

Genetic variation of fibre components in a genetic resource collection of winter oilseed rape (*Brassica napus* L.)

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Summary

Fibre components were investigated in a diversity set of 294 genotypes of black seeded oilseed rape from various breeding sources. The results showed phenotypic variation for lignin, cellulose and hemicellulose content among the accessions and following Bonferroni correction a significant SNP for lignin content was mapped on chromosome C03 and additional putative QTL were found on A10, A05 and C04. Identified SNPs will help in further understanding the genomic region influencing lignin content in oilseed rape.

Introduction

Fibre content in oilseed rape is a major component reduce the meal quality in the seed. The genetic variation of 3 fibre components was investigated in oilseed rape genetic collections to identify genomic region of interest.

Materials and Methods

- The population comprising 294 diversity sets of black seeded winter oilseed rape sown in 5 environments were genotyped with the Illumina Infinium 60K Brassica SNP array.
- Lignin, hemicellulose and cellulose of open pollinated seed were predicted by NIRS using calibration (Dimov *et al.*, 2012).
- Phenotypic data were analysed with PLABSTAT 3A.
- GWAS was performed in R using Multi locus mixed Linear Model (Segura *et al.*, 2012) on a panel of 15, 211 SNP

Results

a. Phenotypic variation and heritability

- The results shows phenotypic variation for all the 3 components with moderate to high heritability that ranges from 70% in cellulose to 86% in lignin.

Table 1: Phenotypic variation in oilseed rape diversity set (n = 294)

Traits(%)	Lignin	Cellulose	Hemicellulose
Mean± sd	13.60 ± 1.30	2.8 ± 1.54	14.40 ± 1.45
Range	7.64 – 18.4	0.50 – 6.99	10.10 – 17.37
h ² *	86	70	77

h² Broad sense heritability in percentage

b. GWAS Analysis

- One SNP was associated with the Lignin content on C03 explaining 8.3% of the phenotypic variance (fig1).
- There are additional putative QTL found on A10, A05 and C04 (fig 1).
- No association was found for cellulose and hemicellulose (data not shown).

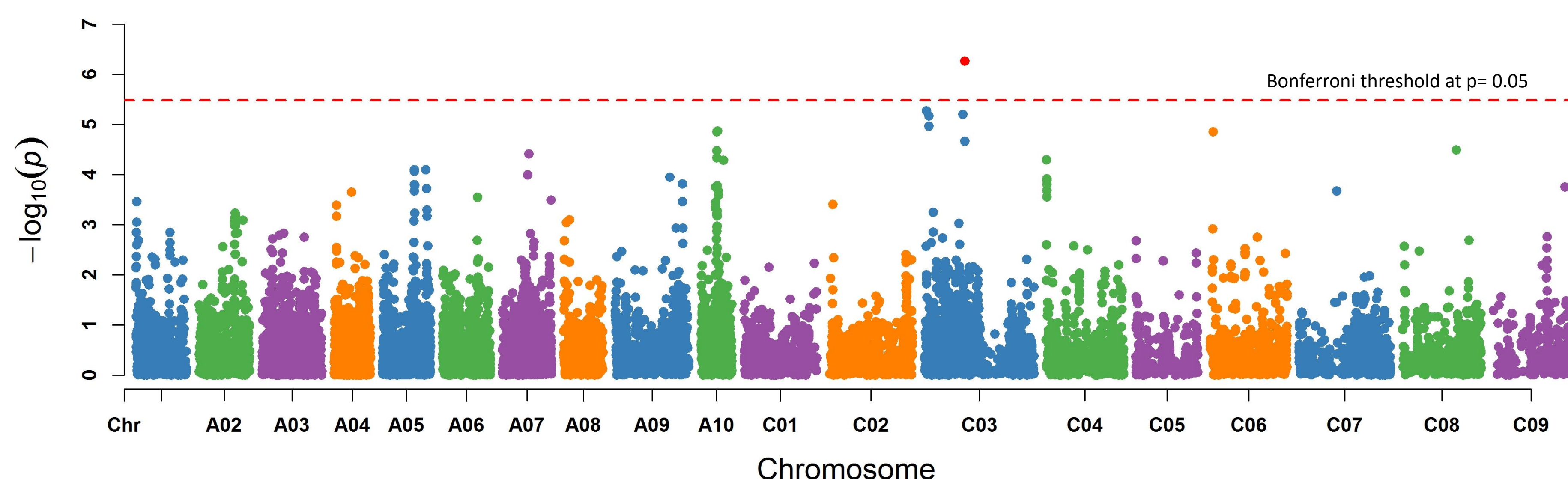
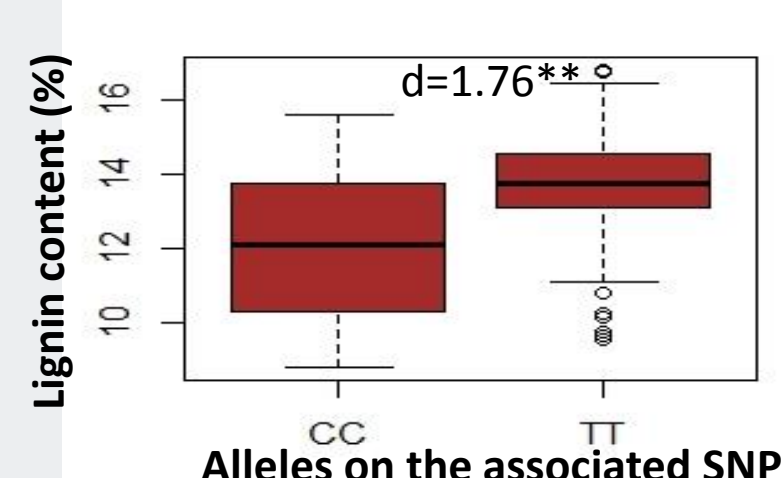


Fig 1: Manhattan plot showing association of 15, 211 SNP markers with the mean lignin content (%) across 5 environments and 294 genotypes

c. Allelic effects of associated SNP

Fig 2: The phenotypic difference of 1.76% for lignin content between CC(17) and TT (277) alleles on the associated SNP Bn.scaff.17298.1-p1064361.

*** Significant at pval= 0.001



Conclusion

- A genome wide association mapped a SNP on chromosome C03 influencing lignin content and 3 other putative QTL on A10, A05 and C04.
- No significant association found for cellulose and hemicellulose for this population of diversity panel.