

# Influence of root anatomical traits in root pathogens and mycorrhizal colonization in maize



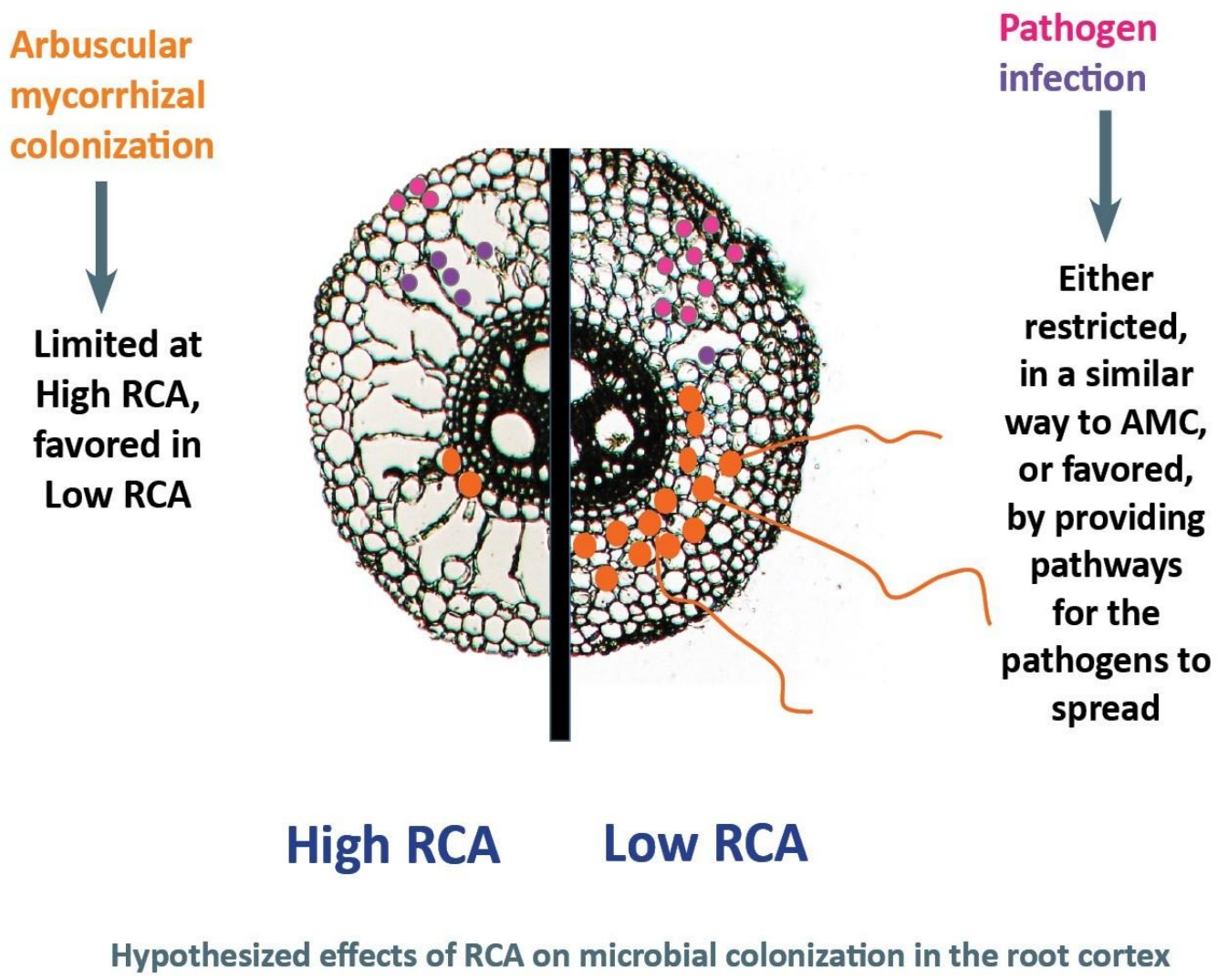
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## Overview

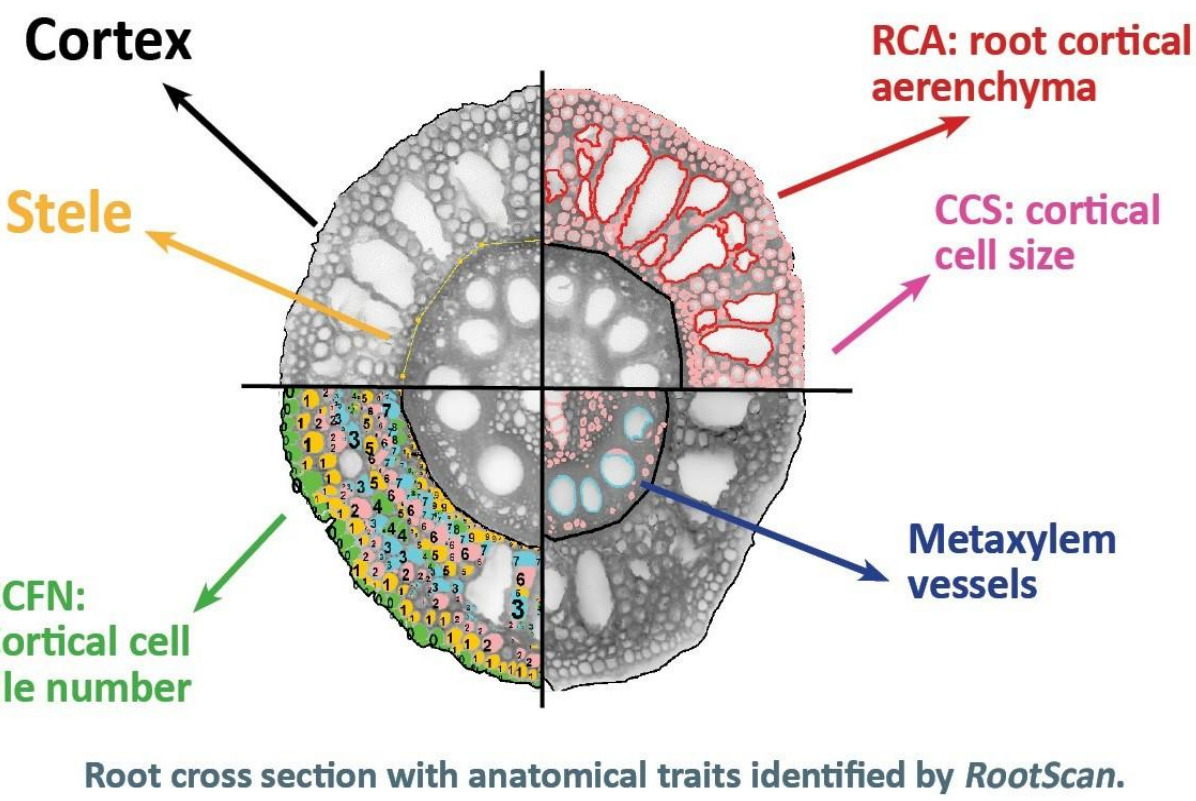
Root anatomical traits impact plant growth by modifying root soil exploration cost and water and nutrient transport. For example, increased root cortical aerenchyma (RCA), and decreased cortical cell file number (CCFN) and cortical cell size (CCS) are traits that improve the acquisition of water and nutrients by reducing the metabolic costs of soil exploration in maize<sup>1,2,3,4</sup>. While there is great potential of these traits as plant breeding targets, especially under nutrient and water stress, the microbial tradeoffs of these and other anatomical traits, need to be considered in the context of sustainable agriculture.

The general objective of this research is to study the effect of anatomical traits on the belowground microbial relations of maize. Two microbial groups are presented: arbuscular mycorrhizal colonization (AMC) and root pathogens, represented by root rots (RR).

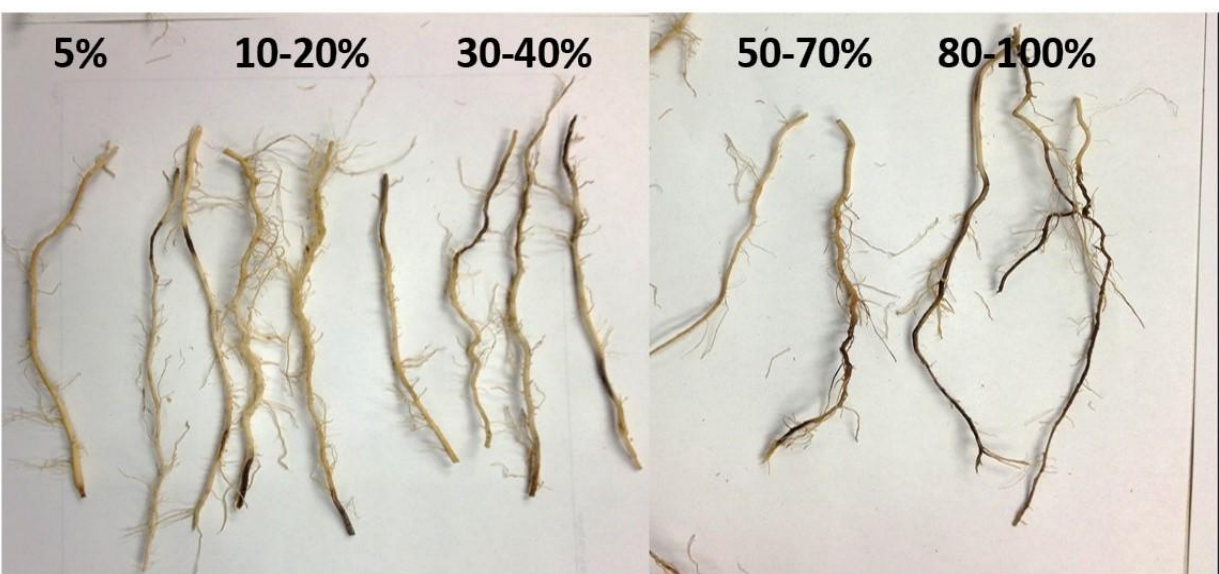


## Methods

We analyzed the effects of RCA, CCFN, CCS, and other anatomical traits on arbuscular mycorrhizal colonization (AMC) and the percent root rot (RR) of field-grown maize roots.



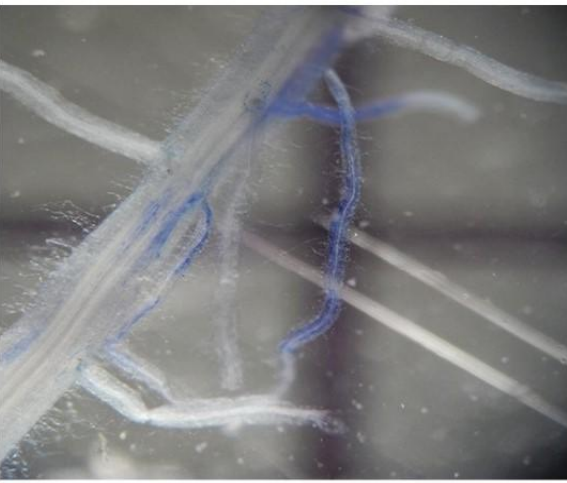
Root cross section with anatomical traits identified by RootScan.



RR scale. Roots were excised 10 cm from the stem and the rot extent rated in segments collected in the second and third whorls of the nodal system. Main axis with their laterals are shown.



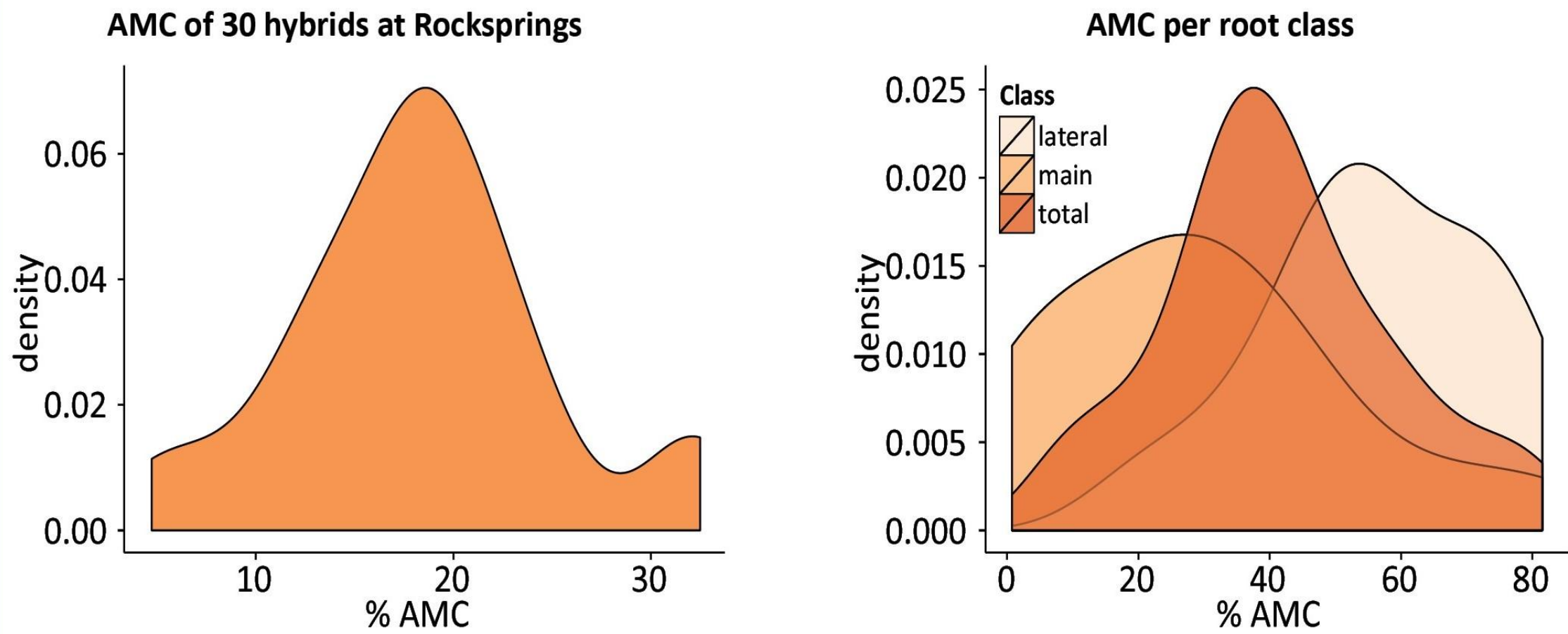
Sampling in the third whorl of the nodal root system. Maize root crown seen from below



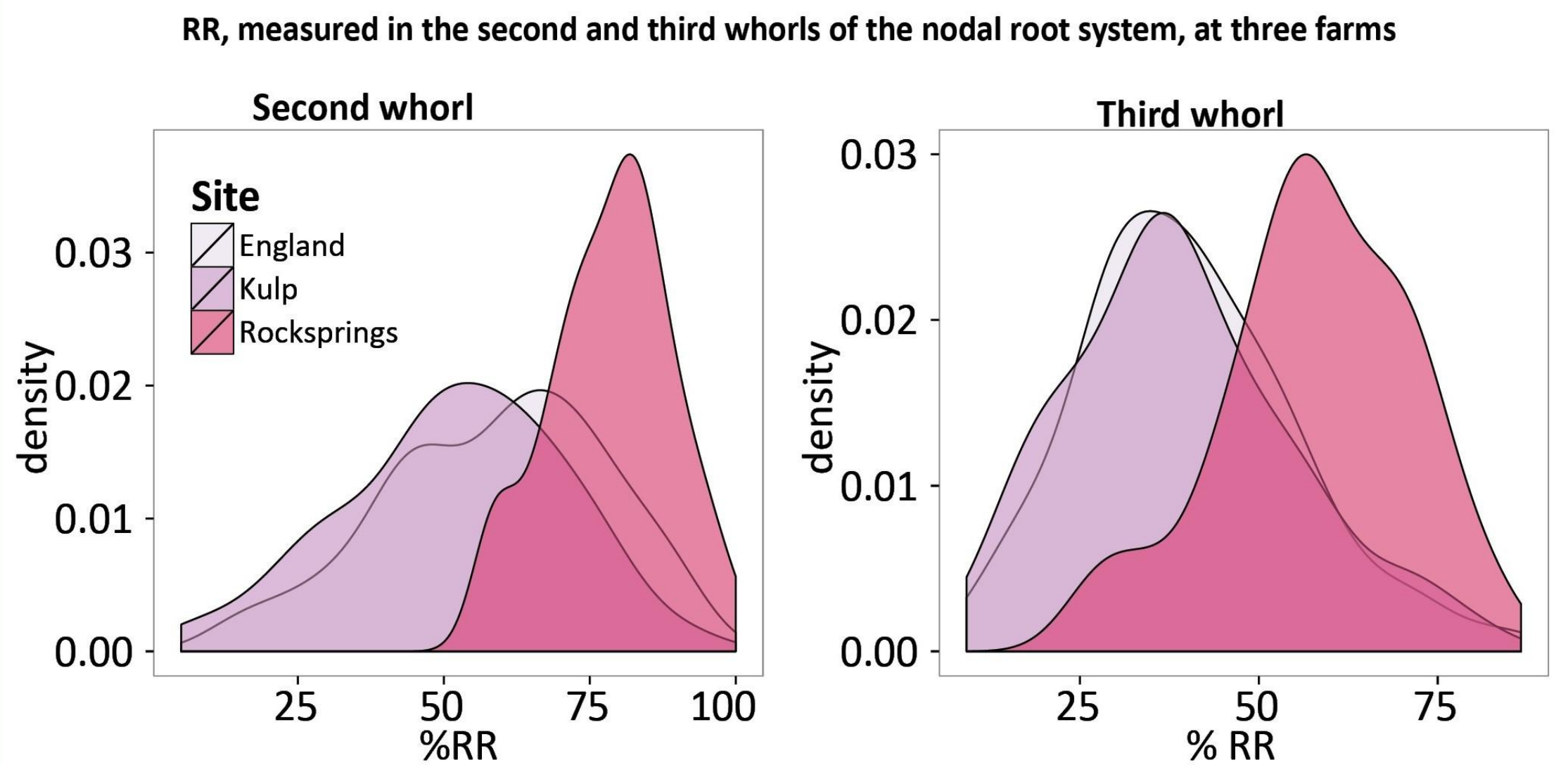
AMC was quantified on cleared and stained roots under the microscope with the gridline intersect method.

Root crowns of 30 commercial hybrid lines were excavated and washed at flowering at three Pennsylvania farms (Rocksprings, Kulp, and England), and sampled for analysis. The software RootScan was used to measure anatomical traits on root cross sections obtained by laser ablation. RR and AMC were measured as shown above.

## Natural variation of Arbuscular Mycorrhizal Colonization and Root Rots in field-grown maize



Density plots of averages per hybrid line, of a total of 30 lines. Root class AMC was separately evaluated in 10 hybrids at one farm. AMC differs among plant genotypes, and root classes (P values < 0.05).



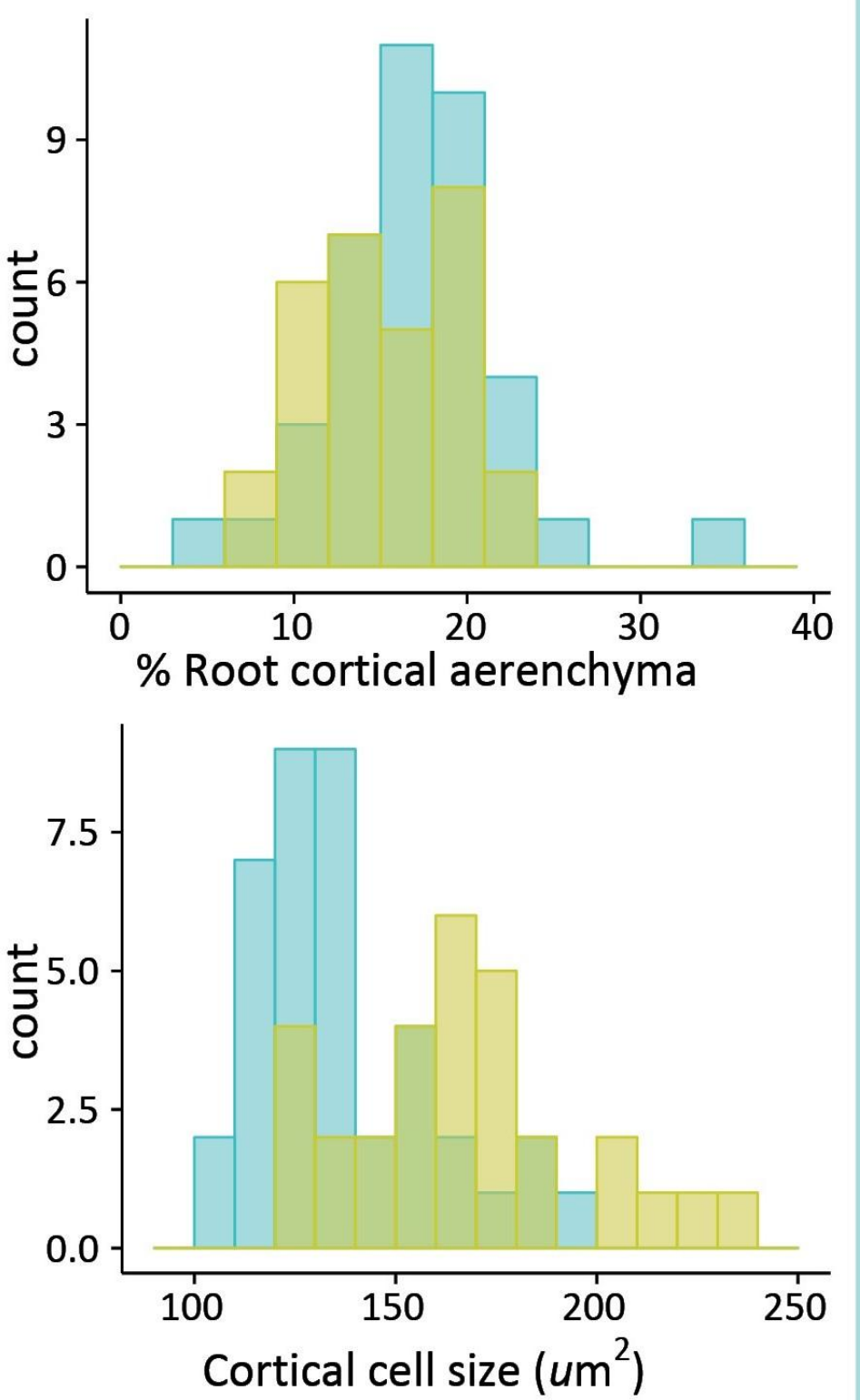
Density plots of averages per hybrid line. RR differs among sites and plant genotypes (P values < 0.05). The more external the whorl in the nodal system, the lower the %RR.

## Natural variation of anatomical traits in 30 lines of hybrid maize and its importance on AMC and RR

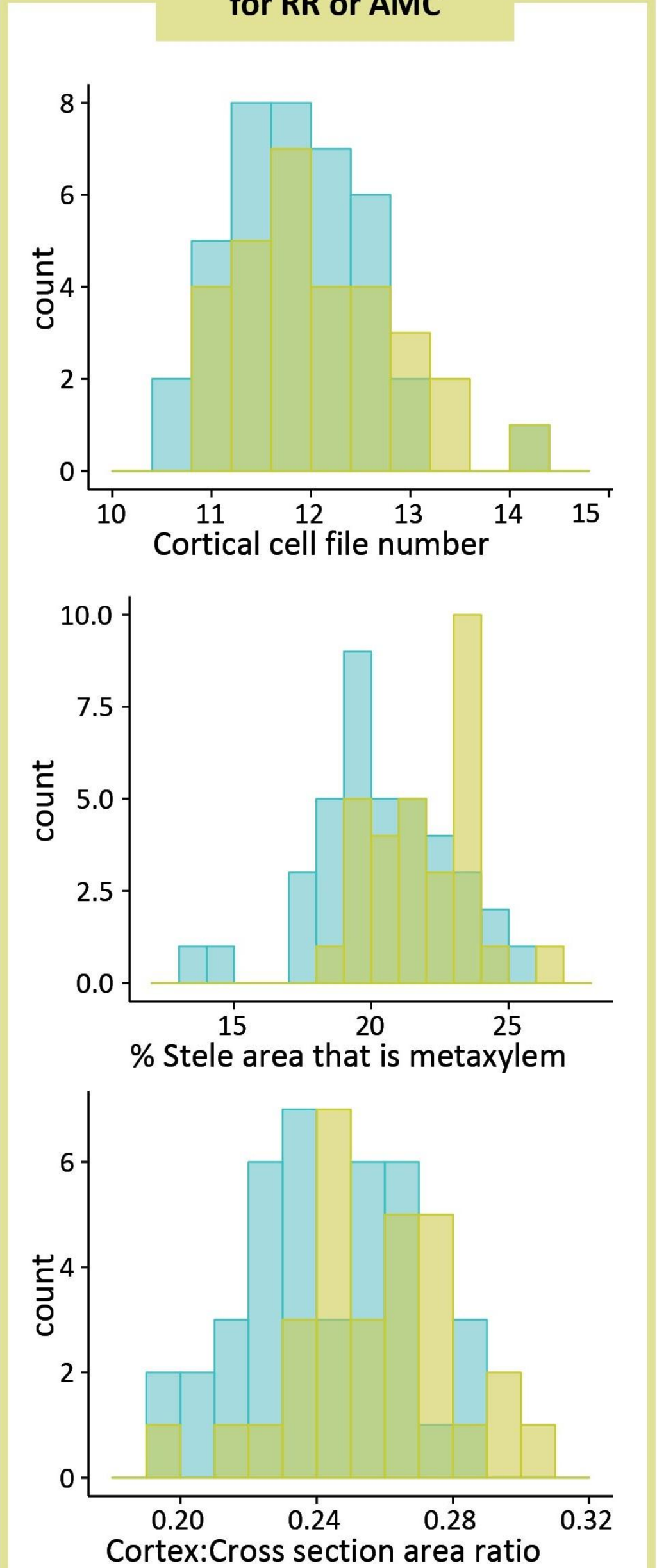
The most important explanatory anatomical variables for RR and AMC were determined with a Random Forest model. 23% of the variability in RR and 10% of the variability in AMC were explained by the most important anatomical traits.

Site: England, Kulp

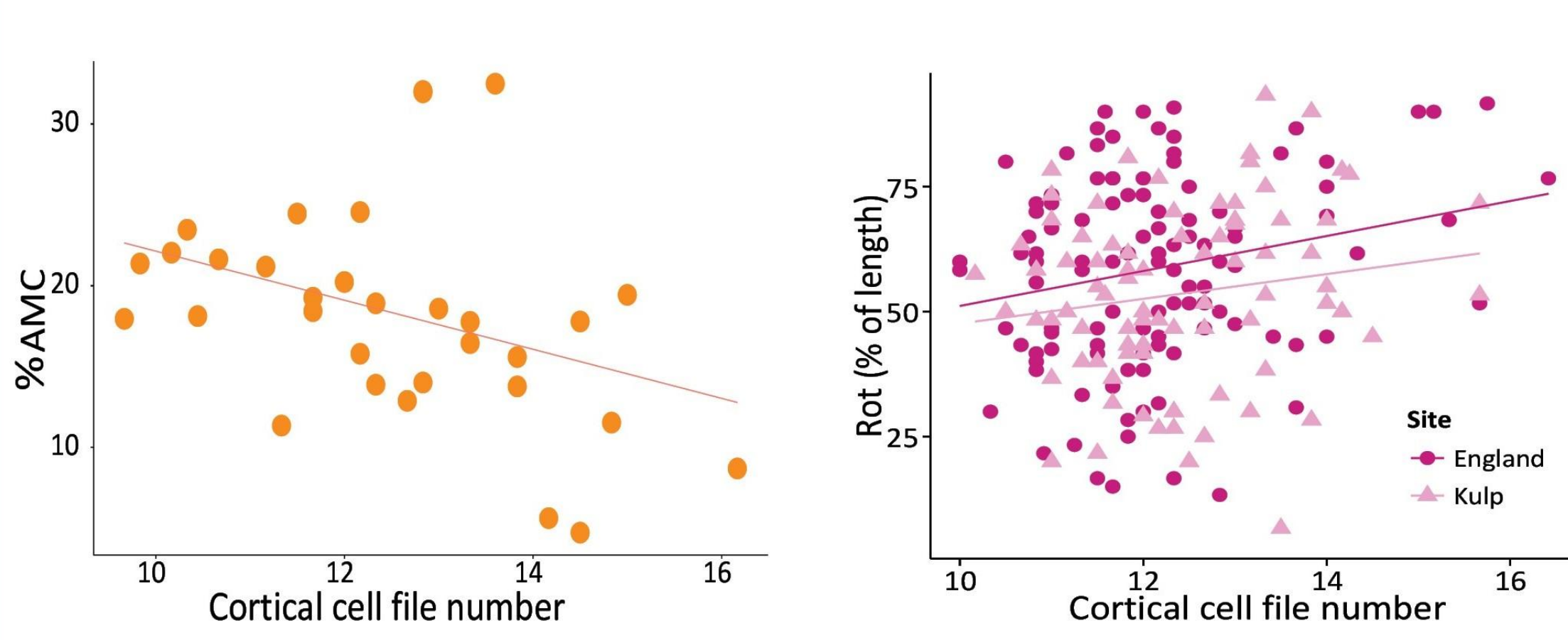
Variables not important for RR or AMC



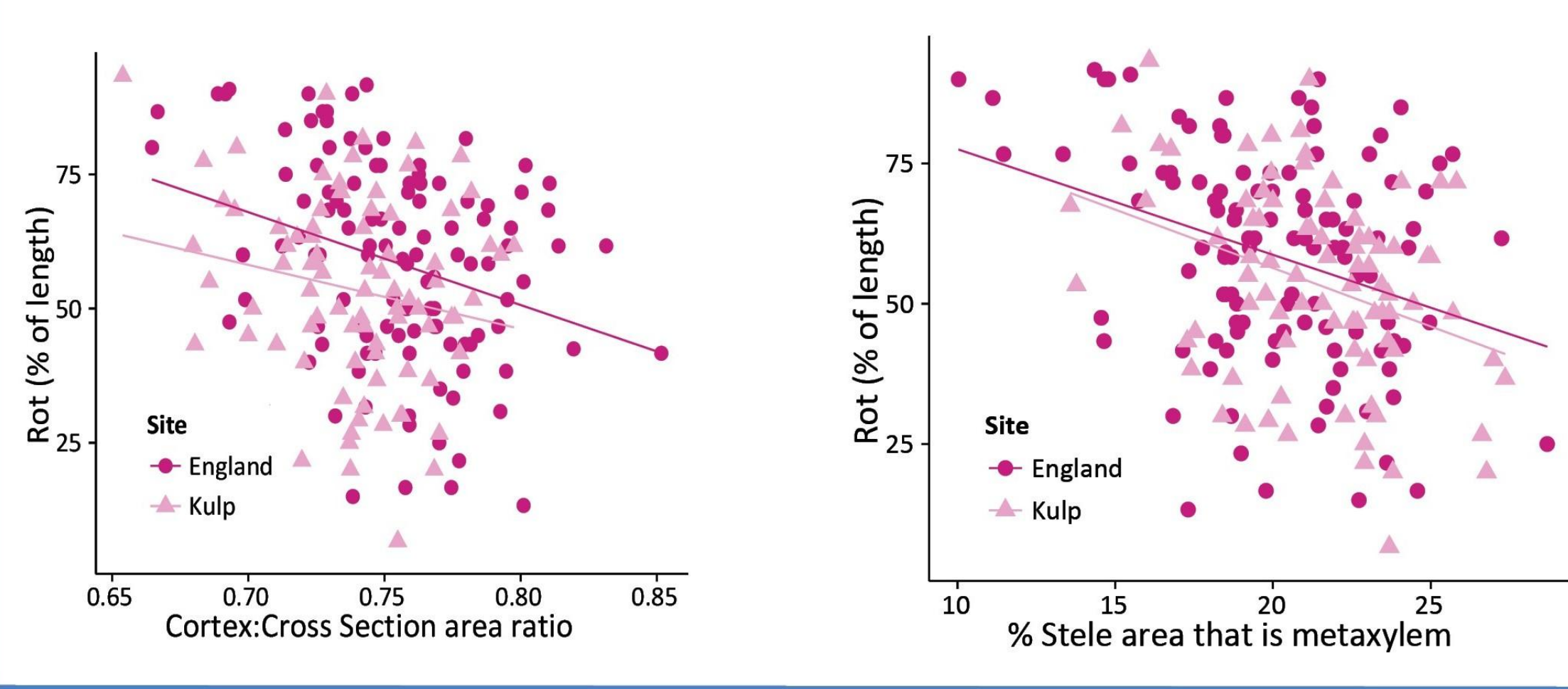
Variables important for RR or AMC



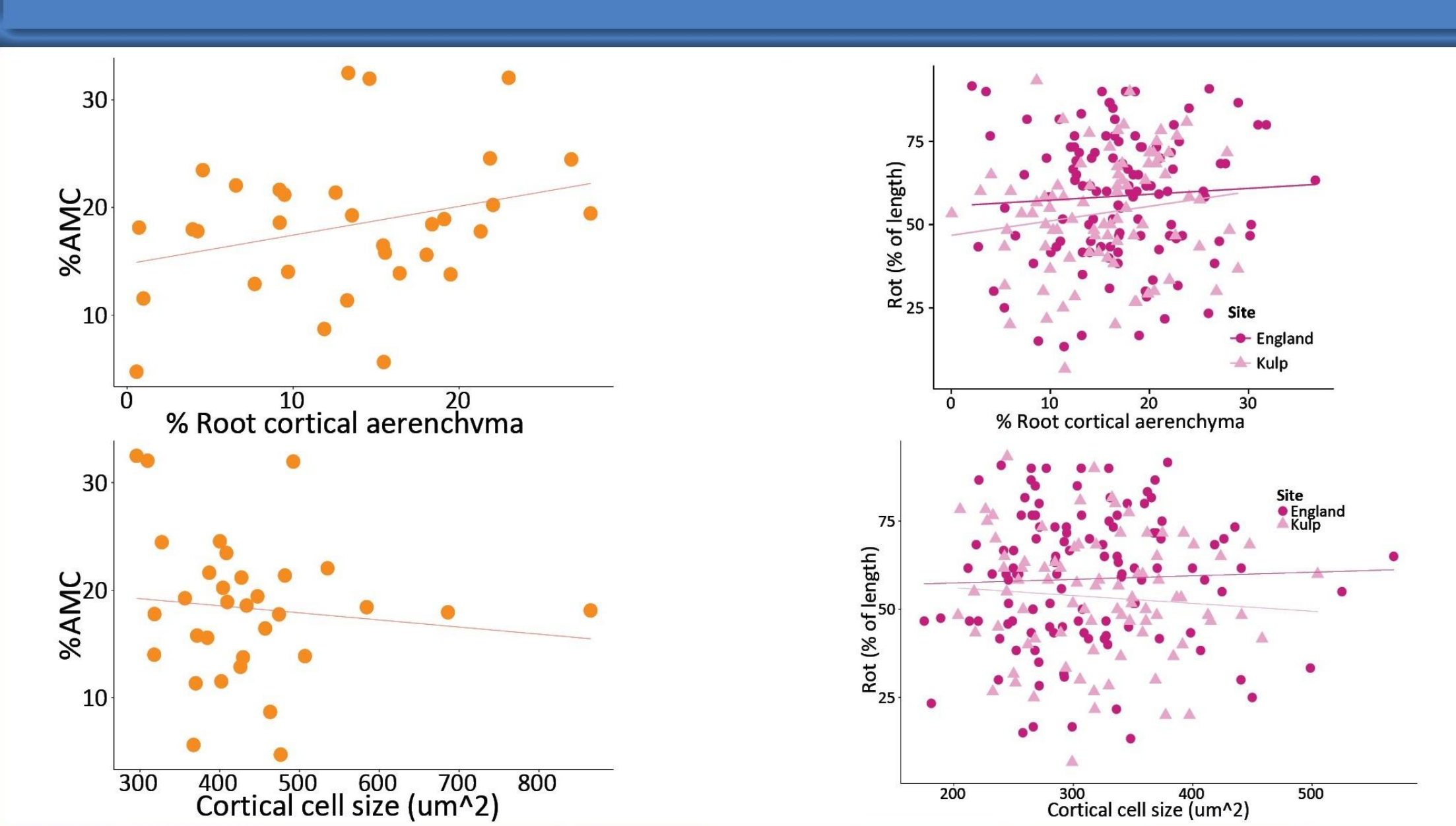
## Cortical cell file number affects AMC and RR in opposite ways



## Decreased xylem and cortex relative areas cause a decrease in RR



## No effect found of RCA and CCS on AMC or RR



## Summary

- AMC of 30 % on average occurred in the main axis of nodal roots of field-grown hybrids at optimum fertilization and watering regimes. Higher values of 50% on average are found in lateral roots.
- RR decreases with root thickness from the inner part to the external part of the root crown.
- Both AMC and RR are affected by site and hybrid line.
- Root anatomical traits explain up to 23% of the variability in RR and AMC, with CCFN affecting the two microbiological processes in opposite ways - roots with more CCFN have more RR and less AMC.
- Xylem and cortex relative areas affect RR but not AMC.
- The evidence suggests that there are no significant microbial tradeoffs of higher RCA and CCS.

## References

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## Acknowledgments

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