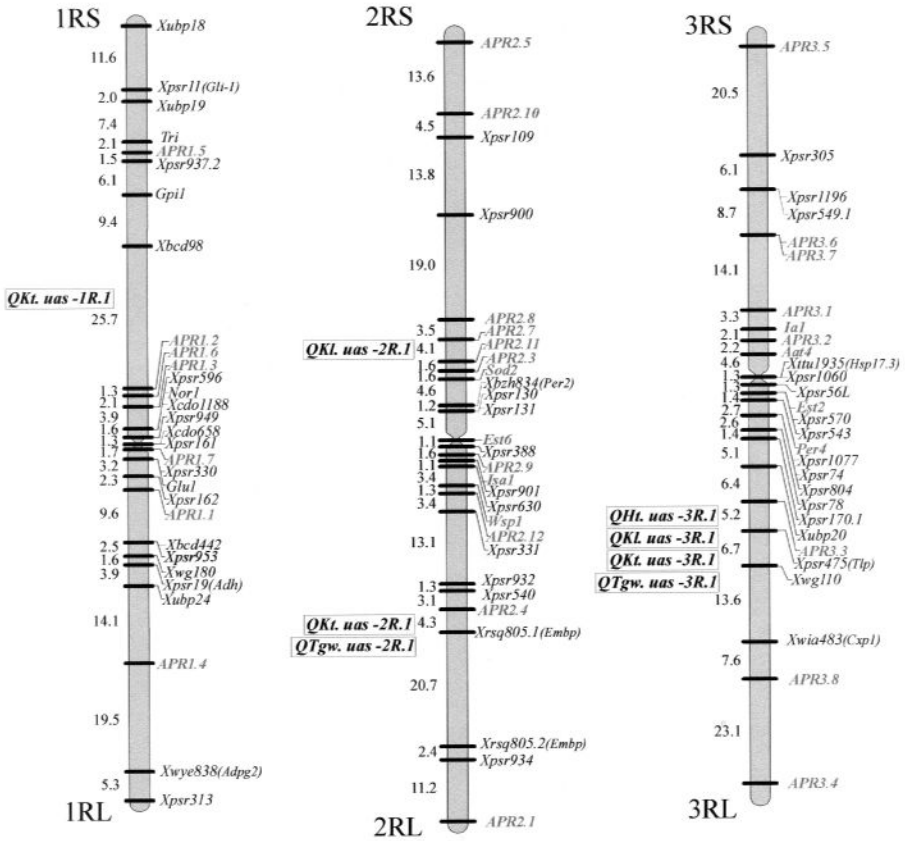
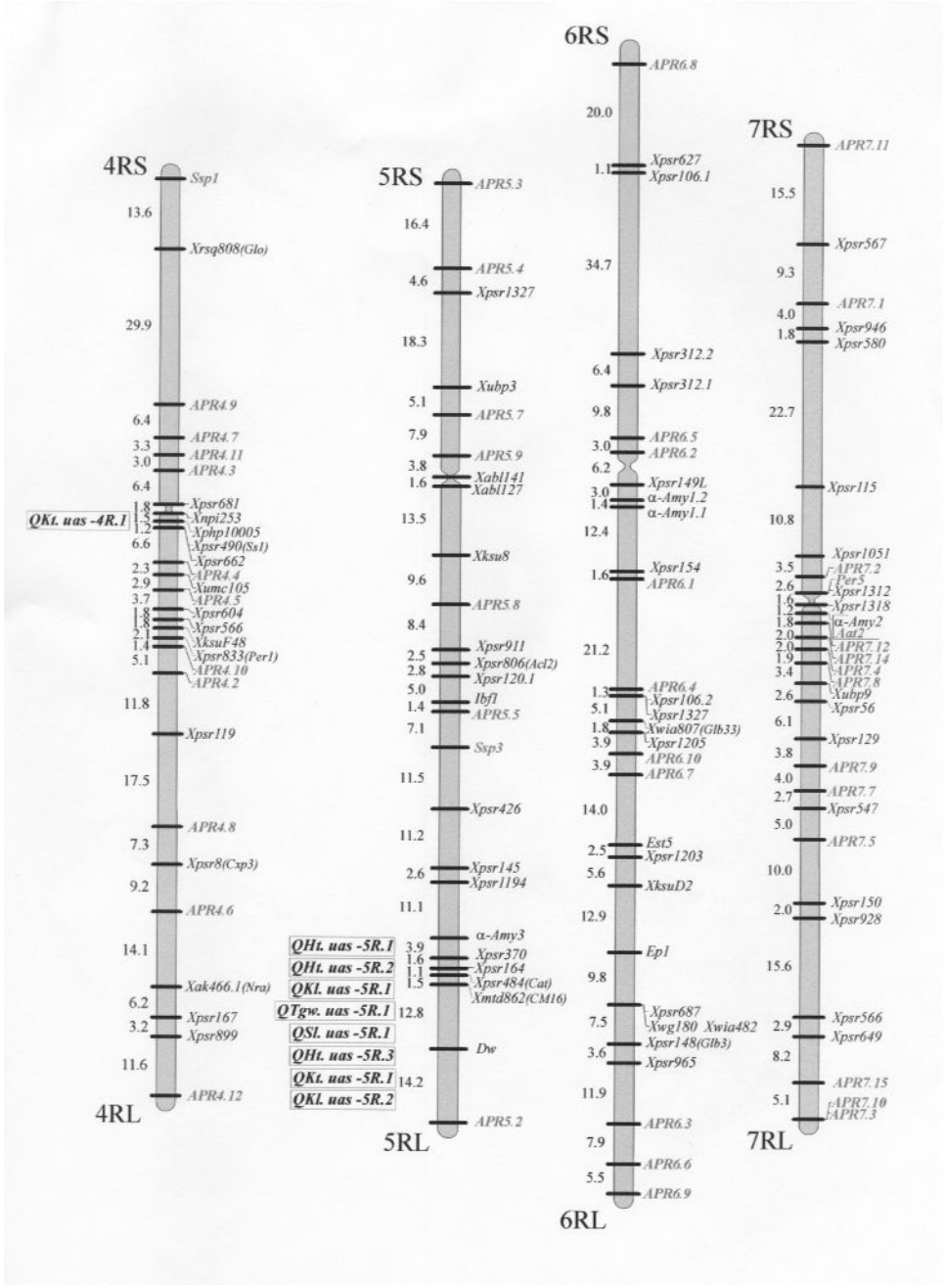


Fig. 1 QTLs controlling traits connected with growth of rye plant detected on a genetic map of rye genome (Masoj© *et al.* 2001), containing RFLP,RADP (*APR*) isoenzyme, protein and mor–phological marker loci. Positionsof QTLs are marked on the left side of the chromosomes (see Table 2 for comparison). The second part of this figure is on the next page


4RS
Ssp1
13.6
Xrsq808(Glo)
29.9
APR4.9
6.4
APR4.7
3.3
APR4.11
3.0
APR4.3
6.4
Xpsr681
1.8
Xnpi253
1.5
Xphp10005
1.2
Xpsr490(Ss1)
6.6
Xpsr662
2.3
APR4.4
2.9
Xumc105
3.7
APR4.5
1.8
Xpsr604
1.8
Xpsr566
2.1
XksuF48
1.4
Xpsr833(Per1)
5.1
APR4.10
APR4.2
11.8
Xpsr119
17.5
APR4.8
7.3
Xpsr8(Cxp3)
9.2
APR4.6
14.1
Xak466.1(Nra)
6.2
Xpsr167
3.2
Xpsr899
11.6
APR4.12
4RL
QKt. uas -4R.1
5RS
APR5.3
16.4
APR5.4
4.6
Xpsr1327
18.3
Xubp3
5.1
APR5.7
7.9
APR5.9
3.8
Xabl141
1.6
Xabl127
13.5
Xksu8
9.6
APR5.8
8.4
Xpsr911
2.5
Xpsr806(Acl2)
2.8
Xpsr120.1
5.0
Ibf1
1.4
APR5.5
7.1
Ssp3
11.5
Xpsr426
11.2
Xpsr145
2.6
Xpsr1194
11.1
α-Amy3
3.9
Xpsr370
1.6
Xpsr164
1.1
Xpsr484(Cat)
1.5
Xmtd862(CM16)
12.8
Dw
14.2
APR5.2
5RL
QHt. uas -5R.1
QHt. uas -5R.2
QKl. uas -5R.1
QTgw. uas -5R.1
QSl. uas -5R.1
QHt. uas -5R.3
QKt. uas -5R.1
QKl. uas -5R.2
6RS
APR6.8
20.0
Xpsr627
1.1
Xpsr106.1
34.7
Xpsr312.2
6.4
Xpsr312.1
9.8
APR6.5
3.0
APR6.2
6.2
Xpsr149L
3.0
α-Amy1.2
1.4
α-Amy1.1
12.4
Xpsr154
1.6
APR6.1
21.2
APR6.4
1.3
Xpsr106.2
5.1
Xpsr1327
1.8
Xwia807(Glb33)
3.9
Xpsr1205
3.9
APR6.10
APR6.7
14.0
Est5
2.5
Xpsr1203
5.6
XksuD2
12.9
Ep1
9.8
Xpsr687
7.5
Xwg180 Xwia482
Xpsr148(Glb3)
3.6
Xpsr965
11.9
APR6.3
7.9
APR6.6
5.5
APR6.9
6RL
7RS
APR7.11
15.5
Xpsr567
9.3
APR7.1
4.0
Xpsr946
1.8
Xpsr580
22.7
Xpsr115
10.8
Xpsr1051
3.5
APR7.2
Per5
2.6
Xpsr1312
1.6
Xpsr1318
1.2
α-Amy2
1.8
Aat2
2.0
APR7.12
2.0
APR7.14
1.9
APR7.4
3.4
APR7.8
2.6
Xubp9
Xpsr56
6.1
Xpsr129
3.8
APR7.9
4.0
APR7.7
2.7
Xpsr547
5.0
APR7.5
10.0
Xpsr150
2.0
Xpsr928
15.6
Xpsr566
2.9
Xpsr649
8.2
APR7.15
5.1
APR7.10
APR7.3
7RL

a long arm of chromosome 3R, showing tight linkage with *Xpsr475* — RFLP marker locus. All these *Ht* loci exhibit high LOD values ranging from 4.7 for *QHt.3R. 1* to 25.7 for *QHt.5R3* (Table 2). Altogether *QHt* loci determine the plant height in as much as 77.2%. The major effect is exerted by the SRI loci, since they are identified as dwarfing gene (genes). Polymorphism at the *QHt. 3R. 1* locus has two times lower effect on plant height than dwarfing gene and its allele present in line RXL1O acts positively on the trait.

Only one QTL controlling spike length was revealed in the region of the *Dwl* dwarfing gene on SRI. This locus determines the trait variation in 40.7% and the allele belonging to RXL1O line reduces the spike length for 9.5 mm on average (Table 2).

QTLs underlying the observed variation of thousand grain weight were mapped on chromosomes 2RL, in a close linkage with the *Xrsq8OS. 1* RFLP marker, on 3RL, adjacent to Xpsr475 locus and on SRI in the region of the *Dwl* gene (Fig 1.). Alleles from line RXL1O contained in a loci on chromosomes 2R and SR have negative effect, while allele of the 3RL locus acts positively (Table 2).

Kernel length was controlled by four QTL5. In the presence of allele from RXL1O line, kernel length is increased by *Kl 2R. 1* and *Kl 3R. 1* loci and decreased by two linked loci from chromosome SRI (Fig. 1, Table 2). A genetic background of kernel thickness was partially the same as that of kernel length. Both traits were controlled by the QTL

from chromosome 3R and the QTL from chromosome SRI. Moreover the allelic effects in each locus were similar for both traits i.e. RXL1O allele from the locus on chromosome 3RI increased both kernel dimensions while allele at SRI acted negatively. Other three genes found to underlay variation in kernel thickness were located on chromosomes 1R, 2R and 4R (Fig. 1, Table 2).

DISCUSSION

The results of this study showed that distal region of chromosome SRI, where a qualitatively distinguished dwarfing gene *Dwl* is located (Devos et at. 1993), contain 1–3 linked QTLs strongly affecting all analysed traits connected with plant growth. This finding is in agreement with earlier reports of Börner *et al.* (1999) and Korzun et at. (2001) obtained on different from ours mapping populations. These authors detected 2–3 linked QTL5 underlying plant height and located in a region of dominant dwarfing gene locus *(Ddwl).* Similar location was found for QTL5 underlying peduncle length and thousand grain weight, which might be explained by pleiotropic effects of the single *Ddwl* locus. Interestingly the dwarfing allele found in our study is recessive, unlike that from mapping population used by Börner et at. (1999). Apparently *Dwl* (Devos *et al.* 1993) or *Ddwl* (Korzun et at. 2001) is a polymorphic locus having both dominant and recessive dwarfing alleles. Another explana–

tion, taking into consideration the appearance of 2–3 QTL5 in the distal region on SRI, might assume that *Dwl* and *Ddwl* are two tightly linked dwarfing genes. Börner et at. (1999) found also on chromosome SRS, near the centromere, QTL affecting spike length. In our study only one locus, linked to *Dwl* on SRI determined spike length.

This paper reveals the existence of a new QTL controlling rye plant growth, which is located on chromosome 3R and linked with the *Xpsr475* RFLP marker. This locus shows pleiotropic effects on four traits related to growth i.e. plant height, thousand grain weight, kernel length and thickness. Allele from line RXL1O enhanced the growth, exhibiting positive additive effects on all four traits. A third chromosomal region containing pleiotropically acting gene is that of chromosome 2R, around the Xrsq8OS.1 RFLP marker. It contains QTL negatively affecting grain weight and kernels thickness. A comparison between genetic systems underlying thousand kernel weight and kernel dimensions shows that they share 2–3 common genes and in addition contain at least 2 independent genetic loci.

It is apparent from the observations of the shape of rye kernel that it can vary, being sometimes short round, short thin, long thick or long thin. The two grain dimensions —length and thickness are not always correlated. This observation is understandable in view of the results of this study. A systems of 4–S QTLs underlying each of the two kernel dimensions are only partially overlapping. The two common loci are those from chromosome SRI and 3RL. The remaining two loci in case of kernel length and three loci for kernel thickness are located in different chromosomal regions and may regulate kernel growth in different ways.

CONCLUSIONS

1. The variation of plant height within DS2 x RXL1O mapping population is controlled by QTLs from two different chromosomal regions. In a distal part of the chromosome SRI, containing known dwarfing gene *Dwl,* 1–3 linked QTLs exist and, in addition, a single QTL on a chromosome 3RI affects growth of rye plants.
2. QTLs from chromosome SRI andlor 3RI exert strong pleiotropic effects on other growth related traits like spike length, thousand grain weight, kernel dimensions.
3. Two partially overlapping gene systems consisting of 4 and S QTL5 underlay kernel length and thickness respectively. Both systems have common genes on chromosomes SRI and 3RI and 2 or 3 additional independent QTL5 on chromosomes 1R, 2R and 4R.

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