



IWGSC Coordinating Committee and Triticeae Genome Workshop

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7-8 April 2011
Prague, Czech Republic



Data Release Principles/Policies

- All BAC libraries “backed up” at CNRGV
- Data depository – URGI
- Sequence submission to Genbank/EMBL
– suggestion – coordinated IWGSC submitter
- How do we achieve the most open data sharing while preserving the opportunity for analyses by data generators and IWGSC sponsors?

Examples: Potato



We are making the draft genome sequence of *Solanum tuberosum* RH and *Solanum phureja* DM1-3 516R44 (CIP801092) available to community prior to publication with the expectation that the community will not encroach on our efforts to analyze and publish a whole genome analysis of potato. Thus, by accepting the terms of this agreement and accessing the associated draft genome sequence data, you are agreeing not to publish whole-genome or whole chromosome scale analyses of the potato genome, analyses of gene families/genome structures/repetitive sequences, comparative analyses with other organisms including other plant genomes, or other analyses such that they encroach and limit our opportunity to publish the findings of our work.

The data may be downloaded and used by those who agree to these terms of release. It should not be further re-distributed or publicly released. Thus, if you wish for someone in your laboratory to use the data, they must all read and agree to the access terms as defined on this web page.

If the data are used in a publication, it should be cited as "Potato Genome Sequencing Consortium."

Examples: Peach



Early Online Access to the Assembled Peach Genome

The International Peach Genome Initiative (IPGI) would like to welcome you to the early online access to the draft assembled and annotated peach genome (peach v1.0). Rest assured, despite the fact that the genome is being made available on April 1, 2010, this is no joke! Before we talk more about the genome itself, let's do some housekeeping regarding data access.

As a public service, and in agreement with the [Fort Lauderdale agreement](#), the peach genome is being made available by IPGI prior to peer-reviewed publication of the data. IPGI and its partners are making this data available with the expectation and desire to publish this data in a reasonable time without preemption by other groups. *By accessing these data, you agree not to publish any articles containing analyses of genes or genomic data on a whole genome or chromosome scale prior to publication by IPGI and/or its collaborators of a comprehensive genome analysis ("Reserved Analyses").* "Reserved analyses" include the identification of complete (whole genome) sets of genomic features such as genes, gene families, regulatory elements, repeat structures, GC content, or any other genome feature, and whole-genome- or chromosome- scale comparisons with other species. If you are interested in collaboration on one of these topics involving the peach genome, please contact one of the project coordinators. Work towards the publication of the peach genome is underway, and we plan to submit a manuscript in the coming months. If you will be employing the data for non-reserved analyses, such as cloning a gene of interest or to analyze a gene family etc., please feel free to do so, we only ask that you reference the International Peach Genome Initiative as your citation.

Excerpt from the Toronto Statement

- **Data analysts/users** should freely analyse released prepublication data and act responsibly in publishing analyses of those data by:
 - Respecting the scientific etiquette that allows data producers to publish the first global analyses of their data set
 - Reading the citeable document associated with the project
 - Accurately and completely citing the source of prepublication data, including the version of the data set (if appropriate)
 - Being aware that released prepublication data may be associated with quality issues that will be later rectified by the data producers
 - Contacting the data producers to discuss publication plans in the case of overlap between planned analyses

Draft Data Release Statement of Agreement

By signing up for access to these data, I hereby agree to the following principles consistent with the Bermuda and Fort Lauderdale agreements on data release and the Toronto Statement: I agree to

- Respect the rights of the data producers and contributors to analyze and publish the first global analyses and certain other reserved analyses of this data set in a peer-reviewed publication. I understand that this includes:
 - Whole chromosome, chromosome arm, or whole genome level analyses on genes, gene families, repetitive sequences;
 - Large-scale intra-specific and inter-specific comparative analysis; and
 - Any other analyses that may limit the opportunity for the IWGSC data producers and contributors to publish the first global analysis.
- Not redistribute, release, or otherwise provide access to the data to anyone else, including anyone else in my lab. The data may be used only by the person signing this statement.
- Contact the IWGSC and data producers to discuss any publication plans that utilize this data to avoid the overlap of any planned analyses.
- Accurately and completely cite the prepublication data, including any applicable version.
- Prior to publication of the reserved analyses, credit “The International Wheat Genome Sequencing Consortium” and the leader, if any, of the relevant chromosome.
- Not patent or in any other way infringe the ownership of the data.

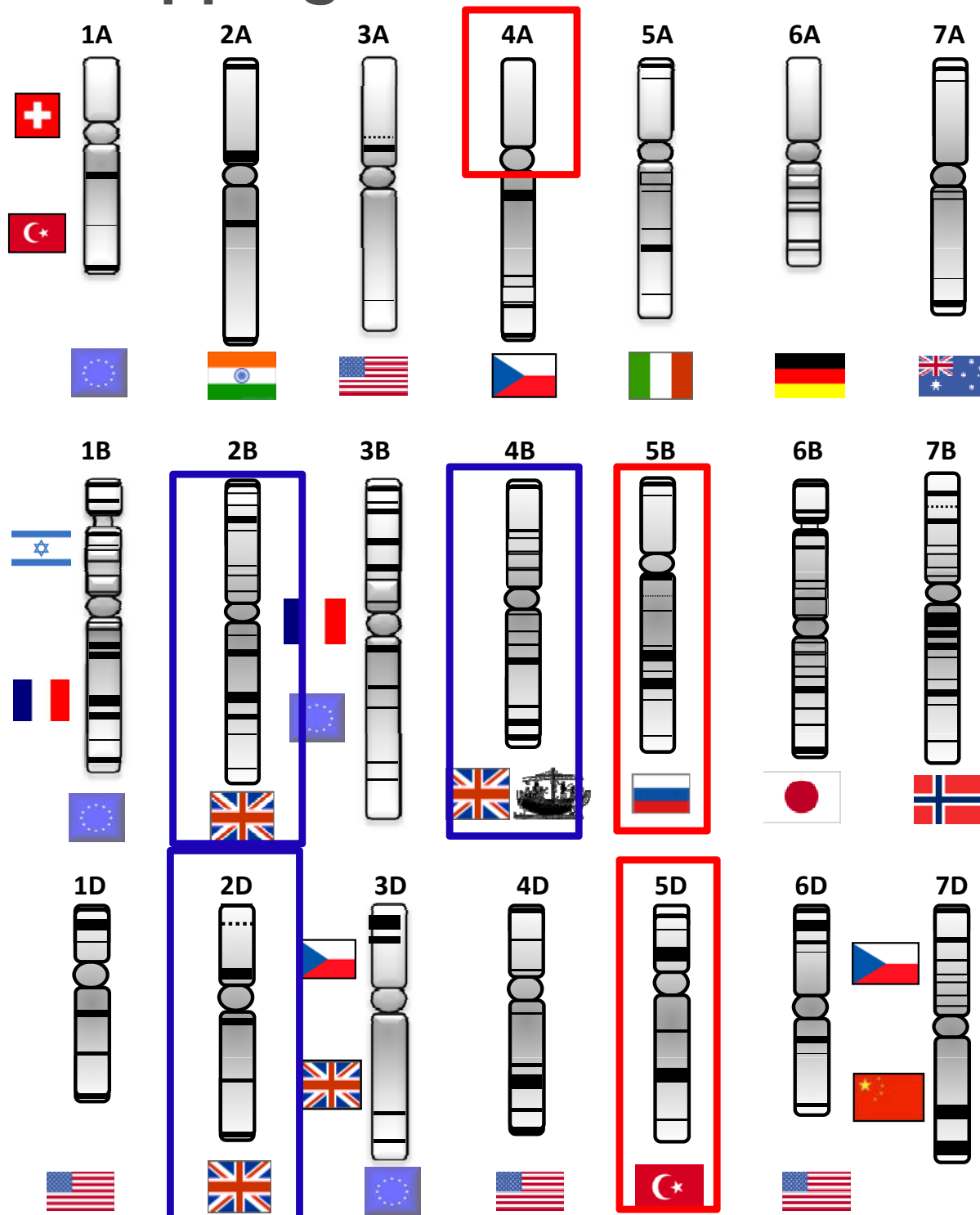
Timeline: Data Release Targets

- Survey sequence reads added to the short-read archive – by December 2011 or six months after assemblies.
- Assemblies?

Next Meetings

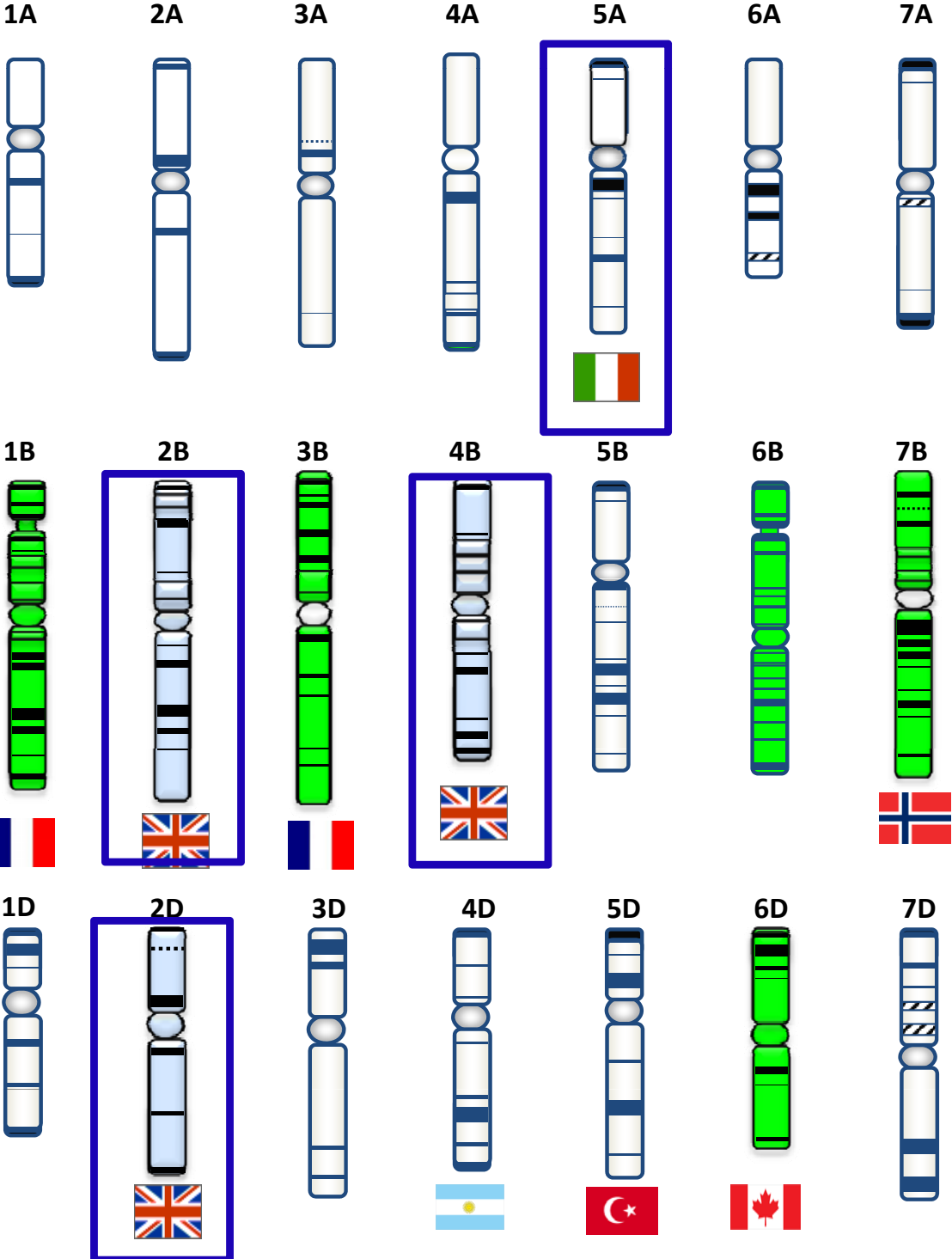
- IWGSC scientific workshop:
4 September 2011, Mexico City, Mexico
 - Topic ideas?
- Coordinating Committee meeting in conjunction with ITMI:
September 2011, Mexico City, Mexico.

Physical mapping of the bread wheat genome



T. aestivum
cv Chinese Spring

MTP sequencing of the bread wheat genome



T. aestivum
cv Chinese Spring

Sponsors





Thank you