Agronomic effects of a reciprocal translocation in a widely grown Spanish barley variety

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Abstract

A large spontaneous reciprocal translocation is present in a widely grown Spanish barley cv. 'Albacete'. It has been hypothesized that high popularity of ‘Albacete’ with farmers, particularly in semi-arid areas where barley is grown under rainfed conditions, may be due to the presence of this translocation. Agronomic effects of this translocation were studied at two locations and two growing seasons in a set of 245 doubled haploid lines derived from the F_1s of four crosses involving 'Albacete'. The results have shown a significant positive main effect of the translocation on the thousand kernel weight and a significant environment by translocation interaction for the thousand kernel weight, lodging and tiller number. However, the results do not support the hypothesis that this chromosomal structural change alone provides an increased adaptation to low-yielding sites.

Keywords: Reciprocal translocation · Barley · Breeding · Adaptation

Introduction

Spontaneous reciprocal translocations seldomly occur in cultivated barley; only a few cases have been described (Konishi and Linde-Laursen 1988). Translocations usually reduce the agronomic value; ‘Albacete’ is the only extensively cultivated barley variety carrying a reciprocal translocation without apparent loss of agronomic value. In Spain it has been grown for decades on up to 1 million ha/year. The reciprocal translocation was identified in a meiotic analysis of semi-sterile F_1 hybrids involving ‘Albacete’ (Luis Cistué, *personal communication*; see also Farré et al (2011)). Farré et al. (2012)

performed a molecular and cytogenetic characterization of the reciprocal translocation and determined the position of the translocation breakpoints. Drought is the main factor limiting the yield of cereals in environments with high temperatures and limited rain during the grain-filling period (López-Castañeda and Richards 1994). It is unknown whether the reciprocal translocation has a positive effect on drought tolerance and other traits that make it worth to be introduced in the barley germplasm. In the present study, 248 doubled haploid (DH) lines from four crosses involving 'Albacete' as one of the parents will be used to phenotypically characterize the effects of the presence of the reciprocal translocation.

Materials and methods

Plant material

Different agronomic traits were evaluated in 245 DH lines of barley derived from the F_1s between 'Albacete' and 'Barberousse', 'Plaisant' and 'Orria' and a DH line derived from 'Plaisant'×'Orria'. 'Albacete' is a variety with a long cycle and an alternative growth habit. It is drought tolerant with a stable grain yield production. 'Barberousse' is known for its good productivity and easy adaptation; it is sensitive to drought. 'Plaisant' shows good adaptation and high-yield under Spanish conditions. 'Orria' is a Spanish variety of CIMMYT origin, well adapted to fertile, rainfed environments. The DH lines were scored for the presence of the reciprocal translocation using molecular data (Farré et al. 2011). The number of lines carrying/not carrying the translocation were 41/54, 18/20, 40/27, 36/9 for A×B, A×O, A×P and A×(P×O), respectively.

Phenotyping

Four field trials were carried out at two rainfed locations in North-Eastern Spain in 2008/2009 and 2009/2010: Gimenells (41º 37'N, 0º 22'E, 248m) and Foradada (41º 51'N, 1º 0'E, 407m). Experiments contained one or two replicates per DH line augmented by four replicated checks in a rectangular set-up. The traits measured were: days to heading, days to jointing, days to maturity, number of spikes in 50 cm, yield, thousand kernel weight (TKW), early vigour, till number, total height and lodging.

Data analysis

For each population the average broad sense heritability was estimated. For each trait, Best Linear Unbiased Estimates (BLUEs) of DH individuals were estimated by removing spatial effects. The BLUEs were further analysed using the mixed model facilities of Genstat version 13 (Payne et al. 2009), heterogeneous variances within population were corrected.

Results and Discussion

(Table 1) Broad sense heritabilities (H^2) ranged from 0.27 to 0.84. A highly significant main effect of the reciprocal translocation was obtained for TKW; DH lines carrying the reciprocal translocation had a greater TKW than those with a standard chromosome arrangement (34.8 vs 32.9 gr, respectively). No significant main effects were found for the other traits. For TKW, lodging and till number a significant environment by translocation interaction was found. More lodging was recorded at Gimenells and for the RT genotypes. Differences in the response of the RT to till number may be associated to specific meteorological conditions. In conclusion, the results do not support the hypothesis that the reciprocal translocation alone provides an increased

adaptation to low-yielding sites; TKW is the only trait which is clearly enhanced by the reciprocal translocation. Future work combining the results from this study with QTL analysis will be carried out to characterize the effects of the reciprocal translocation and QTL simultaneously.

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Table legend

Table 1. a) Summary of the mixed model analysis performed for all the agronomic traits studied comprising 982 genotypes carrying a reciprocal translocation (RT) or the standard chromosome arrangement (no RT) in four trials (the significant levels are based on the Wald test). b) Average values for the two groups in 4 trials (carrying or not the reciprocal translocation).

a)

Source of variation	d.f.[1]	Traits associated to development						Yield and yield components					
		Days to Jointing		**Days to Heading**		**Days to Maturity**		**Nº spikes 50 cm**		**Yield (T/ha)**		**TKW (g)**	
		Wald-test	p-value	Wald-test	p-value	Wald-test	p-value	Wald-test	p-value	Wald-test	p-value	Wald-test	p-value
Environment (E)	3	14689.0	<0.001	62871.4	<0.001	73360.5	<0.001	195.2	<0.001	559.6	<0.001	2982.0	<0.001
Population (Pop)	3	3.8	0.292	27.0	<0.001	4.1	0.263	19.7	<0.001	11.0	0.016	37.4	<0.001
RT	1	0.2	0.625	0.2	0.667	1.5	0.218	2.7	0.103	0.7	0.402	21.0	<0.001
Pop.RT	3	2.3	0.512	2.3	0.518	1.7	0.641	4.8	0.200	1.2	0.768	2.9	0.411
E.Pop	9	13.3	0.040	24.1	0.005	13.3	0.152	14.7	0.024	6.4	0.694	62.8	<0.001
E.RT	3	3.6	0.165	1.7	0.625	1.4	0.713	5.0	0.082	10.6	0.014	17.6	<0.001
E.Pop.RT	9	17.7	0.008	13.5	0.142	1.6	0.996	5.1	0.534	10.6	0.309	23.9	0.005
H^2		0.73		0.84		0.57		0.27		0.60		0.81	

b)

Environment	no RT	RT	no RT	RT	no RT	RT	no RT	RT	no RT	RT	no RT	RT
F-2009/2010	149.5	148.1	183.0	183.1	223.0	223.4	44.5	45.6	4.9	5.1	35.6	37.9
F-2008/2009	-	-	166.6	166.8	196.0	196.3	57.7	55.8	5.4	5.6	29.8	32.3
G-2009/2010	126.9	127.1	161.8	161.9	202.0	202.4	56.4	59.5	6.0	6.3	38.3	40.0
G-2008/2009	109.4	109.2	151.3	151.2	184.6	184.8	-	-	4.7	4.4	27.8	28.4
Average s.e.d	0.63		0.35		0.27		1.80		0.13		0.51	

[1] The degrees of freedom for Days to Jointing, number of spikes in 50 cm, Early Growth and Till Number should be equal to two, as data was not recorded in one trial

(Table 1. Continued)

a)

Source of variation	d.f.[1]	Architecture traits							
		Early Growth		**Till Number**		**Total Height (cm)**		**Lodging**	
		Wald-test	p-value	Wald-test	p-value	Wald-test	p-value	Wald-test	p-value
Environment (E)	3	393.4	<0.001	1357.0	<0.001	176.5	<0.001	231.0	<0.001
Population (Pop)	3	4.1	0.263	13.9	0.005	19.3	<0.001	36.0	<0.001
RT	1	1.3	0.262	1.3	0.263	0.0	0.923	0.1	0.745
Pop.RT	3	1.6	0.662	6.0	0.123	2.0	0.579	1.6	0.654
E.Pop	9	13.0	0.044	20.3	0.003	17.4	0.045	18.3	0.034
E.RT	3	0.5	0.765	12.6	0.002	1.1	0.781	13.7	0.004
E.Pop.RT	9	6.0	0.425	4.7	0.584	7.1	0.624	7.8	0.559
H^2		0.46		0.49		0.41		0.60	

b)

Environment	no RT	RT	no RT	RT	no RT	RT	no RT	RT
F-2009/2010	3.1	3.1	2.7	2.8	90.1	88.7	4.3	4.3
F-2008/2009	-	-	-	-	102.8	104.8	4.78	3.9
G-2009/2010	2.7	2.7	5.2	5.8	93.8	94.1	4.6	5.2
G-2008/2009	3.8	3.7	7.4	7.0	99.0	97.0	6.8	7.2
Average s.e.d	0.09		0.23		1.82		0.41	

[1] The degrees of freedom for Days to Jointing, number of spikes in 50 cm, Early Growth and Till Number should be equal to two, as data was not recorded in one trial