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SCAR and CAPS Markers Linked to Quality Traits (Oil, β-glucan, and Protein Content) in Oat

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Introduction

To improve grain quality for different markets, oat breeders are faced with the challenge of selecting varieties with high and low content of oil, β-glucan, protein and other chemical traits. Each of these traits is controlled by multiple genetic loci.

We report on the development of PCR-based Sequence Characterized Amplified Region (SCAR) and Cleaved Amplified Polymorphic Sequence (CAPS) molecular markers in oat for application in genetic studies and marker assisted selection (MAS) breeding (Rines et al. 2006). A set of 8 markers were designed to target oil content (Orr and Molnar 2007) and a set of 15 markers were designed to target β-glucan and protein content (Orr and Molnar 2008). These more robust markers were developed from Random Amplified Polymorphic DNA (RAPD) markers mapped in the Kanota x Ogle (KO) (Wight et al. 2003) or the Terra x Marion (TM) (De Koeyer et al. 2004) recombinant inbred line (RIL) populations and associated with QTLs for grain quality traits.

Materials and methods

The diagnostic band of each RAPD marker (10 bp RAPD primer) was isolated from an agarose gel and sequenced. For development of the derived SCAR or CAPS marker, multiple PCR primers (20-25bp) were designed and optimal PCR conditions determined. Then the best combination was tested for polymorphism and mapped on the KO or TM mapping populations, using post-amplification restriction enzyme digestion if necessary.

Results and discussion

Based on QTL studies reported in the literature, 5 RAPD markers were identified as linked to 4 TM QTLs for oil content and a 6th and a 7th RAPD marker were linked to homologous or homoeologous regions. Likewise 7 RAPD markers are linked to β-glucan content QTLs and 2 others to homologous or homoeologous regions. SCAR or CAPS markers were developed from each and mapped in either KO or TM (Table). While many of the new markers map to the same loci as the original RAPD markers, others map to homologous or homoeologous genomic regions and still others to regions not known to be orthologous to the original RAPD regions.

The naked (*N1*) locus on the TM5 linkage group and several other genomic regions are associated with QTLs for multiple traits (Table), either due to clustering of independent genetic loci or due to pleiotrophic affects. Thus 3 of the new markers are associated with both oil and β-glucan content and 9 with protein content.

Similar results have been obtained for numerous SCARs for other traits (Orr and Molnar, unpublished).

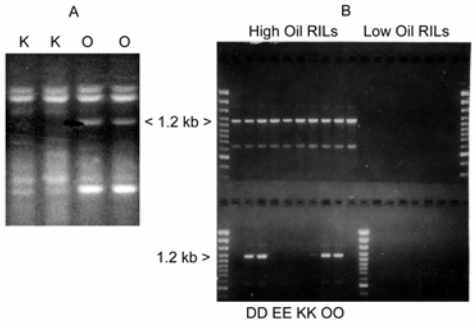

Figure: PCR amplification products separated by electrophoresis in agarose gels give more complex banding patterns for a RAPD marker (A) than for the derived SCAR marker (B). In panel A, RAPD primer ubc364 produces a 1.2kb product with genomic DNA of oat variety 'Ogle' (lanes 3 and 4) but not with 'Kanota' (1 and 2). This polymorphic band was used to design new SCAR primers. Panel B shows products obtained with SCAR marker ubc364os primers and genomic DNAs of 'Dal' (lanes 23 and 24), 'Exeter' (25 and 26), 'Kanota (27 and 28), and 'Ogle' (29 and 30). All high oil content RILs of the Dal x Exeter population produce the 1.2 kb band (2 to 11) but none of the low oil content RILs (12 to 22) indicating that this SCAR has potential for MAS for oil content. Lanes 1, 20, 21, and 32 are molecular weight standards and lane 31 is a control sample lacking any genomic DNA.

SCAR or CAPS Marker	Map Location (Linkage Group) Linkage to published QTL indicated by underlining	
	Original RAPD	Derived SCAR
Oil Content QTLs		
ubc121ms	TM11	TM15
ubc167s	TM15	
ubc167ts (*Hinf I*) #		TM15
ubc167ms (*Hpa II*) #		TM15
ubc185s * #	TM5	TM5
ubc186s	TM15	TM15
ubc189s *	TM4_16	TM8
ubc198s #	TM15	TM15
ubc364os * #	KO15	KO11_41+20
β-Glucan Content QTLs		
ubc109as	TM4	KO14, TM unlinked
ubc109bs	TM2 (KO11 / KM11)	TM2 (KO11 / KM11)
ubc118mbs	Unknown	TM19 (KO3+38)
ubc159as #	TM5	TM5
ubc179os	TM11	KO2 (TM21), [KO3]
ubc185s * #	TM5	TM5
ubc189s *	TM4_16	TM8, KO13
ubc221as	KO17	KO24_26_34
ubc254s	KO5	KO3+38
ubc263s #	TM14	KO2 (TM21), [KO3]
ubc264kas #	TM1 (KO33)	KO17
ubc267s	TM18	TM18
ubc352ks	KO19+27	KO19+27
ubc352os	KO22_44+18, (TM5); TM27	KO22_44+18, (TM5); TM27
ubc360s #	KO33	
ubc360s (*Taq1*)		KO2 (TM21), [KO3]
ubc364os * #	KO15	KO11_41+20
ubc372s	KO3	KO3
ubc375s	KO20	
ubc375s (*DdeI*)		KO20

Notes: * These 3 SCARs are linked to both oil and β-glucan content QTLs.
These 9 SCAR or CAPS markers are linked to protein content QTLs.

Conclusions

These PCR-based markers have potential to service as anchor markers for comparative mapping, to define homologous and homoeologous relationships in oat, to investigate the complex genetics of grain quality traits, and for marker assisted oat breeding.

Our SCAR and CAPS markers complement marker development that has been done by other research groups and several new initiatives, such as DArT and SSR markers, which are underway to increase the number and utility of PCR-based markers in oat.

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