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THE PGR NETWORKS IN FRANCE: COLLABORATION OF USERS AND THE GENETIC RESOURCE CENTRE ON SMALL GRAIN CEREALS

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Plant genetic resources (PGR) have been used in breeding programs for many decades to produce modern varieties by introducing genes of interest, in particular, resistance genes. Nevertheless, these resources remain underestimated if we focus on abiotic stress tolerance or new agricultural techniques, which consider productivity with regard to the environment. In recent years, new users, such as scientists and farmers, have discovered diverse sources of interest for screening and exploiting natural diversity conserved in PGR collections.

In the case of the French cereals PGR Network, a share of the responsibility, based on the knowledge and ability of network members, has been decided in order to better promote the use of PGR. The main species of *Triticum* (wheat), *Hordeum* (barley), *Secale* (rye), \times *Triticosecale* (triticale), *Avena* (oat) genera and their wild relatives are held in the collection. By combining phenotypic and genotypic data, the whole genetic resource collection has been structured into smaller functional groups of accessions, in order to facilitate the access and meet the increasing number of different requirements for the distribution of adapted samples of accessions.

New panels are being processed to give breeders and scientists new useful tools to study, for instance, stress resistance or to develop association studies. All these data obtained from the French small grain cereal Network will be progressively available through the INRA Genetic Resource Website (<http://urgi.versailles.inra.fr/siregal/siregal/welcome.do>).

Key words: cereals, genetic resources, data management, seed distribution.

Introduction

For about one century, plant genetic resources (PGR) were traditionally used by breeders in their breeding programs in order to introduce traits and genes of interest in improved material and, then, to create new cultivars. This context is changing with the occurrence of new constraints, due to environmental conditions (i.e. climate changes, rules with respect to environmental conditions during production) and to the evolution of socio-economic demands. At the same time, new tools to investigate PGR diversity were introduced (Paux *et al.*, 2010). There has been a renewed interest for PGR expressed by new users (for instance, scientists who can now describe PGR diversity at new scales as genomic, proteomic and metabolic) in order to search for new

alleles for new targets. This attraction also concerns farmers, gardeners and private individuals who are more interested in cultivated biodiversity. This may be represented by landraces or old varieties that they want to use directly for organic farming or for specific adaptations to human nutrition.

In this context, considering the fact that the largest part of our collection is under-estimated for these new aims and targets, we need to define different way to promote genetic resources from the INRA collection. These management activities must be able to answer to the socio-economic evolution of agriculture and to the development of basic scientific knowledge in genetics. To achieve these two aims, responsibility must be shared between actors managing the genetic resources in order to better promote and act on them.

Management of Genetic Resources in France

The INRA Plant Breeding Division supports eleven Genetic Resources Centers (GRC) plus one in the French Indies for tropical species such as yam. These GRC belong to the French IBISA network. Each one of these GRC is focused on a specific group of species. The main missions of these GRC are the **characterization of resources** (passport data, genetic markers, agronomic criteria of interests), the stock management, ensuring the quality control (identity, viability and sanitary condition) and the management and diffusion of **scientific and technical information related to genetic resources**.

Small grain collection. In the case of small grain cereals, the Genetic Resources Centre (GRC) held in Clermont-Ferrand gathers accessions of major species of agricultural interest belonging to genus *Triticum* (wheat), *Hordeum* (barley), *Secale* (rye), \times *Triticosecale* (triticale) *Avena* (oat), and their wild relatives.

The bread wheat (*Triticum aestivum*) collection is made up of 11 500 cultivated lines, as landraces, breeding lines, elite's lines and registered cultivars. A third of these wheats has French origin, the second third comes **from Europe and the last one is from the rest of the world**, with about ninety different countries represented. Among French material, the collection gathers old varieties, or «**landraces**» **from the 19th century**, the first French varieties bred in France (Vilmorin's collection), as well as the last «**elite**» **lines from the end of 20th century**. **The wide coverage of a breeding period allows retracing the history of bread wheat selections in France**, given that the pedigree is known. Besides these patrimonial resources, foreign material is composed of genetic resources more traditional. This whole collection is described for agro-morphological traits - height, spike descriptors (awn, hairiness), growth habit, lodging and resistance to major diseases (mildews, rusts) (Roussel *et al.*, 2004). An estimation of some technological parameters linked to bread-making quality has been realised by a NIRS methodology (Roussel *et al.*, 2005) on most of the accessions. A molecular diversity analysis has also been done on 4 000 accessions to characterize the allelic diversity with 42 microsatellites loci spread across the genomes (one by chromosome arm). From this study, a worldwide bread wheat core

collection, namely INRA372CC, was defined by Balfourier *et al.* (2007), from INRA in order to propose to scientists a subsample of a reasonable size with maximized allelic diversity. The core collection captures more than 98% of the genetic diversity conserved in the whole wheat GRC collection. This core collection was deeply phenotyped for about 30 different agronomical, biochemical and technological traits (Bordes *et al.*, 2008) linked to bread making quality. It was also genotyped with about one thousand molecular markers (DART, SNP and SSR) spread over the genome, in order to determine its genetic structure (Horvath *et al.*, 2009). By introducing this core collection in different scientific projects, 8 times in France and abroad, more data can be analyzed and used to develop association analyses. Currently this subsample is characterized for flour and dough quality (Bordes *et al.*, 2011), nitrogen use efficiency, grain protein and earliness (Rousset *et al.*, 2010; Le Gouis *et al.*, 2012). **These projects have been supported by industrial processors, cereal breeders and French National Agency for Research.**

Besides this bread wheat collection, the small grain CRG holds 2800 durum wheats and relatives, 450 *Aegilops* sp. and also conserves about 6 500 scientific lines used for cytogenetic and genomic studies; this includes aneuploid, addition, deletion or substitution lines, interspecific hybrid, and recombinant inbred line populations used for molecular mapping work.

The GRC also maintains a barley (*Hordeum vulgare*) collection with around 6 500 accessions. It is mainly composed of traditional genetic resources, and it is a national reference for all French landraces, obsolete and improved accessions, breeding material and French acquisitions from Morocco. This collection is well documented for pedigree, as well as agronomic descriptors for two thirds of the barley varieties. This barley collection contains very specific and important material (as semi-dwarf) with quantitative traits of interest for disease resistance and malting.

Since triticale (\times *Triticosecale*) is a cereal species recently developed by man, landraces do not exist. On the other hand, all the rye and bread wheat variability is available to breed new «**primary**» triticale. So, only some varieties, recently bred, are conserved in the collection as well as scientific material used to breed primary triticale. This collec-

tion gathered about a thousand triticale varieties, or breeding lines mainly originated from France and Europe. The collection both comprises hexaploid (*×Triticosecale neoblaringhemii*; advanced varieties) and octoploid form (*×Triticosecale rimpaii*; primary triticale), for which an evaluation is in process.

For oat (*Avena sativa*), collection gathered around 1200 varieties cultivated in France, for the most part with a French origin (65 %). The rest of the collection comes mainly from Germany, North America, Sweden and the United-Kingdom. This collection with patrimonial value had been evaluated during two European projects – GENRES CT99-106 (Katsiotis *et al.*, 2008) and AGRI GENRES 870/2004 (Germeier *et al.*, 2011). As well as agronomic traits, an estimation of biochemical characteristics (protein and cellulose) has been done by NIRS methodology.

Rye (*Secale cereale*) collection contains 85 local populations native mainly to Massif Central (France) and Portugal, too. This small collection has a patrimonial values and does not represent the past French rye diversity, which has probably disappeared.

All these genetic resources (around 25 000 accessions) constitute a useful genebank, as well,

for basic genomic studies and applied breeding approaches. It allows for preservation of the existing diversity. In the same way, these resources are a useful tool for the development of new cultivars by modern breeding methodologies to comply with new targets for food supplies.

Management of collection. Management of small grain genetic resources in France is mainly done by two partners. The public sector, represented by INRA, who developed a national scientific network on cereal research of 108 full time permanent staff. This network is organized according to the available tools and abilities with a main head unit in Clermont-Ferrand (GDEC unit), coordinating the scientific projects on genomics, genetic resources and breeding, in concert with others INRA units (Fig. 1).

The second partner is the private sector that represented by UFS, the French Union of Seeds composed by 110 French seed corporations, from an international group to family-owned businesses. It covers all seed species. For small grain cereal section, 12 private breeders are concerned by genetic resource management. The network is made of their 12 locations, where they developed facilities for phenotyping and breeding activities. This multi-location network appears as a good tool to

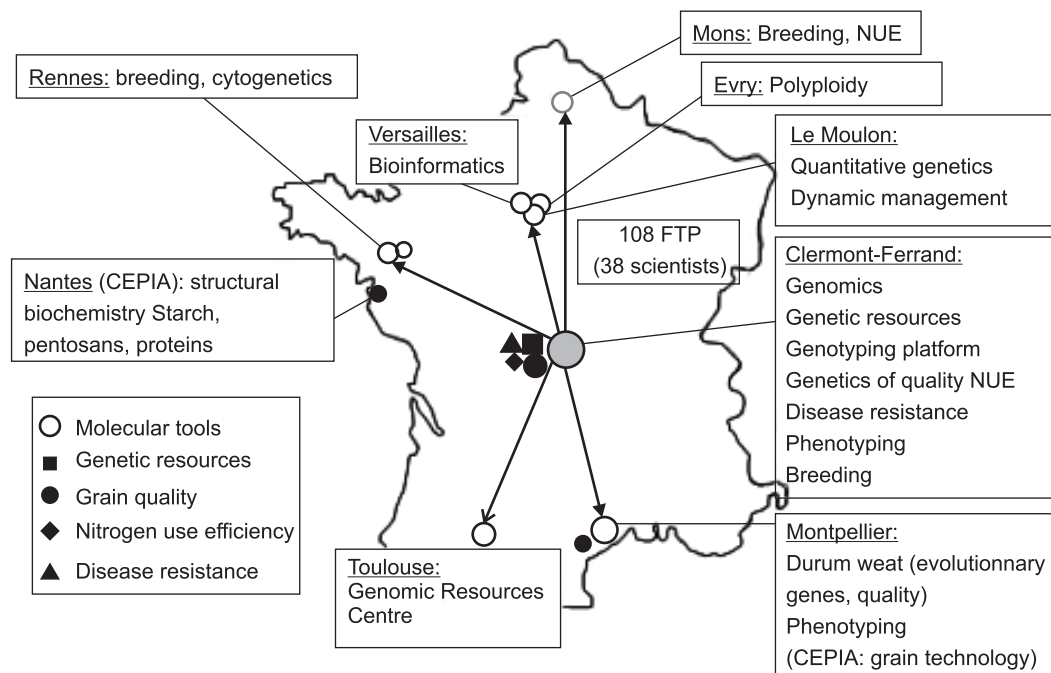


Fig. 1. INRA scientific network.

measure genotype by environment (G×E) interactions in phenotyping activities (Fig. 2).

The management of genetic resources on small grain cereals is shared between these two main actors. All the in-deep phenotyping activities are made by the private breeders' network that can realize a useful characterisation of genetic diversity in contrasting environmental conditions for biotic and abiotic stresses. Activities of pre-breeding, such as inter-specific crosses and enrichment of diversity, are also devoted to the private breeders. Finally, they have facilities to manage, for specific projects, big multiplications of seeds in large quantities when necessary.

In parallel, INRA GDEC Clermont-Ferrand unit shelters the Genetic Resources Centre (http://www.clermont.inra.fr/umr1095_eng/Teams/Technical-and-Experimental-Platforms/Genetic-Resources-Centre) which manages, with the help of the experimental unit, the primary characterisation of the accessions, such as days to flowering, height, growth habit, diseases resistances and so on. The Genetic Resources Centre carries out the multiplication, conservation and distribution of the seed batch. To insure traceability, GRC manages

all data in appropriate databases and organizes a quality management system. Furthermore, thanks to its high-throughput genotyping platform and to technological lab facilities, molecular and technological characterisation of diversity may be also performed in INRA-GDEC units.

From the whole network collections, different sub-collections or subsamples of accessions were defined by the main actors of plant genetic resources management. In bread wheat, barley and triticale species, we have defined specific collections (i.e. national collections) made of those accessions historically used in France for breeding programs during the last century. In the case of bread wheat, it is the collection of 1783 accessions which was officially declared in 2010 by the FAO as France's contribution to the **International Treaty on Plant genetic Resources for Food and Agriculture**. This National Bread wheat collection is currently characterised for both molecular and agronomical traits in a common evaluation project, between the GDEC unit and the UFS genetic resources network, supported by the French Ministry in charge of agriculture and fishing. This project consists of 3 work packages (WP). In the first one, twelve

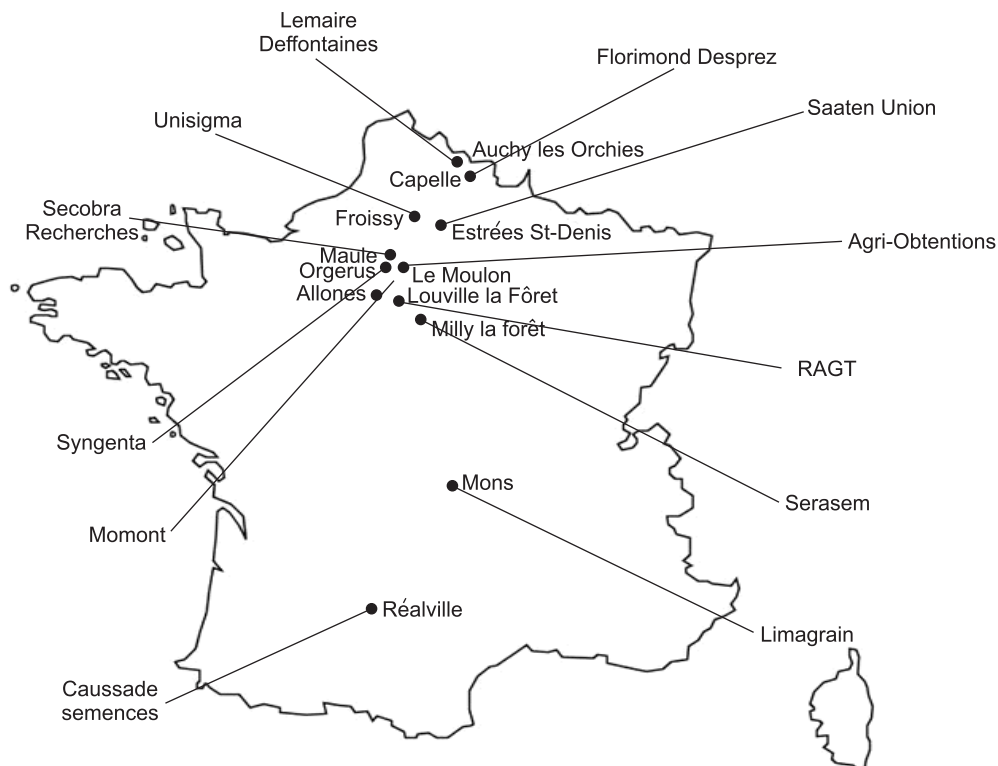


Fig. 2. UFS network on small grain genetic resources.

private breeders have to evaluate, during 3 years, the collection in field nurseries in their multisite evaluation network. In the second, WP2, INRA of Clermont-Ferrand is in charge of genotyping the whole collection with a set of 42 microsatellites markers. And finally, a third WP is a common task of data analysis. The aim is to analyze the structure of the whole collection in order to use this information for a subsequent project, association analyses on a sample set.

Distribution of samples

After five years, the number of samples distributed by the GRC had increased by 290 % (from 1656 to 4857 samples) while the number of requests was

quite stable (Fig. 3). Each request includes a Transfer Material Agreement. An increase number of requests is mainly due to an increased number of plant genetic resource network activities. Each year 20 per cent of the distributed samples are sent abroad.

Table 1 shows the number of samples distributed by species function of requester's type during 2005–2010 periods. In terms of the numbers of samples distributed, first of all we have the breeders from French or foreign private companies. During these five years, an exponential increase of private company requests has been received, due to both the PGR activities and to the core collection publication and the FAO participation.

The «Research institutes», which included broad types of research teams and a wide variety

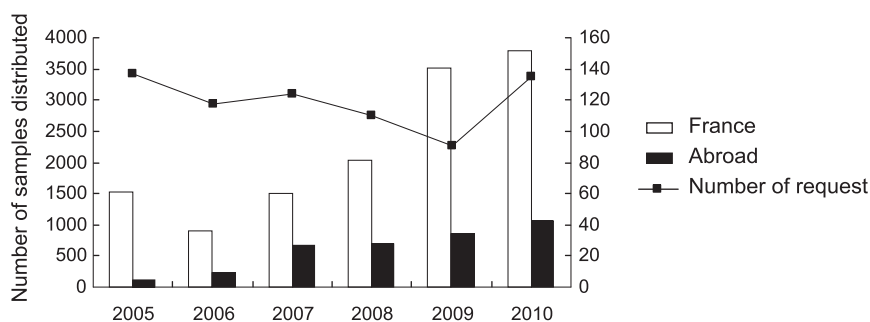


Fig. 3. Number of requests and samples distributed during the five last years (2005–2010).

Table 1

Number of sample distributed by requester type for different species, on 2005–2010 periods

Genus/species	Breeders	Farmers	Research institutes	Others
<i>Aegilops</i> L.	3	13	160	13
<i>Triticum</i> L.				
<i>T. monococcum</i>	25	29	51	18
<i>T. timophevi</i>	4	7	3	5
<i>T. turgidum</i>	78	189	523	57
<i>T. turgidum turgidum</i>	7	85	34	22
<i>T. turgidum durum</i>	12	48	122	19
<i>T. aestivum</i>	5923	1178	5568	378
<i>T. aestivum spelta</i>	19	49	138	10
<i>T. aestivum aestivum</i>	5893	1122	5411	360
<i>Hordeum</i> L.	1766	320	131	53
× <i>Triticosecale</i> Wittm.	1	1	46	11
<i>Secale</i> L.	2	27	15	18
<i>Avena</i> L.	89	118	95	33
Total	7891	1882	6592	586

of projects, from «field to laboratory», are the next ones. These institutes are French, European and abroad and can be held by public institutions or private companies.

«Farmers» category includes diverse kinds of farming. Half of these farmers belong to an association called «Reseau Semences Paysannes», which is a militant association. These farmers want to develop their own network for exchanges of material in order to promote local varieties. Besides this network, we also have farmers dealing with organic farming, mixed farming and who directly sell their final product – for instance, beer or bread.

Finally, «Others» include associations, non-governmental organization, botanic garden, museum, agricultural college and private individuals.

Requests concern mainly *Triticum* species, and, in a less important part, *Hordeum* species. Wheat relatives are mostly used by research institutes. This can be explained by the research of genes of interest in the ancestries in order to insert them by interspecific crosses. Another interest with this material is to illustrate the historical pedigree of wheat for public exhibition.

Bread (*T. aestivum*) and hard wheat (*T. durum*) are both used by research institutes for genetic analysis, breeding but also for interspecific crosses.

Breeders asked mainly for barley and bread wheat for their breeding programs. This focus is partly due to the genetic resource network organisation and trial evaluation set-up each year.

During these five years, French farmers interests were mainly focused on bread wheat and rivet wheat (*T. turgidum*), with the hope to restore

ancestral bread making quality. The other species are more and more required, due to new aims, such as straw for roofs in ecological construction projects. This is the case for rye and old varieties of bread wheat.

The Biological status of accessions distributed is shown in Table 2. Requests from scientists concern landraces, old varieties, modern varieties as well as breeder lines. Research institutes can deal with inappropriate material such as wild or landrace accessions thanks to their experimentation capabilities.

For their breeding programs, private companies have the same kind of interest between modern varieties and breeders lines, and they have less interest in landraces or old varieties. Breeders are searching for material close to modern varieties with low plant heights and well characterized disease resistance. Requests are focused on adapted material which could allow integrating new genes of interest with fewer ancestral burdens.

In the case of farmers, a particular interest is placed on landraces and old varieties, which correspond to 90 % of the requests. Indeed, farmers and in particular baker-farmers look for varieties with a lower gluten content. These varieties are not adapted to the industrial bread-baking process, but they respond well to old bread-baking practices. Use of straw for litter, cattle feed or ecological construction is another aspect to take into account. For these purposes, farmers need not-reduced height plants, as landrace or old varieties.

As shown in Table 3, the origin of material requested is highly dependent on a requester's type.

Table 2

Number of distributed samples by requester type according to their biological status, between 2005 and 2010

Type	Breeders	Farmers	Research institutes	Others	Total
Wild	23 (0,3 %)	20 (1,1 %)	182 (2,8 %)	25 (4,3 %)	250 (1,5 %)
Landraces/old varieties	1396 (17,7 %)	1651 (87,7 %)	2591 (39,3 %)	476 (81,2 %)	6114 (36,1 %)
Modern varieties	3373 (42,7 %)	155 (8,2 %)	2268 (34,4 %)	54 (9,2 %)	5850 (34,5 %)
Breeder line	3093 (39,2 %)	24 (1,3 %)	1313 (19,9 %)	8 (1,4 %)	4438 (26,2 %)
Population	2 (0 %)	29 (1,5 %)	18 (0,3 %)	18 (3,1 %)	67 (0,4 %)
Unknown	4 (0,1 %)	3 (0,2 %)	220 (3,3 %)	5 (0,9 %)	232 (1,4 %)
Total	7891	1882	6592	586	16951

Table 3

Geographical origin of requested samples between 2005 and 2010

Geographical origin	Breeders	Farmers	Research institutes	Others	Total
French	5501 (69,7 %)	1390 (73,9 %)	2867 (43,5 %)	458 (78,2 %)	10216 (60,3 %)
European	1890 (24 %)	283 (15 %)	1759 (26,7 %)	34 (5,8 %)	3966 (23,4 %)
Aboard	472 (6 %)	170 (9 %)	1732 (26,3 %)	67 (11,4 %)	2441 (14,4 %)
Unknown	28 (0,4 %)	39 (2,1 %)	234 (3,5 %)	27 (4,6 %)	328 (1,9 %)
Total	7891	1882	6592	586	16951

Scientists inquire about French material, as well as European and abroad. They can delve further into the description of genetic resources diversity, and they can search more extensively into material adapted or unadapted to European environmental conditions.

Almost 90 % of material used by breeders from the GRC includes French or European accessions. These accessions are well adapted to French environmental conditions and are easier to utilize in breeding programs.

This tendency is higher in the «farmers» category, with strong links to territories. Three quarters of samples distributed to farmers include French varieties. They often search for varieties from their areas or varieties cultivated by their grandparents.

To make available the PGR collection to any users, a national website called, «SIREGal» (<http://urgi.versailles.inra.fr/siregal/siregal/welcome.do>), is in progress. In this website, users have access to the passport data, with information on pedigree, country of origin and some primary evaluation data – growth class, plant height or resistance to some diseases. In the future, a relationship with a molecular database will be available, thanks to a link based on the accession number. A picture book of the collection is also in progress with a special focus on national collections being planned.

Thanks to this website, orders can be made directly by this web interface and sent directly to GRC in INRA Clermont-Ferrand. For now, the national collection of bread wheat (1783 accessions) and barley (461 accessions) are available in SIREGal. This website is not only dedicated to small grain cereals, but it receives information on all other PGR Networks maintained by INRA units. Other crop species are available, too, such as maize, grain legumes and fruit and vegetables species.

Conclusion

As illustrated by the increased number of distributed samples, the French PGR network on small grain cereals appears to be quite effective and satisfactory for a larger number of requesters. In the following years, the main efforts will be focused both on the characterisation of the accessions and on the development of interconnected databases, in order to increase the use of genetic resources. For instance, a new project of evaluation of small grain PGR will be initiated in the «Breedwheat» project, in sharing tasks and responsibilities between public and private breeders. This project, supported by the French Government in the framework of the big program, «Biotechnology and Bioresources», started in 2011 and will be closed in 2020. In this project, devoted to bread wheat, new genomic tools will be developed by INRA in order to genotype the whole bread wheat GRC collection; from the whole collection, two panels of accessions will be defined for biotic (fungal disease resistances) and abiotic stress tolerance (drought, low input fertilizer) and, subsequently, multiplied and phenotyped by private breeders for specific traits in their multilocation network during three years. A genomic selection program will be developed, while a specific task will be devoted to bioinformatics and data management. Finally association analysis will be carried out at the end of the project, in relation to the different partners.

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СЕТЬ ГЕНЕТИЧЕСКИХ РЕСУРСОВ ВО ФРАНЦИИ: СОТРУДНИЧЕСТВО МЕЖДУ ПОЛЬЗОВАТЕЛЯМИ И ЦЕНТР ГЕНЕТИЧЕСКИХ РЕСУРСОВ ЗЕРНОВЫХ КУЛЬТУР

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Генетические ресурсы растений (ГРР) многие десятилетия использовались селекционерами в селекционных программах для получения современных сортов путем введения целевых генов (в частности генов устойчивости к болезням). Тем не менее ГРР все еще остаются недооцененными при работе с устойчивостью к абиотическому стрессу и над новыми сельскохозяйственными подходами, рассматривающими продуктивность во взаимосвязи с условиями окружающей среды. В последнее время интерес к изучению и использованию природного разнообразия, законсервированного в коллекциях генетических ресурсов растений, проявляют новые пользователи ГРР-коллекций, а именно ученые и фермеры, открывшие интересующие их новые и разнообразные источники. Для более эффективного использования ГРР было принято решение разделить обязанности по работе в Сети генетических ресурсов злаковых растений Франции в зависимости от знаний и возможностей членов Сети. В коллекции содержатся основные виды родов *Triticum* (пшеница), *Hordeum* (ячмень), *Secale* (рожь), ×*Triticosecale* (тритикале) и *Avena* (овес), а также их дикие сородичи. Ввиду растущего спроса на образцы, содержащиеся в коллекции, а следовательно, необходимости более эффективной

работы с ней, вся коллекция на основании сочетания данных по фенотипу и генотипу поделена на небольшие, но более функциональные группы образцов. Ведется работа со все новыми группами образцов, для того чтобы дать селекционерам и ученым новые полезные инструменты исследования, например, для работ по устойчивости к стрессу или по ассоциативному картированию. Все полученные таким образом в Сети генетических ресурсов злаковых растений Франции данные будут появляться в открытом доступе на сайте генетических ресурсов INRA (<http://urgi.versailles.inra.fr/siregal/siregal/welcome.do>).

Ключевые слова: злаковые культуры, генетические ресурсы, управление информационными ресурсами, распространение семян.