

QTLs Associated with Breeding Characteristics in Oat DH Mapping Population

Tanhuanpää P¹, Kiviharju E^{1*}, Manninen O¹, Schulman A^{1,2}, Kalendar R², Eurola M¹, Hietaniemi V¹, Jalli M¹, and Pietilä L³

¹MTT Agrifood Research Finland, FI-31600 Jokioinen, Finland

²MTT/BI Plant Genomics Laboratory, Institute of Biotechnology, FI-00014 University of Helsinki, Finland

³Boreal Plant Breeding Ltd, FI-31600 Jokioinen, Finland

* corresponding author: elina.kiviharju@mtt.fi



INTRODUCTION

All the maps reported for hexaploid oat have been constructed using recombinant inbred lines (RILs). Another permanent population type is a doubled haploid (DH) population. Compared to RILs, DHs contain no residual heterozygosity. DHs have been applied for mapping in several cereal species, but in oats production of DH mapping population has only recently started to be an option.

MATERIALS AND METHODS

A mapping population of 137 DH plants was generated through anther culture¹ of F₁ plants from the cross between cvs. Aslak and Matilda. A linkage map was built using DNA markers including microsatellites, RAPDs, SRAPs, AFLPs, ISSRs, IRAPs, and REMAPs. Joinmap 3.0⁴ was used for map construction (LOD score mainly 9.0).

Several agronomic and quality traits were analyzed from field trials in years 2005 (1 m² plots with four replicates) and 2006 (6 m² plots with three replicates)(Fig. 1). Leaf blotch disease (caused by *Pyrenophora avenae*) resistance was also evaluated in a greenhouse test with two different isolates. NQTL version 26-Nov-2001³ was used for QTL analysis. Both simple interval mapping (SIM) and simplified composite interval mapping (sCIM) were used.

RESULTS AND DISCUSSION

A DH linkage map of 28 linkage groups consisting of 625 markers was built². The total map size was 1526 cM. QTLs associated with all of the traits studied were found (Table 1 and Fig. 2), and the number of QTLs affecting each trait varied from one to seven. Usually same QTLs were discovered in different years (e.g. two β -glucan QTLs) but sometimes additional QTLs were found in 2005 which is not surprising because quantitative traits are affected by environment, and climatic conditions in 2005 and 2006 were quite different.

Some chromosomal regions affected more than one trait, e.g. QTLs in linkage groups 7 and 11 affected both oil and protein content. It is difficult to differentiate between one QTL having an influence on both these traits and two QTLs situating close to each other. The alleles that had a positive effect on the trait were often derived from either parent (e.g. in β -glucan from Aslak, in oil content from Matilda) but in some traits both parents contributed favourable alleles (e.g. protein content).

Markers closely linked to the traits can be used in marker-assisted selection for more efficient oat breeding.



Fig.1. Oat DH lines in the field.

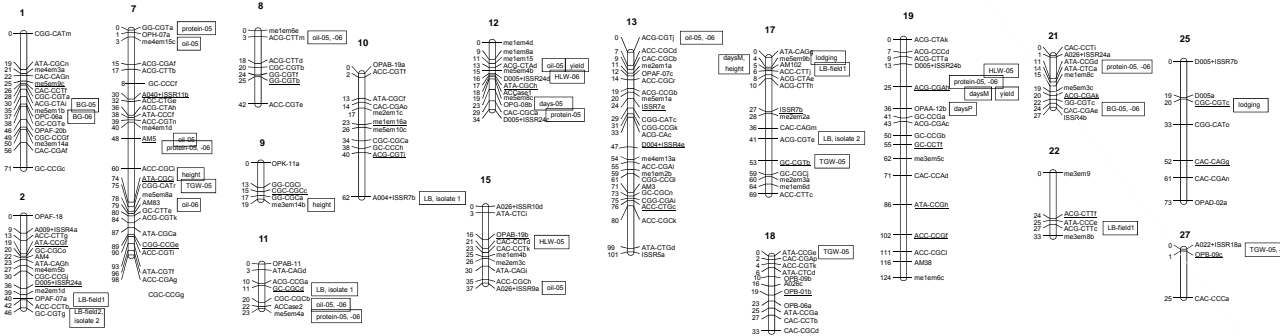


Fig. 2. Linkage groups of oat (not all groups and markers included) with QTLs affecting β -glucan (BG), oil content, protein content, leaf blotch disease resistance (LB; field1=at the beginning of infection, field2= at the maximal infection, isolate 1 and 2 from greenhouse tests), hectoliter weight (HLW), thousand grain weight (TGW), yield, height, lodging, growing time from sowing to maturity (DaysM) and to panicle (DaysP). Background markers are underlined.

REFERENCES

1. Kiviharju E, Moisaner S, Laurila J (2005): Improved green plant regeneration rates from oat anther culture and the agronomic performance of some DH lines. *Plant Cell Tiss Organ Cult* 81: 1-9.
2. Tanhuanpää P, Kalendar R, Schulman AH, Kiviharju E (2008): The first doubled haploid linkage map for cultivated oat. *Genome* (in press).
3. Tinker NA, Mather DE (1995): MQTL: Software for simplified composite interval mapping of QTL in multiple environments. *J Quant Trait Loci* 1.
4. Van Ooijen JW, Voorrips RE (2001): Joinmap 3.0, Software for the calculation of genetic linkage maps. Plant Research International, Wageningen, the Netherlands.

QTL in linkage group	relative allele	R ²
<i>Beta-glucan 2005</i>		
7	matilda	0.20
11	aslak	0.22
17	aslak	0.37
<i>Beta-glucan 2006</i>		
8	matilda	0.19
21	aslak	0.34*
<i>oil 2005</i>		
7	matilda	0.13
11	matilda	0.20
12	matilda	0.14
13	matilda	0.25
15	matilda	0.15
19	matilda	0.14
<i>oil 2006</i>		
11	matilda	0.02
13	matilda	0.22
15	matilda	0.12
19	matilda	0.26
21	matilda	0.12
<i>Leaf Blotch - isolate 1</i>		
11	matilda	0.19
17	matilda	0.34
<i>Leaf Blotch - isolate 2</i>		
11	aslak	0.15
17	aslak	0.25
<i>Leaf Blotch - field 1</i>		
8	aslak	0.25
11	aslak	0.23
15	aslak	0.35
<i>Leaf Blotch - field 2</i>		
11	aslak	0.10
15	aslak	0.28
17	aslak	0.38
<i>Height 2005</i>		
11	matilda	0.11
13	matilda	0.14
17	matilda	0.10
19	aslak	0.15
21	aslak	0.17
<i>Height 2006</i>		
11	matilda	0.02
13	matilda	0.11
17	matilda	0.15
19	aslak	0.10
21	aslak	0.16
<i>HLW 2005</i>		
11	matilda	0.03
13	matilda	0.13
17	matilda	0.16
19	aslak	0.15
21	aslak	0.17
<i>HLW 2006</i>		
11	matilda	0.10
13	matilda	0.11
17	matilda	0.10
19	aslak	0.15
21	aslak	0.16
<i>Yield 2005</i>		
11	matilda	0.10
13	matilda	0.11
17	matilda	0.10
19	aslak	0.15
21	aslak	0.16
<i>Yield 2006</i>		
11	matilda	0.12
13	matilda	0.11
17	matilda	0.10
19	aslak	0.15
21	aslak	0.16
<i>DaysM to maturity 2005</i>		
11	matilda	0.11
13	matilda	0.25
17	matilda	0.28
19	aslak	0.28*
<i>DaysM to panicle 2005</i>		
11	matilda	0.17
13	matilda	0.21
17	matilda	0.17
19	aslak	0.14
21	aslak	0.20

Table 1. QTLs in the DH oat linkage map. Threshold for SIM / sCIM presented. Linkage groups in bold contain a QTL based both on SIM and sCIM. R²=the amount of variation explained by the QTL, *=total amount of variation explained.