Genetic determinants of malting quality traits in a barley population representative of elite breeding in South America

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BACKGROUND

- **Barley is second spring crop in Uruguay and malt is among the country's 10 main export products**
- **High malting quality requirements from the industry**
- **Local varieties with high yield/adaptation but medium malting quality.**
- **European high quality/yield varieties with limited adaptation in suboptimal environments.**

GOALS

- **Determine the genomic regions associated with the main malting quality parameters of barley in European/Uruguayan crosses (representative of local breeding programs) in Southern cone of South America conditions.**
- **Identify favorable alleles for these quality parameters**

MATERIALS & METHODS

- Germplasm: 145 genotypes from 4 crosses with 5 parents (CLE 267 and CLE 268 (local lines), Kalena, Conchita and Livia (european lines) representative of the crossing schemes of local breeding programs.
- Phenotype : Field trials in 3 location (Figure 1) during 2015. Micromalting in Automatic Micromalting System of Phoenix Systems in the Laboratorio Tecnológico del Uruguay (LATU) (Figure 2). Barley protein content (PG, %), malt extract (EX, % dry base), soluble nitrogen (NS, mg/100grs)) and β-glucan (BG, ppm; Figure 3) were measured.
- Genotype: 6220 SNPs from the Illumina 50K iSelect array (Bayer et al. 2017) included in the genome-wide association studies. The analyses were performed using Eigenstrat model (Price *et al.,* 2006) using the *lmem.gwaser* R package (Gutierrez *et al.,* 2016) and a threshold LOD significance of 3 was used.
- Phenotypic variance explained (PVE) by each QTL was estimated by fitting a multilocus model with all significant markers using *relmatLmer* function from *lme4QTL* R package (Ziyatdinov et al. 2018).

Figure 1. Location of field experiments (up-down) 1: "Dr. Mario A. Cassinoni" Exp. Station (EEMAC); 2: Maltería Oriental S.A. Exp. Field (MOSA); 3: "La Estanzuela" Exp. Station (INIA).

Figure 2. Automatic Micromalting System (LATU)

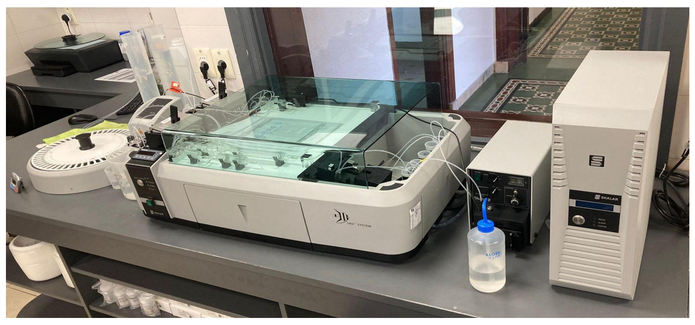

Figure 3. Skalar model SAN++ equipment (with module to measure BG, sampler SA1000, fluorometer SA6310) in Malteria Oriental S.A.

RESULTS & DISCUSSION

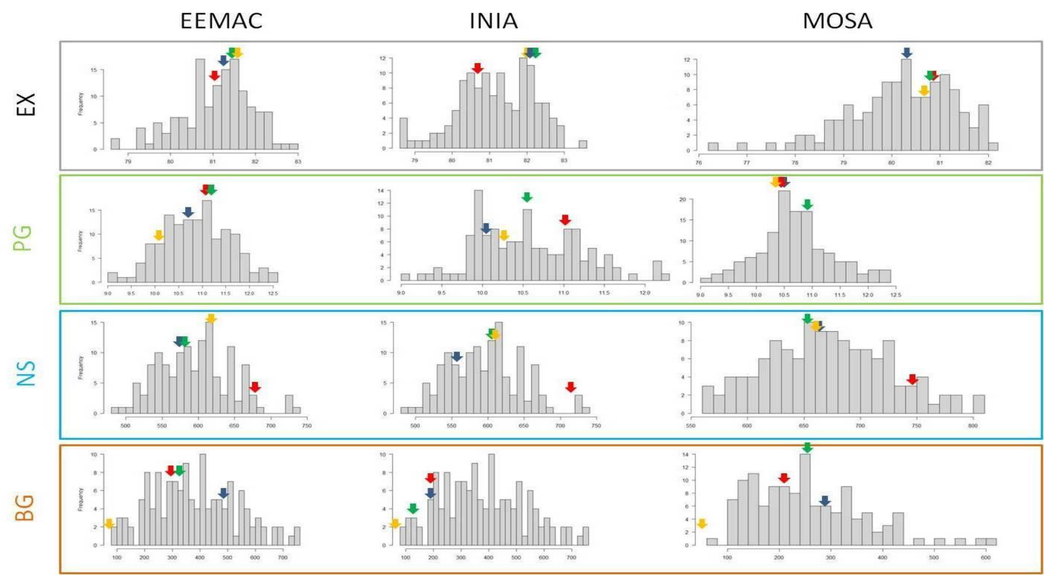

Figure 4. Histogram of the phenotypic values of the four traits analyzed. The phenotypic values of the parents are indicated with arrows: blue: Conchita, green: Kalena; yellow; Livia; red: CLE 267; ND: CLE 268.

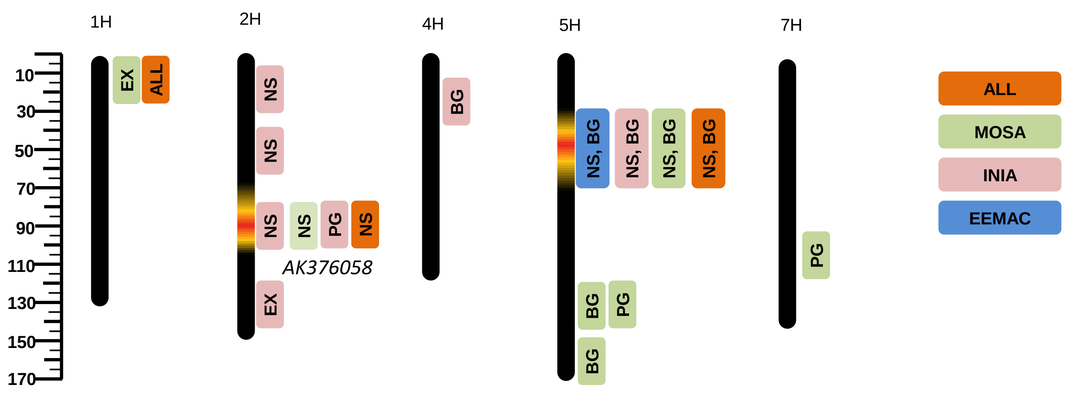

Figure 5. QTLs and two QTLs hotspots (yellow-red), associated traits and in which location were detected

Table 1. QTLs locations, their phenotypic variance and parent`s favorable haplotype. Significative value of the most significative marker of the QTL; *p-value <0.001, **p-value <0.0001 y ***p-value <0.00001.

Trait	Chr.	cM	PVE (%)				Parent Favorable Haplotype
			EEMAC	INIA	MOSA	ALL	
EX	1H	9.92			13.04 **		CLE 267
	1H	15.08				8.39*	CLE 267/268
	2H	142.63		7.49 *			CLE 268/Conchita
	5H	41.74				10.82 *	Kalena
NS	2H	24.50		10.78 *			CLE 267
	2H	40.08		10.89 *			CLE 267
	2H	80.03			13.78 *	18.39**	CLE 267/268/Livia
	2H	92.78		11.07*			CLE 267
	5H	50.00	9.41 *	9.46 *	13.41 *	14.87 ***	CLE 267/Conchita/Kalena/Livia
PG	2H	80.03		19.12 *			CLE 267/268/Livia
	2H	89.80		19.32 **			CLE 267/268
	5H	139.24			13.94 *		Conchita/ Livia/Kalena
	7H	108.78			10.00 *		CLE 267/268/Kalena
BG	4H	24.38		7.27 *			CLE 267/Conchita/Kalena/Livia
	5H	44.17		10.64 *	11.13 *		ND
	5H	50.00	14.62 **			15.94 *	CLE 267/Conchita/Kalena/Livia
	5H	135.95			11.60 *		ND
	5H	151.25			17.56 *		CLE 267/Livia

- **Twenty four QTLs detected for the four traits analyzed. NS and BG showed the highest number of detected association (9 and 7 respectively).**
- **Hotspot on 2H associated to NS and PG in barley. It is in the same zone were the gene *AK376058* which encodes for the enzyme glycoside hydrolases (family 28) with important impact on malt modification.**
- **Hotspot on 5H associated to NS and BG.**
- **We detected no linked QTLs with favorable alleles in repulsion (e.g. QTLs for NS and BG detected in 50 cM in 5H with favorable alleles in both cases).**
- **Both parental types (European and Uruguayan contributed favorable alleles)**

In a context of elite * elite crosses genetic differences are more subtle and the ability to detect relevant QTLs is reduced, although the germplasm is representative and the results are applicable to select lines by local breeding programs in the zone.

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