

From: [Scott Allen Jackson](#)
To: [rajeev varshney](#)
Cc: [Steven Cannon](#); [Lutz Froenicke \(lfroenicke@ucdavis.edu\)](#); [Jeremy Schmutz](#); [Scheffler Scheffler](#); [Richard Michelmore](#); [Peggy Ozias-Akins](#); [David Bertoli](#); [Howard Valentine](#); [Xin LIU](#); [Mark Burrows](#); [Soraya Bertoli](#); [David Bertoli](#); [Schnell, Ray](#); [Victor Nwosu](#); [Rich Wilson](#); [Brian Abernathy](#); [Baozhu Guo](#); [Corley Holbrook](#); [Ran Hovav](#); [Sudhansu Dash](#); [Ethalinda Cannon](#); [Nathan Weeks](#); [Andrew D. Farmer](#); [Longhui Ren](#); [Huang, Wei \[AGRON\]](#); [Kale, Sandip \(ICRISAT-IN\)](#); [Pandey, Manish K \(ICRISAT-IN\)](#); [Agarwal, Gaurav \(ICRISAT-IN\)](#)
Subject: Re: Diploid annotations for review - revisions, updates
Date: Wednesday, August 27, 2014 8:44:02 AM

This seems reasonable to me, too. -scott

On Aug 26, 2014, at 10:40 PM, Varshney, Rajeev (ICRISAT-IN)
<R.K.Varshney@CGIAR.ORG> wrote:

Thanks very much, Steven. I agree with your approach and suggestion.

Dear all: I would like to use this message to update you all on the other activity that we have undertaken. With an objective to identify the markers easily assayable for breeding applications, we have also searched genomes (AA and BB) for insertion and deletions. Please see the message below and attached file. We are in process of identify chromosome/ genome specific indel markers that can be easily scored for genetics and breeding applications.

Again this stuff can be included in Marker section (along with SSRs) in the genome MS. We can have a few supplementary tables on statistics as well as primer sequence.

Many thanks and kind regards

Rajeev

Begin forwarded message:

From: sandip kale <sandipmkale@gmail.com>
Subject: InDel identification between A and B genomes of peanut
Date: August 25, 2014 at 4:53:13 PM GMT+5:30
To: Manish Pandey <manishgenetics@gmail.com>
Cc: Gaurav Agarwal <gaurav.iari@gmail.com>, "Varshney, Rajeev (ICRISAT-IN)" <R.K.Varshney@CGIAR.ORG>

Hello Sir,

Attached herewith the summary of InDels identified between peanut A and B genomes.

The following steps were used for InDel identification

1. The MUGSY software was used for InDel identification assuming these two genomes are closely related
2. The output was parsed to obtain InDel sizes using perl script (the perl script was procured from Dr. Jingjing)

Total 1045015 insertions and 953715 deletions were obtained, out of which, 269974 insertions and 245250 deletions were present on same chromosomes of A and B genomes while rest were present on different chromosomes.

	Total	Same_chromosome	Different_chromosome
Insertions	1045015	269974	775041
Deletions	953715	245250	708465

We would like to discuss the results and further plans with Rajeev sir and you

Kindly let us know the your availability

Thanking you

With best

Sandip and Gaurav

On Aug 27, 2014, at 4:17 AM, Cannon, Steven
<Steven.Cannon@ARS.USDA.GOV> wrote:

PGC group,

Another update. As Ethy was submitting scaffolds to GenBank (still underway; waiting for some information from BGI, and then more QC), we learned of several redundant scaffolds — that is, scaffolds present in both the pseudomolecules and in the remaining “unplaced” scaffold set, for both of the species. There were eleven redundant scaffolds in *A. duranensis* and in *A. ipaensis*.

Beyond these twelve scaffolds, we identified a number of other very low-quality scaffolds in the “unplaced” set, which I would also like to remove. These have no genes, and contain < 2000 bases of non-N sequence or are > 80% Ns.

Although it would be OK for the GenBank submission to diverge from the 1.0 assembly (leading eventually to a new assembly version), I think it will be best

to correct (remove) these duplicated scaffolds from the “unplaced” scaffolds in the current assembly. The change doesn’t affect any of the pseudomolecules. My strong preference is therefore to leave the overall assembly version as 1.0, but to make a dated update to the “all-scaffolds” file and to the files with unplaced scaffolds.

A small additional complication is that the scaffold removals will also affect the gene models (903 MAKER genes in *A. duranensis* and 354 MAKER genes in *A. ipaensis*, and similar changes for GLEAN). However, I think this also should be OK, since we (this group) should be the only set of people who have the gene models (i.e. they haven’t been made public yet).

Analyses that are sensitive to total assembly sequence or the full gene set may need to be re-run (although the total sequence changing will be less than 0.1%, and no changes in the pseudomolecules). I would not expect aggregate or summary statistics to change.

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Please let us know if you have any questions or concerns, or if you find any problems.

Steven

From: <Cannon>, Steven Cannon <steven.cannon@ars.usda.gov>
Date: Monday, July 21, 2014 at 5:13 PM
To: Lutz Froenicke <lfroenicke@ucdavis.edu>, Jeremy Schmutz <jschmutz@hudsonalpha.org>, "Scheffler, Brian" <Brian.Scheffler@ARS.USDA.GOV>, "<rwmichelmore@ucdavis.edu>" <rwmichelmore@ucdavis.edu>, Peggy Ozias-Akins <pozias@uga.edu>, David Bertioli <djbertioli@gmail.com>, Howard Valentine <hvalentine@peanutsusa.com>, "Jackson, Scott" <sjackson@uga.edu>, "Michelmore, Richard" <rwmichelmore@ucdavis.edu>, "Liu, Xin" <liuxin@genomics.org.cn>, "mburow@tamu.edu" <mburow@tamu.edu>, "Bertioli, Soraya" <Soraya.Bertioli@embrapa.br>, "Bertioli, David" <david.bertioli@pq.cnpq.br>, "Schnell, Ray" <Ray.Schnell@effem.com>, "Nwosu, Victor" <victor.nwosu@effem.com>, Richard Wilson <rfwilson@mindspring.com>, "Varshney, Rajeev (ICRISAT-IN)" <r.k.varshney@cgiar.org>, Brian Abernathy <bla@uga.edu>, "Guo, Baozhu" <Baozhu.Guo@ARS.USDA.GOV>, "Holbrook, Corley" <Corley.Holbrook@ARS.USDA.GOV>, Ran Hovav <ranh@volcani.agri.gov.il>
Cc: Sudhansu Dash <sdash@iastate.edu>, Ethalinda Cannon <ekcannon@iastate.edu>, Nathan Weeks <weeks@iastate.edu>, Andrew Farmer <adf@ncgr.org>, Longhui Ren <lhren@iastate.edu>, "Huang, Wei [AGRON]" <weih@iastate.edu>, Steven Cannon <steven.cannon@ars.usda.gov>
Subject: Diploid annotations for review - revisions, updates

PGC group,

Here is an update on annotation work from the IA and NM groups.

Briefly:

- Some MAKER gene models have been demoted
- New functional descriptions for both MAKER and GLEAN models
- New browser tracks, with functional descriptions
- New analysis/comparison of the MAKER and GLEAN (BGI) models ...
- ... which suggests (I think) that both the MAKER and GLEAN models should be used/promoted
- Question for the group about when and how to release these (i.e. remove password protection).

Any accompanying news releases? Time this release with any events (perhaps the November meeting)?

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What's new:

- In the MAKER annotation, we "demoted" 1164 Aradu and 1553 Araip genes to the "lowqual_or_TE" set. This is

Longhui Ren's work here, resulting from sleuthing to find why there were more Araip models than for Aradu.

It seems that – as David B has mentioned – there has been a greater proliferation and diversification of transposable

elements in *A. ipaensis*. The repeat masking in the MAKER gene modeling was apparently not as thorough or

as unbiased as for the GLEAN (BGI) masking, so MAKER picked up some additional "genes" in *A. ipaensis*.

Even so, there are some apparently significant differences in the gene complements of the two genomes.

- For both the MAKER and GLEAN annotations, the functional descriptions have been updated, in the *.AHRD.* files.

These annotations were gathered using the "Automated Assignment of Human Readable Descriptions"

(AHRD) tool, by Andrew Farmer, using the following search targets:

Arabidopsis v10, Medicago v4.0,

soybean v. Glyma.Wm82.a2.v1, and InterProScan 5.3-46.0 (targeting UniProt90 (2014) and Gene Ontology (2014)).

There are two variants of the *.AHRD.* files: the full AHRD results in

*.AHRD.csv, and an abbreviated,

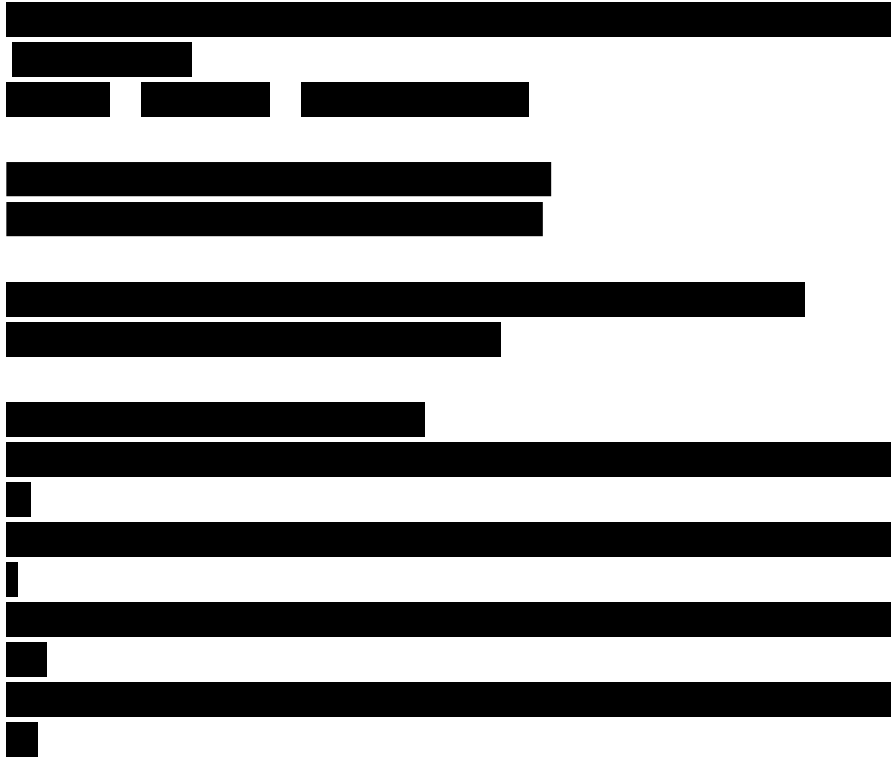
two-column format in *.AHRD.slim .

- The README files have been updated accordingly.

- The browser tracks for the MAKER and GLEAN models now have functional

descriptions.

(The links below are ones you have seen before, but the contents have been updated. If you are working with the annotation sets below (*.tar.gz), please download these again. Although the gene models are the same, the annotations are new, as is the separation into “good” vs. “demoted” sets.)



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Some analysis about the similarities and differences between MAKER and GLEAN (Sudhansu):

Approximately two thirds of the MAKER and GLEAN gene models correspond (overlap). Specifically ...

- In Aradu 26533 GLEAN genes (out of 37842 total, 70%) overlap with 25203 MAKER genes (out of 38149 total, 66%) in 27099 cases of overlap.
- In Araip 26910 GLEAN mRNA models (out of 39303 total, 68.5%) overlap with 25738 MAKER gene models (out of 42883 total, 60%) in 27629 cases of overlap.

Each method seems to provide additional apparently “real” that the other misses. Specifically ...

- There are significant numbers of “good” genes (with high AHRD scores) in both the “MAKER-only” and “GLEAN-only” sets. AHRD assigns a “quality” score ranging from 0 to 4 stars, with 4 being the best. In Aradu, about 2.5% of the MAKER only genes (331/12946) are 4-star and about 3.5% (393/11309) of the GLEAN-only genes are 4-star.

There are also frequently differences in gene fragmentation and structure (informal observation from looking at the browser).

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Please let us know if have any questions or spot any problems!
Steven and group

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