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QTL ANALYSIS OF YIELD-RELATED MORPHOLOGICAL TRAITS AND RESISTANCE TO POWDERY MILDEW IN AN INTROGRESSVE LINE OF BREAD WHEAT

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The introgressive line 8/1, a derivative of the susceptible spring wheat cultivar 'Tähti' and *Triticum militinae* (2n=28 AtAtGG), is characterized by improved resistance to *Blumeria graminis* ssp. *tritici*. Altogether, the line carries *Triticum militinae* translocations on seven chromosomes (Figure 1), including translocations involved in adult plant resistance to powdery mildew on chromosomes 4A (*Xwmc232-Xgwm160)*, 5A *(Xgwm666-Xcfa2185)* and 7A (*Xbarc70*), responsible for 54%, 23%, and 18% of the quantitative trait of adult plant powdery mildew resistance, respectively (Jakobson et al., 2006, TAG 112:760 and unpublished data).

The plants of the line 8/1 are higher than those of the original spring wheat cultivar 'Tähti', the spike is longer and of low compactness (speltoid type) with high rachis fragility and low grain threshability (Table 1). The line 8/1 is also characterized by slower rate of development compared to 'Tähti', the delay in ear-emergence being about 5 days.

For breeding purposes, the high resistance to powdery mildew in line 8/1 should be separated from undesirable morphological traits.

QTL mapping of several morphological traits was carried out in two mapping populations developed for the resistance QTL analysis: i), a single-seed descendant F2 mapping population from a cross of the resistant line 8/1 with cultivar Tähti (134 plants, 2002) and ii), a doubled haploid (DH) mapping population developed from the same cross (135 lines).

Both the F2 mapping population and the DH population were grown in the field, the first in 2002 and the latter in 2006 and 2007; in 2009, DH plants were planted in a controlled environment. Both populations were evaluated for plant height, spike length, kernel weight per spike, a thousand kernel weight, spikelet number per 10 cm of spike (compactness). In 2009, DH population plants were additionally evaluated for ear-emergence time, rachis fragility and grain threshability.

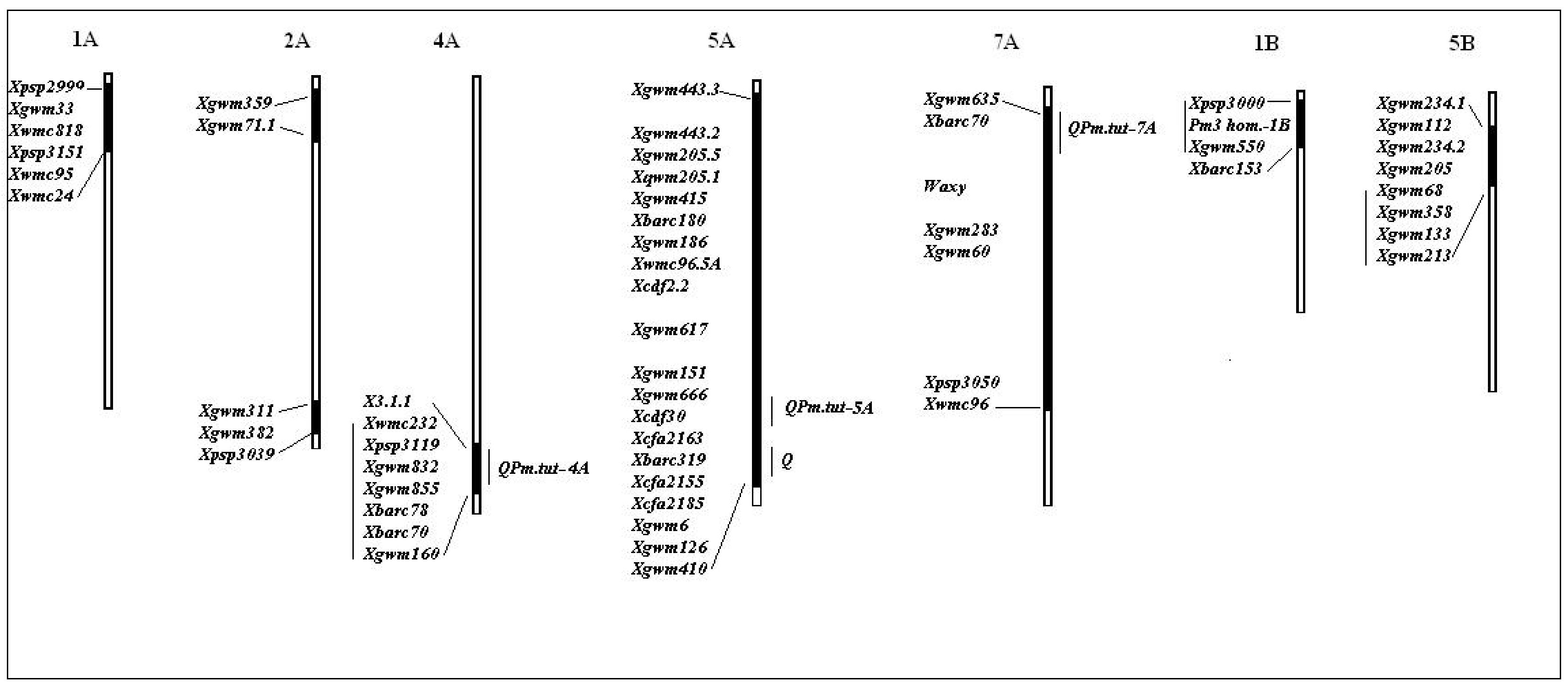

Fig. 1. *T. militinae*-originating translocatons in the genome of the introgressive line 8/1 DH

Year	Lines	Number of plants		Plant height (cm)	Spike length (cm)	Spikelet number	Compactness (spikelet number per 10 cm of spike)	Grain number per spike	Grain weight per spike (grams)	Thousand kernel weight (grams)	Threshability (%)	Rachis fragility (%)	Ear-emergence time (days)
2006	Tähti			107.0	8.3	18.6	22.4	47.7	2.0	42.4			
	8/1			111.9	10.1	17.0	16.9	43.7	2.1	46.6			
	DH	66	mean	109.0	9.5	18.0	19.2	41.4	1.6	39.5			
			range	74.0-128.0	7.1-11.8	12.6-20.0	15.1-24.6	21.0-54.6	0.7-2.2	23.2-50.3			
2007	Tähti			82.1	8.0	17.5	22.0	40.9	1.5	37.2			
	8/1			92.1	9.9	16.4	16.6	42.8	1.5	34.4			
	DH	119	mean	83.4	8.5	15.5	18.4	35.5	1.3	34.8			
			range	50.6-99.4	5.6-10.4	11.0-17.6	14.7-23.1	15.8-48.2	0.3-2.0	15.7-46.5			
2009	8/1			130.0	14.0	20.0	14.3	48.0	2.1	44.7	69.2	48.0	77.0
	Tähti			117.0	10.3	21.0	20.4	41.4	2.0	48.6	99.5	5.0	72.0
	DH	135	mean	114.8	10.9	22.3	21.0	32.0	1.5	44.2	90.7	8.0	76.2
			range	67.0-147	5.2-15.7	16-.0-25	14.7-34.6	20.3-46.5	0.3-2.6	19.4-56.1	22.0-100.0	3.8-33.0	65.0-88.0

Table 1. Mean performance and range of traits of the parental lines and mapping populations measured in the 3 years

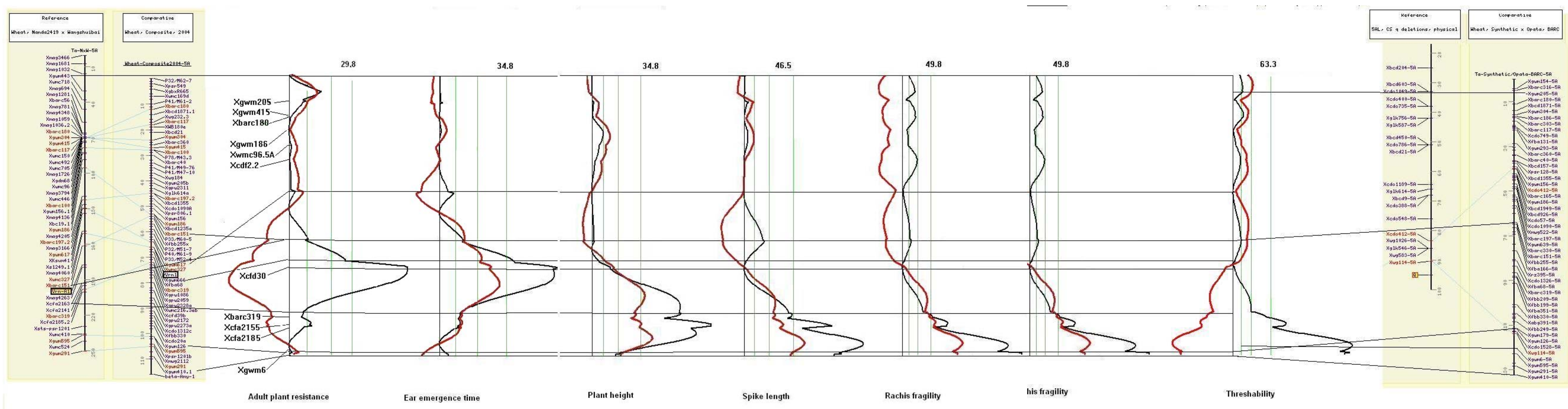

Fig. 2. Effect and position of QTLs for morphologial traits and for adult plant resistance to powdery mildew on chromosome 5A (DH population in 2009, *MapManager QTX*, simple interval mapping, free regression model). Black line – likelihood ratio statistic, red line – additive effect. Green vertical lines represent the suggestive, significant and highly significant LRSs. Critical LRS statistic values for highly signifiant level are given above.

The three *T. militinae* translocations responsible for the high adult plant powdery mildew resistance in line 8/1 were all involved in the modification of some of the analyzed morphological traits. Below, only the highly significant (***) and significant (**) effects are listed.

The 4A translocation carrying the main QTL for resistance was involved in the delayed ear-emergence (13% of the trait variation,), low threshability and high rachis fragility (10% and 9%, respectively, both **). The translocation also affected spike length (13%, ***) and compactness (8%, **). We have no recombinant plants in this translocated region.**

In the region of *Xpsp3001-Xpsp3050* of the long translocation on chromosome 7A, *T. militinae* alleles affected the same morphological characteristics (10% of the delay in ear-emergence, 17-18% of threshability and rachis fragility, 12% of higher spike length, all *). This region is well separated from the *Xbarc70* region of the resistance QTL.**

All analyzed morphological traits were affected by the *T. militinae* alleles on the almost fully substituted chromosome 5A. In the line 8/1, this chromosome was resposible for 28% of the delay in ear-emergence, and 11% (*Xgwm415- Xbrc180*) + 23% (*Xcfa2163-Xfa2155*) + 46% (*Xgwm6-Xgwm410*) of the low threshability (all *). Similarly to chromosome 7A, rachis fragility was affected by the same regions as threshability (15%, 25%, and 54%, respectively, all ***) on chromosome 5A. The (*Xgwm415- Xbrc180*) and (*Xgwm6-Xgwm410*) regions on chromosome 5A also had a lowering effect on the thousand-kernel-weight (15% (***) and 14% (**), respectively).**

In the *Q* gene region (*Xgwm6-Xgwm410*) on chromosome 5A, the *T. militinae* allele also strongly affected the compactness of the spike (30%,*) and spike length (33%, ***, Figure 2). Recombinant DH plants carrying the resistance QTL originating from *T. militinae* and the common wheat allele in the *Q* gene region have been identified.**

However, the major QTL affecting ear emergence time was mapped on the *T. militinae* 5A chromosome translocation in the region of adult plant resisance QTL betweem the loci *Xbarc151* and *Xcda2163* (DH population 2009, Figure 2). In 2006 and 2007, QTLs for spike length and plant height were detected in the same region (data not shown). A gene determining the spring/winter growth habit or vernalization response, *Vrn-A1*, has been mapped on chromosome 5A in the region of *Xbarc151-Xgwm666*, and has been shown to have a primary effect in controlling ear-emergence time similarly to the *Q* gene (Kato et al. 1999). It has been supposed that in most situations later flowering plants tend to be taller simply due to their extended life cycle, and allelic variation at *Vrn-A1* could regulate plant height (Kato et al. 1999, TAG 98:472).

In conclusion, ear-emergence/plant height/spike length QTLs have been mapped in the region of the QTL for adult plant powdery mildew resistance on chromo-some 5A. A QTL for seedling resistance has also been detected in the same region (data not shown). Fine mapping of this region is needed to decide whether the *Vrn-A1* gene supposedly responsible for the altering of ear emergence/plant height/spike length, might affect the resistance.