

CryoWEB: Web software for the documentation of the cryo-preserved material in animal gene banks

Zhivko Duche^v*, Truong Van Chi Cong, Eildert Groeneveld

Institute of Farm Animal Genetics, Friedrich-Loeffler-Institut, Hoeltystrasse 10, 31535 Neustadt, Germany; Zhivko Duche^v - Email: zhivko.duchev@fli.bund.de; *Corresponding author

Received February 8, 2010; Accepted September 27, 2010; Published November 1, 2010

Abstract:

Many countries in the world have set up national domestic conservation programmes and collections of long-term storage of cryo-preserved animal genetic material. We have developed a web based software - CryoWEB for the documentation of such collections. The software is generally applicable to all livestock breeds, independent of the donor's species and the type of preserved material. The software can record basic herd-book information for the donor animal, the structure of the storage facilities, description of the stored samples and their distribution within the gene bank. It also traces the movements of the sample vessels within the storage facilities and the usage of sample units. The outputs implemented in CryoWEB address the informational needs of the gene bank manager in her everyday tasks.

Availability: CryoWEB is publicly available at <http://cryoweb.tzv.fal.de>

Keywords: CryoWEB, animal gene banks, documentation, Open Source

Background:

Conservation of the genetic diversity is one of the important concerns in the modern animal breeding. The 'Global Plan of Action' adopted at the United Nations Interlaken Conference on Animal Genetic Resources stipulates the setup on national gene banks worldwide. Here, CryoWEB can be used right away to serve as the electronic register.

In many countries a national conservation programme has been set-up, usually as a combination of the in situ, ex situ in vitro and ex situ in vivo methods. As part of these programmes a long-term collection of cryo-preserved animal genetic material from various breeds is established, e.g. in Brazil [1], USA [2], or France [3]. Such collections are supposed to serve as a source of material for recovering breeds in distant future, or for supportive breeding. Therefore, the collection comprises various types of material, ranging from semen and embryos [5] to somatic cells [6]. The frozen material is usually duplicated in more than one storage location for security reasons.

A consistent documentation system has been recognized (e.g. in [6]) as an integral part of every gene bank. Such a system should collect and keep enough data for the successful identification and usage of the samples. This is a very important issue as the utilization of the stored material takes place long time after the collection when the access to primary data may be not possible. Therefore, the documentation system should contain at least a minimum data set to meet the following requirements:

For any sample chosen from the database, the user should be able to find the material in the storage facilities.

From the label on any vessel in the storage facilities the user should be able to find the information for the sample in the database.

For any sample identification there should be an exhaustive description of

the protocol used for freezing the material and the procedures to be followed when thawing.

Sometimes the gene bank management organization prefers to develop a new documentation system, including specific traits relevant to the local testing and production procedures, e.g. a "days to market" field in the USA animal-GRIN database [2]. Such systems require significant investments both in terms of funding and time for the initial development. On the other hand, in many gene banks the curators want to start recording data immediately, i.e. there is a demand for a uniform documentation system, which is easy to set up and use everywhere. The here presented Open Source software CryoWEB was developed with the intention to be a generally applicable gene bank documentation system. It can be used uniformly across species, material types and storage facilities.

Methodology:

CryoWEB was developed in the Institute of Farm Animal Genetics (FLI) in Germany on the basis and concepts of the CryoIS software [4] used for the Dutch gene bank. Several of the main blocks were preserved, but major improvements were introduced. First of all CryoWEB is intended to be used "out of the box", whereas CryoIS had to be customized. Secondly, the whole system was changed from desktop to a Web application. Finally, nationalization options and access control were introduced.

The main concept of CryoWEB is "less is more". The system requests from the user a minimum set of data, which is available for all species and essential for the gene bank management. Nevertheless, the user can still store additionally all data she considers valuable. This is done in the form of archives of files, where heterogeneous information can be included, e.g. birth certificate of the donor, material transfer agreement, performance test results, health certificate, etc.

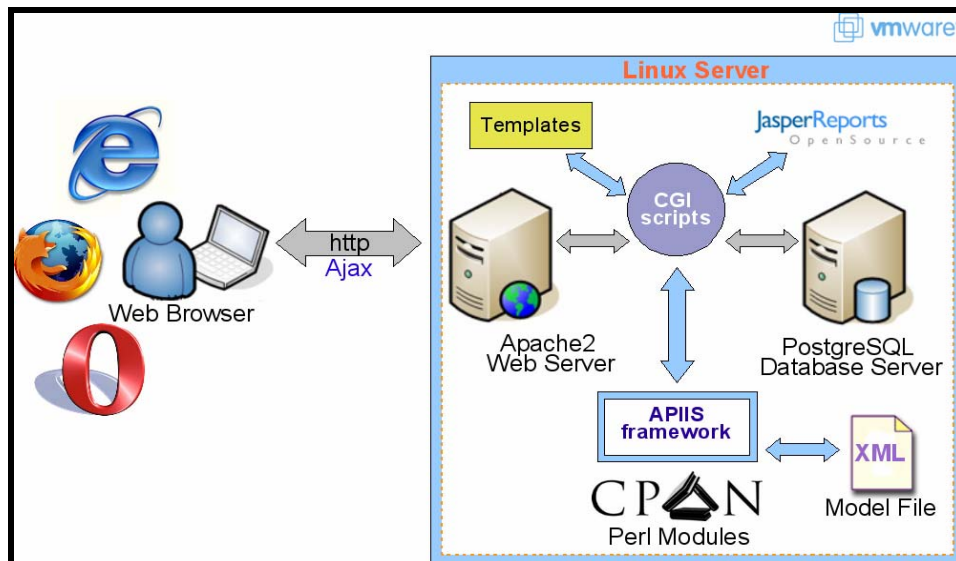


Figure 1: Application architecture of CryoWEB. The complete linux server can be encapsulated in a virtual appliance.

Input:

The data entry is logically grouped in four main blocks comprising several Web forms each. In the *Animals* block herdbook data about the donors and their pedigree may be recorded. In the *Storage Facilities* block the user specifies the structure of the tanks and freezers. In the *Samples* block the user enters data for the production and the freezing of the material, its distribution within the storage, moving and usage. The *Contacts* block provides a directory of people and organizations linked with the gene bank. The minimum data set fields are marked on each form.

Output:

CryoWEB has two types of outputs – screen outputs and reports for printing. In each data entry block the user can search and view stored data. A tree-view browsing of the hierarchy of storage locations is also developed.

The system can generate also a ready-to-print reports in PDF format. These include inter alia general gene bank statistics, information about a donor and all its samples, complete inventory of the storage facilities, history of movements in period, tracing a sample. There is also an option to export cumulated annual statistics per breed and material type for the EFABIS [7] network. However, this export is not based on the automated synchronization protocol used in the network [8], as the user must be able to correct manually the totals with the data from gene banks that use other software.

Software platform:

The software was written in Perl and runs under GNU Linux operating system, using PostgreSQL for database management system and Apache2 for web server. CryoWEB utilizes also several Perl modules from Comprehensive Perl Archive Network (CPAN) and the JasperReports framework for the outputs part. The application model of CryoWEB is given in **Figure 1**.

Distribution options:

CryoWEB is released under the GPL license and therefore the source code is freely available. Before installing this code and setting up a web page the user must have all required software (e.g. web server, additional Perl modules) in place. This assumes system administration knowledge which is not always available. To reduce the complexity of setting a complete Web system to a simple installation of a stand-alone application we offer second distribution option – virtual appliance. This is a virtual machine, where all the required software (including CryoWEB) is already installed and can be executed on Windows and Linux platforms using one of the free players from VMWare or VirtualBox.

Applications:

The CryoWEB software is installed as national gene bank information system in Netherlands, Slovakia, Slovenia, Austria, Switzerland, Iceland, Georgia, Estonia, Finland, Germany and Greece.

Acknowledgements:

The development of CryoWEB was partially supported by the European Commission, Directorate-General for Agriculture and Rural Development, under Council Regulation (EC) No 870/2004 (Action 20 - EFABISNET).

References:

- [1] A da S Mariante *et al. Livest Sci* **120**:204 (2009)
- [2] H Blackburn *Livest Sci* **120**:196 (2009)
- [3] <http://www.cryobanque.org/index.php?lang=en>
- [4] E Groeneveld *et al. Livest Prod Sci* **89**:297 (2004)
- [5] G.Gandini *et al. Genet Sel Evol* **39**:465 (2007) [PMCID: PMC2682823]
- [6] E Groeneveld. *AGRI* **36**:1(2005)
- [7] <http://efabis.net>
- [8] Z Ducheve & E Groeneveld *Bioinformatics* **1**:146 (2006) [PMID: 17597877]

Edited by P. Kanguane

Citation: Ducheve *et al. Bioinformatics* 5(5): 219–220 (2010)

License statement: This is an open-access article, which permits unrestricted use, distribution, and reproduction in any medium, for non-commercial purposes, provided the original author and source are credited.