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A B73 x Gaspé Introgression Library Reveals Ample Genetic Variability for Root System Architecture and Water Use Efficiency in Maize

INTRODUCTION

Collections of nearly isogenic lines where each line carries a delimited portion of a donor source genome into a common recipient genetic background are known as introgression libraries and have already shown to be instrumental for the dissection of quantitative traits. By means of marker-assisted backcrossing, we have produced an introgression library using the extremely early-flowering maize (Zea mays L.) variety Gaspe Flint and the elite line B73 as donor and recipient genotypes, respectively, and utilized this collection to investigate the genetic basis of agronomic traits related with WUE and roots characteristics.

Root architecture traits are crucial for crop productivity, especially under drought but the genetic control in the field is incompletely known. The "shovelomics" method of field excavation of mature root crowns followed by manual phenotyping enables a relatively high throughput as needed for breeding and quantitative genetics.

The objectives of this study were to optimize a protocol for maize root phenotyping in the field, to map QTLs for root trait architecture in the field in the B73 x Gaspé Flint introgression library and to investigate the relationship between root traits and grain yield under drought.

METHODS

The IL collection was genotyped using a SNP array based on the ILLUMINA Infinium technology. The collection was grown in a replicated field trial at two water regimes (well-watered, WW, and water-stressed, WS) at Horta, Ravenna. Forty traits covering phenology, plant architecture, yield, and root architecture were analyzed. Root architecture was investigated by means of shovelomics (Trachsel et al. 2011, Plant and Soil) coupled with software-assisted digital image analysis (REST, Colombi et al. 2015, Plant and Soil), for a total of c. 1,400 analyzed root images.

RAR	Root angle - REST
FFA	Fill factor on arc - REST
MFD	Mean fractal dimension - REST
AREA	Area - REST
MW	Maximal width - REST
DWMW	Depth, at which "maximal width" is located - REST
TPSL	Total projected structure length - REST
RAS	Root angle - score
RMS	Root mass - score
DS	Depth - score
BRN0	Brace root number at soil level
BRN1	Brace root number at above-ground node 1
BRN2	Brace root number at above-ground node 2
BRN3	Brace root number at above-ground node 3
RDW	Root dry weight

Based on REST (7 traits)

Manual measurements, visual scores (8 traits)

NDRE	NDRE
NDVI	NDVI
MF	Male flowering
FF	Female flowering
ASI	ASI
SPAD	SPAD
ST	Stress
SC	Stomatical conductance
TL	Transition leaf
SG	Stay green
PH	Plant height
TEH	Top ear height
PN	Plant nodes
EW	Ear weight
EPP	Ear per plant
KR	Kernel row
EL	Ear lenght
ED	Ear diameter
CD	Cob diameter
KT	Kernel type
TW	Test weight
KWPE	Kernel weight per ear
GY	Grain yield
HI	Harvest index
TKW	Thousand kernel weight

Morpho-physiological (13 traits)

Yield and yield-related traits (12 traits)

Plot preparation
1. Three representative plants per plot
2. Stem cut at c. 0.3 m from soil level

Digging
Plants were manually digged using a spade

Washing

photos

RESULTS AND DISCUSSION

By comparing B73 and Gaspè Flint, approx. 39% of the SNP present on the array resulted polymorphic, indicating that this SNP array is extremely informative for genotyping this collection. By extending the analysis to the 73 IL lines, the coverage of the Gaspé Flint genome is high with a mean value of 3.3 introgressions per IL line and an average length of 39 Mb (corresponding to approx. 25 cM of Gaspé Flint genome introgressed into B73). A total of 327 independent bins have been identified with three main gaps on chromosome 6 (106 Mb), 7 (123 Mb) and 9 (107 Mb) in telomeric regions of the respective chromosomes.

The stress imposed in the WS experiment resulted in significantly lower plant height (-12%), yield (-42%) and thousand kernel weight (-14%) and longer anthesis-silking interval (+8%) when compared with WW. As to the root system architecture, in WS statistically significant lower root dry weight and root area and higher number of brace roots were observed. A strong negative correlation was found between stay green and stress index with grain yield, yield related traits and plant height, as expected but also with root area and other root traits. Additionally, a positive high correlation was observed between visually or manually scored root traits and corresponding traits based on software-based analysis (0.6-0.8) (Figure2). Hereditability for visual score traits was 72-80% while for REST traits was 54-81%.
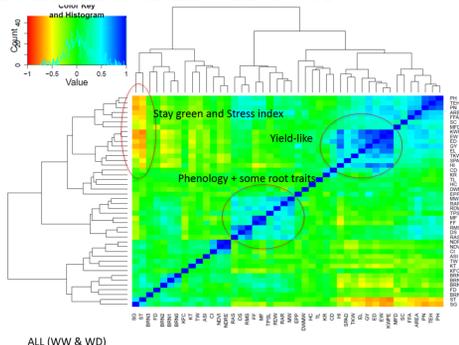

Figure 1. Correlation between traits.

A total of 107 QTLs for 33 traits were identified (30 refers to root traits, 40 to morphological traits and 54 to ear morphology and yield related traits). QTLs for flowering time previously mapped in the same population (Salvi et al., 2011, BMC Plant Biol) have been confirmed and two important QTL for root mass and angle on chromosome 1 (1.03, Landi et al., 2002, Maydica) and chromosome 2 (2.04, Giuliani et al., 2005) have been confirmed. For most of the root traits Gaspé provided the minus allele. Some of the QTL were clustered together, and chromosome 1, 2 and 8 (Figure 2) were found to influence most of the root traits analyzed. Only limited overlap between root and yield components QTLs have been detected: chromosome 1 (1,02: BRN1, TKW; 1.03-1.04: RDW, AREA, EPP), chromosome 2 (RAR, TKW) and chromosome 4 (RAS, CD).
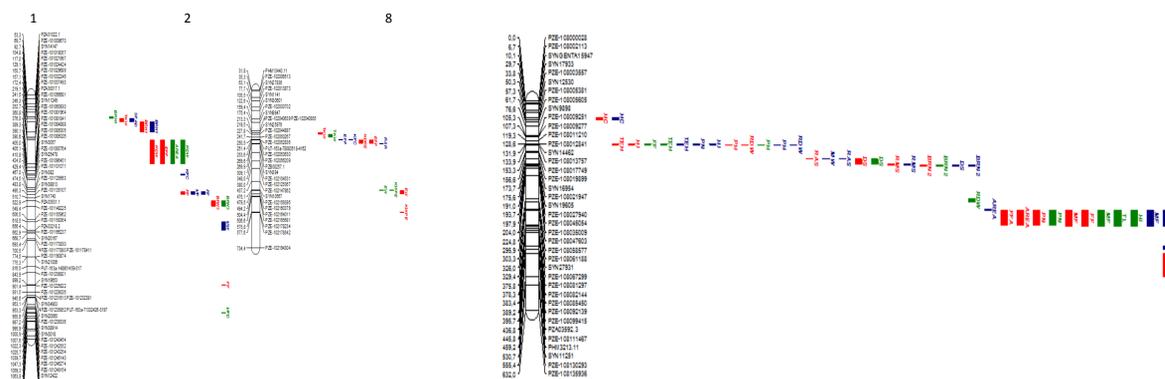

Figure 3. QTL for brace root angle on chr. 2

IL 159-7-2-1   B73

Figure 2. QTL results for chromosome 1, 2 and 8.

CONCLUSION AND PERSPECTIVES

A protocol for maize root phenotyping in the field have been optimized using shovelomics coupled with software-based analysis of digital photos. REST software gave us very good correlation between corresponding visual scored and software measured traits. Overlapping between root traits and yield components has been identified on chromosome 1 and 2 and 4. Together with information based on hydroponics and pot experiments for the same population, these results should contribute to unveil the role of root architecture variation on maize yield.

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