

Report of a Working Group on *Beta* and the World *Beta* Network

Fourth Joint Meeting, 20-22 June 2012, Cappelle-en-Pévèle, France
L. Maggioni, L. Frese and E. Lipman





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The European Cooperative Programme for Plant Genetic Resources (ECPGR) is a collaborative programme among most European countries aimed at contributing to national, sub-regional and regional programmes in Europe to rationally and effectively conserve *ex situ* and *in situ* Plant Genetic Resources for Food and Agriculture and increase their utilization. The Programme, which is entirely financed by the member countries, is overseen by a Steering Committee composed of National Coordinators nominated by the participating countries and a number of relevant international bodies. The Coordinating Secretariat is hosted by Bioversity International. The Programme operates through nine networks in which activities are carried out through a number of permanent working groups or through ad hoc actions. The ECPGR networks deal with either groups of crops (cereals; forages; fruit; oil and protein crops; sugar, starch and fibre crops; vegetables) or general themes related to plant genetic resources (documentation and information; *in situ* and on-farm conservation; inter-regional cooperation). Members of the working groups and other scientists from participating countries carry out an agreed workplan with their own resources as inputs in kind to the Programme.

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Patellifolia plant in its natural surroundings east of Tazacorte, La Palma, Spain. Courtesy of © L. Frese, Julius Kühn-Institut, Quedlinburg, Germany.

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http://www.ecpgr.cgiar.org/networks/sugar_starch_fibre_crops/beta/beta_meeting_2012/presentations_beta2012.html

INTRODUCTION

The fourth joint meeting of the World *Beta* Network (WBN) and of the Working Group on *Beta* of the European Cooperative Programme for Plant Genetic Resources (ECPGR) was held during 20-22 June 2012 in Cappelle-en-Pévèle, France. It was hosted by the company Florimond Desprez.

Lothar Frese, Chair of the Working Group, opened the meeting by welcoming the 33 participants from 17 countries. He thanked the ECPGR Secretariat and Florimond Desprez for the efficient organization of the meeting.

Bruno Desprez welcomed all the participants; he briefly described the facilities at Florimond Desprez and wished the participants a fruitful meeting.

Lorenzo Maggioni, ECPGR Coordinator, welcomed the ECPGR Working Group and the WBN participants, and thanked Bruno Desprez and the Florimond Desprez staff for their invitation, hospitality and financial contribution to the meeting.

Lothar Frese reminded the participants that this meeting, the fourth in its series, brings together people from various disciplines, bound by the common wish to work together for the conservation and use of plant genetic resources of a crop of global importance. The Group intends to work together to share knowledge, according to each one's availability and capacity.

He presented the agenda for the three days, reminding the Group of the target of defining the conservation priorities and the plans for a joint management of the available resources. This can be better achieved through the generation of knowledge on the distribution, genetic diversity and genetic structure of the *Beta* populations.

PART I. WORLD *BETA* NETWORK MEETING

Geographic distribution

Opening remarks: *Beta maritima*: the origin of beets

B.V. Ford-Lloyd

The book "*Beta maritima*: the origin of beets" by E. Biancardi, L. Panella and R.T. Lewellen was published in 2012 by Springer. It summarizes existing knowledge and offers stimulus for future research; it thus serves as a resource for the Group. The book is a unique text entirely dedicated to sea beet and its descendants, offering narrative experiences of researchers who have investigated sea beet populations around the world and worked with its wild plants.

B. Ford-Lloyd thought that the book was an incentive for the Group in its reflection on how it can organize itself for the conservation of *Beta* in the near future. The Group's first priority should be to ensure that conservation of beet continues in Europe, since the plant is of European origin. Technology is helping conservation. Next-generation sequencing supports the genetic population studies on which conservation priorities are based. High throughput transcriptomic and gene expression studies will soon be possible as well.

The Working Group on *Beta* should continue to facilitate conservation efforts in Europe. In this context, the Group should remain alert to the changes that ECPGR is undergoing. The International Database for *Beta* (IDBB) still exists but there are not enough resources to

improve and develop it beyond the achievements obtained through recent EU-funded projects. The IDBB still needs to be integrated with the database created by the AEGRO project (An Integrated European *In Situ* Management Work Plan: Implementing Genetic Reserves and On Farm Concepts), including data from the Global Biodiversity Information Facility (GBIF), herbarium data, etc.

Distribution and conservation status of Beta and Patellifolia species in the Macaronesian region

A. Santos Guerra

According to the checklists from Azores (Silva et al. 2005)¹, Cabo Verde (Sánchez-Pinto et al. 2005)², the Canary Islands (Acebes Ginovés et al. 2010)³ and Madeira-Salvagens (Jaardim and Menezes de Sequeira 2008)⁴, four species of *Beta* (*B. macrocarpa*, *B. patula*, *B. vulgaris* and *B. vulgaris* subsp. *maritima*), and three of *Patellifolia* (*P. patellaris*, *P. procumbens* and *P. webbiana*) are present in these territories. *B. patula* and *P. webbiana* must be considered as endemic species for Madeira and the Canary Islands, respectively. Further research is required to know the exact representation at different archipelagos to resolve the problems of the complex *P. webbiana* and the polymorphic *P. procumbens* or to expand the area of some species. Strikingly, *P. procumbens* (IUCN category LC) has not yet been reported for the island of Fogo in the Cabo Verde archipelago.

Due to the halophilous or halo-nitrophilous character of most of these species, their distribution is relegated to littoral or lowlands areas and is related to human activities. In a few cases, some plants can be present at higher altitude (for example, *P. patellaris* in the Caldera de Taburiente National Park, La Palma, Canary Islands). This aspect should be taken into account for preserving some of these populations and studying their evolution, especially within protected areas (national, natural and rural parks, etc.) and in relation to the impact of human presence.

Discussion

M.C. Duarte thought that conservation should be focused on species and populations that are rare and live at the margins of the distribution area.

-
- ¹ Silva L, Pinto N, Press B, Rumsey F, Carine M, Henderson S, Sjögren E. 2005. List of vascular plants (Pteridophyta and Spermatophyta). In: Borges PAV, Cunha R, Gabriel R, Martins AF, Silva L, Vieira V, editors. A list of terrestrial fauna (Mollusca and Arthropoda) and flora (Bryophyta, Pteridophyta and Spermatophyta) from the Azores. Direcção Regional do Ambiente de Madeira and Universidade dos Açores, Horta, Angra do Heroísmo and Ponta Delgada. pp. 131-156.
 - ² Sánchez-Pinto L, Rodríguez M^aL, Rodríguez S, Martín K, Cabrera A, Marrero MC. 2005. Pteridophyta, Spermatophyta. In: Arechavaleta M, Zurita N, Marrero MC, Martín JL, editors. Lista preliminar de especies silvestres de Cabo Verde (hongos, plantas y animales terrestres). Consejería de Medio Ambiente y Ordenación Territorial, Gobierno de Canarias. pp. 38-57.
 - ³ Acebes Ginovés JR, León Arencibia MC, Rodríguez-Navarro ML, Del Arco Aguilar M, García A, Gallo A, Pérez de Paz PL, Rodríguez Delgado O, Martín Osorio VE, Wildpret De La Torre W. 2010. Pteridophyta, Spermatophyta. In: Arechavaleta M, Rodríguez S, Zurita N, García A, editors. Lista de especies silvestres de Canarias (hongos, plantas y animales terrestres). Gobierno de Canarias, Santa Cruz de Tenerife. pp. 119-172.
 - ⁴ Jaardim R, Menezes de Sequeira M. 2008. Lista das plantas vasculares (Pteridophyta and Spermatophyta). In: Borges PAV, Abreu C, Franquinho Aguiar AM, Carvalho P, Jardim R, Melo I, Oliveira P, Sérgio C, Serrano ARM, Vieira P, editors. A list of the terrestrial fungi, flora and fauna of Madeira and Selvagens archipelagos. Direcção Regional do Ambiente de Madeira and Universidade dos Açores, Funchal and Angra do Heroísmo. pp. 157-178.

A. Santos clarified that *Beta* is not a priority for the botanic garden La Orotava in Tenerife and that not enough seed is kept available for distribution. However, the botanic garden in Gran Canaria has a good seed bank.

L. Frese wondered whether a true sample was used for the sequencing of *P. webbiana*, since the only site where this species can be confirmed is in a military area in La Isleta, Gran Canaria, and other occurrences have not been taxonomically confirmed. A. Santos thought that it should be possible to obtain a permit to collect new seed from the original source.

Survey of in situ resources of *Beta vulgaris* subsp. *maritima* in Ireland

D. Grogan

The purpose of the survey was to establish the extent of changes since 1987 to native *Beta vulgaris* subsp. *maritima* populations represented in *ex situ* genebank collections. Its other aim was to establish contacts with relevant local authorities, making them aware of the presence of populations of this crop wild relative in the Areas of Scientific Interest and the Special Areas of Conservation under their control.

Location names and coordinates obtained from the International Database for *Beta* yielded 43 unique sites from which seed was collected in 1987. The survey was carried out in two periods between 2003 and 2007. Each site was surveyed across 500-1000 m of shoreline, as appropriate. Plant populations were estimated, a GPS point reference was taken for 10 representative plants at each site, and digital photographs were taken to record the extent of these habitats and threats to these sites.

On the east, south and southwest coasts, the majority of *in situ* populations were at least as good as found in 1987, and were not under any immediate threat of destruction. However, on the west coast, north of Galway Bay, no plants were found at two locations; there are now no recorded populations present from north of Galway Bay to Carlingford Lough on the north-east coast. Evidence of the negative impact of coastal erosion and human activity on habitats was evident at all sites.

International evaluation of *ex situ* genebank accessions has indicated that useful resistance genes are present in Irish populations, and molecular investigation of selected accessions has confirmed that Irish material is genetically closer to north-western European ecotypes than to those from the Mediterranean area.

Geographic structure of genetic diversity

Structural and content diversity of mitochondrial genome in gynodioecious beet: a comparative genomic analysis

A. Darracq, J.S. Varré, L. Maréchal-Drouard, A. Courseaux, V. Castric, P. Saumitou-Laprade, S. Oztas, P. Lenoble, B. Vacherie, V. Barbe, P. Touzet

Cytoplasmic male sterility (CMS) is a common feature in Angiosperms. This sexual polymorphism where hermaphrodites and females coexist in populations is called gynodioecy. It is believed to be the output of the genomic conflict between the mitochondrion that produces male sterility factors and the nucleus that counteracts by restoring male fertility. Wild beet, *B. vulgaris* subsp. *maritima*, is a gynodioecious species where different CMS systems have been described. The nearly whole sequences of five new mitochondrial (mt) genomes in the *Beta* genus were presented: four from *B. vulgaris* and one from *B. macrocarpa*, a sister species belonging to the same *Beta* section. Results were pooled with those from two previously sequenced genomes of *B. vulgaris* and from previously

studied genome diversity at the species level arriving at a total of 7 mt genomes, with 3 CMSs and 3 non-CMSs from *B. vulgaris*. The phylogenetic analysis revealed that CMSs and non-CMSs formed separate clades. The two groups of mt genomes – CMSs and non-CMSs – were therefore compared, and it was found that the CMS lineage might have evolved rapidly in sequence and structure (Darracq et al. 2011).⁵

Molecular analyses of *Beta vulgaris* subsp. *maritima* accessions of the Greek Genebank

P. Ralli, O. Koutita, K. Tertivanidis and G. Skaracis

Wild beet is a proven valuable source of desirable traits for sugar beet breeding programmes. Detailed characterization of such available material is a prerequisite for its efficient exploitation. The objective of this study was to investigate, by means of molecular markers, the genetic diversity in certain wild beet accessions preserved at the Greek Genebank. Thirty-four accessions of the sea beet (*B. vulgaris* L. subsp. *maritima* (L.) Arcang.) collected from different regions of Greece were included in the study. Random amplified polymorphic DNA (RAPD) markers were used. Following a preliminary evaluation of 60 random 10-mer primers, 21 such primers manifesting polymorphism (an average of 6.5 bands per primer) were further analysed. Bulked DNA samples from five individual plants per accession were amplified with these primers. A total of 218 bands were detected out of which 136 (62.3%) were polymorphic. Genetic similarity, based on Jaccard's coefficient, was estimated between the different accessions. The association between the accessions was assessed by two multivariate analyses: UPGMA (unweighted pair group average) and PCORDA (principal coordinate analysis). Very similar grouping (three main groups/subgroups) was achieved by both the clustering and ordination approach. Good correlation was observed between such grouping and the geographical distribution data of the accessions. Thus, the use of these and other sea beet populations collected throughout Greece can be planned more effectively.

Evaluation of genetic diversity and root traits of sea beet accessions of the Adriatic Sea coast

P. Stevanato, D. Trebbi, E. Biancardi, G. Cacco, J. M. McGrath, M. Saccomani

Thirty-nine sea beet (*B. vulgaris* L. subsp. *maritima* (L.) Arcang.) accessions of the Adriatic coast were screened genetically and for their adaptive morpho-functional root traits in order to identify new sources of abiotic resistances for sugar beet breeding programmes. Genetic diversity was evaluated with 21 microsatellites markers, which identified 44 polymorphic alleles. Two main clusters of sea beet were identified: the West and the East Adriatic coast groups, with the latter showing higher genetic diversity.

Among sea beet accessions with desirable root traits, four accessions have proved to be useful for sugar beet (*B. vulgaris* (L.) subsp. *vulgaris*) breeding aimed at improving the tolerance to nutritional stresses. Lastovo (ID 29) and Zut (ID 34) accessions were characterized by the highest values of root elongation rate (RER), total root length (TRL), fine root length (FRL) and root surface area (RSA), still maintaining a high value of root tips density (RTD), while Grado (ID 21) and Portic (ID 23) accessions were characterized by the highest RTD, but low values of RER, TRL, FRL and RSA.

⁵ Darracq A, Varré JS, Maréchal-Drouard L, Courseaux A, Castric V, Saumitou-Laprade P, Oztas S, Lenoble P, Vacherie B, Barbe V, Touzet P. 2011. Structural and content diversity of mitochondrial genome in beet: a comparative genomic analysis. *Genome Biology and Evolution* 3:723–736.

Genetic structure analysis of Moroccan wild beet germplasm

Y. El Bahloul, F. Gaboun

Wild genetic resources of beet are widespread along the Atlantic coast, Mediterranean region and a part of Asia. Very little is known about existing species and their genetic structure in Morocco. The objectives of this study were to identify the main existing species and to undertake a genetic evaluation. Collection trips for *Beta* have been conducted since 2005, covering different climatic regions along the Atlantic coast and from inland areas. Nineteen populations from the collection were evaluated for genetic diversity. Eight *B. maritima*, six *B. macrocarpa* and five *P. patellaris* populations were analysed using 12 polymorphic microsatellite markers.

High genetic diversity was observed between and within populations of each studied group. Allelic richness was about 5.13 for *B. macrocarpa*, 5.07 for *B. maritima* and 1.6 for *Patellifolia*. An analysis of functional correspondence showed a low population genetic structure for *B. macrocarpa* and *B. vulgaris* subsp. *maritima*. In contrast, *Patellifolia* presented very highly structured populations. Gene flow was significant within *B. macrocarpa* despite its being a self-pollinated plant; it is probably due to seed transfer and transportation. Gene flow within and between populations of *B. vulgaris* subsp. *maritima* is the result of both seed and pollen migration. Gene flow was very low within the *Patellifolia* group as it is a highly autogamous species.

The evaluated germplasm presents high genetic diversity. The Moroccan collection is of great interest for introgression of genes of interest into cultivated beet.

Drought physiology of sugar beet compared with its wild relative *B. vulgaris* subsp. *maritima*

(abstract provided by authors, who were unable to attend the meeting)

E.S. Ober, D. Johnston

Insufficient soil moisture limits sugar beet (*B. vulgaris* subsp. *vulgaris*) yields in the UK and other water-limited areas. It was hypothesized that the wild maritime relative *B. vulgaris* subsp. *maritima*, which often thrives in saline and dry habitats, may have desirable drought tolerance traits that could be introgressed into elite sugar beet germplasm. To test this hypothesis, the performance of commercial sugar beet hybrids was compared with *maritima* accessions under well-watered and water-limited conditions. Various physiological and morphological features related to drought tolerance were studied in sugar beet and *maritima* types from Corsica, England and Greece in both field and glasshouse experiments. In the field experiments, *maritima* types maintained greater turgor, net photosynthesis, stomatal conductance and transpiration rate than sugar beet, especially under water-limited conditions. However, *maritima* types had a lower total dry weight (TDW), water-use efficiency (WUE) and radiation-use efficiency (RUE) than sugar beet. This suggests that the whole plant net photosynthesis and/or the conversion of fixed CO₂ into dry matter was smaller in *maritima* types than in sugar beet. The percentage decrease in TDW and relative growth rate (RGR) due to water-limited conditions was similar in both *Beta* types, suggesting that sugar beet had similar tolerance to stress as *maritima*. In the glasshouse experiment, similar leaf water potentials, net photosynthesis, stomatal conductance and transpiration rate were obtained in both *Beta* types. As in the field experiment, *maritima* had lower TDW and WUE than sugar beet. However, the percentage decrease in TDW and RGR due to water-limited conditions was smaller in *maritima* than in sugar beet. This may have been due to the faster onset of water deficit in the glasshouse compared with the field experiments. It was concluded that the *maritima* accessions studied were not more drought tolerant than sugar beet. Further work has shown that sufficient diversity for drought tolerance exists within

elite sugar beet germplasm to enable breeding progress. However, the *maritima* accessions did show greater osmotic adjustment than the hybrids, which deserves further investigation.

Biogeographical determinants of population structure in *B. nana*

C.M. Richards, A.L. Fenwick, B.C. Hellier, L. Panella, L. Frese

Beta nana is a rare alpine species endemic to Greece. It is a crop wild relative of cultivated beet (*B. vulgaris* subsp. *vulgaris*) and is an important genetic resource for breeding cold tolerance and other traits. A plant exploration conducted in 2005 found 26 occurrences of this wild beet on six mountain locations that span three phytogeographical zones in Greece, from Mount Olympus in the north to Mount Taygetos in the south. In addition to seed, leaf materials from about 30 individual plants were collected at each mountain location. These samples were used to estimate genetic diversity and differentiation patterns, using co-dominant simple sequence repeat (SSR) loci. Specifically, these genotypic data were used to estimate the hierarchical genetic structure across these discrete alpine habitats in Greece and to estimate ongoing and historic demographic and gene flow patterns linking these sites. Importantly these patterns of genetic differentiation were compared with environmental niche models for the species.

Spatial and genetic data were integrated to assess the impact of various climate models on the range of this specialized species and to identify regions of critical conservation priority.

Preliminary work on tissue from plants grown from seed collected at Mounts Olympus, Giona, Vardousia and Parnassos showed results similar to Nagamine and Ford-Lloyd (1989)⁶, who had found five unique and invariant allozyme alleles compared with other species. High overall inbreeding associated with locus information was detected by SSR markers in populations at nine sites comprising 180 individuals. Population-specific variation with SSRs also showed huge inbreeding, with some populations showing no variation. Genotypic data have shown that if loci are polymorphic, almost all the diversity is partitioned among the populations of different mountain tops.

Discussion

A. Tan pointed out that protocols for germination of *B. nana* need to be developed.

B. Ford-Lloyd remarked that a better understanding of the ecology of this species would be useful for gauging the effects of climate change. At present, this species cannot be easily grown outside its natural habitat.

Project discussion: Genetic diversity and gene flow in *B. nana*

(led by L. Panella and P. Ralli)

P. Ralli presented a proposal for a research study for *in situ* conservation of *B. nana* on Mount Olympus, to be carried out in collaboration with the protection services of the Olympus National Park. It is important to know that Mount Olympus is a National Park and it belongs to the Natura 2000 protected area network. The location is also close to the genebank, which is an advantage. The threat from human activities or from grazing is more limited here than in other areas where *B. nana* was detected. However, climatic and environmental changes can be a more immediate threat, since this species is adapted to conditions of low atmosphere pressure, oxygen concentration and temperature, and high relative humidity. The purpose of the project would be the detection of appropriate areas for *in situ*

⁶ Nagamine T, Ford-Lloyd BV. 1989. New genetic markers in a wild species of beet (*Beta nana* Boiss. et Heldr.): prospects for utilization. *Plant Breeding* 102:344–347 (doi: 10.1111/j.1439-0523.1989.tb01268.x).

conservation of *B. nana* and monitoring of *B. nana* populations that were located during previous expeditions (Dale 1980⁷, 1981⁸; Frese et al. 2009⁹), as well as surveying of additional areas.

The proposed plan for the study includes:

- Detailed mapping of *B. nana* populations in the studied areas, as well as in other areas of Greece;
- Regular monitoring and recording of demographic parameters of populations;
- Periodic observations and measurements of the ecological environment;
- Conservation actions in populations that are at risk in specific habitats;
- Complementing *in situ* conservation with *ex situ* measures by sampling and safe maintenance of seeds in the Greek Genebank;
- Phenotypic characterization, agronomic evaluation and genetic study of identified populations, including the study of the reproductive system and of factors affecting germination ability;
- Documentation of the acquired information (collection and passport data, field observations, population monitoring data, etc.) in a database.

Recommendations

- It was agreed that the establishment of three genetic reserves for *B. nana* is – in the light of the results presented by L. Panella – obviously not sufficient and that genetic reserves should be established on all mountains in Greece where this species occurs. It was noted that the limited genetic variation within sites is a threat to the species in itself as it indicates limited adaptability. The participants recommended the establishment of a first genetic reserve on Mount Olympus and investigation of the distribution of genetic diversity within the three sites located at different altitudes, which the Greek Genebank had recently revisited.
- The Greek Genebank was invited to submit a *B. nana* project proposal to the ECPGR Secretariat so that the small action funds already earmarked for this work could be released. The ECPGR WG on *Beta* and the WBN will backstop a national *B. nana* project proposal by a supporting letter.
- ERA-NET calls for proposals should be tracked. Greece could consider applying for European Rural Development Funds, specifically referring to EC Regulation 1974/2006 which provides detailed rules for the application of Regulation 1698/2005 and stipulates support in its Article 27.4(b) “to preserve plant genetic resources naturally adapted to the local and regional conditions and under threat of genetic erosion”.

Workplan

- The WG Chair will support the Greek *B. nana* project proposal with a supporting letter **(by end July 2012)**.
- The Greek Genebank will submit as soon as possible a proposal to the ECPGR Secretariat for the use of available funds from the ECPGR Networks’ budget (€ 2600). This will include sampling of plants on Mount Olympus, to be carried out in **September 2012**.

⁷ Dale MFB. 1980. Report on 1980. Survey on *B. nana* in Greece. Copy available at the Greek Genebank, Thessaloniki.

⁸ Dale MFB. 1981. Report on 1981. Collection of *B. nana* in Greece (Supplement to 1980 report). Copy available at the Greek Genebank, Thessaloniki.

⁹ Frese L, Hannan R, Hellier B, Samaras S, Panella L. 2009. Survey of *Beta nana* in Greece. In: Frese L, Maggioni L, Lipman E, editors. Report of a Working Group on *Beta* and World *Beta* Network. Third Joint Meeting, 8-11 March 2006, Puerto de la Cruz, Tenerife, Spain. Bioversity International, Rome, Italy. pp. 45-52.

Project discussion: Genetic diversity and gene flow in *Patellifolia* species

(led by A. Santos Guerra and B.V. Ford-Lloyd)

A. Santos confirmed that *Patellifolia* species are protected in many areas, but no organization is working on this genus in the Canary Islands. The competent authority for protection of the island's flora is the Canarian authorities.

L. Panella commented that 66 accessions of three *Patellifolia* species are present in the Germplasm Resources Information Network (GRIN, USA). The concern is that *P. webbiana* may not really be *webbiana*; collaboration was invited for the identification of *Patellifolia* with appropriate genetic markers.

L. Frese reported that, using a flow cytometer, JKI observed 3x and 4x types in a *P. patellaris* sample taken at Marrakesh.

B. Ford-Lloyd suggested collecting single plant samples of *Patellifolia* species in the Canary Islands and Madeira. L. Frese reminded that this had already been done; the samples are now stored either as dry leaves or DNA-probes at the Julius Kühn-Institut (JKI). The set of SSR markers used to analyse the variation within *B. patula* did not work in *Patellifolia*. He offered to do routine analysis on *Patellifolia* material, but also wished to see a more comprehensive cooperative project being developed on this issue with the objective of detecting SSR markers suited to describe the genetic diversity in the genus *Patellifolia*.

Recommendation

- There was general agreement that any further research on *Patellifolia* should include taxonomically clearly defined standard accessions of *P. patellaris*, *P. procumbens* and *P. webbiana*. The *P. procumbens* accession used in the genome sequencing project by the Universities of Bielefeld, Barcelona and Dresden should be verified for validation. The offer from L. Frese to organize a meeting to draft a project proposal was welcomed. The project could either focus on *Patellifolia* research aspects or expand the scope of research to the *Corollinae* section. ECPGR funds allocated to the small action on *B. patula* (€ 5000) could be used for this purpose. Forthcoming calls of ERA-NET and BiodivERsA (<http://www.biodiversa.org/>) should be tracked.¹⁰

Workplan

- Depending on feedback from interested potential partners (to be received by **end July 2012**), L. Frese will organize a meeting to prepare a project on *Patellifolia*, *Beta* section *Corollinae*, along with *B. nana* (taxonomic aspects, genetic diversity).

Utilization, conservation and documentation

Fine-mapping of rhizomania resistance using an in situ population of *B. vulgaris* subsp. *maritima*

F.J. Kopsch-Obuch, S.L.M. Frerichmann and G. Capistrano-Gößmann

Rhizomania is one of the most severe sugar beet (*B. vulgaris*) diseases worldwide, including Germany, leading to a loss in sugar yield of up to 80%. The causal agent of this disease is the beet necrotic yellow vein virus (BNYVV), which is transferred by the soil-borne

¹⁰ The BiodivERsA partners have decided to launch their fourth joint call for research proposals on "Invasive Species and Biological Invasions" with a focus on alien invasive species, planned to be launched in early November 2012, with a closing date in mid-February 2013.

plasmodiophoromycete *Polymyxa betae*. Rhizomania is controlled by the use of resistant sugar beet varieties. Resistance is conferred mainly by the two resistance genes *Rz1* and *Rz2*. While the origin of *Rz1* is still unknown, *Rz2* has been derived from the *B. vulgaris* subsp. *maritima* accession WB42. This accession was collected from a wild beet population that still exists *in situ* nearby Kalundborg, Denmark. Low linkage disequilibrium (LD) is assumed as this population is segregating for *Rz2* and has undergone many generations of cross-pollination and recombination. The wild population along the coastal line of Kalundborg was re-sampled, providing a genetic resource that is very suitable for high-resolution mapping of *Rz2*. This project is aimed at (i) fine-mapping of *Rz2* in *B. vulgaris* subsp. *maritima*, (ii) map-based cloning of *Rz2* and (iii) sequence-based search for new sources of rhizomania resistance. More than 200 test cross families were produced from 200 distinct wild beets and a rhizomania-susceptible CMS sugar beet line. These test cross families are being phenotyped for rhizomania resistance, and various marker systems are employed for fine-mapping of *Rz2*. Preliminary results were presented.

Discussion

The study was received by the meeting as an exemplar case showing the value, also for genetic studies, of *in situ* conservation of entire populations of crop wild relatives. Even though the area under study had already been proposed for the establishment of a genetic reserve, the results show that the existing genetic diversity for rhizomania resistance is also distributed outside the limits of the proposed genetic reserve. Therefore, it will be worthwhile revisiting the extension of the proposed genetic reserve.

Evaluation of resistance to *Cercospora* leaf spot, *Rhizoctonia* root rot and *Aphanomyces* root rot in Japanese elite breeding lines

K. Taguchi, K. Okazaki, H. Takahashi

The Japanese elite breeding lines were derived mainly from ancestral cultivars, which could have originated from only about ten kinds of open-pollinated varieties (OPVs) (Taguchi et al. 2006)¹¹ that were included in the hybrid breeding programme launched at least 50 years ago for creating useful parental lines. Considering that it is a very important task to conserve the genetic diversity of the germplasm for the future, 63 elite breeding inbred lines (ILs) were assessed for resistance to three major diseases: *Cercospora* leaf spot (CLS), *Rhizoctonia* root rot (RHR) and *Aphanomyces* root rot (APR) at the National Agricultural and food Research Center, Hokkaido Agricultural Research Center (NARO/HARC).

Analysis of resistance data, assessed on a NARO/HARC scale of 0-5, indicated significant differences between the ILs. Clear variations of disease indices were recorded: 3.3 ± 0.4 for CLS, 4.5 ± 0.5 for RHR and 1.7 ± 1.0 for APR. The broad-sense heritability was estimated at above 90% in each evaluation. There were some strong resistant lines in ILs, the ratios of which were 9% for CLS, 3% for RHR and 27% for APR. The proportion of APR-resistant lines was relatively high, while only a few CLS- and RHR-resistant lines were observed among the ILs. The variation of resistances could be explained in part by the pedigree relationships between the ILs and their ancestral OPVs. Some lines were observed with higher resistance than in the standard strong varieties. These highly resistant lines will be useful for the disease resistance breeding programme. Eight additional lines showed medium resistance to the three diseases and can also be used for resistance breeding.

¹¹ Taguchi K, Nakatsuka K, Takahashi H, Okazaki K, Yoshida T. 2006. Relationship between the Coefficient of Parentage and Sugar Yield in Sugar Beet F1 Hybrid. *Breeding Research* 8:151–159. (In Japanese).

Genetic control of bolting in *B. vulgaris*

A.E. Müller, S. Vogt, W. Zhang, N. Dally, G. Schulze-Buxloh, M. Lommel, G. Weyens, M. Lefebvre, B. Wahl, A. Schechert, C. Jung

Natural accessions of *B. vulgaris* such as sea beets (*B. vulgaris* L. subsp. *maritima*) comprise annual forms that bolt and flower within a single growing season without requirement for vernalization as well as iteroparous perennials that require vernalization. The annual habit is controlled by the bolting locus B (Munerati 1931¹²). The vernalization response of cultivated biennial forms such as the sugar beet (*B. vulgaris* L. subsp. *vulgaris*) is mediated by *BvFT1* (FLOWERING LOCUS T1), which acts as a floral repressor and is downregulated by vernalization. Flowering in annuals and vernalized biennials also depends on expression of the floral promoter gene *BvFT2*, which is induced under long-day conditions (Pin et al. 2010¹³). Current studies aim to understand the genetic network that governs life cycle and bolting control in beet, with applications for plant breeding including suppression of vernalization-responsiveness to enable winter cultivation. Using a large F2 population derived from a cross between an annual and a biennial beet and a map-based cloning approach, the team developed a set of molecular markers that cosegregate with B and anchor a 0.9 Mb BAC contig to the genetic map of the B locus. Whole BAC sequencing identified *BvBTC1* (BOLTING TIME CONTROL 1) as a strong candidate gene. A functional analysis of *BvBTC1* demonstrated its pivotal role in life cycle control in beet as well as an unexpected role in biennials. A haplotype analysis in wild and cultivated beets further suggested that domestication of beet involved selection of a rare *BvBTC1* allele. Besides the B locus, a genetic survey of biennial genotypes derived from ethyl methanesulfonate (EMS) mutagenesis of an annual accession by linkage mapping in newly developed F2 populations identified two additional, previously unknown loci B2 and B4 that co-regulate annual bolting in wild beets (Büttner et al. 2010¹⁴, Abou-Elwafa et al. 2011¹⁵). In a complementary approach, additional components of the floral transition gene network in beet are being identified by genome-wide transcript profiling. An integrated model for the genetic control of bolting in beet was presented.

Home garden beets in Turkey

A. Tan

Gardens have existed in Turkey since ancient times. Traditional Turkish houses always had a garden, no matter what the size of the house. These gardens are not only important sources of food, fodder, fuel, medicines, spices, ornamentals, construction materials and income, they also provide microenvironments for the conservation of a wide range of different vegetable and even fodder beets, since Turkey is one of the centres of origin and domestication for beet and holds wide diversity of both wild beets and cultivated beets that have been grown for centuries. For this reason, beets in home gardens were investigated. Since home gardens are considered as a niche within an agroecosystem, study sites were selected in the

¹² Munerati O. 1931. L'eredità della tendenza alla annualità nella comune barbabietola coltivata. Zeitschrift Pflanzenzüchtung 17:84–89.

¹³ Pin PA, Benlloch R, Bonnet D, Wremerth-Weich E, Kraft T, Gielen JJJ, Nilsson O. 2010. An antagonistic pair of *FT* homologs mediates the control of flowering time in sugar beet. Science 330:1397-1400.

¹⁴ Büttner B, Abou-Elwafa SF, Zhang W, Jung C, Müller A. 2010. A survey of EMS-induced biennial *Beta vulgaris* mutants reveals a novel bolting locus which is unlinked to the bolting gene *B*. Theoretical and Applied Genetics. 121:1117-1131.

¹⁵ Abou-Elwafa SF, Büttner B, Kopisch-Obuch FJ, Jung C, Müller AE. 2011. Genetic identification of a novel bolting locus in *Beta vulgaris* which promotes annuality independently of the bolting gene *B*. Molecular Breeding, published online November 22, 2011, DOI 10.1007/s11032-011-9671-x.

agroecological zones that contain significant biological diversity. Common sampling procedures were applied to assess the extent of species diversity maintained in home gardens; the study sites were then surveyed for in-depth study. Local knowledge associated with this diversity, ethno-botanical diversity based on local taxonomy used by growers, socio-economic status and local seed management systems were also recorded. The recorded beet species and forms of local beet cultivars were also characterized, using agromorphological traits.

Very diverse forms of leaf beets, root beets and even fodder beets were grown in the home gardens and were sometimes associated with wild maritime beets and wild *Corollinae* species. Growers, especially women, play a key role in managing this diversity in agroecosystems. Such maintenance of diversity is a very valuable complement to *ex situ* conservation. It is not uncommon to find more than 50 plant species in a single garden.

Conservation of intraspecific diversity in genetic reserves for wild beets

L. Frese, M.C. Duarte, M. Veloso

The status of wild species belonging to the gene pool of cultivated beets was assessed by Bilz et al. (2011)¹⁶ using the International Union for Conservation of Nature (IUCN) Red List Criteria (IUCN 2001, cited in Bilz et al. 2011). The results indicate that 50% of these wild species are threatened by extinction to varying degrees: *Beta patula* (critically endangered, CR), *B. macrocarpa* (endangered, EN), *B. adanensis* (= *B. vulgaris* subsp. *adanensis*, valid name) (vulnerable, VU), *B. nana* (VU), and *Patellifolia webbiana* (CR). There is therefore an urgent need to conserve the intraspecific diversity of these species in their natural habit (*in situ*) with the objective of increasing their conservation status to the level of least concerned (LC). The genetic reserve conservation technique was suggested by Maxted et al. (1997)¹⁷ as a way of preserving intraspecific diversity. With the aim of identifying priority genetic reserve sites, Kell et al. (2012)¹⁸ developed and tested the crop gene pool strategy in the context of the AEGRO project (<http://aegro.jki.bund.de/aegro/>). A case study on the gene pool of cultivated beets provided a basis for decision-making (Frese et al., AEGRO working document¹⁹). On this basis, 26 locations in the EU-27 were proposed as suited for the establishment of genetic reserves for *Beta* and *Patellifolia* species. The Genetic Reserve Information System (GenResIS²⁰) developed by the University of Madrid provides detailed information on the locations of the recommended sites and their ecogeographic variables. In close cooperation with the national and local nature conservation agencies, action plans now need to be developed for integrating the management plans of genetic reserves with those of

¹⁶ Bilz M, Kell S, Maxted N, Lansdown RV. 2011. European Red List of Vascular Plants. Publications Office of the European Union, Luxembourg.

¹⁷ Maxted N, Hawkes JG, Ford-Lloyd BV, Williams TW. 1997. A practical model for *in situ* genetic conservation. In: Plant Genetic Conservation: The In Situ Approach. Maxted N, Ford-Lloyd BV, Hawkes JG, editors. Chapman and Hall, London. pp. 339–367.

¹⁸ Kell SP, Maxted N, Frese L, Iriondo JM. 2012. *In situ* conservation of crop wild relatives in Europe: a strategy for identifying priority genetic reserve sites. In: Agrobiodiversity Conservation: Securing the diversity of Crop Wild Relatives and Landraces. Maxted N, Dulloo ME, Ford-Lloyd BV, Frese L, Iriondo JM, Pinheiro de Carvalho MÂA, editors. CABI Publishing, Wallingford, UK. pp. 7–19.

¹⁹ Frese L, Pinheiro de Carvalho MÂA, Duarte MC. 2011. Crop case study *Beta* L. (including *Patellifolia* A.J. Scott et al.). Annex 07 of the final report of the AEGRO project (<http://aegro.jki.bund.de/aegro/index.php?id=174>).

²⁰ GenResIS. 2012. Genetic Reserve Information System (<http://www.agrobiodiversidad.org/>).

Natura 2000 protected sites, similar to the action plans prepared for *B. patula* (Pinheiro de Carvalho and Frese, AEGRO working document²¹).

The 26 sites were selected on the basis of geographic, climatic and genetic data and proposed to the best knowledge. They form the first components of species-specific networks of plant occurrences presumed to represent a significant part of the intraspecific diversity of threatened wild beet species. The network can be expanded to ensure the existence of a wide genetic base, which is essential for the adaptive evolution and persistence of the species that are important genetic resources for plant breeding. More investigations into the ecogeographic patterns of intraspecific diversity are required to better inform the decisions taken in favour of or against specific sites and plant occurrences.

Discussion on suggested genetic reserve sites for Beta and Patellifolia

(led by L. Frese and M.C. Duarte)

The discussion clarified that the selection system of the suggested reserve sites has been only partially successful, since certain interesting sites are missing from the lists; also, more information should be used (such as molecular genetic data) to revise the site list.

Implementation of the genetic reserves concept remains difficult in its last stages, which involve follow-up with local authorities; the WG could play a significant role here.

Recommendations

- The list of proposed genetic reserves should be revised and the network of genetic reserves should be expanded through cooperation with non-EU representatives.
- *In situ* and *ex situ* management of *Beta* germplasm should exemplarily be linked using recommended genetic reserve sites (i.e. samples of *B. patula* from the genetic reserve sites should be deposited in the genebank of Madeira).

Workplan

- Each country representative should revise the list of proposed genetic reserves and send comments to L. Frese by end 2012. The list of proposed sites is available from the Genetic Resources Information System (GenResIs) of the AEGRO project (www.agrobiodiversidad.org/aegro).
- Representatives from Armenia, Azerbaijan, Georgia, Iran, Russian Federation and Turkey will apply the 4-steps methodology developed by the AEGRO project and suggest sites for genetic reserves for species of the Beta section Corollinae, by end 2013.
- Country delegates will ensure that *ex situ* samples are collected from each proposed genetic reserve site and deposited in the respective country genebank. These samples should also be proposed to the respective National Coordinators for inclusion in the European Collection and therefore be flagged in the European Plant Genetic Resources Catalogue (or European Internet Search Catalogue, EURISCO) as being part of AEGIS (before the end of 2013).

Introduction to the AKER project

B. Desprez and K. Henry

AKER is the name of a French research initiative on “New strategies for the use of the exotic variability, based on genomic tools (sugar beet as a model plant)”. The project responds to the need to become more competitive in the international sugar market. The competitive

²¹ Pinheiro de Carvalho MÂA, Frese L. 2011. *Beta patula* Aiton genetic reserve action plan. Annex 10 of the final report of the AEGRO project (<http://aegro.jki.bund.de/aegro/index.php?id=174>).

advantage of other players like Brazil compared with Europe can be reduced in the future not only because of increasing costs of production in Brazil, but also through genetic improvement that can be achieved through this project. Current barriers to yield increase in Europe are losses caused by leaf diseases; also, it is impossible to adopt genetically modified crops as they are not accepted by the public, as opposed to the case in competitor countries. Since the genetic variability currently used in sugar beet is increasingly narrow, the use of the existing variability needs to be improved to speed up genetic progress. A favourable factor is the possibility of optimally utilizing world genetic variability by using available informatics and genomic methodologies. A group of players in France is determined to invest in this crop, which is of commercial interest and has a relatively simple genome.

The objectives of the project include:

1. To obtain improved genetic material;
2. To improve access to genetic material, optimizing genetic diversity that is available and can be rapidly used to reach new targets;
3. To provide access to molecular tools and new technologies to accelerate creation of improved genomes;
4. To provide access to improved phenotyping tools and methodologies;
5. To train new human resources in the use of novel genomic techniques;
6. To establish a public-private collaboration on root beet as a model plant.

The project involves the French National Institute for Agronomical Research (Institut National de la Recherche Agronomique, INRA), Florimond Desprez Veuve & Fils (sugarbeet breeder), the Variety and Seed Study and Control Group (Groupe d'Etude et de contrôle des Variétés Et des Semences, GEVES), various French universities and research institutions, and the Confederation of Sugar Beet Growers (Confédération Générale des Planteurs de Betteraves, CGB) as well as the Sugar Factory Union (Syndicat National des Fabricants de Sucre).

The project started by requesting over 3000 accessions from the genebanks. Out of the received accessions, 15 will be selected as holders of the necessary variability. These will be crossed with elite lines, and 200 individuals from each crossed population (i.e. a total of 3000 hybrids) will then be selected for further genotyping and phenotyping. New phenotyping systems will need to be developed for monitoring all plant growth phases. Bioinformatics for data integration will be used to establish new breeding algorithms and prediction tools. Training and teaching components will be embedded in the project.

The project used EURISCO to identify around 9000 accessions in European genebanks. Of these, 3185 were selected on the basis of geographic distribution.

Thirty-nine institutions were contacted; 12 gave positive answers, 3 negative answers, 2 are under negotiation, 22 gave no answer. Problems were therefore identified in this exercise, since EURISCO does not necessarily provide information on available seed, updated addresses of the institutions or names of relevant contact persons. It was also surprising to meet restricted genetic resources policies in some cases (Kew Gardens, UK; Vavilov Institute, Russian Federation; China).

Introduction to the PGR Secure project

B.V. Ford-Lloyd

PGR Secure is an EU-funded project on "Novel characterization of crop wild relative and landrace resources as a basis for improved crop breeding" (<http://www.pgrsecure.org/>). The aim is to research novel characterization techniques and conservation strategies for

European crop wild relative and landrace diversity, as a means of enhancing crop improvement by breeders to ensure continued food security in the face of changing consumer demand and climate change. The project, coordinated by the University of Birmingham, UK, involves partner institutions from Finland, Germany, Italy, the Netherlands, Spain, UK, as well as Bioversity International, the European Association for Plant Breeding Research (EUCARPIA) and the Nordic Genetic Resource Center (NordGen). The project is developed in close collaboration with the ECPGR *In situ* and On-farm Conservation Network. Among the anticipated results, the project is expected to help develop national and regional crop wild relative and landrace conservation strategies. Information on important traits in this material will be made available through a portal, and collaboration between breeders and conservationists to facilitate the use of these traits will be promoted. With focus on *Avena*, *Beta*, *Brassica* and *Medicago*, a model will also be developed to predict whether unknown accessions are resistant or susceptible to pests and diseases.

Web components for genetic resources site, observation methodology and evaluation data

C.U. Germeier

Web-based components were developed for the AEGRO and AVEQ (*Avena* genetic resources for quality in human consumption) projects. In the case of AEGRO, a Population Level Information System (PLIS) was developed for model crops (e.g. *Beta*), as well as an integrated model for *in situ* and *ex situ* data. As part of PLIS, a Web application was developed for information on already known sites and additional tools supporting *in situ* field work. Concepts were also proposed for data exchange and for the integration of project results in existing information systems (e.g. the European Central Crop Databases, ECCDBs). Historical occurrence (distribution) data have also been integrated in the System. Biological data sources for *Beta* accessions were derived from GBIF, EURISCO, pcGRIN and the IDBB. Geographic data sources were taken from EUROSTAT and Natura 2000. This has allowed an analysis of occurrences of *Beta* within and outside protected areas.

In the case of AVEQ, Web solutions were developed for managing cooperative multisite genetic resources evaluation and facilitate the inclusion of project data into a central database by promoting standardized ways of documentation and data generation. These solutions have allowed online description of field experiments and treatments, online field plan generation, download of pdf and Excel templates, and spreadsheet upload with routine calculations (e.g. emergence, yield, seed weight).

The future use of information tools envisages that:

- The user community should be able to manage the database itself by using the online tools;
- Users should be able to adapt and further develop these tools themselves for their purposes with the source code available in an open source repository.

The following next step is proposed:

- All source codes developed for AEGRO and AVEQ will be made available in CropForge together with journal publications.

New project ideas proposed for further development and funding include:

- Mobile apps for using the IDBB in exploration and monitoring of *in situ* crop wild relative resources;
- Using and improving the online tools developed for AVEQ in a *Beta* evaluation and characterization project;

- Updating passport data and/or stronger integration with EURISCO and GRIN passport data.

Discussion on the role of European information systems (service to projects, information flow between systems)

The discussion focused on the importance of user-friendly information systems that are able to service the user community effectively. The practice of certain national genebanks to restrict or complicate access to information on accessions – even though they are listed in EURISCO – was widely criticized. These difficulties met by users, when reported to the wider public, can backfire on the sustainability of publicly funded plant genetic resources systems.

Data exchange between information systems holding data on *Beta* is still inadequate. The diversity of systems – each new project builds a new database – is a problem for the genetic resources user community.

The tools developed for the *Avena* Database could be implemented in the IDBB, in case the Group considers it important. If so, the necessary funds should be raised. There is some concern that the building of huge centralized systems (such as EURISCO and GENESYS) will discourage interest and investment in the maintenance of central crop databases. The Working Group on *Beta* could therefore prepare a project for the development of the IDBB and submit it to appropriate donors for funding.

Recommendation and Workplan

- The WG Chair and the IDBB Manager should prepare **as soon as possible** a project proposal that aims to guarantee the future sustainability and further development of the IDBB.

Posters

The posters listed below were presented.

Note: The asterisk (*) preceding a title indicates that the poster is available online

(http://www.ecpgr.cgiar.org/networks/sugar_starch_fibre_crops/beta/beta_meeting_2012/posters.html).

- * **Assessment of genetic diversity by SSR markers in sugar beet in the context of breeding for salt tolerance**

Z. Abbasi, A. Arzani, M. Majidi, M. Nachtigall, L. Frese

- * **Population differentiation in *Beta vulgaris* subsp. *maritima* measured with Delta**

L. Frese, M. Enders, M. Nachtigall, E.M. Gillet, H.-R. Gregorius

Mitochondrial minisatellite polymorphism of cultivated beets: fodder beet as the probable source of the owen cytoplasm

T. Kubo, D. Cheng, Y. Yoshida, M. Matsunaga, Y. Honma, T. Mikami

- * **Variability of morphological and economic traits of selected *Beta* accessions**

K. Kuzdowicz

- * **Application of real-time PCR and RT-PCR methods for quantification of BNYVV in selected wild accessions from the genus *Beta* - development of the relative approach**
A. Litwiniec, M. Gońska

- * **Nuclear DNA content and chromosome number of selected wild species from the genus *Beta***
A. Litwiniec, I. Jędrzejczyk

The features of *ex situ* and *in situ* conservation of *Beta* in Armenia
D. Melikyan

The morphological features of *Beta* varieties cultivated in Armenia and their adaptation to local conditions
D. Melikyan

- * **Resistance to beet cyst nematode (*Heterodera schachtii*) in hybrids derived from crosses of sugar beet with wild relatives**
A. Rajabi, S. Vahedi, S.B. Mahmoudi, M. Aghaeizadeh

- * **Development and evaluation for drought tolerance of family lines derived from sugar beet × fodder beet crosses**
D.F. Taleghani, A. Rajabi, M. Aghaezadeh, M.R. Orazizadeh, S.B. Mahmoudi, M. Mesbah, M. Ahmadi

Marker assisted selection of maintainer lines against Owen type CMS in sugar beet
K. Taguchi, M. Moritani, T. Mikami, T. Kubo

PART II. ECPGR BETA WORKING GROUP MEETING

General briefing on ECPGR

L. Maggioni

Participants were updated on the status of the ECPGR Programme of the ongoing Phase VIII (2009-2013). The budget of the *Beta* WG and the planned use of this budget were presented:

- Fourth *Beta* Working Group meeting (2012): € 9680
- Sampling of *B. nana* for geneflow analysis five years after the last visit to the Olympus site (2012): € 3100
- Monitoring of a genetic reserve of *B. patula*, Madeira, including working visit of the Portuguese partner (2013): € 5000
- Network Coordinating Group Meeting and ECCDB Manager Meetings (2009 and 2013): € 12 255.

The Coordinator cautioned that unspent funds of the WG will not be immediately available for new activities. The Secretariat would have to submit an application to the Steering Committee (SC), requesting approval for the use of these funds. Currently, unspent funds have been frozen by the SC, given that a few member countries still have outstanding dues.

The participants were informed about the outcome of the ECPGR Independent External Review (July 2010) and about the process followed by the SC for taking decisions at their next meeting in December 2012 on the future of the ECPGR, based on the "Options paper" being prepared by the ECPGR Executive Committee. The new goal and objectives of the ECPGR, as agreed by the SC in Bratislava (December 2010), were presented.

Report of the Working Group Chair, review of the workplan

L. Frese

The elements of the workplan were summarized and progress reported.

1. Identification of target populations for *in situ* conservation should explore the feasibility of creating genetic reserves as soon as possible.
Progress: A total of 26 occurrences have been identified within the framework of the AEGRO project. The recommended sites are located in Denmark, France, Germany, Greece, Italy, Portugal and Spain.
2. Develop a data model and module for *In Situ* Management (ISM). Develop and agree on a descriptor list for ISM.
Progress: Completed as part of AEGRO.
3. Organize a technical meeting focused on the development of a descriptor list and a data model.
Progress: Activity was cancelled.

4. Solve certain taxonomic problems.

Progress: There was some discussion on problems related to the identification of *Patellifolia* species between the Botanic Garden of Tenerife, the University of Birmingham and the Julius Kühn-Institut in response to the paper of Thulin et al. (2010).²²

5. Inclusion of additional characterization and evaluation data into the IDBB: the IDBB Manager will not request data. It is the task of the institutions producing data to submit them to the IDBB.

Progress: A data set was offered by the Armenian member. The IDBB Manager invested time to ensure the technical online availability of the information system by migrating the database from the old server to a new one. There is no staff capacity available for updating the system.

6. Establishment of a baseline of genetic diversity data for monitoring.

Progress: About 1000 plants were sampled starting from July 2008; DNA probes were produced from the samples and part of them (only section *Beta*) were analysed by the JKI using SSR markers. *B. nana* accessions collected by a joint USDA–ARS, GGB and JKI plant exploration team in Greece in 2005 were analysed in a similar way. The results on *B. nana* and *B. patula* were published.^{23,24} The work needs to be continued.

7. Provide USDA–ARS, Pullman with the duplicate samples (Germany, Greece, UK) of F. Dale's *B. nana* collecting mission, 1980-1981.

Progress: Some seeds have been exchanged between the Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), Gatersleben, Germany and USDA–ARS.

Update on AEGIS

L. Maggioni

The history of the establishment of AEGIS, its milestones and its key components were presented. Thirty countries are now members and 43 genebanks have signed Associate Membership Agreements with their respective National Coordinators. The scope of the European Collection was described, and the main elements of the AEGIS Quality System (AQUAS) were outlined. In line with the AQUAS principles, the Group had already developed in the past a seed increase protocol for wild and cultivated *Beta* germplasm, and areas for developing a quality concept had been identified: germplasm acquisition; status of acquired material; regeneration; post-harvest; pre-storage; germination capacity and storage conditions.

²² Thulin M, Rydberg A, Thiede J. 2010. Identity of *Tetragonia pentandra* and taxonomy and distribution of *Patellifolia* (Chenopodiaceae). *Willdenowia* 40:5-11.

²³ Frese L, Nachtigall M, Enders M, Pinheiro de Carvalho MAA. 2012. *Beta patula* Ait. genetic diversity analysis. In: Maxted N, Dulloo ME, Ford-Lloyd BV, Frese L, Iriondo JM, Pinheiro de Carvalho MAA, editors. *Agrobiodiversity Conservation: Securing the diversity of Crop Wild Relatives and Landraces*. CAB International, Wallingford, UK. pp. 45-51.

²⁴ Panella L, Fenwick A, Frese L, Hellier B, Richards CM. 2010. Genetic diversity within and among populations of *Beta nana*. 72nd IIRB Congress – 72e Congrès de l'IIRB – 72. IIRB Kongress. 22-24 June 2010, Copenhagen, Denmark. Abstract 3.26:177-179

A few points for action by the WG were proposed, as follows:

1. Agree on the process of identifying *Beta* accessions for the European Collection;
2. Compile first lists of possible AEGIS accessions;
3. Decide whether crop-specific standards are needed beyond the current FAO draft list of technical standards for seed crops/species and, if so, plan for their elaboration.

Criteria for the definition of *Beta* accessions for the European Collection

Ayfer Tan introduced the subject, indicating that all available data sources should be used to identify the existing *Beta* accessions in European genebanks. EURISCO records 8224 accessions from 28 European genebanks, while the IDBB records 10 485 accessions held in 28 genebanks worldwide. In order to select appropriate accessions for inclusion in the AEGIS European collection, she proposed merging of the lists from EURISCO and the IDBB, and starting the sorting of accessions held in countries that have signed the AEGIS Memorandum of Understanding (MoU). The second step would be to check completeness of a minimum amount of data (at least "Species" and "Accession name" or "Collecting number" or "Donor number" or "Other number" or "Country of origin"). Accessions without species name, unclear species and hybrids should not be considered. The lists could then be divided into sub-sections and candidate accessions could first be selected from the smaller subsections. Obvious duplicates could be identified, and Most Appropriate Accessions (MAAs) among duplicates could be selected on the basis of criteria such as:

- Quality of passport data
- Quality of management standards of holding institutes
- Minimum number of regeneration cycles
- Health status (checked for seed-borne/quarantine diseases)
- Existence of characterization and evaluation data
- Whether the accession is maintained in the country where it was collected or originated
- Accession history
- Storage facilities
- Minimum germination % standards used by holder (International Seed Testing Association, ISTA; AQUAS)
- Monitoring germination % by holder (Revised Genebank Standards for the Conservation of Orthodox Seeds, RGBSO; AQUAS).

Other crop-specific criteria that could be used to select those accessions that have been properly regenerated could be the following:

- Number of seeds or approximate size of the original sample;
- Number of plants used in the regeneration plots;
- Pollination method (controlled);
- Number of plants collected in the regeneration plots (minimum 10?).

However, the information for these criteria may not have been recorded or may not be easily available. The general problem is that lack of data or wrong data make it very difficult to select material.

Discussion

The Group considered that the analysis of the databases in the proposed way and with so many criteria would be difficult to achieve without funding support. The alternative

suggested was to start focusing on those accessions that were selected in the past for GenRes projects and now for the AKER project. These accessions are rich in data and have already been selected through some criteria. Moreover, full sets of characterization data are not required to select accessions that need to be preserved as a priority. For example, accessions belonging to the taxa included in the IUCN Red List (*B. nana*, *B. patula* and *B. webbiana*) would all need to be conserved in the European Collection. The taxa related to the proposed *in situ* conservation sites were also suggested as appropriate. This type of choice would also establish a link between *in situ* and *ex situ* conservation, thereby bringing their complementarity into effect.

Regarding the possibility of sorting out accessions on the basis of their taxonomy, it was pointed out that the taxonomy currently used by the N.I. Vavilov Research Institute for Plant Industry (VIR, St Petersburg) does not match other taxonomies such as GRIN; a parallel between the two should be established.

Recommendation

- The first group of accessions to be proposed for inclusion in the European Collection should be selected from the *Beta* Core Collection and the AKER collection. Accessions of threatened species should also be included.

Workplan

- Under the guidance of the IDBB Managers, a list of candidate accessions to be included in the European Collection will be compiled **by end 2012**, using the *Beta* Core Collection, AKER collection and accessions of threatened species. All concerned country representatives and/or curators will support the IDBB Managers' activity. The WG Chair will then submit the agreed list to all the concerned National Coordinators, suggesting inclusion of the respective accessions into AEGIS.
- Lothar Frese, with the assistance of Maria Cristina Duarte, will compare the VIR and GRIN taxonomies for *Beta* and provide a list of matching relationships for all relevant taxa **by end 2013**.

Discussion on generic genebank standards and on the need to agree on crop-specific standards

(introduced by A. Tan)

Following a request of the FAO Commission to update existing standards for orthodox and non-orthodox seeds, and for clonally propagated plants, the FAO drafted the "Revised Genebank Standards for the Conservation of Orthodox Seeds". This document (www.fao.org/docrep/meeting/022/MB179E.pdf) was discussed by the FAO Commission during its meeting in July 2011; it will be finalized and discussed again at the Sixth Session of the Intergovernmental Technical Working Group on Plant Genetic Resources for Food and Agriculture in November 2012. In this document, standards are defined for acquisition, drying and storage, seed viability monitoring, regeneration, characterization, documentation, distribution, safety-duplication and security/personnel.

Ayfer Tan suggested that the FAO Genebank Standards could be adopted as they are, and that the genebanks should attempt to follow them. The WG on *Beta* had already developed a crop-specific "Seed increase protocol" and collected the available regeneration guidelines in the form of country protocols, all available on the *Beta* WG's Web site (http://www.ecpgr.cgiar.org/networks/sugar_starch_fibre_crops/beta/other_wg_documents.html).

The existing protocols are judged to be sufficiently developed and, when followed, ensure quality of conservation of *Beta* germplasm. Guidelines for the multiplication of *B. nana* are, however, missing and should be developed.

Recommendation

- The FAO “Genebank Standards for the Conservation of Orthodox Seeds” combined with the *Beta* WG “Seed increase protocol” should be checked by the WG curators to confirm whether they can be adopted by the WG and proposed for approval as part of the AEGIS Quality System (AQUAS). The only missing element is a regeneration protocol for *B. nana*, which should be developed by the WG.

Workplan

- Lothar Frese will request Barbara Hellier (USDA-ARS) to provide information or possibly a protocol for the regeneration of *B. nana* **by end 2012**.
- Under the coordination of the WG Chair, all *Beta* WG curators will check the validity of the seed increase protocol for *Beta* and inform the WG Chair of their analysis, **by end 2012**.

Final discussion

L. Frese summarized the recommendations and workplan items that emerged from the discussions at the meeting. The agreed workplan items are compiled in Appendix I (pp. 25-26).

Workplan

- The scientific proceedings of this meeting, including the contributions of all the authors, will be published by JKI. Papers for inclusion in the proceedings will be submitted to L. Frese **by 3 September 2012**.

CONCLUSION

Election of new Chairs of the Working Group on *Beta* and World *Beta* Network

Lothar Frese was reconfirmed as the Chair of the Working Group on *Beta*. He agreed to act as the Chair until the end of 2013 and suggested the new Chairperson be elected via electronic media.

Yasmina El-Bahloul was elected as the new Chair of the World *Beta* Network.

Closing remarks

The participants visited the laboratories of Florimond Desprez. On behalf of the participants, the new Chair warmly thanked Bruno Desprez for the excellent organization, financial support of some participants and the splendid hospitality that contributed to a pleasant and productive meeting. All participants concurred that the Working Group gained momentum as the meeting facilitated the exchange of some very new and exciting research results. Special thanks were addressed to Valérie Fortin and all the staff of Florimond Desprez involved in the organization of the meeting. Special thanks were also addressed to Lorenzo Maggioni (representing the ECPGR) for the financial and logistic support, and his

contributions to the meeting. He was asked to convey special thanks to Lidwina Koop and Elinor Lipman for their excellent help. The last meeting took place in 2006; given the many ongoing activities in the field of conservation and utilization of genetic resources and related research projects, the Group suggested that such meetings be held every two or three years. The Chair of the ECPGR WG and of the WBN took note of this suggestion. The meeting was closed by the Chair who thanked all participants for their valuable contributions to the meeting and wished all participants a safe journey home.

APPENDICES

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Appendix I. Workplan 2012-2013

(Agreed at the Fourth Joint Meeting of the ECPGR Working Group on *Beta* and the World *Beta* Network, 20-22 June 2012, Cappelle-en-Pévèle, France)

Activities	Responsibility	Deadline
Beta nana project proposal		
Support the Greek <i>B. nana</i> project proposal with a supporting letter.	WG Chair	End July 2012
Submit a proposal to the ECPGR Secretariat for the use of available funds from the ECPGR Networks' budget (€ 2600). This will include sampling of plants on Mount Olympus, to be carried out in September 2012.	Parthenopi Ralli	As soon as possible (in time for sampling to be done in September 2012)
Patellifolia project		
Inform Lothar Frese of their interest in a project on <i>Patellifolia</i> , section <i>Corollinae</i> , and including <i>B. nana</i> (taxonomic aspects, genetic diversity)	Interested potential partners	End July 2012
Organize a meeting to prepare the project, depending on feedback received	Lothar Frese	End 2013
Genetic reserve sites for <i>Beta</i> and <i>Patellifolia</i>		
Revise the list of proposed genetic reserves and send comments to Lothar Frese. The list of proposed sites is available from the Genetic Resources Information System (GenResIs) of the AEGRO project www.agrobiodiversidad.org/aegro	Country representatives of the ECPGR WG	End 2012
Apply the 4-steps methodology developed by the AEGRO project and suggest sites for genetic reserves for species of the section <i>Corollinae</i> .	Representatives from Armenia, Azerbaijan, Georgia, Iran, Russian Federation and Turkey	End 2013
Ensure that <i>ex situ</i> samples are collected from each proposed genetic reserve site and deposited in the respective country genebank. These samples should also be proposed to the respective National Coordinators for inclusion into the European Collection and therefore be flagged in EURISCO as being part of AEGIS.	Country delegates	End 2013
IDBB		
Prepare a project proposal for guaranteeing the future sustainability and further development of the IDBB.	WG Chair and IDBB manager	As soon as possible

Activities	Responsibility	Deadline
Determination of <i>Beta</i> accessions for the European Collection		
Compile a list of candidate accessions to be included in the European Collection using the <i>Beta</i> Core Collection, AKER collection and accessions of threatened species.	IDBB Managers, with support from all concerned country representatives and/or curators	End 2012
Submit the agreed list to all the concerned National Coordinators, suggesting inclusion of the respective accessions into AEGIS.	WG Chair	End January 2013
Compare the VIR and GRIN taxonomies for <i>Beta</i> and provide a list of matching relationships for all relevant taxa.	Lothar Frese, with the assistance of Maria Cristina Duarte	End 2013
Crop-specific standards - regeneration		
Request Barbara Hellier (USDA-ARS) to provide information or possibly a protocol for the regeneration of <i>B. nana</i> .	Lothar Frese	End 2012
Check the validity of the seed increase protocol for <i>Beta</i> and inform the WG Chair of the analysis http://www.ecpgr.cgiar.org/networks/sugar_starc_h_fibre_crops/beta/other_wg_documents.html	All <i>Beta</i> WG curators, under the coordination of the WG Chair	End 2012
Publication of the proceedings		
Provide papers to be included in the proceedings of the meeting to Lothar Frese	All authors	By 3 September 2012
Publish scientific proceedings of this meeting	Lothar Frese plus co-editors	2013

Appendix II. Acronyms and abbreviations

AEGIS	A European Genebank Integrated System
AEGRO	An Integrated European <i>In Situ</i> Management Work Plan: Implementing Genetic Reserves and On Farm Concepts (<i>EU project</i>)
AQUAS	AEGIS Quality System
AVEQ	<i>Avena</i> genetic resources for quality in human consumption (<i>EU project</i>)
BNYVV	Beet Necrotic Yellow Vein Virus
CGB	Confédération Générale des Planteurs de Betteraves (Confederation of root beet farmers), France
CIN	Centro di Ricerca per le Colture Industriali (Research Institute for Industrial Crops), Italy
CMS	Cytoplasmic Male Sterility
CWR	Crop Wild Relative
ECCDB	European Central Crop Database
ECPGR	European Cooperative Programme for Plant Genetic Resources
EU	European Union
EUCARPIA	European Association for Plant Breeding Research
EURISCO	European Internet Search Catalogue
FAO	Food and Agriculture Organization of the United Nations, Italy
GBIF	Global Biodiversity Information Facility
GEVES	Groupe d'Etude et de contrôle des Variétés Et des Semences (Variety and Seed Study and Control Group), France
GGB	Greek Genebank, Thermi-Thessaloniki, Greece
GPS	Global Positioning System
GRIN	Germplasm Resources Information Network, USA
ICIA	Instituto Canario de Investigaciones Agrarias, Tenerife
IDBB	International Database for <i>Beta</i>
IHAR	Plant Breeding and Acclimatization Institute, Poland
IL	Inbred line
INRA	Institut National de la Recherche Agronomique (National Institute for Agronomical Research), France
IPK	Institut für Pflanzengenetik und Kulturpflanzenforschung (Institute of Plant Genetics and Crop Plant Research), Gatersleben, Germany (<i>now the Leibniz Institute of Plant Genetics and Crop Plant Research</i>)
ISM	<i>In Situ</i> Management
ISTA	International Seed Testing Association
IUCN	International Union for Conservation of Nature
JKI	Julius Kühn-Institut, Quedlinburg, Germany

MAA	Most Appropriate Accession (<i>for AEGIS</i>)
MoU	Memorandum of Understanding
NordGen	Nordic Genetic Resource Center
RAPD	Random amplified polymorphic DNA
RGBSO	Revised Genebank Standards for the Conservation of Orthodox Seeds
SBSI	Sugar Beet Seed Institute, Karadj, Iran
SSR	Simple sequence repeat
USDA-ARS	United States Department of Agriculture-Agricultural Research Service, USA
VIR	N.I. Vavilov Research Institute of Plant Industry, St Petersburg, Russian Federation
WBN	World <i>Beta</i> Network

Appendix III. Agenda

**Fourth Meeting of the ECP/GR Working Group on Beta
and the World Beta Network
20-22 June 2012, Cappelle-en-Pévèle, France**

Tuesday, 19 June

Arrival of participants

Wednesday, 20 June

09:00-09:30	Registration
09:30-10:00	Welcome and Introduction
	Geographic distribution
10:00-10:25	Opening remarks: <i>Beta maritima</i> : The origin of beets (B.V. Ford-Lloyd)
10:25-10:50	Distribution and conservation status of <i>Beta</i> and <i>Patellifolia</i> species in the Macaronesian region (A. Santos Guerra)
10:50-11:15	Coffee break
11:15-11:40	Survey of <i>in situ</i> resources of <i>Beta vulgaris</i> subsp. <i>maritima</i> in Ireland (D. Grogan)
	Geographic structure of genetic diversity
11:40-12:05	Comparative genomics of mitochondrial genomes of beet (P. Touzet)
12:05-12:30	Molecular analyses of <i>Beta maritima</i> accessions of the Greek Genebank (P. Ralli)
12:30-14:30	Lunch
14:30-14:55	Evaluation of root morpho-functional traits and genetic diversity of sea beet accessions along the Adriatic Sea coastline (P. Stevanato)
14:55-15:20	Genetic structure analysis for Moroccan wild beet germplasm (Y. El Bahloul)
15:20-15:45	Genetic diversity of <i>Beta nana</i> populations across Greek mountains (L. Panella)
15:45-16:15	Coffee break
16:15-16:45	Project discussion: Genetic diversity and gene flow in <i>Beta nana</i> (led by L. Panella, P. Ralli)
16:45-17:15	Project discussion: Genetic diversity and gene flow in <i>Patellifolia</i> species (led by A. Santos Guerra, B.V. Ford-Lloyd)
19:30	Joint dinner

Thursday, 21 June

	Utilization, conservation and documentation
09:00-09:25	Fine-mapping of rhizomania resistance using an <i>in situ</i> population of <i>Beta vulgaris</i> subsp. <i>maritima</i> (F. Kopsisch-Obuch)
09:25-09:50	Evaluation of resistance to <i>Cercospora</i> leaf spot, <i>Rhizoctonia</i> root rot and <i>Aphanomyces</i> root rot in Japanese elite breeding lines (K. Taguchi)
09:50-10:15	The genetic control of bolting in <i>Beta vulgaris</i> (A. Müller)
10:15-10:45	Coffee break
10:45-11:10	Home garden beets of Turkey (A. Tan)
11:10-11:35	Conservation of intraspecific diversity in genetic reserves for wild beets (L. Frese, M.C. Duarte and M. Veloso)
11:35-12:00	Discussion on suggested genetic reserve sites for <i>Beta</i> and <i>Patellifolia</i> (led by L. Frese and M.C. Duarte)
12:00-13:30	Lunch
13:30-15:30	Poster presentation and visit of the company Florimond Desprez
15:30-15:50	Introduction of the AKER project (company Florimond Desprez)
15:50-16:10	Introduction of the PGR Secure project (B.V. Ford-Lloyd)
16:10-16:30	Web components for genetic resources site, observation methodology and evaluation data (C. Germeier)
16:30-17:00	Discussion on the role of European information systems (service to projects, information flow between systems)
18:45-20:00	Guided tour in Lille before joint dinner
20:00	Joint dinner

Friday, 22 June

	ECPGR Beta Working Group meeting
09:00-09:15	General briefing on ECPGR (L. Maggioni)
09:15-09:30	Report of the Working Group Chair, review of the Workplan (L. Frese)
09:30-10:00	Update on AEGIS (L. Maggioni)
10:00-10:30	Coffee
10:30-11:30	Criteria for the definition of <i>Beta</i> accessions for the European Collection (introduced by A. Tan)
11:30-12:00	Discussion on generic genebank standards and on the need to agree on crop-specific standards (introduced by A. Tan)
12:00-13:00	Final discussion, recommendations and conclusions
13:00-14:30	Lunch
14:30-15:00	Election of new Chair and Vice-Chair of the ECPGR Beta Working Group Election of the Executive Secretary of the WBN Closing remarks
Afternoon	Departure of participants

Appendix IV. List of participants

Fourth Meeting of the ECP/GR Working Group on Beta and the World Beta Network 20-22 June 2012, Cappelle-en-Pévèle, France

N.B. Contact details of participants updated at the time of publication. The composition of the Working Group is subject to changes. The full list, constantly updated, is available from the Beta WG's Web page (http://www.ecpgr.cgiar.org/networks/sugar_starch_fibre_crops/beta.html)

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