

## **The first International Tomato Finishing Workshop was held 16th and 17th April 2007 at Wellcome Trust Genome Campus, UK.**

The purpose of the meeting was to ensure that finishing standards are uniform over all chromosomes. Delegates from France, Italy, the Netherlands, Spain, the USA and the UK attended, giving representation for 8 out of the 12 *S.lycopersicum* chromosomes being finished across the consortium.

Below is an outline of the topics covered.

It is essential that these issues remain active as discussion points - please use this e-mail forum (tomato-finishing-L) to continue the discussion so we can conclude some of the issues and amend the standards document accordingly.

The workshop started with a tour of the Wellcome Trust Sanger Institute (WTSI) campus followed by presentations on the main principles of mapping and finishing approaches at the WTSI. This opened the discussion to the recently updated tomato genome finishing standards document available on SGN at <http://www.sgn.cornell.edu/solanaceae-project/sol-bioinformatics>

[http://docs.google.com/View.aspx?docid=dggs4r6k\\_1dd5p56](http://docs.google.com/View.aspx?docid=dggs4r6k_1dd5p56)

From these discussions the following issues were raised - these are in no particular order;

### 1. QA exercise

It was decided that this was necessary to do as part of the project. There was some discussion about how this would be approached and what checks would be beneficial. It will likely be coordinated centrally - but with multiple centres taking part.

Checks will include; -Restriction digest analysis

- Visual checks on the databases
- Checks on regions that will have tags in Genbank
- Utilisation of the FES (when available) to check integrity of the clone assemblies

### 2. Sequencing over uni-directional regions with the opposite strand

This was debated as it appeared in the original standards document but there is extensive evidence that regions covered by uni-directional Big Dye terminators that are of good quality are not prone to problems. We are keen to take opinions from all on this so we can reach an agreement.

### 3. Single Clone regions

There was debate about the reasonable attempts that should be made across these regions before we can add a tag to be visible in Genbank. We are keen here as well to take comments. Should we attempt to cover these? Should we attempt to sequence the single sub-clone in both strands before adding a tag to Genbank?

### 4. Reasonable attempts and tags for the Genbank submission.

We have discussed some of the regions we feel need to have a tag added to the Genbank submission. In addition we talked about the attempts that should be made of such regions before tags are added. A separate document will be circulated to this alias shortly with the suggested tags and attempts with some of the more detailed discussion points involved.

## 5. Protocols

There was some discussion about use of particular chemistries for specific problems. We hope to circulate more detailed information shortly.

## 6. New Tools on SGN

Lukas Mueller demonstrated some of the new tools available on SGN for viewing maps and finished sequence data and also for blasting the various tomato repeat sets.

## 7. Use of restriction digest data is essential

There was a great deal of discussion about restriction digest analysis for BAC clones to assist with the finishing process and to verify the final clone assembly.

## 8. BAC overlaps

This was discussed and the thoughts were that the overlap length to aim for could be reduced to 2kb. 500bp would be a minimum. In either case this is after the overlap has been verified on the map. Submissions made to Genbank that are finished uniquely without entire overlaps included should be tagged in Genbank to make clear that the finished sequence does not represent the entire insert of the original BAC clone.

## 9. Contamination screen is essential

Each centre should be screening for contamination of bacterial transposons and vector. An additional screen is performed by SGN when BACs are uploaded.

## 10. TPF and AGP files to be submitted to SGN by all by end of June

Once there is one file from each centre then we can review how often an upload will be practical and beneficial for the project. Each project should upload a first version of the files by the end of June, 2007.

## 11. Date for the 2nd International Tomato Finishing Workshop

There was agreement about the benefit of the finishing participants meeting together in this way. A provisional date for the next workshop has been set for February 2008. The workshop will most likely be held in Europe. Wellcome Trust Sanger Institute would be happy to host this again but if any country wishes to make an alternative offer then please make your intentions known.

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