X-Virus-Scanned: amavisd-new at
X-Spam-Flag: NO
X-Spam-Score: -2.56
X-Spam-Level:
X-Spam-Status: No, score=-2.56 tagged_above=-10 required=5 tests=[AWL=0.038,
BAYES_00=-2.599, HTML_MESSAGE=0.001]
Subject: Sorghum composition slide for conference call
Date: Mon, 4 Aug 2008 11:32:18 -0700
X-MS-Has-Attach: yes
X-MS-TNEF-Correlator:
Thread-Topic: Sorghum composition slide for conference call
Thread-Index: AcjzVY+KkS9TqPziTxi2udlzRuZEOgDCUJxQ
From: "Walter Nelson" <wnelson@ceres-inc.com>
To: <wlr@tamu.edu>,
<jmullet@tamu.edu>
Cc: "Edgar Haro" <eharo@ceres-inc.com>,
"Spencer Swayze" <sswayze@ceres-inc.com>,
"Peter Mascia" <pmascia@ceres-inc.com>,
"Bonnie Hames" <bhames@ceres-inc.com>,
"Simpson, Shay" <shay-simpson@tamu.edu>,
"Baltensperger, David" <dbaltensperger@ag.tamu.edu>,
"Patricia Klein" <pklein@tamu.edu>,
"Avant, Bob" <bavant@tamu.edu>,
"Schuerman, Peter L." <PSchuerman@tamu.edu>,
<bmccutchen@tamu.edu>,
"Juerg Blumenthal" <jblumenthal@tamu.edu>
X-Virus-Scanned: amavisd-new at tamu.edu

Bill and John (and others),

Looking forward to speaking to you all this afternoon.

Walter

From: Simpson, Shay [mailto:shay-simpson@tamu.edu]
Sent: Thursday, July 31, 2008 2:37 PM

To: Baltensperger, David; wlr@tamu.edu; jmullet@tamu.edu; Patricia Klein; Avant, Bob; Schuerman, Peter L.; ahelms@tamu.edu; bmccutchen@tamu.edu; Juerg Blumenthal; Edgar Haro; Walter Nelson; Spencer Swayze
Cc: Slovacek, Jackie; j-young@tamu.edu; Penn, Nancye B; Nelson, Michelle
Subject: Ceres Aug. 4 - Agenda
Importance: High

All:

Attached please find the agenda for the conference call with Ceres this coming Monday.

I scheduled HEEP conference room 437 for our Texas A&M group to meet in.

For those that are not in College Station, the call in number is

888-296-6500

After the tone dial 801464#.

Walter, please forward this email to your group with Ceres as I don't have all of their email addresses.

Thanks,

Shay

Shay L. Simpson

Project Manager, Bioenergy Program

Texas AgriLife Research

979-845-6315 Tel

shay-simpson@tamu.edu

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fax: 979-862-4790

>X-Virus-Scanned: amavisd-new at neo-proxy-3.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.599
>X-Spam-Level:
>X-Spam-Status: No, score=-2.599 tagged_above=-10 required=5
> tests=[BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Use of structure
>Date: Thu, 7 May 2009 11:37:30 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Use of structure
>Thread-Index: AcnHiWhm4y3RaiSITi2+IOLaugDQfwHuS/Gg
>From: "Xuefeng Ma" <xma@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>Hi, Trish,
>
>I was very busy last week and I have not try your file. Do you still
>want me to implement you file and it may be helpful to compare the
>result from you?
>
>Xuefeng
>
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Monday, April 27, 2009 3:39 PM
>To: Xuefeng Ma
>Cc: John Bouck
>Subject: RE: Use of structure
>
>Xuefeng
>
>The extra column is the geographic information that I stuck in in the
>column right next to the line names. This column can easily be
>removed as it is an optional column. The genotype data is fine as I
>have opened it in structure and done several test runs with the
>data. Thus all you need to do is remove the column directly to the
>right of the line names. Does that make sense?
>
>Trish
>
>
>
>At 05:13 PM 4/27/2009, Xuefeng Ma wrote:
> >Hi, Trish,

> >
> >Please let me know if you have more questions.
> >
> >Xuefeng
> >
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Monday, April 27, 2009 2:51 PM
> >To: Xuefeng Ma
> >Subject: RE: Use of structure
> >
> >Xuefeng

> > >Xuefeng
> > >
> > >
> > >-----Original Message-----
> > >From: John Bouck
> > >Sent: Monday, April 27, 2009 2:25 PM
> > >To: Patricia Klein
> > >Cc: Xuefeng Ma
> > >Subject: RE: Use of structure
> > >
> > >Hi Trish,
> > >
> > >I do not run this program here - this is usually used by Xuefeng
>here.
> > >
> > >Xuefeng - can you please help Trish by suggesting parameters and take
>a
> >

> > >Thanks,
> > >John
> > >
> > >-----Original Message-----
> > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > >Sent: Monday, April 27, 2009 12:00 PM
> > >To: John Bouck
> > >Subject: Use of structure
> > >
> > >John

> > >P.S.S. Hope your long drive back to CA went okay and you have now
> > >recuperated from the trip.
> > >
> > >
> > >
> > >
> > >
> > >
> > >Dr. Patricia Klein
> > >Associate Professor
> > >Institute for Plant Genomics and Biotechnology TAMU 2123 Texas
>AgriLIFE
> >
> > >Research Texas A&M University College Station, TX 77843-2123
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X-Virus-Scanned: amavisd-new at
X-Spam-Flag: NO
X-Spam-Score: -2.598
X-Spam-Level:
X-Spam-Status: No, score=-2.598 tagged_above=-10 required=15
tests=[BAYES_00=-2.599, HTML_MESSAGE=0.001]
Subject: RE: Illumina 30bp sequences
Date: Wed, 26 Mar 2008 10:00:36 -0700
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: Illumina 30bp sequences
Thread-Index: AciPXsuTkdnKvhqZTQGDenQ4bBS4aQAA+dig
From: "Timothy Swaller" <tswaller@ceres-inc.com>
To: "Patricia Klein" <pklein@tamu.edu>,
"John Bouck" <jbouck@ceres-inc.com>
X-Virus-Scanned: amavisd-new at tamu.edu

Thanks Patricia.

Can you also give us the restriction site that was cut, so that we can narrow down the BLAST matches a bit?
We can 1st locate these sites within the genome and expect matches in only these windows.

Tim

From: Patricia Klein [mailto:pklein@tamu.edu]
Sent: Wednesday, March 26, 2008 9:31 AM
To: John Bouck
Cc: Timothy Swaller
Subject: Illumina 30bp sequences

John

Take care,
Trish

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>X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.599
>X-Spam-Level:
>X-Spam-Status: No, score=-2.599 tagged_above=-10 required=5
> tests=[BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Use of structure
>Date: Mon, 27 Apr 2009 15:54:41 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Use of structure
>Thread-Index: AcnHiWhm4y3RaiSITi2+IOLaugDQfwAALrXw
>From: "Xuefeng Ma" <xma@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>Cc: "John Bouck" <jbouck@ceres-inc.com>

>Xuefeng
>
>
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Monday, April 27, 2009 3:39 PM
>To: Xuefeng Ma
>Cc: John Bouck
>Subject: RE: Use of structure
>
>Xuefeng

>Trish
>
>
>
>At 05:13 PM 4/27/2009, Xuefeng Ma wrote:
> >Hi, Trish,

> >Please let me know if you have more questions.
> >
> >Xuefeng
> >
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Monday, April 27, 2009 2:51 PM
> >To: Xuefeng Ma
> >Subject: RE: Use of structure
> >
> >Xuefeng

> >Trish
> >
> >

> > >Xuefeng
> > >
> > >
> > >-----Original Message-----
> > >From: John Bouck
> > >Sent: Monday, April 27, 2009 2:25 PM
> > >To: Patricia Klein
> > >Cc: Xuefeng Ma
> > >Subject: RE: Use of structure
> > >
> > >Hi Trish,
> > >
> > >I do not run this program here - this is usually used by Xuefeng
>here.
> > >
> > >Xuefeng - can you please help Trish by suggesting parameters and take
>a
> >
> > >look yourself?
> > >I believed that Structure would be able to accommodate geographic
> > >origin in some capacity - can you please comment.
> > >
> > >Thanks,
> > >John
> > >
> > >-----Original Message-----
> > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > >Sent: Monday, April 27, 2009 12:00 PM

> > >To: John Bouck
> > >Subject: Use of structure
> > >
> > >John

> > >Thanks

> > >P.S.S. Hope your long drive back to CA went okay and you have now
> > >recuperated from the trip.
> > >
> > >
> > >
> > >
> > >
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>X-Virus-Scanned: amavisd-new at neo-proxy-3.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -1.801
>X-Spam-Level:
>X-Spam-Status: No, score=-1.801 tagged_above=-10 required=5 tests=[AWL=0.699,
>	BAYES_00=-2.599, RDNS_NONE=0.1, SPF_PASS=-0.001]
>Authentication-Results: os-mail-4.tamu.edu;
>dkim=neutral (message not signed) header.i=none
>X-HAT: SG SUSPECTLIST_NO_SBRS, P $THROTTLED_NO_SBRS, L IncomingMail
>X-SRBS: None
>X-EXTLoop1: 1
>X-IronPort-Anti-Spam-Filtered: true
>X-IronPort-Anti-Spam-Result:
>ApwEAKOf8UpB2vnI/2dsb2JhbACEc5UusyuCFAmORAKBMIEigRZTBItu
>X-IronPort-AV: E=Sophos;i="4.44,682,1249275600";
>   d="scan'208";a="3254426"
>Subject: RE: Gantt Chart
>Date: Wed, 4 Nov 2009 15:41:37 -0800
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Gantt Chart
>Thread-Index: AcpUy3RSNSdYZqYWTRqqTYviUDEvkAI3GKsA
>From: "Timothy Swaller" <tswaller@ceres.net>
>To: "Patricia Klein" <pklein@neo.tamu.edu>
>
>Hi Trish.
>I discussed the current Ghantt chart with John
>at the IPMB. I will make a version 2 and resend for review and discussion.
>After I send out the version 2, I will schedule
>some time to catch up and go over this with you.
>
>In general I am using this chart in its simplest
>means (tasks and timelines). The original chart
>was straight out of the contract with the red
>indicating that there were no timelines in the contract for these line items.
>
>I am hoping to get version 2 out to both you and
>John by next week and schedule a call later next week or the week after.
>
>Thanks for the patience
>
>Tim
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@neo.tamu.edu]
>Sent: Saturday, October 24, 2009 10:00 AM
>To: Timothy Swaller
>Subject: Re: Gantt Chart
>
>Tim
>
>I did not get a chance to get with John this
>past week to dicuss the Gantt chart details. I
>think he might have been too busy getting ready
>for this upcoming IPMB meeting. Perhaps when
>you get back to CA and things slow down a bit
>for you (if they ever do), you and I could talk
>on the phone to go over some of the terms at the
>bottom of the chart so that I better understand
>what they mean and what you are looking for with
>regards to the activities that I am directly working on.
>
>I am sure that John can provide an updated
>progress report on what we have been doing when

>the two of you meet, but I would like to have a
>better understanding of the chart for future meetings that we have.
>
>Thanks
>Trish
>
>
>----- Original Message -----
>From: "Timothy Swaller" <tswaller@ceres.net>
>To: "John Mullet" <jmullet@tamu.edu>, "Patricia Klein" <pklein@tamu.edu>
>Sent: Friday, October 23, 2009 10:09:13 AM GMT -06:00 US/Canada Central
>Subject: RE: Gantt Chart
>
>
>
>
>Sounds good John.
>
>See you in St. Louis.
>
>
>
>my cell
>
>805-410-2873
>
>
>
>Tim
>
>
>
>
>
>From: John Mullet [mailto:jmullet@tamu.edu]
>Sent: Wednesday, October 21, 2009 5:29 AM
>To: Patricia Klein
>Cc: Timothy Swaller
>Subject: Re: Gantt Chart
>
>
>
>Trish and Tim,
>
>
>
>
>
>Trish and I will discuss this before I head to
>the IPMB. I can give you an update while there.
>
>
>
>
>
>My schedule is pretty flexible early in the
>week. How about trying to meet near the
>conference registration desk at about noon on Monday and talk over lunch?
>
>
>
>
>
>My cell number is 979-229-9666.
>
>
>
>
>
>Thanks,

>
>
>
>
>
>John
>
>
>
>
>
>
>
>
>
>
>On Oct 20, 2009, at 10:43 AM, Patricia Klein wrote:
>
>
>
>
>
>
>Tim
>
>That would work for me. I just need for John to
>confirm that it will work for him.
>
>Thanks and hope you get everything done before IPMB.
>
>Trish
>
>
>
>At 10:38 AM 10/20/2009, Timothy Swaller wrote:
>
>
>
>Thanks Patricia.
>I am hopelessly busy this week due to the IPMB
>next week. Is it poss ble for you and John to
>take a look and possibly John would have a free
>hour next week to sit down with me and go over this.
>
>John, do you have an idea of your schedule next
>week at the IPMB and do you have any free time to meet and discuss this?
>
>Thanks
>Tim
>
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Thursday, October 15, 2009 10:14 AM
>To: Timothy Swaller; John Mullet
>Subject: Re: Gantt Chart
>
>Tim
>
>I looked at it briefly but haven't gone over it
>with John yet. Unfortunately we have a grant
>proposal due this week and we were both working
>on it for the last few weeks. I now believe John
>is out of town for the rest of the week so my
>guess is it won't be until next week that he and
>I can discuss what you sent. Perhaps we could
>schedule some type of conference call for later
>next week? Sorry I can't give you more details
>right now. As soon as John is back from his trip, I will ta k with him.
>
>Thanks
>Trish
>

>
>
>At 10:55 AM 10/15/2009, Timothy Swaller wrote:
>
>Hi John and Patricia.
>Hope all is well, I here there has been a significant amount of rain lately.
>
>Have you had a chance to look over the Gantt
>chart I sent out and do you have any questions/comments on it?
>
>Stay dry
>Tim
>
>Timothy Swaller
>Director, IT and Genomics
>Office: 805.376.6545
>tswaller@ceres.net
>
><135224f3.gif>
>Ceres, Inc. ~ The Energy Crop Company Â®
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>--
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>Texas A&M University
>College Station, TX 77843-2123

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X-Virus-Scanned: amavisd-new at
X-Spam-Flag: NO
X-Spam-Score: -2.598
X-Spam-Level:
X-Spam-Status: No, score=-2.598 tagged_above=-10 required=5
tests=[BAYES_00=-2.599, HTML_MESSAGE=0.001]
X-Virus-Scanned: amavisd-new at tamu.edu
X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
Subject: Illumina Platform
Date: Fri, 12 Dec 2008 08:07:21 -0800
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: Illumina Platform
Thread-Index: Aclcc7ZJNBbtHomPTDqOhR4AKPxDJg==
From: "Timothy Swaller" <tswaller@ceres-inc.com>
To: "Patricia Klein" <pklein@tamu.edu>,
<jmullet@tamu.edu>

Good to see you both again.
Came across an article today in Nature Methods.
thought it was interesting.

“A large genome center’s improvements to the Illumina sequencing system”
vol.5 No. 12, Dec. 2008, p. 1005

Discusses some changes they have made to the library prep phase to make it more efficient.

Tim

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Sr. Manager
Genomic Technologies
Ceres, Inc.
(805) 376-6504 x1109
www.ceres.net

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X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
X-Spam-Flag: NO
X-Spam-Score: -2.412
X-Spam-Level:
X-Spam-Status: No, score=-2.412 tagged_above=-10 required=5 tests=[AWL=0.186, BAYES_00=-2.599, HTML_MESSAGE=0.001]
X-Virus-Scanned: amavisd-new at tamu.edu
X-Greylist: from auto-whitelisted by SQLgrey-1.7.6
Subject: RE: A&M Ceres MAS/MAB/mapping strategy discussion
Date: Thu, 12 Feb 2009 07:28:23 -0800
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: A&M Ceres MAS/MAB/mapping strategy discussion
Thread-Index: AcmNICY3fGvQ8oXOT+6soRq9rFmIYgABlHCw
From: "Walter Nelson" <wnelson@ceres.net>
To: "Patricia Klein" <pklein@tamu.edu>

Thanks Patricia. Will see if Bill has any conflicts and then will try to confirm everything.

Walter

From: Patricia Klein [mailto:pklein@tamu.edu]
Sent: Thursday, February 12, 2009 6:40 AM
To: John Mullet; Walter Nelson
Cc: Bill Rooney
Subject: Re: A&M Ceres MAS/MAB/mapping strategy discussion

April 3rd would work for me as well.

Thanks
Trish

At 07:45 AM 2/12/2009, John Mullet wrote:

> Yes, April 3rd will work for me.
>
> John
> On Feb 12, 2009, at 7:42 AM, Walter Nelson wrote:
>
> > John Bouck mentioned he's got something starting on the 9th. How about April 3rd?
> >
> > W

From: John Mullet [mailto:jmullet@tamu.edu]
Sent: Thursday, February 12, 2009 5:37 AM
To: Walter Nelson
Cc: Bill Rooney; Patricia Klein
Subject: Re: A&M Ceres MAS/MAB/mapping strategy discussion

Walter,

I will be traveling April 6-8. Could we try later that week or early the next?

Thanks,

John
On Feb 12, 2009, at 7:32 AM, Walter Nelson wrote:

> John, Patricia and Bill,
>
> The primary constraint I got on scheduling this was from Bill to put it after April 1. I wanted to propose to you Monday, April 6. While the Ceres people would be there all day, I don't expect you all need to be present the whole time. We can put an agenda together that can cover various topics and still work for your schedules. I think the idea was to keep it relatively informal as well (i.e. no extensive slide decks required, only for explanation to facilitate discussion etc...) John B and Jeff also specifically mentioned wanting to see the labs as well for example.
>
> Please let me know if April 6 would work for you and, if not, let me know what day(s) would. I'd mainly just like to have it sometime before the next quarterly at the end of April.
>
> Thanks,
>
> Walter

Walter E Nelson
Ceres, Inc.
1535 Rancho Conejo Blvd.
Thousand Oaks, CA 91320
voice: (805)376-6548
www.ceres.net

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Dr. Patricia Klein
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>Subject: RE: Information from last phone discussion
>Date: Tue, 20 Nov 2007 13:08:22 -0800
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Information from last phone discussion
>Thread-Index: AcgojAgdHWSS5JeBRXSYqATV93PKegDLNkIg
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>X-Virus-Scanned: amavisd-new at tamu.edu
>
>Thanks Trish,

>Enjoy your thanksgiving,
>John
>
>
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Friday, November 16, 2007 12:05 PM
>To: John Bouck
>Subject: Information from last phone discussion
>
>
>
>John,

>Thanks
>Trish
>
>
>
>
>
>
>Dr. Patricia Klein
>Associate Professor
>Institute for Plant Genomics and Biotechnology TAMU 2123 Texas
>Agricultural Experiment Station Texas A&M University College Station, TX
>77843-2123
>
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>
>**********
>
>This email message is for the sole use of the intended recipient(s)
>and may contain confidential and privileged information. Any
>unauthorized review, use, disclosure or distr bution is
>proh bited. If you are not the intended recipient, please contact
>the sender by reply email and destroy all copies of the original
>message. Ceres, Inc. declines any liability for any viruses or
>other potentially harmful code which may be transmitted by or
>accompanying this email or any attachment.
>
>**********

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>X-Virus-Scanned: amavisd-new at neo-proxy-2.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.412
>X-Spam-Level:
>X-Spam-Status: No, score=-2.412 tagged_above=-10 required=5 tests=[AWL=0.187,
>	BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Use of structure
>Date: Mon, 27 Apr 2009 14:25:22 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Use of structure
>Thread-Index: AcnHaut+ppc9eceIR/SktQiuYMzP7QAE289g
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>Cc: "Xuefeng Ma" <xma@ceres-inc.com>
>
>Hi Trish,
>
>I do not run this program here - this is usually used by Xuefeng here.
>
>Xuefeng - can you please help Trish by suggesting parameters and take a
>look yourself?
>I believed that Structure would be able to accommodate geographic origin
>in some capacity - can you please comment.
>
>Thanks,
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Monday, April 27, 2009 12:00 PM
>To: John Bouck
>Subject: Use of structure
>
>John

>P.S.S. Hope your long drive back to CA went okay and you have now
>recuperated from the trip.
>
>

>
>
>
>
>Dr. Patricia Klein
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X-Virus-Scanned: amavisd-new at neo-proxy-2.tamu.edu
X-Spam-Flag: NO
X-Spam-Score: -0.495
X-Spam-Level:
X-Spam-Status: No, score=-0.495 tagged_above=-10 required=5
tests=[BAYES_00=-2.599, HTML_MESSAGE=0.001, RDNS_NONE=0.1,
TRACKER_ID=2.003]
X-HAT: SG SUSPECTLIST_NO_SBRS, P $THROTTLED_NO_SBRS, L tamu-relay
X-SRBS: None
X-EXTLoop1: 1
X-IronPort-Anti-Spam-Filtered: true
X-IronPort-Anti-Spam-Result: Aq4EABTNm0pB2vnI/2dsb2JhbACCLCrXFYQaBYpT
X-IronPort-AV: E=Sophos;i="4.44,307,1249275600";
d="scan'208,217";a="12959319"
Subject: NextGen data
Date: Mon, 31 Aug 2009 13:21:29 -0700
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: NextGen data
thread-index: AcoqbdGmS/L6yK4ES2S39YuWfQxUzwAADj8QAABoE/AAAA8H8AACD8+Q
From: "Timothy Swaller" <tswaller@ceres.net>
To: "Patricia Klein" <pklein@tamu.edu>,
<jmullet@tamu.edu>

Hi Patricia and John.

Tim

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Ceres – Texas AgriLife Meeting Agenda draft
Quarter 2008Q4
December 9, 2008
Ceres (1535 Rancho Conejo Blvd)
Thousand Oaks, CA

Agenda:

6:00	Depart
7:00	Dinner (Piatti)

Attendees:

CERES	**Texas AgriLife**
Edgar Haro	John Mullet
Spencer Swayze	Bill Rooney
Walter Nelson	Peter Schuerman
Peter Mascia	Patricia Klein
John Bouck	Jürg Blumenthal

Tim Swaller	David Baltensperger
Bonnie Hames	Shay Simpson
Jeff Gwyn	

>X-Virus-Scanned: amavisd-new at
>X-Spam-Flag: NO
>X-Spam-Score: -2.54
>X-Spam-Level:
>X-Spam-Status: No, score=-2.54 tagged_above=-10 required=5 tests=[AWL=0.059,
>	BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: Draft Meeting agenda for Ceres - Texas A&M quarterly
>Date: Fri, 5 Dec 2008 14:25:12 -0800
>X-MS-Has-Attach: yes
>X-MS-TNEF-Correlator:
>Thread-Topic: Draft Meeting agenda for Ceres - Texas A&M quarterly
>Thread-Index: AclWOdWE0OngHVw0S9GM4yRa9G/PRQA7R4nw
>From: "Walter Nelson" <wnelson@ceres-inc.com>
>To: "John Mullet" <jmullet@tamu.edu>,
>	"Bill Rooney" <wlr@tamu.edu>,
>	"Patricia Klein" <pklein@tamu.edu>,
>	"Juerg M Blumenthal" <JBlumenthal@ag.tamu.edu>,
>	"Edgar Haro" <eharo@ceres-inc.com>,
>	"Jeff Gwyn" <jgwyn@ceres-inc.com>,
>	"Timothy Swaller" <tswaller@ceres-inc.com>,
>	"John Bouck" <jbouck@ceres-inc.com>,
>	"Bud Wylie" <bwylie@ceres-inc.com>
>Cc: "Shay Simpson" <shay-simpson@tamu.edu>,
>	"Bob Avant" <bavant@dsmail.tamu.edu>,
>	"McCutchen, Bill" <bmccutchen@tamu.edu>,
>	"Schuerman, Peter L." <PSchuerman@tamu.edu>,
>	"Peter Mascia" <pmascia@ceres-inc.com>,
>	"Richard Flavell" <rflavell@ceres-inc.com>,
>	"Michael Stephenson" <mstephenson@ceres-inc.com>,
>	"Kimberly Norton" <knorton@ceres-inc.com>
>
>
>Hello Everyone,
>
>Attached is a draft agenda for our meeting on Tuesday. Please take a
>look at it and let me know if you'd like to make any adjustments.
>
>The conference number we will use is:
>1 866 339 1399 (toll free)
>1 334 323 1808 (International)
>MEETING NUMBER: *9042546*
>
>Shay, please forward to anyone on the A&M side that I missed.
>
>Looking forward to seeing everyone here next week.
>
>Best regards,
>
>Walter
>
>
>
>
>Walter E Nelson
>Ceres, Inc.
>1535 Rancho Conejo Blvd.

>Thousand Oaks, CA 91320
>voice: (805)376-6548
>www.ceres.net
>
>
>-----Original Message-----
>From: John Mullet [mailto:jmullet@tamu.edu]
>Sent: Thursday, December 04, 2008 9:58 AM
>To: Walter Nelson
>Cc: Shay Simpson
>Subject: Meeting agenda
>
>Hi Walter,

>Thanks,
>
>John
>

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>X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -1.999
>X-Spam-Level:
>X-Spam-Status: No, score=-1.999 tagged_above=-10 required=5 tests=[AWL=0.500,
>	BAYES_00=-2.599, RDNS_NONE=0.1]
>X-HAT: SG SUSPECTLIST_NO_SBRS, P $THROTTLED_NO_SBRS, L tamu-relay
>X-SRBS: None
>X-EXTLoop1: 1
>X-IronPort-AV: E=Sophos;i="4.44,506,1249275600";
>   d="pdf'?mpp'32?scan'32,208,32";a="32916625"
>Subject: RE: sweet sorghum genotyping
>Date: Mon, 5 Oct 2009 08:02:36 -0700
>X-MS-Has-Attach: yes
>X-MS-TNEF-Correlator:
>Thread-Topic: sweet sorghum genotyping
>Thread-Index: Aco9Tpu1SQ5fin5hTdiNOR7TNS3K2gIfRNfw
>From: "Timothy Swaller" <tswaller@ceres.net>
>To: "John Mullet" <jmullet@tamu.edu>,
>	"Patricia Klein" <pklein@tamu.edu>
>Cc: "Walter Nelson" <wnelson@ceres.net>,
>	"Jeff Gwyn" <jgwyn@ceres-inc.com>
>
>Hi John and Patricia.
>I believe Walter may have discussed a need I have to fill out a more
>formal tracking and progress update. I have prepared a template of the
>current projects taken from the agreement as a starting point, but I was
>hoping to build on this by modifying and revising based on your
>knowledge of what has been done and agreed on to date. Please look this
>over. (I apologize for the redundancy, since I believe you had done a
>similar exercise with John Bouck as well)
>What is your opinions on the best path forward to fill this out, there
>are several possibilities? Conference call with video, I could take a
>trip to TX, etc.
>I will also be attending the IPMB in St. Louis from the 25-30, so if
>either of you are attending, this may be an opportunity to sit down and
>walk through this or just have dinner and talk.
>
>Thanks
>Tim
>
>included in .pdf and .mpp
>
>
>-----Original Message-----
>From: John Mullet [mailto:jmullet@tamu.edu]
>Sent: Thursday, September 24, 2009 12:38 PM
>To: Walter Nelson; Timothy Swaller
>Cc: Bill Rooney; Jeff Gwyn; Richard Flavell
>Subject: sweet sorghum genotyping
>
>Walter and Tim,

>Thanks,
>
>John
>
>

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>X-Virus-Scanned: amavisd-new at neo-proxy-2.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.599
>X-Spam-Level:
>X-Spam-Status: No, score=-2.599 tagged_above=-10 required=5
> tests=[BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: from auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: SNP file for R07007 vs R07020
>Date: Tue, 7 Jul 2009 15:28:53 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: SNP file for R07007 vs R07020
>Thread-Index: Acn/UU3VOq2kdmDVS22zUJikLhFJiAAACFrA
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>

>This week is lost due to local meetings - how about Monday at 3:00 your
>time?
>
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Tuesday, July 07, 2009 3:22 PM
>To: John Bouck
>Subject: RE: SNP file for R07007 vs R07020
>
>John

>Thanks
>Trish
>
>
>
>At 05:09 PM 7/7/2009, you wrote:
> >Trish,
> >

> >Are you up for a call next week?
> >
> >John
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Tuesday, June 30, 2009 7:17 AM
> >To: John Bouck
> >Subject: RE: SNP file for R07007 vs R07020
> >
> >John

> >Trish
> >
> >
> >
> >At 07:37 PM 6/29/2009, you wrote:
> > >Trish,
> > >
> > >How's the heat? Our guys in CS are just constantly griping about it
>-
> > >are they just wimps?

> > >Input welcomed,
> > >John
> > >
> > >-----Original Message-----
> > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > >Sent: Friday, June 19, 2009 11:42 AM
> > >To: John Bouck
> > >Subject: RE: SNP file for R07007 vs R07020

> > >Trish

> > >
> > >
> > >
> > >At 01:28 PM 6/19/2009, you wrote:
> > > >Remaining information needed: T3x8$AM
> > > >
> > > >John
> > > >
> > > >-----Original Message-----
> > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > >Sent: Friday, June 19, 2009 11:23 AM
> > > >To: John Bouck
> > > >Subject: RE: SNP file for R07007 vs R07020
> > > >
> > > >John
> > > >
> > > >You are going to have to remind what the address of the FTP site
> > > >is. I can't seem to remember and can't find any documentation. I
> > > >may need to call you for a password. I am in now if you want to
>call
> > > >me with the information.
> > > >
> > > >Trish
> > > >
> > > >
> > > >
> > > >At 01:10 PM 6/19/2009, you wrote:
> > > > >Great,

> > > > >Look forward to talking next week.
> > > > >
> > > > >John
> > > > >
> > > > >-----Original Message-----
> > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > >Sent: Friday, June 19, 2009 11:03 AM
> > > > >To: John Bouck
> > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > >
> > > > >John

> > > > >Thanks
> > > > >Trish
> > > > >
> > > > >
> > > > >
> > > > >At 07:39 PM 6/18/2009, you wrote:
> > > > > >You've done rio? Is that data you can share?
> > > > > >
> > > > > >John
> > > > > >
> > > > > >-----Original Message-----
> > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > >Sent: Thursday, June 18, 2009 2:30 PM
> > > > > >To: John Bouck
> > > > > >Subject: RE: SNP file for R07007 vs R07020

> > > > > >Trish
> > > > > >
> > > > > >

> > > > > >
> > > > > >-----Original Message-----
> > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > >Sent: Thursday, June 18, 2009 8:31 AM
> > > > > >To: John Bouck
> > > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > > >
> > > > > >John
> > > > > >
> > > > > >As far as I can tell that should work for me. No worries
>about
> > >teh
> > > > > >rescheduling. I too am busy so I totally understand. I may

> > > > > > >
> > > > > > > >Thanks
> > > > > > > >Trish
> > > > > > > >
> > > > > > > >At 10:17 AM 6/18/2009, you wrote:
> > > > > > > > >Trish - I'm really sorry to do this again but my schedule
>is
> > > > >being
> > > > > > > >taken
> > > > > > > > >over by others and I have yet another last minute conflict.
> > > > > > > > >
> > > > > > > > >Maybe we should shoot for Monday afternoon at 3:00 your
>time
> >-
> > > > >things
> > > > > > > > >should quiet down next week.
> > > > > > > > >
> > > > > > > > >Best,
> > > > > > > > >John
> > > > > > > > >
> > > > > > > > >-----Original Message-----
> > > > > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > > > > >Sent: Wednesday, June 17, 2009 8:22 AM
> > > > > > > > >To: John Bouck
> > > > > > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > > > > > >
> > > > > > > > >John
> > > > > > > > >
> > > > > > > > >That time tomorrow should work just fine.
> > > > > > > > >
> > > > > > > > >Thanks
> > > > > > > > >Trish
> > > > > > > > >
> > > > > > > > >
> > > > > > > > >
> > > > > > > > >At 10:10 AM 6/17/2009, you wrote:
> > > > > > > > > >Trish,
> > > > > > > > > >
> > > > > > > > > >I have an external meeting that is now planned for the
>same
> > > > >time
> > > > > > > >as
> > > > > > > > >our
> > > > > > > > > >meeting later today. Can we move our discussion to
> >tomorrow
> > > >at
> > > > > > >3:00
> > > > > > > > > >your time?
> > > > > > > > > >
> > > > > > > > > >Sorry for the late notice,
> > > > > > > > > >John
> > > > > > > > > >
> > > > > > > > > >-----Original Message-----
> > > > > > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > > > > > >Sent: Tuesday, June 09, 2009 1:53 PM
> > > > > > > > > >To: John Bouck
> > > > > > > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > > > > > > >
> > > > > > > > > >Sounds good, I will put that time on my calendar and be
> > > >waiting
> > > > > > >for
> > > > > > > > >your
> > > > > > > > > >call.
> > > > > > > > > >
> > > > > > > > > >Trish
> > > > > > > > > >
> > > > > > > > > >
> > > > > > > > > >At 03:47 PM 6/9/2009, you wrote:
> > > > > > > > > > >Great - how about Wednesday at 4:00 your time?
> > > > > > > > > > >

> > > > > > > > > >John
> > > > > > > > > >
> > > > > > > > > > >-----Original Message-----
> > > > > > > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > > > > > > >Sent: Tuesday, June 09, 2009 1:46 PM
> > > > > > > > > > >To: John Bouck
> > > > > > > > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > > > > > > > >
> > > > > > > > > > >John
> > > > > > > > > > >
> > > > > > > > > > >I will be around next week as of now so whenever you
>want
> > > >to
> > > > > >talk
> > > > > > > > > > >just give me a heads up on day/time.
> > > > > > > > > > >
> > > > > > > > > > >Trish
> > > > > > > > > > >
> > > > > > > > > > >
> > > > > > > > > > >
> > > > > > > > > > >At 03:44 PM 6/9/2009, you wrote:
> > > > > > > > > > >Hi Trish,
> > > > > > > > > > >
> > > > > > > > > > >We've started getting our heads around this - would
>be
> > > >fun
> > > > > >to
> > > > > > > > > > >discuss,
> > > > > > > > > > >unfortunately I'm traveling for the next several
>days.
> > > >Are
> > > > > > >you
> > > > > > > > > > >free
> > > > > > > > > > >next Wednesday or Thursday?
> > > > > > > > > > >
> > > > > > > > > > >John
> > > > > > > > > > >
> > > > > > > > > > >-----Original Message-----
> > > > > > > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > > > > > > >Sent: Wednesday, May 20, 2009 9:27 AM

> >know.
> > > > >Let
> > > > >me
> > > > > > > > > > >know how it all turns out.
> > > > > > > > > > >
> > > > > > > > > > >Thanks
> > > > > > > > > > >Trish
> > > > > > > > > > >
> > > > > > > > > > >
> > > > > > > > > > >
> > > > > > > > > > >
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> > > > > > > > > > >Dr. Patricia Klein
> > > > > > > > > > >Associate Professor
> > > > > > > > > > >Institute for Plant Genomics and Biotechnology
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> > > > > > > > > > >Texas AgriLIFE Research
> > > > > > > > > > >Texas A&M University
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> > > > > > > > > > >phone: 979-862-6308
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> > > > > > > > > > >Dr. Patricia Klein
> > > > > > > > > > >Associate Professor
> > > > > > > > > > >Institute for Plant Genomics and Biotechnology
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> > > > > > > > > > >Dr. Patricia Klein
> > > > > > > > > > >Associate Professor
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>X-Virus-Scanned: amavisd-new at neo-proxy-2.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.599
>X-Spam-Level:
>X-Spam-Status: No, score=-2.599 tagged_above=-10 required=5
>	tests=[BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: from auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: SNP file for R07007 vs R07020
>Date: Tue, 7 Jul 2009 15:09:09 -0700
>X-MS-Has-Attach:

>Thread-Index: Acn5jXbsa0vgh+LRRsK3AaUhWmbBrwFwXqrQ
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>

>Are you up for a call next week?
>
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Tuesday, June 30, 2009 7:17 AM

>Thanks
>Trish
>
>
>
>At 07:37 PM 6/29/2009, you wrote:
> >Trish,
> >
> >How's the heat? Our guys in CS are just constantly griping about it -
> >are they just wimps?

> >Input welcomed,
> >John
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Friday, June 19, 2009 11:42 AM
> >To: John Bouck

> >Trish
> >
> >
> >
> >At 01:28 PM 6/19/2009, you wrote:
> > >Remaining information needed: T3x8$AM
> > >
> > >John
> > >
> > >-----Original Message-----
> > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > >Sent: Friday, June 19, 2009 11:23 AM

> > >John
> > >
> > >You are going to have to remind what the address of the FTP site
> > >is. I can't seem to remember and can't find any documentation. I
> > >may need to call you for a password. I am in now if you want to call
> > >me with the information.
> > >
> > >Trish
> > >
> > >
> > >
> > >At 01:10 PM 6/19/2009, you wrote:
> > > >Great,

> > > >Look forward to talking next week.
> > > >
> > > >John
> > > >
> > > >-----Original Message-----
> > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > >Sent: Friday, June 19, 2009 11:03 AM

> > > >Thanks
> > > >Trish
> > > >
> > > >
> > > >
> > > >At 07:39 PM 6/18/2009, you wrote:
> > > > >You've done rio? Is that data you can share?
> > > > >
> > > > >John
> > > > >
> > > > >-----Original Message-----
> > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > >Sent: Thursday, June 18, 2009 2:30 PM

> > > > > >Trish
> > > > > >
> > > > > >At 10:17 AM 6/18/2009, you wrote:
> > > > > > >Trish - I'm really sorry to do this again but my schedule is
> > > >being
> > > > > >taken
> > > > > > >over by others and I have yet another last minute conflict.
> > > > > > >
> > > > > > >Maybe we should shoot for Monday afternoon at 3:00 your time
>-
> > > >things
> > > > > > >should quiet down next week.
> > > > > > >
> > > > > > >Best,
> > > > > > >John
> > > > > > >
> > > > > > >-----Original Message-----
> > > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > > >Sent: Wednesday, June 17, 2009 8:22 AM

> > > > > > >John
> > > > > > >
> > > > > > >That time tomorrow should work just fine.
> > > > > > >
> > > > > > >Thanks
> > > > > > >Trish
> > > > > > >
> > > > > > >
> > > > > > >
> > > > > > >At 10:10 AM 6/17/2009, you wrote:
> > > > > > > >Trish,
> > > > > > > >
> > > > > > > >I have an external meeting that is now planned for the same
> > > >time
> > > > > >as
> > > > > > >our
> > > > > > > >meeting later today. Can we move our discussion to
>tomorrow
> > >at
> > > > > >3:00
> > > > > > > >your time?
> > > > > > > >
> > > > > > > >Sorry for the late notice,
> > > > > > > >John
> > > > > > > >
> > > > > > > >-----Original Message-----
> > > > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > > > >Sent: Tuesday, June 09, 2009 1:53 PM

> > > > > > > >Sounds good, I will put that time on my calendar and be
> > >waiting
> > > > > >for
> > > > > > >your
> > > > > > > >call.
> > > > > > > >

> > > > > > > >Trish
> > > > > > > > >
> > > > > > > > >
> > > > > > > > >At 03:47 PM 6/9/2009, you wrote:
> > > > > > > > >Great - how about Wednesday at 4:00 your time?
> > > > > > > > > >
> > > > > > > > > >John
> > > > > > > > > >
> > > > > > > > > >-----Original Message-----
> > > > > > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > > > > > >Sent: Tuesday, June 09, 2009 1:46 PM
> > > > > > > > > >To: John Bouck
> > > > > > > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > > > > > > > >
> > > > > > > > > > >John
> > > > > > > > > > >
> > > > > > > > > > >I will be around next week as of now so whenever you want
> > >to
> > > > >talk
> > > > > > > > > > >just give me a heads up on day/time.
> > > > > > > > > > > >
> > > > > > > > > > > >Trish
> > > > > > > > > > > > >
> > > > > > > > > > > > > >
> > > > > > > > > > > > > >
> > > > > > > > > > > > > >At 03:44 PM 6/9/2009, you wrote:
> > > > > > > > > > > > > > >Hi Trish,
> > > > > > > > > > > > > > > >
> > > > > > > > > > > > > > > >We've started getting our heads around this - would be
> > >fun
> > > > >to
> > > > > > > > > > > > > > > >discuss,
> > > > > > > > > > > > > > > > >unfortunately I'm traveling for the next several days.
> > >Are
> > > > >you
> > > > > > > > > > > > > > > >free
> > > > > > > > > > > > > > > > >next Wednesday or Thursday?
> > > > > > > > > > > > > > > > >
> > > > > > > > > > > > > > > > >John
> > > > > > > > > > > > > > > > >
> > > > > > > > > > > > > > > > >-----Original Message-----
> > > > > > > > > > > > > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > > > > > > > > > > > > >Sent: Wednesday, May 20, 2009 9:27 AM

> > > > > > > > > > > > > > > > >John

> > > > > > > > > >Thanks
> > > > > > > > > >Trish
> > > > > > > > > >
> > > > > > > > > >
> > > > > > > > > >
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>X-Virus-Scanned: amavisd-new at neo-proxy-2.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.599
>X-Spam-Level:
>X-Spam-Status: No, score=-2.599 tagged_above=-10 required=5
> tests=[BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Use of structure
>Date: Thu, 7 May 2009 13:07:58 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>thread-topic: Use of structure
>thread-index: AcnPS4ezpW+dhPNvSKa27+MSQfN+wwAA1emQ
>From: "Xuefeng Ma" <xma@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>No problem.
>I will keep the program running, and deliver you the result next week. I
>need to pre-run many times to determine k, and then run the same k many
>times again. The final results will be a permutation average from
>CLUMPP.
>
>Xuefeng
>
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Thursday, May 07, 2009 12:36 PM
>To: Xuefeng Ma
>Subject: RE: Use of structure
>
>Xuefeng
>
>If you have time that would be great. Since this is not my area of
>expertise any guidance that I could get from you would be most helpful.
>
>thanks
>Trish
>
>
>At 01:37 PM 5/7/2009, you wrote:
> >Hi, Trish,
> >
> >I was very busy last week and I have not try your file. Do you still
> >want me to implement you file and it may be helpful to compare the
> >result from you?
> >
> >Xuefeng
> >
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Monday, April 27, 2009 3:39 PM
> >To: Xuefeng Ma
> >Cc: John Bouck
> >Subject: RE: Use of structure
> >

> >data. Thus all you need to do is remove the column directly to the
> >right of the line names. Does that make sense?
> >
> >Trish
> >
> >
> >
> >At 05:13 PM 4/27/2009, Xuefeng Ma wrote:
> > >Hi, Trish,
> > >

> > >Please let me know if you have more questions.
> > >
> > >Xuefeng
> > >
> > >
> > >-----Original Message-----
> > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > >Sent: Monday, April 27, 2009 2:51 PM
> > >To: Xuefeng Ma
> > >Subject: RE: Use of structure
> > >
> > >Xuefeng

> > >Trish
> > >
> > >

> > > >Xuefeng
> > > >
> > > >
> > > >-----Original Message-----

> > > >From: John Bouck
> > > >Sent: Monday, April 27, 2009 2:25 PM
> > > >To: Patricia Klein
> > > >Cc: Xuefeng Ma
> > > >Subject: RE: Use of structure
> > > >
> > > >Hi Trish,
> > > >
> > > >I do not run this program here - this is usually used by Xuefeng
> >here.
> > > >
> > > >Xuefeng - can you please help Trish by suggesting parameters and
>take
> >a
> > > >
> > > >look yourself?
> > > >I believed that Structure would be able to accommodate geographic
> > > >origin in some capacity - can you please comment.
> > > >
> > > >Thanks,
> > > >John
> > > >
> > > >-----Original Message-----
> > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > >Sent: Monday, April 27, 2009 12:00 PM
> > > >To: John Bouck
> > > >Subject: Use of structure
> > > >
> > > >John

> > > >P.S.S. Hope your long drive back to CA went okay and you have now
> > > >recuperated from the trip.
> > > >
> > > >

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> > > >
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>X-Spam-Score: -2.599
>X-Spam-Level:
>X-Spam-Status: No, score=-2.599 tagged_above=-10 required=5
>	tests=[BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: from auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Question about GGT
>Date: Thu, 9 Jul 2009 08:01:21 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Question about GGT
>Thread-Index: AcoAmax9fzOFaGwlQmSfhaKHpi0RfQAC2Kgw
>From: "Xuefeng Ma" <xma@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>

>Hope it helps.
>
>Xuefeng
>
>
>
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Thursday, July 09, 2009 6:32 AM
>To: Xuefeng Ma
>Subject: RE: Question about GGT
>

>Thanks
>Patricia
>
>
>At 05:56 PM 7/8/2009, you wrote:

> >FYI, I will be off in China about 6 weeks since tomorrow. I am glad to
> >catch any more questions if you have by tomorrow morning.

> >
> >Regards,
> >
> >Xuefeng
> >
> >
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Wednesday, July 08, 2009 3:39 PM
> >To: Xuefeng Ma
> >Subject: RE: Question about GGT
> >
> >Xuefeng

> >
> >
> >
> >At 01:23 PM 5/21/2009, you wrote:
> > >I do not have any problems.
> > >You can build the file either through the file Builder or format and
> > >copy from excel. If you use file builder, a map file and a loc file
>are
> > >needed. If you format in excel, it is very easy to copy in, but you
>do
> > >not have the flexibility to sort markers.
> > >
> > >No limitations for the numbers of plants and markers to load IN, but
> > >there is a column restriction if you download OUT as excel (you will
> > >lose any data beyond 256 column, because the build-in excel is still
> >the
> > >2003 version). However, you can get around it by exporting through
>txt
> > >file.
> > >
> > >Xuefeng
> > >
> > >
> > >-----Original Message-----
> > >From: John Bouck
> > >Sent: Thursday, May 21, 2009 11:11 AM
> > >To: Xuefeng Ma
> > >Subject: FW: Question about GGT
> > >
> > >Is this performance problem what you would expect?
> > >
> > >John
> > >
> > >-----Original Message-----
> > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > >Sent: Thursday, May 21, 2009 9:46 AM
> > >To: John Bouck
> > >Subject: RE: Question about GGT
> > >
> > >John,

> > >Thanks
> > >Trish
> > >
> > >
> > >
> > >At 10:41 AM 5/21/2009, you wrote:
> > > >Yes this should work. Xuefeng does this for looking at diversity
> > > >analysis - certainly most of the powerful tools in GGT for data
> > >analysis
> > > >are around pedigrees and population analysis so it is not
>surprising
> > > >that it is a focus of the documentation.
> > > >
> > > >Are you able to get the data in?
> > > >If it is something you can share we could take a look.
> > > >
> > > >John
> > > >
> > > >-----Original Message-----
> > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > >Sent: Thursday, May 21, 2009 8:25 AM
> > > >To: John Bouck
> > > >Subject: Question about GGT
> > > >
> > > >John,
> > > >
> > > >I have a quick question about graphical genotyping. I have
>installed
> > > >GGT32 on my windows machine and have read over the manual. As I
>read
> > > >over it, it sounds as if I need my individuals to come from some
>type
> > > >of population. However, we are working with diverse genotypes and
> > > >not individuals from a population. Do you know if GGT will work
>for
> > > >this? I have my markers across 13 different genotypes and would
>like
> > > >to graphically display this data but don't quite see how GGT will
>do
> > > >that as I don't have a population type to enter. I don't see this
> > > >mentioned in the manual. Any comments/suggestions would be
> > >appreciated.
> > > >
> > > >Thanks
> > > >Trish
> > > >
> > > >
> > > >
> > > >
> > > >
> > > >
> > > >
> > > >
> > > >Dr. Patricia Klein
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>X-Virus-Scanned: amavisd-new at neo-proxy-3.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.361
>X-Spam-Level:
>X-Spam-Status: No, score=-2.361 tagged_above=-10 required=5 tests=[AWL=0.238,
>	BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: SNP file for R07007 vs R07020
>Date: Fri, 19 Jun 2009 11:10:01 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: SNP file for R07007 vs R07020
>Thread-Index: AcnxCDdq9XK7h+d/SsW/x/9sdAkcgwAAB5VQ
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>Great,
>
>If you can drop the sequence with quality scores onto the FTP site we
>set up earlier that would be easiest.
>
>Look forward to ta king next week.
>
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Friday, June 19, 2009 11:03 AM
>To: John Bouck
>Subject: RE: SNP file for R07007 vs R07020
>
>John
>
>Yes I can share the Rio data. What would you like and how would you
>like to get it. I can give you the sequence file with the quality
>scores if that is how you want it. I don't know if it would be too
>big to send in an email or not.
>
>I did ta k with John about the sweet sorghum project and this is what
>he told me. All of the money for the sweet sorghum program that was
>added into the Ceres project goes to Bill for breeding work. Thus no
>money was allocated for marker work and therefore, he doesn't have
>plans to do any sweet sorghum genotyping. If we want to discuss this
>at a quarterly meeting with Bill, Jeff, and the rest of us, that
>would be fine, but for now that is how the project is written and the
>budget allocated.
>
>Thanks
>Trish
>
>
>
>At 07:39 PM 6/18/2009, you wrote:
> >You've done rio? Is that data you can share?
> >
> >John
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Thursday, June 18, 2009 2:30 PM
> >To: John Bouck
> >Subject: RE: SNP file for R07007 vs R07020
> >

> >John
> >
> >Haven't done any thus far except Rio. I think the plan at first was
> >to get some of the Ceres PS lines done as well as mapping population
> >parents. Sweets would likely come after these.
> >
> >Trish
> >
> >
> >At 04:24 PM 6/18/2009, you wrote:
> > >Sounds l ke a good idea let me know when you have analyzed what you
> > >want. Are you guys doing any sweets? I'm curious to see the
>variation
> > >between sweet and non-sweets.
> > >
> > >John
> > >
> > >-----Original Message-----
> > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > >Sent: Thursday, June 18, 2009 8:31 AM
> > >To: John Bouck
> > >Subject: RE: SNP file for R07007 vs R07020
> > >
> > >John
> > >
> > >As far as I can tell that should work for me. No worries about teh
> > >rescheduling. I too am busy so I totally understand. I may even
> > >have additional PS genotypes analyzed by then. We finished a run
> > >this week that contained an additional 8 PS lines (R07008, R07012,
> > >R07108, R07030, R07034, R07042, R07045 and R07045) in addition to the
> > >anthracnose mapping parents. I am trying to get that data through
> > >the analysis pipeline so I can see how these lines compare to the
> > >R07007 and R07020. Perhaps we should have the call once I have that
> > >data analyzed which should be sometime next week? Just let me know
> > >your thoughts on this.
> > >
> > >Thanks
> > >Trish
> > >
> > >At 10:17 AM 6/18/2009, you wrote:
> > > >Trish - I'm really sorry to do this again but my schedule is being
> > >taken
> > > >over by others and I have yet another last minute conflict.
> > > >
> > > >Maybe we should shoot for Monday afternoon at 3:00 your time -
>things
> > > >should quiet down next week.
> > > >
> > > >Best,
> > > >John
> > > >
> > > >-----Original Message-----
> > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > >Sent: Wednesday, June 17, 2009 8:22 AM
> > > >To: John Bouck
> > > >Subject: RE: SNP file for R07007 vs R07020
> > > >
> > > >John
> > > >
> > > >That time tomorrow should work just fine.
> > > >
> > > >Thanks
> > > >Trish
> > > >
> > > >
> > > >
> > > >At 10:10 AM 6/17/2009, you wrote:
> > > > >Trish,
> > > > >
> > > > >I have an external meeting that is now planned for the same time

>as
> > >our
> > > > >meeting later today. Can we move our discussion to tomorrow at
> >3:00
> > > > >your time?
> > > > >
> > > > >Sorry for the late notice,
> > > > >John
> > > > >
> > > > >-----Original Message-----
> > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > >Sent: Tuesday, June 09, 2009 1:53 PM
> > > > >To: John Bouck
> > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > >
> > > > >Sounds good, I will put that time on my calendar and be waiting
>for
> > > >your
> > > > >call.
> > > > >
> > > > >Trish
> > > > >
> > > > >
> > > > >At 03:47 PM 6/9/2009, you wrote:
> > > > > >Great - how about Wednesday at 4:00 your time?
> > > > > >
> > > > > >John
> > > > > >
> > > > > >-----Original Message-----
> > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > >Sent: Tuesday, June 09, 2009 1:46 PM
> > > > > >To: John Bouck
> > > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > > >
> > > > > >John
> > > > > >
> > > > > >I will be around next week as of now so whenever you want to
>talk
> > > > >just give me a heads up on day/time.
> > > > > >
> > > > > >Trish
> > > > > >
> > > > > >
> > > > > >
> > > > >At 03:44 PM 6/9/2009, you wrote:
> > > > > >Hi Trish,
> > > > > >
> > > > > >We've started getting our heads around this - would be fun to
> > > > >discuss,
> > > > > >unfortunately I'm traveling for the next several days. Are
>you
> > > >free
> > > > > >next Wednesday or Thursday?
> > > > > >
> > > > > >John
> > > > > >
> > > > > >-----Original Message-----
> > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > >Sent: Wednesday, May 20, 2009 9:27 AM
> > > > > >To: John Bouck
> > > > > >Subject: SNP file for R07007 vs R07020
> > > > > >
> > > > > >John
> > > > > >
> > > > > >I uploaded a file with the name
> > > > > >R07007_R07020_SNP.final.pairwised.unique.052009.xls. This is
> >an
> > > > > >excel file of ~5000 potential SNPs/INDELs found between
>R07007
> > >and

> > > > > > >R07020. I highlighted in yellow some potential markers that
> >are
> > > > >also
> > > > > > > >present in some of the other 11 genotypes examined and thus I
> > > >would
> > > > > > > >consider to be of high quality "real" polymorphisms. In pink
> >are
> > > > > > > >markers where the polymorphism was found only between R07007
> >and
> > > > > > > >R07020 and thus I wouldn't have as much confidence that these
> >are
> > > > > > > >"real" polymorphisms. I did this for some markers on chr. 1
> > > >only.
> > > > >I
> > > > > > > >hope this gives you enough information to design some Taqman
> > > >assays
> > > > > > > >to test. If you need additional info please let me know.
>Let
> >me
> > > > > > > >know how it all turns out.
> > > > > > > >
> > > > > > > >Thanks
> > > > > > > >Trish
> > > > > > > >
> > > > > > > >
> > > > > > > >
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>X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -0.739
>X-Spam-Level:
>X-Spam-Status: No, score=-0.739 tagged_above=-10 required=5
> tests=[BAYES_20=-0.74, HTML_MESSAGE=0.001]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>x-cr-hashedpuzzle: AV8q AjSV AzwK A04k BSSn CYoX CvL1 DeGV EVm4 FJUK
>FUnp FuIu F9Ec Hu73 J77L
>K0Ng;1;cABrAGwAZQBpAG4AQAB0AGEAbQB1AC4AZQBkAHUA;Sosha1_v1;7;{FAABB3A7-F6F0-4065-82FF-87ADD7A179B7};
agBiAG8AdQBjAGsAQABjAGUAcgBlAHMALQBpAG4AYwAuAGMAbwBtAA==;Tue,
>10 Mar 2009 17:51:06 GMT;QwBlAHIAZQBzACAAcwBwAHIAZQBhAGQAcwBoAGUAZQB0AA==
>Subject: Ceres spreadsheet
>Date: Tue, 10 Mar 2009 10:51:06 -0700
>x-cr-puzzleid: {FAABB3A7-F6F0-4065-82FF-87ADD7A179B7}
>X-MS-Has-Attach: yes
>X-MS-TNEF-Correlator:
>Thread-Topic: Ceres spreadsheet
>Thread-Index: AcmhqMmx4cUG+a8hTBGbzon55m150A==
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>Trish,
>
>It was a pleasure to discuss some interesting bioinformatics with
>you earlier today. Attached is the spreadsheet that we discussed on
>the phone. The latter tabs are easier to work with.
>
>The frequency column indicates the ratio of sequencing reads with
>each polymorphism and the reference sequence column should indicate
>the position on the sorghum chromosome where the polymorphism is found.
>
>Look forward to discussing further in the future,
>John
>
>

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X-Virus-Scanned: amavisd-new at neo-proxy-2.tamu.edu
X-Spam-Flag: NO
X-Spam-Score: -2.35
X-Spam-Level:
X-Spam-Status: No, score=-2.35 tagged_above=-10 required=5 tests=[AWL=0.248,
BAYES_00=-2.599, HTML_MESSAGE=0.001]
X-Virus-Scanned: amavisd-new at tamu.edu
X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
Subject: FW: Meeting invitation: Geospiza - John B.
Date: Tue, 24 Mar 2009 14:03:06 -0700
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: Meeting invitation: Geospiza - John B.
Thread-Index: AcmsraXakZVnaAKMQhmYuJ7j1SUkTQAFhPAA
From: "John Bouck" <jbouck@ceres-inc.com>
To: "Patricia Klein" <pklein@tamu.edu>

Contact info for the meeting tomorrow at 4:00 your time.

Thanks for joining, should be interesting and I look forward to your insight to what they've done as well.

John

From: Darrell Reising [mailto:messenger@webex.com]
Sent: Tuesday, March 24, 2009 11:08 AM
To: John Bouck
Subject: Meeting invitation: Geospiza - John B.

Hello ,

Darrell Reising invites you to attend this online meeting.

Topic: Geospiza - John B.
Date: Wednesday, March 25, 2009
Time: 2:00 pm, Pacific Daylight Time (GMT -07:00, San Francisco)
Meeting Number: 803 883 176
Meeting Password: seattle

Please click the link below to see more information, or to join the meeting.

To join the online meeting
---
1. Go to https://geospiza.webex.com/geospiza/j.php?

ED=105457587&UID=86280587&PW=7f07d3c4284809000710065c
2. Enter your name and email address.
3. Enter the meeting password: seattle
4. Click "Join Now".

To join the meeting on iPhone

Go to wbx://geospiza.webex.com/geospiza?MK=803883176&MPW=3151a8f227c0e11fd9a7fd1aa24ebfee734503dea095c22c3b2fae09d62eeb25

Don't have the iPhone WebEx application yet?
Go to http://itunes.apple.com/WebObjects/MZStore.woa/wa/viewSoftware?id=298844386

To join the teleconference only

AT Teleconference Information;

US Toll Free - 866.866.2244
International - 1.404.260.1415

Participant Code - 9548312

For assistance
---
1. Go to https://geospiza.webex.com/geospiza/mc
2. On the left navigation bar, click "Support".

You can contact me at:

1-206-6334403

To add this meeting to your calendar program (for example Microsoft Outlook), click this link:
https://geospiza.webex.com/geospiza/j.php?ED=105457587&UID=86280587&ICS=MI&LD=1&RD=2&ST=1&SHA2=tiI8GFJ2-DLEZCj0ozOLxnyFRp53gXntyXR58B03q64=

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X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
X-Spam-Flag: NO
X-Spam-Score: -2.123
X-Spam-Level:
X-Spam-Status: No, score=-2.123 tagged_above=-10 required=5 tests=[AWL=0.375,
BAYES_00=-2.599, HTML_MESSAGE=0.001, RDNS_NONE=0.1]
X-HAT: SG SUSPECTLIST_NO_SBRS, P $THROTTLED_NO_SBRS, L tamu-relay
X-SRBS: None
X-EXTLoop1: 1
X-IronPort-AV: E=Sophos;i="4.44,718,1249275600";
d="pdf'?gif'147?mpp'147,32?scan'147,32,208,217,147,32";a="46702322"
Subject: revised Genomics Gantt chart
Date: Tue, 10 Nov 2009 15:02:13 -0800
X-MS-Has-Attach: yes
X-MS-TNEF-Correlator:
Thread-Topic: revised Genomics Gantt chart
Thread-Index: AcpiWkXVdJ+lYcehS3q5RnfSDm58Iw==
From: "Timothy Swaller" <tswaller@ceres.net>
To: "Patricia Klein" <pklein@tamu.edu>,
"John Mullet" <jmullet@tamu.edu>
Cc: "Jeff Gwyn" <jgwyn@ceres-inc.com>,
"Walter Nelson" <wnelson@ceres.net>

Hi Trish and John.
I revised this chart based on the conversation I had with John at the IPMB.
I have indicated in red items we should spend a bit of time discussing at the next quarterly to ensure we are in alignment and if these items add significant value to the program given the resources available. Also the genome platform needs to have a bit of discussion on how to optimize the communication and learning between groups.

I would like to, if possible, get this Gantt chart to a level where we are actually visualizing quarter by quarter what objectives were completed and what objectives are being targeted next. I do not want this to be onerous, but the better we can track and have transparency within the program, the better we can ensure this program is being utilized optimally with both groups obtaining significant value.

Thanks
I will try to schedule a call next week to discuss.

Tim

Timothy Swaller

Director, IT and Genomics
Office: 805.376.6545
tswaller@ceres.net

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1535 Rancho Conejo Blvd. ~ Thousand Oaks, CA 91320 USA
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TAMU 2123
Texas AgriLIFE Research
Texas A&M University
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phone: 979-862-6308
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>Subject: RE: Information from last phone discussion
>Date: Tue, 11 Dec 2007 09:00:58 -0800
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Information from last phone discussion
>Thread-Index: AcgojAgdHWSS5JeBRXSYqATV93PKegO/Dovw
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>Cc: "Nickolai Alexandrov" <nicka@ceres-inc.com>,
> "Spencer Swayze" <sswayze@ceres-inc.com>
>X-Virus-Scanned: amavisd-new at tamu.edu
>
>Hi Patricia,
>
>Thanks for this summary of chromosome 3. We had previously performed
>gene predictions on the earlier releases of Sorghum and are currently
>working on the September release. The plan is to be able to compare
>notes and discuss the annotation with you when you're here next week.
>In the spreadsheet you provide the genomic start and stop as well as the
>top two blast hits. The easiest comparison for us between the sets will
>be at the protein level and this is difficult for us to extract from the
>genomic information you provided without knowing the exon structure and
>reading frame - is it possible to share the protein sequences from the
>gene predictions? This will make the comparison much easier.
>
>I'm looking forward to your visit next week - I hope we will have time
>for informal discussions and I'd enjoy showing you some of the things we
>are up to as well.
>
>Regards,
>John
>
>==========
>John Bouck, Ph.D.
>Director of Information Technology
>Ceres, Inc.
>1535 Rancho Conejo Blvd
>Thousand Oaks, CA 91320
>+1-805-376-6509
>==========
>
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Friday, November 16, 2007 12:05 PM
>To: John Bouck
>Subject: Information from last phone discussion
>
>
>
>John,
>
>Per our last Ceres/TAMU phone discussion on Nov. 12th, I am sending you
>an annotation file from sorghum chr. 3 as well as our 96-well DNA
>extraction protocol. In the excel annotation file, I have taken ~5Mbp
>from the end of sorghum chr. 3 and run this through FGENESH and then
>BLASTed the resulting protein sequences to the rice peptide database,
>the nr database and the rice pseudomolecules. I have then parsed out
>the top two hits from each database and added in some of our genetic
>marker and sorghum EST data from our genetic and physical maps. Please
>let me know if this all makes sense. This region was selected since it
>contains a gene (AltSB) that encodes a gene involved in aluminum
>tolerance in sorghum that we recently helped map base clone. The gene
>is #267 in this list. As we discussed on the phone, our lab is not

>annotating the entire sorghum genome. We have taken the JGI annotations
>for the 10 sorghum pseudomolecules (from the sbi1 download of Sept. 07)
>and done similar BLAST analyses to see what the genes might be. Then
>when we are in a trait locus of interest we go in and use other programs
>such as FGENESH and RiceGAAS and look at how these programs would
>annotate the same region. We then compare all of these to see what
>might have been missed by one program or another and to look for
>candidate genes worth pursuing.
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>Genogrinder machine. This is a pretty crude DNA extraction protocol but
>the DNA is clean enough for our microsatellite PCR reactions. We
>haven't tried any SNP assays with this DNA. The yield is pretty
>consistent if we start with similar tissue amounts. We have worked with
>leaf tissue and taken punches and have also worked with very young
>seedlings grown for a few days in moistened germination paper and taken
>sections of the hypocotyl. Both work well. Please let me know if you
>have any further questions.
>
>Thanks
>Trish
>
>
>
>
>
>
>Dr. Patricia Klein
>Associate Professor
>Institute for Plant Genomics and Biotechnology TAMU 2123 Texas
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>
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>X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.599
>X-Spam-Level:
>X-Spam-Status: No, score=-2.599 tagged_above=-10 required=5
>	tests=[BAYES_00=-2.599]
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>X-Greylist: from auto-whitelisted by SQLgrey-1.7.6
>X-Greylist: from auto-whitelisted by SQLgrey-1.7.6
>X-Greylist: from auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: CSREES-DOE Genomics Feedstock proposal
>Date: Wed, 11 Feb 2009 05:46:59 -0800
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: CSREES-DOE Genomics Feedstock proposal
>Thread-Index: AcmMTmsx7M672UpqSVmXnuw+Voo77QAADchQ
>From: "Walter Nelson" <wnelson@ceres.net>
>To: "John Mullet" <jmullet@tamu.edu>
>Cc: "Bill Rooney" <wlr@tamu.edu>,
>	"Bonnie Hames" <bhames@ceres-inc.com>,
>	"Steven Thomas" <sthomas@ceres-inc.com>,
>	"Patricia Klein" <pklein@tamu.edu>
>
>Thanks John. I found the discussion very useful and appreciated your
>keeping an eye out on additional funding opportunities to help our
>project. My apologies as well for not getting a response to you more
>quickly.
>
>Let's be sure to discuss the composition and conversion mapping project
>in the April meeting and the quarterly to see what other things we can
>do to accelerate it.
>
>Best regards,
>
>Walter
>
>
>
>-----Original Message-----
>From: John Mullet [mailto:jmullet@tamu.edu]
>Sent: Wednesday, February 11, 2009 5:40 AM
>To: Walter Nelson
>Cc: Bill Rooney; Bonnie Hames; Steven Thomas; Patricia Klein
>Subject: CSREES-DOE Genomics Feedstock proposal
>
>Hi Walter,
>
>Thank you for discussing the possibility of getting DOE to fund an
>AgriLIfe/ Ceres collaboration on QTL mapping the basis of variation in
>bioenergy sorghum composition and conversion traits. I apologize for
>not getting this discussion going sooner. Because the proposal is due
>on 2/18, I have decided that we should wait until next year to submit a
>proposal on this topic. In the meantime, we will have the opportunity
>to collect additional preliminary data and advance our populations to
>make the proposal stronger.
>
>Best regards,
>
>John

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>X-Virus-Scanned: amavisd-new at neo-proxy-3.tamu.edu
>X-Spam-Flag: NO
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>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: Ceres - analysis
>Date: Wed, 11 Mar 2009 09:52:35 -0700
>X-MS-Has-Attach: yes
>X-MS-TNEF-Correlator:
>Thread-Topic: Ceres - analysis
>Thread-Index: AcmiacbwnTu2g11VS6+Snl61/iHDTg==
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>Patricia,
>
>I have spoken with a company (Geospiza) who has
>an analysis service they provide for processing
>next generation sequencing information. They
>essentially will take the sequence and quality
>scores and set up an analysis pipeline and
>provide results back to us. Attached is a
>flier. They have offered to demonstrate a
>couple of test runs for free. Their approach
>requires a sequenced template so the Ceres
>experiments are not appropriate as there is no
>genomic sequence available for the two species we examined.
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>couple lanes from the 112008 run to them and see
>what they come up with. By the way, they want
>to sell this service (of course) and have a list
>price of 500 dollars per lane. Presumably this is negotiable…
>
>Let me know if this is might be useful or if
>there are other experiments that are of more
>interest. I'd like to compare what they can do
>with something we've looked at to see what the accuracy and benefit might be.
>
>John
>

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>Subject: RE: Information from last phone discussion
>Date: Wed, 12 Dec 2007 08:51:17 -0800
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Information from last phone discussion
>Thread-Index: Acg80EpSWOjIYJjGRyqGym9XAZbwxAADqOhg
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>X-Virus-Scanned: amavisd-new at tamu.edu
>
>Thanks for this Trish - it will be interesting to see the similarities
>in what we do. Yes, your approach makes sense to focus in on the areas
>of interest.
>
>Look forward to chatting next week.
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Wednesday, December 12, 2007 7:04 AM
>To: John Bouck
>Cc: Nickolai Alexandrov; Spencer Swayze; John Mullet
>Subject: RE: Information from last phone discussion
>
>John,
>
>Attached is the output file from FGENESH using the 5Mbp from the end of
>sbi1_chr3. I believe it contains all of the information that you are
>looking for. As I mentioned previously we are not annotating the entire
>sorghum genome sequence since DOE and others (Gramene, JGI, Paterson
>group, etc) will be doing this (and will likely have the funding to do
>so). Our approach has been to use programs like FGENESH and RiceGAAS to
>do an initial annotation on regions containing QTL that we are mapping.
>This provides us with a quick scan of the region to begin the hunt for
>potential candidate genes.
>
>I look forward to talking with you more about this next week and to get
>a look at some of the things that Ceres is working on.
>
>Take care,
>Trish
>
>
>At 11:00 AM 12/11/2007, John Bouck wrote:
> >Hi Patricia,
> >
> >Thanks for this summary of chromosome 3. We had previously performed
> >gene predictions on the earlier releases of Sorghum and are currently
> >working on the September release. The plan is to be able to compare
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> >Regards,

> >John
> >
> >=========================
> >John Bouck, Ph.D.
> >Director of Information Technology
> >Ceres, Inc.
> >1535 Rancho Conejo Blvd
> >Thousand Oaks, CA 91320
> >+1-805-376-6509
> >=========================
> >
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Friday, November 16, 2007 12:05 PM
> >To: John Bouck
> >Subject: Information from last phone discussion
> >
> >
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> >John,
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> >Thanks
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X-Virus-Scanned: amavisd-new at
X-Spam-Flag: NO
X-Spam-Score: -2.598
X-Spam-Level:
X-Spam-Status: No, score=-2.598 tagged_above=-10 required=5
tests=[BAYES_00=-2.599, HTML_MESSAGE=0.001]
X-Virus-Scanned: amavisd-new at tamu.edu
X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
Subject: Illumina Analysis
Date: Fri, 12 Dec 2008 08:20:22 -0800
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: Illumina Analysis
Thread-Index: AclcdYf00ODEypw6Qa+IPvOVLrP0lQ==
From: "Timothy Swaller" <tswaller@ceres-inc.com>
To: "Patricia Klein" <pklein@tamu.edu>

Patricia.
These are some of the analysis programs that were featured at the conference I attended sponsored by Illumina.

Maq	(Mapping and Assembly with Quality) is an algorithm, developed at the Sanger center, for assembling Next Gen reads onto a reference sequence
Velvet	algorithms for de novo short read assembly using de Bruijn graphs
Alta-cyclic	base-caller for next-gen sequencing reads (improves N50 contig length by more than 50%)
Bowtie	**an ultrafast, memory-efficient, open source short read aligner**

Tim

Timothy Swaller
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X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
X-Spam-Flag: NO
X-Spam-Score: -1.854
X-Spam-Level:
X-Spam-Status: No, score=-1.854 tagged_above=-10 required=5 tests=[AWL=-0.745,
BAYES_05=-1.11, HTML_MESSAGE=0.001]
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X-Greylist: from auto-whitelisted by SQLgrey-1.7.6
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Subject: A&M Ceres MAS/MAB/mapping strategy discussion
Date: Thu, 12 Feb 2009 05:32:20 -0800
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: A&M Ceres MAS/MAB/mapping strategy discussion
Thread-Index: AcmNFlR0QjxEDREbT22j8LsmmwFBbw==
From: "Walter Nelson" <wnelson@ceres.net>
To: "John Mullet" <jmullet@tamu.edu>,
"Patricia Klein" <pklein@tamu.edu>,
"Bill Rooney" <wlr@tamu.edu>

John, Patricia and Bill,

I have discussed with John and Bill the interest from some of our scientists here at Ceres to have a more focused/dedicated discussion about the marker and mapping work going on in the program. The idea was to be able to spend more time on the various marker and mapping activities, timing and screening of the various populations, implementation of using the markers, discuss the solexa platform etc.... and not in the typical crammed 1-2 hour summary during the quarterly.

The primary constraint I got on scheduling this was from Bill to put it after April 1. I wanted to propose to you Monday, April 6. While the Ceres people would be there all day, I don't expect you all need to be present the whole time. We can put an agenda together that can cover various topics and still work for your schedules. I think the idea was to keep it relatively informal as well (i.e. no extensive slide decks required, only for explanation to facilitate discussion etc...) John B and Jeff also specifically mentioned wanting to see the labs as well for example.

Please let me know if April 6 would work for you and, if not, let me know what day(s) would. I'd mainly just like to have it sometime before the next quarterly at the end of April.

Thanks,

Walter

Walter E Nelson
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>X-Virus-Scanned: amavisd-new at neo-proxy-3.tamu.edu
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>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Ceres - analysis
>Date: Fri, 13 Mar 2009 17:46:13 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Ceres - analysis
>Thread-Index: Acm bp+n9ENMRIWnTpuMUDao7TX+oQBzxh9w
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>Sorry for the delayed response.
>
>Good idea to have a single genotype - I also wanted to toss at them a
>lane that needed to be de-convoluted to see what they could do. Unless
>you object, I'll send them lane 1 and lane 2 - this would then be a
>complex multiplexing problem as well as a simpler assembly problem.
>
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Wednesday, March 11, 2009 10:25 AM
>To: John Bouck
>Subject: Re: Ceres - analysis
>
>John
>
>It might be interesting to have them look at
>lanes 2 and 7 from the 112008 run. These are
>only one genotype (IS3620c) digested with HpaII
>and then sequenced from that site. All of the
>useful sequences should start with TATCGG from
>these two lanes. It would be interesting to see
>how the data looks for these two lanes using
>their service. Let me know what you think.
>
>Trish
>
>
>At 11:52 AM 3/11/2009, you wrote:
> >Patricia,
> >
> >I have spoken with a company (Geospiza) who has
> >an analysis service they provide for processing
> >next generation sequencing information. They
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X-Virus-Scanned: amavisd-new at
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X-Spam-Score: -2.563
X-Spam-Level:
X-Spam-Status: No, score=-2.563 tagged_above=-10 required=5 tests=[AWL=0.035,
BAYES_00=-2.599, HTML_MESSAGE=0.001]
Subject: IBERS contact
Date: Thu, 14 Aug 2008 06:37:06 -0700
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: IBERS contact
Thread-Index: Acj+EtgMdEBHU81kScC2zJcMkCcsVw==
From: "Walter Nelson" <wnelson@ceres-inc.com>
To: <jmullet@tamu.edu>,
"Bill Rooney" <wlr@tamu.edu>,
"Patricia Klein" <pklein@tamu.edu>,
"Juerg Blumenthal" <jblumenthal@tamu.edu>
Cc: "Peter Schuerman" ,
"Bob Avant" <bavant@dsmail.tamu.edu>,
"McCutchen, Bill" <bmccutchen@tamu.edu>
X-Virus-Scanned: amavisd-new at tamu.edu

John, Bill, Patricia and Juerg,

I wanted to let you know that in the near future you will likely be contacted by Iain Donnison from IBERS (The Institute of Biological, Environmental & Rural Sciences, formerly known as IGER). IBERS is research institute located in Wales and has been doing breeding and research in forages as well as many other areas for the past 100 years or so. It is one of the "sister" institutions in the UK along with John Innes, Rothamsted etc....

As you may or may not know, IBERS is our research partner for miscanthus much like A&M for sorghum and Noble for switchgrass. We have not yet publically announced the relationship due to some considerations in the UK that are in the process of being resolved, some of which are similar to those resolved when Ceres and A&M began our project together. Although news of our interaction with IBERS has leaked out in various circles, I would ask that you nevertheless keep this knowledge as confidential.

A group from IBERS will be in the US in mid/late September visiting a few research locations and they have expressed interest in contacting and visiting you as well to discuss research and breeding in bioenergy crops writ large. We of course are happy for the interaction and felt it a good idea to formally notify you of our working with them in advance of a possible visit. I have already given Iain your names and email addresses.

We also wanted to let you know that we view this as a typical interaction between public research groups and not facilitated directly by us. Hence, if you are not available for a visit, Ceres completely understands and there will be no hard feelings whatsoever.

That also means that confidentiality agreements between A&M and Ceres do not apply to discussions you have with IBERS and should be taken into consideration when deciding what to talk about. However, because IBERS is a great research team and institution (as you know, we only do germplasm collaborations with the best research teams and

institutions in the world), we want to make sure both groups get the most out of the interaction. Since I currently oversee both collaborations, I can say that there are some interesting synergies between your work and theirs. Should you figure out a time and schedule a visit, we should discuss a bit in advance to figure out a way to facilitate the best interaction possible. I have said essentially the same thing to them.

Please let me know if you have any questions.

Best regards,

Walter

Walter E Nelson
Ceres, Inc.
1535 Rancho Conejo Blvd.
Thousand Oaks, CA 91320
voice: (805)376-6548
www.ceres.net

Dr. Patricia Klein
Associate Professor
Institute for Plant Genomics and Biotechnology
TAMU 2123
Texas AgriLIFE Research
Texas A&M University
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phone: 979-862-6308
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X-Virus-Scanned: amavisd-new at
X-Spam-Flag: NO
X-Spam-Score: -2.551
X-Spam-Level:
X-Spam-Status: No, score=-2.551 tagged_above=-10 required=5 tests=[AWL=0.047,
BAYES_00=-2.599, HTML_MESSAGE=0.001]
Subject: FW: Quarterly Meeting
Date: Mon, 14 Jul 2008 06:31:28 -0700
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: Quarterly Meeting
Thread-Index: AcjP93L4RmZqvYXdRKuuPgqHS3H4CAANedkgAA2kTuAFVFIxsA==
From: "Walter Nelson" <wnelson@ceres-inc.com>
To: "Simpson, Shay" <shay-simpson@tamu.edu>
Cc: "Bill Rooney" <wlr@tamu.edu>,
"John Mullet" <jmullet@tamu.edu>,
"Patricia Klein" <pklein@tamu.edu>
X-Virus-Scanned: amavisd-new at tamu.edu

Hi Shay,

I hope this note finds you well.

I was wondering if you'd had the chance to discuss some of these proposed dates for the next quarterlies by everyone there at . I wanted to be sure to schedule them in advance so that everyone has time set aside and we don't have any surprises.

If we follow the proposed list below, a phone call discussion is about 3 weeks away. My week for August the 4th is open as of now. As I mentioned, I think participation by phone for most will be fine, though I was thinking I may be in CS regardless that week so can adjust to be present from Ceres. At this point I would say to just pick a day that works for you and I will work with Edgar to schedule around it.

Thanks,

Walter

From: Walter Nelson
Sent: Tuesday, June 17, 2008 3:36 AM
To: 'shay-simpson@tamu.edu'
Cc: Spencer Swayze; Bob Avant
Subject: RE: Quarterly Meeting

Hi Shay,

Good to hear from you. Thanks for the note. We should indeed schedule some quarterly meetings.

>X-Virus-Scanned: amavisd-new at
>X-Spam-Flag: NO
>X-Spam-Score: -2.555
>X-Spam-Level:
>X-Spam-Status: No, score=-2.555 tagged_above=-10 required=5 tests=[AWL=0.044,
>	BAYES_00=-2.599]
>Subject: RE: Visit next week
>Date: Wed, 14 May 2008 11:39:12 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Visit next week
>Thread-Index: Aci1xz1LlGCo/l0vQY2RW3L2dw8XjgAKl+og
>From: "Walter Nelson" <wnelson@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>,
>	"John Mullet" <jmullet@tamu.edu>
>X-Virus-Scanned: amavisd-new at tamu.edu
>
>Patricia and John,
>
>Friday will work fine for me. I am presently flexible on the time.
>Just let me know what works best for you and I will set it aside on my
>calendar.
>
>Thanks!
>
>Walter
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Wednesday, May 14, 2008 6:33 AM
>To: John Mullet; Walter Nelson
>Subject: Re: Visit next week
>
>Walter and John,
>
>Friday would work better for me. I am on a search committee for Soils
>and Crop Sciences and we will be interviewing our 2nd candidate on
>Wednesday and Thursday of next week. If we could set up a schedule for
>Friday that should not present any conflicts at this time.
>
>Thanks
>Trish
>
>
>At 07:35 AM 5/14/2008, John Mullet wrote:
> >Hi Walter,
> >
> >Excellent, lets set up a time to meet. I will also coordinate your
> >visit with Patricia Klein so you can get a sense of our sorghum genome
> >map and bioinformatics platform.
> >
> >I have a potential conflict on Thursday afternoon, so lets try either
> >for Wednesday, possibly late morning (11am - 1pm)) or early afternoon
> >(1pm-3pm) or Friday late am or early afternoon depending on Trish's
> >schedule.
> >
> >I suggest we review the following Ceres funded activities related to
> >this topic:
> >
> >1. Illumina-based genotyping platform development (JM).
> >2. Informatics related to Illumina data (PK).
> >3. Map-based cloning activity related to Ma5/Ma6 (JM).
> >4. MAS activity related to Ma5/Ma6 (PK).
> >5. Sorghum genome sequence/map platforms (PK).

> >
> >Thanks,
> >
> >John
> >
> >Trish - let me know if you are available either Wednesday or Friday
> >(May 23).
> >
> >
> >
> >On May 13, 2008, at 5:35 PM, Walter Nelson wrote:
> >
> >>Hi John,
> >>
> >>Hope this note finds you well.
> >>
> >>I am going to be in College Station May 21st through May 24th (Weds
> >>thru Sat). I'm not sure if you are going to be available, but one of
> >>the things I have been meaning to do is to spend some time with you
> >>and/or Patricia to continue some of the discussions below as well as
> >>to get a better feel for the mapping and marker side of the program
> >>activities.
> >>Also, I've actually never been to your labs despite being in CS a few
> >>times now.
> >>
> >>The reason this comes to mind is that I feel that integrating the MAB
> >>and genomics portions of our research with our breeding activities is
> >>one of the bigger challenges we face but also presents one of the
> >>bigger opportunities. While I understand all of these things in
> >>principle, I feel that I need to get my mind wrapped around them even
> >>more in order to make more of a difference with their implementation.
> >>
> >>Let me know if you will be around and have time. I absolutely
> >>understand if you are busy. I will only be unavailable on Wednesday
> >>night and Thursday morning as I let Spencer talk me into speaking at
> >>his panel at a conference in Houston.
> >>
> >>Best regards,
> >>
> >>Walter
> >>
> >>-----Original Message-----
> >>From: John Mullet [mailto:jmullet@tamu.edu]
> >>Sent: Tuesday, April 22, 2008 2:04 PM
> >>To: Walter Nelson
> >>Subject: Re: Mapping populations question
> >>
> >>Walter,
> >>
> >>All the time, but often with several populations. That is why I asked
>
> >>whether you were mapping markers or traits. For traits/QTL mapping,
> >>one needs to make a population that segregates for that trait. This
> >>is what Ceres is funding TAMU to do for example with genes that
> >>control flowering time and biomass traits (both population
> >>construction and QTL mapping).
> >>
> >>Lets follow up tomorrow,
> >>
> >>John
> >>
> >>
> >>On Apr 22, 2008, at 2:56 PM, Walter Nelson wrote:
> >>
> >>>Thanks John, I think that answers my question, but I may need to
> >>>understand it a bit better....
> >>>
> >>>So all the screening done when looking for a trait to map (e.g.
> >>>drought or flowering time) to correlate to a location is done with
> >>>one

> >>
> >>>population? Do you ever do things like, for example, take a high
> >>>lignin line and a low lignin line, cross and make a population to
> >>>screen and try to track that exact QTL or locus associated with
> >>>lignin? Maybe not a good example as those pathways are well known,
> >>>but
> >>
> >>>you get the idea.
> >>>
> >>>If it's a long answer, feel free to hold till tomorrow and we can
> >>>chat
> >>
> >>>during one of the breaks.
> >>>
> >>>Thanks!
> >>>
> >>>Walter
> >>>
> >>>
> >>>Walter E Nelson
> >>>Product Manager
> >>>Ceres, Inc.
> >>>office (805) 376-6548
> >>>mobile (805) 410-0503
> >>>
> >>>sent via Treo
> >>>
> >>>-----Original Message-----
> >>>From: John Mullet <jmullet@tamu.edu>
> >>>Sent: Tuesday, April 22, 2008 9:15 AM
> >>>To: Walter Nelson <wnelson@ceres-inc.com>
> >>>Cc: Patricia Klein <pklein@tamu.edu>
> >>>Subject: Re: Mapping populations question
> >>>
> >>>Walter,
> >>>
> >>>Do you mean a population for mapping the genetic map position of DNA
> >>>markers? If so, we routinely use our BTx623/IS3620C population of
> >>>~132 RILs and this could also be used by Ceres.
> >>>
> >>>Thanks,
> >>>
> >>>John
> >>>On Apr 22, 2008, at 11:02 AM, Walter Nelson wrote:
> >>>
> >>>>John,
> >>>>
> >>>>One thing that came up yesterday that I wanted to mention for the
> >>>>meeting was an inquiry on my end about mapping populations being
> >>>>used
> >>
> >>>>or that are available for marker identification in sorghum.
> >>>>
> >>>>If possible, could we discuss this a bit tomorrow either as part of
> >>>>the meeting or at dinner?
> >>>>
> >>>>Thanks!
> >>>>
> >>>>Walter
> >>>>
> >>>>
> >>>>
> >>>>
> >>>>Walter E Nelson
> >>>>Ceres, Inc.
> >>>>1535 Rancho Conejo Blvd.
> >>>>Thousand Oaks, CA 91320
> >>>>voice: (805)376-6548
> >>>>www.ceres.net
> >>>

> >>
> >
>
>
>
>
>
>
>Dr. Patricia Klein
>Associate Professor
>Institute for Plant Genomics and Biotechnology TAMU 2123 Texas AgriLIFE
>Research Texas A&M University College Station, TX 77843-2123
>
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I was thinking we should actually schedule the next 4 of them so that we can get them on everyone's calendars and give them plenty of warning as this is something I have not done well so far.

My thinking was the following:

- A brief quarterly update during the week of August 4th, perhaps mostly by phone, to make up for full July schedules
- A larger, "full" quarterly in mid to late September, where Ceres will come to College Station (I chose this as Bill asked that we schedule major things after August 15th and a September visit should allow us to see the nurseries right before harvest. We should check with Bill on the harvest timing).
- TAMU comes to Ceres in mid to late December (on or about the week of Dec 15th, presumably after students get out)
- Ceres visits TAMU in March
- At that point, we just schedule them every three months a year in advance...June, September, December, March etc...

What do you think?

Best regards,

Walter

Walter E Nelson
Ceres, Inc.
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Thousand Oaks, CA 91320
voice: (805)376-6548
www.ceres.net

From: Spencer Swayze
Sent: Monday, June 16, 2008 8:53 PM
To: Walter Nelson
Subject: FW: Quarterly Meeting

Walter,

I believe this one is for you. Have a great week.

Best regards,

Spencer P. Swayze

Manager of Business Development

Ceres, Inc. "*The Energy Crop Company*™"

sswayze@ceres-inc.com

Office: (805) 376-6508

Mobile: (805) 407-8799

www.ceres.net

-----Original Message-----
From: Simpson, Shay [mailto:shay-simpson@tamu.edu]
Sent: Monday, June 16, 2008 2:25 PM
To: Spencer Swayze
Cc: Avant, Bob
Subject: Quarterly Meeting

Spencer:

We talked briefly about the need to plan the next quarterly meeting a few weeks ago when you were in town with the BOD meeting. I'd like to get the ball rolling on setting the agenda and meeting topics for our next meeting. Looking at July schedules, I am seeing a full month and wondering if we can look at the week of August 4. What is your preference for location, dates, etc?

Thanks,

Shay

Shay L. Simpson

Project Manager, Bioenergy Program

Texas AgriLife Research

979-845-6315 Tel

shay-simpson@tamu.edu

Dr. Patricia Klein
Associate Professor
Institute for Plant Genomics and Biotechnology
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fax: 979-862-4790

X-Virus-Scanned: amavisd-new at neo-proxy-3.tamu.edu
X-Spam-Flag: NO
X-Spam-Score: -0.921
X-Spam-Level:
X-Spam-Status: No, score=-0.921 tagged_above=-10 required=5 tests=[AWL=-0.912,
BAYES_05=-1.11, EXTRA_MPART_TYPE=1, HTML_MESSAGE=0.001,
RDNS_NONE=0.1]
X-HAT: SG SUSPECTLIST_NO_SBRS, P $THROTTLED_NO_SBRS, L tamu-relay
X-SRBS: None
X-EXTLoop1: 1
X-IronPort-Anti-Spam-Filtered: true
X-IronPort-Anti-Spam-Result: AugEAIHi1kpB2vnI/2dsb2JhbACCKyrITAmPLwKCTIFiBIpu
X-IronPort-AV: E=Sophos;i="4.44,566,1249275600";
d="gif'147?scan'147,208,217,147";a="38403970"
Subject: Gantt Chart
Date: Thu, 15 Oct 2009 08:55:29 -0700
X-MS-Has-Attach: yes
X-MS-TNEF-Correlator:
Thread-Topic: Gantt Chart
Thread-Index: AcpNr+tH2UIJ6aerQ2ahud57pY3K2Q==
From: "Timothy Swaller" <tswaller@ceres.net>
To: "John Mullet" <jmullet@tamu.edu>,
"Patricia Klein" <pklein@tamu.edu>

Hi John and Patricia.
Hope all is well, I here there has been a significant amount of rain lately.

Have you had a chance to look over the Gantt chart I sent out and do you have any questions/comments on it?

Stay dry
Tim

Timothy Swaller
Director, IT and Genomics
Office: 805.376.6545
tswaller@ceres.net

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Texas A&M University
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phone: 979-862-6308
fax: 979-862-4790

X-Virus-Scanned: amavisd-new at neo-proxy-2.tamu.edu
X-Spam-Flag: NO
X-Spam-Score: -1.664
X-Spam-Level:
X-Spam-Status: No, score=-1.664 tagged_above=-10 required=5 tests=[AWL=-0.166,
BAYES_00=-2.599, EXTRA_MPART_TYPE=1, HTML_MESSAGE=0.001,
RDNS_NONE=0.1]
X-HAT: SG SUSPECTLIST_NO_SBRS, P $THROTTLED_NO_SBRS, L tamu-relay
X-SRBS: None
X-EXTLoop1: 65.218.249.200
X-IronPort-Anti-Spam-Filtered: true
X-IronPort-Anti-Spam-Result: Av8EABwJAUtB2vnI/2dsb2JhbACCJirGRgmNOQKCUIFqBIw4
X-IronPort-AV: E=Sophos;i="4.44,751,1249275600";
d="gif'147?scan'147,208,217,147";a="48391805"
Subject: Gantt chart
Date: Mon, 16 Nov 2009 08:15:23 -0800
X-MS-Has-Attach: yes
X-MS-TNEF-Correlator:
Thread-Topic: Gantt chart
Thread-Index: Acpm1/++BewicbWkRGunWR0/2wy8SQ==
From: "Timothy Swaller" <tswaller@ceres.net>
To: "Patricia Klein" <pklein@tamu.edu>,
"John Mullet" <jmullet@tamu.edu>

Hi Trish and John

Do you both have any free time later this week to discuss the current version of the Gantt chart?

I was thinking either
Thursday (11/19) morning 9am PST
Thursday (11/19) afternoon 1pm PST
Friday (11/20) morning 9am PST

Do any of these work or fit better with your schedules?
Feel free to suggest alternate as well.

Thanks
Tim

Timothy Swaller
Director, IT and Genomics
Office: 805.376.6545
tswaller@ceres.net

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X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
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X-Spam-Score: -1.499
X-Spam-Level:
X-Spam-Status: No, score=-1.499 tagged_above=-10 required=5
tests=[BAYES_00=-2.599, EXTRA_MPART_TYPE=1, HTML_MESSAGE=0.001,
RDNS_NONE=0.1, SPF_PASS=-0.001]
Authentication-Results: os-mail-1.tamu.edu; dkim=neutral (message not signed) header.i=none
X-IronPort-Anti-Spam-Filtered: true
X-IronPort-Anti-Spam-Result: AqIEANdIiUpB2vnI/2dsb2JhbACCKivEVgmOcQKCSoFNBYog
X-IronPort-AV: E=Sophos;i="4.43,398,1246856400";
d="gif'147?scan'147,208,217,147";a="1336139"
Subject: Sorghum Illumina Data
Date: Mon, 17 Aug 2009 12:14:16 -0700
X-MS-Has-Attach: yes
X-MS-TNEF-Correlator:
Thread-Topic: Sorghum Illumina Data
thread-index: AcofbulVNV5Sk4zqRIOLDw+tyMi9Jw==
From: "Timothy Swaller" <tswaller@ceres.net>
To: "Patricia Klein" <pklein@tamu.edu>
Cc: <jmullet@tamu.edu>

Hi Patricia.
I have taken over the management and analysis of the integration of the IT and Genomics information including the Illumina data coming from TAMU and was wondering if you could send me an update on all runs (files) that have been transferred to us to-date. If you could also indicate for these genotypes how they are related (if they are) and any phenotypic descriptors would be very helpful.

Also, has there been agreement on the other genotypes that will be processed and what timeframe we will be receiving these.
I assume all data is being transferred over the VPN (http://files155.cyberlynk.net/client/).

Thanks for the help.
Tim

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X-Virus-Scanned: amavisd-new at
X-Spam-Flag: NO
X-Spam-Score: -2.598
X-Spam-Level:
X-Spam-Status: No, score=-2.598 tagged_above=-10 required=5 tests=[AWL=-0.000,
BAYES_00=-2.599, HTML_MESSAGE=0.001]
Subject: Next-generation base caller
Date: Mon, 18 Aug 2008 10:30:21 -0700
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: Next-generation base caller
Thread-Index: AckBWBcP6XFoarYERsWmuwHhPg1wfA==
From: "Timothy Swaller" <tswaller@ceres-inc.com>
To: <jmullet@tamu.edu>,
"Patricia Klein" <pklein@tamu.edu>
X-Virus-Scanned: amavisd-new at tamu.edu

Hi Patricia / John

Just wanted to share an article I just read about a next-generation base-caller that seems to be a good improvement from the Illumina base-caller.
Of course, additional testing would be necessary to determine this reliably.

The article is in
Yaniv Erlich, et al. Alta-Cyclic: a self-optimizing base caller for next-generation sequencing. **Nature Methods**. Vol. 5 No. 8. Aug. 2008. p. 679.

This program may help on read length and # of useable reads.

Tim

_____
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phone: 979-862-6308
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X-Virus-Scanned: amavisd-new at
X-Spam-Flag: NO
X-Spam-Score: -2.598
X-Spam-Level:
X-Spam-Status: No, score=-2.598 tagged_above=-10 required=5 tests=[AWL=-0.000,
BAYES_00=-2.599, HTML_MESSAGE=0.001]
Subject: Next-generation base caller
Date: Mon, 18 Aug 2008 10:30:21 -0700
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: Next-generation base caller
Thread-Index: AckBWBcP6XFoarYERsWmuwHhPg1wfA==
From: "Timothy Swaller" <tswaller@ceres-inc.com>
To: <jmullet@tamu.edu>,
"Patricia Klein" <pklein@tamu.edu>
X-Virus-Scanned: amavisd-new at tamu.edu

Hi Patricia / John

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Yaniv Erlich, et al. Alta-Cyclic: a self-optimizing base caller for next-generation sequencing. **Nature Methods**. Vol. 5 No. 8. Aug. 2008. p. 679.

This program may help on read length and # of useable reads.

Tim

_____
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fax: 979-862-4790

X-Virus-Scanned: amavisd-new at neo-proxy-3.tamu.edu
X-Spam-Flag: NO
X-Spam-Score: -1.499
X-Spam-Level:
X-Spam-Status: No, score=-1.499 tagged_above=-10 required=5
tests=[BAYES_00=-2.599, EXTRA_MPART_TYPE=1, HTML_MESSAGE=0.001,
RDNS_NONE=0.1, SPF_PASS=-0.001]
Authentication-Results: os-mail-1.tamu.edu; dkim=neutral (message not signed) header.i=none
X-IronPort-Anti-Spam-Filtered: true
X-IronPort-Anti-Spam-Result:
AuQEAFCTikpB2vnI/2dsb2JhbACCJi+VNrEpCZAFAoIwARmBTQWBTohc
X-IronPort-AV: E=Sophos;i="4.43,403,1246856400";
d="jpg'145?scan'145,208,217,145";a="2845077"
Subject: RE: Sorghum Illumina Data
Date: Tue, 18 Aug 2009 11:46:30 -0700
X-MS-Has-Attach: yes
X-MS-TNEF-Correlator:
Thread-Topic: Sorghum Illumina Data
thread-index: AcogJOGR2+rbFnWbTcupmLtODHHRrQAD0DPw
From: "Timothy Swaller" <tswaller@ceres.net>
To: "Patricia Klein" <pklein@tamu.edu>

Thanks Trish.
What you explain below would be greatly appreciated.

Tim

From: Patricia Klein [mailto:pklein@tamu.edu]
Sent: Tuesday, August 18, 2009 9:57 AM
To: Timothy Swaller
Subject: RE: Sorghum Illumina Data

Tim

I will reupload the sequence files for the following:

R07007
R07008
R07012
R07018
R07020
R07030
R07034
R07042

R07045
R07054
Rio
BTx623 (multiple samples based on DGA restriction enzyme depth)
IS3620c (multiple samples based on DGA restriction enzyme depth)
SC748-5
P850029

Of course the first 10 are materials that have been designated as Ceres lines from the 2007 screening performed by Bill. The 10 lines chosen thus far were for picked either because they are being advanced in Bill's breeding program or because they represented a diverse group (based on the SSR dendrogram) from the 07 materials. John can likely give you a few more details of these next week.

Rio was chosen since it is a sweet sorghum and has been used in Bill's breeding program as well.

BTx623 and IS3620c are the parents of our high density genetic mapping population and they are the materials that all testing has been performed on for the DGA genotyping method.

SC748-5 and P850029 are parents to the anthracnose population.

When I upload the sequence files, I will also need to upload a text document that explains some information about the files. For example, we have used 3 different restriction enzymes for digital genotyping analysis (DGA) depending on the depth of coverage we are looking at. You will need to know what enzyme was used for each sample. In addition, most of the sequences start with a 3 or 4 base pair ID tag to identity the line and this will need to be parsed out before analyzing the sequences. You will need to know what the ID tag is on each of the lines so that you can parse it out. Once I get this information written up, I will begin the upload. It will likely take some time since there are numerous files and they are big but I will send you another email once the process is started.

Does this all make sense?

Trish

At 10:20 AM 8/18/2009, you wrote:

Thanks Trish for the quick response on this.

If it is not too much trouble, could you send or re-send all data over the VPN. We are having a bit of trouble locating and understanding some of the current data files here and this seems like an ideal time for us to rebuild and/or reprocess all of this data. We have been working on this NGS analysis pipeline.

As mentioned previously with each experiment (run) could you indicate the genotype and possibly why it was selected. Also, if it has any relation with other genotypes that have been run. Phenotypic information is always nice as well.

Thanks again for your help and I will see you next week at the quarterly.

Tim

From: Patricia Klein [mailto:pklein@tamu.edu]
Sent: Monday, August 17, 2009 12:48 PM
To: Timothy Swaller
Subject: Re: Sorghum Illumina Data

Tim

Some of the data that was last transferred was incorrectly identified to John Bouck (some lanes were switched in the Illumina run and I wasn't aware of this until after I had uploaded the data). I contacted John as we were supposed to have a phone conversation and I was going to discuss this with him, but I never heard from him. I later learned he had left the company. Thus it might be best to not work with the last set of data uploaded and let me resend the data. I believe that data was for 8 R07 lines. I was uploading to the site you indicate below but upon checking now the Tamu directory is empty. At this point, I am not quite sure what to do since I can't see what was uploaded anymore and thus I don't know exactly what your group is working with. I didn't upload on a regular basis, it was just something that John and I were beginning to explore. If you could advise me on how you want to proceed I would be happy to resend you the data and properly identify it. Currently, we have run several different lines through our digital genotyping pipeline including several of the R07 lines (10 lines), parents of mapping populations (includes the parents of our high density map, parents of anthracnose population, parents of one of our flowering time populations), Rio (sweet sorghum), and a few others. I believe I had sent him data on R07007 and R07020 and this data was properly identified. I also sent data on Rio which should be fine as well. The last data was for the other 8 R07 lines done to date. These were R07008, R07012, R07018, R07030, R07034, RR07042, R07045 and R07054. These were the lines that were misidentified but we now have the proper identification so I could resend that data. I am pretty sure that is all of the data that I uploaded at this point in time. Once I hear back from you I can send the data. As far as additional genotypes that will be processed, that is something that we typically discussed with John at our quarterly meetings. John Mullet's lab is doing the actual sample prep work and then my lab does the analysis after the run. Thus John Mullet is the one who has been identifying the genotypes that go on a particular run. John and John had been discussing this, but I am not sure that any agreement had ever been reached. You may want to contact John Mullet about this or we could discuss it further at the quarterly meeting next week. I know that John Bouck had expressed an interest in specifying some particular genotypes that would be of interest to Ceres but again I am not sure if he ever sent John that list. Much of what John Mullet has put into the pipeline thus far has been related to Bill's bioenergy breeding program which of course feeds into the Ceres program. Looking forward to hearing from you on how best to proceed.

Thanks
Trish

At 02:14 PM 8/17/2009, you wrote:

Hi Patricia.
I have taken over the management and analysis of the integration of the IT and Genomics information including the Illumina data coming from TAMU and was wondering if you could send me an update on all runs (files) that have been transferred to us to-date. If you could also indicate for these genotypes how they are related (if they are) and any phenotypic descriptors would be very helpful.

Also, has there been agreement on the other genotypes that will be processed and what timeframe we will be receiving these.

I assume all data is being transferred over the VPN (http://files155.cyberlynk.net/client/).

Thanks for the help.
Tim

Timothy Swaller
Director, IT and Genomics
Office: 805.376.6545
tswaller@ceres.net

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1535 Rancho Conejo Blvd. ~ Thousand Oaks, CA 91320 USA
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X-Virus-Scanned: amavisd-new at neo-proxy-3.tamu.edu
X-Spam-Flag: NO
X-Spam-Score: -1.499
X-Spam-Level:
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tests=[BAYES_00=-2.599, EXTRA_MPART_TYPE=1, HTML_MESSAGE=0.001,
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Authentication-Results: os-mail-2.tamu.edu; dkim=neutral (message not signed) header.i=none
X-IronPort-Anti-Spam-Filtered: true
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X-IronPort-AV: E=Sophos;i="4.43,402,1246856400";
d="jpg'145?scan'145,208,217,145";a="2589082"
Subject: RE: Sorghum Illumina Data
Date: Tue, 18 Aug 2009 08:20:18 -0700
X-MS-Has-Attach: yes
X-MS-TNEF-Correlator:
Thread-Topic: Sorghum Illumina Data
thread-index: AcofdARM2Swhpl9eTKOj92iJ2WjwgAAom48w
From: "Timothy Swaller" <tswaller@ceres.net>
To: "Patricia Klein" <pklein@tamu.edu>
Cc: "Walter Nelson" <wnelson@ceres.net>

Thanks Trish for the quick response on this.

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>X-Virus-Scanned: amavisd-new at neo-proxy-3.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.327
>X-Spam-Level:
>X-Spam-Status: No, score=-2.327 tagged_above=-10 required=5 tests=[AWL=0.272,
>	BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: SNP file for R07007 vs R07020
>Date: Thu, 18 Jun 2009 17:39:12 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: SNP file for R07007 vs R07020
>Thread-Index: AcnwW+YPAoyL6HP7SS6iyHMUjOmP7wAD5wYA
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>You've done rio? Is that data you can share?
>
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Thursday, June 18, 2009 2:30 PM
>To: John Bouck
>Subject: RE: SNP file for R07007 vs R07020
>
>John
>
>Haven't done any thus far except Rio. I think the plan at first was
>to get some of the Ceres PS lines done as well as mapping population
>parents. Sweets would likely come after these.
>
>Trish
>
>
>At 04:24 PM 6/18/2009, you wrote:
> >Sounds l ke a good idea let me know when you have analyzed what you
> >want. Are you guys doing any sweets? I'm curious to see the variation
> >between sweet and non-sweets.
> >
> >John
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Thursday, June 18, 2009 8:31 AM
> >To: John Bouck
> >Subject: RE: SNP file for R07007 vs R07020
> >
> >John
> >
> >As far as I can tell that should work for me. No worries about teh
> >rescheduling. I too am busy so I totally understand. I may even
> >have additional PS genotypes analyzed by then. We finished a run
> >this week that contained an additional 8 PS lines (R07008, R07012,
> >R07108, R07030, R07034, R07042, R07045 and R07045) in addition to the
> >anthracnose mapping parents. I am trying to get that data through
> >the analysis pipeline so I can see how these lines compare to the
> >R07007 and R07020. Perhaps we should have the call once I have that
> >data analyzed which should be sometime next week? Just let me know
> >your thoughts on this.
> >
> >Thanks
> >Trish

> >
> >At 10:17 AM 6/18/2009, you wrote:
> > >Trish - I'm really sorry to do this again but my schedule is being
> >taken
> > >over by others and I have yet another last minute conflict.
> > >
> > >Maybe we should shoot for Monday afternoon at 3:00 your time - things
> > >should quiet down next week.
> > >
> > >Best,
> > >John
> > >
> > >-----Original Message-----
> > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > >Sent: Wednesday, June 17, 2009 8:22 AM
> > >To: John Bouck
> > >Subject: RE: SNP file for R07007 vs R07020
> > >
> > >John
> > >
> > >That time tomorrow should work just fine.
> > >
> > >Thanks
> > >Trish
> > >
> > >
> > >
> > >At 10:10 AM 6/17/2009, you wrote:
> > > >Trish,
> > > >
> > > >I have an external meeting that is now planned for the same time as
> >our
> > > >meeting later today. Can we move our discussion to tomorrow at
>3:00
> > > >your time?
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> > > >Sorry for the late notice,
> > > >John
> > > >
> > > >-----Original Message-----
> > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > >Sent: Tuesday, June 09, 2009 1:53 PM
> > > >To: John Bouck
> > > >Subject: RE: SNP file for R07007 vs R07020
> > > >
> > > >Sounds good, I will put that time on my calendar and be waiting for
> > >your
> > > >call.
> > > >
> > > >Trish
> > > >
> > > >
> > > >At 03:47 PM 6/9/2009, you wrote:
> > > > >Great - how about Wednesday at 4:00 your time?
> > > > >
> > > > >John
> > > > >
> > > > >-----Original Message-----
> > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > >Sent: Tuesday, June 09, 2009 1:46 PM
> > > > >To: John Bouck
> > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > >
> > > > >John
> > > > >
> > > > >I will be around next week as of now so whenever you want to ta k
> > > > >just give me a heads up on day/time.
> > > > >
> > > > >Trish
> > > > >

> > > > >
> > > > >
> > > > >At 03:44 PM 6/9/2009, you wrote:
> > > > > >Hi Trish,
> > > > > >
> > > > > >We've started getting our heads around this - would be fun to
> > > >discuss,
> > > > > >unfortunately I'm traveling for the next several days. Are you
> > >free
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> > > > > >John
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> > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > >Sent: Wednesday, May 20, 2009 9:27 AM
> > > > > >To: John Bouck
> > > > > >Subject: SNP file for R07007 vs R07020
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> > > > > >John
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> > > > > >I uploaded a file with the name
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>X-Virus-Scanned: amavisd-new at neo-proxy-2.tamu.edu
>X-Spam-Flag: NO
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>Subject: RE: SNP file for R07007 vs R07020
>Date: Thu, 18 Jun 2009 08:17:43 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: SNP file for R07007 vs R07020
>Thread-Index: AcnvX2d4CfDb68JyQm2u+EgB77BQ7gAyB3qQ
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
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>X-Spam-Score: -2.387
>X-Spam-Level:
>X-Spam-Status: No, score=-2.387 tagged_above=-10 required=5 tests=[AWL=0.212,
>	BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: SNP file for R07007 vs R07020
>Date: Fri, 19 Jun 2009 11:27:36 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: SNP file for R07007 vs R07020
>Thread-Index: AcnxCvAcXDqAoqAITk2j2sklwPG7KwAAHTjA
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>I think this was it:
>
>http://files155.cyberlynk.net/client
>
>your login was Tamu
>
>I'll send your password in a separate email.
>
>John
>
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>X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.483
>X-Spam-Level:
>X-Spam-Status: No, score=-2.483 tagged_above=-10 required=5 tests=[AWL=0.116,
>	BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: SNP file for R07007 vs R07020
>Date: Fri, 19 Jun 2009 11:28:33 -0700
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>X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.413
>X-Spam-Level:
>X-Spam-Status: No, score=-2.413 tagged_above=-10 required=5 tests=[AWL=0.186,
>	BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Ceres chat
>Date: Tue, 19 May 2009 14:05:20 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>thread-topic: Ceres chat
>thread-index: AcnYxDwLs4vLsIrLTwqAVFcITov43wAAIJfw
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>In thinking about this I wonder how much difference there is in the
>metrics we use for identifying good SNPs for TaqMan assays and the
>process you have set up for identifying SNPs for genotyping purposes.
>
>Probably the best thing is to do a comparison - can you send seq and
>qual files for R07007 and R07020 as well as SNPs you call between these?
>We'll run through the detection process and then see what overlap there
>is between what we think will convert into a good taqman and what you've
>called. I expect we will be more stringent but it will be good to
>understand this.
>
>It will be interesting to compare notes on this.
>
>Does this seem reasonable?
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Tuesday, May 19, 2009 1:52 PM
>To: John Bouck
>Subject: RE: Ceres chat
>
>John,
>
>John Mullet is the one making up the list of genotypes for analysis
>so he might have shared that with Walter, but I am not sure. Yes we
>did include R07007 and R07020 in our March run. So far these are the
>only two bioenergy lines. We also had Rio (sweet sorghum) in a
>recent run. More bioenergy lines including R07008, R07012, R07018,
>R07030, R07034, R07042, R07045 and R07054 are planned for the next
>GAII run assuming that all produce high quality NgoMIV/bioruptor
>template. I would be happy to share that data with you. Can you tell
>me in what format you would like it? I could send you a list of
>locations where we found potential SNPs/INDELs in these two bioenergy
>lines compared with the rest of the 11 genotypes thus far
>examined. Additionally, I could do a quick comparison of just R07007
>vs R07020 to see where they differ as well. Let me know and I can
>try to get you the data you need to enable you to convert some of the
>potential markers into TaqMan assays.
>
>Trish
>
>
>
>At 03:47 PM 5/19/2009, you wrote:
> >Trish,
> >

> >Great, sounds like good progress. It will be interesting to see how
>much
> >multiplexing can be done, even 4 is a big help.
> >
> >I haven't done much with trimming the reads but rather relied upon
>super
> >deep alignments and quality scores to give high quality data. We've
> >converted some 454 data into TaqMan assays with good success but
>haven't
> >had same success with Illumina in a different grass.
> >
> >At one point there was going to be a list of the genotypes shared that
> >you were planning to examine - is this still available, or maybe Walter
> >already has it?
> >
> >Do I recall correctly that you looked at R07007 previously? I'd love
>to
> >test converting SNPs from this approach into TaqMan assays to determine
> >the success of this. It would be fun to compare notes again on the
>same
> >data sets - are you happy to share some data?
> >
> >Regards,
> >John
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Tuesday, May 19, 2009 1:16 PM
> >To: John Bouck
> >Subject: Re: Ceres chat
> >
> >John
> >
> >Analysis of Illumina data is progressing. I am finishing up a set of
> >13 genotypes (a couple bioenergy lines, a sweet sorghum, some drought
> >tolerant lines, Bill's breeding materials, mapping population
> >parents). The next run on the Illumina is scheduled for early June
> >and will contain an additional 17 lines many of which will be
> >bioenergy types from the 2007 work as well as the parents of the
> >anthracnose mapping populations.
> >
> >I have been working out some simulations to determine the right
> >number of genotypes to include per lane when using NgoMIV/bioruptor
> >vs FseI/bioruptor template preparation. The simulations looked good
> >and I believe we can analyze 4 (or possibly 6) genotypes/lane when
> >working with NgoMIV/bioruptor and 24 genotypes/lane when using
> >FseI/bioruptor samples. This will give us an average depth/sequence
> >of 12X. I have also looked at overall error rates using BTx623
> >sequences and believe that when we sequence, we should cut off the
> >bottom 1/4 of the sequences (ie those sequences counted less than 1/4
> >of the average depth - below 3X when we sequence to 12X avg depth)
> >which will give us high quality data with a low error rate. At our
> >meeting in April I had mentioned that we were trimming back the
> >bottom 1/3 of the sequences but after more analysis, it looks like
> >the bottom 1/4 is better.
> >
> >I would be happy to ta k with you about all of this further if you
> >need more information or have additional questions. Just let me
> >know. I am available both tomorrow and Friday to visit. Next week
> >is crazy for me as my son graduates from high school next Friday and
> >then has his Eagle Scout Court of Honor on Saturday. I will be
> >taking a few days off to get ready for my family to visit and prepare
> >things.
> >
> >Take care
> >Trish
> >
> >
> >
> >At 11:55 AM 5/19/2009, you wrote:

> > >Trish,
> > >
> > >How are things in CS?
> > >
> > >I was hoping to follow up with you on the SNP discovery in 50
> > >sorghum lines. How is this going? Perhaps we can chat later in the
> >week.
> > >
> > >Hope all is well,
> > >John
> >
> >
> >
> >
> >
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X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
X-Spam-Flag: NO
X-Spam-Score: -2.599
X-Spam-Level:
X-Spam-Status: No, score=-2.599 tagged_above=-10 required=5 tests=[AWL=-0.001,
BAYES_00=-2.599, HTML_MESSAGE=0.001]
X-Virus-Scanned: amavisd-new at tamu.edu
X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
Subject: RE: Use of structure
Date: Wed, 20 May 2009 14:13:06 -0700
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
thread-topic: Use of structure
thread-index: AcnPS4ezpW+dhPNvSKa27+MSQfN+wwKQ4lFQAAAkzPA=
From: "Xuefeng Ma" <xma@ceres-inc.com>
To: "Patricia Klein" <pklein@tamu.edu>
Cc: "Xuefeng Ma" <xma@ceres-inc.com>

There are three sheets in the file.

From: Xuefeng Ma
Sent: Wednesday, May 20, 2009 2:12 PM
To: 'Patricia Klein'
Cc: John Bouck; Timothy Swaller
Subject: RE: Use of structure

Hi, Trish,

Here is the structure/clumpp result. One of the population, Q2, can be a sub-pop of Q3.
Please let me know if you have questions.

Xuefeng

-----Original Message-----
From: Patricia Klein [mailto:pklein@tamu.edu]
Sent: Thursday, May 07, 2009 12:36 PM
To: Xuefeng Ma
Subject: RE: Use of structure

Xuefeng

If you have time that would be great. Since this is not my area of
expertise any guidance that I could get from you would be most helpful.

thanks
Trish

At 01:37 PM 5/7/2009, you wrote:
>Hi, Trish,
>
>I was very busy last week and I have not try your file. Do you still
>want me to implement you file and it may be helpful to compare the
>result from you?
>
>Xuefeng
>
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Monday, April 27, 2009 3:39 PM
>To: Xuefeng Ma
>Cc: John Bouck
>Subject: RE: Use of structure
>
>Xuefeng
>
>The extra column is the geographic information that I stuck in in the
>column right next to the line names. This column can easily be
>removed as it is an optional column. The genotype data is fine as I
>have opened it in structure and done several test runs with the
>data. Thus all you need to do is remove the column directly to the
>right of the line names. Does that make sense?
>
>Trish
>
>
>
>At 05:13 PM 4/27/2009, Xuefeng Ma wrote:
> >Hi, Trish,
> >
> >I am happy to go through your data.
> >First, there is a minor formatting error. You have 109 columns in the
> >file. This might be an error because you have formatted the data as
> >diploid, which should be EVEN columns. This has to be fixed because
> >allele heterozygous/homozygous states may change if there is a column
> >shift.
> >
> >The log probability can be found from the "simulation Summary". The K
> >and Ln P(D) are the two the most needed columns to look at. Usually we
> >are seeking a lower K with higher Ln P(D).
> >
> >Since the materials are all sorghum R lines that may have involved in
> >backcross from common gene pools, the following two models should fit:
> >Use Admixture Model
> >Allele Frequencies are Correlated among Pops
> >

> >Please let me know if you have more questions.
> >
> >Xuefeng
> >
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Monday, April 27, 2009 2:51 PM
> >To: Xuefeng Ma
> >Subject: RE: Use of structure
> >
> >Xuefeng
> >
> >I found a blank marker entry in the file I sent earlier for txp57 in
> >line R.08010. I wanted to correct it and resend you the data file in
> >case you get a chance to look at it in structure.
> >
> >Trish
> >
> >
> >At 04:36 PM 4/27/2009, you wrote:
> > >There are a few parameters needs to be determined from testing.
> > >Burning: with this samples size, you need at least 10,000.
> > >Reps: at least 10,000,
> > >Number of population: need to be tested based on pre-runs. The
>largest
> > >relative log possibility is the one you need to select while
> > >considering some trade off of number of K.
> > >
> > >All other parameters are optional depending on case. If you are not
> > >sure if the origin shaped the germplasms, it is better to leave it is
> > >unknown.
> > >
> > >You file is lost during email transfer. How many alleles are
>generated
> > >from the 54 markers?
> > >
> > >Xuefeng
> > >
> > >
> > >-----Original Message-----
> > >From: John Bouck
> > >Sent: Monday, April 27, 2009 2:25 PM
> > >To: Patricia Klein
> > >Cc: Xuefeng Ma
> > >Subject: RE: Use of structure
> > >
> > >Hi Trish,
> > >
> > >I do not run this program here - this is usually used by Xuefeng
>here.
> > >
> > >Xuefeng - can you please help Trish by suggesting parameters and take
>a

> >
> > >look yourself?
> > >I believed that Structure would be able to accommodate geographic
> > >origin in some capacity - can you please comment.
> > >
> > >Thanks,
> > >John
> > >
> > >-----Original Message-----
> > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > >Sent: Monday, April 27, 2009 12:00 PM
> > >To: John Bouck
> > >Subject: Use of structure
> > >
> > >John
> > >
> > >I have downloaded structure and am trying to use in on the 100 lines
> > >that have thus far been put into the Ceres breeding program from Bill
> > >Rooney. The lines were screened with 54 SSRs from around the genome.
> > >I have correctly formatted the data so that it goes into structure
>and
> > >have done one run so I know that the data is formatted okay. I have
> > >also included geographic origin of the material as as added entry in
>my
> >
> > >data file. Since I have never worked with this program I am a bit
> > >unsure of what types of parameters I should be testing to see if the
> > >output makes sense. Would you mind somewhat guiding me through my
> > >first run of the program. Additionally I have attached the data
> > >formatted for structure to this email so that you can also take a
>look
> > >at it in structure.
> > >
> > >Thanks
> > >Trish
> > >
> > >P.S. The data is formatted so that all data for a given sample is on
> > >one row of the file. There are 101 individuals (included BTx623) and
> > >54 markers. There were 15 different countries of origin (file shows
> > >16 as those that I had no information for, I marked as 0) and finally
> > >missing data is coded as a -9.
> > >
> > >P.S.S. Hope your long drive back to CA went okay and you have now
> > >recuperated from the trip.
> > >
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>X-Spam-Flag: NO
>X-Spam-Score: -2.599
>X-Spam-Level:
>X-Spam-Status: No, score=-2.599 tagged_above=-10 required=5 tests=[AWL=-0.001,
>	BAYES_00=-2.599, HTML_MESSAGE=0.001]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Use of structure
>Date: Wed, 20 May 2009 14:11:40 -0700
>X-MS-Has-Attach: yes
>X-MS-TNEF-Correlator:
>thread-topic: Use of structure
>thread-index: AcnPS4ezpW+dhPNvSKa27+MSQfN+wwKQ4lFQ
>From: "Xuefeng Ma" <xma@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>Cc: "John Bouck" <jbouck@ceres-inc.com>,
>	"Timothy Swaller" <tswaller@ceres.net>
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> > > >
> > > >-----Original Message-----
> > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > >Sent: Monday, April 27, 2009 12:00 PM
> > > >To: John Bouck
> > > >Subject: Use of structure
> > > >
> > > >John
> > > >
> > > >I have downloaded structure and am trying to use in on the 100 lines
> > > >that have thus far been put into the Ceres breeding program from Bill
> > > >Rooney. The lines were screened with 54 SSRs from around the genome.
> > > >I have correctly formatted the data so that it goes into structure
> >and
> > > >have done one run so I know that the data is formatted okay. I have
> > > >also included geographic origin of the material as as added entry in
> >my
> > >
> > > >data file. Since I have never worked with this program I am a bit
> > > >unsure of what types of parameters I should be testing to see if the
> > > >output makes sense. Would you mind somewhat guiding me through my
> > > >first run of the program. Additionally I have attached the data
> > > >formatted for structure to this email so that you can also take a
> >look
> > > >at it in structure.
> > > >
> > > >Thanks
> > > >Trish
> > > >
> > > >P.S. The data is formatted so that all data for a given sample is on
> > > >one row of the file. There are 101 individuals (included BTx623) and
> > > >54 markers. There were 15 different countries of origin (file shows
> > > >16 as those that I had no information for, I marked as 0) and finally
> > > >missing data is coded as a -9.
> > > >
> > > >P.S.S. Hope your long drive back to CA went okay and you have now
> > > >recuperated from the trip.
> > > >
> > > >
> > > >
> > > >
> > > >
> > > >
> > > >Dr. Patricia Klein
> > > >Associate Professor
> > > >Institute for Plant Genomics and Biotechnology TAMU 2123 Texas
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X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
X-Spam-Flag: NO
X-Spam-Score: -1.665
X-Spam-Level:
X-Spam-Status: No, score=-1.665 tagged_above=-10 required=5 tests=[AWL=-0.167,
BAYES_00=-2.599, EXTRA_MPART_TYPE=1, HTML_MESSAGE=0.001,
RDNS_NONE=0.1]
X-HAT: SG SUSPECTLIST_NO_SBRS, P $THROTTLED_NO_SBRS, L tamu-relay
X-SRBS: None
X-EXTLoop1: 1
X-IronPort-Anti-Spam-Filtered: true
X-IronPort-Anti-Spam-Result: At4EAHJ23UpB2vnI/2dsb2JhbACCJy3IagmPCgKCTIFjBIsD
X-IronPort-AV: E=Sophos;i="4.44,592,1249275600";
d="gif'147?scan'147,208,217,147";a="40913044"
Subject: RE: Gantt Chart
Date: Tue, 20 Oct 2009 08:38:42 -0700
X-MS-Has-Attach: yes
X-MS-TNEF-Correlator:
Thread-Topic: Gantt Chart
Thread-Index: AcpNuvMSTRJbKi36Q1mBuc/f92u2BgD4CMHw
From: "Timothy Swaller" <tswaller@ceres.net>
To: "Patricia Klein" <pklein@tamu.edu>,
"John Mullet" <jmullet@tamu.edu>

Thanks Patricia.
I am hopelessly busy this week due to the IPMB next week. Is it possible for you and John to take a look and possibly John would have a free hour next week to sit down with me and go over this.

John, do you have an idea of your schedule next week at the IPMB and do you have any free time to meet and discuss this?

Thanks
Tim

From: Patricia Klein [mailto:pklein@tamu.edu]
Sent: Thursday, October 15, 2009 10:14 AM
To: Timothy Swaller; John Mullet
Subject: Re: Gantt Chart

Tim

I looked at it briefly but haven't gone over it with John yet. Unfortunately we have a grant proposal due this week and we were both working on it for the last few weeks. I now believe John is out of town for the rest of the week so my guess is it won't be until next week that he and I can discuss

what you sent. Perhaps we could schedule some type of conference call for later next week? Sorry I can't give you more details right now. As soon as John is back from his trip, I will talk with him.

Thanks
Trish

At 10:55 AM 10/15/2009, Timothy Swaller wrote:

Hi John and Patricia.
Hope all is well, I here there has been a significant amount of rain lately.

Have you had a chance to look over the Gantt chart I sent out and do you have any questions/comments on it?

Stay dry
Tim

Timothy Swaller
Director, IT and Genomics
Office: 805.376.6545
tswaller@ceres.net

c e r e s

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>X-Virus-Scanned: amavisd-new at neo-proxy-3.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.599
>X-Spam-Level:
>X-Spam-Status: No, score=-2.599 tagged_above=-10 required=5
> tests=[BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Question about GGT
>Date: Thu, 21 May 2009 11:23:30 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>thread-topic: Question about GGT
>thread-index: AcnaNDd/69qFFTvkQ0+1dFUhA/22nwAC0isAAAAV3sA=
>From: "Xuefeng Ma" <xma@ceres-inc.com>
>To: "John Bouck" <jbouck@ceres-inc.com>
>Cc: <pklein@tamu.edu>
>
>I do not have any problems.
>You can build the file either through the file Builder or format and
>copy from excel. If you use file builder, a map file and a loc file are
>needed. If you format in excel, it is very easy to copy in, but you do
>not have the flexibility to sort markers.
>
>No limitations for the numbers of plants and markers to load IN, but
>there is a column restriction if you download OUT as excel (you will
>lose any data beyond 256 column, because the build-in excel is still the
>2003 version). However, you can get around it by exporting through txt
>file.
>
>Xuefeng
>
>
>-----Original Message-----
>From: John Bouck
>Sent: Thursday, May 21, 2009 11:11 AM
>To: Xuefeng Ma
>Subject: FW: Question about GGT
>
>Is this performance problem what you would expect?
>
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Thursday, May 21, 2009 9:46 AM
>To: John Bouck
>Subject: RE: Question about GGT
>
>John,
>
>I now have gotten it to work. I didn't realize that I did not need
>to include any information on the population type. When I have that
>field blank in my imported excel file, it appears to load the data
>without a problem. The only issue I am now having is with the size
>of the data set that it will work with. I have pared the data down
>by chromosome and then have only tried to load markers that are at
>least 100Kbp apart. For chr. 1 that leaves me with 137 markers over
>the 13 individuals. Even this amount of data seems to be giving my
>computer problems. Perhaps I am just not being patient enough (the
>GGT screen has a "busy drawing, please wait ..." message). Do you
>know how many markers Xuefeng has tried to use when drawing
>chromosomes in GGT? Not sure if it is my computer or the program at
>this point.

>
>Thanks
>Trish
>
>
>
>At 10:41 AM 5/21/2009, you wrote:
> >Yes this should work. Xuefeng does this for looking at diversity
> >analysis - certainly most of the powerful tools in GGT for data
>analysis
> >are around pedigrees and population analysis so it is not surprising
> >that it is a focus of the documentation.
> >
> >Are you able to get the data in?
> >If it is something you can share we could take a look.
> >
> >John
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Thursday, May 21, 2009 8:25 AM
> >To: John Bouck
> >Subject: Question about GGT
> >
> >John,
> >
> >I have a quick question about graphical genotyping. I have installed
> >GGT32 on my windows machine and have read over the manual. As I read
> >over it, it sounds as if I need my individuals to come from some type
> >of population. However, we are working with diverse genotypes and
> >not individuals from a population. Do you know if GGT will work for
> >this? I have my markers across 13 different genotypes and would like
> >to graphically display this data but don't quite see how GGT will do
> >that as I don't have a population type to enter. I don't see this
> >mentioned in the manual. Any comments/suggestions would be
>appreciated.
> >
> >Thanks
> >Trish
> >
> >
> >
> >
> >
> >
> >
> >
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>X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.444
>X-Spam-Level:
>X-Spam-Status: No, score=-2.444 tagged_above=-10 required=5 tests=[AWL=0.155,
>	BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Question about GGT
>Date: Thu, 21 May 2009 08:41:42 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>thread-topic: Question about GGT
>thread-index: AcnaKM7nLBcBxxEUTX62GYdvt0YO2QAAVm/Q
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>Yes this should work. Xuefeng does this for looking at diversity
>analysis - certainly most of the powerful tools in GGT for data analysis
>are around pedigrees and population analysis so it is not surprising
>that it is a focus of the documentation.
>
>Are you able to get the data in?
>If it is something you can share we could take a look.
>
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Thursday, May 21, 2009 8:25 AM
>To: John Bouck
>Subject: Question about GGT
>
>John,
>
>I have a quick question about graphical genotyping. I have installed
>GGT32 on my windows machine and have read over the manual. As I read
>over it, it sounds as if I need my individuals to come from some type
>of population. However, we are working with diverse genotypes and
>not individuals from a population. Do you know if GGT will work for
>this? I have my markers across 13 different genotypes and would like
>to graphically display this data but don't quite see how GGT will do
>that as I don't have a population type to enter. I don't see this
>mentioned in the manual. Any comments/suggestions would be appreciated.
>
>Thanks
>Trish
>
>
>
>
>
>
>
>
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X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
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X-Spam-Level:
X-Spam-Status: No, score=-1.499 tagged_above=-10 required=5 tests=[AWL=-0.001,
BAYES_00=-2.599, EXTRA_MPART_TYPE=1, HTML_MESSAGE=0.001,
RDNS_NONE=0.1]
X-HAT: SG SUSPECTLIST_NO_SBRS, P $THROTTLED_NO_SBRS, L tamu-relay
X-SRBS: None
X-EXTLoop1: 1
X-IronPort-Anti-Spam-Filtered: true
X-IronPort-Anti-Spam-Result:
AqQEAP9Mt0pB2vnI/2dsb2JhbACCKyvBUQmOEAKCRYFUBYFYiSM
X-IronPort-AV: E=Sophos;i="4.44,425,1249275600";
d="gif'147?scan'147,208,217,147";a="25102803"
Subject: Sorghum NGS
Date: Mon, 21 Sep 2009 09:54:06 -0700
X-MS-Has-Attach: yes
X-MS-TNEF-Correlator:
Thread-Topic: Sorghum NGS
Thread-Index: Aco63CDsBLurT1DnTeaeIHiBwdjOCA==
From: "Timothy Swaller" <tswaller@ceres.net>
To: "Patricia Klein" <pklein@tamu.edu>,
<jmullet@tamu.com>

Trish/John. How are things?
I am trying to get a list of sorghum lines together that we would be interested in for NGS processing.
In the mean time, are there additional genotypes you are running (within the Ceres/TAMU collaboration) which you will be sending to us?
Is there a scheduled timeframe for processing and data delivery? (sorry I am still catching up on things).

Can you give me a bit of information on the below lines?
Why were they selected and what is their importance? (phenotype information is preferred if available)

R07007
R07008
R07012
R07018
R07020
R07030
R07034

R07042
R07045
R07054
Rio
BTx623
IS3620c
SC748-5
P850029

Was there ever a vision of Ceres using this instrument for other NGS activities we have ongoing internally?
Example. you would provide a service @ some cost or make the instrument available to us for some predetermined time?

Last question: Should I continue to contact both of you for questions or is there 1 point person.

Thanks for the help.
Tim

Timothy Swaller
Director, IT and Genomics
Office: 805.376.6545
tswaller@ceres.net

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X-Virus-Scanned: amavisd-new at neo-proxy-2.tamu.edu
X-Spam-Flag: NO
X-Spam-Score: -2.385
X-Spam-Level:
X-Spam-Status: No, score=-2.385 tagged_above=-10 required=5 tests=[AWL=0.213,
BAYES_00=-2.599, HTML_MESSAGE=0.001]
X-Virus-Scanned: amavisd-new at tamu.edu
X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
Subject: Structure
Date: Wed, 22 Apr 2009 12:21:38 -0700
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: Structure
Thread-Index: AcnDf475WXC/qT2dTgOzlKk0fThung==
From: "John Bouck" <jbouck@ceres-inc.com>
To: "Patricia Klein" <pklein@tamu.edu>

Patricia,

When we met a few weeks ago you expressed interest in an application to look at the structure of populations. I had promised to send a link and then promptly went on vacation…

Anyway, the application we use quite frequently now is this one:
http://pritch.bsd.uchicago.edu/structure.html

Look forward to catching up tomorrow,
John

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X-Virus-Scanned: amavisd-new at
X-Spam-Flag: NO
X-Spam-Score: -2.557
X-Spam-Level:
X-Spam-Status: No, score=-2.557 tagged_above=-10 required=5 tests=[AWL=0.041,
BAYES_00=-2.599, HTML_MESSAGE=0.001]
Subject: RE: Quarterly Meeting Schedule
Date: Tue, 22 Jul 2008 08:22:40 -0700
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: Quarterly Meeting Schedule
Thread-Index: AcjnsNobuxUMXNZSQm2Yb3dNp84dSgDqLJQg
From: "Walter Nelson" <wnelson@ceres-inc.com>
To: "Simpson, Shay" <shay-simpson@tamu.edu>,
"Baltensperger, David" <dbaltensperger@ag.tamu.edu>,
"Bill Rooney" <wlr@tamu.edu>,
"John Mullet" <jmullet@tamu.edu>,
"Patricia Klein" <pklein@tamu.edu>,
"Avant, Bob" <bavant@tamu.edu>,
"Schuerman, Peter L." <PSchuerman@tamu.edu>,
"Helms, Adam" <ahelms@dsmail.tamu.edu>,
"Edgar Haro" <eharo@ceres-inc.com>,
"Juerg M Blumenthal" <JBlumenthal@ag.tamu.edu>
Cc: "Slovacek, Jackie" <j-slovacek@tamu.edu>,
<j-young@tamu.edu>,
"Penn, Nancye B" <npenn@tamu.edu>,
"Nelson, Michelle" <m_nelson@tamu.edu>
X-Virus-Scanned: amavisd-new at tamu.edu

Shay,

Thank you for sending the proposed dates below. They look okay to me, but I am still waiting for a few responses from my end. Also, I am including Edgar Haro (Ceres Sorghum breeder) and Juerg Blumenthal (now running some agronomy work for the program) on this note as they should definitely attend if possible. I already spoke to Edgar and he should be able to do the call. I will let you know if I need any revisions.

Also, as for time for the call, I think 2-3 hours for the call will be plenty as I imagine 30 minutes or so plus discussion for an update per area (breeding, genomics, agronomy) should be fine. I know Bill had also mentioned a discussion about seed scale up on with respect to Ceres awhile back and we could discuss a few licensing matters as well.

Would you like to take a first pass at a meeting agenda or would you like me to?

Thanks,
Walter

From: Simpson, Shay [mailto:shay-simpson@tamu.edu]
Sent: Wednesday, July 16, 2008 7:00 PM
To: Walter Nelson; Baltensperger, David; Bill Rooney; John Mullet; Patricia Klein; Avant, Bob; Schuerman, Peter L.; Helms, Adam
Cc: Slovacek, Jackie; j-young@tamu.edu; Penn, Nancye B; Nelson, Michelle
Subject: Quarterly Meeting Schedule
Importance: High

Walter and all,

(Who have a left off of the recipient list to receive this email?)

Based on the responses I have received so far, the following schedule will fit best in the majority of the respondents calendars for quarterly meeting:

August 4 to have a conference call for brief update – Walter please let us know the time preference and how many hours to hold (2 hours or what?).

September 22 for Ceres to travel to A&M for full-quarterly meeting.

December 11 for A&M to travel to Ceres.

March 9 for Ceres to travel to A&M

Please give me more specific feedback on whether you like these dates or would want to adjust slightly.

Thank you,

Shay

Shay L. Simpson

Project Manager, Bioenergy Program

Texas AgriLife Research

979-845-6315 Tel

shay-simpson@tamu.edu

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Project Timeline

On track | Needs attention | Off track

April 1, 2009

Project Timeline

1, 2009

Q4

>X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
>X-Spam-Flag: NO
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>X-Spam-Level:
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>	BAYES_00=-2.599, FUZZY_VLIUM=0.001]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Geospiza
>Date: Mon, 23 Mar 2009 10:45:18 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Geospiza
>Thread-Index: AcmowZgKPtVVR0tFSaC6V6ctuN4yewAJWDhAAAC8NcAAuURcYAAD3QCw
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>Trish,
>
>Do you want to join me for this? I can't meet until 2:00 that day would
>this time work for you?
>
>John
>
>-----Original Message-----
>From: Reising, Darrell [mailto
>Sent: Monday, March 23, 2009 8:51 AM
>To: John Bouck
>Cc: Olson, N. Eric
>Subject: RE: Geospiza
>
>John - are you available on Wednesday at 1:30 for a WebEx presentation
>of our analysis?
>
>Darrell
>
>Darrell Reising - Director, Core Lab Solutions
>Geospiza, Inc.
>
>+1.206.633.4403 x124
>
>
>
>-----Original Message-----
>From: John Bouck [mailto:jbouck@ceres-inc.com]
>Sent: Thursday, March 19, 2009 4:29 PM
>To: Reising, Darrell; Hodson, Matt
>Subject: RE: Geospiza
>
>Great, there are two lanes of data - one is a multiplexing with the
>first three nt's indicating different pools that were mixed together (16
>pool - I can send the tags if needed). The second is all from one
>genotyping experiment. The goal is to find SNPs and be able to compare
>them. This is a restriction digest approach where the DNA is cut,
>linkers ligated onto the ends and sequence generated from those ends.
>So the expectation is that there will be redundant reads in the genome
>surrounding the appropriate restriction site.
>
>I can explain more thoroughly if it is helpful.
>
>Look forward to learning how you can help us.
>John
>
>-----Original Message-----

>From: Reising, Darrell [mailto
>Sent: Thursday, March 19, 2009 4:05 PM
>To: Hodson, Matt; John Bouck
>Subject: RE: Geospiza
>
>ThanX Matt. We will be back to shortly John.
>
>Darrell
>
>Darrell Reising - Director, Core Lab Solutions
>Geospiza, Inc.

>+1.206.633.4403 x124
>
>
>
>-----Original Message-----
>From: Hodson, Matt
>Sent: Thursday, March 19, 2009 11:36 AM
>To: John Bouck
>Cc: Reising, Darrell
>Subject: Re: Geospiza
>
>John,
>
>I've unzipped them and let Darrell know that your Illumina data and ref
>sequences are ready to go.
>
>Cheers,
>-Matt
>
>-----
>Matt Hodson
>Technical Support Scientist, Geospiza
>(206) 633-4403, Ext. 111
>
>
>
>John Bouck wrote:
> > Matt,
> >
> > I've transferred two zipped files each representing one lane of data
> > from an Illumina sequencing run.
> >
> > Let me know what the next steps are.
> >
> > John
> >
> > -----Original Message-----
> > From: Hodson, Matt [mailto
> > Sent: Tuesday, March 17, 2009 9:52 PM
> > To: John Bouck
> > Cc: darrell; Olson, N. Eric
> > Subject: RE: Geospiza
> >
> > John,
> >
> > Go here
> > http://www.filecatalyst.com/download/files/fcdirect-express.html
> >
> > username = filecatalyst
> > password = fcisfast!
> >
> > and install the 'FileCatalyst Express' application for your platform.
> > The client works just like an ftp client although it's not. Once it's
> > installed use
> >
> > host = 216.139.212.145
> > username = john_bouck
> > pass = jbouck1

> > port = 8008
> > transfer mode = UDP
> >
> > Then just transfer your data over. If you hit in problems let me
>know.
> > Otherwise shoot us an email when the transfer is complete.
> >
> > Cheers,
> > -Matt
> >
> > _____
> > From: John Bouck [jbouck@ceres-inc.com]
> > Sent: Tuesday, March 17, 2009 3:46 PM
> > To: Hodson, Matt
> > Subject: RE: Geospiza
> >
> > Hi Matt,
> >
> > I can access the data through windows or unix - windows is a little
> > easier for me today.
> > I can also burn a DVD if that is easier.
> >
> > John
> >
> > From: Matt Hodson [mailto
> > Sent: Tuesday, March 17, 2009 12:46 PM
> > To: John Bouck
> > Cc: Reising, Darrell
> > Subject: Re: Geospiza
> >
> > Hi John,
> >
> > There are a number of ways to transfer the data to us. Can you tell
>me
> > what platform you are using? This is the computer that has access to
> > your Illumina GA data.
> >
> > Cheers,
> > -Matt
> >
> >
> > -----
> >
> > Matt Hodson
> >
> > Technical Support Scientist, Geospiza
> >
> > (206) 633-4403, Ext. 111
> >
> >
> > Reising, Darrell wrote:
> > Hi John. Let me introduce you to Matt Hodson, our lead support
>manager.
> > He will work with you to get the files to us.
> >
> > We will perform a complementary analysis on two of your fastq files
> > using our Resequencing pipeline. Turn-around time is about a week as
>we
> > add your files to the analysis queue.
> >
> > BTW - can you point me to the link for your Sorghum genome reference?
>I
> > suspect NCBI has it - but if you can point to the ref - that will save
> > us the time to locate.
> >
> > Matt - please connect with John. His phone number is 805.376.6509
> >
> > ThanX
> >
> > Darrell

> >
> > Darrell Reising - Director, Core Lab Solutions
> > Geospiza, Inc.
> >
> > +1.206.633.4403 x124
> >
> >
> > _____
> > From: John Bouck
> > [mailto:jbouck@ceres-inc.com<mailto:jbouck@ceres-inc.com>]
> > Sent: Tuesday, March 17, 2009 8:30 AM
> > To: Reising, Darrell
> > Subject: RE: Geospiza
> >
> > Hi Darrell,
> >
> > I have nailed down two lanes of data that would be of interest for us
>to
> > understand the utility of your pipeline. How should we proceed from
> > here?
> >
> > John
> >
> > From: John Bouck
> > Sent: Wednesday, March 11, 2009 10:03 AM
> > To: 'Reising, Darrell'
> > Subject: RE: Geospiza
> >
> > Hi Darrell,
> >
> > Yes I took a look at the datasets we have available and today they are
> > all from species where we do not have a reference sequence. My
> > recollection from our call is that in order to do SNP discovery the
> > assembly requires a reference. I've also queried one of our
> > collaborators who we are working with on Sorghum (genome sequenced) to
> > find a good test case. For this latter approach here is quick
>summary:
> >
> > Goal - SNP discovery
> > Multiplexing - up to 16 x per lane with sequence tags
> > GA2 platform
> > Genomic DNA
> > RAD approach (restriction digest and sequencing from ends) - not
>really
> > an assembly, more of an alignment
> > Sorghum
> >
> > What we look for - in SNPs
> >
> > Frequency - e.g. number of reads with each variant
> >
> > Quality of nt at SNP
> >
> > Quality of surrounding nts (2 upstream and 2 downstream)
> >
> > Quality of general alignment (no insertions / deletions)
> >
> > We haven't yet selected a specific experiment but expect to in the
>next
> > few days.
> >
> > John
> >
> >
> > From: Reising, Darrell
> > [mailto
> > Sent: Wednesday, March 11, 2009 9:12 AM
> > To: John Bouck
> > Subject: Geospiza
> >

> > Hi John - last we spoke - we were going to take a file or two and run
> > thru our analysis server. Still interested in that?
> >
> > Below is the info that I would need to know to ensure we have the
> > pipeline ready;
> >
> > Platform? - GA Classic or GA2? other?
> >
> > Application? - i.e. RNA-Seq, Tag Profiling, etc.
> >
> > Species? -
> >
> > Sample source? - i.e. tissue, cell line, other
> >
> > Prep kit used?
> >
> > ThanX - look forward to hearing from you.
> >
> > Darrell
> >
> > Darrell Reising - Director, Core Lab Solutions
> > Geospiza, Inc.
> > <mailto >
> >
> > [P] 206.633.4403 x124
> > [C] 425.445.6767
> > [F] 206.633.4415
> >
> > 100 West Harrison
> > North Tower, Suite 330
> > Seattle, WA 98119
> >
> > www.geospiza.com<http://www.geospiza.com/>
> >
> >
> >

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X-Virus-Scanned: amavisd-new at
X-Spam-Flag: NO
X-Spam-Score: -2.598
X-Spam-Level:
X-Spam-Status: No, score=-2.598 tagged_above=-10 required=15
tests=[BAYES_00=-2.599, HTML_MESSAGE=0.001]
Subject: RE: Illumina 30bp sequences
Date: Wed, 26 Mar 2008 11:54:08 -0700
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: Illumina 30bp sequences
Thread-Index: AciPXsuTkdnKvhqZTQGDenQ4bBS4aQAE3a0g
From: "Timothy Swaller" <tswaller@ceres-inc.com>
To: "Patricia Klein" <pklein@tamu.edu>,
<jmullet@tamu.edu>
X-Virus-Scanned: amavisd-new at tamu.edu

Hi Patricia and John

Here is the current software we are using for graphical genotyping. Our datasets are not huge currently so it will be interesting to see with your larger datasets if the software can handle it. I like it because it is quite easy to use and data format are easy excel formats which makes things a bit easier for us as well.

Here is the link for the download.

http://www.plantbreeding.wur.nl/UK/software_ggt.html

Tim

Timothy Swaller
Manager
Sequencing/Molecular Markers
Ceres, Inc.
(805) 376-6504 x1109
www.ceres.net

From: Patricia Klein [mailto:pklein@tamu.edu]
Sent: Wednesday, March 26, 2008 9:31 AM
To: John Bouck
Cc: Timothy Swaller
Subject: Illumina 30bp sequences

John

Attached are two fasta files each containing around 7000-7500 30bp sequences that we obtained from our initial Illumina run. As John indicated we prepared template from two genotypes (BTx623 and IS3620C) using two restriction enzymes and then ligated a sequencing primer containing an ID tag to one side of the template. The templates were sent to Illumina and they generated the data. We received back 33bp sequences but we trimmed the last 3bp from the sequences as we believe many of the differences in these last 3bp were sequencing errors and not 'real' SNP differences. The ID tags added to the two genotypes were ACC for BTx623 and TCA for IS3620C. The four bases after the ID tag (CCGG) are the remainder of the 8bp recognition enzyme that was used for digestion on the one side of the molecule. The naming convention of the sequences (ie BTx_1_441) refers to the genotype (in this case BTx623) followed by a numerical ID (1) followed by the number of times this exact sequence was counted (or sequenced) in the Illumina run (in this case the first sequence was represented 441 times in the data set). I only analyzed the sequences that were counted at least 5 times or more since most of the sequences that were counted only a couple of times or less should be those sequences that contain random sequence errors that were generated during the Illumina run.

We performed a blastn analysis of these sequences to a database of the 3304 JGI sequences in their latest release (ie 10 sorghum psuedomolecules and 3294 super_contigs). We used BLASTN parameters that are for finding short nearly exact matches. These parameters are typically used when searching for oligo sequences and that is why I chose them. The blastn conditions were: blastall -p blastn -b 10 -v 10 -m 0 -I T -e 0.1 -W 7 -r 2 -q -3 -F "m D" -G 5 -E 2

A perfect hit will give an Identity of 27/27 since the first three nucleotides are the synthetic ID key attached to each genotype.

After performing the blast analysis we parsed the output files to give us the total number of hits for a given sequence and then provide information on only the top two hits (ie what the hit was, its start and stop position within a chromosome pseudomolecule or super_contig, the e-value, and identity). This allowed us to see how many of the sequences hit the genome uniquely and how good the second hit was in the cases where the sequence hit mulitple locations within the genome.

Once we finished parsing the data from the two genotypes, we then combined the datasets to attempt to look for possible SNPs and/or indels between BTx623 and IS3620C. For this we wrote a perl script to look for a BTx623 sequence that hit a specific location perfectly (ie 27/27) and then see if an IS3620C sequence hit that same specific location but not perfectly. The script was a bit more detailed than this but hopefully you can get an idea of what I am talking about.

One thing to note in the sequences once you get your BLAST results back. You will notice that in many instances there are multiple BTx623 and/or IS3620C sequences that hit the same specific site within the genome and one of these hits the site perfectly (ie 27/27) but the others hit the site imperfectly (ie 26/27). In a very large proportion of these cases, it appears that the imperfect sequence has a C to A mutation in it. This was very surprising to us because sequencing errors using the Illumina system should be random and thus would occur randomly throughout the 33bp

sequences that we obtained from Illumina. In the C to A mutation cases, we see a significant number of sequences that all had the same C to A mutation in the exact same nucleotide position. We have contacted Illumina about this issue and are trying to see if there was some problem during the sequencing run that caused this to occur.

Let me know if you have any questions. I can also send you my parsed BLAST files and those sequences where I believe I identified a SNP and/or Indel between BTx623 and IS3620C if you want. I didn't attach them to this file as I knew it would be too large.

Take care,
Trish

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>X-Virus-Scanned: amavisd-new at neo-proxy-3.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -1.995
>X-Spam-Level:
>X-Spam-Status: No, score=-1.995 tagged_above=-10 required=5 tests=[AWL=0.604,
>	BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: FW: Access to data
>Date: Thu, 26 Mar 2009 08:30:07 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Access to data
>Thread-Index: AcmuEvm+lPlWr9SeTTaH1jynHG8MuwAFLj3A
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>FYI - feel free to poke around if you have interest.
>
>John
>
>-----Original Message-----
>From: N. Eric Olson, PhD [mailto
>Sent: Thursday, March 26, 2009 5:59 AM
>To: John Bouck
>Cc: Darrell Reising
>Subject: Access to data
>
>John,
>
>I have released the results for three of the bar coded samples into your
>
>account. You can log in with the information below. I will release
>more later in the day.
>
>http://analysis.finchlab.com/Finch/Core/folderContents?FOLDER_ID=9;Tab=1
>User: ceres
>Pass: sorghum
>
>Let me know if you have any questions.
>
>Regards,
>Eric

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>X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.134
>X-Spam-Level:
>X-Spam-Status: No, score=-2.134 tagged_above=-10 required=5 tests=[AWL=0.465,
>	BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Geospiza
>Date: Thu, 26 Mar 2009 11:49:25 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Geospiza
>Thread-Index: AcmuFxHPuGm/VUtwTbyy9UaCBk1pFQAK6dDQ
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>Trish,
>
>Yes, my expectation is that we could ta k them into a steep discount
>(40%). Still would be around 2 thousand for looking at a single run.
>I'm not convinced this is the way to go but we're getting desperately
>short on resources (= peoples time) so these outsourcing options are
>becoming more attractive. At an FTE rate of 250 k per year, one week of
>a bioinformatician costs me 5,000 in salary and overhead.
>
>Still seems early but we'll keep an eye on it.
>
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Thursday, March 26, 2009 6:28 AM
>To: John Bouck
>Subject: Re: Geospiza
>
>John
>
>I agree. For a full 7 lane run it would cost
>$3500 which might eventually be worth the cost
>but right now I don't feel they have enough stuff
>for DNA sequencing/SNP analysis to warrant that
>cost. Perhaps as they develop more tools it
>might be worth the cost. Additionally we
>sometimes run the same sample in multiple lanes
>and then combine the data prior to downstream
>analysis. If they only charged $500 for the
>combined lanes then that might also help with the cost.
>
>Thanks
>Trish
>
>
>
>At 07:34 PM 3/25/2009, you wrote:
> >Thanks for joining us on the call Trish - I
> >forget if I mentioned this but their model is to
> >charge per lane of data run through their
> >analysis pipeline. The list price is 500 bucks
> >per lane - presumably this is negotiable. I
> >don't know about you but I spent a least a few
> >hundred bucks of my own time mucking around with
> >the data. Not to mention time spent cleaning my hard drive.
> >

> >However, it seems like early days for these guys,
> >John
>
>
>
>
>
>
>Dr. Patricia Klein
>Associate Professor
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X-Virus-Scanned: amavisd-new at
X-Spam-Flag: NO
X-Spam-Score: -2.539
X-Spam-Level:
X-Spam-Status: No, score=-2.539 tagged_above=-10 required=5 tests=[AWL=0.059,
BAYES_00=-2.599, HTML_MESSAGE=0.001]
X-Virus-Scanned: amavisd-new at tamu.edu
X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
Subject: Topics for discussion at the next quarterly meeting
Date: Wed, 26 Nov 2008 13:46:50 -0800
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: Topics for discussion at the next quarterly meeting
Thread-Index: AclQEH0cEmmbRw1+R9yck5rIKJGKcA==
From: "Walter Nelson" <wnelson@ceres-inc.com>
To: "Bill Rooney" <wlr@tamu.edu>,
"John Mullet" <jmullet@tamu.edu>,
"Patricia Klein" <pklein@tamu.edu>,
"Juerg M Blumenthal" <JBlumenthal@ag.tamu.edu>
Cc: "Bob Avant" <bavant@dsmail.tamu.edu>,
"McCutchen, Bill" <bmccutchen@tamu.edu>,
"Peter Schuerman" <
"Simpson, Shay" <shay-simpson@tamu.edu>,
"Edgar Haro" <eharo@ceres-inc.com>

Bill, John, Juerg and Patricia,

I hope this note finds everyone well and getting ready for (or already started having) a few days off for the holidays.

I wanted to send you all a quick note regarding something I had mentioned at our last quarterly, that being the idea of using the next quarterly as a sort of "Year 1 review" of the activities in the collaboration. Our thinking was to have a point-by-point technical overview of the activities that are described in the workplan of the research agreement. The goal would be to see how things have progressed since we began a year ago, whether they are going to plan, and what everyone's thoughts are on what, if anything, we should be doing differently. I think this will also be helpful for some of the new additions to our team here at Ceres (i.e. Jeff Gwyn and Mike Stephenson, to name but two).

Also, we have reviewed the two proposals sent to us and are interested in discussing them further. However, since you will only be here one day, we felt in-depth discussions about them should probably be at times separate from the quarterly, probably in College Station in the next month or two.

What we would like though during the quarterly would be a bit more information about the proposals. For the Intergeneric Hybridization project, a summary of what data is currently available (e.g. results/pictures of crosses

completed, cytogenetics done to date, relative percentages of "good" crosses and off-types etc...) would be very useful to us. For the Germplasm Mining project, more detail about how this project would be done technically (e.g. using the Illumina system?) as there were some questions about that based on the reading of the proposal.

I will put an agenda together with Shay early next week, but wanted to relate these topics as early as possible so as to catch you before any presentations are prepared. Don't hesitate to drop me a line if you have any questions.

Thanks and have a wonderful holiday weekend!

Best regards,

Walter

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1535 Rancho Conejo Blvd.
Thousand Oaks, CA 91320
voice: (805)376-6548
www.ceres.net

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>X-Virus-Scanned: amavisd-new at neo-proxy-3.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.599
>X-Spam-Level:
>X-Spam-Status: No, score=-2.599 tagged_above=-10 required=5
>	tests=[BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Use of structure
>Date: Mon, 27 Apr 2009 15:13:09 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Use of structure
>Thread-Index: AcnHgrV31jrsSYP1RkmQ/Uh+vS/xDQAADDdg
>From: "Xuefeng Ma" <xma@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>Cc: "John Bouck" <jbouck@ceres-inc.com>
>
>Hi, Trish,
>
>I am happy to go through your data.
>First, there is a minor formatting error. You have 109 columns in the
>file. This might be an error because you have formatted the data as
>diploid, which should be EVEN columns. This has to be fixed because
>allele heterozygous/homozygous states may change if there is a column
>shift.
>
>The log probability can be found from the "simulation Summary". The K
>and Ln P(D) are the two the most needed columns to look at. Usually we
>are seeking a lower K with higher Ln P(D).
>
>Since the materials are all sorghum R lines that may have involved in
>backcross from common gene pools, the following two models should fit:
>Use Admixture Model
>Allele Frequencies are Correlated among Pops
>
>Please let me know if you have more questions.
>
>Xuefeng
>
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Monday, April 27, 2009 2:51 PM
>To: Xuefeng Ma
>Subject: RE: Use of structure
>
>Xuefeng
>
>I found a blank marker entry in the file I sent earlier for txp57 in
>line R.08010. I wanted to correct it and resend you the data file in
>case you get a chance to look at it in structure.
>
>Trish
>
>
>At 04:36 PM 4/27/2009, you wrote:
> >There are a few parameters needs to be determined from testing.
> >Burning: with this samples size, you need at least 10,000.
> >Reps: at least 10,000,
> >Number of population: need to be tested based on pre-runs. The largest
> >relative log possibility is the one you need to select while
> >considering some trade off of number of K.
> >

> >All other parameters are optional depending on case. If you are not
> >sure if the origin shaped the germplasms, it is better to leave it is
> >unknown.
> >
> >You file is lost during email transfer. How many alleles are generated
> >from the 54 markers?
> >
> >Xuefeng
> >
> >
> >-----Original Message-----
> >From: John Bouck
> >Sent: Monday, April 27, 2009 2:25 PM
> >To: Patricia Klein
> >Cc: Xuefeng Ma
> >Subject: RE: Use of structure
> >
> >Hi Trish,
> >
> >I do not run this program here - this is usually used by Xuefeng here.
> >
> >Xuefeng - can you please help Trish by suggesting parameters and take a
>
> >look yourself?
> >I believed that Structure would be able to accommodate geographic
> >origin in some capacity - can you please comment.
> >
> >Thanks,
> >John
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Monday, April 27, 2009 12:00 PM
> >To: John Bouck
> >Subject: Use of structure
> >
> >John
> >
> >I have downloaded structure and am trying to use in on the 100 lines
> >that have thus far been put into the Ceres breeding program from Bill
> >Rooney. The lines were screened with 54 SSRs from around the genome.
> >I have correctly formatted the data so that it goes into structure and
> >have done one run so I know that the data is formatted okay. I have
> >also included geographic origin of the material as as added entry in my
>
> >data file. Since I have never worked with this program I am a bit
> >unsure of what types of parameters I should be testing to see if the
> >output makes sense. Would you mind somewhat guiding me through my
> >first run of the program. Additionally I have attached the data
> >formatted for structure to this email so that you can also take a look
> >at it in structure.
> >
> >Thanks
> >Trish
> >
> >P.S. The data is formatted so that all data for a given sample is on
> >one row of the file. There are 101 individuals (included BTx623) and
> >54 markers. There were 15 different countries of origin (file shows
> >16 as those that I had no information for, I marked as 0) and finally
> >missing data is coded as a -9.
> >
> >P.S.S. Hope your long drive back to CA went okay and you have now
> >recuperated from the trip.
> >
> >
> >
> >
> >
> >
> >
> >Dr. Patricia Klein

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>Associate Professor
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>Research Texas A&M University College Station, TX 77843-2123
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fax: 979-862-4790

>X-Virus-Scanned: amavisd-new at neo-proxy-2.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.599
>X-Spam-Level:
>X-Spam-Status: No, score=-2.599 tagged_above=-10 required=5
>	tests=[BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Use of structure
>Date: Mon, 27 Apr 2009 14:36:54 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Use of structure
>Thread-Index: AcnHaut+ppc9eceIR/SktQiuYMzP7QAE289gAAAk77A=
>From: "Xuefeng Ma" <xma@ceres-inc.com>
>To: "John Bouck" <jbouck@ceres-inc.com>,
>	"Patricia Klein" <pklein@tamu.edu>
>
>There are a few parameters needs to be determined from testing.
>Burning: with this samples size, you need at least 10,000.
>Reps: at least 10,000,
>Number of population: need to be tested based on pre-runs. The largest
>relative log possibility is the one you need to select while considering
>some trade off of number of K.
>
>All other parameters are optional depending on case. If you are not sure
>if the origin shaped the germplasms, it is better to leave it is
>unknown.
>
>You file is lost during email transfer. How many alleles are generated
>from the 54 markers?
>
>Xuefeng
>
>
>-----Original Message-----
>From: John Bouck
>Sent: Monday, April 27, 2009 2:25 PM
>To: Patricia Klein
>Cc: Xuefeng Ma
>Subject: RE: Use of structure
>
>Hi Trish,
>
>I do not run this program here - this is usually used by Xuefeng here.
>
>Xuefeng - can you please help Trish by suggesting parameters and take a
>look yourself?
>I believed that Structure would be able to accommodate geographic origin
>in some capacity - can you please comment.
>
>Thanks,
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Monday, April 27, 2009 12:00 PM
>To: John Bouck
>Subject: Use of structure
>
>John
>
>I have downloaded structure and am trying to use in on the 100 lines
>that have thus far been put into the Ceres breeding program from Bill

>Rooney. The lines were screened with 54 SSRs from around the genome. I
>have correctly formatted the data so that it goes into structure and
>have done one run so I know that the data is formatted okay. I have
>also included geographic origin of the material as as added entry in my
>data file. Since I have never worked with this program I am a bit
>unsure of what types of parameters I should be testing to see if the
>output makes sense. Would you mind somewhat guiding me through my first
>run of the program. Additionally I have attached the data formatted for
>structure to this email so that you can also take a look at it in
>structure.
>
>Thanks
>Trish
>
>P.S. The data is formatted so that all data for a given sample is on
>one row of the file. There are 101 individuals (included BTx623) and
>54 markers. There were 15 different countries of origin (file shows
>16 as those that I had no information for, I marked as 0) and finally
>missing data is coded as a -9.
>
>P.S.S. Hope your long drive back to CA went okay and you have now
>recuperated from the trip.
>
>
>
>
>
>
>Dr. Patricia Klein
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>X-Virus-Scanned: amavisd-new at neo-proxy-2.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.226
>X-Spam-Level:
>X-Spam-Status: No, score=-2.226 tagged_above=-10 required=5 tests=[AWL=0.372,
> BAYES_00=-2.599, FUZZY_VLIUM=0.001]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Illumina data analysis
>Date: Fri, 27 Feb 2009 15:17:10 -0800
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Illumina data analysis
>Thread-Index: AcmZMKUJR7CWkQ0hQwWdKq+OOUOSDwAAKJ5w
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>Great, 10:30 your time, 8:30 Pacific on Friday March 6 - I will call you
>on the number below.
>
>Look forward to ta king,
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Friday, February 27, 2009 3:09 PM
>To: John Bouck
>Subject: RE: Illumina data analysis
>
>John,
>
>After 10am central time is fine for me. Why don't we set it up for
>10:30am my time. Will that work? Can you call me? My number is on
>my signature below.
>
>Trish
>
>
>
>At 05:01 PM 2/27/2009, you wrote:
> >Next Friday is a good day to chat. The morning is easier - anytime
> >after 10:00 your time would work well.
> >
> >Below is short summary of a recent assembly from the 11208_GAII run -
> >this is sequence number 1 extracted for the AAC tag. I'm just listing
> >the chromosome fragments below as the scaffold list appears to be not
>as
> >interesting. I pulled 403 high quality SNPs from this assembly.
> >
> >Look forward to chatting.
> >
> >John
> >==
> >
> > Count Average length
> >Reads 703,399 27
> >Matched 635,643 27
> >Not matched 67,756 27
> >References 230 3,103,018
> >==
> >Reference Length # Matches # Forward Matches #
> >Reversed Matches # Paired-end Matches Min coverage Max
> >coverage
> >chr_1 73,840,631 108,262 52,737 55,525 0 0 385

> >chr_2 77,932,606 78,044 39,843 38,201 0 0 344
> >chr_3 74,441,160 88,963 45,159 43,804 0 0 329
> >chr_4 68,034,345 73,469 34,185 39,284 0 0 1,726
> >chr_5 62,352,331 39,393 21,099 18,294 0 0 306
> >chr_6 62,208,784 51,852 26,925 24,927 0 0 277
> >chr_7 64,342,021 44,115 20,662 23,453 0 0 290
> >chr_8 55,460,251 35,225 18,590 16,635 0 0 320
> >chr_9 59,635,592 48,717 24,929 23,788 0 0 342
> >chr_10 60,981,646 57,635 26,502 31,133 0 0 281
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Friday, February 27, 2009 2:38 PM
> >To: John Bouck
> >Subject: Re: Illumina data analysis
> >
> >John
> >
> >Yes I certainly would be interested in your analysis. I am kind of
> >tied up with things most of next week but would likely have time next
> >Friday, March 6th. Would that work for you?
> >
> >Thanks
> >Trish
> >
> >
> >
> >At 04:22 PM 2/27/2009, you wrote:
> > >Patricia,
> > >
> > >I hope all is well there in Texas.
> > >I was reminded recently that you had provided us some data from some
> > >experiments you had run on your Illumina sequencing machine. We
> > >have been trying a couple of software packages including one from a
> > >company called CLC and I took the opportunity to examine some of the
> > >data you shared. I've done an assembly against the sorghum genome
> > >and identified some SNPs. As always, a little analysis raises more
> > >questions than it answers and I was curious to talk with you and
> > >share experiences.
> > >
> > >Let me know if you have interest and time to chat,
> > >John
> > >
> > >==========
> > >John Bouck, Ph.D.
> > >Director of IT and Bioinformatics
> > >Ceres, Inc.
> > >1535 Rancho Conejo Blvd
> > >Thousand Oaks, CA 91320
> > >+1-805-376-6509
> > >==========
> > >
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> >
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>X-Virus-Scanned: amavisd-new at neo-proxy-2.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -1.108
>X-Spam-Level:
>X-Spam-Status: No, score=-1.108 tagged_above=-10 required=5
>	tests=[BAYES_05=-1.11, FUZZY_VLIUM=0.001, HTML_MESSAGE=0.001]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: Illumina data analysis
>Date: Fri, 27 Feb 2009 14:22:35 -0800
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Illumina data analysis
>Thread-Index: AcmZKePiaeeuBbaiSLe5bWjamxDWiQ==
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>Patricia,
>
>I hope all is well there in Texas.
>I was reminded recently that you had provided us some data from some
>experiments you had run on your Illumina sequencing machine. We
>have been trying a couple of software packages including one from a
>company called CLC and I took the opportunity to examine some of the
>data you shared. I've done an assembly against the sorghum genome
>and identified some SNPs. As always, a little analysis raises more
>questions than it answers and I was curious to talk with you and
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>Let me know if you have interest and time to chat,
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>X-Virus-Scanned: amavisd-new at neo-proxy-2.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -1.853
>X-Spam-Level:
>X-Spam-Status: No, score=-1.853 tagged_above=-10 required=5 tests=[AWL=0.745,
>	BAYES_00=-2.599, FUZZY_VLIUM=0.001]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Illumina data analysis
>Date: Fri, 27 Feb 2009 15:01:26 -0800
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Illumina data analysis
>Thread-Index: AcmZLEiBAex/eVwZSY+u3bCzpIjLCAAAaqiA
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>Next Friday is a good day to chat. The morning is easier - anytime
>after 10:00 your time would work well.
>
>Below is short summary of a recent assembly from the 11208_GAII run -
>this is sequence number 1 extracted for the AAC tag. I'm just listing
>the chromosome fragments below as the scaffold list appears to be not as
>interesting. I pulled 403 high quality SNPs from this assembly.
>
>Look forward to chatting.
>
>John
>=======================================
>
>	Count	Average length
>Reads	703,399	27
>Matched	635,643	27
>Not matched	67,756	27
>References	230	3,103,018
>=======================================
>Reference	Length	# Matches	# Forward Matches	#
>Reversed Matches	# Paired-end Matches	Min coverage	Max
>coverage
>chr_1	73,840,631	108,262	52,737	55,525	0	0	385
>chr_2	77,932,606	78,044	39,843	38,201	0	0	344
>chr_3	74,441,160	88,963	45,159	43,804	0	0	329
>chr_4	68,034,345	73,469	34,185	39,284	0	0	1,726
>chr_5	62,352,331	39,393	21,099	18,294	0	0	306
>chr_6	62,208,784	51,852	26,925	24,927	0	0	277
>chr_7	64,342,021	44,115	20,662	23,453	0	0	290
>chr_8	55,460,251	35,225	18,590	16,635	0	0	320
>chr_9	59,635,592	48,717	24,929	23,788	0	0	342
>chr_10	60,981,646	57,635	26,502	31,133	0	0	281
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Friday, February 27, 2009 2:38 PM
>To: John Bouck
>Subject: Re: Illumina data analysis
>
>John
>
>Yes I certainly would be interested in your analysis. I am kind of
>tied up with things most of next week but would l kely have time next
>Friday, March 6th. Would that work for you?
>
>Thanks
>Trish

>
>
>
>At 04:22 PM 2/27/2009, you wrote:
> >Patricia,
> >
> >I hope all is well there in Texas.
> >I was reminded recently that you had provided us some data from some
> >experiments you had run on your Illumina sequencing machine. We
> >have been trying a couple of software packages including one from a
> >company called CLC and I took the opportunity to examine some of the
> >data you shared. I've done an assembly against the sorghum genome
> >and identified some SNPs. As always, a little analysis raises more
> >questions than it answers and I was curious to talk with you and
> >share experiences.
> >
> >Let me know if you have interest and time to chat,
> >John
> >
> >==========
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> >
>
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X-Virus-Scanned: amavisd-new at
X-Spam-Flag: NO
X-Spam-Score: 0
X-Spam-Level:
X-Spam-Status: No, score=x tagged_above=-10 required=15 tests=[]
Subject: Map visualization
Date: Thu, 27 Mar 2008 08:45:32 -0700
X-MS-Has-Attach: yes
X-MS-TNEF-Correlator:
Thread-Topic: Map visualization
Thread-Index: AciQIZcJ1MV4o0xGQwqBz+hcVfvq9g==
From: "John Bouck" <jbouck@ceres-inc.com>
To: "Patricia Klein" <pklein@tamu.edu>,
"John Mullet" <jmullet@tamu.edu>
Cc: "Timothy Swaller" <tswaller@ceres-inc.com>,
"Walter Nelson" <wnelson@ceres-inc.com>
X-Virus-Scanned: amavisd-new at tamu.edu

Patricia, John,

Thanks for sending the sequences from Solexa, we're taking a look to see how we can represent these - hope to be able to show something to talk about in a week or two.

Below are two screen grabs from an application which shows chromosome relationships. We're finding this a convenient way to see gross relationships and then zoom into the gene level. If you look closely one can make out a track that we've put in, I don't recall what this represents but conceptually it could represent anything from marker presence to expression level.

Hope this helps give an idea of what we're thinking will be useful - it likely requires an explanation so feel free to call or we can discuss at our next opportunity.

John

==========<?xml:namespace prefix = o ns = "urn:schemas-microsoft-com:office:office" />

<?xml:namespace prefix = st1 ns = "urn:schemas-microsoft-com:office:smarttags" />John Bouck, Ph.D.

Director of Information Technology

Ceres, Inc.

1535 Rancho Conejo Blvd

Thousand Oaks, CA 91320

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==========

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>X-Virus-Scanned: amavisd-new at neo-proxy-3.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.599
>X-Spam-Level:
>X-Spam-Status: No, score=-2.599 tagged_above=-10 required=5
> tests=[BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: from auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: SNP file for R07007 vs R07020
>Date: Tue, 30 Jun 2009 08:26:46 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: SNP file for R07007 vs R07020
>Thread-Index: Acn5jXbsa0vgh+LRRsK3AaUhWmbBrwACMqkg
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>Great, thanks Trish - I'll dig into it.
>
>Yes there was only one file that you had sent previously. Is it the
>newer base caller from Illumina that has this skewing problem? Did it
>exist in the older base caller?
>
>Thanks again, look forward to sharing notes and observations,
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Tuesday, June 30, 2009 7:17 AM
>To: John Bouck
>Subject: RE: SNP file for R07007 vs R07020
>
>John
>
>I put a new file on the ftp site this morning. It is called
>Rio_s3_NgoMIV_37bp_seqs.txt. It is the original Rio sequences
>without the 4bp ID trimmed from the 5' end. For these sequences we
>had to start using N's in the ID tags so that we would get an equal
>distribution of A,C,G and T at the first 2 base positions in the
>sequence as skewed base distribution at positions 1 and 2 within a
>sequence can cause base calling issues with the Illumina
>software. Therefore, in this file the 'good' Rio sequences should
>begin with either NNTCCCGGC (ID tag 1 followed by the partial NgoMIV
>site) or NNGACCGGC (ID tag 2 followed by the partial NgoMIV
>site). Let me know if you have an additional questions.
>
>Thanks
>Trish
>
>
>
>At 07:37 PM 6/29/2009, you wrote:
> >Trish,
> >
> >How's the heat? Our guys in CS are just constantly griping about it -
> >are they just wimps?
> >
> >Hey, I'm having a hard time with the seqs you up-loaded, looking at the
> >reads they seem to have the same name. Attached is an example - the
> >first two are the old format you had sent and the bottom two are the
> >newer format. Not having a unique ID for the seqs is causing me
> >problems - do you have a set with alternative naming? I can make
> >something up but this will surely cause some problems later...
> >

> >Input welcomed,
> >John
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Friday, June 19, 2009 11:42 AM
> >To: John Bouck
> >Subject: RE: SNP file for R07007 vs R07020
> >
> >Okay I just started transferring a Rio sequence/quality file to
> >you. This was treated the same way as the R07007 and R07020 DNA (ie
> >digested with NgoMIV, adapters added and sequence obtained from the
> >NgoMIV partial site remaining [CCGGC]. I have already removed the ID
> >tag from the 5'end of these sequences so there is just a 33bp
> >sequence tag remaining.
> >
> >Trish
> >
> >
> >
> >At 01:28 PM 6/19/2009, you wrote:
> > >Remaining information needed: T3x8$AM
> > >
> > >John
> > >
> > >-----Original Message-----
> > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > >Sent: Friday, June 19, 2009 11:23 AM
> > >To: John Bouck
> > >Subject: RE: SNP file for R07007 vs R07020
> > >
> > >John
> > >
> > >You are going to have to remind what the address of the FTP site
> > >is. I can't seem to remember and can't find any documentation. I
> > >may need to call you for a password. I am in now if you want to call
> > >me with the information.
> > >
> > >Trish
> > >
> > >
> > >
> > >At 01:10 PM 6/19/2009, you wrote:
> > > >Great,
> > > >
> > > >If you can drop the sequence with quality scores onto the FTP site
> >we
> > > >set up earlier that would be easiest.
> > > >
> > > >Look forward to talking next week.
> > > >
> > > >John
> > > >
> > > >-----Original Message-----
> > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > >Sent: Friday, June 19, 2009 11:03 AM
> > > >To: John Bouck
> > > >Subject: RE: SNP file for R07007 vs R07020
> > > >
> > > >John
> > > >
> > > >Yes I can share the Rio data. What would you like and how would
> >you
> > > >like to get it. I can give you the sequence file with the quality
> > > >scores if that is how you want it. I don't know if it would be too
> > > >big to send in an email or not.
> > > >
> > > >I did talk with John about the sweet sorghum project and this is
> >what
> > > >he told me. All of the money for the sweet sorghum program that

>was
> > > >added into the Ceres project goes to Bill for breeding work. Thus
>no
> > > >money was allocated for marker work and therefore, he doesn't have
> > > >plans to do any sweet sorghum genotyping. If we want to discuss
>this
> > > >at a quarterly meeting with Bill, Jeff, and the rest of us, that
> > > >would be fine, but for now that is how the project is written and
>the
> > > >budget allocated.
> > > >
> > > >Thanks
> > > >Trish
> > > >
> > > >
> > > >
> > > >At 07:39 PM 6/18/2009, you wrote:
> > > > >You've done rio? Is that data you can share?
> > > > >
> > > > >John
> > > > >
> > > > >-----Original Message-----
> > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > >Sent: Thursday, June 18, 2009 2:30 PM
> > > > >To: John Bouck
> > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > >
> > > > >John
> > > > >
> > > > >Haven't done any thus far except Rio. I think the plan at first
> >was
> > > > >to get some of the Ceres PS lines done as well as mapping
> >population
> > > > >parents. Sweets would likely come after these.
> > > > >
> > > > >Trish
> > > > >
> > > > >
> > > > >At 04:24 PM 6/18/2009, you wrote:
> > > > > >Sounds like a good idea let me know when you have analyzed what
> >you
> > > > > >want. Are you guys doing any sweets? I'm curious to see the
> > > >variation
> > > > > >between sweet and non-sweets.
> > > > > >
> > > > > >John
> > > > > >
> > > > > >-----Original Message-----
> > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > >Sent: Thursday, June 18, 2009 8:31 AM
> > > > > >To: John Bouck
> > > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > > >
> > > > > >John
> > > > > >
> > > > > >As far as I can tell that should work for me. No worries about
> >teh
> > > > > >rescheduling. I too am busy so I totally understand. I may
>even
> > > > > >have additional PS genotypes analyzed by then. We finished a
>run
> > > > > >this week that contained an additional 8 PS lines (R07008,
> >R07012,
> > > > > >R07108, R07030, R07034, R07042, R07045 and R07045) in addition
>to
> > >the
> > > > > >anthracnose mapping parents. I am trying to get that data
> >through
> > > > > >the analysis pipeline so I can see how these lines compare to
>the

> > > > > >R07007 and R07020. Perhaps we should have the call once I have
> > >that
> > > > > >data analyzed which should be sometime next week? Just let me
> >know
> > > > > >your thoughts on this.
> > > > > >
> > > > > >Thanks
> > > > > >Trish
> > > > > >
> > > > > >At 10:17 AM 6/18/2009, you wrote:
> > > > > > >Trish - I'm really sorry to do this again but my schedule is
> > >being
> > > > > >taken
> > > > > > >over by others and I have yet another last minute conflict.
> > > > > > >
> > > > > > >Maybe we should shoot for Monday afternoon at 3:00 your time
>-
> > > >things
> > > > > > >should quiet down next week.
> > > > > > >
> > > > > > >Best,
> > > > > > >John
> > > > > > >
> > > > > > >-----Original Message-----
> > > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > > >Sent: Wednesday, June 17, 2009 8:22 AM
> > > > > > >To: John Bouck
> > > > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > > > >
> > > > > > >John
> > > > > > >
> > > > > > >That time tomorrow should work just fine.
> > > > > > >
> > > > > > >Thanks
> > > > > > >Trish
> > > > > > >
> > > > > > >
> > > > > > >
> > > > > > >At 10:10 AM 6/17/2009, you wrote:
> > > > > > > >Trish,
> > > > > > >
> > > > > > > >I have an external meeting that is now planned for the same
> > >time
> > > > >as
> > > > > >our
> > > > > > > >meeting later today. Can we move our discussion to
>tomorrow
> >at
> > > > >3:00
> > > > > > > >your time?
> > > > > > >
> > > > > > > >Sorry for the late notice,
> > > > > > > >John
> > > > > > >
> > > > > > > >-----Original Message-----
> > > > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > > > >Sent: Tuesday, June 09, 2009 1:53 PM
> > > > > > > >To: John Bouck
> > > > > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > > > > >
> > > > > > > >Sounds good, I will put that time on my calendar and be
> >waiting
> > > >for
> > > > > > >your
> > > > > > > >call.
> > > > > > > >
> > > > > > > >Trish
> > > > > > > >
> > > > > > > >
> > > > > > > >At 03:47 PM 6/9/2009, you wrote:

> > > > > > > > > >Great - how about Wednesday at 4:00 your time?
> > > > > > > > > >
> > > > > > > > > >John
> > > > > > > > > >
> > > > > > > > > >-----Original Message-----
> > > > > > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > > > > > >Sent: Tuesday, June 09, 2009 1:46 PM
> > > > > > > > > >To: John Bouck
> > > > > > > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > > > > > > >
> > > > > > > > > >John
> > > > > > > > > >
> > > > > > > > > >I will be around next week as of now so whenever you want
> >to
> > > > >talk
> > > > > > > > > >just give me a heads up on day/time.
> > > > > > > > > >
> > > > > > > > > >Trish
> > > > > > > > > >
> > > > > > > > > >
> > > > > > > > > >
> > > > > > > > > >At 03:44 PM 6/9/2009, you wrote:
> > > > > > > > > > >Hi Trish,
> > > > > > > > > >
> > > > > > > > > >We've started getting our heads around this - would be
> >fun
> > > > >to
> > > > > > > > > >discuss,
> > > > > > > > > > >unfortunately I'm traveling for the next several days.
> >Are
> > > > >you
> > > > > > > > > >free
> > > > > > > > > > >next Wednesday or Thursday?
> > > > > > > > > >
> > > > > > > > > > >John
> > > > > > > > > >
> > > > > > > > > > >-----Original Message-----
> > > > > > > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > > > > > > >Sent: Wednesday, May 20, 2009 9:27 AM
> > > > > > > > > > >To: John Bouck
> > > > > > > > > > >Subject: SNP file for R07007 vs R07020
> > > > > > > > > >
> > > > > > > > > > >John
> > > > > > > > > >
> > > > > > > > > > >I uploaded a file with the name
> > > > > > > > > > >R07007_R07020_SNP.final.pairwised.unique.052009.xls.
> >This
> > > > >is
> > > > > > > > > >an
> > > > > > > > > > >excel file of ~5000 potential SNPs/INDELs found between
> > > > >R07007
> > > > > > > > > >and
> > > > > > > > > > >R07020. I highlighted in yellow some potential markers
> > > > >that
> > > > > > > > > >are
> > > > > > > > > >also
> > > > > > > > > > >present in some of the other 11 genotypes examined and
> >thus
> > > > >I
> > > > > > > > > >would
> > > > > > > > > > >consider to be of high quality "real" polymorphisms.
>In
> > > > >pink
> > > > > > > > > >are
> > > > > > > > > > >markers where the polymorphism was found only between
> > > > >R07007
> > > > > > > > > >and
> > > > > > > > > > >R07020 and thus I wouldn't have as much confidence that
> > > > >these
> > > > > > > > > >are

> > > > > > > > > >"real" polymorphisms. I did this for some markers on
> >chr.
> > >1
> > > > > >only.
> > > > > > >I
> > > > > > > > > >hope this gives you enough information to design some
> > >Taqman
> > > > > >assays
> > > > > > > > > >to test. If you need additional info please let me
>know.
> > > >Let
> > > > >me
> > > > > > > > > >know how it all turns out.
> > > > > > > > > >
> > > > > > > > > >Thanks
> > > > > > > > > >Trish
> > > > > > > > > >
> > > > > > > > > >
> > > > > > > > > >
> > > > > > > > > >
> > > > > > > > > >
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> > > > > > > > > >
> > > > > > > > > >
> > > > > > > > > >Dr. Patricia Klein
> > > > > > > > > >Associate Professor
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>X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.366
>X-Spam-Level:
>X-Spam-Status: No, score=-2.366 tagged_above=-10 required=5 tests=[AWL=0.233,
>	BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: domain auto-whitelisted by SQLgrey-1.7.6
>Subject: RE: Quick question about RNA-seq
>Date: Mon, 30 Mar 2009 13:17:33 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Quick question about RNA-seq
>Thread-Index: AcmxbQdLomDuSN16RK+QsxZJs0lmsAAABoqg
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>Hi Trish,
>
>Sure, my favorite was the CLC bio genomics workbench. This is a
>commercial tool but there is a free month-long demo version that they
>could try out. This was handy because the parameters for searching for
>SNPs were more accessible. If they want to share a few files I'd be
>happy to do a quick analysis and send assembly info or SNPs. We've also
>downloaded but not yet used significantly the velvet program which is a
>free tool for de novo assembly - from the Sanger center I believe. They
>also have a snp discovery tool - although from the demo the other day it
>seemed to have a high number of false positives.
>
>I also had good experience assembling one monocot against another - I
>don't know off hand if there are closely related species to Rose that
>have been sequenced (dicot I believe). Would be worth a try though
>because I was able to assemble twice as much against a genome as de
>novo.
>
>Even without the genome we ended up with a megabase of cDNA sequence
>from one experiment and many SNPs. Changed our position instantly from
>sequence poor to plenty to work with for genotyping.
>
>Expression information was easy to extract from these experiments as
>well - simple matter of counting reads.
>
>Hope this is helpful info - happy to talk directly if that helps,
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Monday, March 30, 2009 12:21 PM
>To: John Bouck
>Subject: Quick question about RNA-seq
>
>John
>
>When you guys did the small RNA-seq test run on your 'unsequenced'
>genome, what program did you use for assembly of the short
>sequences? I have a colleague who wants to try this method on rose
>and there is no genome sequence for rose. Since I believe that you
>indicated that your group had success assembling contigs representing
>the gene transcripts I was hoping you could share some ideas on the
>assembly process.
>
>Thanks
>Trish
>

>
>
>
>
>
>
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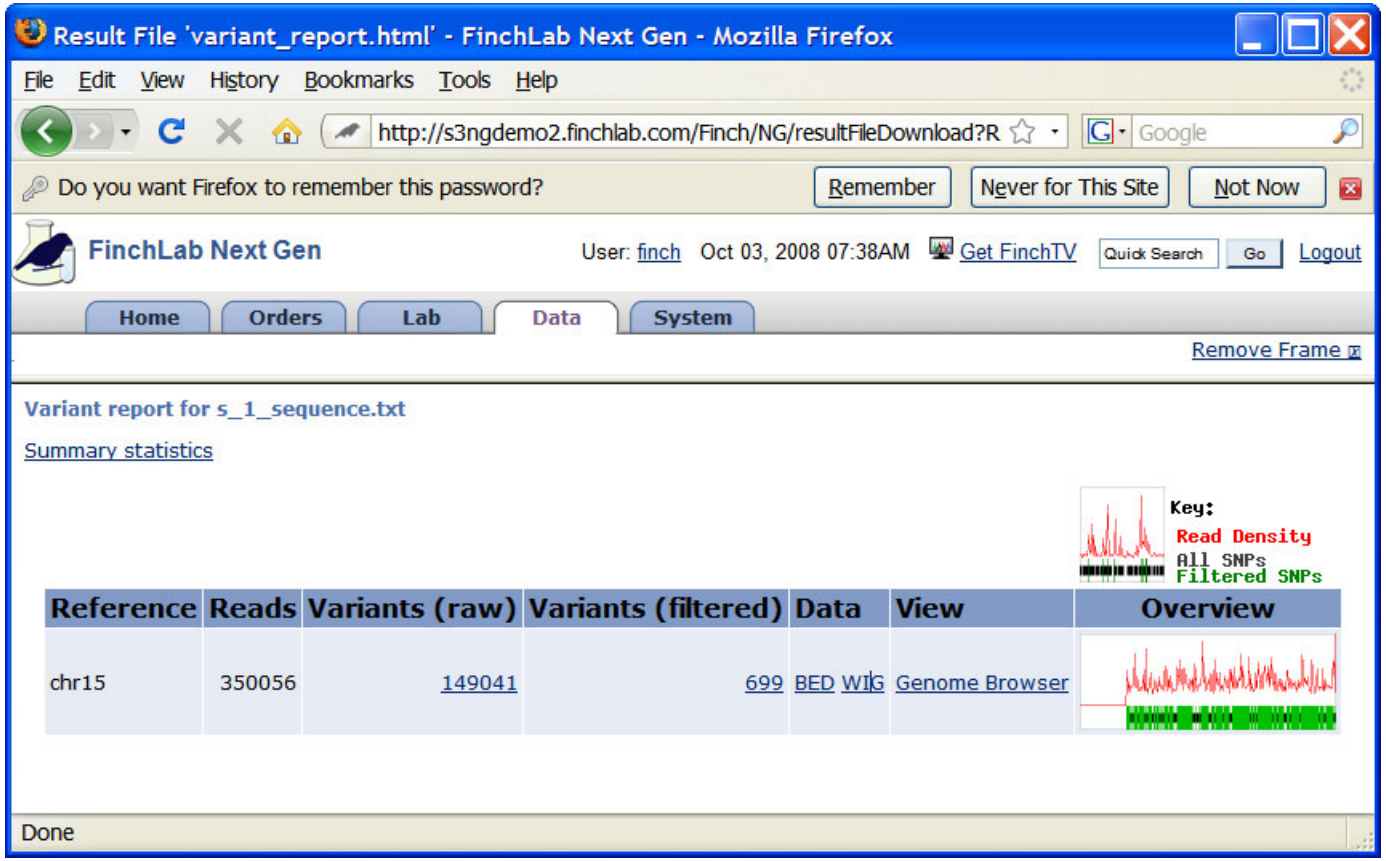
Results: From Instrument

Results from Illumina GA instrument without analysis pipeline:

```
>HWI-EAB661_3_Day2_8_1_879_236
GTAGGTTTTCTGCTTAGGAGTTTAA
>HWI-EAB661_3_Day2_8_1_601_362
GCAGTCCAAATGTTTTTGAGATGGC
>HWI-EAB661_3_Day2_8_1_897_362
GATGAGTATAATTACCCCAAAAAGA
>HWI-EAB661_3_Day2_8_1_881_223
GGACTGGTTTAGATATGAGTCACAT
>HWI-EAB661_3_Day2_8_1_555_244
GTCTACTGCTCGCGTTGCGTCTATT
>HWI-EAB661_3_Day2_8_1_550_234
GAGCTTAATAGAGGCCAAAGCGGTC
>HWI-EAB661_3_Day2_8_1_514_233
GCAGAAGAAAACGTGCGTCAAAAAT
>HWI-EAB661_3_Day2_8_1_606_240
GAATGTTTATAGGTCTGTTGAACAC
>HWI-EAB661_3_Day2_8_1_622_342
GATATGTATGTTGACGGCCATAAGG
>HWI-EAB661_3_Day2_8_1_888_233
GAGACAAATAATCTCTTTAATAACC
>HWI-EAB661_3_Day2_8_1_557_342
GTTCCAAGTATCGGCAACAGCTTTA
>HWI-EAB661_3_Day2_8_1_907_368
GTTATAGATATTCAAATAACCCTGA
>HWI-EAB661_3_Day2_8_1_882_549
GCATGGGTGATGCTGGTATTAAATC
>HWI-EAB661_3_Day2_8_1_888_323
GTTTTCTTCATTGCATTCAGATGGA
>HWI-EAB661_3_Day2_8_1_565_223
GATTTGGAGGCATGAAAACATACAA
>HWI-EAB661_3_Day2_8_1_589_351
GTCCGATGCTGTTCAACCACTAATA
>HWI-EAB661_3_Day2_8_1_243_645
GATGTTTTCCGTTCTGGTGTTTCGT
>HWI-EAB661_3_Day2_8_1_607_356
GTCACAGGTTGCGCCGCCAAAACGT
>HWI-EAB661_3_Day2_8_1_911_362
```

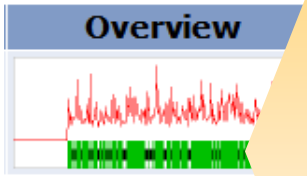

geospiza

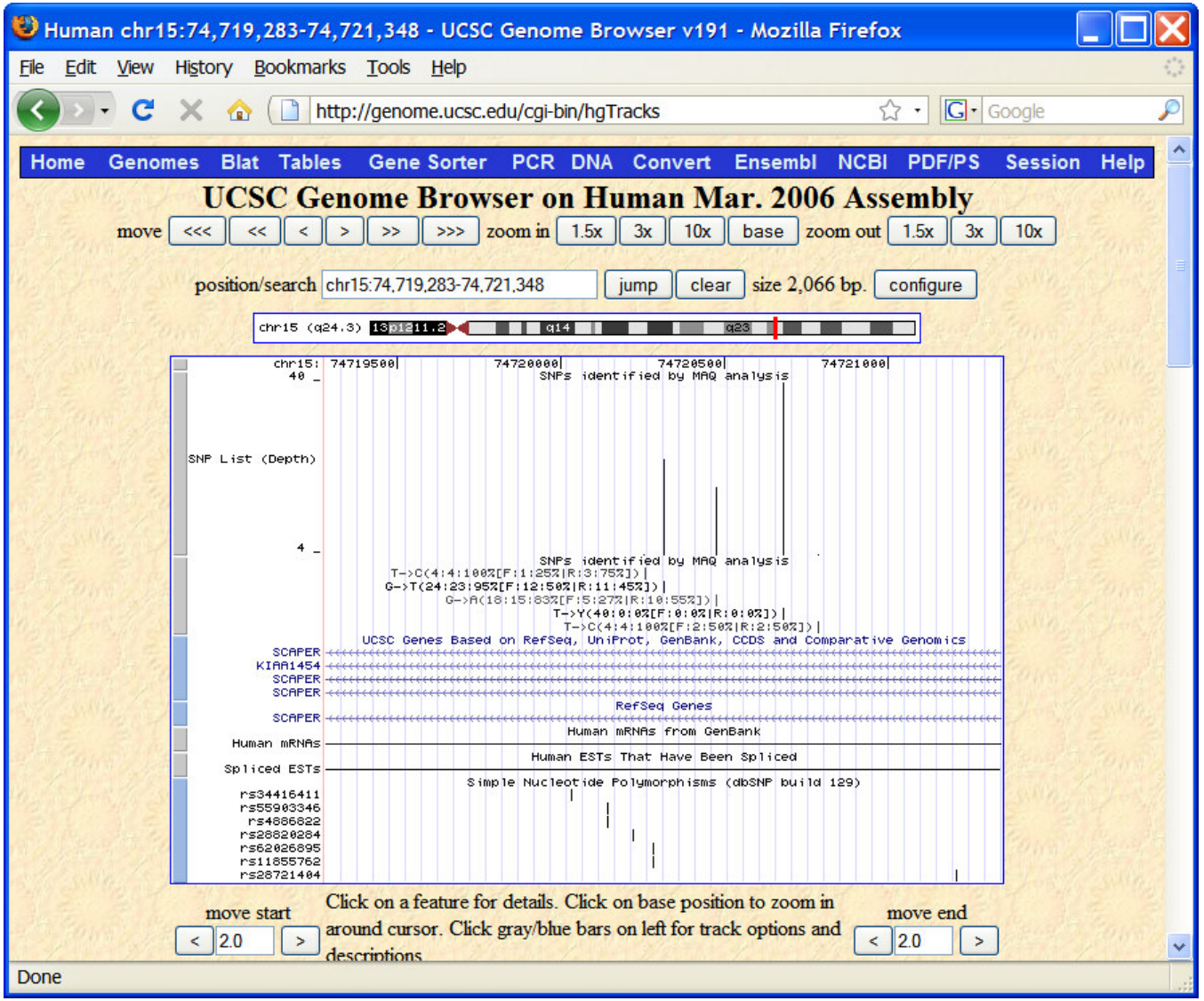
Results: Resequencing Pipeline



geospiza

Results: Resequencing Pipeline





geospiza

>X-Virus-Scanned: amavisd-new at neo-proxy-2.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -2.599
>X-Spam-Level:
>X-Spam-Status: No, score=-2.599 tagged_above=-10 required=5
> tests=[BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: delayed 00:12:04 by SQLgrey-1.7.6
>Subject: RE: Question about GGT
>Date: Wed, 8 Jul 2009 15:56:34 -0700
>X-MS-Has-Attach:
>X-MS-TNEF-Correlator:
>Thread-Topic: Question about GGT
>Thread-Index: AcoAHPXLyUI/7QdrQyKdPNz/inxr8AAAVsxg
>From: "Xuefeng Ma" <xma@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>Hi, I am glad to help
>YES. GGT can handle heterozygous.
>For general marker analyses, including diversity, linkage
>disequilibrium, etc. it should not have any problem.
>The only thing you need to pay attention is when you run marker-trait
>association. In this case, proper value should be set in order to get a
>meaningful result when considering dominant or co-dominant cases.
>
>FYI, I will be off in China about 6 weeks since tomorrow. I am glad to
>catch any more questions if you have by tomorrow morning.
>
>Regards,
>
>Xuefeng
>
>
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Wednesday, July 08, 2009 3:39 PM
>To: Xuefeng Ma
>Subject: RE: Question about GGT
>
>Xuefeng
>
>Sorry to bother you with this but I have a question about using GGT
>for looking at the marker data for my diverse sorghum genotypes. Can
>GGT handle markers that are heterozygous? It doesn't look l ke it
>can but I just wanted to make sure that I wasn't missing
>something. I appreciate your help.
>
>Patricia
>
>
>
>At 01:23 PM 5/21/2009, you wrote:
> >I do not have any problems.
> >You can build the file either through the file Builder or format and
> >copy from excel. If you use file builder, a map file and a loc file are
> >needed. If you format in excel, it is very easy to copy in, but you do
> >not have the flexibility to sort markers.
> >
> >No limitations for the numbers of plants and markers to load IN, but
> >there is a column restriction if you download OUT as excel (you will
> >lose any data beyond 256 column, because the build-in excel is still
>the
> >2003 version). However, you can get around it by exporting through txt

> >file.
> >
> >Xuefeng
> >
> >
> >-----Original Message-----
> >From: John Bouck
> >Sent: Thursday, May 21, 2009 11:11 AM
> >To: Xuefeng Ma
> >Subject: FW: Question about GGT
> >
> >Is this performance problem what you would expect?
> >
> >John
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Thursday, May 21, 2009 9:46 AM
> >To: John Bouck
> >Subject: RE: Question about GGT
> >
> >John,
> >
> >I now have gotten it to work. I didn't realize that I did not need
> >to include any information on the population type. When I have that
> >field blank in my imported excel file, it appears to load the data
> >without a problem. The only issue I am now having is with the size
> >of the data set that it will work with. I have pared the data down
> >by chromosome and then have only tried to load markers that are at
> >least 100Kbp apart. For chr. 1 that leaves me with 137 markers over
> >the 13 individuals. Even this amount of data seems to be giving my
> >computer problems. Perhaps I am just not being patient enough (the
> >GGT screen has a "busy drawing, please wait ..." message). Do you
> >know how many markers Xuefeng has tried to use when drawing
> >chromosomes in GGT? Not sure if it is my computer or the program at
> >this point.
> >
> >Thanks
> >Trish
> >
> >
> >
> >At 10:41 AM 5/21/2009, you wrote:
> > >Yes this should work. Xuefeng does this for looking at diversity
> > >analysis - certainly most of the powerful tools in GGT for data
> >analysis
> > >are around pedigrees and population analysis so it is not surprising
> > >that it is a focus of the documentation.
> > >
> > >Are you able to get the data in?
> > >If it is something you can share we could take a look.
> > >
> > >John
> > >
> > >-----Original Message-----
> > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > >Sent: Thursday, May 21, 2009 8:25 AM
> > >To: John Bouck
> > >Subject: Question about GGT
> > >
> > >John,
> > >
> > >I have a quick question about graphical genotyping. I have installed
> > >GGT32 on my windows machine and have read over the manual. As I read
> > >over it, it sounds as if I need my individuals to come from some type
> > >of population. However, we are working with diverse genotypes and
> > >not individuals from a population. Do you know if GGT will work for
> > >this? I have my markers across 13 different genotypes and would like
> > >to graphically display this data but don't quite see how GGT will do
> > >that as I don't have a population type to enter. I don't see this

> > >mentioned in the manual. Any comments/suggestions would be
> >appreciated.
> > >
> > >Thanks
> > >Trish
> > >
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> > >
> > >
> > >
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> >
> >Dr. Patricia Klein
> >Associate Professor
> >Institute for Plant Genomics and Biotechnology
> >TAMU 2123
> >Texas AgriLIFE Research
> >Texas A&M University
> >College Station, TX 77843-2123
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> >phone: 979-862-6308
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>X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
>X-Spam-Flag: NO
>X-Spam-Score: -1.999
>X-Spam-Level:
>X-Spam-Status: No, score=-1.999 tagged_above=-10 required=5 tests=[AWL=0.500,
>	BAYES_00=-2.599, RDNS_NONE=0.1]
>X-HAT: SG SUSPECTLIST_NO_SBRS, P $THROTTLED_NO_SBRS, L tamu-relay
>X-SRBS: None
>X-EXTLoop1: 1
>X-IronPort-AV: E=Sophos;i="4.44,506,1249275600";
>   d="pdf'?mpp'32?scan'32,208,32";a="32916625"
>Subject: RE: sweet sorghum genotyping
>Date: Mon, 5 Oct 2009 08:02:36 -0700
>X-MS-Has-Attach: yes
>X-MS-TNEF-Correlator:
>Thread-Topic: sweet sorghum genotyping
>Thread-Index: Aco9Tpu1SQ5fin5hTdiNOR7TNS3K2gIfRNfw
>From: "Timothy Swaller" <tswaller@ceres.net>
>To: "John Mullet" <jmullet@tamu.edu>,
>	"Patricia Klein" <pklein@tamu.edu>
>Cc: "Walter Nelson" <wnelson@ceres.net>,
>	"Jeff Gwyn" <jgwyn@ceres-inc.com>
>
>Hi John and Patricia.
>I believe Walter may have discussed a need I have to fill out a more
>formal tracking and progress update. I have prepared a template of the
>current projects taken from the agreement as a starting point, but I was
>hoping to build on this by modifying and revising based on your
>knowledge of what has been done and agreed on to date. Please look this
>over. (I apologize for the redundancy, since I believe you had done a
>similar exercise with John Bouck as well)
>What is your opinions on the best path forward to fill this out, there
>are several possibilities? Conference call with video, I could take a
>trip to TX, etc.
>I will also be attending the IPMB in St. Louis from the 25-30, so if
>either of you are attending, this may be an opportunity to sit down and
>walk through this or just have dinner and talk.
>
>Thanks
>Tim
>
>included in .pdf and .mpp
>
>
>-----Original Message-----
>From: John Mullet [mailto:jmullet@tamu.edu]
>Sent: Thursday, September 24, 2009 12:38 PM
>To: Walter Nelson; Timothy Swaller
>Cc: Bill Rooney; Jeff Gwyn; Richard Flavell
>Subject: sweet sorghum genotyping
>
>Walter and Tim,
>
>I needed to fill up the next Illumina genotyping run so to get us
>started on sweet sorghums, I included the following materials that we
>already had DNA for (mainly early introductions into the U.S.).
>
>Chinese Amber
>Orange
>Sourless
>Honey
>Sumac
>Gooseneck

>Collier
>Keller
>Della
>
>Once you decide on the additional sweet sorghum materials of interest,
>we will get DNA isolated and put them on a subsequent run.
>
>Thanks,
>
>John
>
>

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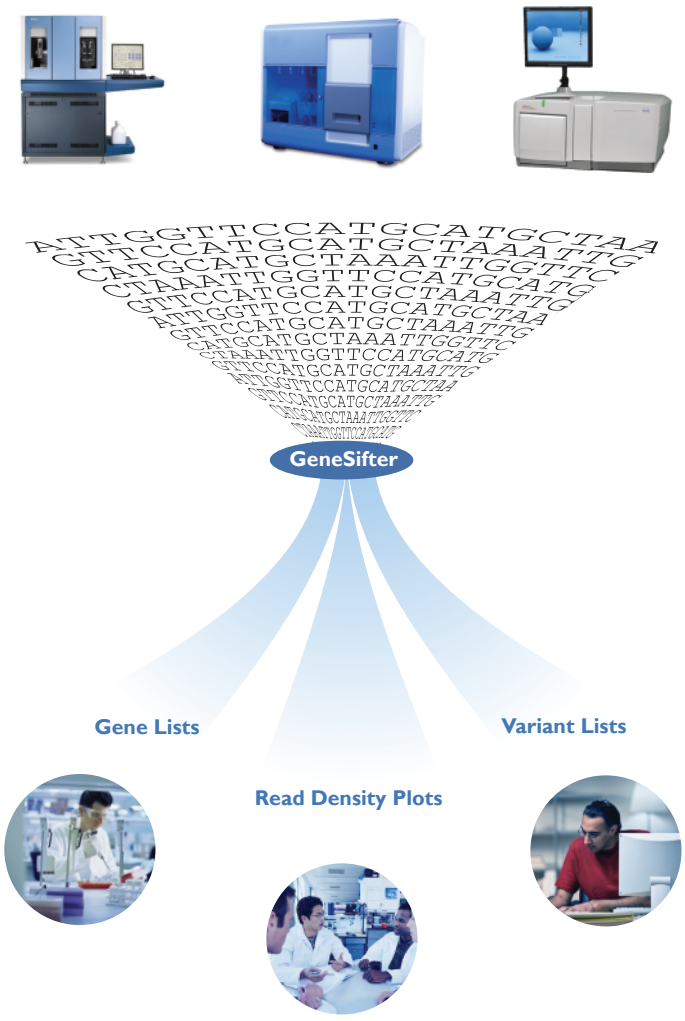
Geospiza GeneSifter™ Data Analysis: Transforming Data into Information

Geospiza takes raw data from any sequencing platform and transforms it into usable information based on your application. You can then access your information through an intuitive web interface anytime, anywhere or download it into a universal file format for further analysis.

Selected Applications

- *RNA Seq*
- *Tag Profiling*
- *ChIP-Seq*
- *Variant Analysis*
- *Digital Gene Expression*
- *Small RNA Analysis*
- *Methylation Analysis*
- *Resequencing*
- *Mutation Discovery*
- *De novo assembly*



Get Your Results When, Where and How You Want Them

geospiza™
FROM SAMPLE TO RESULTS™

Complete Data Workflow Management with Unparalleled Ease-of-Use

Verifiable Results

Geospiza provides a clear line of sight through every stage of sample preparation, sample processing and data delivery - continuing through every phase of data analysis to give you and your team verifiable confidence in your results.

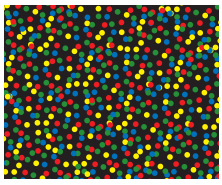
Geospiza and the Three Phases of Data Analysis

Next Gen data workflows involve three distinct phases of work:

1. Primary data analysis involves converting image data to sequence data.
2. This step involves aligning the sequences from the primary data analyses to reference data.
3. Summaries of the alignment information from multiple samples may be compared to produce scientific understanding.

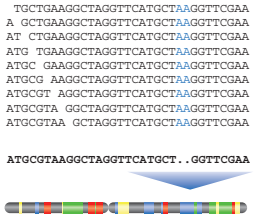
Each phase has a discrete analytical process and we call these phases primary data analysis, secondary data analysis and tertiary data analysis.

Geospiza offers the only product that manages the entire data workflow by consolidating raw data from every Next Generation Sequencing Platform, through secondary data analysis to provide gene lists, read density plots, variant lists or universal file formats in support of custom tertiary data analysis.



Instrument: Primary Data Analysis

Primary data analysis involves converting image data to sequence data. The sequence data can be in familiar "ACTG" sequence space or less familiar color space (SOLiD) or flow space (454). Primary data analysis is commonly performed by software provided by the data collection instrument vendor and it is the first place where quality assessment about a sequencing run takes place.



Application: Secondary Data Analysis

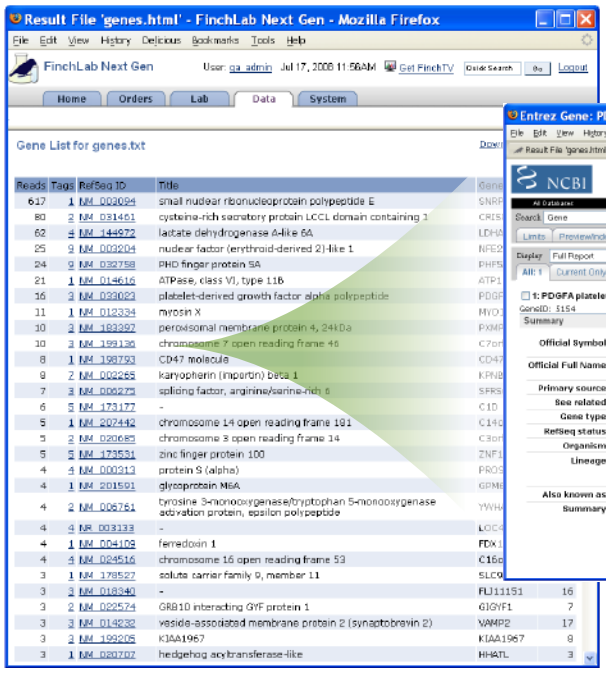
Secondary data analysis creates the data sets that will be further used to develop scientific information. This step involves aligning the sequences from the primary data analyses to reference data. Reference data can be complete genomes, subsets of genomic data like expressed genes, or individual chromosomes. Reference data are chosen in an application specific manner and sometimes multiple reference data sets will be used in an iterative fashion.

This is where Geospiza excels. We provide an easy-to-use interface for all common secondary analysis applications. Secondary analysis is critical because it allows you to look at data from each sample in a biological context as well as translating it into common formats such as BED and WIG.

Experiment: Tertiary Data Analysis

Tertiary data analysis represents the third phase of the Next Gen workflow. This phase may involve a simple activity like viewing a data set in a tool like a genome browser so that the frequency of tags can be used to identify promoter sites, patterns of variation, or structural differences. In other experiments, like digital gene expression, tertiary analysis can involve comparing different data sets in a similar fashion to microarray experiments.

Data Analysis with Best-of-Breed Algorithms for any Application



Gene list from RNA-Seq highlight gene expression levels

Navigate from your gene list to detailed reference information in a single click

From Data to Information

To help you get the information you need, we turn raw data into meaningful information such as gene lists, read depth, WIG files, SNPs and BED files. The GeneSifter analysis pipeline integrates state of the art alignment algorithms like MAQ and Mapreads, and converts files into more understandable formats.

These more understandable formats mean that instead of searching through millions of data, you can find out which are the most expressed genes in your RNA library. Then, you can intuitively link out to annotation or drill down to find out more specific data for a particular gene. For example, with ChIP-Seq a summary of graphical chromosome overviews allows you to visually identify regions of interest.

GeneSifter not only takes the raw data and transforms it into processed application data, but also summarizes the data to highlight the most interesting and important information for you.

Open Platform Supports Community Standards

To help you get the information you need, Geospiza makes use of best of breed tools available. We provide built-in links to the NCBI database and the UCSC Genome Browser. As part of this extensible framework, you can export data at other convenient points within the application for further or custom analysis.

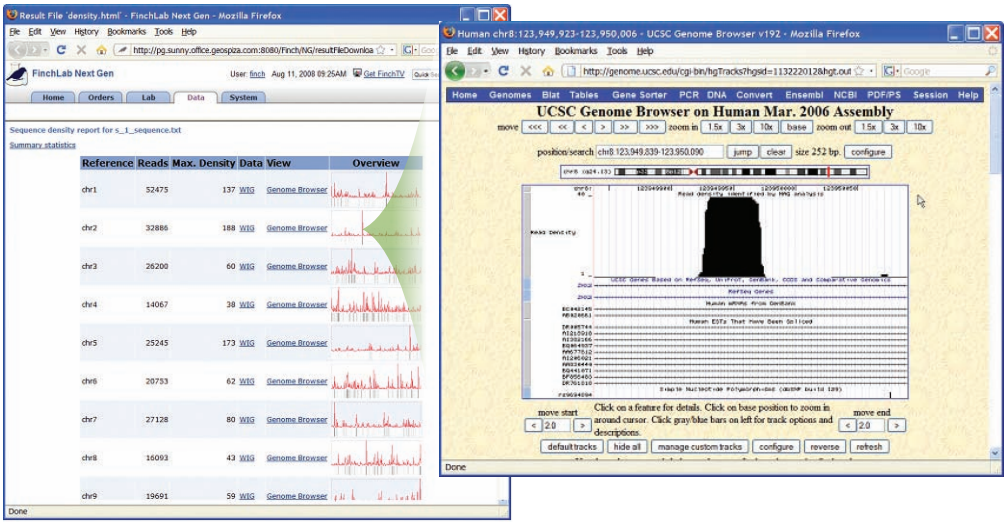
Selected Algorithms

- *Eland*
- *MAQ*
- *Mapreads*
- *Newbler*
- *SOAP*
- *Velvet*

Selected File Formats

- *WIG*
- *FASTA*
- *Chromatograms AB1*
- *CS FASTA*
- *Fragment Files*
- *SCF Chromatograms*
- *BED*
- *Gene List*
- *Other Standard Formats*

Open Platform and Rapid Development Keep You Ahead of the Curve



An Example with ChIP-seq

To perform a ChIP-seq experiment, you need to have a Next Gen sequencing instrument. You will also need to have the ability to run an alignment program and work with the resulting data to get your results. This is easier said than done. Once the alignment program runs, you might have to also run additional programs and scripts to translate raw output files to meaningful information.

If you do this yourself, you have to learn the nuances of the alignment program, how to run it different ways to create the data sets, and write the scripts to create the HTML reports, graphs, and wig files.

With GeneSifter, you can skip those steps. You get the same results by clicking a few links to sort the data, and a few more to select the files, run the pipeline, and view the summarized results. You can also click a single link to send the data to the UCSC genome browser for further exploration.

Faster Analysis

GeneSifter provides analysis services that can accelerate analysis that would take hours or days on your laptop - so that you have the results in minutes. Complex command line programs become easy with select options from pull down menus.

Stay Current with Geospiza

As new algorithms and applications become available, we quickly update GeneSifter so that you always have access to the latest tools.

GeneSifter has an innovative web-based architecture that enables rapid development and updates, which are seamlessly available to our hosted customers. We release new features and capabilities over 8 times a year. With Geospiza, you know that you will always have access to the most current technology.

Supported Platforms

Applied Biosystems:

- *Capillary Electrophoresis and SOLiD Sequencers*

Illumina:

- *Genome Analyzer*

Roche:

- *Genome Sequencer FLX™ System*

Helicos:

- *Single Molecule Sequencer*

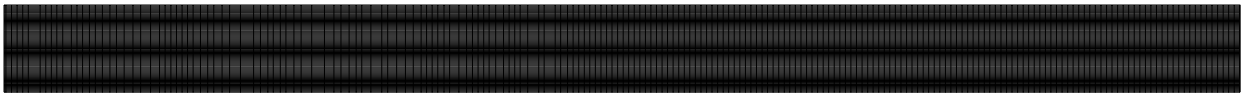
Supported Browsers

- ***Firefox***
- ***Internet Explorer***
- ***Safari***

geospiza™
FROM SAMPLE TO RESULTS™

Geospiza, Inc.
www.geospiza.com
info@geospiza.com

	Start	Finish	Duration	Work	Cost	% Complete	% Work Complete
1	Mon 9/3/07	Fri 8/31/12	1305d?	0h	$0 00	15%	0%



X-Virus-Scanned: amavisd-new at neo-proxy-3.tamu.edu
X-Spam-Flag: NO
X-Spam-Score: -1.756
X-Spam-Level:
X-Spam-Status: No, score=-1.756 tagged_above=-10 required=5 tests=[AWL=0.742,
BAYES_00=-2.599, HTML_MESSAGE=0.001, RDNS_NONE=0.1]
X-HAT: SG SUSPECTLIST_NO_SBRS, P $THROTTLED_NO_SBRS, L tamu-relay
X-SRBS: None
X-EXTLoop1: 65.218.249.200
X-IronPort-Anti-Spam-Filtered: true
X-IronPort-Anti-Spam-Result:
AtsEABINAUtB2vnI/2dsb2JhbACCJCzHO4xhgkGBewSBbYpACw
X-IronPort-AV: E=Sophos;i="4.44,751,1249275600";
d="ics'?scan'208,217";a="5865125"
Subject: GoToMeeting Invitation - Gantt Discussion
Date: Mon, 16 Nov 2009 08:32:56 -0800
X-MS-Has-Attach:
X-MS-TNEF-Correlator:
Thread-Topic: GoToMeeting Invitation - Gantt Discussion
Thread-Index: Acpm2nM8Dq/YsVtuSb2Oy89AqCSp/AAAAAMA
From: "Timothy Swaller" <tswaller@ceres.net>
To: "John Mullet" <jmullet@tamu.edu>,
"Patricia Klein" <pklein@tamu.edu>

When: Thursday, November 19, 2009 1:00 PM-2:00 PM (GMT-08:00) Pacific Time (US & Canada).

Where: N/A

Note: The GMT offset above does not reflect daylight saving time adjustments.

~~*~*~*~*~*~*~*~*~*

1. Please join my meeting.

https://www2.gotomeeting.com/join/636549115

2. Join the conference call:

ACCESS (Dial-In) NUMBERS:

8664890573 (Toll-free North America)

2053540119 (International)

MEETING NUMBER: *6389180*

Meeting ID: 636-549-115

GoToMeeting®

Online Meetings Made Easy™
Content-class: urn:content-classes:calendarmessage
Content-Type: text/calendar;
method=REQUEST;
name="meeting.ics"
Content-Transfer-Encoding: 8bit

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>X-Virus-Scanned: amavisd-new at neo-proxy-1.tamu.edu
>X-Spam-Flag: NO
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>X-Spam-Level:
>X-Spam-Status: No, score=-2.599 tagged_above=-10 required=5
> tests=[BAYES_00=-2.599]
>X-Virus-Scanned: amavisd-new at tamu.edu
>X-Greylist: delayed 00:12:05 by SQLgrey-1.7.6
>Subject: RE: SNP file for R07007 vs R07020
>Date: Mon, 29 Jun 2009 17:37:42 -0700
>X-MS-Has-Attach: yes
>X-MS-TNEF-Correlator:
>Thread-Topic: SNP file for R07007 vs R07020
>Thread-Index: AcnxDaeR6VnG9vMmRfKXDXZiKzddkwIDK6/g
>From: "John Bouck" <jbouck@ceres-inc.com>
>To: "Patricia Klein" <pklein@tamu.edu>
>
>Trish,
>
>How's the heat? Our guys in CS are just constantly griping about it -
>are they just wimps?
>
>Hey, I'm having a hard time with the seqs you up-loaded, looking at the
>reads they seem to have the same name. Attached is an example - the
>first two are the old format you had sent and the bottom two are the
>newer format. Not having a unique ID for the seqs is causing me
>problems - do you have a set with alternative naming? I can make
>something up but this will surely cause some problems later...
>
>Input welcomed,
>John
>
>-----Original Message-----
>From: Patricia Klein [mailto:pklein@tamu.edu]
>Sent: Friday, June 19, 2009 11:42 AM
>To: John Bouck
>Subject: RE: SNP file for R07007 vs R07020
>
>Okay I just started transferring a Rio sequence/quality file to
>you. This was treated the same way as the R07007 and R07020 DNA (ie
>digested with NgoMIV, adapters added and sequence obtained from the
>NgoMIV partial site remaining [CCGGC]. I have already removed the ID
>tag from the 5'end of these sequences so there is just a 33bp
>sequence tag remaining.
>
>Trish
>
>
>
>At 01:28 PM 6/19/2009, you wrote:
> >Remaining information needed: T3x8$AM
> >
> >John
> >
> >-----Original Message-----
> >From: Patricia Klein [mailto:pklein@tamu.edu]
> >Sent: Friday, June 19, 2009 11:23 AM
> >To: John Bouck
> >Subject: RE: SNP file for R07007 vs R07020
> >
> >John
> >
> >You are going to have to remind what the address of the FTP site

> >is. I can't seem to remember and can't find any documentation. I
> >may need to call you for a password. I am in now if you want to call
> >me with the information.
> >
> >Trish
> >
> >
> >
> >At 01:10 PM 6/19/2009, you wrote:
> > >Great,
> > >
> > >If you can drop the sequence with quality scores onto the FTP site we
> > >set up earlier that would be easiest.
> > >
> > >Look forward to talking next week.
> > >
> > >John
> > >
> > >-----Original Message-----
> > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > >Sent: Friday, June 19, 2009 11:03 AM
> > >To: John Bouck
> > >Subject: RE: SNP file for R07007 vs R07020
> > >
> > >John
> > >
> > >Yes I can share the Rio data. What would you l ke and how would you
> > >like to get it. I can give you the sequence file with the quality
> > >scores if that is how you want it. I don't know if it would be too
> > >big to send in an email or not.
> > >
> > >I did talk with John about the sweet sorghum project and this is what
> > >he told me. All of the money for the sweet sorghum program that was
> > >added into the Ceres project goes to Bill for breeding work. Thus no
> > >money was allocated for marker work and therefore, he doesn't have
> > >plans to do any sweet sorghum genotyping. If we want to discuss this
> > >at a quarterly meeting with Bill, Jeff, and the rest of us, that
> > >would be fine, but for now that is how the project is written and the
> > >budget allocated.
> > >
> > >Thanks
> > >Trish
> > >
> > >
> > >
> > >At 07:39 PM 6/18/2009, you wrote:
> > > >You've done rio? Is that data you can share?
> > > >
> > > >John
> > > >
> > > >-----Original Message-----
> > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > >Sent: Thursday, June 18, 2009 2:30 PM
> > > >To: John Bouck
> > > >Subject: RE: SNP file for R07007 vs R07020
> > > >
> > > >John
> > > >
> > > >Haven't done any thus far except Rio. I think the plan at first
>was
> > > >to get some of the Ceres PS lines done as well as mapping
>population
> > > >parents. Sweets would likely come after these.
> > > >
> > > >Trish
> > > >
> > > >
> > > >At 04:24 PM 6/18/2009, you wrote:
> > > > >Sounds like a good idea let me know when you have analyzed what
>you

> > > > >want. Are you guys doing any sweets? I'm curious to see the
> > >variation
> > > > >between sweet and non-sweets.
> > > > >
> > > > >John
> > > > >
> > > > >-----Original Message-----
> > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > >Sent: Thursday, June 18, 2009 8:31 AM
> > > > >To: John Bouck
> > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > >
> > > > >John
> > > > >
> > > > >As far as I can tell that should work for me. No worries about
>teh
> > > > >rescheduling. I too am busy so I totally understand. I may even
> > > > >have additional PS genotypes analyzed by then. We finished a run
> > > > >this week that contained an additional 8 PS lines (R07008,
>R07012,
> > > > >R07108, R07030, R07034, R07042, R07045 and R07045) in addition to
> > >the
> > > > >anthracnose mapping parents. I am trying to get that data
>through
> > > > >the analysis pipeline so I can see how these lines compare to the
> > > > >R07007 and R07020. Perhaps we should have the call once I have
> > >that
> > > > >data analyzed which should be sometime next week? Just let me
>know
> > > > >your thoughts on this.
> > > > >
> > > > >Thanks
> > > > >Trish
> > > > >
> > > > >At 10:17 AM 6/18/2009, you wrote:
> > > > > >Trish - I'm really sorry to do this again but my schedule is
> > >being
> > > > >taken
> > > > > >over by others and I have yet another last minute conflict.
> > > > > >
> > > > > >Maybe we should shoot for Monday afternoon at 3:00 your time -
> > >things
> > > > > >should quiet down next week.
> > > > > >
> > > > > >Best,
> > > > > >John
> > > > > >
> > > > > >-----Original Message-----
> > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > >Sent: Wednesday, June 17, 2009 8:22 AM
> > > > > >To: John Bouck
> > > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > > >
> > > > > >John
> > > > > >
> > > > > >That time tomorrow should work just fine.
> > > > > >
> > > > > >Thanks
> > > > > >Trish
> > > > > >
> > > > > >
> > > > > >
> > > > > >At 10:10 AM 6/17/2009, you wrote:
> > > > > > >Trish,
> > > > > > >
> > > > > > >I have an external meeting that is now planned for the same
> > >time
> > > > >as
> > > > > >our
> > > > > > >meeting later today. Can we move our discussion to tomorrow

>at
> > > >3:00
> > > > > > >your time?
> > > > > > > >
> > > > > > > >Sorry for the late notice,
> > > > > > > >John
> > > > > > > >
> > > > > > > >-----Original Message-----
> > > > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > > > >Sent: Tuesday, June 09, 2009 1:53 PM
> > > > > > > >To: John Bouck
> > > > > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > > > > >
> > > > > > > >Sounds good, I will put that time on my calendar and be
>waiting
> > > >for
> > > > > > >your
> > > > > > > >call.
> > > > > > > >
> > > > > > > >Trish
> > > > > > > >
> > > > > > > >
> > > > > > > >At 03:47 PM 6/9/2009, you wrote:
> > > > > > > > >Great - how about Wednesday at 4:00 your time?
> > > > > > > > >
> > > > > > > > >John
> > > > > > > > >
> > > > > > > > >-----Original Message-----
> > > > > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > > > > >Sent: Tuesday, June 09, 2009 1:46 PM
> > > > > > > > >To: John Bouck
> > > > > > > > >Subject: RE: SNP file for R07007 vs R07020
> > > > > > > > >
> > > > > > > > >John
> > > > > > > > >
> > > > > > > > >I will be around next week as of now so whenever you want
>to
> > > >talk
> > > > > > > >just give me a heads up on day/time.
> > > > > > > > >
> > > > > > > > >Trish
> > > > > > > > >
> > > > > > > > >
> > > > > > > > >
> > > > > > > > >At 03:44 PM 6/9/2009, you wrote:
> > > > > > > > > >Hi Trish,
> > > > > > > > > >
> > > > > > > > > >We've started getting our heads around this - would be
>fun
> > > >to
> > > > > > > >discuss,
> > > > > > > > > >unfortunately I'm traveling for the next several days.
>Are
> > > >you
> > > > > > > >free
> > > > > > > > > > >next Wednesday or Thursday?
> > > > > > > > > > >
> > > > > > > > > > >John
> > > > > > > > > > >
> > > > > > > > > > >-----Original Message-----
> > > > > > > > > > >From: Patricia Klein [mailto:pklein@tamu.edu]
> > > > > > > > > > >Sent: Wednesday, May 20, 2009 9:27 AM
> > > > > > > > > > >To: John Bouck
> > > > > > > > > > >Subject: SNP file for R07007 vs R07020
> > > > > > > > > > >
> > > > > > > > > > >John
> > > > > > > > > > >
> > > > > > > > > > >I uploaded a file with the name
> > > > > > > > > > >R07007_R07020_SNP.final.pairwised.unique.052009.xls.
>This

> >is
> > > >an
> > > > > > > > > >excel file of ~5000 potential SNPs/INDELs found between
> > > >R07007
> > > > >and
> > > > > > > > > >R07020. I highlighted in yellow some potential markers
> >that
> > > >are
> > > > > > > >also
> > > > > > > > > >present in some of the other 11 genotypes examined and
>thus
> >I
> > > > >would
> > > > > > > > > >consider to be of high quality "real" polymorphisms. In
> >pink
> > > >are
> > > > > > > > > >markers where the polymorphism was found only between
> >R07007
> > > >and
> > > > > > > > > >R07020 and thus I wouldn't have as much confidence that
> >these
> > > >are
> > > > > > > > > >"real" polymorphisms. I did this for some markers on
>chr.
> >1
> > > > >only.
> > > > > > > >I
> > > > > > > > > >hope this gives you enough information to design some
> >Taqman
> > > > >assays
> > > > > > > > > >to test. If you need additional info please let me know.
> > >Let
> > > >me
> > > > > > > > > >know how it all turns out.
> > > > > > > > > >
> > > > > > > > > >Thanks
> > > > > > > > > >Trish
> > > > > > > > > >
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Subject: Request for information on sorghum SSR primer sequences
To: <pklein@tamu.edu>

Dear Dr Klein,

Greetings from ICRISAT-Patancheru!

I am seeking information on primer sequences for a number of sorghum SSR markers from the Xtxp series that were developed at TAMU after the publications by Kong et al. (2000) and Bhattramakki et al. (2000), and have been included in several published studies, but the primer sequences are not available from any public source (so far as I have been able to find).

Essentially these are the Xtxp series SSR markers from TAMU having serial numbers above 358. A good number of these are included in one of the linkage maps among the supplemental files accompanying the recent article by Mace et al. (2009) that provided a consensus sorghum map that includes DArT markers.

I am particularly interested in these as Dave Jordan has advised me of two that flank the ms3 genetic male sterility locus. My group would like to use these to support ICRISAT's sorghum breeding team by rapidly transferring the recessive ms3 gene to elite genetic backgrounds that we are using as recurrent parents in our marker-assisted backcrossing programs.

I am aware of two recent publications that provided large amount of sorghum SSR primer information, but am particularly seeking information on these markers as their association with the ms3 gene is already established.

Please let me know if it would be possible to provide this primer sequence information to ICRISAT.

Sincerely yours,

C Tom Hash
Principal Scientist (Breeding)
ICRISAT-Patancheru, Hyderabad
Andhra Pradesh 502 324
India
Email: c.hash@cgiar.org
Tel: +91-40-3071-3322 (direct) or +91-40-3071-3071 extn 2322
Fax: +91-40-3071-3074

-----Original Message-----
From: Sharma, Arun [mailto:asharma@tamu.edu]
Sent: Tuesday, May 26, 2009 8:37 PM

To: Hash, C (ICRISAT-IN)
Cc: Patricia Klein
Subject: Re: Request for a letter of support

Dear Tom,

Our NSF grant ended an year ago and therefore, no one is updating the marker information on sorgblast.tamu.edu website. I think Trish would be the right person to contact in this regard as she is the only one in TAMU sorghum genomics group who curates all the markers information. If you send her the name of the markers you are interested in, she might be able to get you the primer sequences.

I am copying this e-mail to her so she is aware that you might contact her.

Thanks!

Kind regards,
-Arun

----- Original Message -----
From: "C Hash (ICRISAT-IN)" <C.HASH@CGIAR.ORG>
To: "Arun Sharma" <asharma@tamu.edu>
Sent: Tuesday, May 26, 2009 9:32:41 AM GMT -06:00 Guadalajara / Mexico City / Monterrey
Subject: RE:

Dear Arun,

...

On another matter, I've been trying to find information on some sorghum SSR primer pairs developed at TAMU (post Kong et al and Bhattramakki et al) and have not been having any success. Could you advise me whether there is any publicly accessible site where primer sequence information on these more recently developed sorghum SSR primer pairs is available? I've seen several publications in which these additional markers have been reported as mapped, but am unable to find primer sequence information for them. Alternatively, if there is no publicly-available website ... where this information is available, who would you recommend that I contact seeking this information? Should I contact John Mullet, Patricia Klein, Robert Klein, or someone else?

All for now.

Best regards,

C Tom Hash

ICRISAT-Patancheru

-----Original Message-----
From: Sharma, Arun [mailto:asharma@tamu.edu]
Sent: Tuesday, May 26, 2009 7:56 PM
To: Hash, C (ICRISAT-IN)
Subject: Re: Request for a letter of support

Dear Dr. Hash,

Sorry, it took me so long to get back with the draft letter of support for my permanent residence petition in the US. Please find attached a word file with the draft letter. I would need TWO hard copies of the letter on your letter head with your signature. Please send the letter by post at the below mentioned address. Also, please e-mail your resume as I am required to attach that along with the letters. Please let me know if you have any questions.

POSTAL ADDRESS
Arun Sharma
1100 Hensel Dr., Apt# V2F,
College Station, TX 77840
USA

I truly appreciate your help in this regard.

Sincerely,
-Arun
==========
Arun Sharma
Research Scientist
Institute for Plant Genomics and Biotechnology
Borlaug Center
TAMU 2123
Texas A&M University
College Station, TX 77843-2123

phone: 979-862-4802
fax: 979-862-4790
email: asharma@tamu.edu

----- Original Message -----
From: "C Hash (ICRISAT-IN)" <C.HASH@CGIAR.ORG>
To: "Arun Sharma" <asharma@neo.tamu.edu>
Sent: Wednesday, December 17, 2008 10:10:30 AM GMT -06:00 Guadalajara / Mexico City / Monterrey
Subject: RE: Request for a letter of support

Dear Arun,

I'd be glad to provide the support letter and would greeatly appreciate you providing a draft that I can then personalize.

Wishing you all the best.

Sincerely yours,

C Tom Hash

Subject: RE: Request for information on sorghum SSR primer sequences
To: "Patricia Klein" <pklein@tamu.edu>

Dear Patricia,

Sorry for my delay in getting back to you--my notes on this were buried and took a while to resurface.

Sincerely yours,

Tom

C Tom Hash
Principal Scientist (Breeding)
ICRISAT-Patancheru, Hyderabad
Andhra Pradesh 502 324
India
Email: c.hash@cgiar.org
Tel: +91-40-3071-3322 (direct) or +91-40-3071-3071 extn 2322
Fax: +91-40-3071-3074

-----Original Message-----
From: Patricia Klein [mailto:pklein@tamu.edu]
Sent: Tuesday, June 30, 2009 1:57 AM
To: Hash, C (ICRISAT-IN)
Subject: Re: Request for information on sorghum SSR primer sequences

Tom

As Arun mentioned we don't update our sorgblast3 site any longer as we no longer have the funds from NSF to do so. Can you tell me what particular SSRs (ie the txp #'s) you are interested in around ms3? I can't send you a complete list for every marker developed above txp358 since these have been developed by numerous students, post-docs, etc in either my group, John Mullet's group or Bob Klein's group and I don't have all of the information for each SSR. If you can send me the txp numbers for those that flank the ms3 gene that you refer to, then I can try to see who created them and find out if I can send you the sequences. Some of the SSRs that have been developed by different individuals are being used to map-base clone genes for specific research projects so I am not sure exactly what I will be able to provide. However, no one is currently working on ms3 so it shouldn't be a problem to send the primer sequences flanking that locus.

Thanks
Patricia

At 07:09 AM 6/23/2009, you wrote:
>Dear Dr Klein,
>
>Greetings from ICRISAT-Patancheru!
>
>I am seeking information on primer sequences for a number of sorghum SSR
>markers from the Xtxp series that were developed at TAMU after the
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