From: **Andrew Don Nguyen** adnguyen@uvm.edu
Subject: Re: picea sequencing
Date: January 19, 2016 at 10:59 PM
To: Lau, Matthew K. matthewklau@fas.harvard.edu

AN

Hey Matt, do we have space to sequence the 7 colonies? Or should I stick to the 4 (picea,miamiana,ashmeadi,floridana)?
Quoting "Lau, Matthew K." <matthewklau@fas.harvard.edu>:

> Hi Andrew, sounds good!
>
> Matt
>
> On Tue, Jan 19, 2016 at 6:22 PM, Andrew Nguyen
> <andrew.nguyen@uvm.edu<mailto:andrew.nguyen@uvm.edu>>
> wrote:
>
>
> Hey Matt,
>
> I have a colony of picea, miamiana, ashmeadi, and floridana. If we
> have
> more space, I can include fulva, tennensseensis, lamellidens. I can
> send
> you colonies as soon as this week or the next.
>
> Best,
> Andrew Nguyen
> Ph.D. Candidate
> Department of Biology, University of Vermont
> Room 211, Marsh Life Science Building
> 109 Carrigan Drive
> Burlington, Vt 05405
> website: https://adnguyen.github.io/
>
> "A Keats and a Newton, listening to each other, might hear the
> galaxies
> sing.? ~Richard Dawkins

On 2016-01-15, 3:29 PM, "Lau, Matthew K." <matthewklau@fas.harvard.edu> wrote:

> Hi Sara and Andrew, the sequencing that we?re contracting is going to use
> jumping libraries. Let me know if you want more details, and I can forward the final contract (once the Broad Institute signs it).
>
> Currently, I?m set to sequence a total of 6 samples; and I would like at
> least two of those to be A. rudis. If you have live or -80 frozen whole colonies with several hundred workers, we have room to accommodate at
> least one sample of each of all three of those species (picea, ashmeadi
> and floridana). Also, it seems like sequencing miamiana would be good if
> you have frozen or live whole colonies.
>
> Cheers,
> Matt
>
> > On Jan 14, 2016, at 10:19 AM, Sara Cahan <scahan@uvm.edu> wrote:
> >
> > Just to clarify here - have you contracted for both regular paired-end
> > and mate pair/jump library sequencing, or just the paired-end? We already have some paired-end data for picea, and I want to make sure we
> > are gaining something extra by sequencing picea along with yours. If
> > you are not yet doing the longer-spanning libraries, we'd prefer to send
> > you either ashmeadi or floridana to help with Andrew's work.
> >
> > Thanks

Thanks,
Sara

-----Original Message-----
From: Andrew Nguyen [mailto:andrew.nguyen@uvm.edu]
Sent: Thursday, January 14, 2016 9:46 AM
To: Lau, Matthew K.; Sara Cahan
Cc: Ellison, Aaron; Nicholas Gotelli
Subject: Re: picea sequencing

Hey Matt,

Do we need more picea material?

Also, is there space/money for other species?

Best,
Andrew Nguyen
Ph.D. Candidate
Department of Biology, University of Vermont Room 211, Marsh Life
Science Building
109 Carrigan Drive
Burlington, Vt 05405
website: https://adnguyen.github.io/

"A Keats and a Newton, listening to each other, might hear the galaxies
sing.² ~Richard Dawkins

On 2016-01-13, 5:50 PM, "Lau, Matthew K." <matthewklau@fas.harvard.edu>
wrote:

> Hey Sara and Andrew, we're moving forward with genome

Hey Sara and Andrew, we're moving forward with genome sequencing down
here. We¹re probably a few weeks away (paper work has been inordinately
slow), but I want to give you guys plenty of time to pull together and
ship A. picea (or other) samples down to us if you are able to.

Happy belated New Year to everyone up there!

Cheers,

Matt

> On Dec 10, 2015, at 3:13 PM, Lau, Matthew
> <matthewklau@fas.harvard.edu>
> wrote:
>
> Hi Sara and Andrew, I just finished a bit of Q & A with the Broad Institute folks, and here¹s short version of their response to my question of whether or not the Illumina sequences will be sufficient
> for using as a reference genome for the SNPs:
>
> "This assembly will likely (no guarantee!) be on average composed of
> 5-10kb contigs and would capture somewhere between 80-98% of the
> genome
> (again thats my educated guess). Not knowing a lot about insect
> genes,
> I would imagine that you would be able to do a de novo annotation and
> call genes effectively in those contigs that are larger than gene size.
> With this annotated genome you very likely could align data from other organisms and call SNPs and also have information about which

genes
these SNPs came from. If that seems sufficient for your SNP calling
purposes, then you're probably okay even though the reference won't
be
optimal."

This is without considering that we can do additional sequencing using Jumping Libraries. I still need to get a quote from them for that, but I went ahead and told them to start a work order for us.

Currently, the work order is going to be for six samples, all of which would be A. rudis but we can add your samples into the pipeline
as well.
It would be great to get your A. picea (or any other Aphaenogaster
species you might have on hand) sequenced as well. To get your
samples
into the pipeline, I would need you to ship me whole colonies ³winnowed² down to ants as clean as possible, weighed and frozen at
-80C. Something on the order of a couple hundred ants or more would
be
best (my notes say my sample weighed about 125mg.

Cheers,
Matt