Revision of activity plans

1. **Website (**[**http://www6.inra.fr/wdi**](http://www6.inra.fr/wdi)**)**

**Structure of the website and contributors**

*Leaders names are in bold*

* Guidelines
  + SNPs (**Pierre**, Aravind, Ute, Imma, Pierre, Sophie, Raphaël, Nacer)
  + Genomic annotations (Pierre, Aravind)
  + Phenotypes (**Cyril**, Alex, Caterina, Laurel, Rosemary, Cyril)
  + Germplasm (**Rosemary**, Alex, Caterina, Laurel, Rosemary, Cyril)
  + Gene expression (**Laurel**, Alex, Caterina, Laurel, Rosemary, Cyril)
  + Genetic & Physical maps (**Michael**, Carme, Richard, Effie, Loïc)
* Use cases
* Surveys (Imma, Esther)
* About (**Imma**, Vassilis, Alex)

**Pending actions**

* SNPs : Introduction, best practices, tools, examples
* Genomic annotations: Introduction, best practices, tools, examples
* Phenotypes: Introduction, best practices, tools, examples
* Germplasm: Introduction, best practices, tools, examples
* Gene expression: Introduction, best practices, tools, examples
* Genetic & Physical maps: Best practices, tools, examples
* Use cases: a name for the last use case

2. Different data type related actions and follow up

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| **Data types** | **Actions** | **Participants** | **External experts** |
| **Physical maps** | Check for conversion tools GFF2 to GFF3. | Thomas, Michael |  |
|  | Search for feedback from experts concerning the use of GFF3 to handle genetic maps (in CMaP) and the metadata settings (marker, QTL, maps description) | Thomas, Michael |  |
|  | Have a look at the format from Graingenes |  |  |
|  | Search for details about linking requirements (e.g use the same marker naming standards). This point should be discussed with IWGSC EWG | Michael |  |
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| **Data types** | **Actions** | **Participants** | **External experts** |
| Genetic maps | Identify a minimal set of metadata to handle markers, QTL, maps (type, population, etc.) |  |  |
|  | Find experts that can help in clarifying if GFF3 is also used for genetic maps by CMap | Thomas, Michael |  |
|  | What happens with the markers data if GFF3 is recommended? | Thomas, Michael |  |
|  | Are the QTL information managed in GFF3? | Thomas, Michael |  |
|  |  |  |  |
| **Data types** | **Actions** | **Participants** | **External experts** |
| Phenotypes | Work on a metadata schema starting with IWIS and BMS | Rosemary, Cyril, Imma, Alex, Catarina, Sophie | RDA Metadata IG |
|  | Work on the standardization of traits - Ontologies of traits are/may be used (e.g plant ontology, crop ontology, etc.). Look at how to improve references to those ontologies should be improved | Rosemary, Laurel, Sophie | Elizabeth Arnaud, Marie-Angélique |
|  | Some pieces of data come from external resources e.g NCBI taxon names and IDs. Look at how to improve reference to external resources. |  |  |
|  | Think about making IDs public and retrievable. |  |  |
|  | Ontologies: the group recommends the use of Crop Ontology as a starting point. Anything to do regarding this point (guidelines, etc.)? |  |  |
|  | How about validators for the data filling of phenotypes fields? |  |  |
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| **Data types** | **Actions** | **Participants** | **External experts** |
| Germplasm | Check for compatibility with Genesys and Grin global | Rosemary | Elizabeth |
|  | Check with Elisabeth Arnaud the availability of a user friendly format for DWC Germplasm (a MPCD-like format) and if not, make a proposal | Cyril |  |
|  | Synonyms and Linked Data on IDs: propose a format for generating URIs for each organization. |  |  |
|  | Questions about provenance and contextual metadata should be asked to the “Genetic resources expert working group” of the Wheat Initiative | Michael |  |
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| **Data types** | **Actions** | **Participants** | **External experts** |
| Gene expression | Check for existing conversion tools from one data format to another | Laurel et al |  |
|  | Vocabularies:Microarray Ontology (MO), MGED ontology, Gene Ontology (a standard for the functional analysis). Should we do something about this question (guidelines, etc.)? |  |  |
|  | Shall we adapt the ENCODE-derived standards outlined here: [ENCODE\_BCBC\_RNA-Seq\_Standards](https://www.betacell.org/documents/administered/about/guidelines/ENCODE_BCBC_RNA-Seq_Standards_V01_20110503.pdf) |  |  |
|  |  |  |  |
| **Data types** | **Actions** | **Participants** | **External experts** |
| SNPs | Develop a metadata scheme which should be published and maintained by the Wheat Initiative. Starting list of fields based on GNPIS that could be completed with additional metadata from EBI and ENA. | Pierre? (not sure) |  |
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| **Data types** | **Actions** | **Participants** | **External experts** |
| Genomic annotations | Analyse the existing conversion tools GFF3 to RDF. | Pierre, Aravind |  |
|  | Guidelines for filling content for Column 9 “attributes”; these attributes are not specified at the moment |  |  |
|  | What ontologies (Gene Ontology? others?) to fill the column 9 |  |  |