

**From:** Lau, Matthew matthewklau@fas.harvard.edu  
**Subject:** Re: Broad Inquiry about Ant Whole Genome Sequencing  
**Date:** September 3, 2015 at 5:50 PM  
**To:** Sarah Young stowey@broadinstitute.org  
**Cc:** Jim Bochicchio jboch@broadinstitute.org



Hi Sarah, thanks! Very nice to meet you and Jim, both.

My recollection is that you said Anopheles' genome is about 250Mb, so from my inexperienced perspective, ~80% of the genome doesn't seem too bad.

Thanks again,  
Matt

On Sep 3, 2015, at 1:46 PM, Sarah Young  
<[stowey@broadinstitute.org](mailto:stowey@broadinstitute.org)> wrote:

Hi Matt,

It was a pleasure meeting you yesterday. I wanted to follow up with some stats that we got for the Anopheles genomes. While this is no guarantee that Ant will behave similarly, it does give you a sense for how some insects have behaved previously. Quality of assembly will depend on three things which I mentioned - bias in sequencing (not usually a problem unless extreme GC or amplified DNA), repeats in the genome, and polymorphism. For your genomes I suspect that polymorphisms will be the biggest factor in how well these come together. The anopheles genomes here are really some of the "worse" genomes we've seen as far as high levels of polymorphism.

In a sample of 15 genomes, on average we assembled 193Mb of the genome. We had approximately 6k scaffolds and 14k contigs. There is a very high standard deviation here though: the best samples gave us roughly 3k contigs, and the worst gave us 30k contigs. Scaffold N50s were on average over 4Mb though (indicating that a lot of the genome is contained in big pieces). Contig N50s (meaning stretches without any gaps) on average were 70kb.

Let me know if you have any other questions I can answer!

~Sarah

On Wed, Sep 2, 2015 at 12:51 PM, Jim Bochicchio  
<[jboch@broadinstitute.org](mailto:jboch@broadinstitute.org)> wrote:

Hi Jenn

Ok, no problem.

Thanks  
Jim

On Wed, Sep 2, 2015 at 12:50 PM, Jennifer Wineski  
<[jwineski@broadinstitute.org](mailto:jwineski@broadinstitute.org)> wrote:

My apologies Jim- Matt and I had a separate email, and he confirmed for this afternoon. I will meet Matt in the lobby when he arrives and bring him up to the conference room.

Thank you,

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On Wed, Sep 2, 2015 at 12:43 PM, Jim Bochicchio  
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Hi Jim, great, here you go! Let me know any of these are off-base or insufficient in detail.

| How much material do you have for each sample?

...the more material as you have for each sample.

Our ants usually produce  $1.6 \pm 0.05$  nano-grams / micro-liter (mean  $\pm$  SE).

Again, we have and can get lots (tens or hundreds) of ants.

| Estimated sizes of genomes?

The genome of the most taxonomically similar species is 3.9 Mbp: <http://hymenopteragenome.org/pogonomyrmex/>

| Is the chromosome number known?

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| Are plasmids expected in addition to the chromosome(s)?

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| Is the ploidy known?

If they are female, which is what we would like sequenced, they should be diploid.

| Is the repeat content and/or structure known?

The *Pogonomyrmex* genome is the best indication of the this.

Thanks,  
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On Aug 28, 2015, at 2:21 PM, Jim Bochicchio  
<[jboch@broadinstitute.org](mailto:jboch@broadinstitute.org)> wrote:

Hi Matt

Ok, Jenn (cced) can help us set up a meeting. Can you send us the information below for your samples:

1. Host organism (ant species) and tissue type (antennae, head, etc.)

How much material do you have for each sample?  
Estimated sizes of genomes?  
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Subject: Re: Broad Inquiry about Ant Whole Genome Sequencing  
Date: September 3, 2015 at 1:47 PM  
To: Lau, Matthew matthewklau@fas.harvard.edu  
Cc: Jim Bochicchio jboch@broadinstitute.org

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<[matthewklau@fas.harvard.edu](mailto:matthewklau@fas.harvard.edu)> wrote:

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**From:** Jim Bochicchio [jboch@broadinstitute.org](mailto:jboch@broadinstitute.org)  
**Subject:** Re: Broad Inquiry about Ant Whole Genome Sequencing  
**Date:** September 2, 2015 at 12:52 PM  
**To:** Jennifer Wineski [jwineski@broadinstitute.org](mailto:jwineski@broadinstitute.org)  
**Cc:** Lau, Matthew [matthewklau@fas.harvard.edu](mailto:matthewklau@fas.harvard.edu), Sarah Young [stowey@broadinstitute.org](mailto:stowey@broadinstitute.org)

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JB

No problem, do you have access to the Broad Institute? If not, have the front desk call me when you get here and I will come down to meet you.

Thanks  
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Thanks Jim (i.e. not Jenn, sorry!).

Sent using [CloudMagic](#)

On Wed, Sep 02, 2015 at 12:46 PM, Jim Bochicchio  
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<[matthewklau@fas.harvard.edu](mailto:matthewklau@fas.harvard.edu)> wrote:

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Let me know if there's a good time in there that works for you.

Best,  
Matt

On Aug 28, 2015, at  
2:02 PM, Jim

Bochicchio  
<[jboch@broadinstitute.org](mailto:jboch@broadinstitute.org)> wrote:

Hi Matthew

Great to meet you!  
Allow  
me to introduce  
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We received your  
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Jim Bochicchio  
Product Manager  
Broad Technology  
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Broad Institute  
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USA

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Website:

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**From:** Lau, Matthew matthewklau@fas.harvard.edu  
**Subject:** Re: Broad Inquiry about Ant Whole Genome Sequencing  
**Date:** September 2, 2015 at 12:48 PM  
**To:** Jim Bochicchio jboch@broadinstitute.org  
**Cc:** Jennifer Wineski jwineski@broadinstitute.org, Sarah Young stowey@broadinstitute.org

---



Thanks Jim (i.e. not Jenn, sorry!).

Sent using [CloudMagic](#)

On Wed, Sep 02, 2015 at 12:46 PM, Jim Bochicchio  
<[jboch@broadinstitute.org](mailto:jboch@broadinstitute.org)> wrote:

Ok

On Wed, Sep 2, 2015 at 12:45 PM, Lau, Matthew  
<[matthewklau@fas.harvard.edu](mailto:matthewklau@fas.harvard.edu)> wrote:

Hey Jenn, no I never got the invite. No worries though, be there shortly.

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**From:** jwineski@broadinstitute.org  
**Subject:** Re: Broad Inquiry about Ant Whole Genome Sequencing  
**Date:** September 1, 2015 at 7:41 PM  
**To:** Lau, Matthew matthewklau@fas.harvard.edu

---



Hi Matt,

Thanks so much for your message! I booked the kalahari room on the 8th floor of the 75 Ames street building. When you arrive, please ask for me and will be happy to meet you in the lobby.

Thank you!

Jenn

Sent from my iPhone

On Sep 1, 2015, at 7:26 PM, Lau, Matthew  
<[matthewklau@fas.harvard.edu](mailto:matthewklau@fas.harvard.edu)> wrote:

Hi Jenn, just wanted to check on the best place to meet tomorrow. I'll be on Harvard Main Campus tomorrow, so I can come to you, just let me know where.

Thanks!

Matt

On Aug 31, 2015, at 11:52 AM, Jennifer Wineski  
<[jwineski@broadinstitute.org](mailto:jwineski@broadinstitute.org)> wrote:

Great! Thank you very much. I will send an invitation shortly.

Thanks!

Jenn

On Mon, Aug 31, 2015 at 11:51 AM, Lau, Matthew  
<[matthewklau@fas.harvard.edu](mailto:matthewklau@fas.harvard.edu)> wrote:

Hi Jenn, that would work for me!

Thanks.



Matt

On Aug 31, 2015, at 11:19 AM, Jennifer Wineski  
<[jwineski@broadinstitute.org](mailto:jwineski@broadinstitute.org)> wrote:

Hi Matt,

Would you be able to meet with Jim and Sarah, on Wednesday,  
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Thank you,

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**Subject:** Re: Broad Inquiry about Ant Whole Genome Sequencing  
**Date:** August 31, 2015 at 11:53 AM  
**To:** Lau, Matthew [matthewklau@fas.harvard.edu](mailto:matthewklau@fas.harvard.edu)

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PHOTOGRAPHY COURSE

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