Biomass

• Sample all plots (5 N rates and x replicates).

• Count the number of stalks in the centre 10 m of rows 3 and 4

• Collect all the stalks and tops from a quadrat 5m long \* 2 crop rows.

• Put aside a subsample of 20 stalks and tops for partitioning. Weigh the rest, and discard.

• Weigh the remaining 20 stalk sample (and add that weight to the estimate of total biomass from the harvested area). Then partition those 20 stalks into:

o Millable stalk

o Tops which includes cabbage and green leaves

 To determine between millable stalk and cabbage cut between the 5th and 6th dewlaps for stalks that have not flowered or the 7th and 8th dewlaps for stalks that have flowered

 Include all green leaves, even those attached to the millable stalk into the top sample

• Weigh each component separately and record weights

o Weight of 20 millable stalks

o Weight of 20 tops

Biomass N uptake

* For each plot (5 N rates and x replicates), randomly select 5 millable stalks and 5 tops from the partitioned material above.
* To minimise cross-contamination, mulch stalks and tops in batches if possible rather than alternating individual stalk-top-stalk samples.
* Discard the first mulched material to remove any carry-over from previous samples.
* Collect a subsample of the mulched material and record the fresh weight
* Fresh weight mulched millable stalk sample
* Fresh weight mulched top sample
* Dry subsamples in an oven set at 60oC and record dry weight
* Dry weight mulched millable stalk sample
* Dry weight mulched top sample
* Calculate moisture content
* Moisture content % = ((net fresh weight – net dry weight) / net fresh weight) \* 100
* Grind dry millable stalk and top samples (pass through <2 mm sieve) in batches if possible to minimise cross-contamination.
* Discard the first ground material to remove any carry-over from previous samples.
* Collect a 20g subsample from the ground millable stalks and tops.
* Send samples to DSITI for analysis of N concentration and 15N/14N determination.
* N export to mill in stalk
* During the final crop harvest, randomly select billets from each plot. Mulch and collect a subsample of the mulched material.
* Record the fresh weight
* Dry subsamples in an oven set at 60oC and record dry weight
* Calculate moisture content
* Grind samples (pass through <2 mm sieve) Discard the first ground material to remove any carry-over from previous samples.
* Collect a 20g subsample.
* Send samples to DSITI for analysis of N concentration.

Of course, as soon as I sent this to Jayson, being first cab off the rank, all the local issues and practicalities came home to bite us and compromises had to be made. Key among them were

(i) Plot layout considerations. Jayson has treatments in long strips that occupy the full length of the field. Taking 1 quadrat out of that area was unlikely to be a good representation, or correlate well with yields determined off the full strip. Ideally there would have been biomass assessments from the top, middle and bottom of these strips to obtain an average for each strip (plot). However for some reason Jayson protested about pushing a break across the middle of the co-operators field, and so the compromise was a sample taken 20-30m in from each of the top and bottom of the strip and managed separately.

(ii) Sample size. Instead of my suggested 5m \* 2 rows at each sampling point, we compromised and harvested 5m \* 1 row at each end. It produced the same total area cut, but was from 2 separate areas in the plot. I still worry that this will give us too much variability in crop biomass, and by default N uptake, but we shall see when the data comes in. As a partial fix, Jays counted stalks in 10m of crop row but only harvested 5m. That way we have some sort of check if the stalk count in our harvested area was way below the larger counted area. We may be able to use covariates or other approaches to account for this that way.

(iii) Sub sample for partitioning. Given the halving of the individual biomass plots to 5m \* 1 row, we also halved the number of stalks that were split into tops&trash v stalk (ie. 10 stalks stripped)

Otherwise I think everything else has gone as per the original description. Sampling time for the biomass cuts should be as close to max N uptake as possible, which would be at approx. 9 months of age….or in the case of the Burdekin trial, just before lodging got out of hand.

I think we need to be consistent with our biomass sampling methodology across sites, because to get a good estimate of crop N content you need good estimates of biomass production/unit area. Without that, and N concentrations in tops/stalk become a lot less informative from the perspective of NUE.

Interested to hear how close others are to taking biomass samples. Phil is eagerly waiting to get some plant samples for N analyses, but knowing when they might be coming will hopefully head off any nasty shock (or analytical delays) at that end.