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Living Carbon OSU field trial

Sampling description for field RNA analysis

Sampling.

1. Population narrowed to events: 5A (transgenic), 4A(transgenic), 5C,(transgenic) 13-15E(transgenic), 2H(transgenic), 16-20,(escape) 8-9D,(escape) CT3 (wild type)
2. Population narrowed to trees within 1 standard deviation of the mean tree height (as measured at end of 2022 gro season)
3. Early season sampling:
   1. Draw 6 IDs per event (these IDs also included in metabolite sampling)
4. Late season sampling.
   1. 3 samples drawn from the set of early samples.
   2. 3 samples drawn from the population not included in the early samples.

(rationale: Wanted to have some independent samples for early and late season because this was thought to give best estimate of the mean expression with respect to event. (sampling two separate populations is more representative than sampling one on two occasions)

Wanted some repeat measurements to answer the question of how gene expression changes with respect to sampling date.)

1. Procedure in the field
   1. Find branch on south side of tree
   2. Locate a mature and expanded leaf (should be free of fine hairs along petiole) – often in range of leaf 8-15 but this can vary by tree)
   3. Record stomatal conductance and photosystem II efficiency with Li600
   4. Take 4 leaf punches from leaf, place in tube and put on liquid nitrogen.