

**From:** [Scott Allen Jackson](#)  
**To:** [Daniel O'Connor](#)  
**Cc:** [Steven Cannon](#)  
**Subject:** Re: peanut assemblies  
**Date:** Monday, July 21, 2014 9:15:24 PM  
**Importance:** High

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Hi Dan, Publication should wait until the gneome is published. Hopefully that is 2015:) also, you may want to check with Rajeev Varshney as I think they too were developing some enrichment tools, possibly with Roche.

scott

On Jul 21, 2014, at 7:04 PM, Daniel O'Connor <[d.oconnor@uq.edu.au](mailto:d.oconnor@uq.edu.au)> wrote:

Hi Steven & Scott,

I am working towards getting the enrichment of my poor and excellent blanching accessions organised in the near future.

I would like make sure that I have permission to supply data from the progenitor preliminary gene models to Roche Nimblegen for the design of the enrichment probes.

There will be no publications on any of this until 2015. I understand that I will need to work with the PGC to ensure all the correct protocol publications are followed.

Thanks very much for your time.

Regards

**Dan O'Connor**

**Research Scholar**

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<https://twitter.com/doconnor1874>

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**From:** Cannon, Steven [<mailto:Steven.Cannon@ARS.USDA.GOV>]  
**Sent:** Thursday, 17 July 2014 12:22 AM  
**To:** Daniel O'Connor

**Subject:** Re: peanut assemblies

Hi Dan,

I'm glad the APRES meeting was good. I'd like to have been able to go.

Looking forward to seeing you in Georgia in November -

Steven

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**From:** Daniel O'Connor <[d.oconnor@uq.edu.au](mailto:d.oconnor@uq.edu.au)>  
**Date:** Tuesday, July 15, 2014 at 11:42 PM  
**To:** Steven Cannon <[steven.cannon@ars.usda.gov](mailto:steven.cannon@ars.usda.gov)>  
**Subject:** RE: peanut assemblies

Hi Steven,

I had a very worthwhile trip to APRES last week and caught up with a few of the breeders and molecular biologists which was great.

Howard Valetine mentioned that you will be running a PeanutBase workshop at AAGB which will be great.

Just getting my name down early as that will be very relevant for me.

Hope all is well.

Cheers,

Dan.

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**From:** Cannon, Steven [<mailto:Steven.Cannon@ARS.USDA.GOV>]  
**Sent:** Wednesday, 2 July 2014 11:14 AM  
**To:** Scott Allen Jackson; Daniel O'Connor  
**Subject:** Re: peanut assemblies

Seems fine to me too, although there has been no public release of the gene models yet, so I think it would be best to make a note that these are provisional gene models, still under review by the PGC.

The gene models have held up pretty well to scrutiny so far, but not perfectly. There seem to be a larger proportion of transposon-like gene models in the *A. ipaensis* MAKER gene models than in *A. duranensis*. I need to get a report about this to the PGC and then have a discussion about how to proceed: whether to do some additional filtering, or let them go as-is and keep the problems in mind during downstream analyses.

Steven

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**From:** Scott Allen Jackson <[sjackson@uga.edu](mailto:sjackson@uga.edu)>  
**Date:** Tuesday, July 1, 2014 at 6:55 PM

**To:** Daniel O'Connor <[d.oconnor@uq.edu.au](mailto:d.oconnor@uq.edu.au)>  
**Cc:** Steven Cannon <[steven.cannon@ars.usda.gov](mailto:steven.cannon@ars.usda.gov)>  
**Subject:** Re: peanut assemblies

fine iwth me.  
scott

On Jul 2, 2014, at 7:16 AM, Daniel O'Connor <[d.oconnor@uq.edu.au](mailto:d.oconnor@uq.edu.au)> wrote:

Hi Scott & Steve,  
I wanted to put in a couple of slides about the gene models in my talk at APRES.  
Is this OK, with regards to publications etc?  
Cheers,  
Dan.

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**From:** Scott Allen Jackson [<mailto:sjackson@uga.edu>]  
**Sent:** Tuesday, 17 June 2014 5:34 PM  
**To:** Daniel O'Connor  
**Cc:** Steven Cannon  
**Subject:** Re: peanut assemblies  
**Importance:** High

Hi Dan, I don't know what the exact timeline will be. We will likely be updating the genome assembly in the next year as well which will lead to improved gene models too. I suspect this is longer than you want to wait and if I were you I would go ahead with what we have now as it should be immediately useful for your intentions.

If you wanted to do some informatic work, you could take the two annotations and either do a subtractive, or additive, calculation

scott

On Jun 16, 2014, at 8:29 AM, Daniel O'Connor <[d.oconnor@uq.edu.au](mailto:d.oconnor@uq.edu.au)> wrote:

Hello Scott,

Steven Gannon suggested I contact you about the gene models of *A. duranensis* & *A. ipaensis* available on Peanutbase.

I am Dan O'Connor, a PhD student from the University of Queensland, Australia, and I am part of Robert Henry's group. I met you briefly at AAGB in China last year.

The email trail below will explain my query but I will summarise as best I can.

I would like to develop markers for the blanching trait in the cultivated peanut. I have a good phenotyping technique but now want to get the molecular work done using the US minicore collection, which we have here.

We have extracted genomic DNA from 12 good blanching accessions and 12 poor blanching accessions. Our plan is to pool both good and poor accessions, enrich the DNA using a NimbleGen protocol, and then send for NGS, most probably using the Illumina platform.

I would like to base by target regions for enrichment using the gene models develop by the PGC which are currently available on Peanutbase. I understand these are preliminary models and may change. I am wondering what the timeline may be for the updated gene models through the PGC? I see more gene models and annotations were added earlier this month. I will need to make a decision soon on when to use these models for my enrichment protocol in designing the target probes.

Any advice would be greatly appreciated.

Thanks very much for your time and hopefully I can catch up with you at APRES next month.

Regards

**Dan O'Connor**

**Research Scholar**

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<https://twitter.com/doconnor1874>

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**From:** Cannon, Steven [<mailto:Steven.Cannon@ARS.USDA.GOV>]  
**Sent:** Friday, 13 June 2014 10:22 PM  
**To:** Daniel O'Connor  
**Subject:** Re: peanut assemblies

Hi Dan,

I'm glad the gene models are being helpful.

I haven't received reports of systematic problems – which is a good sign. On the other hand, I don't know how much attention the gene models have received yet. We received gene models from BGI this week. It is possible that a comparison with those will identify some problems. My guess is that both sets will ultimately be made available, with one of them being recommended as the primary set for analysis.

If a Nimblegen array is going to be generated (or really, any resource that will receive a lot of downstream attention and use), I think it will be important to keep the others in the consortium in the loop. I think Scott Jackson would be the first point of contact for coordinating. Can you do that before proceeding?

Unfortunately, I won't be at APRES, but will be at the fall AAGB meeting.

Best wishes,  
Steven

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**From:** Daniel O'Connor <[d.oconnor@uq.edu.au](mailto:d.oconnor@uq.edu.au)>  
**Date:** Friday, June 13, 2014 at 3:20 AM  
**To:** Steven Cannon <[steven.cannon@ars.usda.gov](mailto:steven.cannon@ars.usda.gov)>  
**Cc:** Agnelo Furtado <[a.furtado@uq.edu.au](mailto:a.furtado@uq.edu.au)>, Graeme Wright <[gwright@pca.com.au](mailto:gwright@pca.com.au)>, Robert Henry <[robert.henry@uq.edu.au](mailto:robert.henry@uq.edu.au)>, RCN Rachaputi <[rao.rachaputi@uq.edu.au](mailto:rao.rachaputi@uq.edu.au)>  
**Subject:** RE: peanut assemblies

Hi Steven,

Hope you are having a good week.

I am progressing OK with my design for gene enrichment using the provisional models that you have directed to me previously. I have attached the annotations for Aradu.A01 which were downloaded from Peanutbase yesterday. This is the type format I will need to provide Nimblegen for the probe design. I have found Peanutbase an excellent resource, keep up the great work.

As you discuss below these gene models may not be released or be modified quite substantially.

I am just wondering what the timeline may be updated gene models through the PGC? I see more gene models and annotations were added earlier this month. I will need to make a decision soon on when to use these models for my enrichment protocol in designing the target probes.

As always, your input is greatly appreciated and hopefully I can catch up with you in

person at APRES.

Regards,  
Dan.

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**From:** Cannon, Steven [<mailto:Steven.Cannon@ARS.USDA.GOV>]  
**Sent:** Saturday, 24 May 2014 7:29 AM  
**To:** Daniel O'Connor  
**Cc:** Agnelo Furtado; Graeme Wright; Robert Henry; RCN Rachaputi  
**Subject:** Re: peanut assemblies

Hi Dan et al.,

I will point you at the provisional gene models. Please note the caveats: it is quite possible that these will change before public release; and it is even possible that these won't be released at all, but the group will instead promote a different annotation set. **Provisional** is key; use with caution. (And of course the standard caveats will apply about publication: check with the PGC group: any large-scale analysis of the data will need to be published first by the consortium).

That said, good luck to you, and please let me know if you have any questions.

Steven

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... provisional gene models for the diploids. These are refinements on the MAKER gene predictions from Andrew from a few weeks ago. I have assigned what I think are reasonable stable gene identifiers and assembly/annotation version descriptors, and have done some filtering against low-quality and TE-like genes.

<http://peanutbase.org/files/private/annotation/maker/Aradu.V14167.a1.M1.tar.gz>

<http://peanutbase.org/files/private/annotation/maker/Araip.K30076.a1.M1.tar.gz>

User / pass: Arachis / diploids

I won't repeat here what is in the README or gene\_naming\_scheme document, but these provide quite a bit of information (the same files are in both tar-balls above).

I think it would be best if the group worked with these files for at least several weeks before making them public. We may find problems that should be corrected before release, or may make format changes or add descriptive information (e.g. predicted functional information). In fact, we ought to have time with both the BGI and MAKER models together, to assess similarities and differences. The group may decide to promote only one of the model sets (or may provide access to both).

Please let us know if you have questions or encounter anything fishy (that is, at least [adf@ncgr.org](mailto:adf@ncgr.org) and [steven.cannon@ars.usda.gov](mailto:steven.cannon@ars.usda.gov)).

A good weekend to you -

Steven

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**From:** Daniel O'Connor <[d.oconnor@uq.edu.au](mailto:d.oconnor@uq.edu.au)>  
**Date:** Monday, May 19, 2014 at 6:32 PM  
**To:** Steven Cannon <[steven.cannon@ars.usda.gov](mailto:steven.cannon@ars.usda.gov)>  
**Cc:** Agnelo Furtado <[a.furtado@uq.edu.au](mailto:a.furtado@uq.edu.au)>, Graeme Wright <[gwright@pca.com.au](mailto:gwright@pca.com.au)>, Robert Henry <[robert.henry@uq.edu.au](mailto:robert.henry@uq.edu.au)>, RCN Rachaputi <[rao.rachaputi@uq.edu.au](mailto:rao.rachaputi@uq.edu.au)>  
**Subject:** RE: peanut assemblies

Hi Steven,

Thanks very much for the update. Everything looks to be progressing well.

I will keep working on my gene predictions using FGENESH and then use the finalised gene models to assess the accuracy of the predictions.

Thanks very much for your assistance.

Regards,

Dan.

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**From:** Cannon, Steven [<mailto:Steven.Cannon@ARS.USDA.GOV>]  
**Sent:** Friday, 16 May 2014 3:35 AM  
**To:** Daniel O'Connor  
**Subject:** Re: peanut assemblies

Hi Dan,

I apologize for my delayed response. It's been a busy week, getting summer students started and other things.

There are preliminary annotations. Final gene names haven't been assigned, and some gene calls will likely be demoted and removed. So I could point you at the gene models, with the big caveat that work on these early-stage gene models probably wouldn't be publishable, since they will be revised or replaced (at least the IDs will be replaced).

I suspect we will have finalized gene models within about two weeks. Those won't be released publicly, but could be used for analysis within the group – holding any publications until the genes/annotations are publicly released and described.

What do you think – would you rather get “early-early” access, or wait for a bit more stability?

Steven

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**From:** Daniel O'Connor <[d.oconnor@uq.edu.au](mailto:d.oconnor@uq.edu.au)>  
**Date:** Monday, May 12, 2014 at 5:01 AM  
**To:** Steven Cannon <[steven.cannon@ars.usda.gov](mailto:steven.cannon@ars.usda.gov)>

**Subject: Re: peanut assemblies**

Hi Steven,

Hope everything is going well for you over there.

I am currently attempting to use the diploid assemblies to nominate regions, containing genes, for enrichment of genomic DNA for the cultivated peanut.

Just wondering if you have any ideas or may be able to let me know who would be the best person to contact on gene prediction.

Unfortunately, bioinformatics isn't my strong point, although I am working on it, at the moment.

I see there has been an updated release of the diploid sequences which is great.

Any advice would be greatly appreciated.

Regards,

Dan.

Sent from my iPad

On Mar 24, 2014, at 4:09 AM, "Cannon, Steven" <[Steven.Cannon@ARS.USDA.GOV](mailto:Steven.Cannon@ARS.USDA.GOV)> wrote:

Hi Dan,

The public release of these is still being coordinated. I expect the assemblies to be made available to everyone in about a week.

Since you are a member of the PGC, it should be fine to share these with you – but please keep these strictly to yourself for now. We are so close to the official release that the group is trying to keep things under wraps until there is a coordinated, official announcement.

[http://peanutbase.org/files/genomes/prerelease/Aradu\\_v1.0.tar.gz](http://peanutbase.org/files/genomes/prerelease/Aradu_v1.0.tar.gz)

[http://peanutbase.org/files/genomes/prerelease/Aradu\\_v1.0\\_RM.tar.gz](http://peanutbase.org/files/genomes/prerelease/Aradu_v1.0_RM.tar.gz)

[http://peanutbase.org/files/genomes/prerelease/Aradu\\_v1.0\\_by\\_scaff.tar.gz](http://peanutbase.org/files/genomes/prerelease/Aradu_v1.0_by_scaff.tar.gz)

[http://peanutbase.org/files/genomes/prerelease/Aradu\\_v1.0\\_by\\_scaff\\_RM.tar.gz](http://peanutbase.org/files/genomes/prerelease/Aradu_v1.0_by_scaff_RM.tar.gz)

[http://peanutbase.org/files/genomes/prerelease/Araip\\_v1.0.tar.gz](http://peanutbase.org/files/genomes/prerelease/Araip_v1.0.tar.gz)

[http://peanutbase.org/files/genomes/prerelease/Araip\\_v1.0\\_RM.tar.gz](http://peanutbase.org/files/genomes/prerelease/Araip_v1.0_RM.tar.gz)

[http://peanutbase.org/files/genomes/prerelease/Araip\\_v1.0\\_by\\_scaff.tar.gz](http://peanutbase.org/files/genomes/prerelease/Araip_v1.0_by_scaff.tar.gz)

[http://peanutbase.org/files/genomes/prerelease/Araip\\_v1.0\\_by\\_scaff\\_RM.tar.gz](http://peanutbase.org/files/genomes/prerelease/Araip_v1.0_by_scaff_RM.tar.gz)

User / pass: Arachis / diploids



Directory legend:

RM — RepeatMask-ed, using Arachis repeats provided by David et al.

by\_scaff — The pseudomolecule sequences are in multifasta format, in scaffold chunks. Definition lines give scaffold name and orientation.

Not “by\_scaff” — these pseudomolecule sequences are “entire”, with a single definition line at the top, e.g. >Aradu.A01 or >Araip.B01.

These are big: each is ~150-350 Mb compressed; and up to 1.3 Gb uncompressed. You may not want to get all of them. For example, if you are assessing marker placement on the masked, “entire” pseudomolecules, you probably want Aipa\_v1.0\_RM and Adur\_v1.0\_RM.

Cheers -  
Steven

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**From:** Daniel O'Connor <[d.oconnor@uq.edu.au](mailto:d.oconnor@uq.edu.au)>  
**Date:** Monday, March 17, 2014 at 5:41 PM  
**To:** Steven Cannon <[steven.cannon@ars.usda.gov](mailto:steven.cannon@ars.usda.gov)>  
**Subject:** RE: peanut assemblies

Thanks very much Steven.

Cheers,  
Dan

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**From:** Cannon, Steven [<mailto:Steven.Cannon@ARS.USDA.GOV>]  
**Sent:** Monday, 17 March 2014 9:46 PM  
**To:** Daniel O'Connor  
**Subject:** Re: peanut assemblies

Hi Daniel,

As it turns out, the final assembly proceeded a little more slowly than anticipated (which, I suppose, might have been anticipated – since that’s how things usually happen).

I just finished the assemblies last night, for review, and the core assembly group will have a look at them in the next couple of days and decide how to proceed (i.e. release “as-is” ... or not). Let me ask that group how they would like to handle these, and I will let you know asap — will email this week in any case.

Best,  
Steven

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**From:** Daniel O'Connor <[d.oconnor@uq.edu.au](mailto:d.oconnor@uq.edu.au)>  
**Date:** Sunday, March 16, 2014 at 10:18 PM  
**To:** Steven Cannon <[steven.cannon@ars.usda.gov](mailto:steven.cannon@ars.usda.gov)>  
**Subject:** RE: peanut assemblies

Hi Steven,  
Hope March is treating you well.  
I am just following up on the diploid genomes, as we discussed last month.  
Thanks for your time.  
Regards,  
Dan

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**From:** Cannon, Steven [<mailto:Steven.Cannon@ARS.USDA.GOV>]  
**Sent:** Tuesday, 18 February 2014 11:39 AM  
**To:** Daniel O'Connor  
**Subject:** Re: peanut assemblies

Hi Dan,

That seems wise to me. I'll be in touch in early March (pretty soon!)

Cheers,  
Steven

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**From:** Daniel O'Connor <[d.oconnor@uq.edu.au](mailto:d.oconnor@uq.edu.au)>  
**Date:** Monday, February 17, 2014 at 7:31 PM  
**To:** Steven Cannon <[steven.cannon@ars.usda.gov](mailto:steven.cannon@ars.usda.gov)>  
**Subject:** RE: Steve Cannon Presidential Early Career Award

Hello Steven,

Thanks very much for this update.

After speaking with my supervisors I have decided that it would be best if I wait until March before I follow up again on the diploid genomes.  
I will then contact yourself and Lutz about the data.

Thanks very much for your help and keep up the great work.

Regards

Dan O'Connor  
Research Scholar

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