From:	Seth C. Murray
To:	Wilfred Vermerris; Ana I Saballos
Cc:	Bill Rooney; Stephen Kresovich; Jeff Pedersen; Martha Hamblin; sem30
Subject:	HIF Tissue for RNA - expression sequencing
Date:	Wednesday, November 04, 2009 9:13:39 AM
Attachments:	RNA samples.xlsx

I finished the harvesting of tissue on Monday - given the cool temperatures the plants were in early hard dough stage and still had decent brix.

For each plant that I harvested I collected two samples;
Boot Time point: Flag Leaf and Internode 4
Hard dough: Peduncle and Internode 4
I took the center ~2 inches of internode 4 for RNA extraction and used each end of internode 4 in a handheld juice press to collect brix these two end values were then averaged. These values are reported in the attached spreadsheet.

In preparing to ship these to Florida I have two main questions:

1. Handsqueezed brix values from a single internode are probably not reliable and full of error. However, in the samples I took from family 7, the handsqueezed brix value was higher for the [redacted] allele line than the Rio allele. Should we cherry pick the samples that behaved as we expect (Choose samples with Rio allele having the highest handheld brix, samples with [redacted] allele have lowest brix?). If so we could use Family 12 which behaves closer to what we expect but only has two samples in boot stage. Should we just ignore these handsqueeze values?

2. Should I ship all samples or a subset? There are probably three times more samples than we have money to analyze. If I ship a subset then if something happens we have backups I can reship.

Any thoughts appreciated.

Ana: the hard dough samples (especially the peduncle) are dirty and should be surfaced washed and/or cored to get the pith before RNA extraction if possible. I did not think about this until I was in the field with the liquid nitrogen and only a bandanna to wipe them off.

Thanks,

Seth

----- Original Message -----
From: "Wilfred Vermerris" <wev@ufl.edu>
To: "Bill Rooney" <wlr@tamu.edu>, "Seth C. Murray" <sethmurray@neo.tamu.edu>, "Stephen Kresovich" <sk20@cornell.edu>, "Ana I Saballos" <saballoa@ufl.edu>, "Jeff Pedersen" <Jeff.Pedersen@ars.usda.gov>
Sent: Monday, October 12, 2009 4:02:35 PM GMT -06:00 US/Canada Central
Subject: Map locations of Dwarf1 and Dwarf4?

Dear Steve, Bill, Seth and Jeff,

I was wondering if you are aware of the map locations of dw1 and dw4 in sorghum. If not, are you aware of anybody working on mapping these genes? We are interested in them, but would prefer to not duplicate ongoing efforts.

Thank you,

Wilfred

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