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INTERNATIONAL TREATY ON PLANT GENETIC RESOURCES FOR FOOD AND AGRICULTURE

FIRST MEETING OF THE EXPERT CONSULTATION ON THE GLOBAL INFORMATION SYSTEM ON PLANT GENETIC RESOURCES FOR FOOD AND AGRICULTURE

San Diego, USA, 7-8 September 2015

ANALYSIS OF THE LANDSCAPE AND GENOMICS SURVEYS IN THE CONTEXT OF THE GLOBAL INFORMATION SYSTEM

EXECUTIVE SUMMARY

1. This document has been prepared as an input to facilitate the discussions at the First Consultation on the Global Information System on Plant Genetic Resources for Food and Agriculture. It contains the analysis of the two surveys conducted during 2014 on the main elements of the Global Information System and on current experiences on genomics, phenomics and information exchange.

2. The surveys, designed and circulated in collaboration with other partners and initiatives, collected useful views and information from Contracting Parties and stakeholders, and this document presents the major findings and trends on each of the questionnaires to stimulate the discussion.

3. As part of the documentation for the meeting, the Secretariat has also made available on the Treat y website the inputs received from the other organizations and interested stakeholders.

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I. INTRODUCTION

1. At its Fifth Session, the Governing Body of the International Treaty requested the Secretary through Resolution 10/2013[1], and subject to available resources, to call for an expert consultation on the Global Information System of Article 17.

2. In early 2014, the Secretariat received funds from the Government of Germany to prepare the Consultation and initiated a round of discussions with partner organizations to gather inputs and identify the main areas and elements to be further developed, building on experiences accumulated by those partners and with a view to promote free and open access to data and information in the area of plant genetic resources for food and agriculture.

3. The Annex to the Resolution contains the terms of reference for the consultation, describes its scope and enumerates its objectives. For the preparation of the Consultation, the Secretariat was requested to gather inputs and elaborate a series of background study papers in cooperation with Contracting Parties and relevant stakeholders, including an online survey on the major components of the Global Information System.

4. To collect views and information from Contracting Parties and stakeholders, and in collaboration with other partners and initiatives, the Secretariat prepared and launched in 2014 an online consultation through two surveys:

a. Survey 1 - Landscape Survey on the major components of the Global Information System

b. Survey 2 - Survey on Genomics, Phenomics and Data Sharing and Exchange

5. The present document illustrates the way in which the surveys were prepared and circulated, and also presents the major findings for each one with the aim to stimulate further discussion. The Treaty Secretariat has incorporated some of these elements in the draft vision paper[2].

6. It is foreseen that the online consultation exercises will be repeated from time to time as one of the activities under the collaborative framework of the Global Information System to involve users, stakeholders groups, and relevant initiatives in the development of the functions and services of such system.

II. METHOD

7. Both surveys were structured in the form of online questionaires with one round each and were available online for a little over one month, from 5 July 2014 until the end of August 2014. The questionnaires were published in three UN languages, English, French and Spanish. The Secretariat issued an online notification, which was sent to Contracing Parties and interested stakeholders, requesting them to complete and circulate the two questionaires[3].

8. The Landscape survey was divided into two segments and was mainly addressed to the national focal points of the International Treaty. It was also circulated by email to all of them. It was developed through 17 questions and took an average of 15 minutes to be completed. The survey combined multiple choice questions with questions requiring elaboration and comments.

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[1] Development of the Global Information System on Plant Genetic Resources in the Context of the Article 17 of the International Treaty, IT/GB-5/13/Report, available also at http://www.planttreaty.org/content/resolution-102013-development-global-information-system-plant-genetic-resources-context-arti

[2] IT/COGIS-1/15/2

[3] GB6-0018 –Article 17– Surveys on the GIS. Available in four languages at: http://www.planttreaty.org/content/invitation-complete-and-circulate-two-surveys-context-global-information-system-pgrfa

9. The Second survey was addressed to stakeholders and organizations involved in genomics, phenomics and data-sharing and exchange. It was also promoted through an official notification, and circulated in collaboration with partner organizations to a wider audience, including participants of technical meetings on the subject matter[4]. The survey was structured in four sections and it took, on average, 35 minutes to complete. Not all questions required a reply from the respondents.

10. The questionnaires were used as a tool to implement a multi-stakeholder approach to participative policy-making and introduced different evaluation scales to express desirability and preferences, as well as expected scenarios.

III. THE LANDSCAPE SURVEY ON THE MAJOR COMPONENTS OF THE GLOBAL INFORMATION SYSTEM

a) Respondents

11. The Survey elicited views and opinions from national focal points of the International Treaty on PGRFA and collected responses from 78 participants from all regions, half of them from Europe and Africa as shown in Figure 1. Half of the respondents declared themselves to be the national focal point and the other half said they were officers and staff completing the survey on behalf of their national focal point.

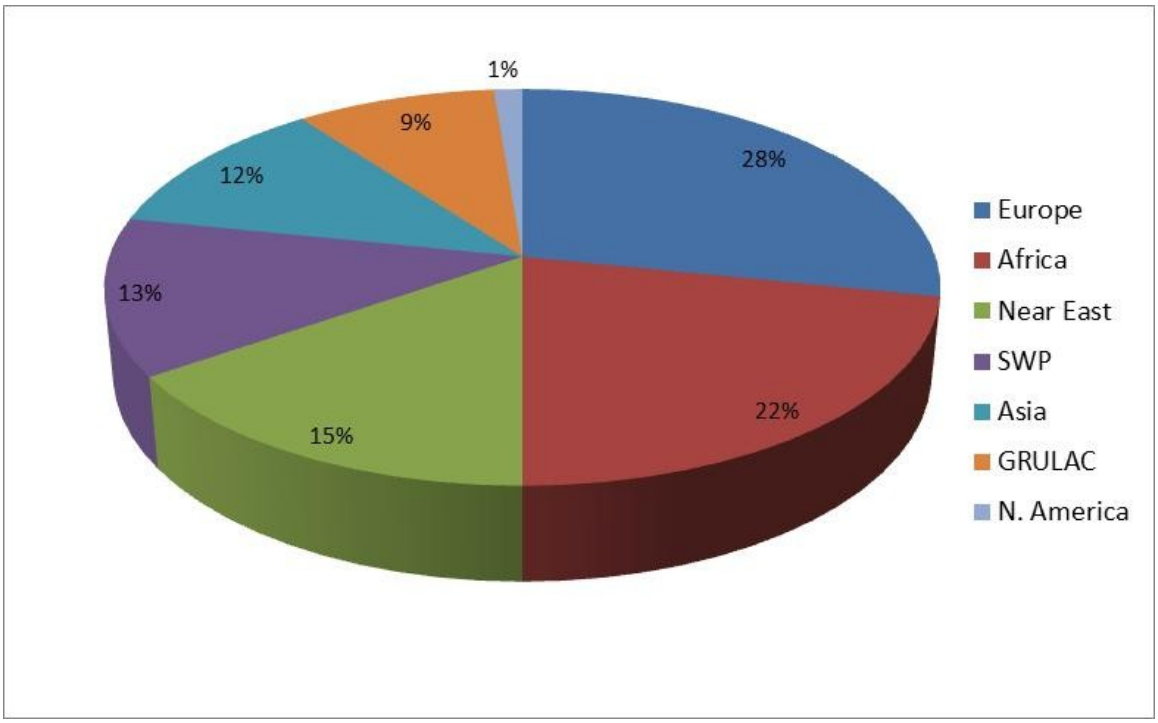

Figure 1: Regional distribution of the respondents.

b) Short Statement and Main Principles

12. As part of its Terms of Reference, the experts of the Global Consultation will advise the Secretariat on the Vision for the future development of the Global Information System referred to in Article 17 of the International Treaty, which will be put forward for the consideration of the

[4] Including the participants of the San Diego Meeting on the advancement of plant genomics, which had previously participated in the SeedSeq meeting in San Diego, and others that have have converged into the DivSeek Initiative.

Governing Body at its Sixth Session. In this regard, the questionnaire presented a short statement on the main elements of the Vision:

> ***The Global Information System will provide a platform of interoperable data and information services on plant genetic resources for food and agriculture;***

13. Then, it requested respondents to express agreement or disagreement, in a five-degree scale, with the following statement, listing a series of principles to be incorporated in the Vision: "***The System will be open, innovative, dynamic, decentralized, collaborative, user-centric, and quality-focused***". As Figure 2 shows, 94% agreed with this vision statement, and nobody expressed any disagreement (the options disagree and strongly disagreed both equal zero).

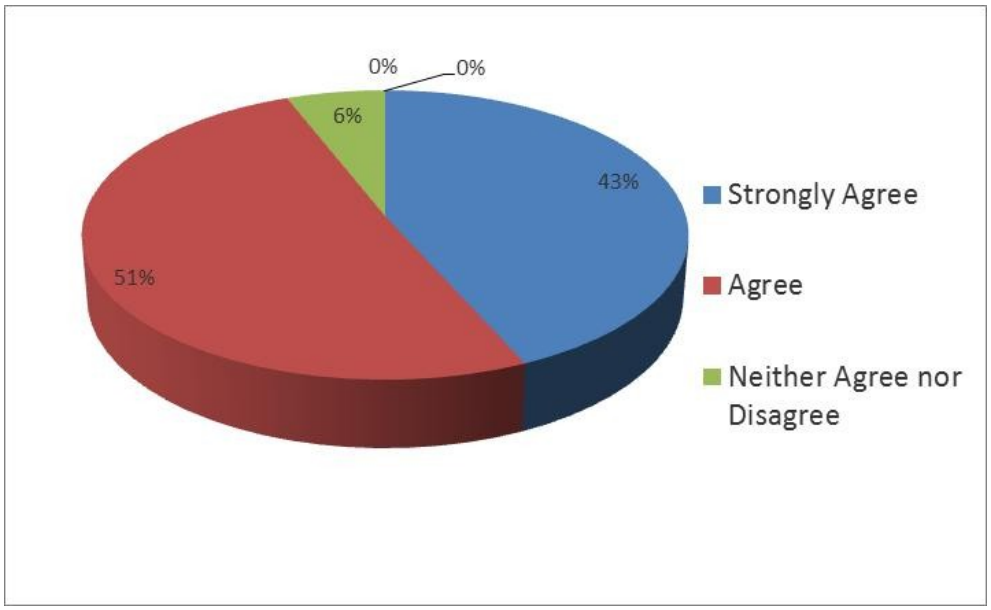

Figure 2: Participants' views on the short statement and the proposed set of principles. No respondent disagreed or showed strong disagreement to the principles listed.

14. Some respondents indicated that, although they supported the principle of decentralization, there is the need for **a central platform at an international level and some sort of core system,** easy to use and understand. Participants also suggested that being user-centric should not be understood as a way to focus uniquely on the needs of the current users, as these may evolve over time.

15. A few users indicated that the ultimate finality of the system should also be incorporated in the opening statement, indicating that *the purpose of the system is to facilitate conservation, utilization and development of agro-biodiversity by integrating ex-situ and in-situ and on-farm information for the benefit of mankind*.

16. Respondents also suggested the consideration and inclusion of additional principles and ideas like: **interoperability** (with other systems) and **free and easy access**, particularly for developing countries with limited internet access and small island states. They indicated that the System should contribute not only to food security, but also to *nutrition and climate change adaptation*. The contribution of authoritative data from National Focal Points or other authorities should also be considered.

c) Top Challenges and Priority Areas

17. The Landscape Survey also listed 13 areas of work to investigate which ones presented the most important and urgent challenges for the Global Information System. Each respondent was allowed to select up to 8 options. The order of priority assigned to these areas is given in Table 1 directly below:

Table 1: Full ranking of challenges listed in order of preference

1	**Link to policy, legal and regulatory information regarding PGRFA at national and international levels.**
2	**Make the material in the Multilateral System more visible and easier to request/order.**
3	**Provide access to technologies for the conservation and sustainable use of Plant Genetic Resources.**
4	**Provide information on existing projects and initiatives working on specific PGRFA.**
5	**Strengthen and support the early warning systems regarding threats to PGRFA.**
6	Agreement on and advocacy of data standards and trait descriptors to encourage data integration across diverse information sources.
7	Provide information on funding opportunities for PGR-related research.
8	Link accession level information to existing scientific literature related to PGRFA.
9	Agreement on and implementation of unique identifiers for PGRFA to unambiguously link germplasm conserved in gene banks or in-situ to a growing body of genetic and phenotypic data stored in otherwise unlinked online databases.
10	Develop a legal framework/licensing scheme for information on PGRFA.
11	Agreement on and testing of a framework that enables tracking of genealogy relationships between materials conserved ex-situ and crop varieties used for food production, in cases where this is feasible and desirable.
12	Link to phyto-sanitary requirements to facilitate the transfer of material.
13	Promote the concept of "open-data" in agriculture and neighbouring fields.

18. The top five challenges, with a score of more than 60 % of the aggregated preferences, are graphically presented in green in Figure 3.

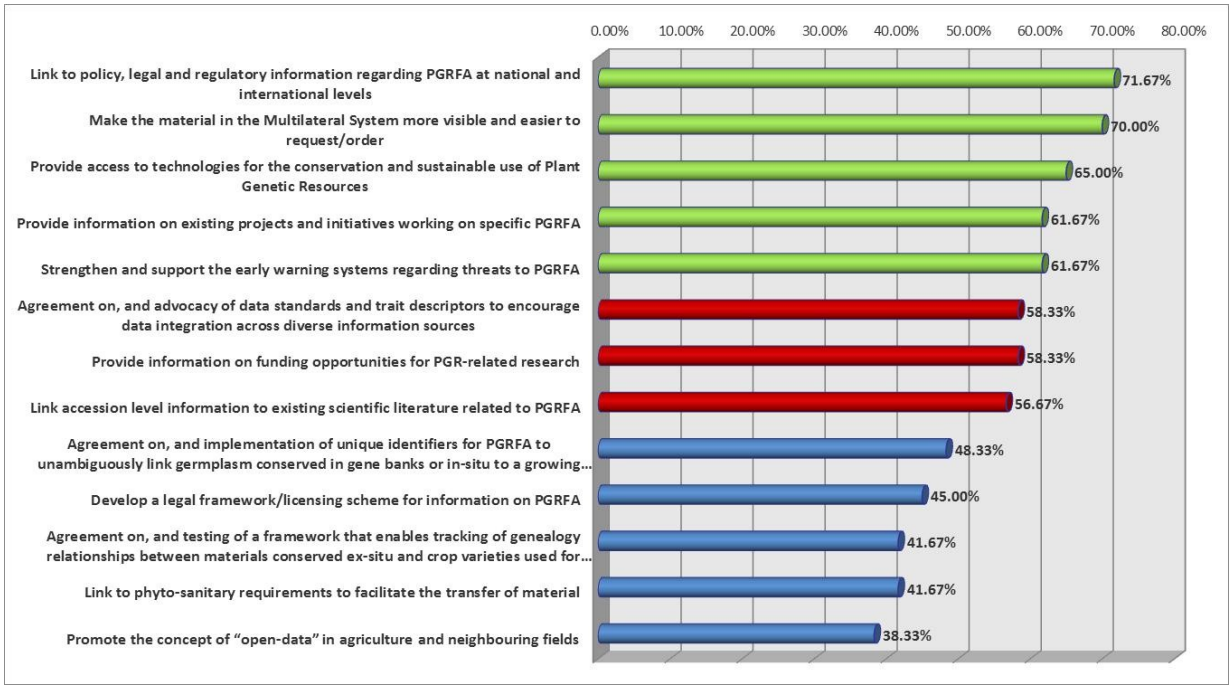

Figure 3: Challenges that should be taken into account when developing the Global Information System, graphically ordered by level of preference.

19. The participants were also given a list of eight possible priorities for the development of tools and associated services and were given the option to select four of them as a top priority. Table 2 presents the results of the raking, while Figure 4 presents a graphic representation of the preferences, which allow us to compare the level of preferences.

Table 2: Ranking of priority areas

1	**Tools to assist in the collection and analysis of characterization and evaluation data.**
2	**Link to geographic information resources holding data on climate, weather, soil, pests and diseases.**
3	**Training of specialized staff on the use of informatics tools and specialized software.**
4	**Tools to facilitate the documentation/dissemination of traditional knowledge associated with PGRFA.**
5	Tools to manage and analyse large-scale genetic diversity and genomics data.
6	Tools to support decision making (identification of potential duplicates, building germplasm subsets, etc).
7	Links to other crop-specific web portals that hold crop-specific genetic or phenotypic data relevant to breeding and research.
8	Tools to assist in the exploration and visualization of genealogy (pedigree).

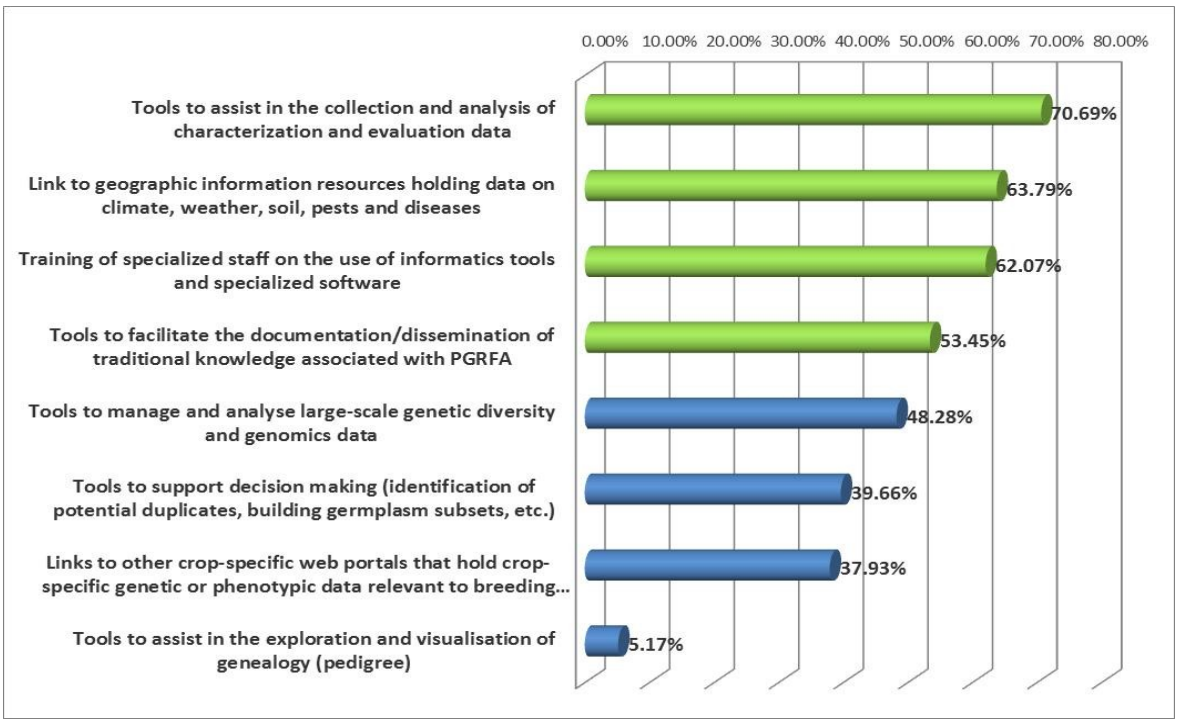

Figure 4: Graphic displaying the Ranking of priority areas.

20. Respondents indicated that they would like additional tools to **facilitate the development of national inventories** on PGRFA and **the reporting of data**, a platform to **connect aspects of**

ex-situ and on-farm conservation, and tools and services for the analysis of **ecogeographic climate and abiotic data** to facilitate trait prioritization of accessions and validation of phenotypes.

d) Interoperability and Main PGRFA Data Sources

21. To the question of whether most of the national organizations make relevant PGRFA data available at no cost, the survey revealed 67% positive answers, as shown in Figure 5. The positive replies to the question on data openness resulted in similar percentage -but surprisingly, 67% of the participants skipped it-. The results are illustrated in Figure 6.

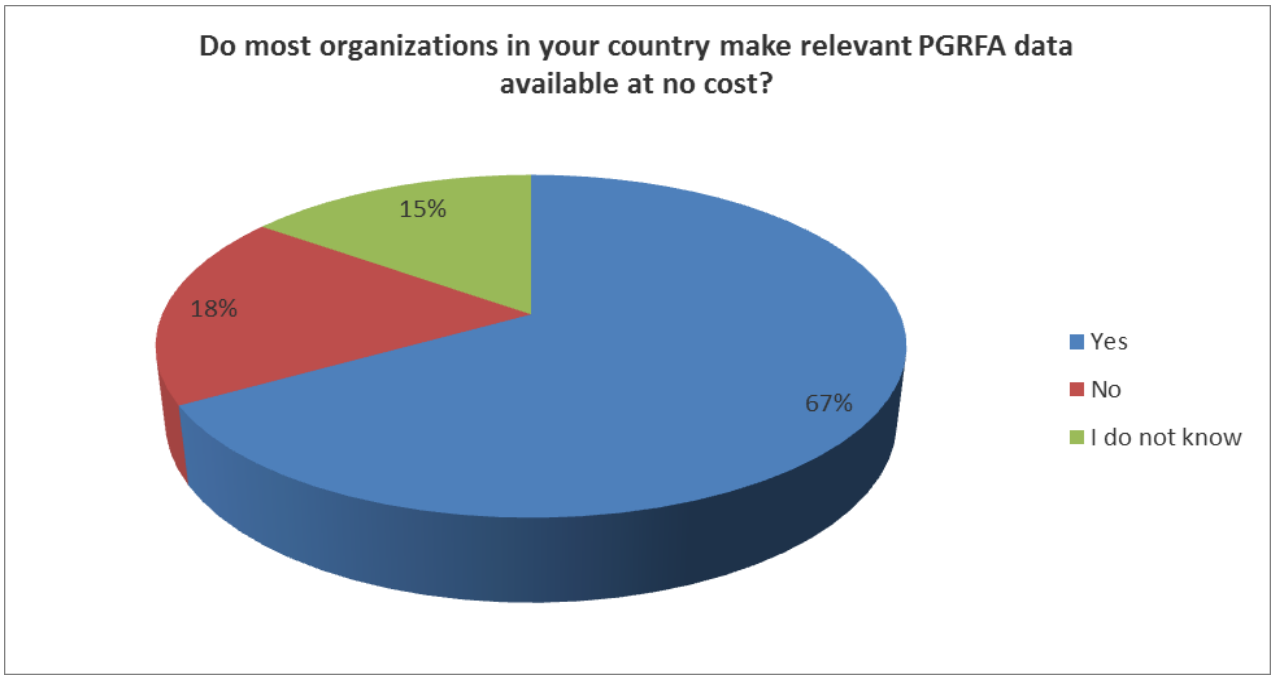

Figure 5: Availability of PGRFA at no cost.

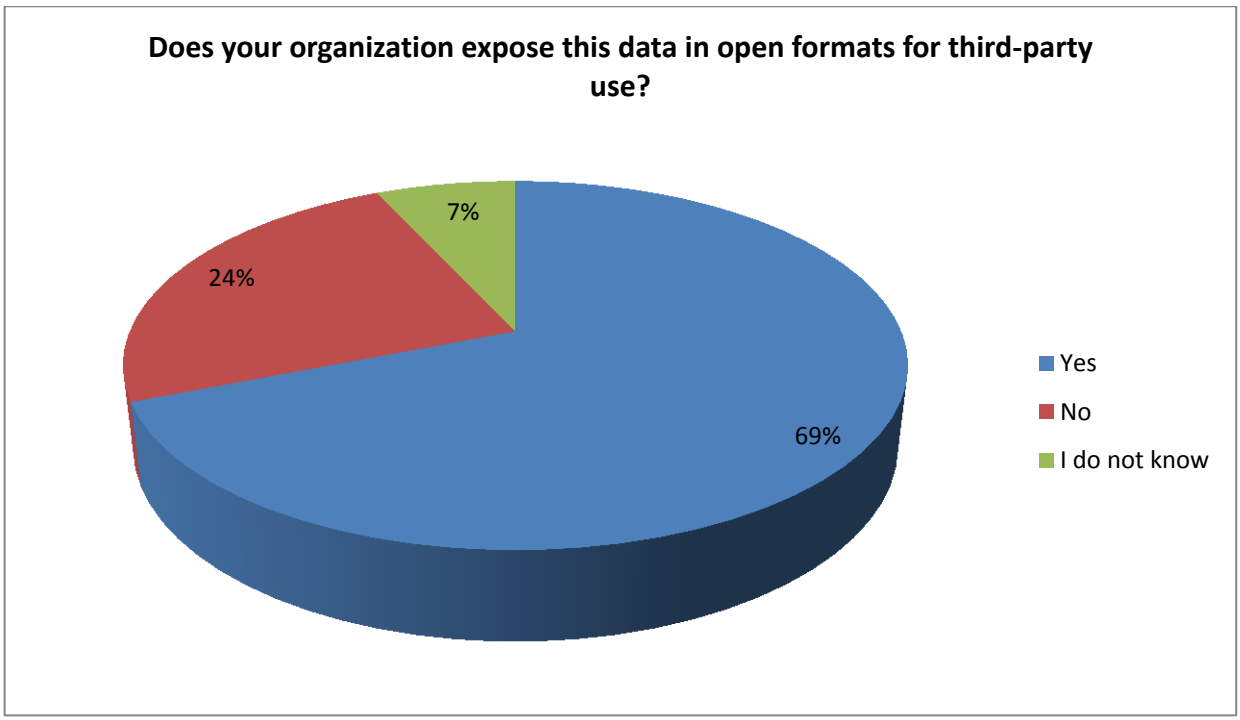

Figure 6: Availability of open data.

22. As much as 80 % of the respondents indicated that the national organizations had submitted data to regional, national or international public repositories, against 13 % negative replies and only 7% declared not to know the answer.

23. The respondents were also asked whether they would like their organization to be contacted in the future in relation to the Global Information System. Almost 60 % of the respondents indicated their willingness to be involved in the development of the Global Information System and indicated some of the areas of interest as shown in Figure 7.

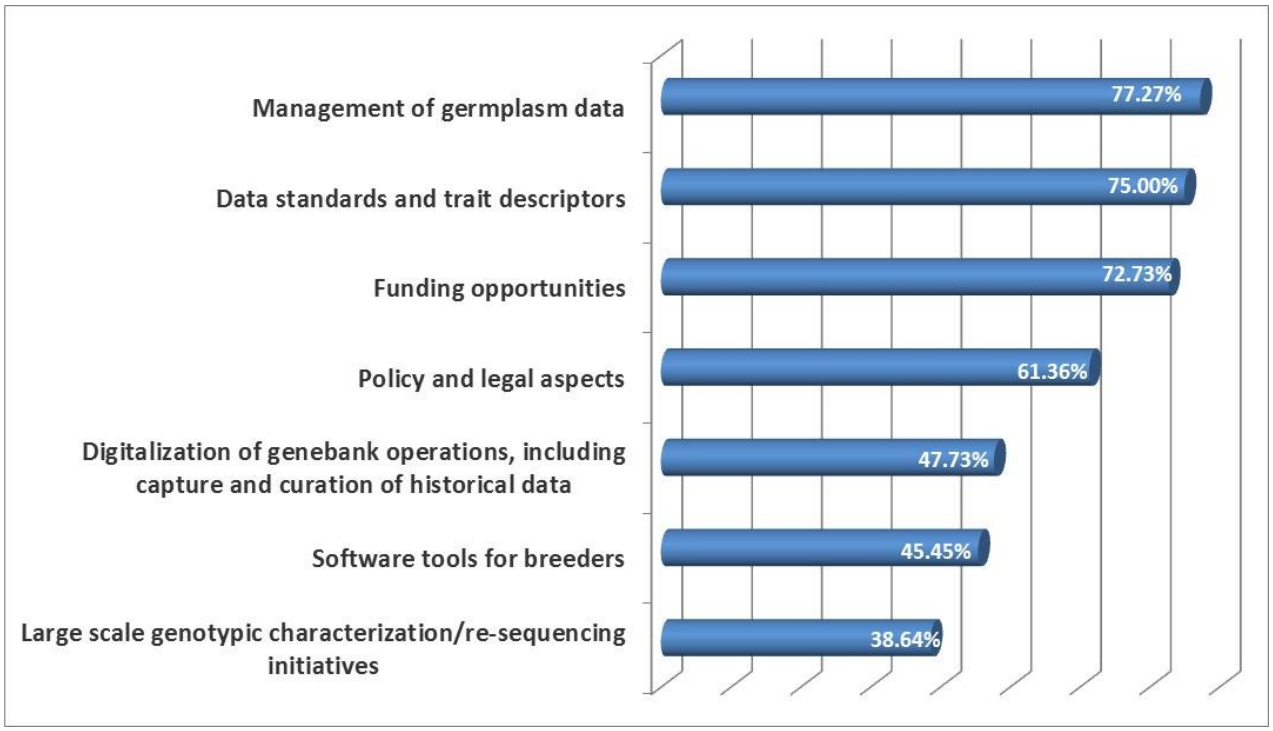

Figure 7: Areas of interest of respondents for future direct corporate involvement with the Global Information System.

24. The questionnaire also asked for information on the **main information sources** used at the country level to access, systematize, manage and share PGRFA and associated data. In addition to the national repositories and genebanks at the national level, a number of international repositories and tools were listed, e.g. Grin Global, Eurisco, Wiews, the Central European crop specific databases, The International Treaty on PGRFA, NordGen Sesto, Genesys, SADC Data and Information System and Dbgermo. Additionally, the respondents indicated other kinds of data sources, such as research journals, the Mansfeld's World Database of Agriculture and Horticultural Crops and websites of various agricultural universities.

IV. THE SURVEY ON GENOMICS, PHENOMICS AND DATA-SHARING AND EXCHANGE

a) Respondents and their Environment

25. The Survey elicited views and opinions from interested stakeholders and collected responses from 46 participants from all regions, most of them through the English version of the questionnaire. In fact, less than 20% of the respondents used the French or Spanish versions.

26. The respondents also provided information regarding the nature of the organizations they were affiliated with. The public sector was clearly the predominant affiliation compared to the private sector, and the national, federal and international levels were the most frequently declared. Most of the respondent indicated working in the research field and over 55% on plant breeding activities.

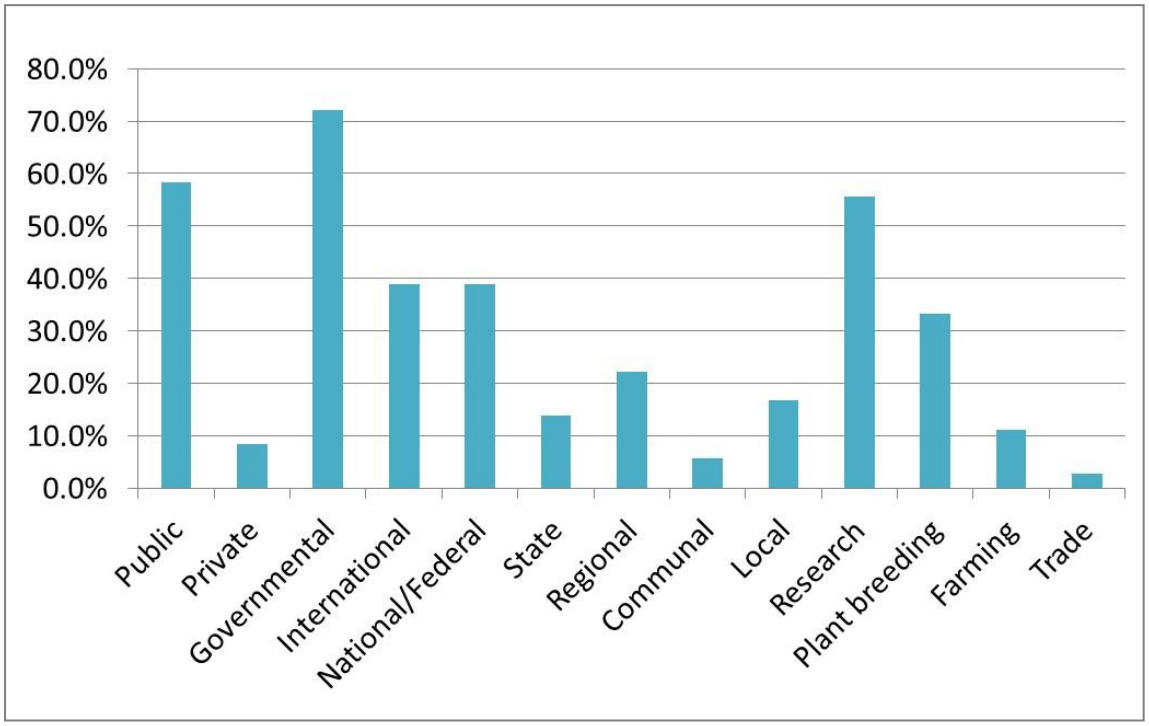

Figure 8: Replies to the question "At what level do you work?"

27. Most of the work undertaken by the respondents is funded by national governments and also through competitive grants. The responses to this question were not mutually exclusive. It is to be noted that only a few of the respondents declared being funded by the private sector (16%) or by foreign governments (13%). The responses are graphically displayed in Figure 9.

28. To the question "Do you directly work with plant genetic resources for food and agriculture (PGRFA)?" 81% of the participants responded positively. Indeed, 67% of the respondents were directly involved in the characterization of PGRFA to determine the expression of highly heritable characterstics for both morphological and agronomic features through phenotypic, genotypic and yield trials activities.

29. To the question of where they source the PGRFA, 87% of the respondents indicated Public seed and genebanks, 51% from local seed and genebanks. Also notable is that 45 percent of the respondents declared that they get the material from collecting missions, as displayed in Figure 10.

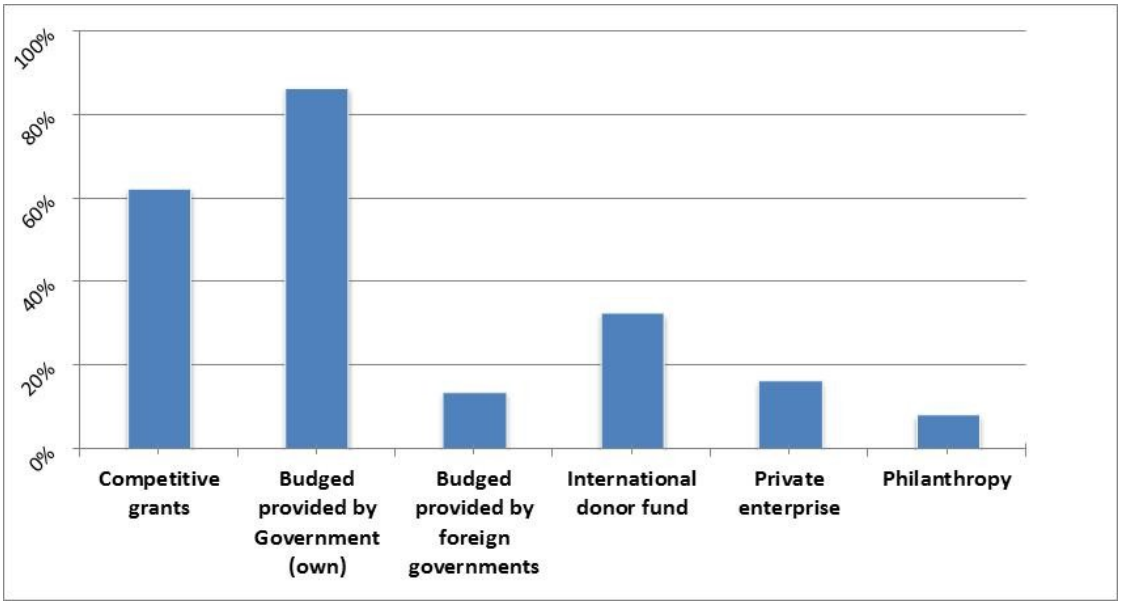

Figure 9: How is your work funded?

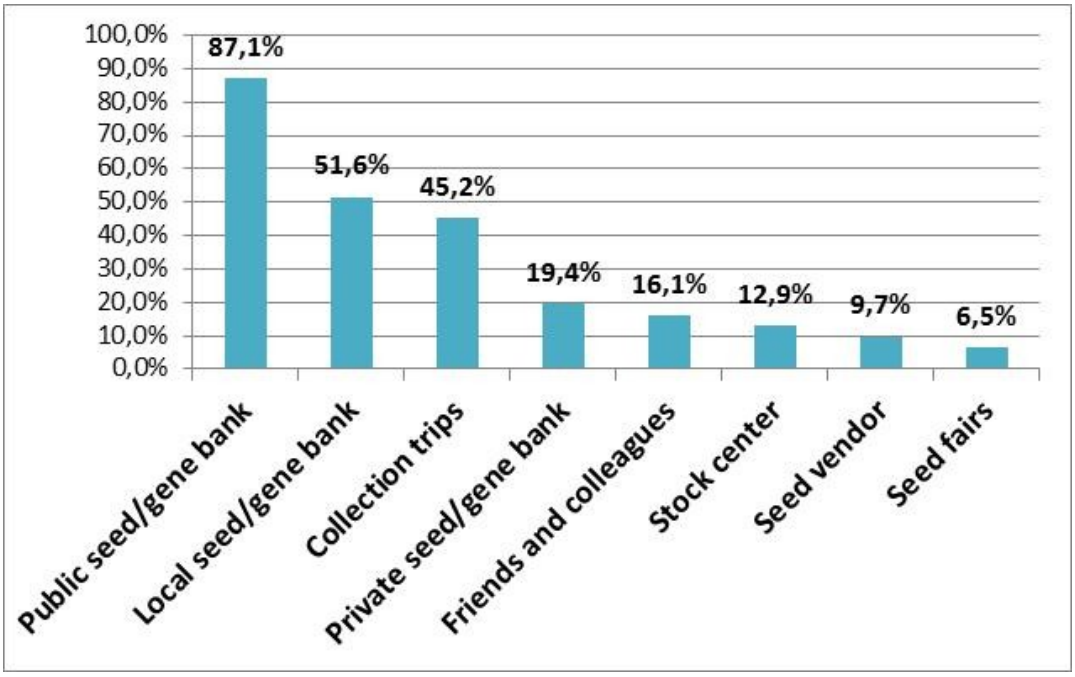

Figure 10: Where do you source your PGRFA?

30. The survey also revealed that 60% of the institutions and research programmes for which the respondents worked were part of a phenotyping, sequencing or genotyping network. In addition to some national or subregional partnerships, these were the initiatives, programmes, consortiums and networks listed: the International Plant Phenomics Network (IPPN); the European Plant Phenotyping Network (EPPN); the European Cooperation in Science and Technology (COST Europe); the International Barley Sequencing Consortium (IBSC); the International Wheat Sequencing Consortium (IWSC); the CGIAR Research Programmes (Maize, Wheat, and Roots Tubers and Bananas, and the Pacific Plant Genetic Resources Network (PPGRN); the wheat Initiative; The SADC Plant Genetic Resources Network; EURoot (Enhancing resource Uptake from Roots under stress in cereal crops); The International Oryza map alignment project (IOMAP); the Drought-tolerant yielding Plants project (DROPS).

31. The respondents also provided a detailed list of funding partners for each institution and programme, which was very diverse, ranging from national institutions to regional and international consortiums, programmes and networks, including FAO, the European Commission, the CGIAR, the World Bank, The Arab Organization for Agricultural Development (AOAD), the International Treaty on PGRFA; the Gates Foundation and other various public institutions based in USA, Australia, Canada and Germany. It is to be noted that the respondents also listed some universities and the private sector.

Knowledge of the Multilateral System (MLS) of Access and Benefit-Sharing

32. All respondent declared to know the International Treaty and only two respondents indicated that they were not familiar with the Standard Material Transfer Agreement (SMTA) of the International Treaty on PGRFA. In fact, 80% of the respondents indicated they were users of the SMTA.

33. When asked about the DivSeek Initiative, 62% declared knowing it and also provided additional information about other similar initiatives: SeedD, Nordic PPP pre-breeding project in perennial ryegrass, the Landrace Pillar of the Wheat Pre-breeding LOLA /Wheat Improvement Strategic Programme/ consortium, the Triticeae Coordinated Agricultural Project (T-CAP), the Breedwheat Project, the QUOATS project, MaizeGDB, PlantGDB, Seeds of Discovery, the WISP Consortium, the Wheat Initiative, The Digital Seed Bank, EVAI and EVAII (both German).

b) Phenotypic Evaluation of PGRFA

34. Plant phenotyping links the genetic background and the environment in which plants develop. The phenotype determines plant performance and productivity and can be measured as biomass and as commercial yield and resource use efficiency. More than 93% of the participants indicated that they or their institutions undertake or are involved with phenotypic evaluation of PGRFA and that their mandates focus on plant breeding; conservation, evaluation, and utilization of PGRFA for food security; the conservation, study and development of local cultivars; the systematic characterization and mobilization of novel, beneficial genetic variation into breeding programs; the assessment of crop diversity, sustainable use of PGRFA and adaptation to climate change. While most respondents work in groups of less than 40 members, some of them indicated that they collaborate in broader networks of researchers, scientists and farmers comprising more than 100 members.

35. While the list of crop species on which the respondents' work is very extensive, the major common answers were: wheat, rice and maize, followed by Arabidopsis, cassava, barley and wild species. Some respondents just indicated cereal and forages.

36. The traits of most interest listed were drought tolerance, pest and disease resistance, improvement of the general yield and nutrition quality. It is to be noted that the list of traits was very long and covered agronomic and morphologic traits related to the structure and function of the plants and the quality of the product. It is to be noted that adaption to local conditions and to climate change were also referred to as some of the trait-related aspects under research.

37. To the question of "What phenotyping standards or descriptor do you use?" the most popular reply, by far, was FAO/Bioversity Multi-crop Passport Descriptors. Other standards were listed among the replies were: The International Union for the Protection of New Varieties of Plants (UPOV), International Association for Cereal Chemistry (IACC), AACC-International Approved Method of Analysis, The Community Plant Variety Office (CPVO) descriptors and the European Native Seed Conservation Network (ENSCONET).

38. Almost 62% of the respondents said they were plant breeders or involved plant breeders in their phenotyping work, and 54% involve farmers. It is worth mentioning that 84% of the respondents work in the field, mainly in green houses. Figure 11 shows the relationship between the "phenotyping" and the "selecting" activities of the respondents, where 73% indicated that they record measurement for every individual and 61% work on selection.

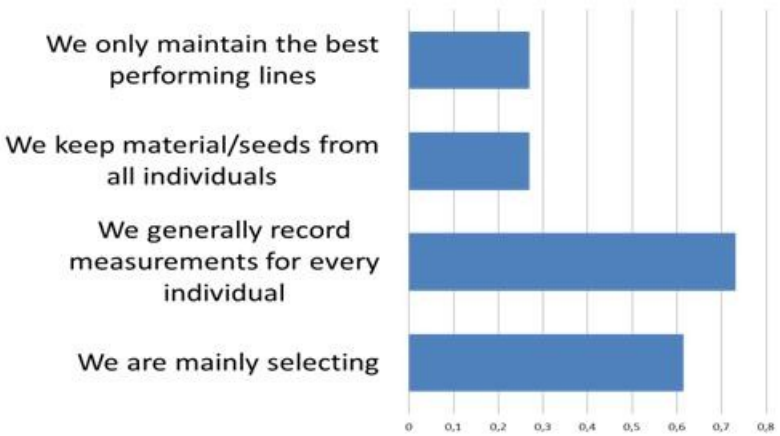

Figure 11: Are you "phenotyping" or are you "selecting?

39. The questionnaire also inquired about the standard phenotyping approach, offering a list of five options that did not excluded each other. The evaluation of the basic morphological and phenological characters, including architecture (88.89%) and the evaluation of agronomic performance under stress (62.96%) were the most popular ones, while the evaluation of agronomic performance under optimum conditions of the resistance to diseases and pests and of quality and nutritional traits accounted for 55% or more of the responses, indicating that they are all relevant.

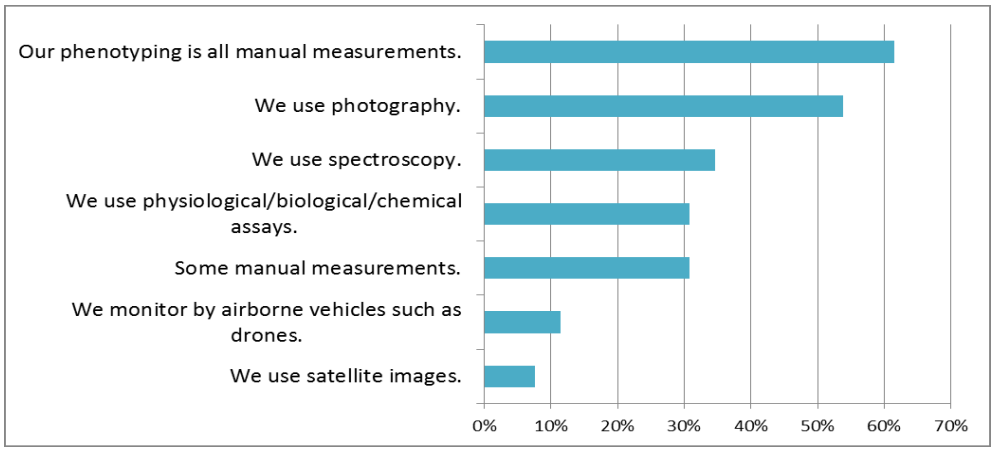

Figure 12: Manually or automated phenotyping.

c) Phenomics: data documentation, local sharing

40. Regarding the documentation of phenomic data, most respondents indicated that the information is kept in excel sheets or in customized relational databases of the institutions where they are kept, including GRIN-CA or tools such as KDDart. It is to be noted that most respondents indicated that data is inserted manually in these systems, although a few of them are using android devices to send the data to the information system. As Figure 13 shows, most data and results are generally connected to specific PGRFA, meaning that data is traceable to a specific batch in an ex-situ collection.

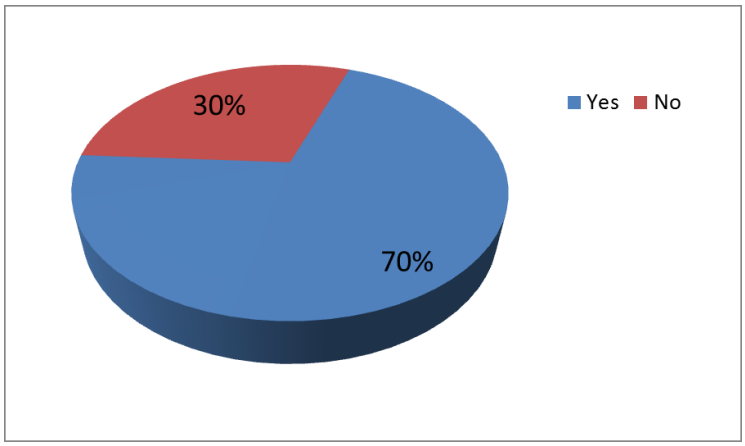

Figure 13: Is phenomic data connected to specific PGRFA in ex-situ collections?

41. Books and publications are also an extended and common method of documentation, and 70% of the respondents said that they publish the results of their research in peer-reviewed journals.

42. Although 93% of the respondents declared that they make the data and results available to plant breeders, high postgraduate students and researchers, only 56% do so with farmers. The main given reasons for sharing this data less with farmers is that "*they are not interested*" or that the information is available to them only "*upon request*". Some respondents indicated lectures, seminars and field demonstrations as additional methods of sharing the results of the analyses with farmers.

d) Genotypic Evaluation of PGRFA

43. More than half of the respondents declared to be undertaking or be involved in genetics and genomics work with PGRFA and, as shown in Figure 14, 14% of them outsource this kind of activities. In fact, partnerships were declared in this area, as many institutions do not have facilities for molecular biology work and they partner with universities and centers with

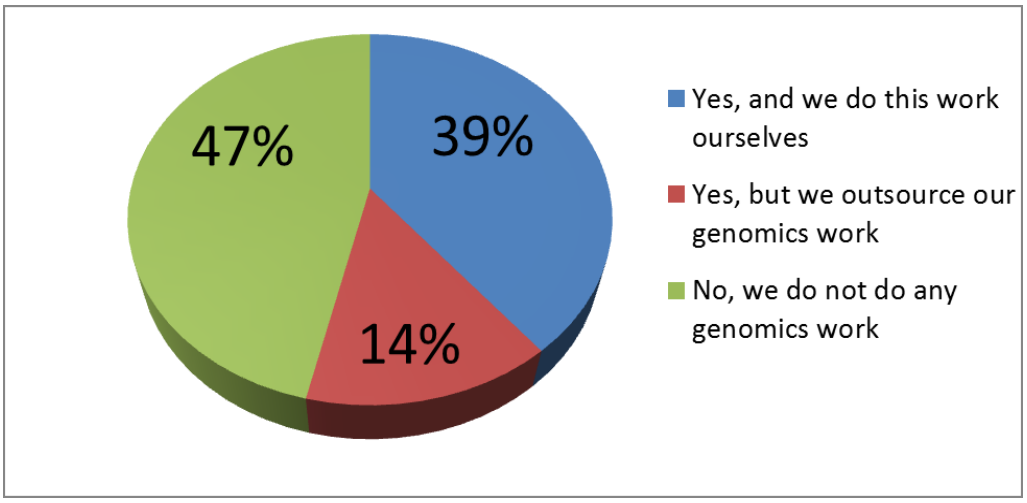

Figure 14: Do you undertake, or are you involved with, genetics, genomics work with PGRFA?

appropriate capacity (e.g. diversity arrays technology). Others indicated that the genomics work was not directly their mandate or that they just simply lack the necessary financial and technical infrastructure and capacity as well as the technical expertise and knowledge.

44. To the question of how the molecular data is documented and kept, individuals provided all kinds of replies, e.g. through customized databases, the data is kept for 10 years, the data is discharged, it depends of the data sets, etc. In a few cases, some institutions have a similar kind of approach for genomic and phenomic data. Seventy two percent of the participants indicated that the results are generally connected to specific PGRFA in an ex-situ collection, very similar to the percentage for phenomics.

45. Regarding the dissemination of the results, 80% of the respondents indicated that they publish molecular biology data in peer-review journals. Nearly all of them said they make the results available to breeders (90%) through various information tools, but also through meetings, conferences and personal contacts. Regarding the sharing of this data with farmers, the responses were the same as those collected on this question regarding phenomic data.

e) Bio-Informatics Data Analysis

46. The study also asked the target audience about the bioinformatics data analysis and revealed that 70% of the respondents require bioinformatics data analysis, with almost 30% of this work being outsourced, as represented in Figure 15. Most of the institutions that undertake this work in-house employ from 2 to 10 technology system administrators and other specialized staff who are trained in this area, and some of them also employ statisticians.

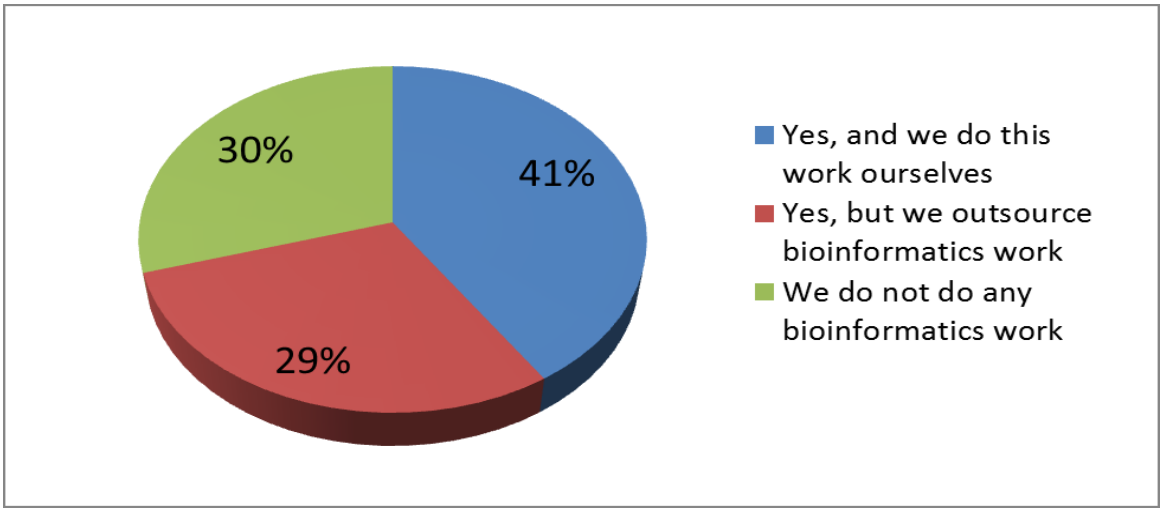

Figure 15: Do your projects require (Bio)Informatics data analysis?

47. When asked about the bioinformatics equipment available, half of the respondent indicated that their institutions use dedicated computers for data storage and one-third said that they use computer cluster sites.

Answer Choices	Responses
Compute cluster on site	33.33%
Dedicated computers for data storage and/or computation	50.00%
Personal computers/Terminals only	8.33%
We are using cloud storage and/or cloud computing	8.33%

Table 3. Type of equipment available for (Bio)Informatics data analysis

48. To investigate the availability of a reference genome sequence for the PGRFA relevant to the work of the respondents, the questionnaire introduced a question on this topic and found that only 36% of the respondents do not have one, but would benefit from it. It also revealed that 18% have a good quality genome reference for their PGRFA and 27% have one, but need improvement.

49. A good 67% of the respondents declared that their institutions frequently use genetic markers, while 45% declared that there are no genetic markers for the PGRFA of their interest.

50. Not much information was collected on the software packages used for the analysis of genomic data. Half of the respondents indicated that their institutions develop their own software. In addition to self-developed tools, the following are used: Burrows-Wheeler Aligner (BWA) for read alignment[5], TopHat, Cufflinks[6] and Augustus gene predictor[7].

51. The most frequent analysis performed by the respondents are: Whole Genome Sequencing (WGS), Genotyping By Sequencing (GBS), Single Nucleotide Polymorphism (SNP) and also diversity analyses, association mapping, selection imprints, allele frequency gradients across environmental clines, genomic prediction/selection, reference genome sequencing for crop wild relatives.

52. The most frequently used standard file formats for storing both the biological sequence and its corresponding quality scores by the respondents were FASTA (over 80%) and FASTQ.

53. One-fourth of the institutions share genomic data with partners and collaborators, but only 15% provide data analysis services to other partners or customers. Most of those partners were from the public sector (71%). It is to be noted that, although a few respondents indicated that their institutions keep logs and tags files internally, most of the data analysis is documented through publications and peer-reviewed journals.

54. Some of the data repositories considered of importance for their work are: the GenBank sequence database of the National Center for Biotechnology Information (NCBI); the European Bioinformatics Institute (EBI); the Ensembl project; Maize GDB; GrainGenes; GRIN and GRIN-CA; IPK and ICRISAT Database; VIR Online catalogue; EURISCO; WIEWS; Taxonomic references; SoyBase; and PeanutBase.

f) Open Data and Data-Sharing

55. Only 52% of the respondents indicated that all data should be open. Some participants indicated that this should be the normal praxis when the work has been publicly funded, but that it should be after a certain period of time during which the primary researcher has a chance to analyze and publish the data analysis.

56. More than 80% of respondents indicated that their data was publicly available or that it could be made available. The key question was whether there are institutional conditions or restrictions that apply to data-sharing. The responses to this question are graphically represented in Figure 16, which shows that nearly one-third of the respondents declare some kind of restrictions, including the precedent of the data generator, the authorization of the head of the organization, donor or project terms, bilateral contracts with companies and other pre-publication agreements. Similar responses apply to the conditions and restrictions imposed by the partners.

57. A variety of different responses were given to the question ‘What do you do with your descendant material of PGRFA you worked on, such as seeds and propagated tissue?’ Results indicated that it depends very much on the initial purpose, and when the material is needed later, a

[5] BWA is a software package for mapping low-divergent sequences against a large reference genome. http://bio-bwa.sourceforge.net/

[6] Cufflinks assembles transcripts, estimates their abundances, and tests for differential expression and regulation in RNA-Seq sample. http://cufflinks.cbcb.umd.edu/

[7] http://augustus.gobics.de/

code or accession number is assigned to it and the material is kept for a few years. In some cases, the material is left in deposit as part of the working collections and the pedigrees are registered.

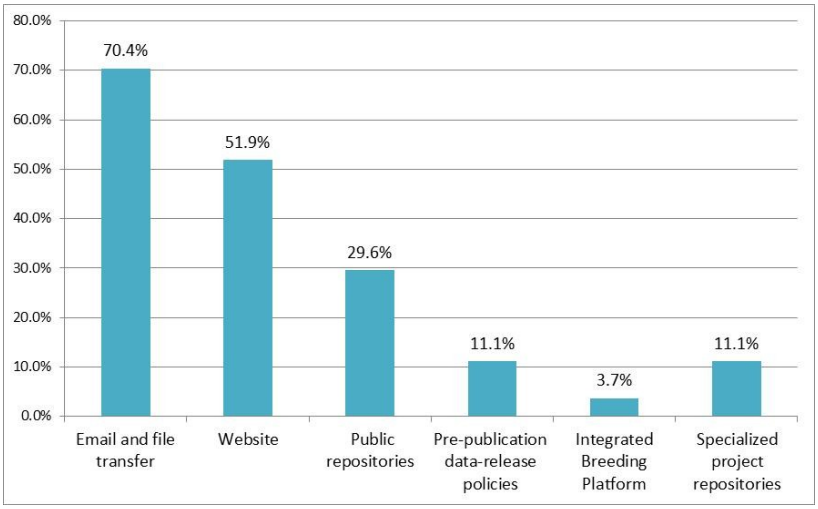

Figure 16: Preferred mechanism for sharing data

58. Regarding the documentation describing the experiment, only 20% of the individuals responded in the affirmative about complying with the "mibbi" Minimum Information Guidelines (E.g., MIAME, MIGS/MIMS, MINSEQE, MIARE, MIAPPE[8]). The data is displayed in Figure 17. The FAO/Bioversity International are clearly the most commonly used data standards.

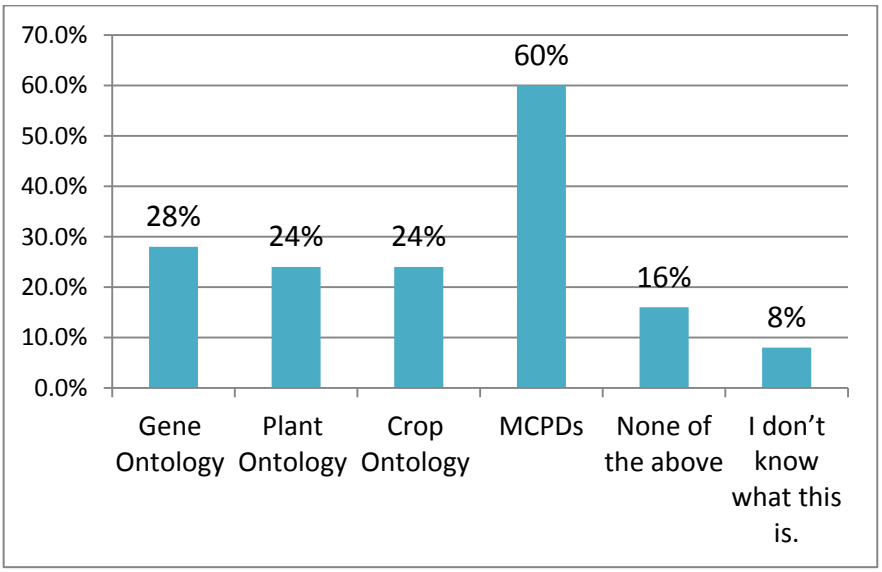

Figure 17: Kind of ontologies and descriptors being used

59. The questionnaire also provided a list of eight data repositories and asked whether data was submitted to them or not. Only four of the eight were selected, with GenBanK selected as the data repository of choice for almost half of the respondents. GenBanK was followed by the Short Read Archive, GEO and iPlant.

[8] http://mibbi.sourceforge.net/portal.shtml

60. A copy of the DivSeek white paper was attached to the questionnaire. The findings of this questionnaire on genomics, phenomics and data sharing and exchange will be considered in the development of DivSeek. It is foreseen that the online consultation exercise will be repeated on a periodic basis and as part of the work under the Global Information System and to the benefit of potential users, stakeholders groups and initiatives, including DivSeek.