The genetic component of variation in phosphorus use by barley is strongly influenced by environment.

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Introduction

Phosphorus (P) is an essential plant nutrient that limits agricultural production on a global scale. It is desirable that the P-use efficiency of agricultural plants be improved. Many plant species are adapted to P-deficiency and have developed a range of mechanisms that enhance their ability to acquire P from soil (Vance et al., 2003) making P-use efficiency a multi-mechanistic trait whose genetic control is likely to be greatly affected by environment (George et al. 2008). Although genotypic variation in P-use efficiency of cereals is reported (Gahoonia & Nielsen, 1996; Manske et al., 2000; Osborne & Rengel, 2002a,b), few studies have investigated this variation in contrasting environmental conditions and the robustness of the genetic component of variation is rarely tested. Here we study the P-use efficiency in an association mapping population of both winter and spring barley. We investigate the impact of a tillage treatment on the robustness of the genetic component of the variation between barley genotypes.

Methods

Screening of association mapping population for shoot P concentration under different cultivation treatments

An association mapping population was grown in the field under two different cultivation treatments of a long-tern field trial. Soil conditions were imposed over a number of years in a field trial located on the SCRI site near Dundee, Scotland (Newton et al, 2008). Five cultivation treatments were established in triplicate in autumn 2003 that imposed different levels of soil disturbance ranging from light to heavy disturbance. Only two of these were used here; minimum tillage to 7 cm depth and conventional plough to 20 cm depth. These treatments provide different physical constraints to root impedance and water availability. Fifteen blocks measuring 33 x 33m were separated from each other by 3m wide strips which were sown with grass seed after the first trial year was sown. Within each block, trial plots measured 1.55m wide by 2.1m long and were sown at 250 seed m^{-2} in early November 2007 or at 360 seed m^{-2} in early April 2008 for winter and spring varieties, respectively. Fifty-six lines of winter barley and 64 lines of spring barley, identified as a population useful for association genetics, were sown to each cultivation treatment.

Shoot sampling and P analysis

Flag leaf samples were taken at growth stage 49 and were freeze dried before milling to a flour. Phosphorus concentration in shoots was determined on milled samples. Concentrations of P in diluted digests were determined by reaction with malachite green (Irving & McLauglin, 1990).

Results

- Winter barley genotypes had significantly ($p<0.05$) greater P concentration in flag leaves than spring barley genotypes (Figure 1).
- Within the spring and winter genotypes there was significant ($P<0.05$) variation in shoot P concentration ranging from 1.7 to 3.0 and 1.5 to 2.5 µg P g-1 DM, respectively (Figure 1).
- Winter barley genotypes (cvs. Avenue, Gleam, Estrel, Pict and Magie) were able to achieve the critical shoot P concentration necessary to achieve 75% maximal growth in this soil under conventional cultivation. In contrast none of the spring genotypes were able to achieve this. Moreover, none of either winter or spring barley varieties passed the critical level in the minimum tillage cultivation treatment (Figure 1).
- In the winter germplasm the minimum tillage cultivation treatment caused a decline in the shoot P concentration while in the spring germplasm there was a slight increase in the average shoot P concentration in the minimum tillage cultivation treatment.
- Only 32% of the winter genotypes fall within the 95% confidence intervals of the relationship between conventional and minimum tillage treatment, while even fewer, only 19%, of the spring genotypes fall within the corresponding confidence interval.

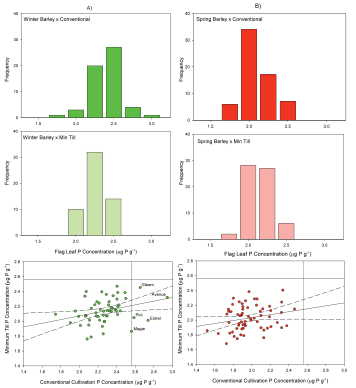

Figure 1. Frequency histograms of shoot P concentration (µg P g-1 DM) for (A) winter barley genotypes (n = 56) and (B) spring barley genotypes (n = 64) grown under conventional plough and minimum tillage cultivation in the field. The relationship of the shoot P-concentration for each genotype between each cultivation treatment is also presented. Regression of the data and 95% confidence intervals for that relationship are presented. Also plotted is the critical P-concentration (2.56 µg P g-1). All data are the mean of three replicates. Only genotypes which show greater P-concentration than the critical to achieve 75% growth on this soil are labelled.

- There was little association between these data and the SNP markers in the winter barley population with three SNP markers showing significant association, which were co-located on the long arm of chromosome 3H but these were only apparent in the minimum tillage treatment (Figure 2).
- There was more association in the spring barley population and again this was more pronounced in the minimum tillage treatment. In the conventional plough treatment there was significant association with 1 and 2 SNP markers on chromosomes 4H and 7H respectively. In contrast, under minimum tillage treatments there were no mutually inclusive associations, but there were five significant associations on chromosome 5H with 3 co-located at the distal end of the long arm (Figure 2).

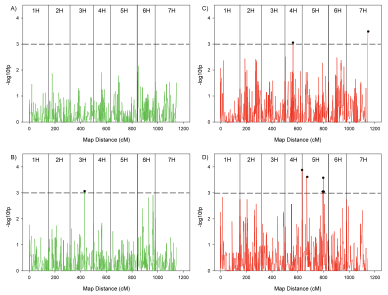

Figure 2. Association mapping analysis of shoot P concentration in spring (C,D) and winter (A,B) varieties of barley under conditions of minimum tillage (B,D) and conventional plough (A,C). Association are made to 1125 SNP markers across all chromosomes of barley. Significant associations are indicated by log10fp values greater than 3 which is indicated by a dashed line and are additionally identified by filled dots. Boundaries of the chromosomes are indicated by vertical lines.

Conclusions

Genotypic variation in P-use efficiency is present in association genetic-mapping populations of barley grown in the field and this variation is meaningful with respect to the ability of a plant to accumulate sufficient P for its growth. However, such variation is not comparable between soil cultivation treatments, where differences in root abiotic stress will have a large impact on root growth and nutrient acquisition. It is therefore important that, when screening for genetic markers for multi-mechanistic traits, such as P-use efficiency, screening is undertaken in a number of environments so that the robustness of the genotypic variation can be tested. Ultimately, it may be possible to use this approach to identify markers for traits that will be applicable for specific environments and deploy these into cultivars which could be tailored for specific management systems.

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