



Networking, partnerships and tools to enhance *in situ*
conservation of European plant genetic resources



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Crop wild relative

Issue 12 September 2020



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Conserving plant genetic resources
for use now and in the future



Editor:
Nigel Maxted

Design by:
Shelagh Kell

Layout by:
rjpdesign.co.uk

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Pyrus syriaca (Wild pear)
in the Southern Palestinian
Territories

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Nigel Maxted

Crop wild relative

Issue 12 September 2020

Contents

1. Editorial	3
2. Designation of genetic reserves for wild celery species in Germany <i>Maria Bönisch and Lothar Frese</i>	4
3. The Italian Network of Biodiversity: searching for CWR in protected areas <i>Valeria Negri, Lorenzo Raggi and Daniela Gigante</i>	8
4. A Nordic network for Crop Wild Relative conservation <i>Heli Fitzgerald, Anna Palmé, Jenny Hagenblad and Jens Weibull</i>	10
5. Finnish crop wild relative networking activities <i>Heli Fitzgerald, Kaija Eisto and Elina Kiviharju</i>	14
6. National network of genetic reserve sites for medicinal, aromatic plants and CWR conservation in Lithuania <i>Juozas Labokas and Birutė Karpavičienė</i>	17
7. The German Network of Genetic Reserves <i>Imke Thormann</i>	23
8. Complementarity analysis for crop wild relatives in the Fertile Crescent <i>Wathek Zair, Joana Magos Brehm, Ahmed Amri, Mauricio Parra Quijano and Nigel Maxted</i>	26
9. Strength through integrating networks: Combining forces for Genetic Resource Conservation across Europe and the Near East <i>Jade Phillips and Nigel Maxted</i>	29
10. Introgression breeding from crop wild relatives in eggplant landraces for adaptation to climate change <i>Jaime Prohens</i>	32

Correspondence address:

Nigel Maxted, School of Biosciences, University of Birmingham, Edgbaston, Birmingham, B15 2TT, UK
Email: n.maxted@bham.ac.uk

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We are pleased to welcome you to Issue 12 of *Crop wild relative*—the second issue to be published in the context of *Farmer's Pride*, a Collaborative Project funded under the EU Horizon 2020 Programme.

The *Farmer's Pride* project (full title: *Networking, Partnerships and Tools to Enhance in situ Conservation of European Plant Genetic Resources*) focuses on building a collaborative network for on-site conservation and sustainable use of Europe's plant diversity for food, nutrition and economic security throughout the region.

Despite these difficult times of global lock-down due to the Covid 19 pandemic, collaborators in the Farmer's Pride project have continued, unperturbed. Eurosite hosted a webinar in June 2020 to highlight the value of crop wild relatives (CWR) in a European and global context and to explain which species are a priority for conservation in Europe and why. The point was clearly made to the protected area manager members of Eurosite that CWR are wild plant species that provide vital diversity for adapting and improving our crops – particularly in the race to combat the adverse impacts of climate change on agricultural production systems. Farmer's Pride project research has shown that a significant number of CWR species occur within protected areas in Europe, including at least two thirds of the highest priority species in need of *in situ* conservation action in the region. The recording can be found here:

https://www.youtube.com/watch?v=jz_eb9lloFU

Also, congratulations to Professor Jose Iriondo and his team at Universidad Rey Juan Carlos, who managed to help establish three new genetic reserves for CWR conservation in the Sierra del Rincón Biosphere Reserve in the rural area of Madrid province working in close collaboration with reserve staff.

A key objective of the Farmer's Pride project is to establish a permanent network for Europe-wide *in situ* conservation of plant genetic resources *in situ* / on-farm conservation sites for crop landraces/farmers' varieties / CWR diversity. As well as to promote and facilitate the use of these conserved resources for the benefit of society. Our ideas are becoming increasingly detailed and we recently produced a Proposal document that outlines our current thinking, see:

<https://more.bham.ac.uk/farmerspride/wp-content/uploads/sites/19/2020/03/Farmers-Pride-Network-Concept.pdf>

Editorial

Further to prepare for network establishment, we are now actively encouraging CWR specialists and Protected Area Managers (along with those managing landraces) to nominate their sites to join the putative Network.

Anyone managing a CWR population can nominate a site and do so simply by complete the following survey:

<https://bham.onlinesurveys.ac.uk/farmers-pride-network-expressions-of-interest>

Within the EU our current thinking is the Network will be supported financially via the EU Green Deal likely via the revised Common Agriculture Policy (CAP). Although the Network will not be restricted to EU countries alone. Sites of European and national significance outside of the EU are also likely to be supported under national Agriculture Bills that mirror the EU Green Deal and which in turn support farmers providing ecosystem service public goods. Therefore, can we persuade you to complete an expression of interest for each site you manage and so nominate CWR (and landrace) populations to join the fledgling network that aims to underpin future food and nutritional security for Europe?

This issue of *Crop wild relative* (issue 12) is focused on reviewing progress in CWR conservation showcasing examples of good practice. The review will commence with establishment of genetic reserves for the 4 wild celery species in Germany (*Apium graveolens*, as well as *Helosciadium repens*, *H. inundatum* and *H. nodiflorum*) (pages 4–7), followed by an article reviewing how to establish the presence of CWR populations in Italian protected areas (pages 8–9), then three summary articles detailing the progress made in CWR conservation in the Nordic countries (pages 10–13), in Finland (pages 14–16, and in Lithuania (pages 17–22). Next is a paper describing the recent establishment of the national network of German genetic reserves (page 23–25), conservation planning

for genetic reserve locations in the Fertile crescent (pages 26–28) and a paper describing the integration of PGR conservation with Forest tree and animal genetic resources conservation (page 29–31). The issue concludes with a paper describing how CWR are being used in eggplant breeding for climate change resilience (pages 32–36).

Crop wild relative is not restricted to reporting research purely within the context of the Farmer's Pride project; we aim to incorporate news and research whether it be from within Europe or elsewhere. We hope you find this issue informative and stimulating and we look forward to receiving your contributions for future issues.



Dr Tamara Smekolova, VIR, St. Petersburg, Russia – an excellent CWR collector, taxonomist and a good friend, who left the 'field' this year. (Photo: N. Maxted).

Designation of genetic reserves for wild celery species in Germany

Maria Bönisch and Lothar Frese

Julius Kühn Institute (JKI) – Federal Research Centre for Cultivated Plants, Institute for Breeding Research on Agricultural Crops, Erwin-Baur-Str. 27, 06484 Quedlinburg, Federal Republic of Germany maria.boenisch@julius-kuehn.de

The conservation technique “genetic reserve” (Jain 1975, Maxted *et al.* 1997a, 1997b) has been applied for the improved protection of wild celery species on behalf of other crop wild relatives (CWR) as part of a project. The aim of the technique is to enable continuous adaptation of species to environmental changes. The prerequisite for this is the comprehensive conservation of the intra-species diversity through the management of their habitats. Between 1997 and today, an impressive number of research projects addressed aspects of the *in situ* conservation strategy. The results (e.g.: Maxted *et al.*, 2016) were used for concept papers (Maxted *et al.*, 2015). Yet, the designation of genetic reserves in Europe was still pending and the practical implementation is lagging behind.

The German Ministry for Food and Agriculture (BMEL) funds projects promoting the application of previously published concepts and tools to be put into practice. During the projects, concepts and tools can be tuned and adapted to practical needs. At the end of the funding period project partners are obliged to transfer the actions into a permanent organizational structure. The implementation of a network of genetic reserves for the

target crop gene pool *Apium* was the aim of such a BMEL-funded model and demonstration project.

Planning of genetic reserves in eight steps

The work plan of the project “Genetic reserves for wild celery species (*Apium* and *Helosciadium*) as a component of a network of genetic reserves in Germany” combined the step-wise methodology for the identification of genetic reserve sites for a target crop gene pool (Kell *et al.*, 2012) with principles of participatory nature conservation project planning (Feige, 2003) (Fig. 1).

The project started with the gathering and processing of distribution data in Germany of the four target species *Apium graveolens* L. ssp. *graveolens*, *Helosciadium repens* (Jacq.) W. D. J. Koch, *H. nodiflorum* (L.) W. D. J. Koch and *H. inundatum* (L.) W. D. J. Koch (steps 1 and 2).

In 2015, experts in the various federal states of Germany visited approximately 350 sites to confirm the existence of the target species, and to assess sites following the minimal quality

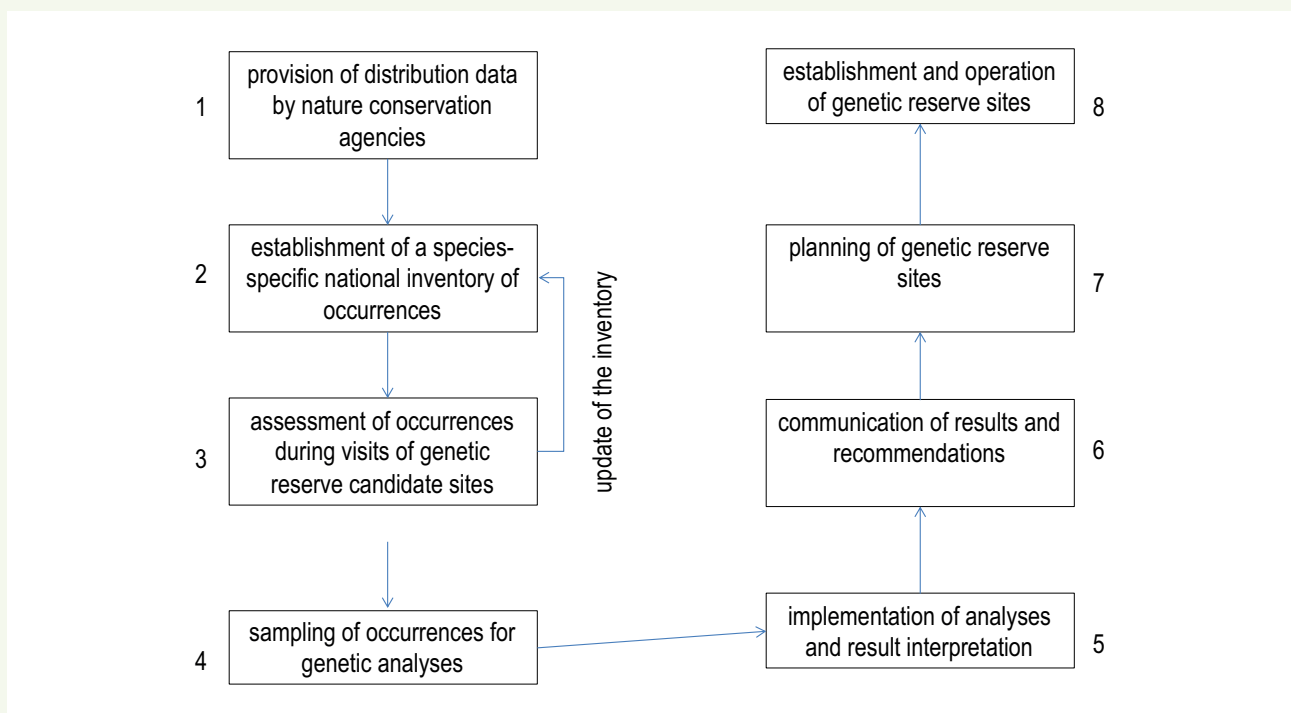


Figure 1. The flow diagram illustrates the work plan.

standards for genetic reserves (Iriando *et al.*, 2012). Subsequently, experts sampled leaves for genetic analysis of approximately 100 sites, which fitted the minimal quality standard best (step 3 to 5) in 2016. The results and recommendations were discussed with stakeholders. In 2018, about 12 occurrences for each wild celery species were finally nominated as genetic reserves based on the results of genetic analyses, together with the condition of the occurrences and sites, their location and the disposition of local stakeholders. The genetic reserves area, which can exist inside or outside of nature reserves, was jointly planned with the responsible local conservation agencies, the coordinating unit of the wild celery specific network (see article from Imke Thormann in this issue) and local stakeholders (6 to 8). Stakeholders were involved in the project planning right from the beginning and were kept informed throughout. A structured discussion with stakeholders open to the results was an important element of the procedure. The process can be divided into an information phase (steps 1 to 5) and participatory project phase (steps 6 to 8). The first five steps, by their nature, are a top-down process, while the final steps should be shaped as a bottom-up process.

In particular, in densely populated countries such as Germany, the competition between land users is high. Competing land users accepted the establishment of a genetic reserve only if the coordinating unit of the wild celery specific network proposed a management plan and an arrangement considering their interests. The proposed genetic reserves for wild celery species were described in specific management plans which included a map showing the growing, migration and transient area (Fig. 2). All stakeholders thus had known beforehand exactly where the genetic reserve is located and how the long-term

operation of the genetic reserve might interfere with their own interests in the same area.

Designation of a genetic reserve

At the end of a successful planning process, local stakeholders willing to support a specific genetic reserve site signed a unilateral declaration of consent. The consent can be withdrawn at any time. During the period of validity, the land owners or land users agree to the management of the genetic reserve and harvesting seeds. A nature conservation agency responsible for the relevant nature reserve, or a permanent institution such as a local government or a non-governmental nature conservation organization, supports the management as far as possible. The willingness of local stakeholders to support the designation and management of a genetic reserve was finally acknowledged with a certificate issued by the Federal Agency for Agriculture and Food (BLE) on behalf of the BMEL (see paper from Imke Thormann).

In the project, we considered a genetic reserve as designated if a declaration of consent has been signed by the land owner and a supporting permanent institution for at least one parcel in the real estate register within the genetic reserve. In this way, 14 genetic reserves had been designated at the end of January 2020. We are currently receiving further signed declarations of consent and are confident that about 45 genetic reserves will be established in the next months -

Lessons learned

To be frank, we had completely underestimated the importance of landowners, who are free to sign a declaration of consent or

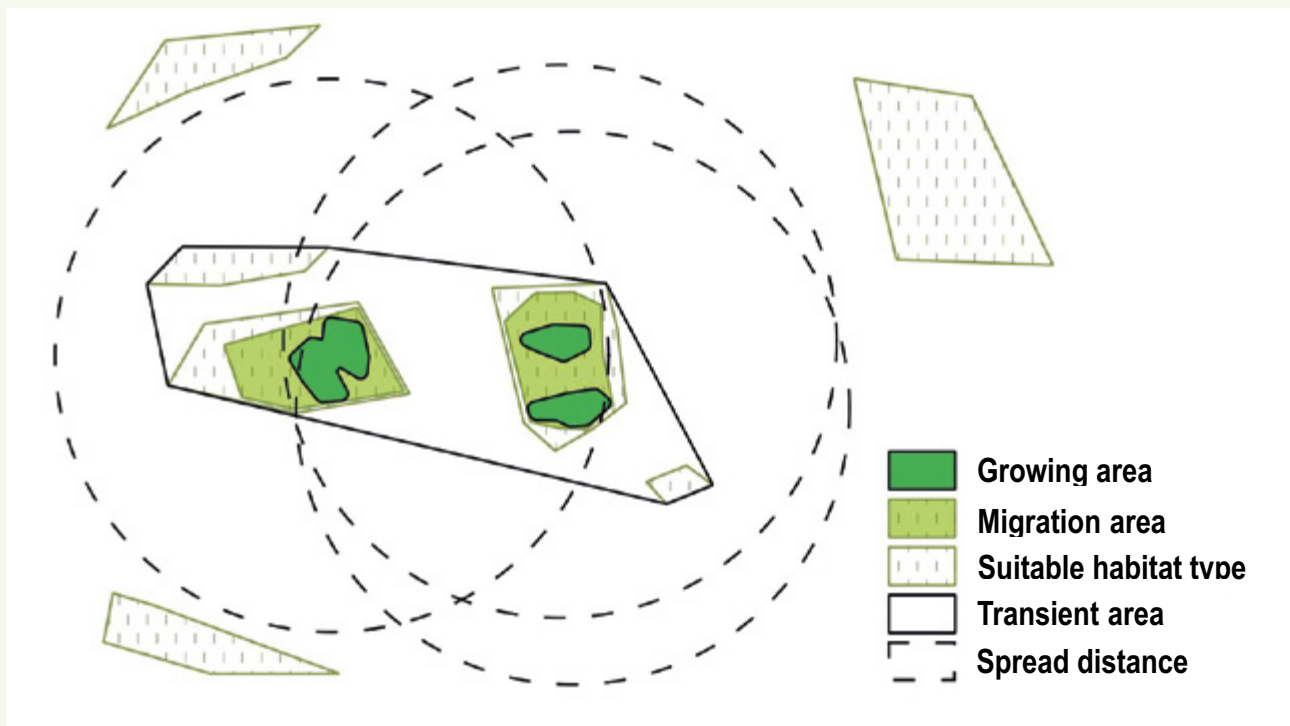


Figure 2. Spatial model of a genetic reserve for wild celery species (modified of Frese *et al.*, 2018).



Genetic reserve for *Apium graveolens* spp. *graveolens* located in a protected area in the state of Saxony-Anhalt. (Photo: M. Bönisch).

not. We had also misjudged the influence of data protection on our work, i.e. the time needed to get access to data required for the project. Further, we had underestimated the time needed for communication with stakeholders at all levels within the cooperation field (Frese *et al.*, 2017) and the necessity of legal advice at the final project stage. The genetic reserve won't be a new category of the nature conservation law. Therefore, the cooperation between the coordinating unit of the wild celery specific network and the local stakeholders is to be based on voluntary participation of stakeholders and at the same time on binding commitments. The declaration of consent developed together with a legal expert fulfills both requirements and it works.

Finally, the time invested into communication via the project website, the project brochure, the participation in meetings of species conservationists, publications in German language in nature conservation journals and countless phone calls have paid off in terms of informing the nature conservation community on the significance of CWR for plant breeding, as well as placing the theme on the political floor. One can debate whether we should have developed a national strategy for CWR *in situ* conservation first. It probably would have taken a few years to reach an agreement between all relevant institutions on a national strategy. This work can still be done. The results of this model and demonstration project show that a network of genetic reserves can also be achieved by starting with a few CWR species. The established network structure can then be extended through an interest driven process supported by project funding. The next series of genetic reserves are likely to be established by a grassland project team, led by the University of Regensburg this year, and other projects will hopefully follow.



Genetic reserve site for *Helosciadium inundatum* located in a protected area in the state of North Rhine-Westphalia. (Photo: M. Bönisch).



Genetic reserve site for *Helosciadium repens* located on a sunbathing lawn maintained by a local community in the state of Brandenburg. (Photo: D. Hanspach).



The six representatives of stakeholder groups receiving a certificate signed by the President of the Federal Office for Agriculture and Food (BLE), Dr. Eiden, acknowledging their active role in the management of the genetic reserves. (Photo: S. Hahn).

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The Italian Network of Biodiversity: searching for CWR in protected areas

Valeria Negri, Lorenzo Raggi and Daniela Gigante

Università degli Studi di Perugia, Borgo Giugno 74, 06121 Perugia (I), valeria.negri@unipg.it

Because of its large mosaic of natural and semi-natural environments, Italy hosts the highest and most significant heritage of biodiversity in continental Europe. A relevant part of this diversity occurs in the 871 Italian protected areas, of which 3,163,590 hectares are land areas. These areas can also be considered as instruments to promote and support forms of economic and social development, while being consistent with the objectives of environmental sustainability.

The Italian Ministry of the Environment set up the Naturaitalia portal (naturaitalia.it), the latest and most comprehensive website on Italy's wildlife and protected areas. Through the Naturaitalia website it is possible to access the Network Nazionale della Biodiversità (National Network of Biodiversity, NNB) a system

of data storing and management designed to support the Italian National Strategy for Biodiversity. The system relies on data and information provided by several subjects accredited at national and international level. The NNB consists of

- a central node, allowing the search and management of alphanumeric and geographic data, and
- peripheral nodes, i.e. databases holding primary data on biodiversity.

Through the Biocase system, it guarantees the interoperability with other international infrastructures (e.g. LifeWatch, GBIF and others) coherently with the guidelines of the INSPIRE Directive (Directive 2007/2/EC of the European Parliament and of the

Home | Il Network | **Dati** | Webgis | Contatti

Home | it | Dati | Plantae | Tracheophyta | Magnoliopsida | Brassicales | Brassicaceae | Brassica | Brassica gravinae Ten. |

Scientific name: Brassica gravinae Ten.

Elenco osservazioni

Numero di elementi totali: 17
Mostra 10 elementi

Filtra:

ID OSSERVAZIONE	NOME SCIENTIFICO	ANNO OSSERVAZIONE	BANCA DATI
43416	Brassica gravinae Ten.	N.D.	Conoscenza delle specie vegetali selvatiche progenitrici di piante coltivate (Crop Wild Relatives - CWR) elencate nel Trattato FAO e presenti (EX SITU) in Italia
44009	Brassica gravinae Ten.	N.D.	Conoscenza delle specie vegetali selvatiche progenitrici di piante coltivate (Crop Wild Relatives - CWR) elencate nel Trattato FAO e presenti (EX SITU) in Italia
44547	Brassica gravinae Ten.	N.D.	Conoscenza delle specie vegetali selvatiche progenitrici di piante coltivate (Crop Wild Relatives - CWR) elencate nel Trattato FAO e presenti (EX SITU) in Italia
45054	Brassica gravinae Ten.	N.D.	Conoscenza delle specie vegetali selvatiche progenitrici di piante coltivate (Crop Wild Relatives - CWR) elencate nel Trattato FAO e presenti (EX SITU) in Italia
51636	Brassica gravinae Ten.	N.D.	Conoscenza delle specie vegetali selvatiche progenitrici di piante coltivate (Crop Wild Relatives - CWR) elencate nel Trattato FAO e presenti (IN SITU) in Italia
52143	Brassica gravinae Ten.	N.D.	Conoscenza delle specie vegetali selvatiche progenitrici di piante coltivate (Crop Wild Relatives - CWR) elencate nel Trattato FAO e presenti (IN SITU) in Italia

Mostrando 1 di 10 di 17 elementi

Precedente 1 2 Prossimo

Vedi su mappa [Download dati](#) Cerca nei dati Citizen Science

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Figure 1. Italian National Network of Biodiversity: results of the data search for *B. gravinae* Ten.

Council of 14 March 2007). With particular reference to CWR, a search tool is available at NNB where information regarding relatives of crops listed in the Annex1 of the *International Treaty on Plant Genetic Resources for Food and Agriculture* can be retrieved by digiting the CWR name. Among others, information includes geographic (latitude and longitude) data that are useful for understanding species distribution over the Italian territory. It is noteworthy that information on protected areas containing the taxon can be downloaded in standard CVS format, allowing easy systematic elaborations.

For example, the results of a search for *Brassica gravinae* Ten. (a near threatened CWR of the *Brassica* genus crops that is rare in Italy) are shown in Figure 1, while a graphical representation of the protected areas where it can be found in Italy and in the Lazio region is shown in Figure 2. The tool can be useful not only to identify protected areas containing CWR of priority interest, but also those with the highest concentration of CWR that deserve particular attention (hotspot identification).

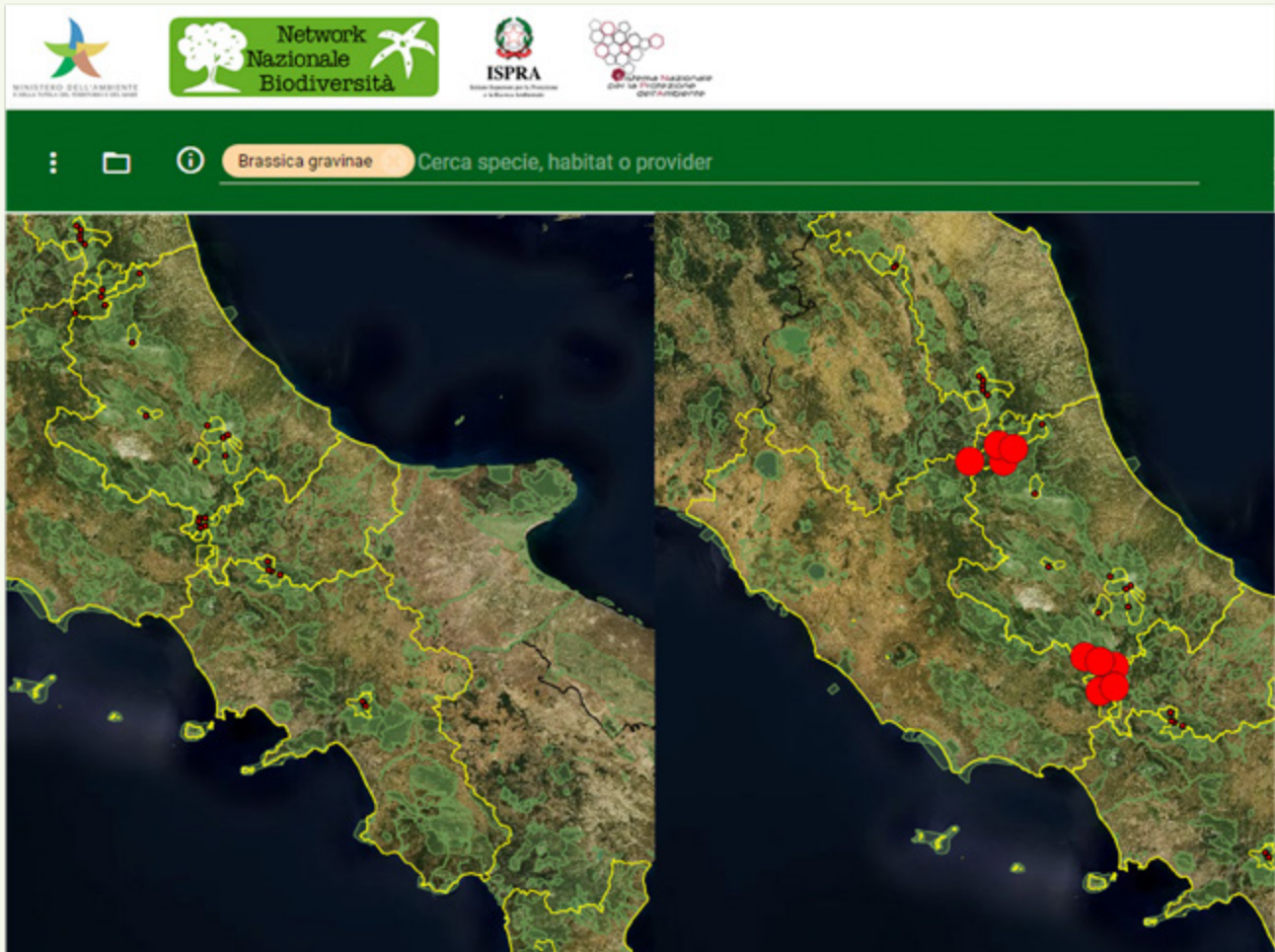


Figure 2. Italian National Network of Biodiversity: map of *B. gravinae* Ten. distribution in Italian protected areas (left) and in the Lazio region protected areas (right, magnification of Lazio Region).



Figure 3. Wild Brassica plants grown at the University of Perugia experimental field. (Photo: Simona Ciancaleoni)

A Nordic network for crop wild relative conservation

Heli Fitzgerald¹, Anna Palmé², Jenny Hagenblad³ and Jens Weibull⁴

¹Finnish Museum of Natural History, LUOMUS, University of Helsinki. heli.fitzgerald@helsinki.fi

²Nordic Genetic Resource Centre (NordGen)

³Department of Physics, Chemistry and Biology, Linköping University

⁴Swedish Board of Agriculture

The Nordic crop wild relative network was initiated within the two projects: 'Ecosystem services: Genetic resources and crop wild relatives' and 'Wild genetic resources – a tool to meet climate change', both funded by the Nordic Council of Ministers. Partners from all the Nordic countries, Denmark, Finland, Iceland, Norway and Sweden, participated in the projects. The main goal was to achieve Nordic synergy in crop wild relative conservation and to facilitate Nordic cooperation, networking and knowledge exchange on crop wild relatives (CWR) topics.

To achieve Nordic synergy on CWR conservation, it was decided to make a conservation plan at the Nordic level. First, a checklist was created including all CWR species of the region. The checklist (Fitzgerald *et al.* 2017) includes all wild taxa of

the same genera as crops, covering over 2,700 CWR related to medicinal, ornamental, forestry, food or forage crops. Food and forage wild relatives were considered the most important CWR groups for the Nordic region, and these categories were prioritised. The checklist was subsequently further prioritised using the socioeconomic value of the crop to which the CWR is related, as well as the potential utilisation value for plant breeding. The resulting checklist consists of 115 priority taxa (Fitzgerald *et al.* 2018) recommended to be prioritised for *in situ* and *ex situ* conservation actions.

The Nordic network also began planning how to best conduct regional *in situ* and *ex situ* conservation of the priority CWR. Currently, no genetic reserves for CWR have been established in the Nordic countries. Within the Nordic project, a regional



Figure 1 Sea kale *Crambe maritima* L. (Photo: Åsmund Asdal).

Nordic CWR in situ conservation plan - complementary network national top sites

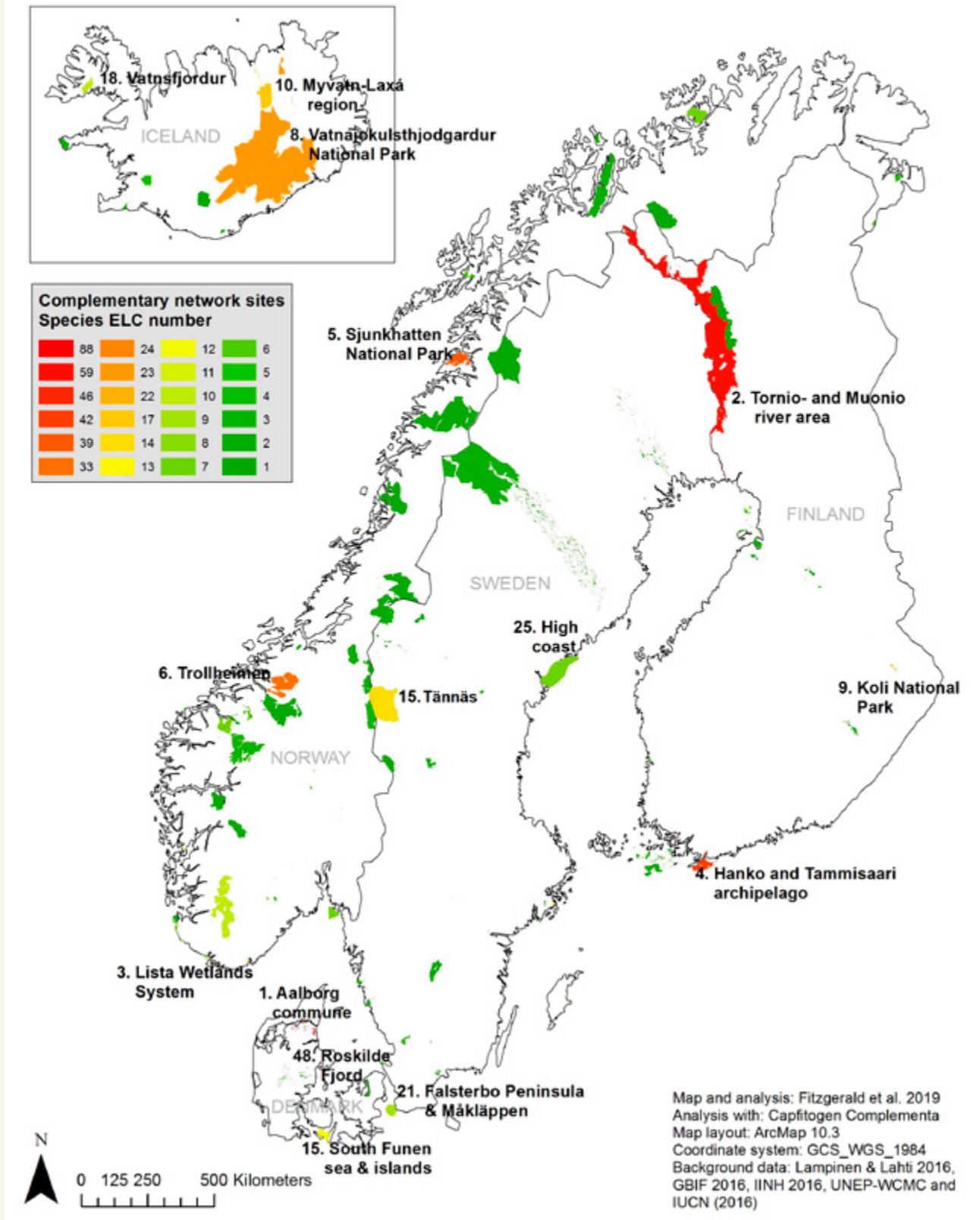


Figure 2. Potential Nordic genetic reserve sites identified in the regional gap analysis – the names of the top three sites in each country given on the map.



Figure 3 Blackthorn or sloe *Prunus spinosa* L. (Photo: Åsmund Asdal).

gap analysis was therefore conducted and complementary conservation areas suitable for genetic reserves were identified in the region (Fitzgerald *et al.* 2019). In conclusion, we recommend that each country evaluate their top three sites for potential establishment as genetic reserves.

Ex situ conservation is already ongoing for CWR taxa in the Nordic countries. The largest seed collection is conserved by NordGen, the Nordic regional genebank for plant genetic resources for food and agriculture. National seedbanks with some priority CWR taxa also exist in the Finnish Museum of Natural History, Finland and the Natural History Museum in Oslo, Norway. For a few of the CWR species on the Nordic priority list, such as timothy and red fescue, large-scale collecting has previously taken place with seeds stored at NordGen. However, most of the species on the priority list have either few populations conserved, or are entirely absent from *ex situ* collections. An *ex situ* gap analysis was conducted to find out how well the existing collections represent diversity in the wild. Additionally, complementary sampling sites were identified, to fill the gaps in *ex situ* collections of the priority species.

During the course of the projects, we also established an informal Nordic network of CWR stakeholders. The project group, including participants from all the Nordic countries, formed the

core of this network. This group was later enlarged by inviting stakeholders to workshops, meetings and by undertaking other communication activities. Stakeholders from both biodiversity conservation and agricultural sides were invited to the workshops, as were representatives of the CWR genetic resource users. Workshops were important channels for knowledge exchange. Discussions were held on the best approach for future actions to ensure CWR conservation in the Nordic region, and led to a set of project recommendations. During one of the workshops, a policy brief (a) Palme *et al.* 2019a) was drafted together with the stakeholders and later delivered to the Nordic Council of Ministers. The policy brief, along with the recommendations in the project report (b) Palme *et al.* 2019), outlines the main principles and needs of CWR conservation in the region.

The implementation of CWR conservation mainly takes place at a national level. Some participating countries have pursued national activities on CWR during the timespan of the Nordic projects, such as national CWR projects carried out both in Finland and in Sweden. Regional co-operation on the *ex situ* conservation side is ongoing, but more work needs to be done to achieve regional co-operation of CWR *in situ* conservation. The informal Nordic CWR network established during the last four years neither has long-term funding, nor is a formal organization. It has been supported exclusively through project

funding and coordinated from NordGen, a Nordic institute dedicated to *ex situ* conservation of seed propagated crops. For *ex situ* conservation of plant genetic resources, there is now a Nordic network including NordGen and the Nordic national genebanks conserving clonal material. Our goal with the network is to continue the work and secure long-term funding, both for *in situ* and *ex situ* conservation stakeholders and activities.

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Figure 4 *Fragaria vesca* L. and *Fragaria viridis* L. in Faerder National Park, Norway. (Photo: Åsmund Asdal).

Finnish crop wild relative networking activities

Heli Fitzgerald¹, Kaija Eisto² and Elina Kiviharju³

¹ Finnish Museum of Natural History, LUOMUS, University of Helsinki. heli.fitzgerald@helsinki.fi

² Metsähallitus Parks and Wildlife Finland

³ Natural Resources Institute Finland.

The Finnish CWR conservation network moved forward when the Natural Resources Institute Finland, Luke; the Finnish Museum of Natural History, University of Helsinki and Metsähallitus, Parks and Wildlife Finland received funding from the Finnish Ministry of Agriculture and Forestry. The first phase of the national crop wild relative conservation project took place during 2017–2018. The aims were to identify the main actors to form a national CWR conservation network; to update the CWR priority list, to identify the priority species ecogeographic diversity in the wild and find potential genetic reserve sites from existing conservation areas and to investigate the background, practical possibilities and options of CWR *in situ* conservation in existing conservation areas.

The second phase of the project is ongoing with further funding from the Finnish Ministry of Agriculture and Forestry in 2019–2020. The work will focus on a pilot *in situ* conservation area that contains a potential future CWR genetic reserve site, and on the other hand planning *ex situ* conservation of the priority species. The main aims are to define the practical actions needed to

establish a CWR genetic reserve in a pilot site and to prepare an overall plan for the National CWR network.

During the first phase, establishment of the potential genetic reserves and their management, monitoring and responsibilities were discussed. A general assessment of the role of protected areas in conservation of CWR species was carried out, including assessment of how the current management measures of protected areas in general maintain the populations of the priority CWR species. It was found that the current restoration and management measures are profitable for several priority CWR species, whereas several other priority species thrive without any active management measures. It seems that the current network of nature protection areas secure populations of many common CWR species. Some CWR species have contrasting management needs compared to the present management practices in existing conservation areas. According to the species distribution data, not all priority species have populations in protected areas. These few species are mainly growing in disturbed habitats and wastelands. The possible



Figure 1. *Myllypuro* meadows in the Nuuksio National Park. (Photo: Heli Fitzgerald).



Figure 2. *Purola* and *Myllypuro* area within the Nuuksio National Park. (Photo: Heli Fitzgerald).

conservation methods of these species growing outside of existing conservation areas needs further investigation.

The national project was carried out in co-operation with Nordic regional project, coordinated by NordGen, 'Wild genetic resources – a tool to meet climate change' which took place at the same time. Both projects gained from the co-operation, for example through the public awareness parts of the projects, such as establishing the Nordic CWR pages and writing plant portraits (NordGen, 2019), printing a CWR brochure (Luke, 2018), developing regional CWR conservation recommendations (Palme *et al.* 2019) and publishing CWR lists and undertaking conservation gap analyses (Fitzgerald *et al.* 2019).

The updated Finnish CWR priority list of 88 taxa (Fitzgerald and Kiviharju, 2018) was based on the Nordic CWR priority list (Fitzgerald *et al.* 2018). Those species on the Nordic list which had established populations in Finland were included, as well as a few additional species not on the Nordic list. The list contains food and forage wild relatives, which are prioritised according to their utilisation potential and socioeconomic value.

The *in situ* gap analysis identified complementary sites with high number of CWR target taxa in existing protected areas. One of the top sites, Nuuksio National Park, was selected as a pilot *in situ* area for the second phase of the project. The National Park area was surveyed during 2019 and populations of the priority CWR taxa were recorded (Figures 1. and 2.). The aims were

to select the target species and populations for conservation and to record habitat conditions and threats to the populations. Another aim was to estimate the availability of the site for long-term conservation and to identify potential areas within the National Park for genetic reserve areas. CWR conservation co-operation with Åland Islands, an autonomous area of Finland, was advanced with visits and meetings during the project (Figures 3. and 4.). Åland Islands have important CWR diversity including CWR taxa not growing in mainland Finland. These CWR populations from Åland Islands were included in the *in situ* and *ex situ* gap analysis.

The network of the main stakeholders established in this project serves as a basis for further discussions of CWR network financial and organizational planning in Finland. It is essential to produce and share knowledge and have both agricultural and environmental experts and administrators join together. Many questions are still open, but the basic work has been done with the Finnish CWR network. Sufficient information has already been collected to help decision making processes, which will need to be made on a Ministry level. Outcomes of the project will be published in the final report and article.

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Figure 3. *Malus sylvestris* in the Ramsholmen conservation area, Åland Islands. (Photo: Heli Fitzgerald).

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Figure 4. Fruits of *Malus sylvestris* and *Malus domestica* x *sylvestris* in Ramsholmen conservation area, Åland Islands (Photo: Heli Fitzgerald).

National network of genetic reserve sites for medicinal, aromatic plants and CWR conservation in Lithuania

Juozas Labokas and Birutė Karpavičienė

Nature Research Centre, Institute of Botany, Žaliųjų Ežerų g. 49, LT-12200 Vilnius, Lithuania

E-mail: juozas.labokas@gamtc.lt (Corresponding author)

INTRODUCTION

The Aichi Biodiversity Target 13 states that “By 2020, the genetic diversity of cultivated plants and farmed and domesticated animals and of wild relatives, including other socio-economically as well as culturally valuable species, is maintained, and strategies have been developed and implemented for minimizing genetic erosion and safeguarding their genetic diversity” (CBD, 2015). It has been estimated that 60–90% of medicinal and aromatic plants in trade are wild collected and that the increase in trade in medicinal and aromatic plants since 1999 is threefold (Jenkins *et al.*, 2018). This suggests that the extent of cultivation of these species should significantly increase to avoid over collection and to mitigate human impact on natural and semi-natural habitats.

Being in a suboptimal climatic zone for most of the globally important crop wild relatives, Lithuania still has a fair amount of medicinal, aromatic and other wild economic plant resources. These present considerable potential for sustainable utilisation if conserved and managed appropriately. And the governmental recognition and support was very timely resulting in Lithuania being one of the first countries in Europe to adopt a Law on National Plant Genetic Resources. Article 8 of the Law states that “For the *in-situ* conservation of national plant genetic resources, genetic reserves, gene conservation areas, seed collection stands shall be established, or populations, groups or single trees shall be selected” (Seimas... 2001). The Law does not include the term ‘crop wild relatives’, which is expected to appear in the amended version of the document. Meanwhile, the term ‘medicinal and aromatic plants’ is widely used.

Thus, having a firm legal support, the research on *in situ* conservation of medicinal and aromatic plant genetic resources has been conducted at the Institute of Botany (currently Nature Research Centre) aiming to establish a national network of genetic sites of medicinal and aromatic plants in Lithuania (Labokas, Karpavičienė, 2018). Here the term ‘medicinal and aromatic plants’ corresponds to the one used in the European Red List assessment, stating that “the term ‘medicinal plant’ has been understood here in a wider sense to include overlapping uses as herbal teas, spices, food, dietary supplements, and cosmetics” (Allen *et al.*, 2014). This implicates that a certain part of the target species is crop wild relatives (CWR) *per se*. On the other hand, many other CWR species, e.g., forage plants, share their habitats with medicinal plants and therefore should be considered for conservation under the same effort in order to reduce overall costs. In this paper we provide a brief overview

of the results achieved so far in establishing a national network of genetic sites of medicinal and aromatic plants and discuss its use for CWR conservation.

RESULTS AND DISCUSSION

Over the period of 2006–2019, a total of 31 genetic sites were selected, evaluated and approved by the order of the Minister of Environment (2020) for long-term conservation of MAP species *in situ*. The establishment of the network was based on the floristic approach to CWR conservation (Magos Brehm *et al.*, 2017). Although distributed unevenly, the established sites represent all major physical geographical areas of Lithuania, from west to east: Coastal Lowland, Žemaičiai Highland, Middle Lithuania Lowland and Baltic Highlands (Figure 1).



***Angelica archangelica* L. is a typical species of natural habitat type 6430 Hydrophilous tall herb fringe communities of plains and of the montane to alpine levels, Verkiai Regional Park near Vilnius, Lithuania. (Photo: J Labokas)**

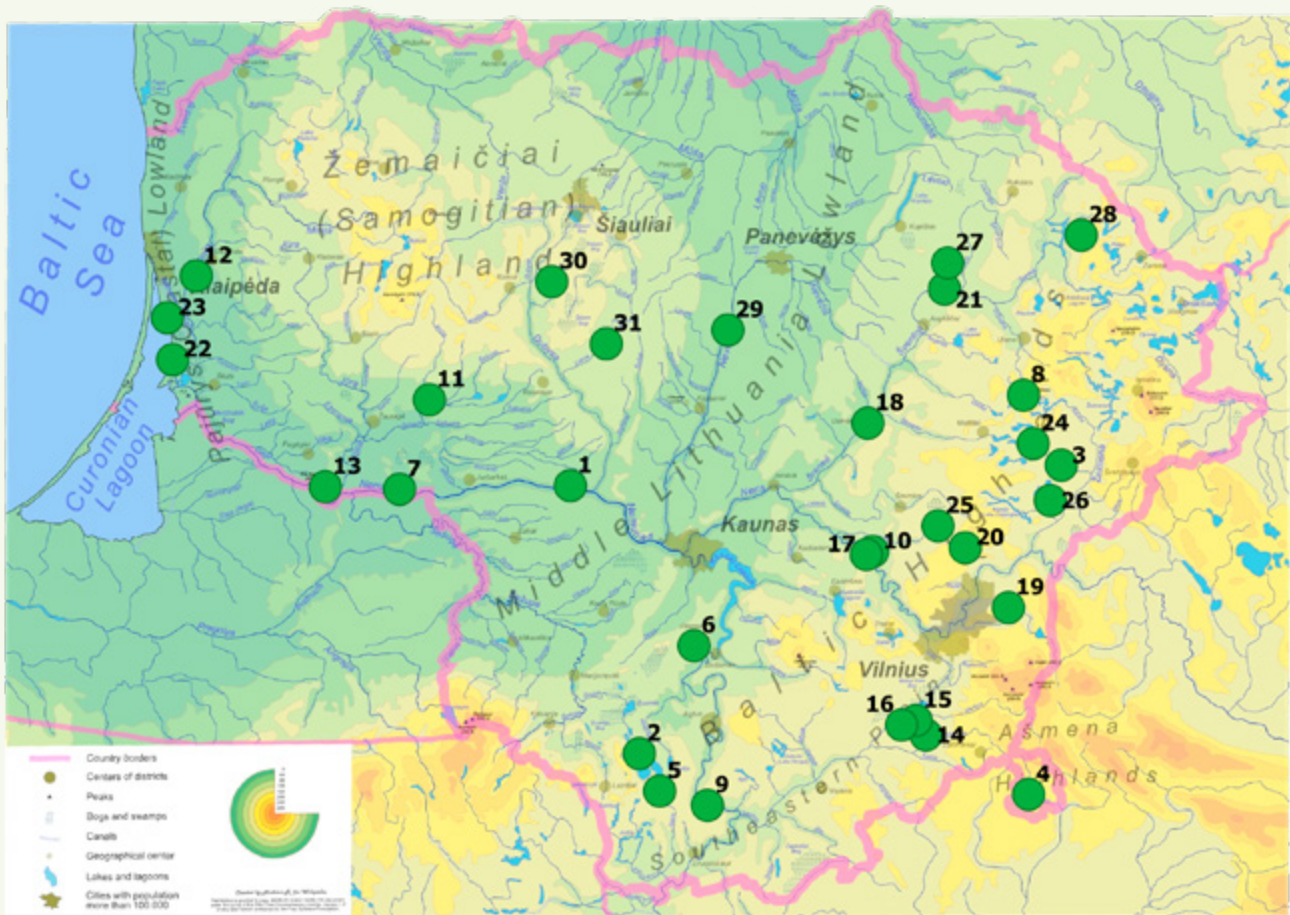


Figure 1. Distribution of genetic sites of MAP species in Lithuania: 1 – Veliuona, 2 – Dusia, 3 – Labanoras, 4 – Dieveniškės, 5 – Bestraigiškė, 6 – Prienai, 7 – Kasikas, 8 – Vorėnai, 9 – Navikai, 10 – Kernavė, 11 – Užšešuviai, 12 – Dovilai, 13 – Bitėnai, 14 – Giria, 15 – Rūdninkai, 16 – Pamerkys Forest, 17 – Kernavė Forest, 18 – Dukstyna Forest, 19 – Rokantai, 20 – Bernotai, 21 – Mikieriai, 22 – Kintai, 23 – Priekulė, 24 – Patramė, 25 – Alka Forest, 26 – Poliesė, 27 – Iženas Bog, 28 – Bradesia, 29 – Krekenava, 30 – Pažerys, 31 – Praviršulio Tyrelis Bog.

From an eco-geographical point of view, as seen in the map, the area of the Baltic Highlands with 17 genetic sites established is represented best, while Žemaičiai Highland with only two sites is the most underrepresented so far. In total, 21 sites (68%) were established in existing protected

areas including regional parks, nature reserves, mounds and other kinds of protected areas. Individual site area varies from 0.4 to 38.0 ha with an average of 7.0 ha and total acreage of 217.2 ha. About 80% of the total acreage is within the existing protected areas (Table 1).

Table 1 Distribution of genetic sites of MAP species by physical geographical areas and protected areas (PA) in Lithuania

Physical geographical area	Total number of sites	Sites in PA		Total area of sites, ha	Area of sites in PA	
		#	%		ha	%
Coastal Lowland	4	3	75	49.5	48.5	98
Žemaičiai Highland	2	2	100	11.9	11.9	100
Middle Lithuania Lowland	8	7	88	44.5	42.7	96
Baltic Highlands	17	12	71	111.3	71.4	64
Total	31	21	68	217.2	174.5	80

Among the major reasons predefining genetic site establishment and distribution pattern are land ownership and land use: only state-owned land which is unused for intensive agricultural activities, afforestation or any other habitat changing purposes, can be selected for genetic site establishment. The guidelines have been developed for genetic site original selection and evaluation based on 10 major criteria pertaining to the categories of species, site and threat assessment (Labokas, Karpavičienė, 2019).

Two groups of sites have been distinguished in terms of the initial selection focus on (1) single species/variety/ecotype or (2) multiple species. A total of nine single species and 22 multiple species sites were established (Table 2). By matching the inventoried priority MAP species with the first version of the national CWR priority list (Labokas *et al.*, 2016) it has been established that each of these sites contain 1 to 16 (7.9 on average) MAP species shared with CWR (see column 6 in

Table 2). The MAP/CWR species represent four use categories: (1) Fruit and berries (genera *Corylus*, *Fragaria*, *Prunus*, *Ribes*, *Rubus*, *Sorbus*, *Vaccinium*, etc.), (2) Vegetables and spices (*Allium*, *Angelica*, *Cichorium*, *Humulus*, *Myrica*, *Origanum*, *Rumex*, *Thymus*, etc.), (3) Forage/fodder (*Trifolium pratense*) and (4) Medicinal/pharmaceutical (*Bistorta major*, *Filipendula ulmaria*, *Hypericum* spp., *Sanguisorba officinalis*, etc.) (Labokas *et al.*, 2016). It should be noted that here we refer to the priority MAP species only. Meanwhile, there are scores of CWR species recorded in the established sites which are generally not considered MAP or at least not priority MAP species, e.g., *Pyrus pyraeaster*, *Ribes alpinum*, *R. spicatum*, *Rubus saxatilis*, *Alopecurus pratensis*, *Festuca* spp., *Lathyrus* spp., *Phleum* spp., *Poa* spp., *Trifolium alpestre*, etc. Species inventory data are available for all sites, and repeated site evaluation is normally carried out every 4–8 years depending on the type of vegetation and habitat.

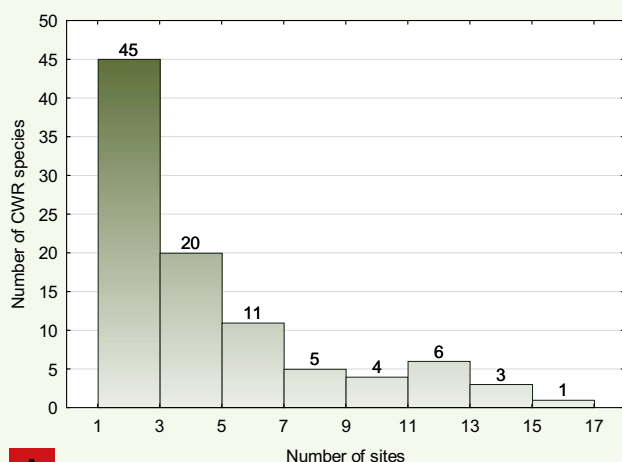


Allium angulosum, a wild relative of garlic, Bitėnai MAP site (No. 13). (Photo by Laima Šveistytė).

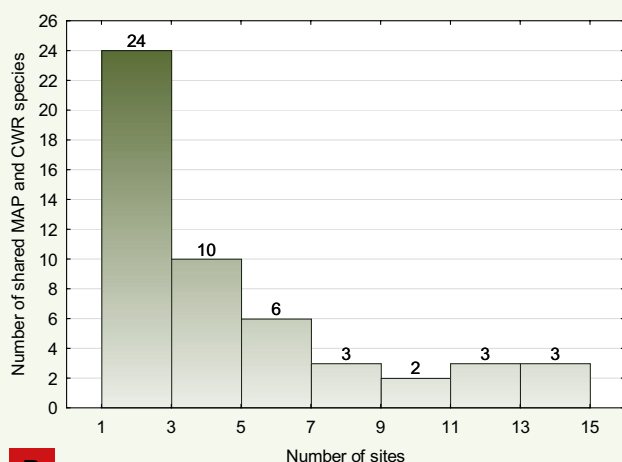
Table 2 Numbers of total vascular plant species, numbers of MAP and CWR priority species in genetic sites with major target species listed. Site numbers correspond to those in Figure 1; site type: M – multispecies, S – single-species.

Site No.	Site type	Total species	MAP	CWR	MAP/CWR	MAP/CWR species with the abundance ≥ 1 estimated on Braun Blanquet (1964) scale
1	M	25	15	10	10	<i>Allium oleraceum</i> , <i>Crataegus monogyna</i> , <i>Fragaria vesca</i> , <i>F. viridis</i> , <i>Origanum vulgare</i> , <i>Primula veris</i> , <i>Prunus spinosa</i>
2	S	39	18	18	11	<i>Allium oleraceum</i> , <i>Crataegus monogyna</i> , <i>Fragaria vesca</i> , <i>F. viridis</i> , <i>Hypericum perforatum</i> , <i>Primula veris</i> , <i>Rubus caesius</i> , <i>Thymus pulegioides</i>
3	S	14	11	3	3	<i>Vaccinium vitis-idaea</i> (incl. var. <i>leucocarpum</i>)
4	M	37	20	12	10	<i>Potentilla erecta</i> , <i>Vaccinium uliginosum</i> , <i>V. vitis-idaea</i>
5	S	37	24	9	9	<i>Corylus avellana</i> , <i>Fragaria vesca</i>
6	S	38	13	7	7	<i>Allium ursinum</i> , <i>Corylus avellana</i> , <i>Ribes nigrum</i>
7	M	32	11	17	8	<i>Allium scorodoprasum</i> , <i>Filipendula ulmaria</i> , <i>Symphytum officinale</i> , <i>Thymus pulegioides</i>
8	M	50	20	17	9	<i>Allium oleraceum</i> , <i>Fragaria vesca</i> , <i>Origanum vulgare</i>
9	M	116	41	31	16	<i>Cichorium intybus</i> , <i>Fragaria vesca</i> , <i>Origanum vulgare</i> , <i>Thymus pulegioides</i>
10	M	73	21	24	8	<i>Cichorium intybus</i> , <i>Fragaria vesca</i> , <i>Helichrysum arenarium</i> , <i>Hypericum perforatum</i>
11	M	57	19	12	7	<i>Bistorta major</i> , <i>Filipendula ulmaria</i> , <i>Hypericum maculatum</i> , <i>Rumex acetosa</i> , <i>Sanguisorba officinalis</i> , <i>Urtica dioica</i>
12	M	37	14	15	7	<i>Allium scorodoprasum</i> , <i>Crataegus monogyna</i> , <i>Fragaria viridis</i>
13	M	48	19	18	9	<i>Allium angulosum</i> , <i>A. scorodoprasum</i> , <i>Fragaria viridis</i>
14	M	33	14	8	7	<i>Filipendula ulmaria</i> , <i>Polemonium caeruleum</i> , <i>Ribes nigrum</i> , <i>Urtica dioica</i>
15	S	37	20	6	5	<i>Thymus serpyllum</i> , <i>Vaccinium vitis-idaea</i>
16	M	32	13	7	5	<i>Ribes nigrum</i> , <i>Urtica dioica</i>
17	M	102	37	34	15	<i>Fragaria viridis</i> , <i>Thymus serpyllum</i>
18	M	95	37	28	12	<i>Fragaria vesca</i> , <i>Origanum vulgare</i> , <i>Rubus caesius</i> , <i>R. idaeus</i> , <i>Sorbus aucuparia</i>
19	M	81	29	23	11	<i>Bistorta major</i> , <i>Filipendula ulmaria</i> , <i>Hypericum maculatum</i> , <i>Polemonium caeruleum</i> , <i>Urtica dioica</i>
20	M	56	17	21	8	<i>Thymus pulegioides</i>
21	M	87	36	21	11	<i>Fragaria viridis</i>
22	M	61	28	18	10	<i>Angelica archangelica</i> , <i>Hypericum perforatum</i> , <i>Rubus plicatus</i> , <i>Rumex acetosa</i> , <i>Sorbus aucuparia</i> , <i>Urtica dioica</i>
23	S	16	8	1	1	<i>Myrica gale</i>
24	S	23	15	5	4	<i>Rubus nessensis</i> , <i>Vaccinium uliginosum</i>
25	S	46	16	5	4	<i>Corylus avellana</i>
26	S	9	9	3	3	<i>Vaccinium uliginosum</i> , <i>Vaccinium vitis-idaea</i>
27	M	25	12	5	4	<i>Menyanthes trifoliata</i> , <i>Vaccinium oxycoccos</i> , <i>V. uliginosum</i>
28	M	61	23	21	8	<i>Helichrysum arenarium</i> , <i>Hypericum perforatum</i> , <i>Rumex acetosa</i> , <i>Thymus pulegioides</i> , <i>Trifolium pratense</i>
29	M	73	30	26	11	<i>Fragaria viridis</i> , <i>Rubus caesius</i>
30	M	74	26	16	6	<i>Bistorta major</i> , <i>Filipendula ulmaria</i> , <i>Potentilla erecta</i>
31	M	23	11	5	5	<i>Menyanthes trifoliata</i> , <i>Potentilla erecta</i> , <i>Vaccinium oxycoccos</i>
Average per site		49.6	20.2	14.4	7.9	
Unique species total		420	122	95	51	

The established sites contain 95 CWR species, or about 53% of the national priority CWR list of 180 species (see Labokas *et al.*, 2016). Meanwhile, only 30 of them, or about 17% of the priority list, are represented by five and more sites (populations) (Figure 2 A) as it has been suggested for *in situ* conservation (Dulloo *et al.*, 2008). And out of 51 shared MAP/CWR species, only 17 species occur in five or more sites (populations) (Figure 2 B). Besides, 19 out of a total 420 vascular plant species occurring within the network are included into the Lithuanian Red Data Book.



A



B

Figure 2 Frequency distribution of priority CWR species occurrence within the network of 31 MAP genetic sites: A – all 95 CWR species inventoried; B – 51 shared MAP/CWR species.

The sites representing high species richness are being increasingly focused on. One of them is Bitėnai MAP site (No. 13) in Rambynas Regional Park, Coastal Lowland area. It contains four species of *Allium*, one of *Fragaria* and many forage plants representing genera *Arrhenatherum*, *Lotus*, *Medicago*, *Mellilotus*, *Phalaris*, *Poa* and *Vicia*. The site has potential to expand in terms of area covered and to meet the most appropriate wild population (MAWP) standards for at least several species mentioned. Moreover, this area has been used for collecting forage plant genetic resources by breeders from the Lithuanian

Institute of Agriculture for a long time ago. Another potential candidate to meet European CWR *in situ* conservation standards is the Krekenava MAP site (No. 29) in Krekenava Regional Park, Middle Lithuania Lowland area. This site contains the following numbers of CWR species: *Allium* (1), *Fragaria* (1), *Humulus* (1), *Ribes* (2), *Rubus* (2) as well as numbers of forage species from genera *Agrostis*, *Dactylis*, *Festuca*, *Medicago*, *Phalaris*, *Phleum*, *Poa*, *Vicia*, *Trifolium*.

CONCLUSION

It is evident that the established national network of MAP genetic sites serves several purposes: to conserve MAP and CWR species, to protect threatened species therein and to provide relevant information for plant genetic resources users, nature conservationists and other stakeholders. This is in congruence with the ECPGR objective 3 *To improve in situ conservation and use of crop wild relatives*, particularly, a step towards its output 3.4 *National and European MAWP networks established* (ECPGR, 2018). The network is being further expanded to cover all physical geographical areas of the country more adequately and to achieve minimum coverage of five populations of most of the target species. Furthermore, a more precise eco-geographic proxy indicator of genetic diversity is available, i.e., there are 10 climatic subareas delimited in Lithuania which could be used for the establishment of CWR genetic reserves to represent as much potential genetic diversity of priority CWR species as possible.

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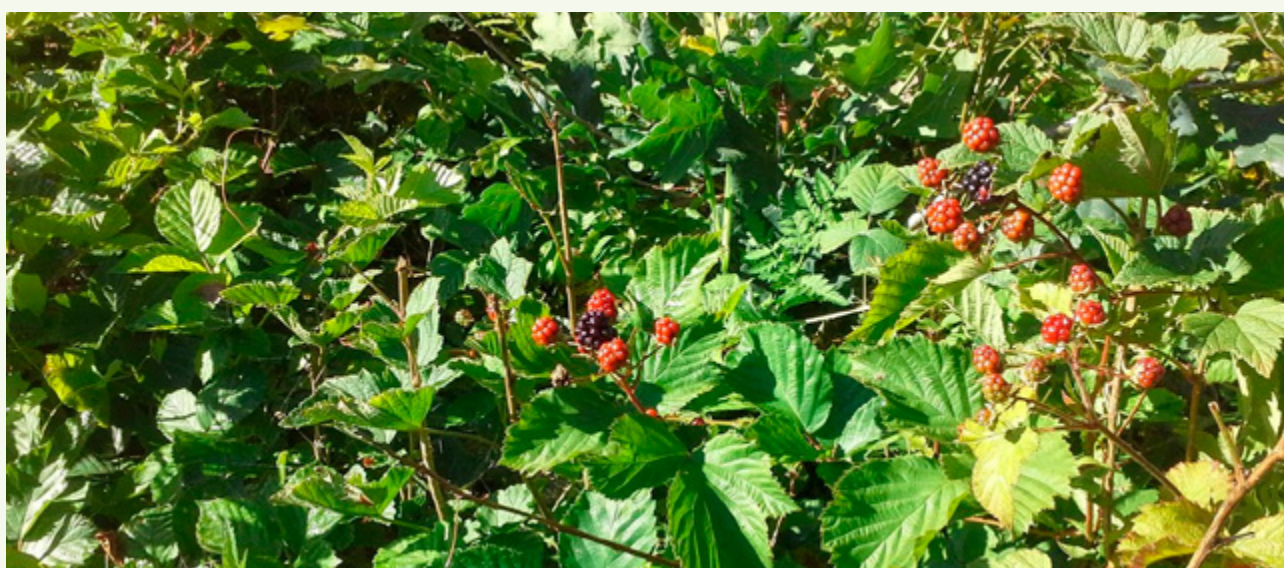
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Trifolium pratense L. is a forage species and a medicinal plant recognized by the World Health Organization (WHO); a four-leaf variation of the species is quite rare, Patramė MAP site (No. 24). (Photo: J Labokas).



A highbush ecotype of *Vaccinium uliginosum* L., a wild relative of blueberries, Poliesė MAP site (No. 26). (Photo: J Labokas).



Fruiting *Rubus plicatus* Weihe et Nees, a wild relative of blackberries – the species occurs only in the Coastal Lowland area of Lithuania; *Ribes spicatum* (in the low right corner), Kintai MAP site (No. 22). (Photo: J Labokas).

The German Network of Genetic Reserves

Imke Thormann

Federal Office for Agriculture and Food, Bonn, Germany

In June 2019, Germany established the first seven genetic reserves for wild celery species. As of February 2020, the number of wild celery genetic reserves had grown to 14 and further reserves will be designated. They constitute the Wild Celery Genetic Reserves Network managed by the Julius Kühn-Institute - Federal Research Centre for Cultivated Plants (JKI).

The Wild Celery Network is part of the “German Network of Genetic Reserves” that has been established in Germany as a framework for *in situ* conservation of priority CWR. The *in situ* conservation of CWR is an area of PGRFA diversity conservation that the German national agrobiodiversity strategy (BMELV 2007) and the National Program for PGRFA (BMEL 2012) clearly address as an important field of action. The ECPGR concept for *in situ* conservation of CWR (Maxted *et al.* 2015), and other key publications (such as Iriondo *et al.* 2008 or Magos Brehm *et al.* 2019) provide a useful basis and reference for implementation.

The German Network of Genetic Reserves has the following objectives:

- Improvement of priority CWR *in situ* conservation in their natural habitats, combined with complementary *ex situ* conservation in gene banks.
- Provision of a framework for coordination, management and integration of CWR *in situ* conservation activities and for raising awareness about the importance of CWR conservation.
- Promotion of CWR utilization through documentation and the provision of freely available *in situ*, *ex situ*, characterisation and evaluation data in national and international information systems.

- Supporting the national PGRFA program in international cooperation and the implementation of the CBD, the 2nd Global Plan of Action for PGRFA, and the International Treaty on PGRFA.
- Supporting the fulfilment of international reporting obligations regarding the implementation of the 2nd Global Plan of Action, the International Treaty, and the State of the World Report on PGRFA.

Structure of the German Network of Genetic Reserves

The structure and current status of the network is visualized in Figure 1. The ‘overall’ network consists of CWR specific networks for priority CWR, such as the Wild Celery Network mentioned above. The CWR specific networks include genetic reserves harbouring populations or plant communities identified based on agreed criteria, and are coordinated by units located at agencies or institutions involved in work with PGRFA such as the JKI in the case of the Wild Celery Network. The overall network is coordinated by the Information and Coordination Centre for Biological Diversity (IBV) of the Federal Agency for Agriculture and Food (BLE).

The coordinating units of the specific networks are established by means of a cooperation agreement between the BLE and the agency or institution that is going to provide the coordinating unit. Genetic reserves within a CWR specific network are designated through a declaration of consent signed by the local stakeholders who contribute significantly to the preservation of the target CWR within the genetic reserve, such as landowners,



Species-rich grassland (Photo by Stefan Schröder, BLE).

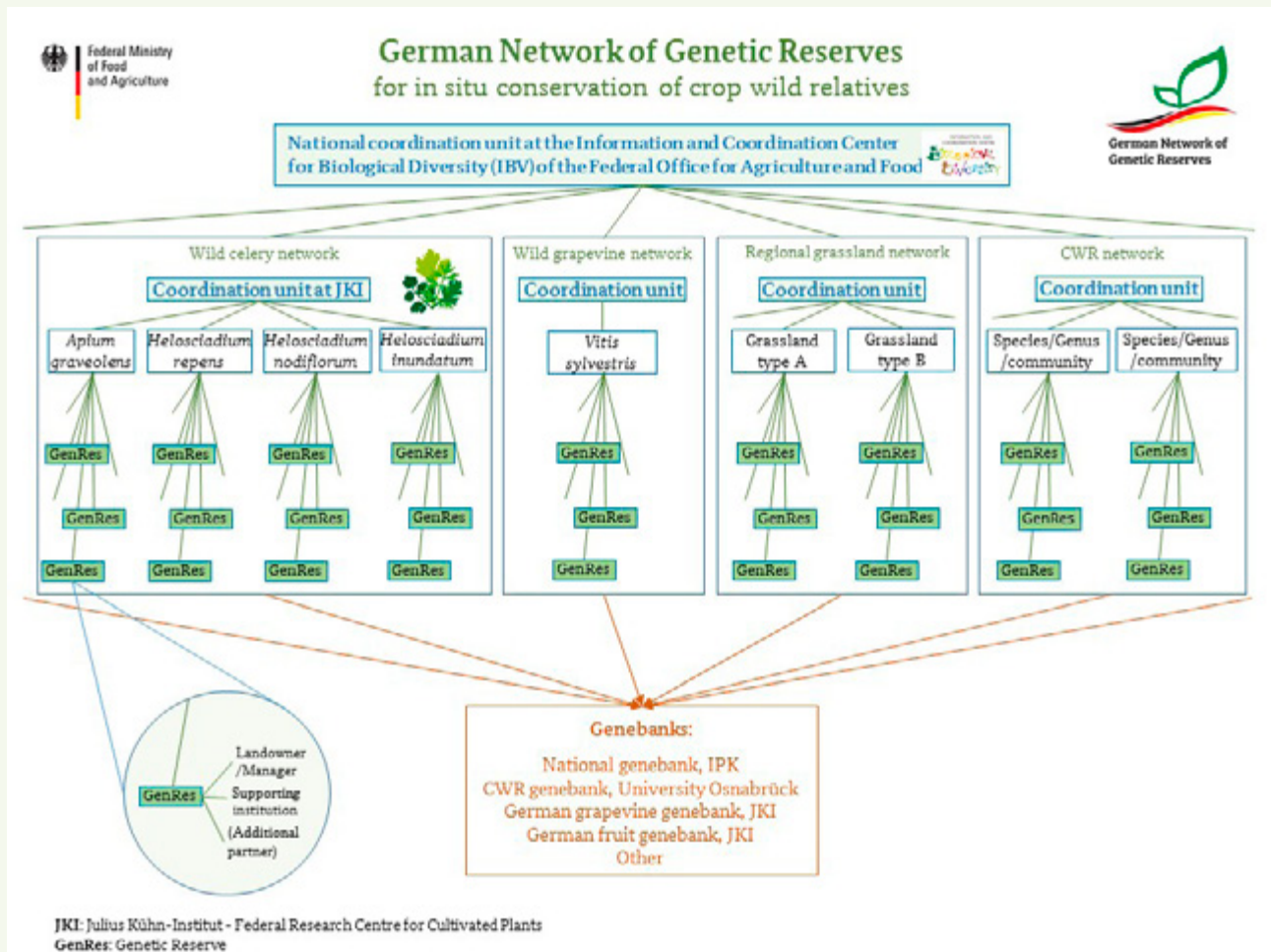


Figure 1: Structure and status of the German Network of Genetic Reserves, February 2020

land managers or local nature conservation agencies (see details below). *Ex situ* accessions of CWR populations shall, where possible, be collected and maintained in gene banks.

Tasks of the coordination units

The national coordination unit BLE/IBV coordinates the integration of the CWR specific networks into the national program for PGRFA and the integration of the national network in all relevant international processes. It is responsible for compiling and including the documentation of all genetic reserves and CWR populations in the national PGRFA inventory, and for providing relevant data to international information systems.

The tasks of a coordinating unit of a CWR specific network include establishing genetic reserves, their documentation, and supporting as far as possible activities within the genetic reserves, in particular the periodic monitoring of populations and, if necessary, the improvement of conservation measures.

Designation of a genetic reserve

The designation as genetic reserve is an important step. The Federal Ministry for Food and Agriculture (BMEL) is prepared to support monitoring activities for priority CWR in genetic reserves. To be designated as genetic reserve, it is currently requested

that a number of minimum requirements be met that ensure the CWR populations can be maintained, necessary conservation measures be carried out and gene bank samples be collected.

The landowner, tenant or land manager should agree that representatives of the specific network-coordinating unit can enter the genetic reserve for data collection, monitoring, collecting of samples and implementation of agreed conservation measures in order to fulfil their tasks within the framework of genetic reserve management. It might be necessary for the coordinating unit to obtain the necessary permits from the local nature conservation authorities. They should furthermore agree that samples of the target CWR species might be collected in accordance with nature conservation law, be stored in a genebank for complementary conservation and be available from the genebank via SMTA and under the conditions of the International Treaty for the purpose of breeding, research and training.

In addition, a permanently operating institution, such as a local nature protection agency or municipality, should agree to support the appropriate management measures for long-term maintenance of the population within the range of its capacities. This institution might at the same time also be the landowner. These agreements are formalised by signing a simple declaration

of consent that has been developed for use within the genetic reserves networks.

The coordinating unit should make the data about the CWR populations occurring in the genetic reserves available to the BLE/IBV, so that the necessary documentation and information about the CWR specific network can be made publically available. For this purpose, descriptor lists are agreed for each specific network.

In recognition of the commitment to the conservation of CWR species as an important part of biological diversity for food and agriculture, and as a contribution to the implementation of the National Program for PGRFA, the local stakeholders that have signed the declaration of consent are awarded with a certificate by the BLE. Landowners or land managers are also welcome to place information plates within the genetic reserve.

Further CWR specific networks

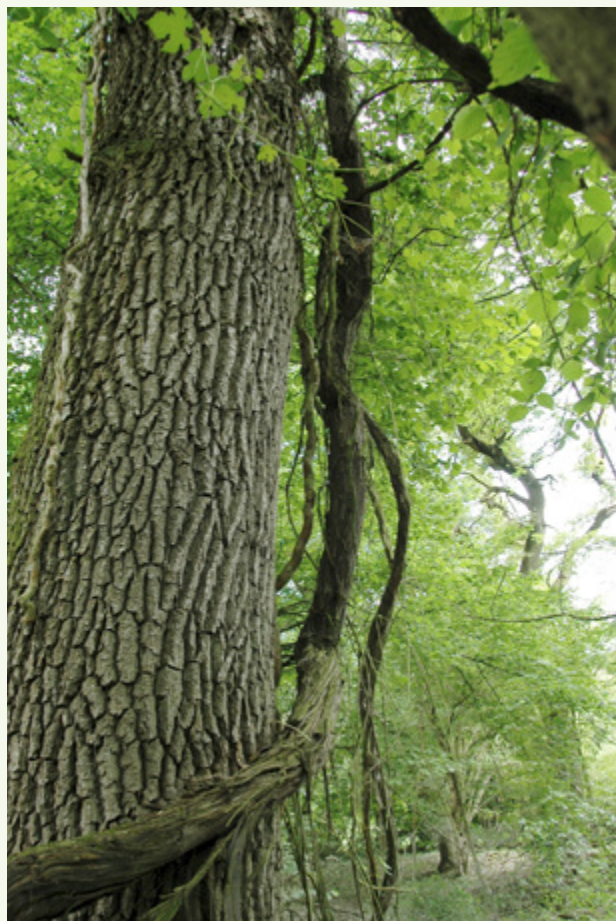
As one result of the project “Identification and Conservation of Historic Old Grasslands”, financed by BMEL and scheduled to be concluded in the first months of 2020, conservation sites for valuable grassland areas have been identified. 27 areas (nine fen meadows, nine oat grass meadows, nine calcareous grasslands) have been proposed as genetic reserves. These should be designated as genetic reserves and become the sub-regional network for grassland genetic reserves in southwest Germany – Swabian Alb and Alpine foothills in Baden-Württemberg.

Building on the project “Survival of the wild grapevine *Vitis sylvestris* C.C. Gmelin in the Rhine floodplains through targeted *in-situ* management” and follow-up research projects, a wild grapevine network is being established. The most important of the wild grapevine sites harbours the only naturally rejuvenating wild grapevine population in Germany on the Rhine island Ketsch (Nick, 2014).

Strategies and methods are being developed about how to expand the national network and to further improve collaboration among the agricultural and environmental sectors. The German Network of Genetic Reserves and the CWR priority list serve as a very useful reference framework for setting up new projects to identify further CWR occurrences or integrating already ongoing conservation actions, such as the wild fruit tree populations managed by the forestry sector.

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**Wild grapevine on the Rhine island Ketsch
(Photo by Stefan Schröder, BLE).**

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Complementarity analysis for crop wild relatives in the Fertile Crescent

Wathek Zair^{1*}, Joana Magos Brehm¹, Ahmed Amri², Mauricio Parra Quijano³ and Nigel Maxted¹

1. School of Biosciences, University of Birmingham, Birmingham, UK

2. Genetic Resources Section, International Centre for Agricultural Research, Dry Areas (ICARDA), Rabat, Morocco.

3. Facultad de Ciencias Agrarias, Universidad Nacional de Colombia sede Bogotá, Bogotá D.C., Colombia.

The Fertile Crescent is a topographically and biologically diverse location of worldwide significance in North East Asia and bordering the eastern coast of the Mediterranean Sea. Its significance comes from it being the global centre of crop origin and diversity (Vavilov, 1926; Willcox, 2012). The region stretches from Jordan, Syria, Palestine/Israel, Lebanon and Turkey, to Iraq (Breasted, 1916; Clay, 1924). It is the global region with the highest concentration of crop wild relatives (CWR) per unit area (Castañeda-Álvarez *et al.*, 2016; Vincent *et al.*, 2019), as well as high crop traditional landrace diversity. CWR are wild plants closely related to crops and therefore provide important sources of novel traits for crop improvement (Maxted *et al.*, 2006), much greater breadth of adaptive trait diversity than cultivars or landraces because they have not passed through the domestication bottleneck (Tanksley and McCouch, 1997; Vollbrecht and Sigmon, 2005). The need to increase food production in the face of climate change has resulted in the increasing use of CWR to provide the required trait diversity (Maxted *et al.*, 2012; FAO, 2015). CWR in the Fertile Crescent are known for their traits associated with drought resistance required to mitigate the adverse impact of climate change (Kelley *et al.*, 2015). However, in the Fertile Crescent, CWR are progressively more threatened by the construction of buildings, infrastructures, roads and railways as well as overgrazing and climate change (El-Beltagy, 2006; Derneg, 2010; Trigo *et al.*, 2010).

The aim of this study is to enhance the conservation of CWR diversity in the Fertile Crescent by identifying species richness and complementarity analysis of 441 priority CWR related to 61 crops and to recommend actions to conserve them more effectively. Passport data for the 441-priority crop wild relative taxa were collated and a total of 30,396 presence points (with latitude and longitude) sourcing from GBIF (2020) and virtual herbarium databases were used in the subsequent analyses. All data was analysed using CAPFITOGEN tools (Parra-Quijano, 2016) and experimental plotting was used to identify locations outside of the study region and then to re-examine the data and either correct the record or exclude them. Further method and results are included in the full version of this article (Zair *et al.*, 2020)

The taxon Richness map for the 441 priority CWR taxa is shown in Figure 2, where the arc of the Fertile Crescent is clearly visible and the Western part of the arc shows a broad concentration of CWR taxa. The complementarity analysis is shown in Figure 3 and indicates the top 25 complementary sites with the top two sites in

Western Anatolian Turkey containing at least 36 CWR taxa each. The next complementarity site is also in Western Anatolian Turkey, not far from the first two. The fourth spot is found inland from Latakia, Syria with the light red square containing from 20 to 35 CWR taxa, a site was established as a CWR genetic reserve here in the 1990s (Figure 4). The fifth, sixth and seventh grids are found in Turkey with the yellow square containing nine to 20 CWR taxa, one in Izmir Province, one in Kumluca Antalya, and one in the South-eastern Anatolia Region near Diyarbakir. There are several priority complementarity grids with the orange colour containing five to nine CWR taxa. The first one is in the Zabadani District in Syria and the remaining in Turkey. On the other hand, Jordan does not have any complementary grids. In Iraq, there is only one containing one to five CWR additional taxa to the network or total number of CWR. In Syria there are three red grid squares containing one to five CWR additional taxa to the network or total number of CWR close to each other at As Suwayda.

The analysis created a regional CWR dataset of occurrence records for CWR conservation planning in North West Asia and the Fertile Crescent. The complementarity analysis using CAPFITOGEN indicated the richest sites to located *in situ* genetic reserves are found in Western Anatolian Turkey. Both the data and methodology applied can be used in setting strategies to conserve CWR genetic resources. This study reported fully in Zair *et al.* (2020) was carried out to help the countries of the Fertile Crescent meet their CBD target of maximising the conservation of CWR



Figure 1. A map showing the countries of the Fertile Crescent.

diversity in their global centre of diversity, so helping address global food and nutritional security.

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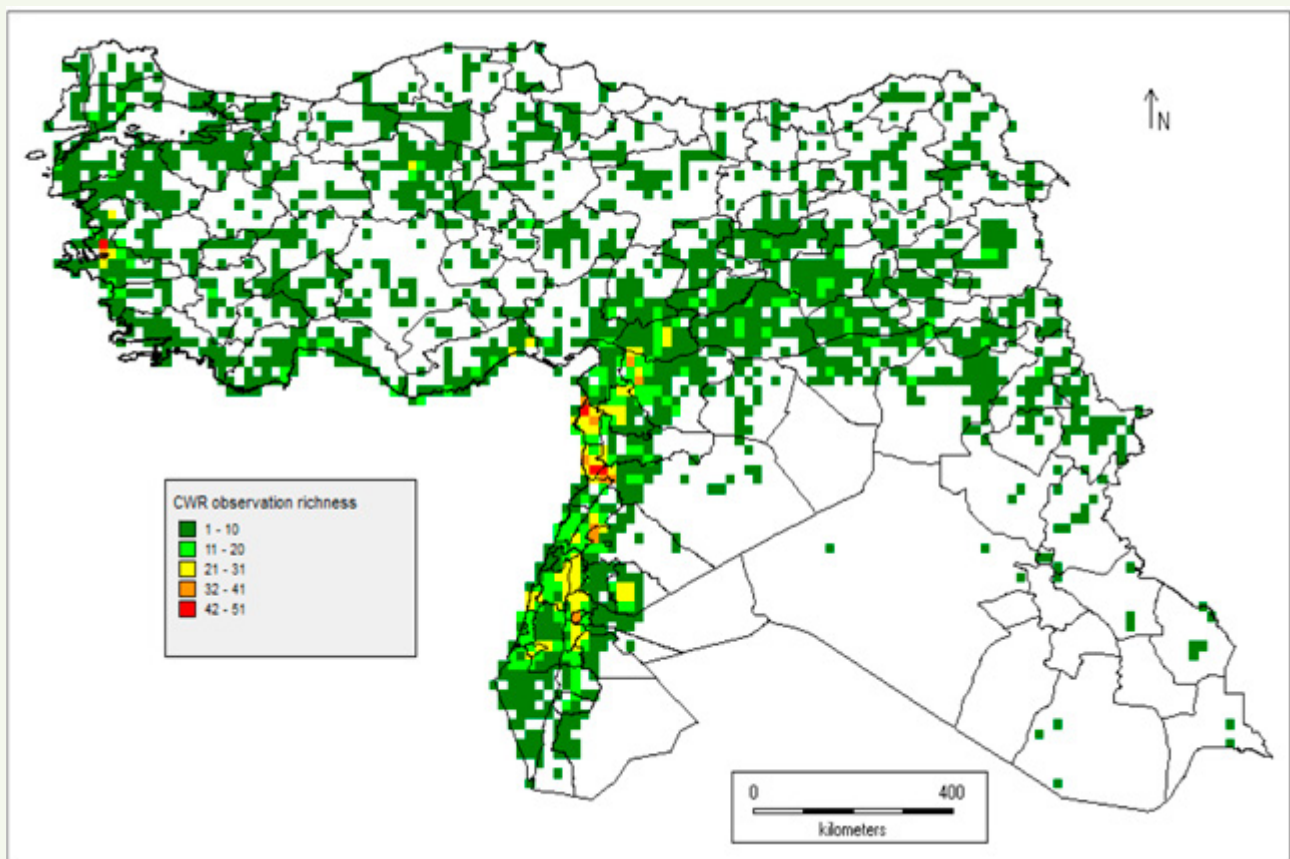


Figure 2. CWR observation richness with a grid cell size of 5 minutes (~9 km²) from Zair *et al.* (2020).

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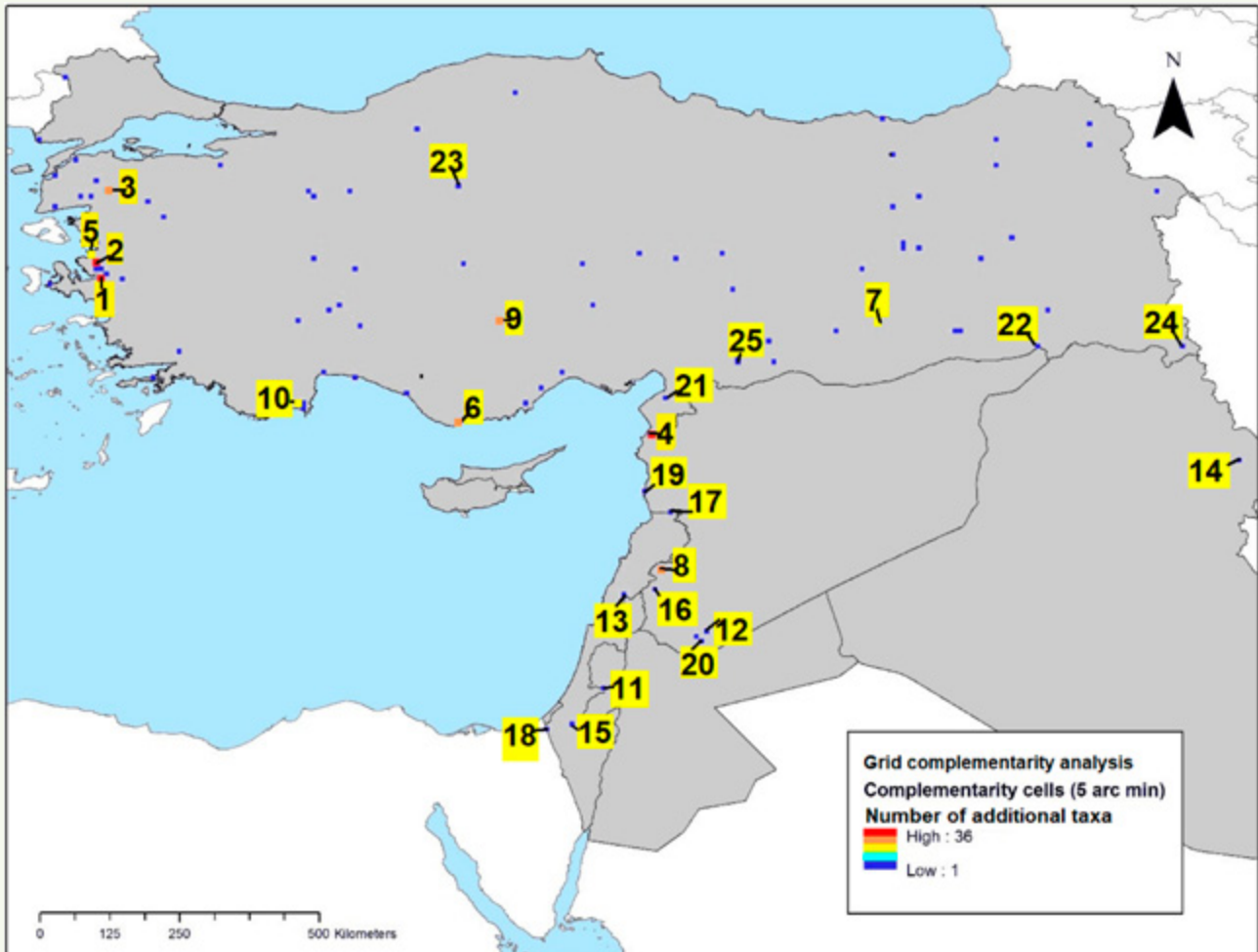


Figure 3. Complementarity analysis with a grid cell of 5 arc minutes (~10 km² at the Equator) from Zair *et al.* (2020).



Figure 4. Genetic reserve established near Qal'at Salah ad Din castle, Latakia, Syria. (Photo: Nigel Maxted).

Strength through integrating networks: Combining forces for Genetic Resource Conservation across Europe and the Near East

Jade Phillips and Nigel Maxted

School of Biosciences, University of Birmingham, Birmingham B15 2TT, UK

The EU H2020 funded GenRes Bridge project aims to strengthen the conservation, use and management of genetic resources across Europe through the integration of crop (CGR), forestry (FGR) and animal genetic resource (AnGR) network activities (genresbridge.eu). The three genetic resource sectors in Europe, as elsewhere, have till this initiative worked independently, which has undoubtedly resulted in duplication of effort, waste of resources and loss of opportunities to enact obvious synergies. The project will promote collaboration and integration across the three pan-European genetic resource networks: the European Cooperative Programme for Plant Genetic Resources (ECPGR), European Forest Genetic Resource Programme (EUFORGEN) and the European Regional Focal Point for Animal Genetic Resources (ERFP). The main project deliverable will be a 'European integrated strategy for the conservation and use of crop, forest and animal genetic resources' designed to bridge the divide between the CGR, FGR and AnGR communities and enhance resource conservation and use efficiency. To support integration GenRes Bridge will also provide user orientated tools and research options to assist implementation of the integrated strategy, ultimately benefiting genetic resource conservation and use, food security and consumer choice.

One such option to assist integrated strategy implementation is to research the coincidence of hotspots of genetic diversity within and across domains throughout the region. Although focusing conservation activities in genetic diversity hotspots has been well studied it has been applied in different ways across the three domains. Plant Genetic Resource (PGR) hotspots have been identified at national (FAO, 2015) and global levels (Vincent *et al.*, 2019, 2013; cwrdiversity.org) and the H2020 Farmers Pride (2020) project is currently working on genetic diversity hotspot identification across Europe. While for the FGR sector EUFORGEN (2019) has developed a Pan-European strategy for genetic conservation of forest trees (de Vries *et al.*, 2015) that includes identification of genetic conservation units composed of tree populations which may act as good sources of diversity for future breeding. While for the AnGR sector, the focus has been more on enhancing *in vivo* and *in vitro* conservation practises and threat assessment (Genetic Resources, 2016).

Researching the coincidence of genetic diversity hotspots within and across domains will be achieved using open source GIS tools. The data used for the analyses is being collected from regional level databases and projects, including GBIF (2020), EUFORGEN (2020), EURISCO (2020), FAO DADIS (2020), IUCN (2020) and the Farmer's Pride project. Figures 1–3 show

the current level of data availability across the region where it is clear there are gaps in the available data found in regional level databases. Consultation with regional coordinators for each domain suggested that the regional databases were going to be the most complete and useable set of data for the scope of this project. National level databases are available and often contain more detailed distribution information, however, recording formats and levels of detail vary between countries and combining data from these sources was not in the scope of this project.

As mentioned, the regional databases for each domain contain data in slightly different formats from each other. EUFGIS (2020) contains georeferenced data on the location of tree stands, which are identified as Genetic Conservation Units across the region. EUFORGEN (2020) has GIS information on the broad distribution range of 110 tree species in Europe. GBIF (2020) and the IUCN (2020) provide GPS coordinate data for tree species distribution. For PGR the EURISCO (2020) database contains GPS coordinates for the original location of the *ex situ* accessions. The Farmers Pride (2020) project will be providing CWR distribution data as GPS coordinates, which will be used with the EURISCO (2020) data (Figure 1) to identify PGR hotspots. The regional animal data in FAO DADIS (2020) is recorded to country level, where number of breeds and species per country is known. Figures 1–3 show a representation of this data for each domain at the broadest data level (i.e. the AnGR data at national level). The figures were created in the freely available QGIS (2020) software. Taxa numbers were calculated from the GPS coordinates for PGR and FGR domains and from the national level presence data for AnGR.

A key challenge in this project will be finding a common and appropriate dimension to represent levels of diversity across all domains and provide sufficient clarity to identify combined hotspots of diversity. The aim is the identification of genetic diversity hotspots for each domain and to establish if these hotspots are coincident. Ecogeographic data (known georeferenced position data) is used as a proxy for genetic diversity within PGR (Parra-Quijano *et al.*, 2016) and for FGR (de Vries *et al.*, 2015), but such data is lacking for AnGR, as is actual genetic diversity data. When drawing conclusions there is also the issue of data unavailability and bias, which is illustrated by Figures 1–3.

What is clear from the data and from a recent project workshop (Rusanen *et al.*, 2019) is that landscape level conservation is likely to be key in targeting the genetic diversity seen across all domains and implementing integrated conservation actions that benefit

Figure 1. Number of plant genetic resources (crop wild relatives and landraces) across Europe and the near East.

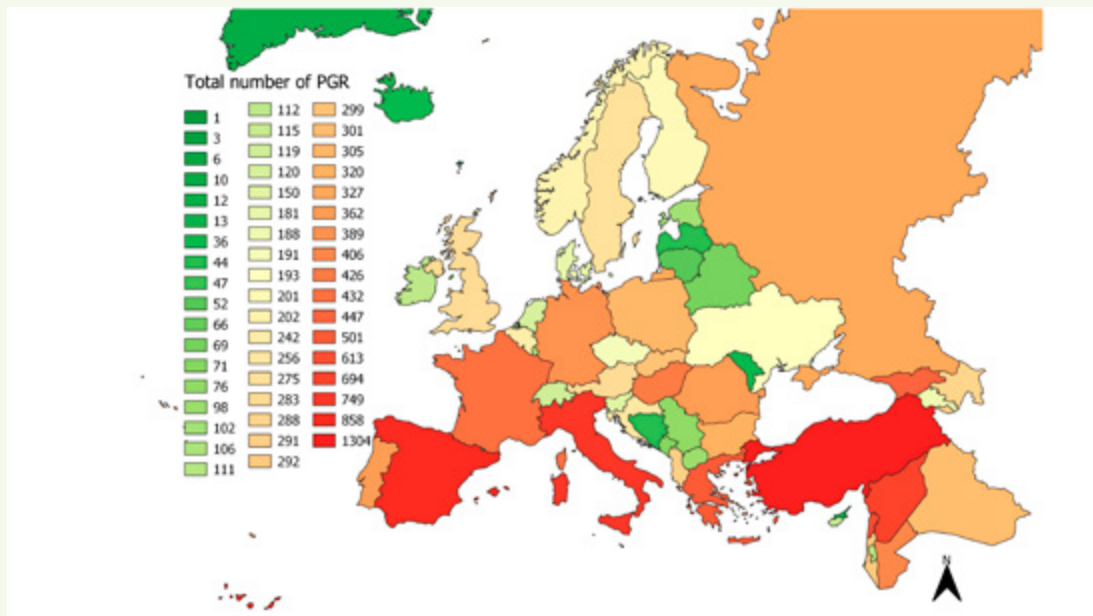


Figure 2. Number of forest genetic resources across Europe and the Near East.

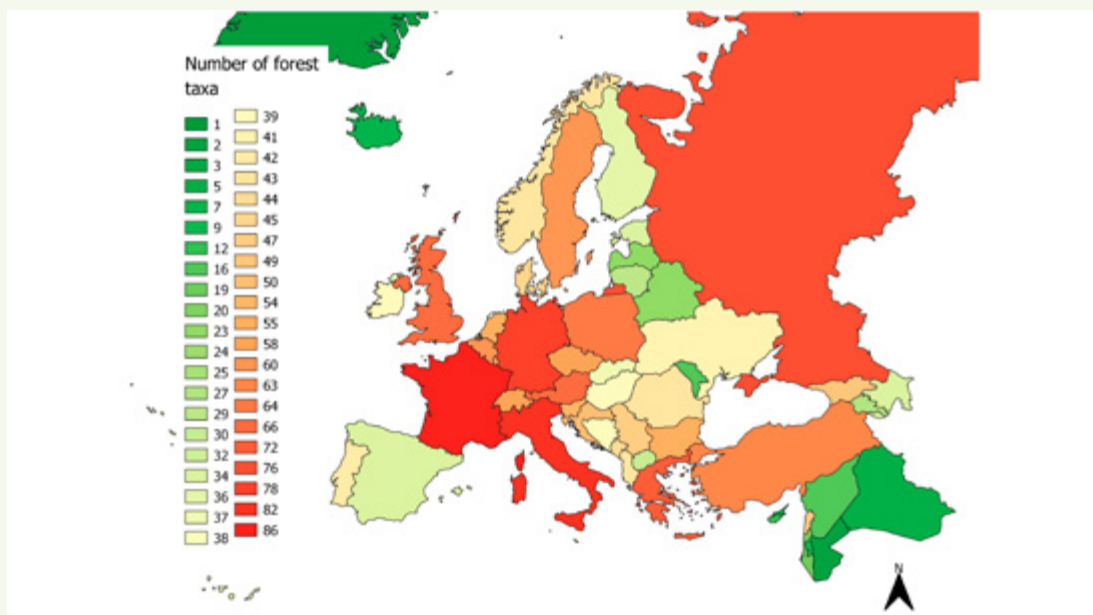
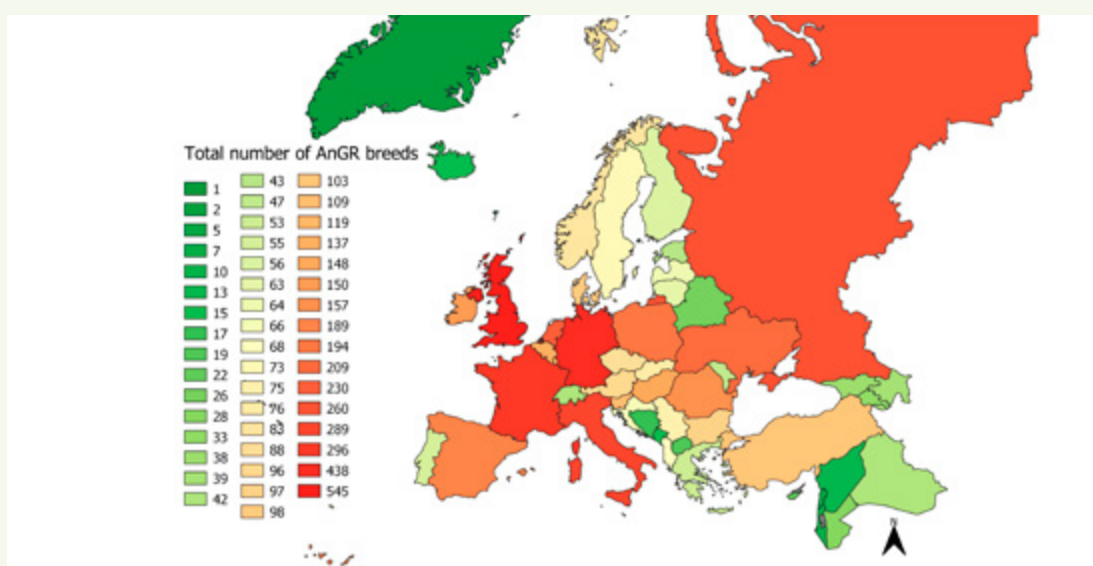


Figure 3. Number of animal genetic resources across Europe and the Near East. Grey indicates no data available.



from possible inter-domain synergies. Different ecogeographic factors may influence the genetic diversity seen within domains and a heterogenous environment is likely to contain a wider range of diversity. Unique genetic diversity traits may also be targeted specifically as it is likely that where unique diversity exists other important traits will be present within the domains.

In terms of implementing landscape level conservation, the Natura 2000 network of reserves is likely to be vital for *in situ* protection of genetic resources across the region. The network covers 18% of EU terrestrial land and offers a haven to Europe's most valuable and threatened species and habitats (Natura, 2020). Furthermore High Nature Value Farmland (HNV) (2020) can be targeted as these areas bring together biodiversity with the continuation of farming and maintenance of farming systems. HNV farmland may contain taxa across all domains in the GenRes Bridge project as well as highlighting the importance of human involvement in genetic resource maintenance.

The GenRes Bridge project will give an insight into ecogeographic data availability and the conservation of genetic resources across domains. This will allow more efficient conservation and thus enable more effective use of genetic resources. The GenRes bridge project encourages and welcomes the involvement of stakeholders within and outside the genetic resource community who will be vital in the creation of an effective and integrated conservation and use strategy www.genresbridge.eu/about-us/stakeholders/.

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Introgression breeding from crop wild relatives in eggplant landraces for adaptation to climate change

M. Plazas¹, P. Gramazio^{1,2}, S. Vilanova¹, A.B. Kouassi³, R.M. Fonseka⁴, M. Rakha^{5,6}, E. García-Forte¹, G. Mangino¹, K.B.A. Kouassi³, H. Fonseka⁷, D. Taher^{6,8}, A. Kouassi³, G. Villanueva¹, A. Arrones¹, D. Alonso¹, and J. Prohens¹

¹Instituto de Conservación y Mejora de la Agrodiversidad Valenciana, Universitat Politècnica de València, Camino de Vera 14, 46022 Valencia, Spain. E-mail: jprohens@btc.upv.es

²Faculty of Life and Environmental Sciences, University of Tsukuba, 1-1-1 Tennodai, Tsukuba 305-8572, Japan. E-mail: gramazio.pietro.gn@u.tsukuba.ac.jp

³Laboratoire de Biotechnologie, Agriculture et Valorisation des Ressources Biologiques, Université Félix Houphouët-Boigny (UFHB), 22 BP 582 Abidjan 22, Côte d'Ivoire. E-mail: abou_kouassi@yahoo.fr

⁴Department of Crop Science, Faculty of Agriculture, University of Peradeniya, Peradeniya 20400, Sri Lanka. E-mail: ramyamf@pdn.ac.lk

⁵Horticulture Department, Faculty of Agriculture, University of Kafrelsheikh, Kafr El-Sheikh, Egypt. E-mail: mdrakha@gmail.com

⁶World Vegetable Center, PO Box 42, Shanhua, Tainan 74199, Taiwan. E-mail: mdrakha@gmail.com

⁷Onesh Agriculture Pvt. Ltd. 100. Kent Road, Colombo 9, Sri Lanka. E-mail: hemalfonseka@yahoo.com

⁸Vegetable Crops Research Department, Agriculture Research Center, Horticulture Research Institute, Giza, Egypt. E-mail: daliataher1981@gmail.com

Eggplant (*Solanum melongena* L.) is an important vegetable in many tropical and subtropical areas of the world. Many of these areas are already suffering dramatic modifications in the current agricultural environment due to climate change (Rosenzweig *et al.*, 2014). Eggplant crop wild relatives (CWR) grow in a wide range of environmental conditions, including desertic areas and other highly stressful environments (Syfert *et al.*, 2016). Some of these wild relatives have been found to be resistant or tolerant to some prevailing diseases and insect pests (Daunay and Hazra, 2012) that might have increased incidence as a result of higher temperatures.

Thanks to the initiative “Adapting Agriculture to Climate Change: Collecting, Protecting and Preparing Crop Wild Relatives” (Dempewolf *et al.*, 2014), we have used eggplant wild relatives for the improvement of eggplant landraces from areas vulnerable to climate change, such as Southeast Asia and West Africa.

Approach used

The approach used in these projects has been the so-called “introgressiomics” (Prohens *et al.*, 2017), which calls for a broad use of CWR for developing multiple introgression breeding materials that can be easily integrated in breeding pipelines. Partners from Côte d'Ivoire, Egypt, Japan, Spain, Sri Lanka, and Taiwan have joined forces to develop and evaluate pre-breeding materials for resistance to biotic and abiotic stress and agronomic, fruit yield and quality traits. Also, several international and local breeding companies from different regions of the world have participated in the evaluation of pre-bred materials with introgressions from wild species.

Development of interspecific hybrids

In a first stage, multiple crosses were performed between six eggplant landraces (three from Côte d'Ivoire and three from Sri Lanka) with 35 wild accessions from 15 wild relatives from the

primary (one species), secondary (11 species) and tertiary (three species) gene pools (Figure 1). A total of 90 hybrid combinations between the six landraces and 14 wild species (all except the tertiary gene pool species *S. sisymbriifolium*) were obtained (Figure 2). For the two other wild species from the tertiary gene pool (*S. elaeagnifolium* and *S. torvum*) embryo rescue was used to obtain the hybrids, which were viable, but completely sterile in the case of the hybrids with *S. torvum*.

Development of backcrosses and introgression lines

As a result of backcrossing of the hybrids to the recurrent cultivated landraces, we developed 48 first backcross (BC1) ; Figure 3 and 36 second backcross (BC2) generations towards the respective *S. melongena* parents involving the primary gene pool species *S. insanum* and eight secondary gene pool species (*S. anguivi*, *S. dasyphyllum*, *S. incanum*, *S. lichtensteinii*, *S. lidii*, *S. linnaeanum*, *S. pyracanthos*, and *S. tomentosum*), as well as the tertiary gene pool species *S. elaeagnifolium*.

A total of 87 progenies of second generations of selfing obtained by single seed descent from individually selected plants for tolerance to drought coming from 14 BC2 generations involving six wild species (*S. anguivi*, *S. dasyphyllum*, *S. incanum*, *S. insanum*, *S. lichtensteinii* and *S. lidii*) were also obtained. These materials are morphologically highly variable (Figure 4) and are potentially of interest for the development of drought-tolerant materials of eggplant.

Marker-assisted selection programmes have been undertaken for the development of introgression lines (ILs) sets with four wild species (*S. elaeagnifolium*, *S. dasyphyllum*, *S. incanum* and *S. insanum*). After several generations of backcross and marker-assisted selection, the first set of fixed introgression lines containing single introgressions of *S. incanum* has been developed (Gramazio *et al.*, 2017). This first set has been



Figure 1 Fruits of eggplant CWR and landraces (large fruits in the center) used for introgression breeding. (Photo: Mariola Plazas).

Figure 2 Leaves and fruits of interspecific hybrids between eggplant and CWR and their respective parents. The left part of the figure displays the leaves of interspecific hybrids between *S. melongena* and *S. insanum* (above), *S. anguivi* (center) and *S. dasyphyllum* (below). The right part of the figure displays the leaves of interspecific hybrids between *S. melongena* and *S. insanum* (above), *S. anguivi* (center) and *S. tomentosum* (below). For both leaves and fruits, the respective parents of interspecific hybrids are included. (Photos: Jaime Prohens).

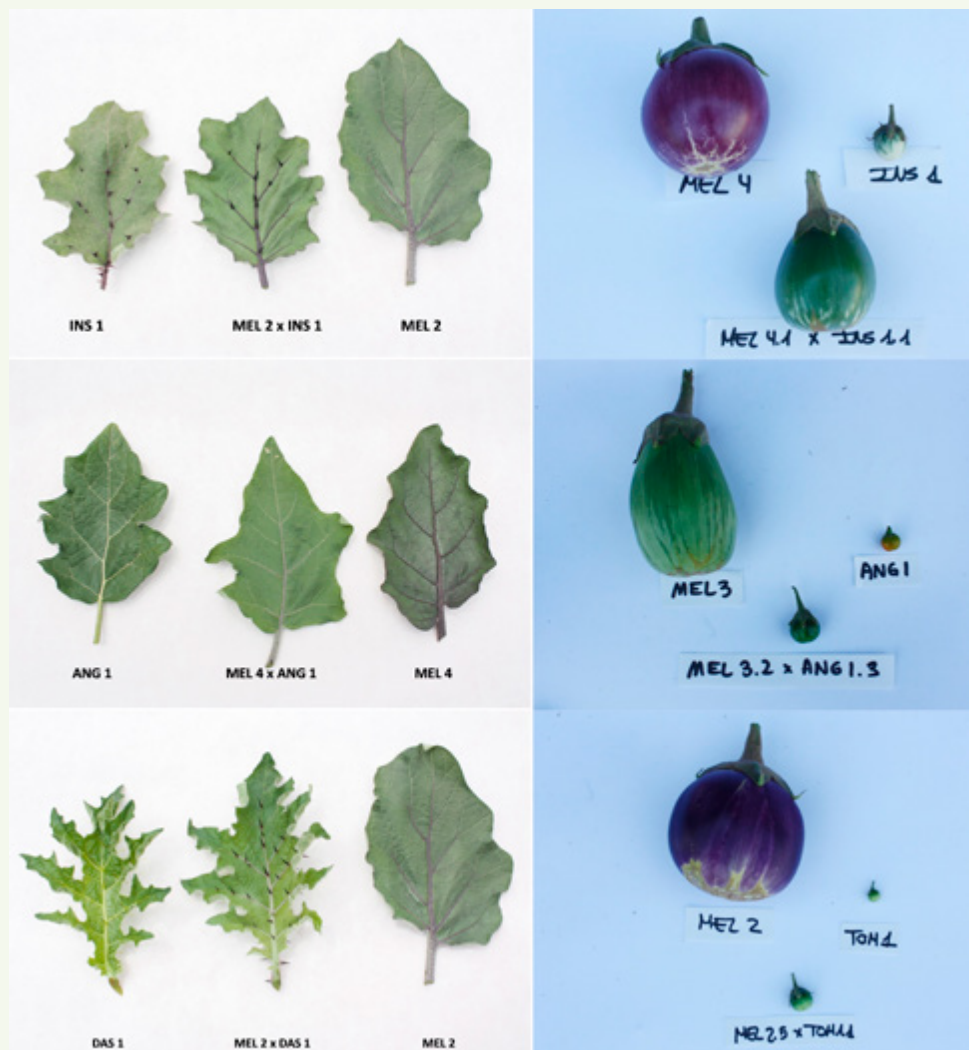


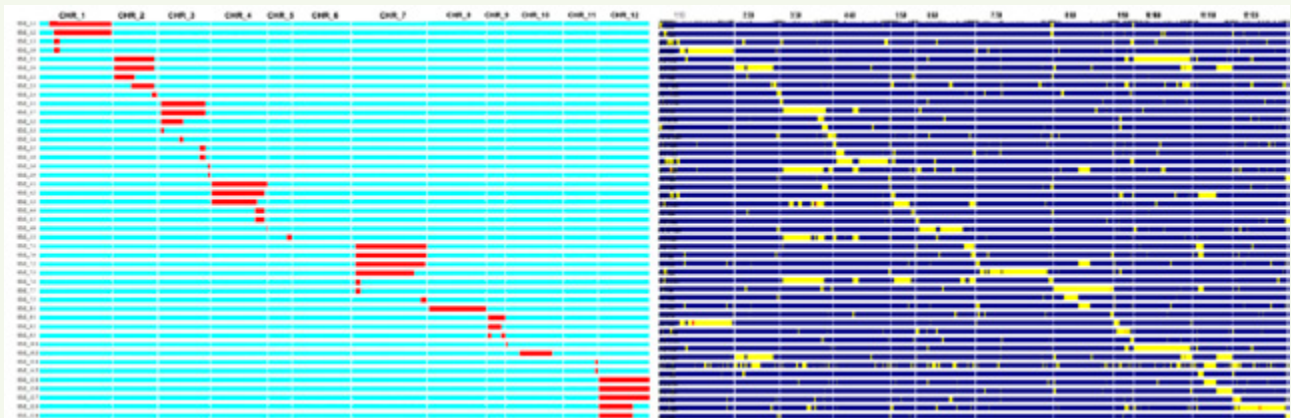


Figure 3 Fruits of four different plants of the first backcross (BC1) of the interspecific (Photo: Mariola Plazas).



Figure 4 Sample of fruits from different BC2S2 progenies between eggplant and accessions of six eggplant CWR (Photo: Jaime Prohens).

Figure 5 Graphical genotypes of fixed introgression lines of *S. incanum* (left) and of the BC4 generation of *S. insanum* (right). Introgressions of *S. incanum* and *S. insanum* are in red and yellow colors, respectively.



completed and at present 51 ILs with *S. incanum*, covering over 70% of the *S. incanum* genome, are available (Figure 5). New crosses and selfings are being performed to complete this set of ILs with *S. incanum*. The programmes with *S. dasyphyllum*, *S. elaeagnifolium* and *S. insanum* are advanced, and BC3 and BC4 generations have been selfed and/or backcrossed again to the *S. melongena* parents to finalize the selection of plants to be selfed for the development of fixed ILs (Figure 5).

Evaluation of materials

Throughout the process of development of eggplant materials with introgressions from CWR, different evaluations have been performed for biotic and abiotic stresses. Drought tolerance was found in several accessions in the CWR *S. anguivi*, *S. dasyphyllum*, *S. insanum*, *S. incanum* and *S. sisymbriifolium* as well as in interspecific hybrids of the three former species with *S. melongena* under different environments (Figure 6). High levels of resistance to different strains of bacterial wilt have been found in *S. sisymbriifolium* and *S. torvum*, while moderate levels of tolerance have been found in accessions of *S. anguivi* and *S. incanum*. Regarding tolerance to insect pests, high levels of resistance to sweet potato whitefly have been found in *S. campylacanthum*, *S. dasyphyllum* and *S. pyracanthos* and *S. tomentosum*, while for two-spotted spider mite the highest levels of resistance have been found in *S. dasyphyllum*, *S. sisymbriifolium* and *S. torvum*. In addition, resistance to spider mite was detected in *S. macrocarpon* and moderate resistance in *S. aethiopicum*.

Some interspecific hybrids were found to be very vigorous and displayed a powerful root system (Figure 7), which may account for increased tolerance to drought, as well as for enhanced vigour of the scion when eggplant is grafted onto vigorous interspecific hybrids of eggplant. Therefore, direct use of interspecific hybrids of eggplant with wild relatives as rootstocks is promising.

Conclusions

Introgression breeding in eggplant landraces from areas particularly susceptible to climate change using a broad range of eggplant CWR could contribute to mitigate the impact

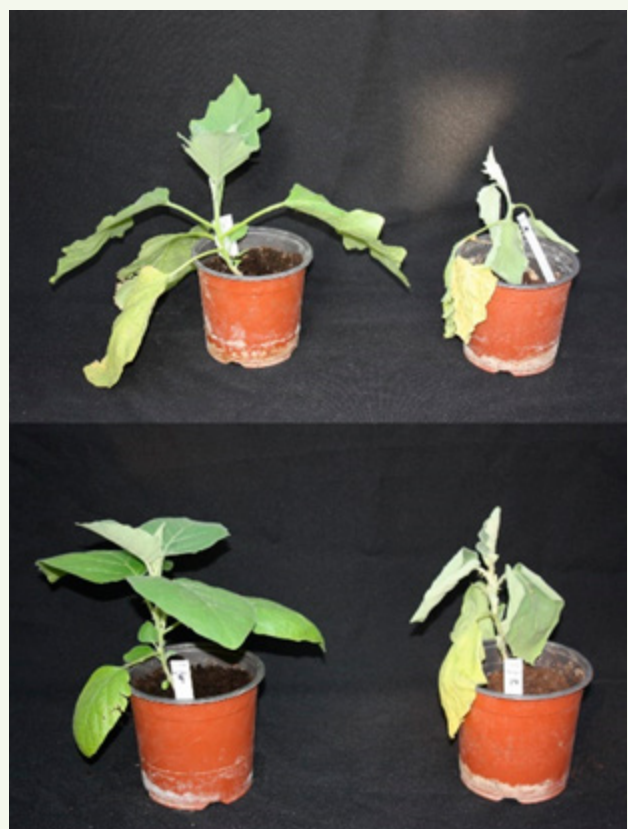


Figure 6 Comparison of the tolerance to water stress of cultivated eggplant (above) and of the eggplant CWR *S. incanum* (right). The plants of the left are the irrigated controls and the plants to the right the non-irrigated ones (Photo: Mariola Plazas).

of climate change in the production of this vegetable. The interspecific hybrids obtained, advanced backcross materials and introgression lines with multiple eggplant CWR are highly promising for broadening the genepool of eggplant and for adapting this crop to climate change. The evaluations performed up to now for tolerance to biotic and abiotic stresses and for other agronomic and quality traits indicate that the development of a new generation of eggplant cultivars with enhanced



Figure 7 Increased vigour for plant vegetative traits and root system in an interspecific hybrid of *S. melongena* with *S. tomentosum* (Photo: Jaime Prohens).

performance under the new environmental conditions resulting from climate change is feasible.

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Book review

Maxted, N., Hunter, D. and Ortiz Rios, R.O., (2020). **Plant genetic conservation**. 560 pp. Cambridge University Press, Cambridge. ISBN 9781139024297.

Plant diversity sustains all animal life, and the genetic diversity within plants underpins global food security for humankind. This text provides a practical and theoretical introduction to the strategies and actions to adopt for conserving plant genetic variation, as well as explaining how humans can exploit this diversity for sustainable development. It initially offers current knowledge on the characterization and evaluation of plant genetic resources. The authors then discuss strategies from *in situ* and *ex situ* conservation to crop breeding, exploring how crop wild relatives can be used to improve food security in the face of increasing agrobiodiversity loss, human population growth and climate change. Each chapter draws on examples from the literature or the authors’ research and includes further reading references. Packed with other useful features such as a glossary, it is invaluable for undergraduate, graduate students and professionals in plant sciences, ecology, conservation biology, genetics, and natural resource management. Drawing on the authors’ wealth of experience, this up-to-date and long-awaited text provides a theoretical and practical introduction to the conservation and utilisation of plant genetic diversity, with a focus on sustaining global food security.

