European Cooperative Programme for Plant Genetic Resources

ECP/GR

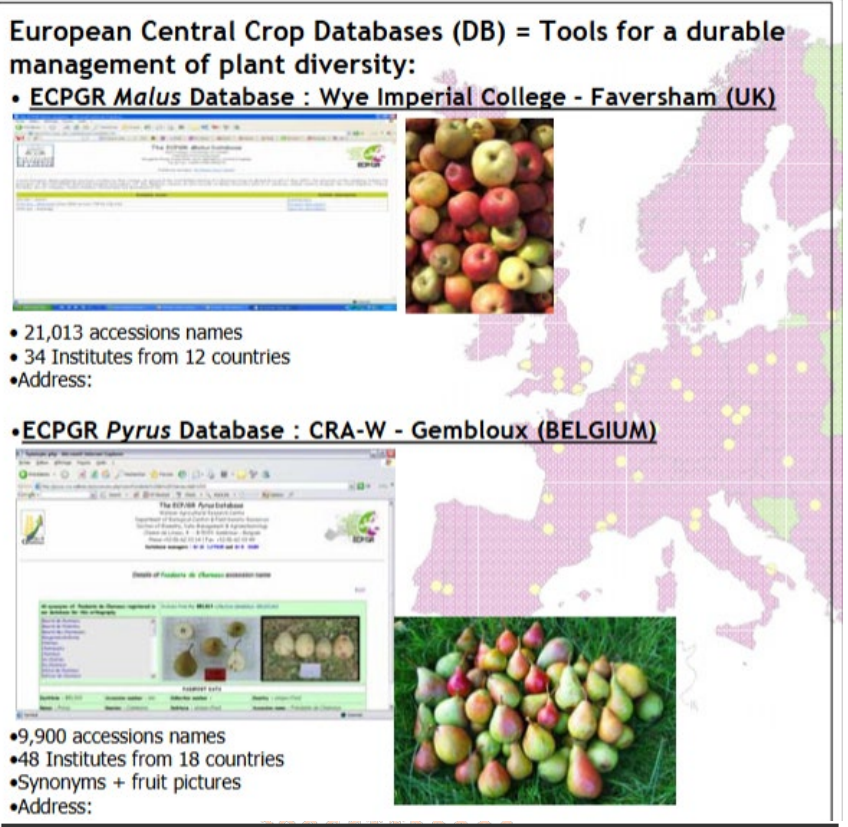
IMPROVEMENT OF FRUIT TREE DATA INCLUSION IN EURISCO

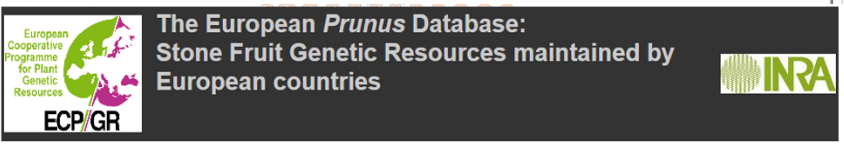
(FRUITTREEDATA)

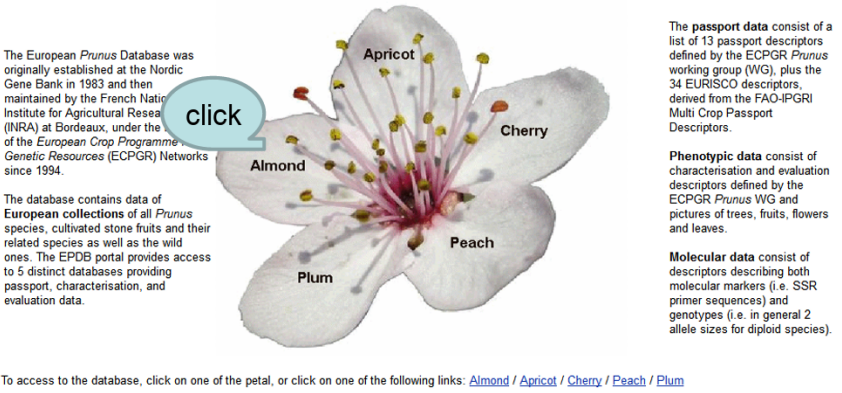
Matthew Ordidge

14th October 2026





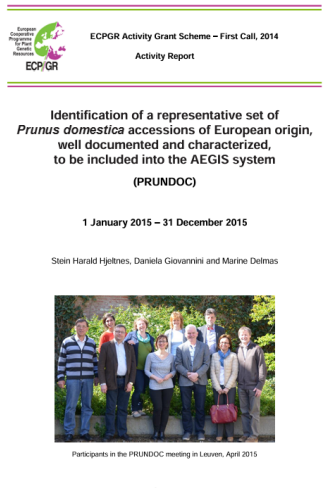




Background (Central Crop Databases)

- Originally developed ~1997 (i.e. pre-EURISCO)
- Aimed* to include additional data types
  - Synonyms
  - Genetic data
  - Photographs
  - Characterization data
- Potential for lack of alignment with EURISCO
- Reliant upon ‘in kind’ support

ECP/GR


ECPGR Activity Grant Scheme – First Call, 2014

Activity Report

Identification of a representative set of *Prunus domestica* accessions of European origin, well documented and characterized, to be included into the AEGIS system

(PRUNDOC)

1 January 2015 – 31 December 2015

Stein Harald Hjeltnes, Daniela Giovannini and Marine Delmas

Participants in the PRUNDOC meeting in Leuven, April 2015

July 2016


ECPGR Activity Grant Scheme – Second Call, 2015

Activity Report

Collaborative action for updating, documenting and communicating the cherry patrimonial richness in EU

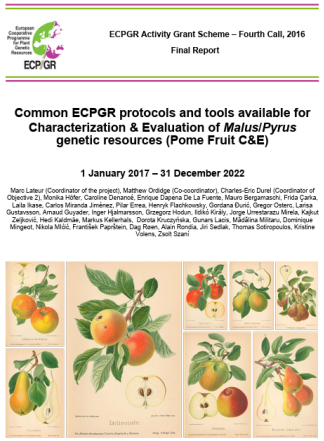
(EU.CHERRY)

March 2016 – February 2017

Marine Delmas, Daniela Giovannini, Sanda Stanivuković, Frantisek Paprstein, Hedi Kaldmäe, Monika Höfer, Gunars Lacis, Matthew Ordidge, Felicidad Fernandez, Marc Lateur, Stephan Weise, Pavlina Drogoudi, Teresa Barreneche

'Büttners Rote Knorpelkirsche' © M. Höfer, JKI

September 2019


ECPGR Activity Grant Scheme – Fourth Call, 2016

Final Report

Common ECPGR protocols and tools available for Characterization & Evaluation of *Malus*/*Pyrus* genetic resources (Pome Fruit C&E)

1 January 2017 – 31 December 2022

Marc Lateur (Coordinator of the project), Matthew Ordidge (Co-coordinator), Charles-Eric Durel (Coordinator of Objective 2), Monika Höfer, Caroline Denanoé, Enrique Dapena De La Fuente, Mauro Bergamaschi, Frida Carka, Laila Ikase, Carlos Miranda Jiménez, Pilar Errea, Henryk Flachkowsky, Gordana Đurić, Gregor Osterc, Larisa Gustavsson, Arnaud Guyader, Inger Hjalmarsson, Grzegorz Hodun, Ildikó Király, Jorge Urrestarazu Mirela, Kajkut Zeljković, Hedi Kaldmäe, Markus Kellerhals, Dorota Kruszyńska, Ounars Lacis, Măd lina Militaru, Dominique Mingeot, Nikola Miloš, František Paprštein, Dag Rasen, Alain Rondia, Jiri Sedlak, Thomas Solinopoulos, Kristine Volens, Zsolt Szani

May 2023


ECPGR Activity Grant Scheme – Fifth Call, 2017

Activity Report

Testing, Use and Alignment of genetic data to distinguish unique and characterized accessions in Prunus (Prunus Alignment)

1 January 2018 - 30 April 2020

Matthew Ordidge, Gunārs Lācis, Marine Delmas, Monika Höfer, Pavlina Drogoudi, Stein Harald Hjeltnes, Hedi Kaldmäe, Torben Toldam-Andersen, Zsuzsanna Békefi, Felicidad Fernández Fernández, Gabriella Sonnante, Hilde Nybom, Dunja Kazija, Daniela Giovannini

Participants in the "Prunus Alignment" meeting in Athens © P. Drogoudi

January 2021

Background (ECPGR Grant Scheme)

ECoHisPy (2014/15)

Expected products/results - 100 historical European pear cultivars verified with common phenotypic and genotypic data and uploaded in the EURISCO catalogue with the AEGIS flag.

PRUNDOC (2015/16)

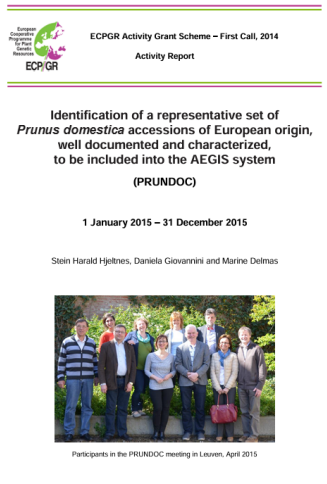
The total number of accessions described was slightly lower than the expected 100: at time of finalising this report, 85 accessions were verified, characterized according to FPDs and prepared for uploading into the European Prunus Database and in EURISCO

EU.Cherry (2016/17)

Action 1. Provide harmonized characterization data of European sweet cherry accessions to be included in EURISCO

Action 2. Prepare transfer of Prunus passport data and Prunus C&E data experience from the EPDB to EURISCO

ECP/GR


ECPGR Activity Grant Scheme – First Call, 2014

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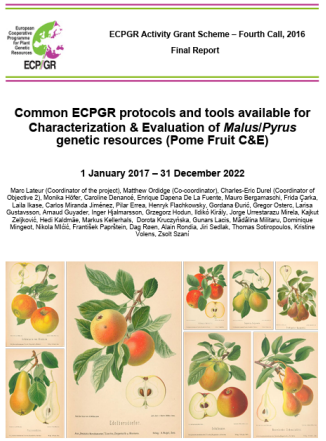
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'Büttners Rote Knorpelkirsche' © M. Höfer, JKI

September 2019

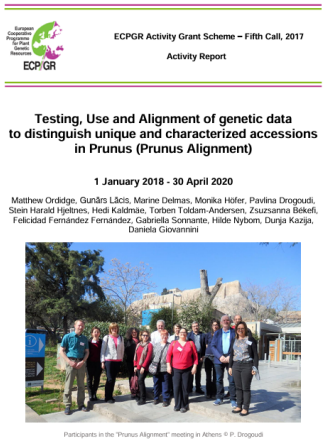

ECPGR Activity Grant Scheme – Fourth Call, 2016

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May 2023


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Participants in the "Prunus Alignment" meeting in Athens © P. Drogoudi

January 2021

Background (ECPGR Grant Scheme)

Pome Fruit C&E (2017/18)

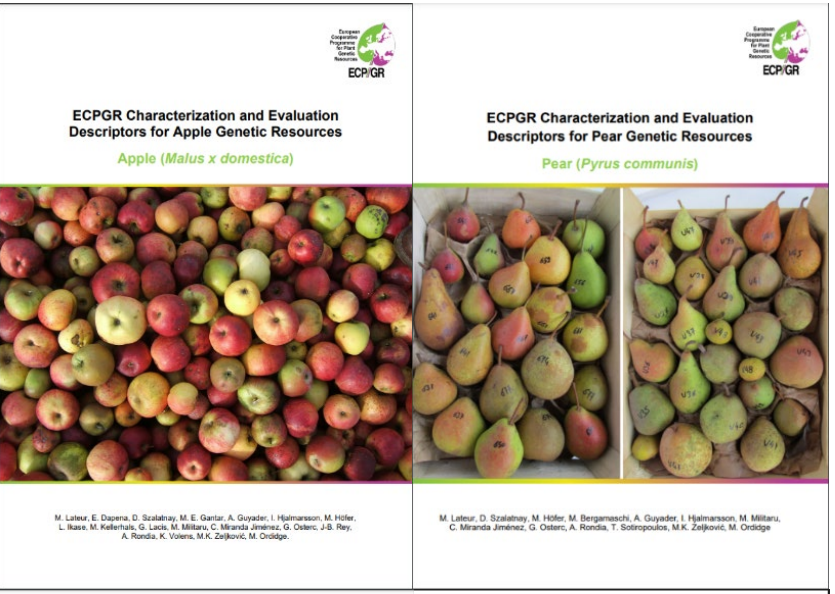
(i) The first objective is to finalize and implement the ECPGR adopted "Characterization and Evaluation descriptors for apple and pear biodiversity"; Compilation of data and adapting method and/or descriptors in line with problems encountered (M13). Adopting final version by the WG, editing documents in electronic version and make it available on the ECPGR and EURISCO websites

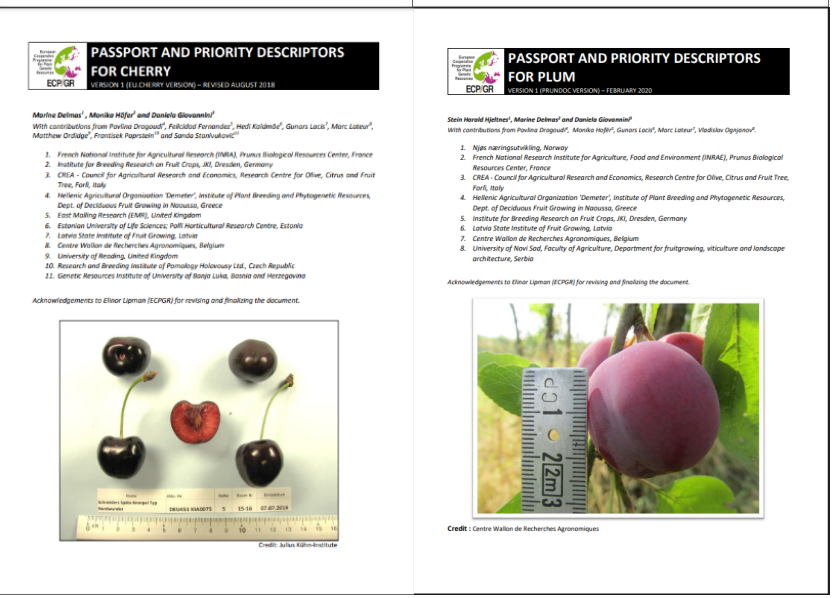
(ii) The second objective is to harmonize SSR data across already genotyped collections of European pear in order to make them available for users and EURISCO.

Prunus Alignment (2018/20)

Additional characterization data for the accessions that were not genotyped have been submitted to the Prunus DB manager.

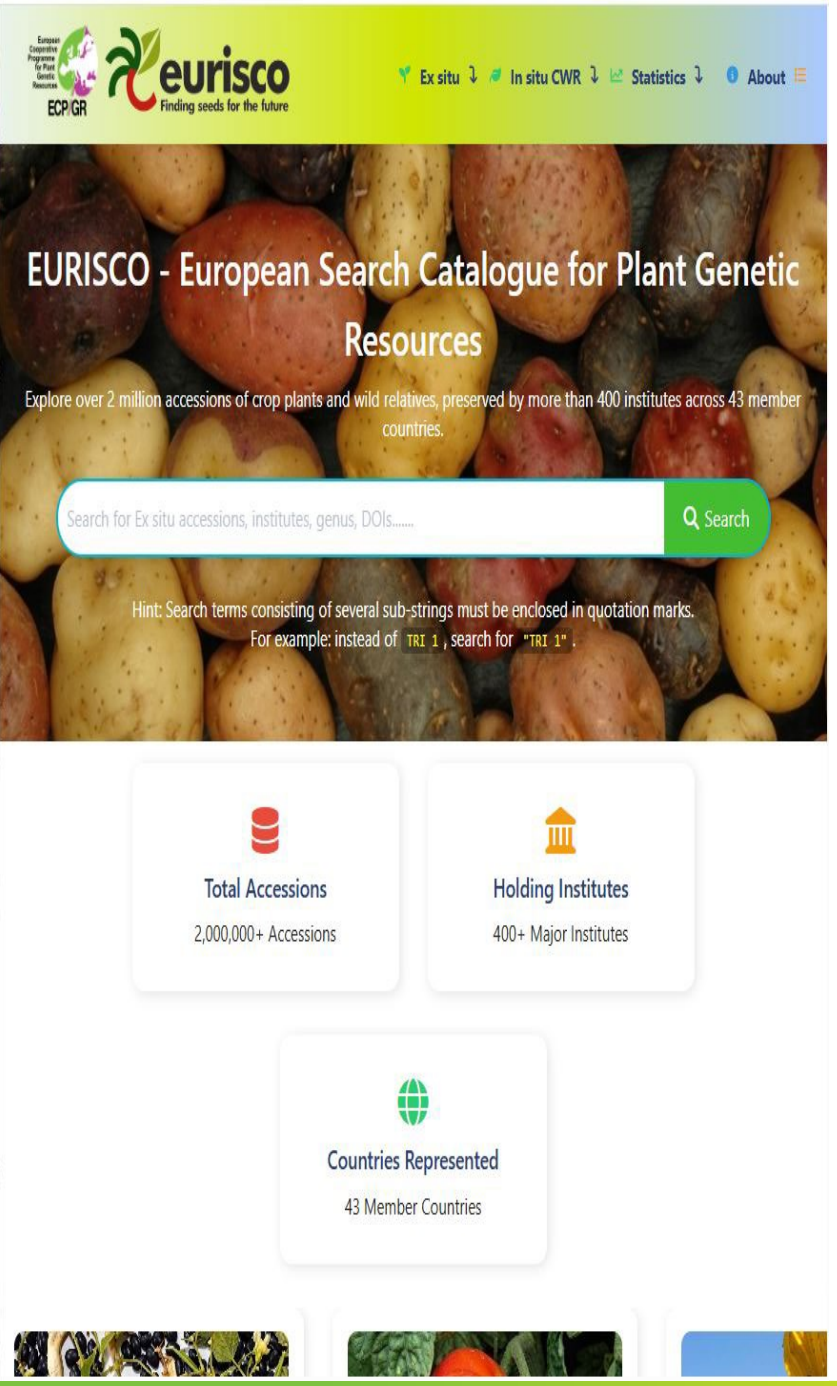
ECP/GR





Background (C&E descriptors)

- Developed (and tested) as part of recent ECPGR projects
- Descriptors prioritized by the Working Groups
- Data collected over many years in some cases



Background (EURISCO)

- Initially developed 2001-2003
- Based on National Focal Points and National Inventories
- Held C&E data since ~2015
- At the time of proposal (September 2021)
  - 16K C&E datapoints for *Malus* (all CZE)
  - 2K C&E datapoints for *Pyrus* (all CZE)
  - 13K C&E datapoints for *Prunus* (CZE and LVA)

ECP/GR

Background (SSR data)

- ECPGR fingerprinting standards established ~2006
- Dataset and alignment expansion (led by INRAE) through EU and ECPGR projects
- Potential for *Malus* (MUNQ), *Pyrus* (PUNQ) and Cherry (CHUNQ) genotype codes to support AEGIS

Molecular characterization of an extensive set of European pear accessions with SSR markers

Caroline Denancé[1], Matthew Ordidge[2], Marc Lateur[3] & Charles-Eric Durel[1]

[1] IRHS, INRA, ACO, UA, 42 Rue Georges Morel, 49070 Beaucouzé, France – caroline.denance@inra.fr
[2] University of Reading, School of Agriculture, Policy and Dev., Whiteknights, PO Box 237, RG6 6AR Reading, United Kingdom
[3] CRA-W, Centre Wallon de Recherches Agronomiques, Plant Breeding & Biodiversity, Rue de Liroux, 4 - 5030 Gembloux, Belgium

One of the major objectives of the ECPGR-funded project "PomeFruit_C&E" [1] is to promote the molecular characterization of European pear collections and proceed to the standardization of the SSR data across collections. Such standardization is required to compare the pear accessions at the European scale and beyond.

Material & Methods

- 19 SSR (11 SSR of ECPGR set [1] + 8 additional SSR)
- 2,593 accessions originating from 20 European countries newly genotyped (green dot)
- Development of dedicated allelic correspondence tables for 2,374 accessions originating from 7 European countries previously genotyped (red dot) [2] [3] [4] [5] [6]



MultiPlex	Marker	LG	Dye	ECPGR set
GP_MP01	EMPc11	11	FAM	x
	CH01f07a	10	NED	x
	CH02b10	2	VIC	x
	CH01h01	17	NED	
	CH05f06	5	PET	
GP_MP02	CH05c06	16	NED	x
	GD147	13	PET	x
	CH01f03b	9	FAM	
	CH02c11	10	NED	
	CH01h10	8	VIC	
GP_MP03	CH03d12	6	NED	x
	EMPc117	7	PET	x
	CH01d08	15	VIC	x
	GD142	9	FAM	
	CH-VF1	1	VIC	
GP_MP04	CH04e03	5	FAM	x
	CH01d09	12	NED	x
	CH03g07	3	VIC	x
	CH04c07	14	VIC	

Table 1. SSR markers used for fingerprinting with linkage group location and multiplex assignment. PCR conditions are available upon request

Country	Institut Acronym	Nb acc.
AL	ABG	10
BA	UNSA	34
	UNIBL-GRI	17
BE	CRA-W	152
BY		9
CH	Fructus	179
CZ	RBIPH	20
DE	JKI	122
DK	UCPH	28
ES	UPNA	156
FI	LUKE	29
FR	INRA	1,067
	UPF	1,035
GB	UoR	549
	FruitID	743
	HHLBT	312

Country	Institut Acronym	Nb acc.
GR	NAGREF	10
HR	HCPHS	10
HU	NARIC	8
IE	ISSA	25
IT	UNIBO	56
	CREA-OFA RM	24
LT	LAMMC	20
LV	LUU	60
NO	NNU	8
PL	InHort	10
RO	RIFG	32
RU	NCRRIHV	48
	VNIISPK	32
SI	UNI-LJ	9
SK	VURV	6
SW	SLU	136
UA	IH NAAS	11

Table 2. List of the collections with numbers of accessions genotyped

Results & Discussion

- 4,912 accessions with at least 9 standardized SSR
- 2,206 unique genotypes (i.e., distinct SSR profiles)
- PUNQ code (Pyrus UNiQue genotype code) assigned for each genotype in order to better characterize any new accession according to this standardized dataset.

Next step

- Analysis of genetic structure
- Analysis of relationship inferences

References: [1] http://www.ecpgr.cgiar.org/working-groups/malus/pyrus/pomefruit-ce/ // [2] Evans et al. (2009) Harmonising fingerprinting protocols to allow comparisons between germplasm collections - *Malus* // *Pyrus*. Acta Hortic // [3] Fernández-Fernández et al. (2010) Final Report of Defra project GC0140 'Fingerprinting the National Apple and Pear Collections'// [4] Sehic et al. (2012) Genetic diversity in a collection of European pear (*Pyrus communis*) cultivars determined with SSR markers chosen by ECPGR. Sci Hortic // [5] Puskás et al. (2015) Molecular and flow cytometric evaluation of pear (*Pyrus* L.) genetic resources of the German and Romanian national fruit collections. Genetic Resources and Crop Evolution. // [6] Urrestarazu et al. (2015) Evaluating the influence of the microsatellite marker set on the genetic structure inferred in *Pyrus communis* L. PLoS ONE // [7] http://www.fruitid.com/#main

XV EUCARPIA Fruit Breeding and Genetics Symposium, Prague, 3-7 June 2019

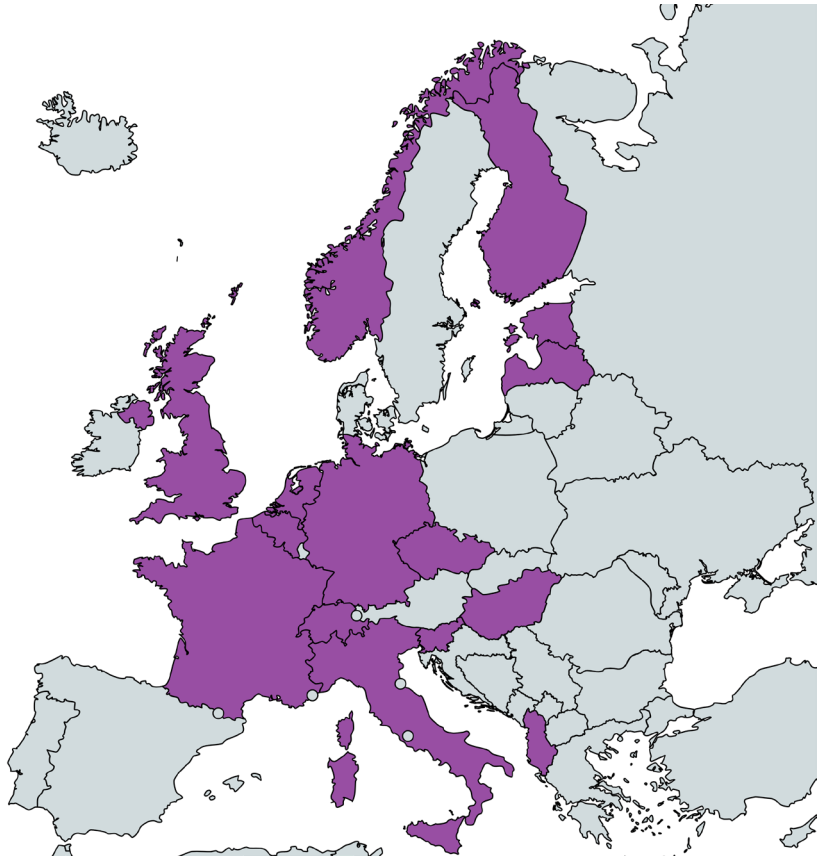
ECP/GR

Three main objectives

- Assessment of the Central Crop Databases (CCDBs)
- Assessment of publicly available C&E data and the accessions missing from EURISCO
- Assessment of the CHUNQ/MUNQ/PUNQ data

ECP/GR

Activity partners



Created with mapchart.net

ECPGR-funded

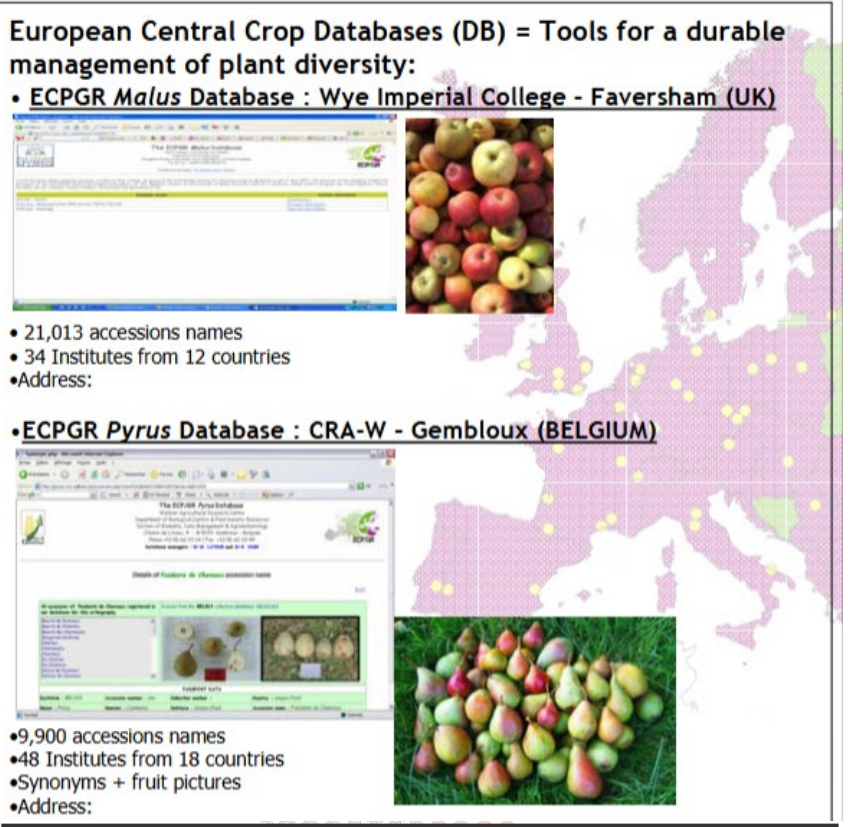
- UK
- Belgium
- Switzerland
- Germany
- Hungary
- Netherlands
- Norway
- Italy
- Czech Republic
- France
- Albania
- Latvia
- Finland
- Slovenia
- Estonia

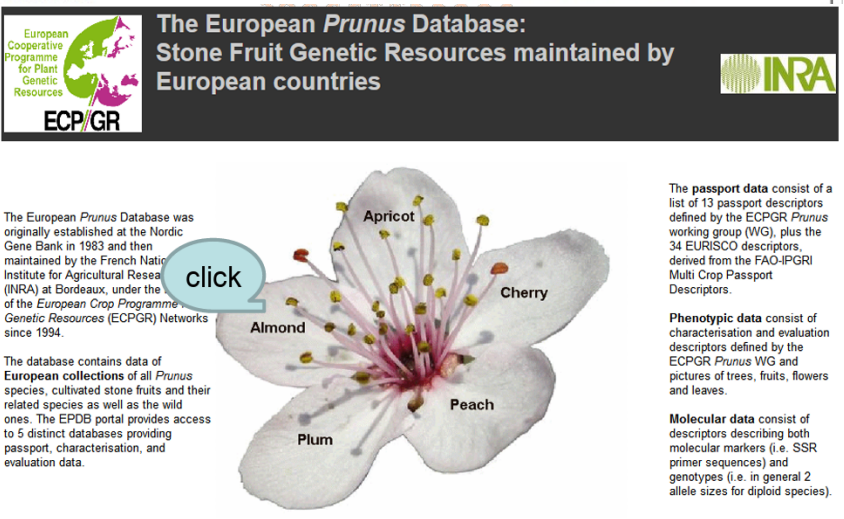
Self-funded

- Germany
- France
- Switzerland

- *Malus*/*Pyrus*
- *Prunus*

ECP/GR

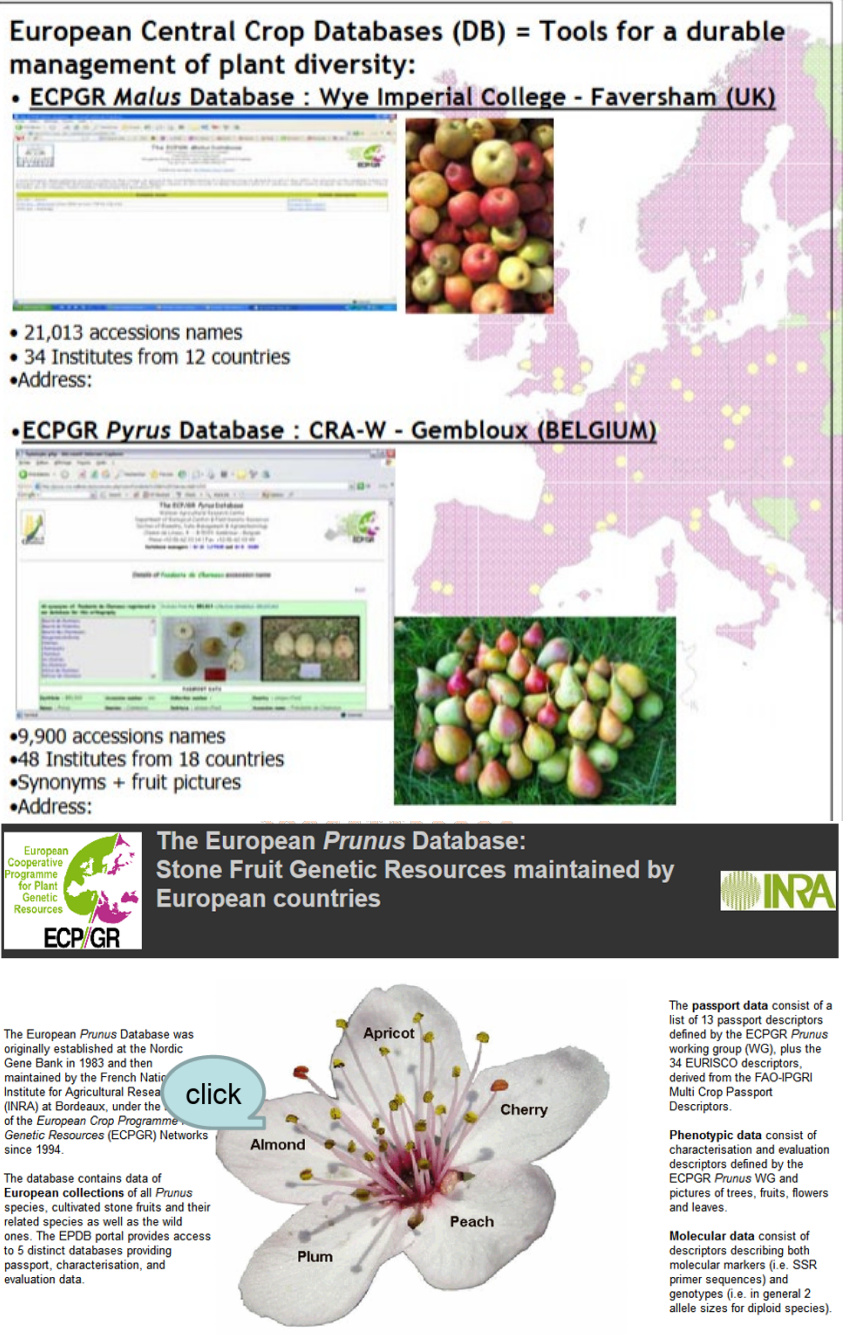




Assessment of the Central Crop Databases

- *Malus* and *Pyrus* were deemed to be outdated
  - No recent updates
  - Not available online
  - Largely accession listings

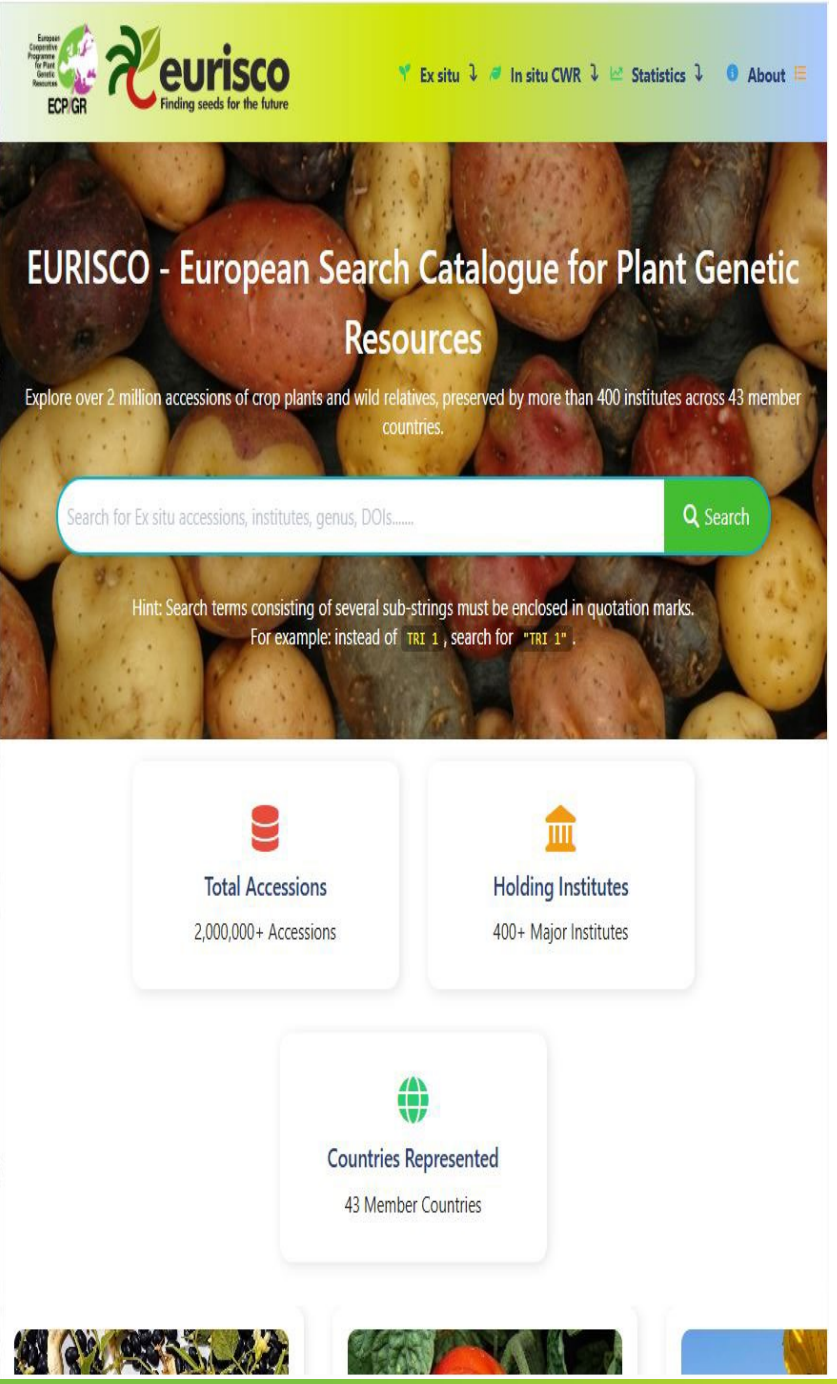
ECP/GR



Assessment of the Central Crop Databases

- *Prunus*DB was considered in more detail
  - Countries represented in the project (~97K datapoints / 7K accessions)
  - Other ECPGR member countries (~47K datapoints / 3K accessions)
  - Countries [currently] outside of ECPGR (~50K datapoints / 4K accessions)
  - The majority of data points were passport data
- Direct comparison to EURISCO was complicated by inconsistencies (e.g. accession no.)
- Various reasons for data not being traceable (project and non-project countries)
  - Collections maintained only to support local breeding program
  - Data had been superseded by move to GRIN-Global
  - Data are held awaiting data sharing agreement
  - Merger or closure of institutes and closure of collections

ECP/GR



Assessment of accessions missing from EURISCO

- Small scale
  - 35 pear accessions (FIN); 38 apple and pear (ITA)

- National scale
  - Re-organization of a Dutch Heritage Collection (NLD)
  - Policy change (to include non-Estonian accessions) (EST)
  - Complete reorganization of data (BEL)
  - Preparation of new data for upload (SVN)
  - Addition of Plant Heritage and discussion with Botanic Gardens (UK)

ECP/GR

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	GD147	13	PET	x
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GP_MP03	CH03d12	6	NED	x
	EMPc117	7	PET	x
	CH01d08	15	VIC	x
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XV EUCARPIA Fruit Breeding and Genetics Symposium, Prague, 3-7 June 2019

Assessment of CHUNQ/MUNQ/PUNQ data

- 226/289 CHUNQ codes appear to be represented within current EURISCO listings.
  - Another 19 are listed through extension by name
  - The majority of codes not represented arose from accessions in France (16), Norway and Sweden (14)and so have the potential to be included within EURISCO.
- Accessions representing 48 CHUNQ codes are at least duplicated within EURISCO.
  - 28 are present at least twice, twelve are present at least three times, six are present at least four times and two are present in at least six countries.
- Direct comparison to EURISCO was complicated by inconsistencies (e.g. accession no.)

ECP/GR

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GP_MP03	CH03d12	6	NED	x
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	CH01d08	15	VIC	x
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GP_MP04	CH04e03	5	FAM	x
	CH01d09	12	NED	x
	CH03g07	3	VIC	x
	CH04c07	14	VIC	x

Table 1. SSR markers used for fingerprinting with linkage group location and multiplex assignment. PCR conditions are available upon request



Country	Institut Acronym	Nb acc.
AL	ABG	10
BA	UNSA	34
	UNIBL-GRI	17
BE	CRA-W	152
BY		9
CH	Fructus	179
CZ	RBIPH	20
DE	JKI	122
DK	UCPH	28
ES	UPNA	156
FI	LUKE	29
FR	INRA	1,067
	UPF	1,035
GB	UoR	549
	FruitID	743
	HHLBT	312

Country	Institut Acronym	Nb acc.
GR	NAGREF	10
HR	HCPHS	10
HU	NARIC	8
IE	ISSA	25
IT	UNIBO	56
	CREA-OFA RM	24
LT	LAMMC	20
LV	LUU	60
NO	NNU	8
PL	InHort	10
RO	RIFG	32
RU	NCRRIHV	48
	VNIISPK	32
SI	UNI-LJ	9
SK	VURV	6
SW	SLU	136
UA	IH NAAS	11

Table 2. List of the collections with numbers of accessions genotyped

Results & Discussion

- 4,912 accessions with at least 9 standardized SSR
- 2,206 unique genotypes (i.e., distinct SSR profiles)
- PUNQ code (Pyrus UNiQue genotype code) assigned for each genotype in order to better characterize any new accession according to this standardized dataset.

Next step

- Analysis of genetic structure
- Analysis of relationship inferences

References: [1] http://www.ecpgr.cgiar.org/working-groups/malus/pyrus/pomefruit-ce/ // [2] Evans et al. (2009) Harmonising fingerprinting protocols to allow comparisons between germplasm collections - *Malus* / *Pyrus*. Acta Hortic // [3] Fernández-Fernández et al. (2010) Final Report of Defra project GC0140 'Fingerprinting the National Apple and Pear Collections'// [4] Sehic et al. (2012) Genetic diversity in a collection of European pear (*Pyrus communis*) cultivars determined with SSR markers chosen by ECPGR. Sci Hortic // [5] Puskás et al. (2015) Molecular and flow cytometric evaluation of pear (*Pyrus* L.) genetic resources of the German and Romanian national fruit collections. Genetic Resources and Crop Evolution. // [6] Urrestarazu et al. (2015) Evaluating the influence of the microsatellite marker set on the genetic structure inferred in *Pyrus communis* L. PLoS ONE // [7] http://www.fruitid.com/#main

XV EUCARPIA Fruit Breeding and Genetics Symposium, Prague, 3-7 June 2019

Assessment of CHUNQ/MUNQ/PUNQ data

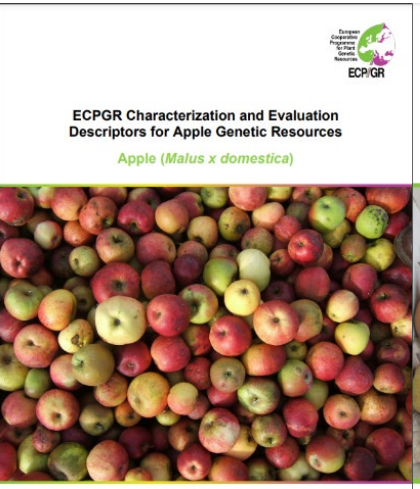
- 10,049 MUNQ codes and 3,848 PUNQ codes have been allocated.
- Accessions held by project partners and listed in EURISCO, represented 3,880 MUNQ codes and 885 PUNQ codes.
  - 6,169 MUNQ codes are not yet confirmed to be represented in EURISCO
  - 2,963 PUNQ codes are not yet confirmed to be represented in EURISCO
- 573 alleles were identified within the MUNQ dataset; 836 alleles were identified within the PUNQ dataset.
  - 153 MUNQ alleles were not confirmed to be represented within EURISCO (of these, 69 were unique and 84 were 'very rare')
  - 307 PUNQ alleles were not confirmed to be represented within EURISCO (of these, 103 were unique, 203 were 'very rare' and one was 'rare')
- All common alleles in the MUNQ and PUNQ systems were shown to be represented within EURISCO.

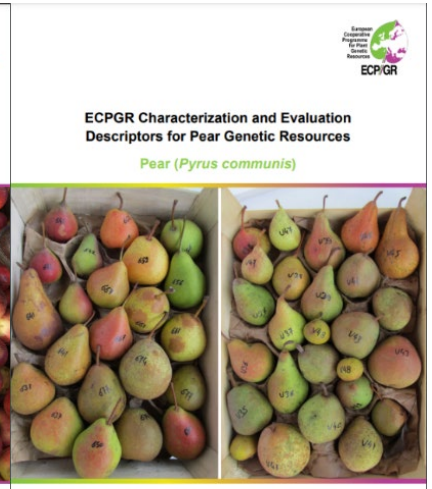
ECP/GR

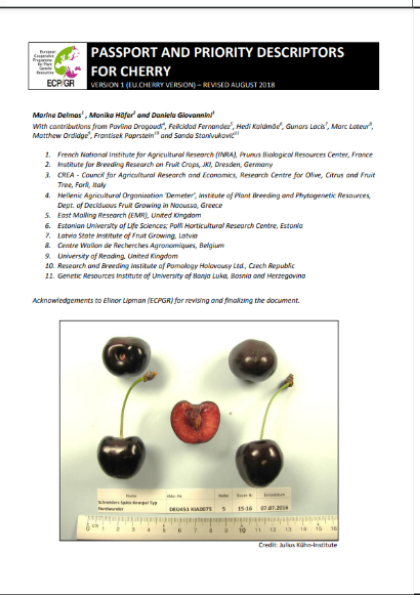


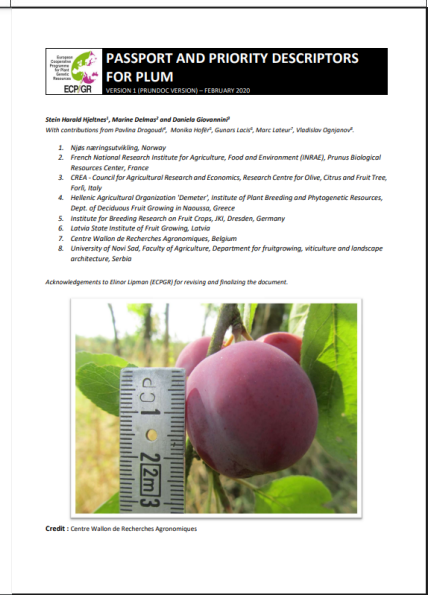
Assessment of publicly available C&E data

Crop	Country	Accessions	Descriptors	Datapoints (approximated due to missing data)
Almond	ITA	8	13	104
Apple	HUN	27	5	135
	ALB	11	47	517
	ITA	76	8	608
	DEU	579	3	1,737
	NLD	102	23	2,000
	LVA	144	33	4,752
	GBR	2002	25	31,550
	CHE	~5600	60*	220,000
			Total	**261,299**
Cherry	ALB	13	22	286
	DEU	12	25	300
	LVA	15	33	495
	ITA	77	8	616
	HUN	412	5	2,060
	GBR	349	14	4,365
	CHE	~970	56*	33,000
			Total	**41,122**





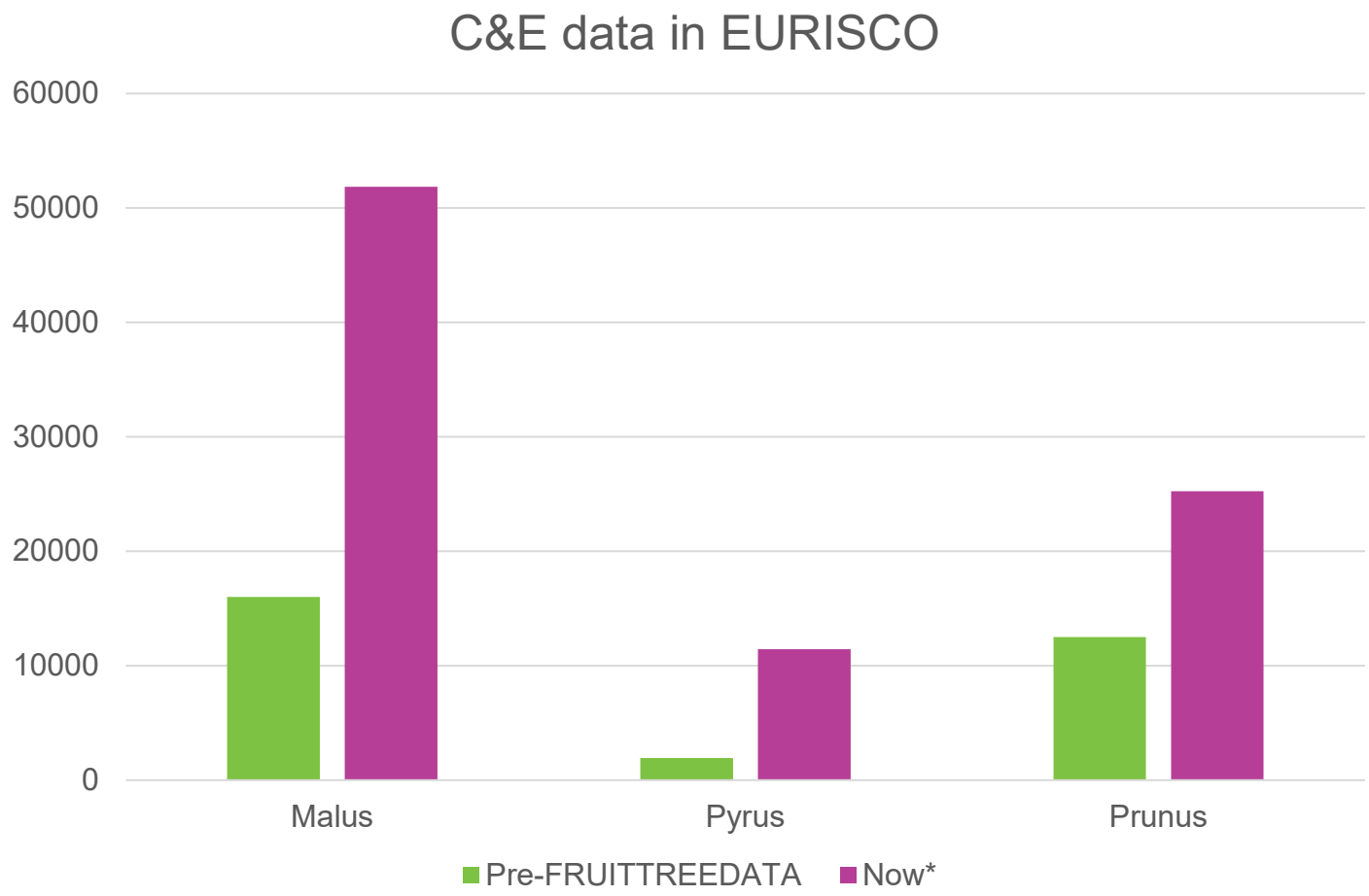




Assessment of publicly available C&E data

Crop	Country	Accessions	Descriptors	Datapoints (approximated due to missing data)
Peach	HUN	150	5	750
	ITA	66	24	1,418
			Total	**2,168**
Pear	DEU	11	16	176
	ALB	14	43	602
	HUN	153	5	765
	GBR	522	25	8,778
	CHE	~2800	59*	130,000
			Total	**140,321**
Plum	DEU	7	18	126
	ITA	33	9	297
	ALB	25	23	570
	HUN	310	6	1,860
	GBR	326	15	4,746
	CHE	~840	56*	37,000
			Total	**44,599**
Prunus spp.	ITA	31	6	186

Improvement of data





Recommendations

- CCDBs be recognised as formally decommissioned from this point onwards
  - Potentially consider options for SSR/genetic fingerprint and image data
  - Some potential further checks for partner and non-partner countries

- Improvement is needed in the linkage between entries in the MUNQ/PUNQ/CHUNQ datasets and EURISCO
  - More comprehensive analysis including all EURISCO entries (analysis was limited to partner countries)

- The range of material within the MUNQ system relative to (known) EURISCO holdings should be considered further
  - Noting that the MUNQ and PUNQ systems are known to include a range of seedlings

ECP/GR



European Cooperative Programme for Plant Genetic Resources
ECP/GR

ECPGR Activity Grant Scheme – Phase X – 5th Call

Activity Report

Improvement of Fruit Tree Data Inclusion in EURISCO

(FRUITTREEDATA)

Period (01/04/2024 – 31/11/2025)

Matthew Ordidge, Mauro Bergamaschi, Andrea Patocchi, Christina Kägi, Monika Höfer, Zsuzsanna Békefi, Sámuel Szilágyi, Willem van Dooijeweert, Stein Harald Hjeltnes, Boris Krska, Jiri Sedlak, Hélène Muranty, Caroline Denancé, Frida Carka, Marine Delmas, Gunars Lacis, Tuuli Haikonen, Gregor Osterc, Hedi Kaldmäe, Marc Lateur, Daniela Giovannini

Recommendations

- Members remain of the view that a clonal identifier on the lines of the MUNQ/PUNQ/CHUNQ coding would be a useful character to include within EURISCO.
  - However, the method for including this remains unclear.
  - We would expect that an equivalent might also be useful for the other clonal crops.

- Suggest that ECPGR/EURISCO continues to consider the most appropriate ways to handle data from multi-year experiments.
  - These are potentially of more relevance to the vegetatively propagated and/or perennial crops where measurement of characters over multiple seasons as part of a single ‘experiment’ is often standard.

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THANK YOU