



Workshop on
“Plant genomics resources and phenotypic data standardisation”
Organised by transPLANT Consortium¹
on 27-28 June 2013
in Poznań, Poland

We are pleased to announce the 2nd transPLANT user training workshop held in Poznań, Poland (Adam Mickiewicz University campus, Dept. of Biology, Umultowska 89, 61-614 Poznań) on 27-28 June 2013.

transPLANT is a consortium of 11 European partners gathered to address the challenges of complex plant genome data integration and to develop a trans-national infrastructure for plant genomic science. For details please visit <http://transplantdb.eu/>.

This second workshop (**see the preliminary program below**) will focus on current developments in plant data resources at transPLANT partner sites, with a special reference to Triticeae, as a lot of exciting but complex data was and is generated at the moment. We will also discuss topics related to standardisation and annotation of plant phenotypic data. The workshop is targeted at (experimental) biologists and breeders who have needs to use these resources in everyday work to interpret own observations. No particular prior (informatics) knowledge are required. In the different sessions we will introduce the partner plant data resources, explain what data is available and how to search, obtain and use this data. The local organizer group is located at Institute of Plant Genetics, Polish Academy of Sciences, Poznań, Poland (www.igr.poznan.pl).

There is NO registration or workshop fee but you will be responsible for your own travel costs, accommodation and local expenses. The number of participants is restricted to 25. The organizers reserve the possibility of selection of participants on the basis of information obtained at application. Details of proposed accommodation and transportation to Poznań will be given later.

If you are interested in that workshop please send the information required in the application form below to Paweł Krajewski, Institute of Plant Genetics PAS, Poznań (pkra@igr.poznan.pl) by 10th May 2013.

Institutions teaching in workshop: Adam Mickiewicz University in Poznań ; EMBL-EBI; MIPS – Helmholtz Center Munich; IPG PAS Poznań

2nd transPLANT user training workshop, 27-28 June 2013

Application form (to be sent to pkra@igr.poznan.pl by 10th May 2013)

Name, surname:

Position:

Affiliation:

Address:

E-mail:

Scientific motivation for attending the workshop (max. 50 words):

¹ The transPLANT project is funded by the European Commission since September 2011 within its 7th Framework Programme under the thematic area "Infrastructures", contract number 283496.

Preliminary programme

Day 1

9:00 Opening

9:05 - 13:00 Plant data resources at HMGU: PlantsDB (HMGU)

*MIPS PlantsDB (<http://mips.helmholtz-muenchen.de/plant/genomes.jsp>) is a database framework for integrative and comparative plant genome research and provides data and information resources for individual plant species (including *Medicago*, *Arabidopsis*, *Brachypodium*, *Sorghum*, maize, rice, barley and wheat). Building up on that, state-of-the-art comparative genomics tools such as CrowsNest are integrated to visualize and investigate syntenic relationships between monocot genomes. Results from novel genome analysis strategies targeting the complex and repetitive genomes of triticeae species (wheat and barley) are provided and cross-linked with model species. The MIPS Repeat Element Database (*mips-REdat*) and Catalog (*mips-REcat*) as well as tight connections to other databases, e.g. via web services, are further important components of PlantsDB.*

Specific topics:

1. Concept of and interactive data access to the barley and wheat genome zippers
2. The barley genome: integration of physical and genetic map, data access and use cases
3. UK wheat 5x WGS+analysis results: concepts to use this new data resource
4. Comparative genomics – from models to crops: exploring synteny, visualization tools (CrowsNest)

Lunch

14:00 – 14:45 Application of new web technologies in biological research and databases (Adam Mickiewicz University, Poznań)

*As biologists venture into bioinformatics, they often have to trade their favorite graphical computer desktop environments for a cumbersome command line versions of very useful scientific programs. Most recently the Web has rapidly evolved into a platform suitable for user-friendly applications that exhibit a level of richness and interaction that could barely be envisioned several years ago. The new web technologies are closing the gap to native applications and fill an important need for the development of data analysis software that provides bioinformatics functionalists to biologists without requiring prior knowledge of programming and scripting languages. We will present design and key technologies underlying some of the recent biological databases and web applications. We show their roles in integration, management and visualization of biological data in mirEX, our latest database of expression levels of *Arabidopsis* pre-miRNAs. We also show the use of different common programming languages to build an Ajax-driven biologist-friendly web applications. Finally, we demonstrate application of our recently-developed web service for annotation of highly-divergent tryptophan-containing Argonaute-binding proteins in grass genomes.*

15:00 - 18:00 Plant data resources at EMBL-EBI: Ensembl Plants (EMBL-EBI)

Ensembl Genomes (<http://www.ensemblgenomes.org>) is an integrative resource for genome-scale data from non-vertebrate species, including plants and plant pathogens. The project exploits and extends the vertebrate-focused Ensembl technology, originally developed for the human genome. Ensembl Plants (<http://plants.ensembl.org>) provides a complementary set of resources for plant

species, providing a consistent set of interactive (web) and programmatic (API and MySQL) interfaces. We currently host 22 plant genomes and provide access to data including: reference sequence, gene models, transcriptional data, polymorphisms and comparative analysis. Since its launch in 2009, Ensembl Genomes has undergone rapid expansion, with the goal of providing coverage of all major experimental organisms, and additionally including taxonomic reference points to provide the evolutionary context in which genes can be understood. Against the backdrop of a continuing increase in genome sequencing activities in all parts of the tree of life, we seek to work, wherever possible, with the communities actively generating and using data, and are participants in a growing range of collaborations involved in the annotation and analysis of genomes.

19:00 Dinner

Day 2

9:00 - 11:00 Methods of standardisation and annotation for plant phenotypic data (IPG PAS)

One of the transPLANT aims is to develop community-accepted standards for data description and submission, covering format, and content and policy. In this part of the workshop we will concentrate on the topics of biological data formatting and annotation possibilities. Currently available tools and Internet resources helpful for these tasks will be presented.

11:00 - 12:00 General discussion

Lunch