Whealbi

Wheat and barley Legacy for Breeding Improvement

Grant agreement number: FP7-613556

Collaborative Project
SEVENTH FRAMEWORK PROGRAMME

Deliverable D6.1

Barley lines with incorporated genetic diversity for useful traits in regions otherwise showing no or very little diversity in elite European spring barley malting varieties

Due date: M48

Actual submission date: M49

Project start date: January 1st, 2014 **Duration:** 60 months

Workpackage concerned: 6

Concerned workpackage leader: KWS

Dissemination level: PU

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Summary

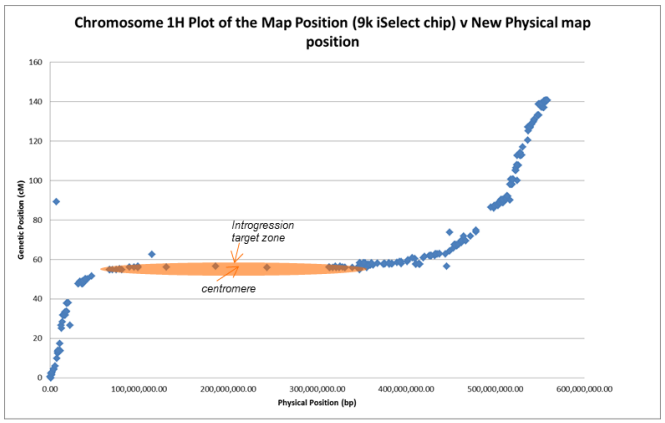
Objectives:

This task will deliver: Barley lines with useful, novel diversity for yield, agronomic, and quality related traits in otherwise conserved genomic regions.

Rationale: Elite spring barley germplasm in Europe is highly interbred and it is known that the gene pool is depleted in genetic diversity. The difficulty for the breeder is not so much finding novel genetic diversity but in finding useful diversity with a positive impact. At the outset we had access to iSel9K SNP chip data enabling the genome analysis of 348 elite spring barley, 346 elite winter barley and 155 exotic old barley cultivars and landraces. This identified regions of the genome that show little or no polymorphism (genetic diversity). It was quickly established that a pattern existed across the genome. For both spring and winter barleys the least diverse region on each chromosome was in the pericentric region. In contrast many landraces were found to show quite different marker patterns (haplotypes) in these same pericentric regions. At this stage 29 landraces were identified (Table 1) that offered a total of 80 novel 'target' haplotypes across the 7 chromosomes. Introgression of each of these into an elite genotype was initiated.

The 29 landraces were crossed and backcrossed to the cultivar KWS Irina (a modern high yielding, widely adapted spring barley suitable for malting and brewing). Each of these target haplotypes could be distinguished from that of KWS Irina using Kaspar SNP markers located close to the centromere. At B1 and B2 Kaspar markers were used to select individuals carrying the target haplotypes.

Exome capture data (generated by Work Package 2 of the Whealbi project) further enabled a detailed analysis of the physical size of the target haplotypes. Figure 1 shows the introgression target for chromosome 1H where the 4cM genetic map distance is shown to actually include about 30% of the physical map distance. Similar relationships were found on all 7 chromosomes.



Results from Exome capture analysis of 1H. *Exome data from JHI, Joanne Russell and Micha Bayer*

Figure 1. Chromosome 1H showing target introgression zone on a genetic v physical map plot

Haplotype Summary April 2016

	Haplotype Identity							
Source Landrace	1H (53 to 56)	2H (64 to 71)	3H (58 to 60)	4H (37 to 45)	5H (47 to 49)	6H (57 to 60)	7H (67 to 69)	
Zephyr M08	3	16					26	
bere 119	25	111	14		33	24	40	
Bere 120		110						
Millenium 219			32					
217	26	106	36			48	66	
Nepal 92 BN 1	42	124	27	65	23	77	84	
Prize Prolific 196		37						
Stat Old 14						49	76	
Binder M8		7				23		
Maja 179	16					55	27	
CraigsTriumph B88 136	46		17	74		40	24	
Donegal landrace 138	6	102	24		33	7	47	
Hanna M08						95		
China Huang Yen		111				3	13	
Cornish 133		23	13			43	24	
NFC Tipple							22	
Webbs Binder 215					24			
Skadu Local Oldings		8						
Morayshire Gold 180	54		23		21	76		
Gotlands 156			29			42		
Golden Archer 147	50	23	24					
Zephyr M08	3	16					26	
Standwell 208							67	
Hen Gymro 165		36						
Earl 139			32					
Eire Six Row 220						92		
Floye		34	30			93	54	
Afghan 1169	50	38	16			120	29	
Camton 129		33					20	
	11	17	13	2	5	16	16	80

Table 1. Haplotype diversity in the pericentric region. Shown by chromosome and landrace source

In order to better inform the introgression targets at B1 from each of the 29 landrace families 20 individuals were selfed and seed sent to New Zealand for multiplication the resulting B1F3 generation was grown in a yield trial in Cambridgeshire, UK replicated in 2016 and 2017. This 384 plot trial was assessed for yield, yield components, agronomic traits and phenology traits. After spatial adjustment of the data (using the array of check genotypes) association analysis was carried out for each target haplotype. It is recognized that at this early generation the analysis is compromised by imperfect markers and imperfect recombination events on each chromosome. Thus the intention of this analysis was the early identification of potentially beneficial haplotype-phenotype combinations. This additional information is then valuable in directing the focus upon these candidate targets for detailed introgression. As an example table 2 shows a summary of the analysis for chromosome 1. For all the component traits of yield considered at least one novel haplotype has been identified as a positive candidate.

Effects summary		1H						
(only sig effects shown)		GDY_1a	HI	BM	S_SL	GNperE	TKW	Tiller
KWS Irina	mean	7.7	48.2	15.9	63.7	19.9	44.0	872.0
Afghan 1169			0.66		-5.94			
Bere-120								
Binder-M8								
Camton-129								
Cornish-133								
Donegal landrace-138					-3.69			98.82
Eire Six Row-220						0.64		
Floye		0.24	1.88					32.62
Golden Archer-147					-4.98	0.67		
Gotlands-156								
Hen Gymro-165						0.99	0.57	
Maja-179_JHI7135_5K					-1.90			40.24
Millenium-219_JHI7112_5K		0.28	3.54		-4.52	1.69	0.58	
Morayshire Gold-180								
Skadu Local "Oldings"								
Standwell-208								
Webbs Naked 2-Row-217				0.63				101.07
Zephyr-M08_JHI7103_5K		0.41	0.55	0.95				

Table 2. Candidate positive effects identified on 1H, showing source of the peri-centric haplotype. Each blank cell in the above table represents a haplotype by trait combination that has a negative or non-significant effect (HI: harvest index; MB: biomass; S_SL: sample stem length; GNperE: grain per ear; TKW: thousand kernel weight; Tiller: tillers per m^2

The exome capture data has enabled us to identify informative SNPs in the target haplotype regions (in silico) and to design Kaspar assays for the efficient selection of each target. This has been done (very simply with a very low fail rate) and employed in the selection of a first batch of B2 individuals carrying candidate introgressions which have been backcrossed and are now at B3F2. Currently B3F2 individuals are being marker selected in order to identify homozygotes for the target introgressions.

There are 30 novel introgression targets in this batch, each of which has a candidate effect associated with it. Self seed at B3F3 will be available in March 2018 completing the introgression phase of the programme. Seed will be delivered to the KWS line breeder for inclusion in ongoing breeding programs in March 2018 and also multiplied to B3F4. Beyond the Fr7 Whealbi project the actual performance of the introgression material will be validated in yield trials by KWS. It is expected that many of the introgressed regions will indeed carry beneficial diversity but many of these will also carry negative effects as well (linkage drag). The outcome from this study will provide the breeder with knowledge of both the benefit and risk together with marker details enabling subsequent breeding to be able to further recombine the region and utilize the beneficial alleles.

Furthermore there is a subsequent batch of introgression lines following one year behind. These will be validated one year later.

Teams involved:

JHI: contributed initial genome data for the background study of elite line, SNP identification from the exome capture data
EI: exome capture data for the landraces

Conclusion

The rich resource offered through the exome capture array opens new opportunities for the enrichment of elite germplasm with material from diverse sources. In this sub-package we have combined directed introgression of diversity with early generation identification of yield related diversity. The process has effectively enabled the introduction of a lot of diversity into the spring barley recipients in a short time frame. This is not fully characterized or validated but the material passes from the pre-breeding phase to the breeding phase with metadata providing the breeder with marker tools and target traits for further enhancement.