Ionomics QTL paper lab meeting

**Rob:**

Confused about how you could have so many overlapping QTLs without high correlations at the phenotypic level

Ecological stoichiometry book

Resource ratio theory - Tilman theory - coexistence is promoted when there are lots of resources available, maybe these would evolve and lead to correlations in nutrient uptake because of these tradeoffs…

Why are some things figures and not tables? Like the genetic correlations could be tables… because there are 18 elements, the figures get really large… try and take out extraneous bits from the figures as much as possible.

**Taslima:**

Could some of the lack of correlation between soil characteristics and plant characteristics be because of the sampling you used? Whole tiller/whole phytomer sampling.

Specific tissue profiles - maybe Na is accumulating in the roots, or leaves, or something. Because you have whole tiller/phytomer sequencing, you can't see that.

Myb also regulates HKT1 - it is the transcription factor that regulates HKT expression.

Add this info to the discussion section too.

Write about some of the implications of the patterns of GxE (relative to the patterns of phenotypic correlations) in the Discussion section

**Bhaskara** - liked the QTL localization and candidate genes result section.

Would be nice to show the ionome differences for parents. (Table 1)

Tone down the introduction talk of local adaptation even more (line 31-32ish)

For PCE, I think having a figure for ionome differences for parents rather than a table.

Add more soil data to the paper:

We have soil data at 20cm depth - 3 under weed cloth samples - on diagonal transect across field - then homogenized and sampled once for each site.