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in

Molina-Cano J.L. (ed.), Christou P. (ed.), Graner A. (ed.), Hammer K. (ed.), Jouve N. (ed.), Keller B. (ed.), Lasa J.M. (ed.), Powell W. (ed.), Royo C. (ed.), Shewry P. (ed.), Stanca A.M. (ed.).
Cereal science and technology for feeding ten billion people: genomics era and beyond

Zaragoza : CIHEAM / IRTA
Options Méditerranéennes : Série A. Séminaires Méditerranéens; n. 81

2008
pages 245

To cite this article / Pour citer cet article

Meskine S., Romagosa I., Comadran J., Russell J.R., Hackett C., van Eeuwijk F., Thomas W.T.B. **Primary root architecture in a diverse set of barley germplasm.** In : Molina-Cano J.L. (ed.), Christou P. (ed.), Graner A. (ed.), Hammer K. (ed.), Jouve N. (ed.), Keller B. (ed.), Lasa J.M. (ed.), Powell W. (ed.), Royo C. (ed.), Shewry P. (ed.), Stanca A.M. (ed.). *Cereal science and technology for feeding ten billion people: genomics era and beyond.* Zaragoza : CIHEAM / IRTA, 2008. p. 245 (Options Méditerranéennes : Série A. Séminaires Méditerranéens; n. 81)

Primary root architecture in a diverse set of barley germplasm

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Most studies on plant adaptation to drought have focused on physiological and morphological measurements taken at the above-ground level; very few studies have been carried out on root characteristics. In this study we report root architecture of a diverse collection of barley genotypes recorded using a gel observation chamber (Bengough *et al*., 2004) at the seedling stage. This non-destructive system allows for a simple measurement of primary seedling root traits based on two dimensional scans that permits a rapid and easy measurement of the spread, length and number of seminal roots. SmartRoot software (Draye *et al*., 2005) was used to semi-automatically process the digital images. A collection of 192 very diverse barley genotypes[1] (83 landraces, 43 old varieties and 66 new varieties from a number of regions around the Mediterranean Basin and the rest of Europe) were phenotyped according to this method. Differences in primary root morphology were related to the geographic origin and to whether or not the genotype was a landrace or a cultivar. Available DArT® marker data for more than 1000 polymorphic loci were used to search for phenotype-marker associations. QTLs, particularly for longest root length and root number, were identified in several chromosomal regions across the barley genome with each character appearing to be under independent genetic control. The most consistent regions appeared to be located on chromosome 5H for both longest root length and root number.

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[1] Contribution of the different partners of the MABDE EU ICA3-CT2002-10026 project, in assembling this germplasm set is highly appreciated, namely Salvatore Ceccarelli and Stefania Grando from ICARDA; Michele Stanca from the Istituto Sperimentale per la Cerealicoltura, Italy; Nicola Pecchioni from the Università di Modena e Reggio Emilia, Italy; Tanner Akar from the Central Research for Field Crops, Turkey; Adnan Al-Yassin from NCARTT, Jordan; Abdelkader Benbelkacem from ITGC, Algeria; Wafaa Choumane from Tishreen University, Latakia, Syria; Mohammed Karrou from INRA, Morocco; and Jordi Bort from the University of Barcelona.