

Meta-analysis of multi-environmental trial data reveals major loci controlling yield related traits in barley in Mediterranean environments



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Using biodiversity to reach the gene

Accurate knowledge of the genomic location of genes controlling important traits is a pre-requisite for the successful deployment of molecular marker technology within a breeding programme. Association genetics benefits from marker saturated genetic maps to effectively use the biodiversity stored in natural populations to fine-map traits of agronomic interest.

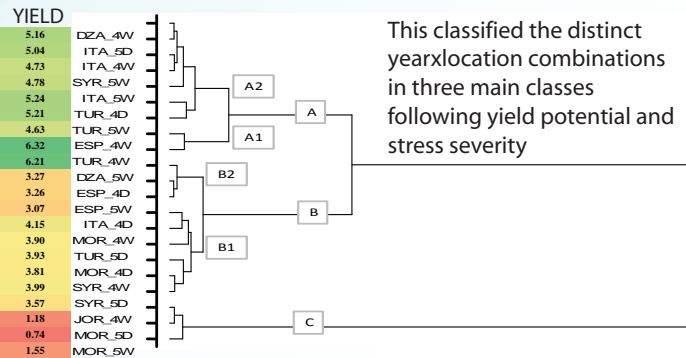
Material & Methods

An association panel consisting of 185 accessions relevant to the barley germplasm cultivated in the Mediterranean basin was used to localize quantitative trait loci (QTL) controlling grain yield and yield related traits.

The germplasm set was genotyped with 1536 SNP markers and tested for associations with phenotypic data gathered over two years for a total of 28 [year x location] combinations under a broad range of environmental conditions.

Environmental clustering

Environment clustering and yield meta-analysis within clusters was performed in order to identify yield main genetic effects linked to the distinct spectra of environmental conditions found in the Mediterranean basin.



Further meta-analysis of these clusters revealed QTL for yield specific to each one of the environmental clusters. Several of the QTL coincide with yield QTL hot-spots reported in the literature in 1H, 4H and 5H.

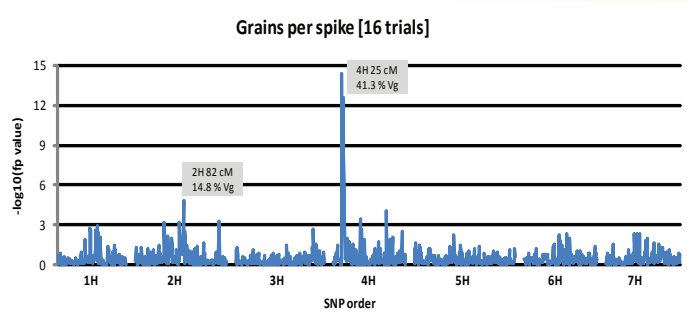
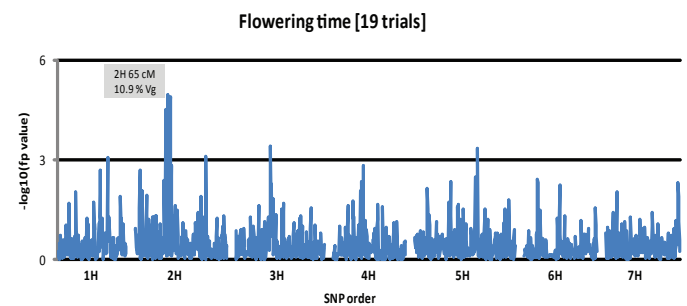
snp id	chrom	pos	YIELD [-LOG10(fp value)]									Genetic effects fp<0.001	
			Z1	A	A1	A2	B	B1	B2	C			
11_20220	1H	107.55	0.53	1.60	3.19	1.22	0.47	0.12	0.75	0.02	-0.33 (A1)		
11_20690	2H	62.82	0.65	0.35	0.49	0.61	2.01	3.35	0.27	0.23	0.16 (B1)		
11_10191	2H	63.53	3.15	1.19	0.56	1.26	1.89	2.50	0.08	1.89	0.18 (Z1)		
11_20833	2H	71.12	2.69	1.60	0.60	1.58	3.07	3.29	0.40	0.57	0.12 (B)	0.16 (B1)	
11_21181	2HL		2.31	1.53	0.24	1.78	0.33	0.84	0.08	3.00	0.14 (C)		
11_20252	3H	6.03	0.96	0.07	0.14	0.15	0.51	0.67	0.42	3.36	-0.16 (C)		
11_21109	3H	51.73	0.88	1.91	3.52	1.39	1.45	0.30	3.31	0.66	-0.55 (A1)	-0.21 (B2)	
11_20866	3H	52.5	1.30	2.72	3.34	2.19	0.76	0.62	0.85	0.06	-0.39 (A1)		
11_11401	3H	58.01	2.27	3.75	1.73	3.71	0.54	1.68	0.51	0.62	-0.19 (A)	-0.19 (A2)	
11_21405	3H	123.68	1.82	1.26	0.51	1.34	3.27	2.35	1.14	0.87	-0.10 (B)		
11_21130	4H	116.85	0.92	1.47	3.17	0.95	0.63	0.40	0.61	0.00	0.42 (A1)		
11_11128	5H	51.6	1.74	1.14	0.15	1.24	2.15	3.06	0.18	0.05	-0.13 (B1)		
11_20367	5H	75.4	0.52	2.06	3.29	1.35	0.06	0.04	0.11	0.14	0.41 (A1)		
11_10104	5H	146	0.38	0.48	0.01	0.65	0.18	0.77	3.26	0.73	0.13 (B2)		
11_10557	5H	147.4	0.16	0.35	0.49	0.25	0.56	0.17	4.43	0.30	0.17 (B2)		
11_11348	7H	70.4	3.26	2.65	0.50	3.22	2.28	2.55	0.35	1.13	0.14 (Z1)	0.18 (A2)	
11_10299	7H	73.75	2.65	3.21	3.35	2.83	1.65	1.42	0.83	0.59	-0.20 (A)	-0.44 (A1)	
11_11291	7H	79.6	2.50	3.14	3.40	2.66	1.51	1.20	0.85	0.58	0.21 (A)	0.46 (A1)	
11_11445	7H	84.92	3.05	2.48	1.52	2.38	3.14	4.18	0.09	0.39	-0.12 (Z1)	-0.13 (B)	
11_10209	7HS		1.72	3.43	1.54	3.47	1.73	1.43	0.91	0.09	0.21 (A)	0.21 (A2)	

Meta-analysis of multi-environmental trial data

Meta-analysis of MET data by fitting a mixed model with kinship estimates detected several QTL for yield and yield related traits.

Trait	SNP	chrom	position	interval (nr*)	-log10(fp)	%Vg	effect	s.e.
Yield	11_10191	2H	63.53	63.53 (2)	3.15	8.29	0.18	0.05
	11_11348	7H	70.4	70.4 (1)	3.26	10.99	0.14	0.04
	11_11445	7H	84.92	84.92 (1)	3.05	10.46	-0.12	0.04
Flowering time	11_10357	1H	100.69	100.69 (1)	3.07	6.84	1.78	0.53
	11_20438	2H	63.53	63.53 (9)	4.95	10.91	-3.40	0.84
	11_20366	2H	128.26	128.26 (1)	3.11	6.88	2.11	0.59
	11_11401	3H	58.01	58.01 (1)	3.42	7.07	1.84	0.55
11_11090	5H	132.63	132.63 (1)	3.32	6.60	2.59	0.74	
Harvest index	11_20603	1H	135.56	135.56 (1)	3.27	11.00	-0.52	0.16
	11_10191	2H	63.53	63.53 (3)	3.64	10.38	0.98	0.27
	11_10918	3H	123.68	123.68 (1)	2.95	12.68	0.52	0.16
Height	11_10376	2H	131.77	131.77 (1)	3.39	8.05	1.53	0.43
	11_20894	5H	2.09	2.09 (1)	2.91	6.09	-1.68	0.52
Thousand kernel weight	11_10796	2H	58.24	58.24 (3)	4.21	9.86	-2.18	0.54
	11_10213	2H	86.63	86.63 (1)	3.08	5.21	-1.50	0.45
	11_20680	4H	26.19	24.59-26.19 (2)	3.49	6.85	2.25	0.62
Grains per spike	11_20121	1H	75.45	75.45 (1)	2.94	8.88	1.36	0.42
	11_10436	2H	62.82	62.82 (1)	3.16	9.01	2.06	0.61
	11_10287	2H	85.92	82.75-86.63 (3)	4.85	14.86	-2.27	0.52
	11_21453	2H	155.3	155.3 (2)	3.28	8.89	-1.36	0.39
	11_20422	4H	24.59	24.59-26.19 (8)	14.35	41.35	4.15	0.53
	11_20610	4H	54.25	54.25-54.98 (3)	3.42	10.42	1.95	0.55
Spikes per m ²	11_20732	4H	92.38	92.38 (1)	4.08	14.69	-1.57	0.39
	11_20422	4H	24.59	24.59-26.19 (5)	4.93	29.52	-20.8	4.74
	11_0553	5H	2.81	2.81 (1)	3.14	12.38	10.54	3.12

Co-localization of several QTL related to yield components traits suggest that major developmental loci may be linked to most of the associations.



Largest QTL for flowering time co-locates with *eam6*, a major locus for heading date in barley for autumn sown conditions. Largest QTL for grains per spike co-locate with *vrs-1* and *Int-C*, two loci involved in the 2/6 row ear types in barley.