Barley Mutant and SNP Databases at SCRI

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SCRI Barley SNP Database

🖉 Barley SNPDB : SCRI Bioinform	natics - Microsoft Internet Explorer provided by S.C.R.I.			general information on the contigs
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Address 🙆 http://germinate.scri.sa	ri.ac.uk/barley_snpdb/		💌 🔁 Go 🛛 Links 🎽	look up a contig
Google - barley snp	🔽 💽 Search 👻 🚿 🕾 O blocked 🛛 🥙 Check 👻 AutoLink 🔹 🗐 AutoFill 🍓 Options 🌛 👸 barley 👸	snp		search affymetrix
SCRI Bioinfor	matics Barley SNP Database		<u>_</u>	contigs using blast
	Balley SNP Database			search affymetrix contigs using keywords
Barley SNPDB Homepage Co	ntact Help Browser Compatibility			choose a data type
main menu	SNP discovery outline			contig abc00076
general information on the contigs	This online database contains information from a project at the SCRI to mine wheat and barley genes for SNPs	which were mapped in barley c	rosses. A synopsis and further details about	primers from abc00076
view linkage maps with	the project can be seen here . An online abstract of the published paper can be seen here .			snps from abc00076
loci derived from affymetrix contigs	Selection of the genes			no map location
look up a contig				display options
search affymetrix contigs using blast	We focused on genes associated with abiotic stress in barley. The reference point for each gene was an EST u Affymetrix probe sets for the Barley1 GeneChip.	nigene from the HarvEST Barley	/ Assembly 21 which was used to design	show list of mutation names
search affymetrix contigs using keywords	Barley germplasm			show good quality sequences with mutations
	A selection of EST unigenes was analyzed for sequence polymorphisms in 8 diverse barley genotypes: OWB D include parents of three doubled haploid mapping populations facilitating linkage mapping of genes and repre- America, as well as a wild barley accession.			show full alignment - including bad quality regions
	Primer design, PCR and sequencing			
	Primers were designed with Primer3 software targeting the 3' ends of unigenes. PCR was carried out on a pa alkaline phosphatase and single-pass sequencing was done with the same primers as PCR using Applied Bi		rmatics < - Microsoft Internet Explorer provided by S.C.R.I. Iools <u>H</u> elp	4
	Sequence analysis	🕒 Back 🔹 🕥 🕣 💌 😰		
	Base calling and sequence assembly was done with phred and phrap . Mutations were identified using polyph	Address 🙆 http://germinate.scr	i.sari.ac.uk/cgi-bin/barley_snpdb/display_contig.cgi?contig=ABC00076	=
	consed .	Google - barley snp	💽 Search 🔹 🧭 🎦 0 blocked 🛛 🖓 Check 👻	<u> </u>
	Polymorphism database	snps from abc00076	_	
		no map location	DNA Sequence of ABC00076	
	Mutations identified by polyphred and the contig alignments were processed using custom-made Perl scripts a	skip to	>ABC00076	
	Reference	details of harvest barley assembly 21 contig	1 CCGCAATCCACCAACCACCATCACCAAATCTCTCTCGCC 61 GCTCCGTCTGTCAGCAATGGAGGTTTCAGGCGCTGCAG	.C.
	Rostoks N, Mudie S, Cardle L, Russell J, Ramsay L, Booth A, Svensson JT, Wanamaker SI, Walia H, Rodriguez		121 AGGGCGCAAGGCCGGCCGGCCGAGGAAGAAGTCAGTGA 181 CCAGTTCCCCGTCGGCCGCATCGGGCGCTACCTCAAGA	ι(
	"Genome-wide SNP discovery and linkage analysis in barley based on genes responsive to abiotic stress." 🛽	sequence of harvest	241 CGGCACCGGTGCCCCGTCTACCTCGCCGCCGTCCTCG	, i
Derlau CNDDD Homonowo Co	wood Illolu	barley assembley 21 contig	301 GGAGCTCGCCGGGAACGCCGCCAAGGACAACAAGAAGA 361 GCTGCTCGCCGTCAGGAACGACGACGAGGAGCTCGGAAAGC	.C.
Barley SNPDB Homepage Co	ntact Help	blast hits to relevant	421 GCACGGCGGCGTGATCCCCAAGATCAACCCGGTGCTGC	Δ.
		databases	481 GGAGGGCAAGGGGCCCAAGTCCCCCCAAGAAGGCCACCA 541 GGCTTAGGAACACGCATAGGTTGATGTAGGTTGCTTAA	
		comments	601 TTGGCTAATGGTGTCGATGTAATCTTTGCTGTTAAGAG	
			661 CCGGAAAAAAAAAAAAAAAAAA	inch Waenningreisen sahr ge-
			BLAST Hits for ABC00076	

Barley SNPDB: SCRI Bioinform	matics< - Microsoft Internet Explorer provided by S.C.R.I.		
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Address 🙆 http://germinate.scri.s	.sari.ac.uk/cgi-bin/barley_snpdb/display_snps.cgi?contig=ABC00076	Go Links 🌺	
Google - barley snp	🔽 💽 Search 🔹 🦪 🖓 0 blocked 🛛 🏘 Check 📼 💐 AutoLink 🔹 🗐 AutoF	🗉 🛃 Options 🄌 👸 barley 👸 snp	
general information on the contigs	Schematic of mutation locations within contig assembl		
view linkage maps with loci derived from affymetrix contigs	(Hover mouse over vertical lines to highlight SNP locations in the table)	·y	
look up a contig	Golden Promise L		
search affymetrix contigs using blast	Golden Promise R HS92 L HS92 R		
search affymetrix contigs using keywords	Lina R Lina L		
choose a data type	Morex L Morex R		
contig abc00076	OWB DIR OWB DIL		
primers from abc00076	Optic L		
snps from abc00076	Optic R OWB R L		
no map location	OWB R R		
display options	Steptoe L Steptoe R		
show list of mutation names			
show good quality sequences with mutations			
	Polymorphic base positions	CMap - Microsoft Internet Explorer provided by S.C.R.I.	
show full alignment - including bad quality	Positions indicated by red arrows are mapped SNPs.	<u>File Edit View Favorites Iools Help</u>	1
regions		🕒 Back 🔹 🕤 🖌 📓 🏠 🔎 Search 🤺 Favorites 🤣 🍰 🕹 🔜 🕶 🔜 🐼 💽 🎉 🦓	
	SNPs detected by primers	Address 🕘 h	Go Links »
		Google - C Search - 🔊 🔊 0 blocked 🎸 Check - 🔨 AutoLink - 🖓 AutoFill 🔽 Options 🖉	
	Consensus sequence positions 788245670029151	CMap Home Maps Map Search Feature Search Matrix Map Sets Feature Types Map Types Evidence Types Species Saved Links Help	
	2 7 8 6 4 0 8 9 4 7 5 7 2 1 0 Golden Promise L01R01 L a_1	Tutorial	
	Golden Promise L01R01 R a_1 A G A C G G T A G T C C A G G		
	HS92 L01R01 L a_1 A G T C G G T A G T C C A G G	Barley Barley SNP	
	HS92 L01R01 R a_1 AGTCGGTAGTCCAGg	Ξ.H	
	Lina L01R01 R a_1 AGACGGTAGTCCAGg	Linkage Group 1H Linkage Group 2H Linkage Group 3H Linkage Group 4H Linkage Group 5H Linkage Group 6H Linkage Group 7H	
1		[56] [80] [70] [59] [75] [49] [57] DEFEND DEFEND DEFEND DEFEND DEFEND DEFEND	

Tel5P scsnp 04538 MWG837 scsnp 15164 scsnp 07301 Ical scsnp 00312 scsnp 00634 scsnp 05789 scsnp 03346 scsnp 0346 scsnp 01834

G1b1 scsnp01834 scsnp01855 scsnp50108 scsnp10477 scsnp06373 scsnp06274 scsnp09099 cMMG706A scsnp16431 scind17753 scsnp11085 scsnp011085

scssr 08238

- Mag + 0-183 cm

Feature Types:

scamp 02622 scamp 10887 scamp 10870 ABG318 scamp 10970 ABG318 scamp 10277 scamp 02116 scamp 10277 scamp 02403 scamp 03677 scamp 02403 scamp 03677 scamp 02403 scamp 03677 scamp 04610 scamp 10375 scamp 046130 scamp 10375 scamp 04537 scamp 05737 sca

- Mag + 0-178 cm

scspr 10559 AB6321 scsnp 16710 BCD 1532 scsnp 01374 scsnp 0294 scsnp 01495 scsnp 01495 scsnp 01495 scsnp 01483 scsnp 01483 scsnp 01834 scsnp 02838 scind 02281 AB6172

- Mag + 0-182 cm

BCD402B scsnp05311 scsnp07112 scsnp00089 scsnp0029 BCD808B scssr20569 ABG484 scind06435 scind07518 scsnp05209 scsnp05209 scsnp05209 scsnp05209 scsnp05809 scsnp01646 BCD4538 ABG319A scsnp0759 scsnp10511 scsnp10311 scsnp0320

0-139 cm

Our Barley SNP Database has been developed to support the Barley SNP projects at SCRI. Currently have information on over 55000 SNP we polymorphisms in 1500 loci in barley, many of which are targeted to genes involved in response to abiotic stress. We have have built our SNP analysis and nomenclature on the EST assembly that was used to constuct the Affymetrix Barley1 Genechip. The database holds a wide range of support information including sequence from standard genotypes, polymorphics sites and Blast analysis to both rice and Arabidopsis. Many of the graphical display elements make use of SVG graphics.



The data set is rapidly expanding as new SNPs are incorporated. We also have recently improved the map displays through the use of CMAP. Currently, we using the resulting increased are resolution and quality of our barley map information to re-analyse the comparative maps of barley and rice. We gratefully acknowledge collaboration in this work with Dr Tim Close's group at UCR and Dr Andreas Graner and Dr Nils Stein at IPK.

Hilds20.1A scsp.07106 scsp.07106 scsp.07106 scsp.07106 scsp.07106 scsp.02805 scsp.02805 scsp.05926 HG530 scsp.04280 A65302 scsp.04280 A6547 scsp.04280 A6547 scsp.04280 scsp.048

- Mag + 0-206 cm

scssr 09398 - ABG3788 - scsnp 00600 DD1.10 ABG3878

AD43307D scsnp 02895 Ldh1 scsnp 01243 scsnp 01797 scsnp 14681 scssr 02093 scsnp 18140

scsnp18140 scsnp04992 scsnp04576 scsnp04576 scsnp04725 RB6474 scsnp0011 HU6934 scsnp0018 scsnp04155 scsnp04135 scsnp04135 scsnp04135 scsnp04135 scsnp04135 scsnp04135 scsnp04135

-scsnp01868 -ABC151A

scsnp 0693

scsnp 01208 scssr 07970 scsnp 14397

scsnp 14397 scsnp 0572 scsnp 05816 scsnp 05816 scsnp 0286 scsnp 0286 scsnp 0286 scsnp 00210 Rez42 ABC3108 scsnp 01865 AB6461A scsnp 15255

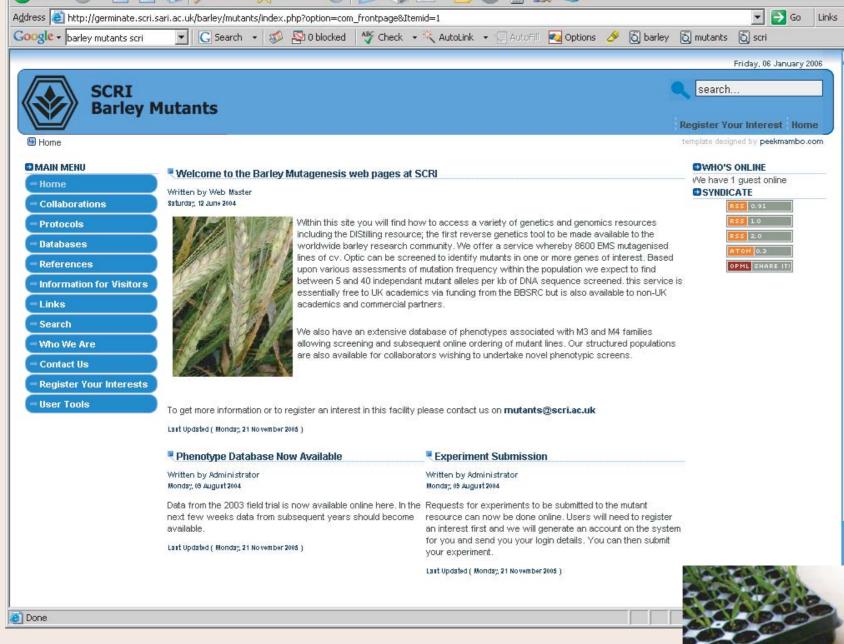
scsnp 15259

http://germinate.scri.sari.ac.uk/barley_snpdb/

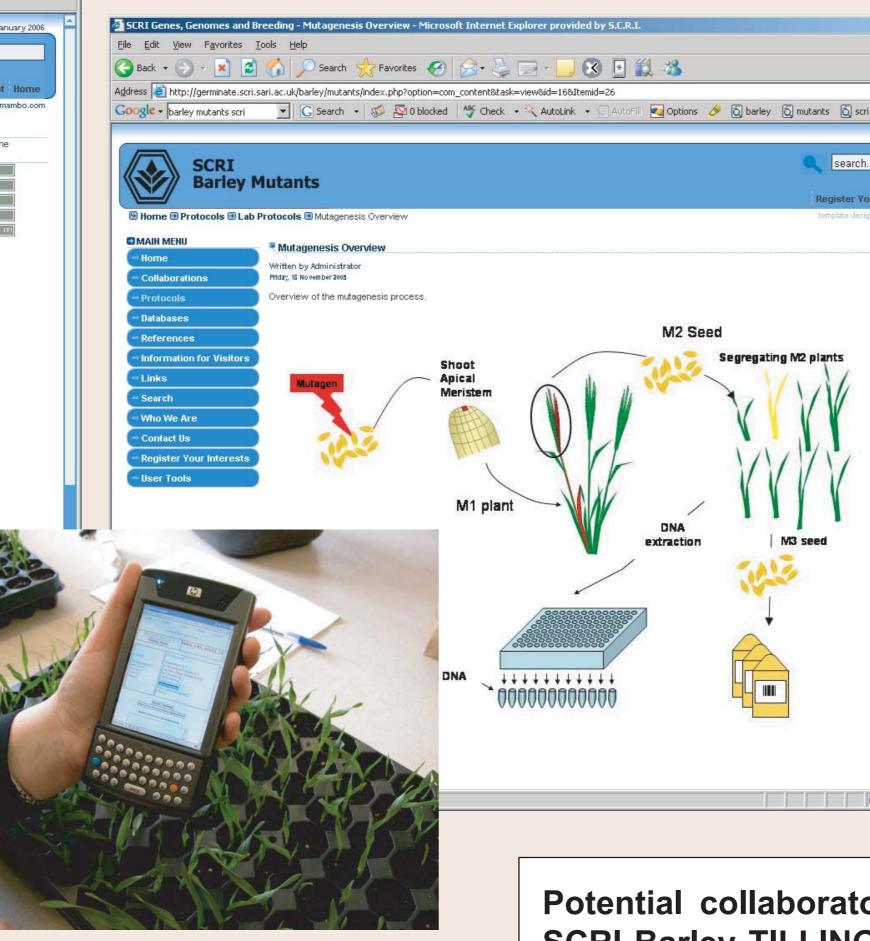
SCRI Barley Mutant Databases

SCRI Genes, Genomes and Breeding - Home - Microsoft Internet Explorer provided by S.C.R.I.	
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The Barley Mutant portal at SCRI has been set up to support the Barley Tilling Project led by Dr Robbie Waugh and Dr David Leader. The portal gives access to our TILLING resources allowing researchers to submit candidate barley genes to the TILLING project and also to monitor the stage of ongoing work. In addition, we also have an extensive online database of visible mutant phenotypes, together with supporting images.







Potential collaborators wishing to make use of the SCRI Barley TILLING resources should either log on the SCRI Barley Mutant Portal (see address below) or email to mutants@scri.ac.uk

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riday, 06 January 20





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