Cite as: Parveaud, C.-E., Lateur, M., Roman, A., Aravanopoulos, P., Van Roozendael, F., Decroocq, V. (2026). Presentation of the FRUITDIV project: exploiting the untapped potential of fruit tree wild diversity for sustainable agriculture. *Proceedings of the 22nd International Conference on Organic Fruit-Growing*, Filderstadt 2026.02.23-25. Ed. FOEKO e.V. 2026: 40-43

Presentation of the FRUITDIV project: exploiting the untapped potential of fruit tree wild diversity for sustainable agriculture

C.-E. Parveaud[1], M. Lateur[2], A. Roman[3], P. Aravanopoulos[4], F. Van Roozendael[2] and V. Decroocq[5]

Abstract

FRUITDIV is a European project (2024-2028) designed to address a critical issue in the agricultural sector: The underutilization and conservation of crop wild relatives (CWRs), particularly those related to fruit trees. CWRs are wild plants that present a high genetic and taxonomic affinity to domesticated crops, and which contain a wealth of untapped genetic diversity. This diversity can provide beneficial traits, such as resistance to pests and diseases, tolerance to drought and salinity, and adaptation to fluctuating climates. Such traits are particularly relevant in low input organic farming systems, because it is much more dependent on the plant material characteristics. This paper gives an overview of the context, aims, methods and first results obtained by the FRUITDIV consortium.

Keywords: fruit tree, wild relatives, *Malus*, *Pyrus*, *Prunus*

Context

Crop wild relatives (CWRs) are wild plant taxa that have a close genetic relationship to domesticated crops, including progenitor species and other species within the same gene pool or taxonomic complex. Next to some undesirable agronomic characters, they hold untapped genetic diversity for beneficial traits like pest and disease resistance, salinity and drought tolerance, and adaptation to marginal lands and fluctuating climates. CWRs and domesticated genetic resources are very important for crop improvement and sustainable agricultural genetic diversity use. Conserving and utilizing CWR genetic resources can lead to more robust and productive crops, playing a role in meeting global climate challenges and food security demands. This approach can reduce pesticide use, as targeted by the European Green Deal's Biodiversity and Farm to Fork strategies. Fruit trees, currently dominated by elite cultivars for high production, prolonged transportability, and shelf life, face a growing range of pests and diseases, and resistance breakdowns in some cases.

The limited understanding and insufficient exploitation of the genetic diversity within Crop Wild Relatives (CWR) are particularly worrying, especially within the fruit sector. Fruit trees, with their long lifespan, are particularly vulnerable to climate change and parasite outbreaks. Habitat fragmentation and global material transfer, severely threaten the sustainable CWR conservation by favouring gene flow between wild and cultivated compartments. Since elite fruit varieties may not perform well under pesticide-free conditions, CWR reservoirs offer opportunities to increase the use of natural resistance sources, enhance genetic diversity in fruit tree breeding programs, and boost diversification in both organic and conventional farming. CWRs can contribute beneficial alleles through conventional breeding or advanced biotechnological methods.

[1] GRAB, FR-26320 Saint-Marcel-lès-Valence, claudeeric.parveaud@grab.fr
[2] CRA-W, BE-5030 Gembloux
[3] Institute of Biological Research Cluj, NIRDBS, RO-400015 Cluj-Napoca
[4] University of Thessaloniki, GR-54006 Thessaloniki
[5] INRAE, UMR BFP, FR-33 882 Villeneuve d'Ornon

However, as global warming accelerates and it takes 20 to 30 years to develop new fruit tree products, urgent answers are needed to ensure food security, sustainable agriculture, and fruit production for the next 50 years. Due to the time- and cost-effective features of fruit tree breeding, research and selection programs are driven by public bodies, with non-academic partners predominantly involved in conserving traditional and ancient varieties, with limited representation of fruit tree CWRs.

European plant conservation initiatives, such as the European cooperative programs for plant genetic resources (ECPGR), list a significant amount of cultivated fruit tree varieties, but few wild genotypes. Fruit tree CWR are significantly under-represented in germplasm collections; many species are either completely missing or are represented by only a few individuals. This insufficient research has impeded their potential for use in breeding. Only a few preliminary studies on specific *Malus* and *Prunus* crop wild related species have been published (*e.g.* Cornille et al., 2012; Groppi et al., 2021, Jacques et al., 2009). While a large fraction of fruit tree CWR species are native to Asia, Europe still hosts populations of *Malus*, *Pyrus*, and *Prunus* CWRs in natural biodiversity hotspots. These hotspots are poorly studied, so far.

Aims

The scientific objectives of FRUITDIV project are:

- Genetically characterise CWR to (i) establish *ex-situ* collections representative of the CWR diversity to be further multiplied in common gardens and (ii) identify key CWR natural populations to be preserved *in-situ*
- Share and develop new and high-throughput (HTP) phenotyping tools and protocols for the evaluation of traits linked to resistance to pests and diseases, and adaptation to low-input cultivation systems in highly contrasted environments
- Integrate CWRs in plant genetic resources (PGR) collections and breeding programs by developing new methods for wild-to-crop translational research
- Promote, through European infrastructures, sustainable data sharing by standardising and giving access to FAIR (Findable, Accessible, Interoperable and Reusable) genotypic and phenotypic Open Data
- Develop pre-breeding material and CWR-adapted methodologies for breeding (marker-assisted introgression of CWR traits of interest, genome-wide selection of favourable and deleterious alleles) at single and multi-trait scales, making use of existing or future multi-site experimental designs and predictive models;
- Foster a more efficient and sustainable conservation of CWR, in situ (in forest reserves), on farms and through NGOs, and enhance stakeholders' awareness of the value and importance of CWR.
- Promote the use of CWR or first-generation pre-breeding material by breeders to disseminate plant material of interest for growers, organic farmers & the fruit tree industry (broad range of usages and cultivation systems).

Methodology

The sampling strategy planned in FRUITDIV includes an inventory of existing *Prunus*, *Malus* and *Pyrus* CWR in PGRC (Plant Genetic Resources Collections) as well as a survey of their ecological niches in Europe. In FRUITDIV, we assume that the European hotspots of biodiversity, that were once refugia for those species during the last glaciation period

(~19,000 years ago), still hold a high level of genetic diversity that is still largely unexplored. Thirty-five biodiversity hotspots are recognised worldwide, all by extremely high levels of endemism and threat. Europe has a major share in only one of these hotspots, the Mediterranean Basin (Hewitt, 2011). Long-term isolation accompanied by relatively constant climatic conditions has led to the accumulation of species in southern Europe over the past millions of years, while temperate and northern Europe are characterised by biodiversity impoverishment in consequence of the glaciation cycles with subsequent range retraction-expansion dynamics of species.

In the context of FRUITDIV, we survey fruit tree CWR in those areas, to characterise them and design sustainable conservation plans. We will extend our inventory to the Caucasus region, to compare genetic diversity between parapatric CWR species (phylogenetically related species that occupy contiguous habitats and are thus potentially in contact). Five Rosaceae fruit tree CWR taxa (i.e. taxonomic groups) will be targeted in FRUITDIV (in bold, the species with a wide-range distribution across Europe that will be the main focus of the survey; in non-bold, the species with a narrower localised distribution):

- *Malus* (***Malus sylvestris***, *M. orientalis*),
- *Pyrus* (***Pyrus pyraster***, *Py. spinosa*, *Py. nivalis*, *Py. eleagrifolia*),
- *Cerasus* (***Prunus avium***)
- *Prunophora* (***Prunus cerasifera***, ***Pr. cocomilia***, *Pr. ramburii*)
- Amygdalus (***Prunus webbii***, *Pr. tenella*, *Pr. scoparia*)

The sixth Rosaceae taxon, the group Armeniaca, has an already established and in-depth genetically characterised core-collection (Groppi et al, 2021). Currently with 300 individuals in its collection, it includes wild representatives of populations of *Pr. armeniaca, Pr. sibirica, Pr. mandshurica, Pr. mume,* and *Pr. brigantina*. It is already established in multiple sites (two in France, one in Greece) and will be shared with other partners in FRUITDIV (one already in establishment phase in Romania). Non-European CWR species, such as *M. sieversii* (from Central Asia) and *M. orientalis* (from Caucasus), already maintained in the German, French and Italian PGR collections, and *Pr. fenzliana, Pr. spinosissima* and *Pr. spartioides* (from the Amygdalus taxon) in the French repository will also be characterised.

Partners involved in FRUITDIV project

Acknowledgements

This project is funded by the European Union under the Grant Agreement no. 101133964. Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union or European Research Executive Agency (REA). Neither the European Union nor the granting authority can be held responsible for them.

References

Cornille A, Gladieux P, Smulders MJ, et al. (2012). New insight into the history of domesticated apple: secondary contribution of the European wild apple to the genome of cultivated varieties. PLoS Genet. 8(5).

Hewitt (2011). *Mediterranean Peninsulas: the evolution of hotspots*. In: Zachos FE, Habel JC (eds) Biodiversity hotspots.

Groppi, A., Liu, S., Cornille, A. *et al.* (2021). Population genomics of apricots unravels domestication history and adaptive events. *Nat Commun* **12**, 3956. https://doi.org/10.1038/s41467-021-24283-6.

Jacques, D., Vandermijnsbrugge, K., Lemaire, S., Antofie, A., Lateur, M. (2009). Distribution and variability of wild apple (*Malus sylvestris* Mill.) in Belgium. *Belgian Journal of Botany*, 142 (1) : 39-49.