Root Architecture in Cotton Cultivars

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Student: Pearl Ly

Supervisors:
Jenny Saleeba, University of Sydney,
Augusto Becerra Lopez-Lavalle, CSIRO Plant Industry

Summary

We have found that cotton root architecture varies with genotype. Additionally, cotton cultivars respond to exposure to the pathogen *Thielaviopsis basicola* with some cultivars showing an increase in root branching and others showing a decrease. Furthermore, degree of root branching was seen to vary with relative resistance to the fusarium wilt pathogen.

1.0 Introduction

An essential component of the plant body is the root system. It provides anchorage and support for the plant to explore its substrate, to absorb water and nutrients and to transport them above ground to the shoot system. Root systems are highly adaptive and responsive to environment flux (Stokes et al, 1996, Annals of Botany 78: 415-421).

The root systems in cotton may vary in different cultivars, for example, cultivars infected with different soil-borne pathogens and cultivars with varying levels of disease resistance may show different root characteristics. The soil-borne black root rot and fusarium (Fov) wilt pathogens have been used in this project to determine whether different disease resistant lines show variations in their root architecture. The root architectures between different genotypes grown under normal conditions are also assessed in this project. More robust roots in cotton cultivars are of great agronomic significance in its potential to protect against cotton diseases without the need for chemicals. Cultivars showing robust root characteristics may be incorporated into new lines.

2.0 Objectives

To determine whether different cotton cultivars, with different levels of disease resistance, have different root architecture.

2.1 Hypotheses

1) Different cultivars of cotton show different root architecture.
2) Root architecture is affected by the presence of a soil-borne pathogen.
3) Root architecture varies with the level of disease resistance.

3.0 Methods and Materials

Two experiments conducted by the University of Sydney consisted of 40 replicates of 10 cultivars (A2/A3, Delta-Emerald, MCU-5, Sicala V2, Sicot-70, Sicot-71, Sicot-80, Sicot-189, Sicot-F1 and Siokra 1-4) grown in random positions in a growth cabinet under 16h long day cycle at temperatures of 28^{o}C - 30^{o}C during the day and 18^{o}C during the night for a period of 4 weeks. The plants were grown in a soil mixture consisting of 2:1:1:1 parts perlite:soil:river sand:peat in black plastic pots and raised on racks to ensure adequate drainage (Beccera Lopez-Lavallez pers comm). In the first experiment, the cultivars were grown without inoculum. The experiment was replicated by the University of Sydney where each sample was inoculated with approximately 5000 spores of cultured *Thielaviopsis basicola* applied at the base of the stem immediately after germination. An additional experiment consisting of 40 replicates of 5 cultivars (A2/A3, Sicot-71, Sicot-189, Sicot-F1 and Siokra 1-4) was conducted by the CSIRO Plant Industry, Canberra, where the plants were inoculated with Fov and grown in a glasshouse for a period of 6 weeks.

The plants were harvested and the characteristics of their root architecture measured including the length of the primary root and the number of primary branch points. A disease index (root blackening) was recorded for inoculated plants to indicate the level and severity of infection by the soil-borne pathogen. The ratio of the number of primary branch points to the length of the primary root (PBPPR) was used in the statistical analysis as this provides a fundamental measure of the primary root structure.

Statistical analysis was performed using SPSS v.15 (SPSS, Chicago). Data was tested for normal distribution using the Kolmogorov-Smirnov test and the data normalised by logarithmic transformation where the data did not follow a normal distribution. Residual maximum likelihood (REML) analysis was used to explain the variation between genotypes. REML is a linear mixed model able to analyse unbalanced data (Patterson and Thompson, 1971 Biometrika 58:545-554). Post hoc tests for multiple pairwise comparisons were performed within REML using the least significant difference (LSD) method.

4.0 Results

4.1 Root Architecture of Cultivars without inoculum

REML analysis of the genotypes grown in normal conditions revealed that the ratio of primary branch points to length of primary root varied significantly between cultivars ($F_{9,341}$=14.570, P<0.001) (Figure 1). This suggests that the root architecture is significantly different between different cultivars of cotton grown without inoculum.

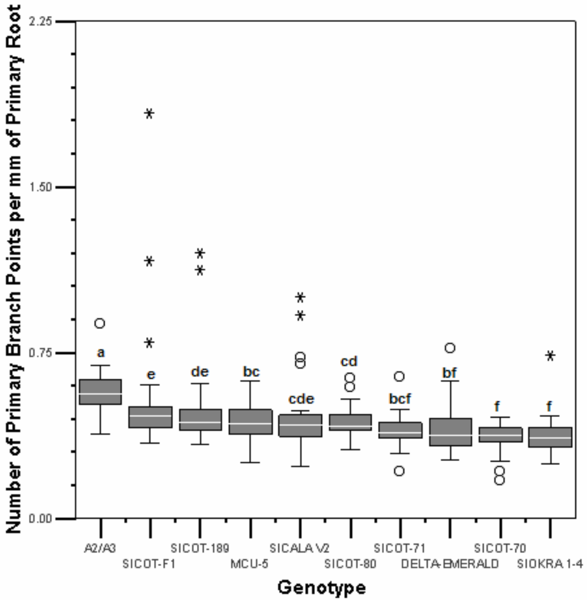

Figure 1: Boxplot of cultivars grown without inoculum showing number of primary branch points to length of primary root. *Boxes* represent interquartile range (IQR); *light centre band* represents median; *whiskers* represent maximum and minimum ratios of PBPPR; *open circles* represent outliers 1.5xIQR and *asterisks* represent outliers 3xIQR. *Lowercase letters* indicate significant differences (P<0.05) between genotypes as determined by post hoc analysis using the LSD method.

The cultivars A2 and A3 show the most robust root architecture and are heavily branched. Siokra 1-4 shows the least number of primary root branches per length of primary root. The Sicot family show similar root architecture to each other as well as the MCU-5, Delta-Emerald and Sicala V2 cultivars without inoculum.

4.2 *The Effect on Cultivars Inoculated with* **T. basicola**

REML analysis revealed that the number of PBPPR for cultivars infected with *T. basicola* varied significantly between genotypes ($F_{9,346}$=12.955, P<0.001) (Figure 2).

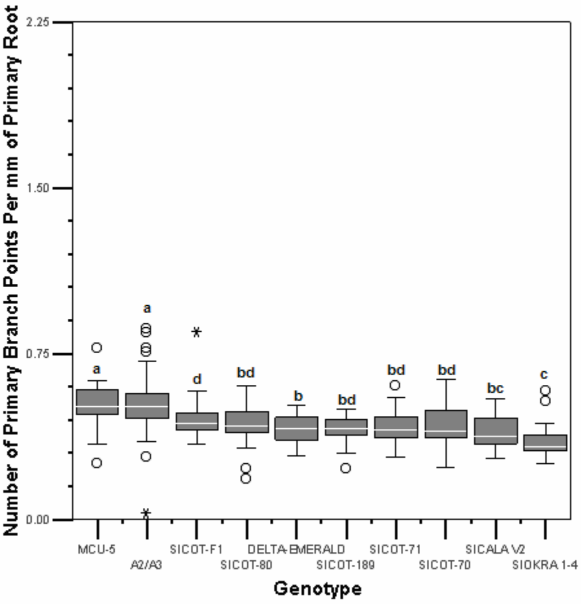

Figure 2: Boxplot of cultivars inoculated with black root rot showing number of primary branch points to length of primary root. *Lowercase letters* indicate significant differences (P<0.05) between genotypes.

The cultivars A2, A3 and MCU-5 show the most branched primary root architecture when inoculated with black root rot. Siokra 1-4 is the least branched cultivar in this condition. Delta-Emerald, Sicala V2 and the Sicot family of cultivars show a medium level of branching.

REML analysis showed that the cultivars MCU-5 ($F_{1,61}$=15.739; P<0.001), Sicot-70 ($F_{1,73}$=9.250; P=0.003) and Sicot-189 ($F_{1,67}$=5.805; P=0.019) are significantly different when grown without inoculum versus inoculation with *T. basicola*. Both MCU-5 and Sicot-70 show an increase in PBPPR in the presence of *T. basicola* whereas in Sicot-189 this is reduced (Figure 3).

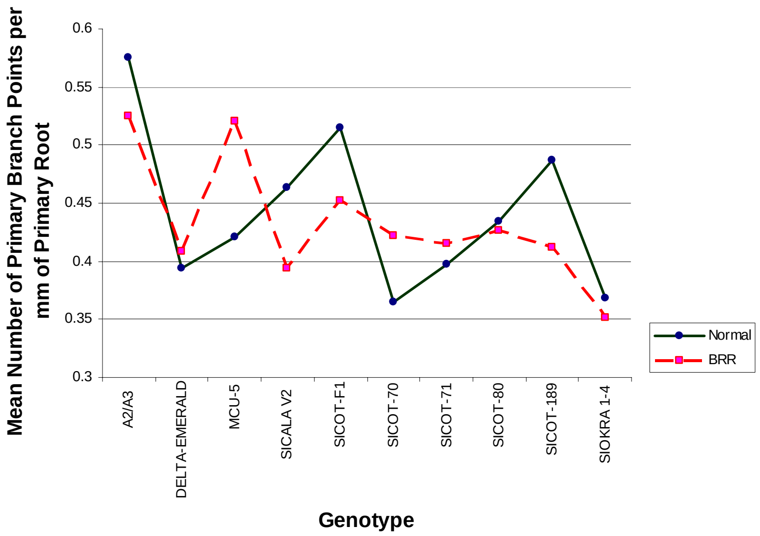

Figure 3: Effect of black root rot on the number of primary branch points per length of primary root on cotton cultivars.

In all cultivars between 5% and 20% of the primary root was infected.

4.3 Root Architecture of Cultivars Inoculated with Fusarium wilt

REML analysis revealed that the effect of infection with the Fov wilt pathogen on number of PBPPR was significant ($F_{4,193}$=56.377, P<0.001) between genotypes (Figure 4).

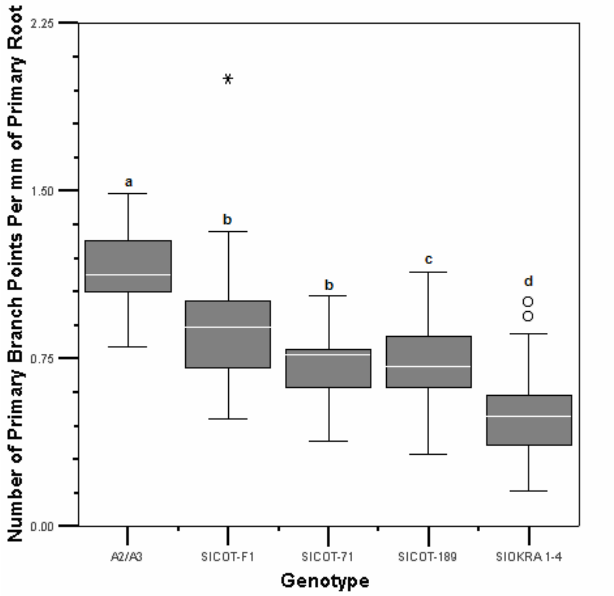

Figure 4: Boxplot of cultivars inoculated with Fov showing number of primary branch points to length of primary root. *Lowercase letters* indicate significant differences (P<0.05) between genotypes.

The cultivars A2 and A3 show the most robust primary root architecture in the presence of Fov. The Sicot cultivars show intermediate root branching and Siokra 1-4 shows the least robust level of primary root branching in the presence of Fov. Root branching mirrors the disease responses of these cultivars to Fov infection. A2, A3 and Sicot-F1 have the highest resistance to Fov infection, Sicot-71 and Sicot-189 have a tolerant response and Siokra 1-4 is sensitive to infection.

5.0 Discussion

There is remarkable variation in the root architecture between cultivars as well as marked similarities. The cultivars A2 and A3 show the most robust root architecture both in normal and perturbed environments. Siokra 1-4 shows the least robust root architecture in normal and perturbed environments. In the presence of the soil-borne pathogens *T. basicola* and Fov, the Sicot family of cultivars show similar root architecture to each other.

Most cultivars show a decreased number of primary branches per mm of primary root with black root rot. The exceptions are MCU-5, Delta-Emerald, Sicot-70 and Sicot-71, which show an increase in the number of primary branch points per mm of primary root.

Since the cultivars inoculated with Fov were grown in different environmental conditions and for a longer duration compared with those grown without inoculum and those inoculated with *T. basicola*, the suitability of statistical analyses between these groups are limited. However, statements may be made about the data obtained within this group. Significant variation in root architecture occurred between genotypes and the degree of resistance to Fov infection varied with root branching.