Inclusion of C&E data in EURISCO – analysis and options

Introduction

The landscape of European PGR documentation is a complex one, with systems at the institutional level, National level and European level. They duplicate each others' data trying to serve the intended users of that information optimally[1]. The combination of passport data from different sources into Central Crop Databases (CCDBs), National Inventories and eventually EURISCO has proven relatively easy. It required the formulation of a standard list of descriptors (MCPD list), a few coding systems (for addresses, origin sites, countries) and obviously the effort of getting the data from the source to the combined database.

Since the beginning of these centralization activities, there have been discussions about also centralizing the characterization and evaluation (C&E) data. Very many of these data have been collected over the years on genebank material, some of them have been computerized, and from that part an even smaller part is available in the public domain. However, apart from a few genebanks, national systems and CCDBs, the centralization of this information has not materialized. This discussion paper, created in the framework of EPGRIS3 activity 2-05[2], will try to analyze why it hardly happened, and if we are going to make it happen, how this could be done.

The original version of this paper was discussed in a group of European PGR documentation experts at a meeting in Bonn on 7 May 2009, and in amended form approved[3].

Conceptual issues

C&E data are the scores of genotypic traits such as flower color, plant height, protein content and mildew resistance. They determine the value of germplasm for use in breeding and research programs, and are therefore of high importance to the user. This implies that molecular fingerprinting data are generally not considered to be C&E data.

C&E data comprise the data resulting from observations on the phenotype of a plant or population. The C-part, characterization, refers to highly heritable (often qualitatively inherited), easily observable traits such as flower color, kernel row number (barley), flowering time, number of shoots, etc. The E-part, evaluation, refers to traits more difficult to observe that often require specific experiments and/or equipment to determine, think of protein content, grain yield, or resistance to a specific pathotype. However, since the line between C and E is rather vague, and many traits can not be classified easily, the C&E data are usually treated as one category of data, especially from the database point of view.

Since C&E data concerns measurements on the phenotype, a number of things need to be known to allow for proper interpretation of an observation:
-    What genotype was scored? Generally this will be – in the PGR community – the population grown from the seeds of an accession, or one or a few random plants from an accession.
-    What trait was scored? This question is easy to answer in a specific case, but often difficult to interpret or standardize. For example, the length of a plant can be called in different ways such as 'plant length', 'plant height', 'growth height', but also names in local languages 'plantlengte' [this is Dutch], abbreviations 'PL', codes 'C021', or it can contain elements of the method of measurement or the environment 'plant length in early season'.

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[1] Refer to vision paper 'The European ex situ PGR Information Landscape' by van Hintum, Begemann and Maggioni as presented at the last ECPGR Steering Committee meeting and available on the EPGRIS3 web site as output of activity 2-06 (http://www.epgris3.eu/EPGRIS3activities.htm#LinkECCDBs)
[2] See EPGRIS3 website www.epgris3.eu/EPGRIS3activities.htm#C&E-Data
[3] For details see EPGRIS3 website www.epgris3.eu/EPGRIS3%2020090507workshop.htm

- How was it scored? Is it an estimate or a precise measurement, is it scored on a nominal, ordinal, interval or ratio scale; whether it is an ordinal scale from 1 to 9, can all classes be used, is it even allowed to score intermediate values between classes (5½).
- When and where was it scored? This is the question relating to the experimental conditions, the experimental design, the location and environment under which the experiment was performed, the genotypes used in the comparison.

These four elements can be called (1) genotype, (2) trait, (3) method, (4) experiment.

It is obvious that these four are not clearly separated. For example, in observations from a single location, the effects of the environmental conditions will be indistinguishable from the effects of the genotype. Since the phenotype is usually the result of both the genotype and the environment, $P=f(G,E)$, information about the environment is required to interpret a score. Saying that a plant is tall might mean that in comparison with other modern varieties in a given environment it is taller than average. But how would it score in comparison with landraces, or in a year with early drought?

This GxE effect is even worse if economically important disease resistances are considered. Here, as a result of the frequently occurring gene-for-gene interaction, different pathotypes causing the infection might result in completely different reactions. Field infections usually are composed of a pallet of pathotypes that varies over time. Only resistance tests under controlled conditions where the inoculum consists of purified and identified pathotypes will probably result in repeatable results. But does that make field observations worthless?

In the end one might conclude that one needs to know so much about the experiment and the genetics of the trait before one can interpret the score, that it makes no sense to generate and use these data. This is obviously not the case. There are a few solutions:
- The first strategy is to choose highly heritable traits whose expression is hardly influenced by the environment. Think of some of the typical 'characterization traits' such as 'row number' for barley or 'crop type' for *Brassica*.
- The second strategy is to standardize the experiment, include standard varieties, prescribe standard experimental design, and control the environment as much as possible in terms of irrigation, soil, disease control. This approach is followed in research to support the registration of new cultivars, but also in regular breeding activities.
- The third strategy is to take the results as they were generated and perform a statistical and/or heuristic analysis to squeeze out as much information about the genotype as possible. This is done for example at CGN to create on-line searchable datasets – one score per accession per trait - from the wide variety of data available from different experiments using different scales with different reliabilities.

So, in general, the first and most important thing is to properly define the variables needed to interpret the score. This will allow comparison of scores within one experiment. To allow comparison of scores over experiments the level of standardization and the level of analysis required will be in balance: the more standardization the less analysis. And, as in all aspects of combination of information from different sources, harmonization or even standardization of terminology makes things much easier.

Experiences with sharing PGR C&E data

Many attempts have been made to make C&E data available on the web. Several genebanks present their C&E data attached to passport data on individual accessions, and few have the possibility to search the C&E information. However, given the apparent importance of these data to the user, the access to this information is low. Also the attempts to combine or centralize C&E data in CCDBs, GRIN and SINGER or the German EVA/EVA2 system have been tedious. Maggioni[4] listed in a 2008 presentation 13 CCDBs with C&E data, however a closer inspection of these databases shows that access to, and the completeness of these data is usually very limited. Here, we'll briefly discuss the approaches and experiences of a few

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[4] Paper 'CCDBs and EURISCO' presented at a EPGRIS3 meeting, March 2008, and available on the EPGRIS3 web site as output of activity 2-06 (http://www.epgris3.eu/EPGRIS3activities.htm#LinkECCDBs)

national genebanks, the CCDBs and the centralized databases SINGER and GRIN. The recent workshop of a group of European PGR documentation experts in Bonn on 7 May 2009 in Bonn presented a more complete picture, the presentations are available on the workshop website.[5]

Looking at national genebanks, only very few allow searching C&E data, some display the data after selecting a specific accession on the basis of passport data. For example, NordGen (Nordic Countries) apparently has the technical ability to display C&E data connected to an accession, however, a 10 minutes search of the database did not result in finding any. At CGN (Netherlands) there is the possibility to download Excel spreadsheets, per crop / trait combination with all C&E data in their database. However these data are made available as they were received, with a variety of scales, methods for measuring and anything else that can vary. To allow the user to search the C&E data while selecting germplasm, for the majority of their crops, the data are synthesized into 'one score per trait per accession' on a scale with no more than five states, to indicate that the reliability of these scores is not very high. The synthesizing effort however is difficult (statistically and biologically) and labor intensive.

Among the large databases that combine data from many sources, the attempts of SINGER to incorporate C&E data have not been successful and EURISCO never even tried. GRIN, on the other hand, provides the user with the possibility to search the C&E data that are available on a standardized scale. The problem here is that apparently any number of observations, on a single accession-trait combination can be included in the database. This can obviously lead to conflicting results. For example, the first fully random search in GRIN resulted in the barley accession PI 383968. This accession had, apart from many other C&E data, two observations for protein content: once 12.38% and once 17.09%. Since also statistics about the experiment that generated the data is accessible, it was possible to find out that in the first experiment it was .2 standard deviation below average of the experiment, whereas in the second it was 2.8 standard deviations above, in other words from average to very high. But at least these data were available, and apparently GRIN had been able to enforce the standardization of the scales.

The situation in the Central Crop Databases varies widely. Most do not have C&E data, but some have, usually originating from an EU project. A few were briefly examined.
- The European Cultivated Potato Database, a database that takes the variety and not the accession as a starting point, has an impressive number of traits that can be searched via an interesting interface. Again a random search: cultivar 'Ariane' showed many traits of which most with only one source or two or more agreeing scores, however 'maturity' was 'intermediate to late' according to one source, 'early to intermediate' according to two others and 'early' according to a fourth source, and the 'dormancy period' was 'short' or 'medium to long' and finally 'yield potential' appeared to be 'medium' to 'very high'. This was only one search, but illustrated a struggle with the same problem as GRIN. The data apparently can be uploaded by contributors directly into the database, provided that the descriptor lists are used.
- The *Vitis* database is also searchable for C&E data, but has a very poor interface. There is a huge list of 72 descriptors, often with names difficult to interpret, such as 'leaf: length p.s. to upper sinus', and the list with scores from which the user can only select one, shows that this part of the data also has not been curated. The random trait 'berry: weight' lists 257 distinct scores, the first 10 being 'm', '0,73', '0,9', '0,97', '1', '1I3', '1,0', '1,02', '1,1' and '1,16'. These data are probably also directly imported, in a similar way as the potato database.
- The European *Avena* Database (EADB) has the most elaborate system for making its C&E data available. There is an apparently extensive set of data and a conceptually well developed interface, though not very user friendly. The approach followed appeared to be at some points similar to CGN, with both the raw data available and so-called 'universal scores' searchable, implying a lot of manual work creating the 'universal scores.
- The European Wheat Database has some C&E data that can be searched in a simple straightforward interface. Apparently the data are collected in a strict format: one score on a pre-defined scale for each of the 21 pre-defined traits per accession. However searching the data showed that few data are available (especially for the disease resistances, no data could be found. The database manager (Iva Faberova) informed us that "Both chairing countries

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[5] For details see EPGRIS3 website www.epgris3.eu/EPGRIS3%2020090507workshop.htm

(CHE and CZE) delivered the main part of information and the third in order is CGN. Those three C&E data sources provided 14655 of total 19222 C&E data ...” and “It is not easy to receive data, even there is morphological information only. The EWDB descriptor list includes a long set of diseases, but nobody is willing to deliver data... Everybody is promising only.”
- The European *Brassica* Database links to the results of two EU projects that are made available in fixed Excel files. Apart from that no C&E data are available.
- The European Barley Database includes searchable C&E data from joint evaluations in an EU project, but it is not easy to find the C&E data. The search interface was developed based on NordGen's 'Dynamic Data Analyser'.

In summary a few observations can be made:
- C&E data are rarely available on genebank websites, and even more rarely searchable.
- Getting the C&E data for centralized databases appears to be very difficult, partly because of the low level of computerization at the provider side, partly because of the labor involved in the required standardization, and possibly partly because of IP issues.
- For centralized databases there are a few approaches, either C&E data are requested in a highly standardized form: a few fixed traits, fixed scales and one score per accession, or the data are made available in a standardized format as they are received. Only the EADB does it in an essentially different way.

A proposal for centralizing access to PGR C&E data

When we discuss exchange of C&E data, it is not feasible to enforce any standardization in terms of experimental design, the use of standards or even the scale of measurement. Standardization only succeeded moderately well in specific projects on *Vitis*, *Avena*, barley and potato due to additional project funds (many coming from EU GENRES 1467/1994 and 870/2004). As a result, the starting point should be the data as they are in the databases.

We can standardize the exchange format, assuming that all data donors are able to export their data in a common format, provided that this is a flexible format. The C&E data of each data source would have to be transformed into this format, with a minimum of data transformation, and uploaded either to the National Focal Point or to EURISCO directly.

EURISCO would, apart from being the current compilation of National Inventories, turn into a repository of European C&E data, strongly increasing the visibility and access to these data. These data would, however, be non-standardized data on a variety of scales, generated in different environments and using all thinkable methods. It will be a challenge to make the data accessible to individual users, and an important role might be played by the Central Crop Database Managers. EURISCO would provide these crop experts with ready access to all (uploaded) C&E data of 'their' crop, ready to be harmonized, analyzed, and made searchable.

As part of the validation of the data to EURISCO, there will have to be a check whether the data correspond to known accessions in EURISCO; this is a prerequisite. Another prerequisite, at the responsibility of the 'uploader' of the data, is that the data are non-confidential: all uploaded data are to be made freely available in the EURISCO-site.

Exchange Format

The exchange format will need to document the minimum information needed to interpret the score. A few elements will need to be covered in the exchange format:
- *Genotype* - The format for C&E data exchange will need to contain information about the genotype characterized. We should assume that this concerns accessions already registered in EURISCO, and the identification can be done via the unique key of EURISCO[6]. In the future Life Science Identifiers (LSID) could be used for this purpose.

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[6] Combined key consisting of the fields NICODE, INSTCODE, ACCENUMB and GENUS

- *Trait* – As long as we do not have and use agreed descriptor lists or ontologies, we'll have to accept the trait names as used by the data providers; what we can ask is to provide an English name of the trait.
- *Method* – A brief description, in English, of the way the trait was scored: first of all the scale that was used, and possibly additional info such as 'the average of five random spikes'.
- *Experiment* – A brief description, in English, of relevant aspects of the experiment: the location plus circumstances such as 'on sandy soil in the Netherlands', 'during multiplication' or 'from a randomized complete block experiment in triplo', 'start of growing season was dark and humid', etc.

This implies that evaluation data would be uploaded in packages consisting of one or more experiments; at this level there could be a generic methodological remark (e.g. the convention for handling variation within accessions). One experiment (with its description) contains *n* genotypes (with their IDs) and *m* traits (with their name and method) and of course *n* x *m* scores or less if not all accessions have data on all traits.

In a relational database this would translate into tables for 'genotype', 'trait' (possibly combined with 'method' or in a one-to-many relation) and 'experiment', all in a one-to-n relation to 'score'.

Obviously, for the purpose of data exchange, this can be implemented in many structures. Probably the most elegant is XML, but 'easier' are Excel spreadsheets, or a set of fixed column text files (as in EURISCO). All these can be relatively easy worked out, demonstrated and implemented. The bottleneck is at the level of the definition of the 'fields'. The list below was discussed and approved by a group of European PGR experts[7]. It is based on the experiences in several genebanks around the world. We will distinguish the four entities described above, combining trait and method, plus one describing the source of the data:

DATASET containing
- UPLOADERCODE – ID-Code, provided by EURISCO, for the registered authorized data provider uploading the data to EURISCO (mandatory)
- DATASET_REMARK – any general remark relevant to all scores in the dataset (max 255 alphanumeric)
- Depending on the upload format an additional ID might be required to link the EXPERIMENTs with the DATASET – needs to be solved when the final formats are described.

EXPERIMENT containing
- EXPERIMENT_NUMBER – unique number in the dataset for the experiment; this number should be unique and persistent for the data provider (mandatory)
- EXPERIMENT_DESCRIPTION – information relevant for the interpretation of the scores in the experiment such as experimental design, experimenter, weather, etc. (max 255 alphanumeric)
- EXPERIMENT_YEAR – the year the experiment was done (started) (4 numeric)
- EXPERIMENT_LONGITUDE – the longitude of the experimental site, provided it was an experiment in the open field (decimal number)
- EXPERIMENT_LATITUDE – the latitude of the experimental site, provided it was an experiment in the open field (decimal number)
- EXPERIMENT_REPORT – a reference to the report of the experiment, either supplied with the data (then only the file name needs to be given, that could be presented as a hot-link in the interface) or the URL of the report or original data (max 100 alphanumeric)

TRAIT containing
- TRAIT_NUMBER – unique, temporary number for the trait in the dataset (mandatory)
- TRAIT_NAME – English name of the trait (max 50 alphanumeric, mandatory)
- TRAIT_REMARK - any general remark that helps interpret the trait (max 255 alphanumeric)

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[7] For details see EPGRIS3 website www.epgris3.eu/EPGRIS3%2020090507workshop.htm

   TRAIT_METHOD – a description of the method for measuring and the scale used (max 255 alphanumeric)

GENOTYPE containing
   GENOTYPE_NUMBER – unique temporary number for the genotype in the dataset (mandatory)
   GENOTYPE_NICODE – see EURISCO (mandatory)
   GENOTYPE_INSTCODE – see EURISCO (mandatory)
   GENOTYPE_ACCENUMB – see EURISCO (mandatory)
   GENOTYPE_GENUS – see EURISCO (mandatory)

SCORE containing
   GENOTYPE_NUMBER – key to GENOTYPE (mandatory)
   EXPERIMENT_NUMBER – key to EXPERIMENT (mandatory)
   TRAIT_NUMBER– key to TRAIT (mandatory)
   SCORE – actual score (max 10 alphanumeric, mandatory)

Some of the mandatory text fields, such as TRAIT_NAME, have to be in English. However, it is generally recommended, for obvious reasons, to only use the English language in the files that are to be uploaded to EURISCO.

Upload mechanism

The upload mechanism should be aligned with the current EURISCO upload mechanism, i.e., the National Focal Points (NFP) should be allowed to upload or delete C&E data. However, in the case of C&E data, it should be possible for a NFP to delegate the uploading task to one or more persons in other organizations, who would be able to upload or delete data originating from their own institution. There will be provisions made at the EURISCO level to accommodate this, possibly including the option for the NFP to revise data uploaded by a delegated uploader before committing.

The mechanism should have the ability to accept any of the agreed formats.

After accepting a file from a uploader, the mechanism should check the integrity of the files: the format and all used codes should be checked. In case of errors, a report should be made available to the uploader, again similar to the current mechanism for passport data.

If the datafile is okay, it can be loaded:
- since the EXPERIMENT_NUMBER is a unique and persistent number for each data supplier, it can be checked whether this experiment already exists in the repository, if so, the already loaded experiment should be replaced,
- the other numbers (TRAIT_NUMBER, GENOTYPE_NUMBER) should be replaced by the existing numbers in case the corresponding data are already in the repository, otherwise a new internal number should be attributed,
- all (new) data should be loaded in the corresponding tables.

A report about the replace and insert actions should be sent to the uploader, via an automated logging system.

Download mechanism

When the data have been centralized, the result will be a very large repository of completely unstandardized but interpretable scores. The managers of the repository will have to create some interfaces allowing potential users to extract that information that (s)he needs. This user will first have to screen and analyze the information before (s)he can make a selection of material.

The download mechanism will need much attention. It should be use-case oriented: different users should be identified and their needs should be described and accommodated.

Initially two major user-groups should be distinguished: (1) the bulk user, such as CCDB managers creating or maintaining a crop specific PGR portal and scientists doing a large survey, and (2) the trait searcher, a breeder or scientist who is looking for a specific trait.

A complicating factor is that EURISCO doesn't have a standardized division in crops. This implies that any user will have to start by selecting accessions, for example of all *Triticum* and *Aegilops*, in all spelling and format versions currently featured in EURISCO. After selecting the accessions, the user should only be confronted with the C&E data on those accessions.

The next step should be the selection of traits. Since trait names are not standardized this might involve long lists of trait-names, and might require a search interface. After selecting the trait(s), the user should be allowed to select the experiments that (s)he would like to get access to. Full text searches in the experiment reports could be an additional way to find the appropriate experiments.

At this point the user should be requested to indicate how the data should be presented or downloaded. This could take many shapes, including the download of entire experiments or the download of matrices with accession times trait/experiment combinations. The display of the selected data in the specified format might become a problem because of the size of the information. In case of download, the required format should be selected (xls, xml or txt), the output should be generated, with appropriate meta information (decoded codes, a readme for the use and interpretation), and made available in a downloadable shape (in a zip file or on a html page with clickable files).

Finally, also the wishes of other systems that might want to use the C&E data in EURISCO, such as ALIS, will be accommodated. For this, and other purposes, it will be desirable to make EURISCO available as a web-service.

Implementation

Getting the C&E data in EURISCO will not be a trivial task, comparable with e.g. the registration of MLS status of the accessions. However, it is of high importance to the user and very timely.

Implementation will require a number of steps:
- Creating ownership in the community of genebanks for the approach to follow by discussing a proposal like this and improving on it, using email correspondence and possibly one or more workshops.
- Agree on and define (the elements of) the mechanisms in detail, including upload formats and functional design of required software and database.
- Get the commitment of a few large potential data donors (NI with access to C&E data) to supply their data in the testing phase (NordGen, CGN, BLE, IPK).
- Build the software required, and test the upload mechanism in collaboration with the committed genebanks.
- Support potential new data donors by approaching them on a personal level, organizing training workshops and/or technical visits.
- Improve on interface and download format in collaboration with selected users.
- Promote the resulting database via publications and/or presentations aimed at the user community (PGR community, plant scientists and breeders).

A prototype, with the data of the 'committed genebanks' and a first download mechanism could be ready in half a year. The total mechanism can be completed in 18 months. The costs would be mainly the coordination of activities, software development and travel funds. Sources for these funds will have to be identified.

Concluding remarks

If we are to centralize C&E data we'll have to accept that these data, as far as they are available in computerized form, vary in all ways possible. Obviously we should try to promote standardization, of both structure and content. The structural part will be dealt with once we start exchanging and centralizing, it can be expected that the exchange format will promote implementation of similar structures in databases. Concerning the content, the first thing to standardize is the trait-names, and a start has been made with the descriptor lists of IPGRI / Bioversity and UPOV, however an expandable trait ontology (with the possibility to cross-reference between the trait names provided by the users and the "standard names") would be very useful. And it would be even better to create joint evaluation programs across European genebanks, possibly in the framework of AEGIS.

Therefore, as a start a pragmatic and cost-effective approach should be followed with activities that can be started right away. But in parallel activities aimed at standardization should be started, aiming at providing appropriate ontologies but also aiming at further standardizing the evaluations themselves, based upon agreed standard varieties, protocols, etc, using all opportunities arising from AEGIS, joint EU projects, and others.

In any case, the proposal above could be implemented tomorrow. And certainly if this proposal is improved with the input of many, it can be expected to be the starting point of an exciting new era for EURISCO.

Acknowledgements

Theo van Hintum, CGN, May 22, 2009

APPENDIX

During the May 7th, 2009 EPGRIS3 meeting in Bonn, Germany[8] a few decisions were made that could not sufficiently be reflected in the text above, or are not sufficiently explicit. These will be listed below:

- Only C&E data of accessions in EURISCO, and thus part of a National Inventory can be uploaded.
- A certified uploader (the EURISCO National Focal Point or a delegate) can upload C&E data on any EURISCO accession (irrespective of the NI it is part of). This is to allow the uploading of the results of EU or other collaborative projects.
- It was considered to add the URL of the original data file in EXPERIMENT, however it was decided not to include it – for the time being.
    Comment by Dag Terje Filip Endresen: More than a URL link to the original data file, I think the URI to a interface of a representation of the original data would be useful (which could include the source data file...). With the URI to for example the web service (preferably standardized to support the C&E data format, but preferably also Darwin Core) at the data provider site, a consumer of C&E data from EURISCO could build his/her own automatic tools to consume the trait observation data. EURISCO providing assistance for the user in discovery of the trait observation datasets, but not necessary in all the full data model richness of each trait dataset. But I am sure that the ability to provide this is some years ahead – at least for the majority of genebanks. A good starting point to stimulate this ability to develop from the data providers could perhaps to allow data providers to share a LSID for each experiment... The LSID could develop in time to be the handle for the interface of the web service sharing a richer version of the trait dataset.
- It is stressed that the numbers for genotype and trait are temporary and will be deleted after insertion in the EURISCO databases, however the number of the experiment (EXPERIMENT_NUMBER in the proposed structure) is persistent and will be used to replace or delete data; any uploader should manage these numbers well.
- Several other potential fields were discussed, however inclusion of additional fields (such as the date, location and observer of a score was rejected for the sake of simplicity – this might be reconsidered in a couple of years.
- In regards the implementation it was decided that
    - Theo van Hintum will update this document and create a website
    - Frank Begemann will circulate the proposal to the ECPGR Documentation and Information Network Coordinating Group and the wider network of CCDB managers and National Focal Points, and ask for feedback.
    - Michael Mackay will check the proposal against other systems such as GRIN, and propose changes to harmonize when needed.
    - Frank Begemann will try to 'feed the proposal into the GIGA process', explore possibilities to benefit from each other's initiative, and possibly integrate them.
    - Based on all feedback, Theo van Hintum, Frank Begemann and Lorenzo Maggioni will prepare a definite proposal.
    - The definite proposal will be distributed by Lorenzo Maggioni to all ECPGR National coordinators for information and comments.
    - After that the details of the elements of the mechanism will have to be worked out in a number of documents (by *to be decided*).
    - Michael Mackay will explore the possibilities to incorporate the proposal in the next phase of GIGA.
    - CGN, NordGen, BLE and IPK committed themselves to deliver the first data sets for developing and testing the infrastructure in Rome.
    At this point we enter the implementation phase. No commitments have been made in this regard but it became apparent that this is a badly needed and widely supported initiative, and its implementation should be high on EURISCOs priority list.

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[8] For details see EPGRIS3 website www.epgris3.eu/EPGRIS3%2020090507workshop.htm