

Mapping of major net-type net-blotch resistance loci in Ethiopian barley line c-23874 and the Russian barley cultivar Zernogradskij 813

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Materials and methods

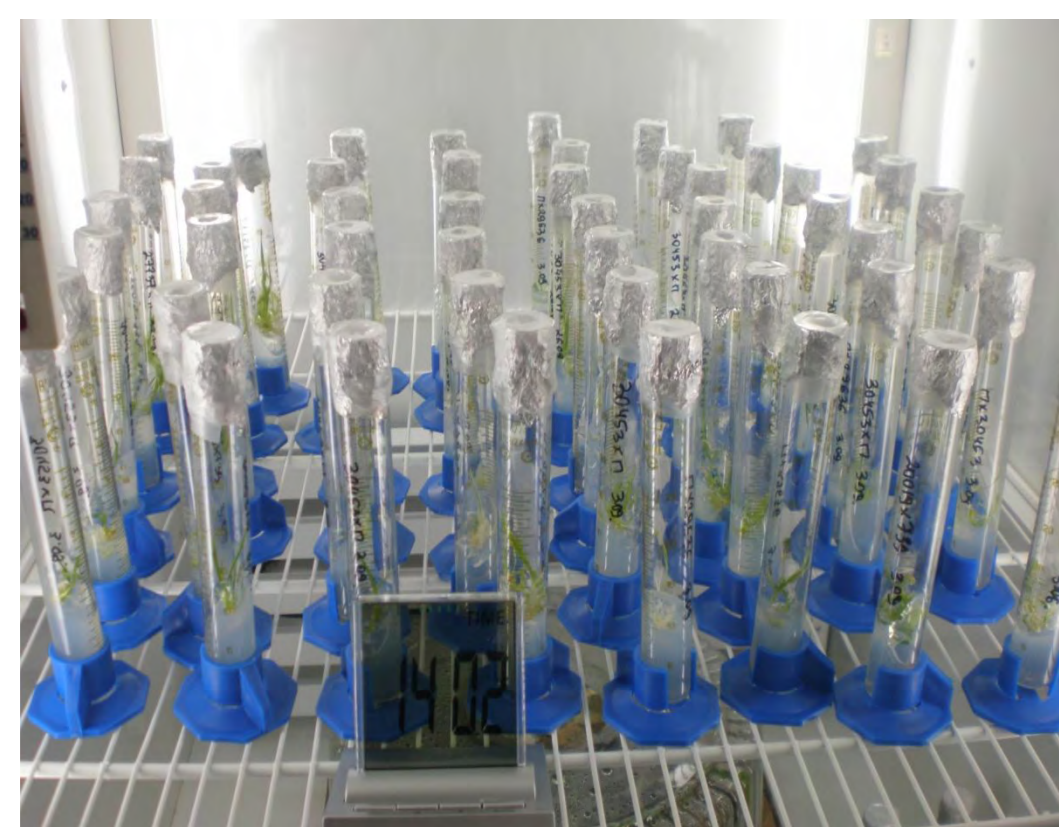


Net blotch caused by *Pyrenophora teres* Drechs f. *teres* is an important barley disease in Russia and elsewhere. Under favorable conditions net blotch can cause significant reductions in both the yield and quality of the crop. Yield losses from this disease on susceptible cultivars in Russia can reach 40% under epidemic conditions.



Table. 1. Two barley mapping populations comprise anther culture-derived doubled-haploid lines (DHLs), were developed.

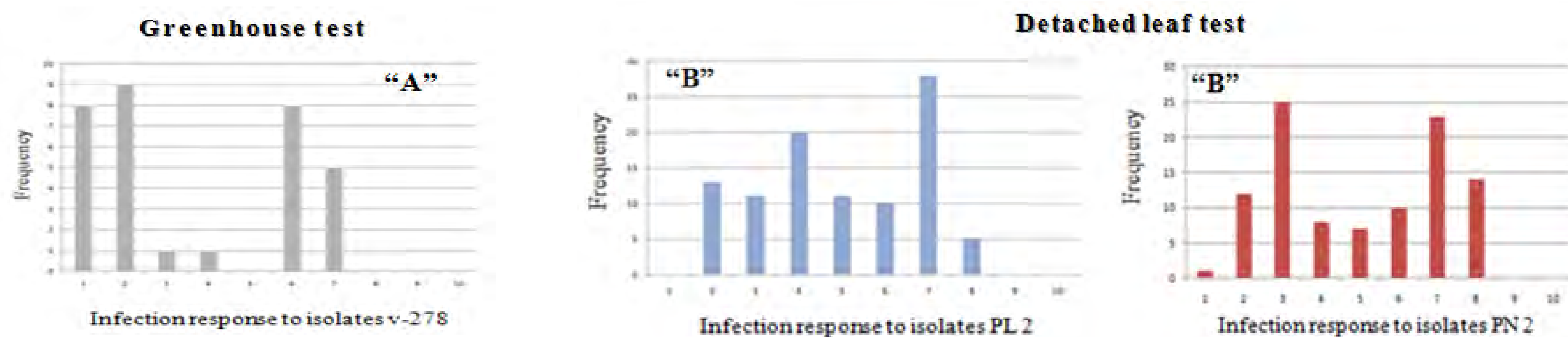
Barley varieties	Origin	Resistance to	
		<i>Pyrenophora teres</i>	<i>Cochliobolus sativus</i>
Mapping population A, 44 DHLs			
Pirkka	Finland	S	S
C-23874	Ethiopia	R	MS
Mapping population B, 114 DHLs			
Rannij 1	Russia (Siberia)	S	R
Zernogradskij 813	Russia (South Region)	R	S



Resistance evaluations were conducted in 2010 in greenhouse of MTT (Finland) and at laboratory conditions (VIZR, Russia) using detached leaf technique. DHLs were screened with one NTN isolate from Finland and two isolates from the Northern part of Russia collected in Leningrad (PL 2) and Novgorod (PN 2) regions in 2010.

Results and discussion

Fig. 1. Frequency of disease reaction incited on the DHLs of two barley populations ("A" and "B") by *Pyrenophora teres* isolates.



Reaction of parental genotypes to isolates PL2 and PN2.



In the greenhouse experiments two parental genotypes c-23874 and Pirkka were inoculated in four replications by isolate v-278 and showed averaged infection types 1.5 and 8 correspondingly

The infection response was recorded on the second leaf, 10 days after inoculation, using the 10-point scale (1)

Scale in greenhouse test



Segregation of resistance to PL 2 and PN 2 isolates in DHLs of "B" population

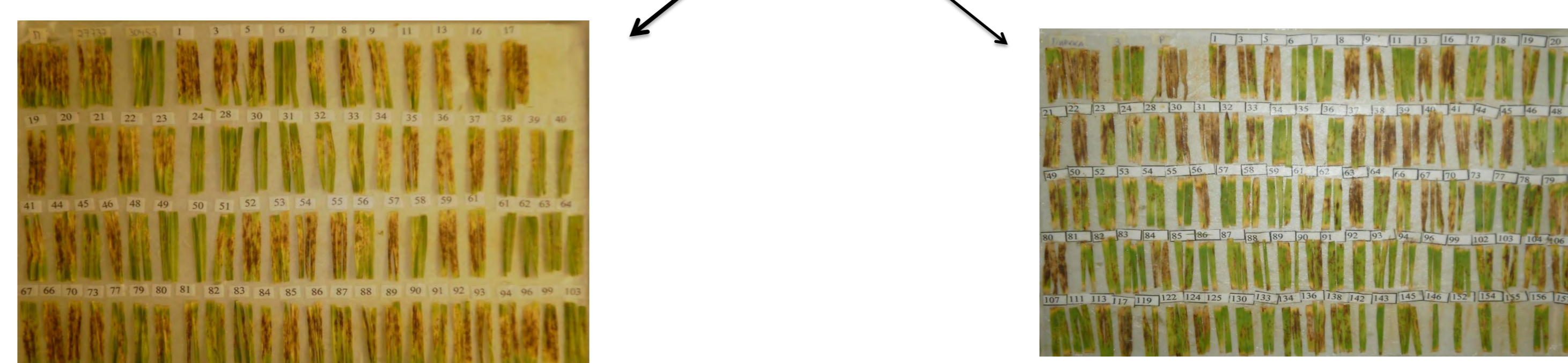


Table. 2. Number of polymorphic SNP markers, used for genotyping two DHLs populations

Chromosomes	Quantity of SNP markers	Polymorphic
Population "A"		
1H	43	12
2H	64	14
3H	55	20
4H	49	12
5H	74	19
6H	55	17
7H	44	14
Bcero:	384	108
Population "B"		
1H	43	18
2H	64	27
3H	55	31
4H	49	20
5H	74	30
6H	55	22
7H	44	16
Bcero:	384	164

The 384 SNP set employed for genotyping of the both DH populations was selected at the JHI and covered all seven barley chromosomes. All 384 SNP markers provided good quality genotype calls for the DHLs, 108 and 164 SNP markers showed polymorphism in population "A" and "B" respectively and were used for mapping. For both populations linkage groups were assembled using the computer program MapManager QTX (2) with an LOD > 3.0 and the Kosambi mapping function (3). In all four replications of the inoculation experiment the highest LOD score (2,9) was associated with the SNP marker 11_11067 located on chromosome 6H (58 cM).

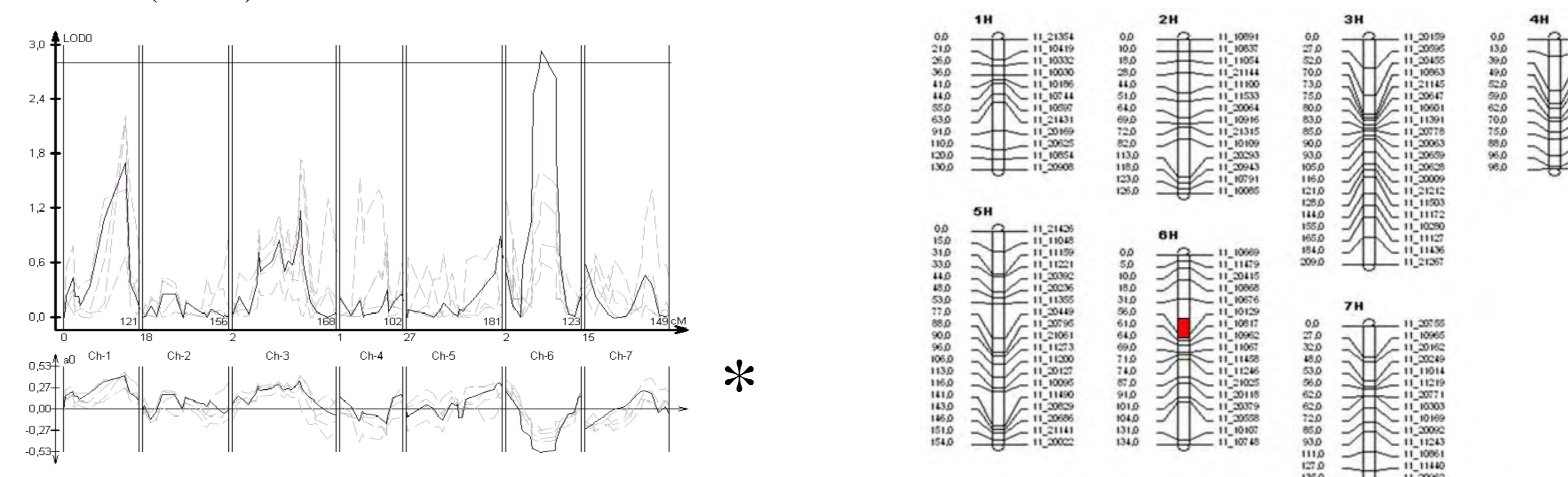


Table. 3. Marker intervals putatively associated with seedling resistance to two isolates of *P. teres* f. *teres* originated from the North of Russia in DH barley population derived from Rannij/ Zernogradskij cross

Isolate	Origin	Exp	Infection response		Effect of QTL in DH progeny			
			Parents		Location of QTL	OTL interval (cM)	Resistance source	LOD/R ²
			Rannij1	Zernogradskij 813				
PL 2	Leningrad region	1	8.2	2.5	5H	4,6-19,9	Zernogradskij	2,4/0,08
		2	7.1	2.2	5H	4,6-19,9	Zernogradskij	3,7/0,12
PN 2	Novgorod region	1	7	2,2	5H	4,6-19,9	Zernogradskij	3,0/0,11
		2	7,2	2,2	5H	4,6-19,9	Zernogradskij	2,7/0,10

* - additive effect of c-23874 allele

Location of major net blotch resistance genes on barley chromosome

To determine the critical LOD threshold, we executed a permutation test with 1000 permutations. A LOD threshold of about 2.7 in this DH population yields an experiment-wise significance level of 0.05. An identical marker interval associated with resistance to NTN was identified for the both isolates on short arm of chromosome 5H explaining 8-12% of the total variation. The interval was flanking by SNP markers 11_20533 and 11_20899 located in 4,6 and 19,9 cM on the Rannij 1/ Zernogradskij 813 genetic map.

Literature cited: 1. Tekauz A. A numerical scale to classify reactions of barley to *Pyrenophora teres* / A. Tekauz // Canad. Journal of plant pathology – 1985 – V.7 – P.181-183. 2. Manly K.F. Map Manager QTX, cross-platform software for genetic mapping/ K.F. Manly, R.H. Cudmore, J.M. Meer// Mammal Genome – 2001- V.12 – P.930-932. 3. Kosambi D.D. The estimation of map distances from recombination values / Ann. Eu-gen. , 12, 1944, p.172–175.