Introduction to CryoWEB and state of implementation in Europe

Zhivko Duchev

Introduction

Since many years the ex situ in vitro conservation is integral part of the national programmes for preservation of livestock genetic diversity. National gene banks were setup in many countries around the globe. These gene banks usually consist of collections of cryo-preserved animal genetic material, intended for short to long term storage and use. The collected genetic material is of various type, mainly semen, but also embryos, oocytes, somatic cells. The collections are usually stored in several duplicating storage sites, to prevent the loss of material in case of disaster.

All the gene bank samples are intended for future use, therefore, an adequate documentation system, keeping track of the collections, must be in place. The documentation should contain consistent data on the samples to support the routine gene bank operations, e.g. sample location, sample identification, current gene bank inventory, use of the material.

Countries organizing a national gene bank have two options in regards establishment of documentation system. These are developing a customized solution, or using an already available uniform tool. In some countries like France and USA[1] the organization managing the gene bank has developed information system tailored to their needs. However, in many cases the effort is concentrated mainly on the organization of the samples collection and storage, and the management prefer to start the documentation as soon as possible with the currently available software.

To meet such demands the open source software CryoWEB[2] was developed in Institute of Farm Animal Genetics (FLI) in Germany. This software is intended to serve as a electronic register of the national collections, uniformly applicable across various species, types of genetic material, storage facilities organizations.

CryoWEB software

The main purpose of CryoWEB is to store and provide all the information needed by the gene bank management in their everyday operations. The data required and stored in CryoWEB allows the manager to:

- find the distribution of each recorded sample in the storage facilities
- get all the information about the sample by the label on its physical storage vessel
- find the procedure to be followed by thawing for each sample
- perform complete or partial inventory of the storage
- identify all samples from a single donor
- keep track of material relocation and use
- virtually browse the storage facilities

In addition the system has options to store additional data which supports the management in taking decisions. These inlude the geographic distribution of the donor animals, search for donor's offspring in the collection, balance of the amount of stored material per animal per breed. And last, but not least the CryoWEB supports also a contact database of all persons and organizations involved with the national gene bank.

The required by CryoWEB dataset per sample is the minimal one, uniformly available across all species and essential for the fulfillment of the gene bank manager's everyday tasks. In other words, the lack of data item in this set will prevent the manager to perform one or more of the operations listed above, e.g. the manager will not be able to find a sample in the storage. In addition to this "passport data", the user has the option to enter non-mandatory data mainly in comments fields, as image or archive of documents. This approach allows the storing additional data in CryoWEB as archive, to keep all relevant data in one place.

The schema of the basic logical blocks for storing required data in CryoWEB is shown in Fig.1.

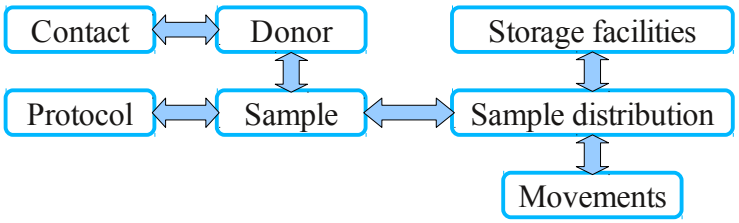

Figure 1. Basic blocks of mandatory CryoWEB data

As expected the central block in the system is the one containing data for the samples. In CryoWEB the term “sample” is used for all the material of one type produced by a given donor on a certain date. Thus, for each sample the system registers its unique identification, the donor animal, the date when the sample was produced and the date when the material was frozen, along with the type of packaging vessel. The sample is linked to a protocol file, where the freezing procedure, the steps to be followed during thawing and the veterinary status are described in detail.

For each donor animal, a minimal species independent data set is collected. The set includes a unique animal's identification, breed, species and gender of the animal. An organization or a person keeping more information is also recorded, e.g. organization which can provide genotype data or breeding value of the donor. These mandatory fields are mark with asterisk in Fig.2.

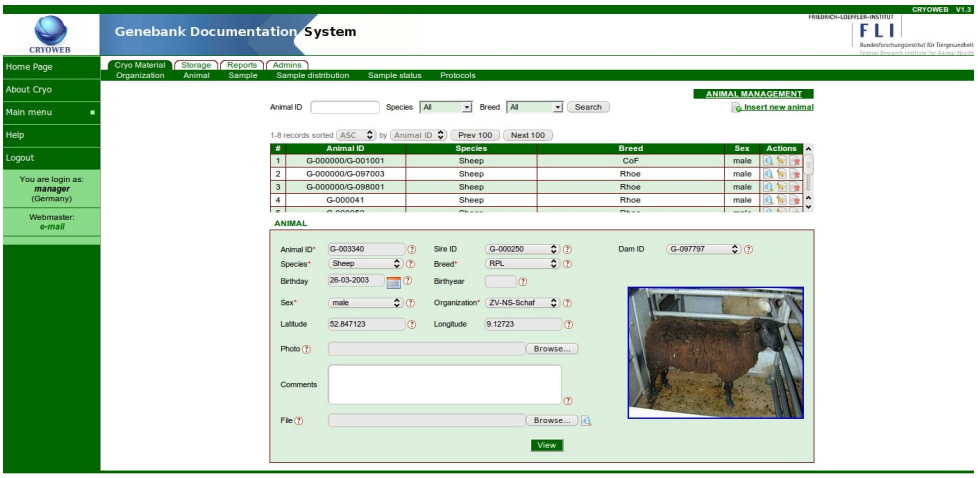

Figure 2. Information about a donor

Each sample is distributed in one or more storage locations. The exact location of the sample in the storage facilities is uniquely identified using a hierarchical addressing. Every single position in the storage is uniformly described in CryoWEB using a hierarchy of five levels. These levels have to be defined by the genebank manager after the initial installation of the system. An example how the levels can be defined for the most common type of storage (using tanks and canisters) follows. The first level is the storage place, e.g. the location of the AI station keeping the samples. The second level is the tank or the freezer, the third one – the canister within the tank, the forth – the level inside the canister and the fifth – the goblet containing the sample vessels The usage of such five levels hierarchy addresses in

CryoWEB allows to describe uniquely each location in most of the standard storage facilities.

Any relocation or usage of the part or the whole sample is also recorded and kept in history. This allows to produce outputs listing cumulated amounts of material which were available each year.

As the name suggest, CryoWEB is web-based information system, thus allowing access to the data from anywhere via the Internet. Since the data collected in the system is considered in some countries not public, the system requires user name and password to access it. The access to the entry web page can be also restricted to certain organizations or networks.

There is also option for translation, allowing the web interface, data content and the outputs to be used in the local language.

More information about the CryoWEB information system can be found on the project web page [3] or in the CryoWEB user's guide [4]. The CryoWEB user's guide is especially useful for the gene bank manager in setting a clear system of rules for preparing the data for entry in the database. Such system is very important and must be followed by every user of the genebank in order to prevent data inconsistencies.

State of implementation in Europe

Within the EFABISnet project[5], the CryoWEB software was installed in ten European countries: Finland, Estonia, Netherlands, Georgia, Slovakia, Slovenia, Austria, Switzerland, Iceland and Ireland. Additionaly, several more countries opted for CryoWEB and the software was also installed in Italy, Poland, Greece, Croatia and Cyprus. Along with Germany, where the software is also used, there are currently 16 European countries (Fig.3) where CryoWEB is installed.

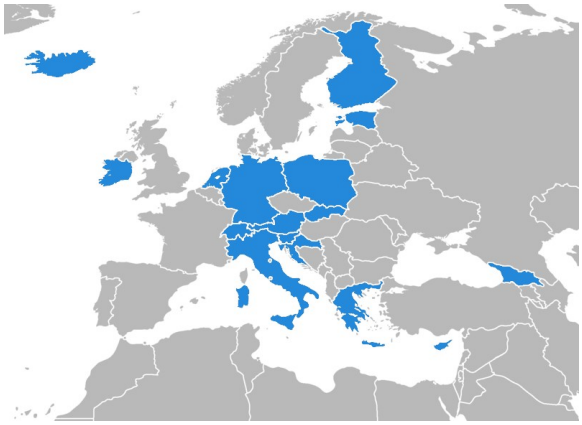

Figure 3. CryoWEB installations in Europe

Thus, now CryoWEB is used in a very heterogeneous set of national setups in terms of gene bank organization, amount and type of stored material, number of included breeds, organization of storage facilities. The software is used for documentation of several national gene banks in Europe, which have already accumulated significant collections, e.g. Netherlands, Austria, Switzerland. In all these countries one of the important issues was the migration of the existing data to the new database. During the migration process the data integrity and completeness was also veryfied and corrected to comply with the standards imposed by CryoWEB.

For some of the countries, e.g. Austria, Slovenia, part of the data were migrated using scripts, and the rest of the required data were entered via the web interface. For the countries having smaller collections, e.g. Estonia, the entering of the data via the web interface was the option of choice.

In other countries, e.g. Ireland, Georgia, which are in process of developing national gene banks CryoWEB was installed as documentation component to start the recording as soon as data are available. In these and other countries CryoWEB was used also as a model of the minimum data set required for successful management of national gene bank collection, i.e. the data set to be recorded

when acquiring and freezing the material.

In some cases CryoWEB was used also for sub-national gene banks. In Finland it is used to keep the data of one part of the national gene bank, the part which is stored in MTT Agrifood Research Finland. In Italy CryoWEB is used for keeping the data of the Italian animal genetic resources cryobank network, a federation of several gene banks. In this setup the data are centrally entered and each participating organization has a read-only access to view the data.

In most of these countries CryoWEB was used "out of the box", however some of the countries, e.g. Italy, Netherlands customized their installations in terms of data content and outputs to fit their specific needs.

Literature

1. Blackburn, H.D., 2009. Genebank development for the conservation of livestock genetic resources in the United States of America, Livestock science, 120, pp. 196-203
2. Duchev *et al., 2010.* CryoWEB: Web software for the documentation of the cryo-preserved material in animal gene banks*,* Bioinformation, 5 (5) 219-220
3. CryoWEB, Genebank Documentation System, http://cryoweb.tzv.fal.de/
4. Duchev *et al., 2010.* CryoWEB. User's Guide and Reference Manual, ISBN 978-3-9813280-0-4
5. EFABISnet,An Integrated Network of Decentralized Country Biodiversity and Genebank Databases, http://efabisnet.tzv.fal.de/