

Prunus Alignment – integrating data for European plum and cherry germplasm



Matthew Ordidge¹ | Gunārs Lācis² | Marine Delmas³ | Monika Höfer⁴ | Pavlina Drogoudi⁵ | Stein Harald Hjeltnes⁶ | Hedi Kaldmäe⁷ | Torben Toldam-Andersen⁸ | Zsuzsanna Békefi⁹ | Felicidad Fernández Fernández¹⁰ | Gabriella Sonnante¹¹ | Hilde Nybom¹² | Dunja Kazija¹³ | Daniela Giovannini¹⁴

Introduction

‘Prunus Alignment’ is a collaborative European project aimed at aligning genetic resources of plum and cherry towards the European Collaborative Program for Plant Genetic Resources (ECPGR) AEGIS concept of ‘A European Genebank Integrated System’. The project aims to build upon progress made in the ECPGR PRUNDOC and EU.CHERRY projects by expanding on the SSR analysis of accessions of local and nationally important plum cultivars, and aligning national datasets of SSR for cherry germplasm collections.

SSR analysis of plum accessions

Plum accessions were first analysed by SSR using capillary electrophoresis, in order to identify and confirm unique genotypes for potential inclusion in the European collection.

Accessions were selected based on prior identification in the ECPGR PRUNDOC project and these were supplemented with newly identified accessions from Estonia, Denmark, Hungary and the UK. A detailed analysis of the findings has been submitted for publication (see below). Loci and samples used for analysis are listed below.

Partner	Samples Analysed		Total	Locus	Size range (bp)
	PRUNDOC	Prunus Alignment			
France	2	16	18	UDP98-407	157-231
Germany	4	3	7	PacA 33	169-254
Greece	4	3	7	CPSTC 026	165-216
Italy	4	10	14	BPPCT 040	118-154
Latvia	3	6	9	BPPCT 007	121-159
Norway	3	2	5	BPPCT 014	186-289
Sweden	5	1	6	BPPCT 034	213-277
Belgium	7	-	7	UDP96-005	92-169
Serbia	4	-	4		
Slovenia	4	-	4		
Estonia	-	5	5		
Denmark	-	5	5		
Hungary	-	6	6		
UK	-	7	7		

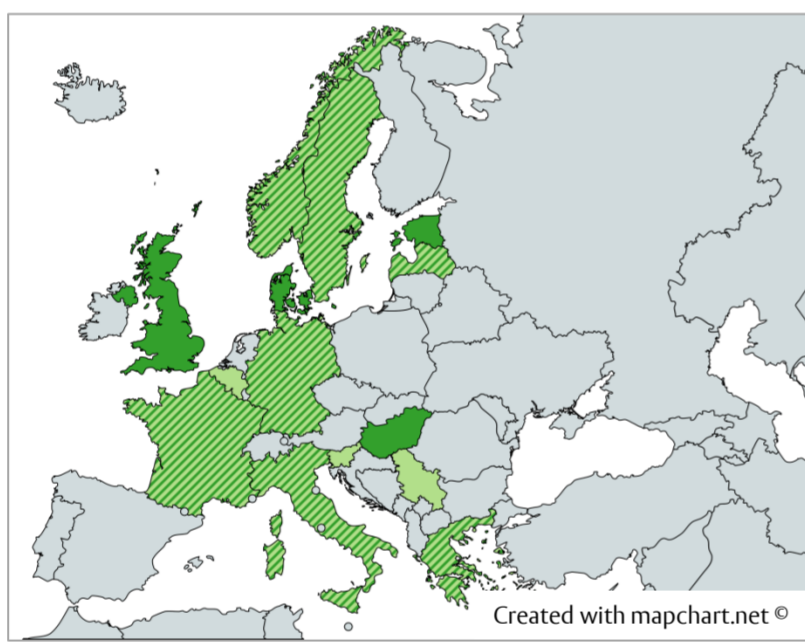


Figure 1. Map showing the origin of accessions. Countries sampled only in PRUNDOC (light green), countries sampled further in Prunus Alignment (striped green), and countries sampled only in Prunus Alignment (dark green) are highlighted.

Acknowledgements

- We would like to specifically thank Jasna Sehic for her technical work in the analysis of SSR profiles.

SSR analysis of plum accessions using High Resolution Melting

A subset of samples will be analysed further using high resolution melt profiles, to evaluate the possibility of using this technique to differentiate genotypic (SSR) profiles within ECPGR.

The main subset of 60 samples will be analysed by HAO-Demeter (in Greece) and a further subset of these will be replicated across labs in Italy (IBBR-CNR and CREA), Latvia and the UK with a view to testing the technique as a tool for germplasm management. Loci used for analysis and partners involved in testing are listed below.

Locus	Size	Partner	Samples	Analysis/Replication
BPPCT034	228	Greece	60	Analysis
BPPCT037	155	Italy ⁽¹¹⁾	24	Replication
PceGA34	155	Italy ⁽¹⁴⁾	24	Replication
PS12A02	200	Latvia	24	Replication
UCD-CH17	188	UK	24	Replication
UDAp-404	181			
UDP96-001	120			

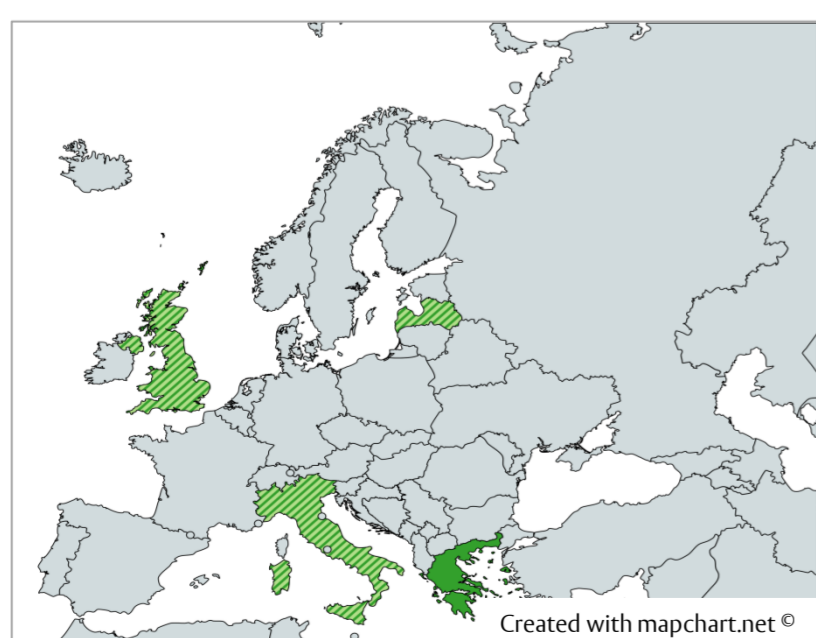


Figure 2. Map showing the distribution of analysis. All samples will be initially analysed in Greece (dark green), followed by replication in partner countries (striped green) as highlighted.

Acknowledgements

- We would like to specifically thank Dr Ioannis Ganopoulos for his technical guidance on this work.

Partners

- University of Reading, School of Agriculture, Policy and Development, Whiteknights, Reading, UK, E-mail: m.ordidge@reading.ac.uk
- Institute of Horticulture, Latvia University of Life Sciences and Technologies, Graudu 1, 3701 Dobeles, Latvia
- INRA-Unité Expérimentale Arboricole, Domaine de la Tour de Rance, 47320 Bourran, France
- Julius Kühn-Institute, Institute for Breeding Research on Fruit Crops, Pillnitzer Platz 3a, D-01326 Dresden, Germany
- HAO-Demeter, Inst. of Plant Breeding and Genetic Resources, 38 R.R. Station, 59035 Naoussa, Greece
- Graminor, Njøsavegen 5, 6863 Leikanger, Norway
- Estonian University of Life Sciences, Polli Horticultural Research Centre, Karski-Nuia, 69104 Viljandimaa, Estonia
- The University of Copenhagen, Dept of Agricultural Sciences, Hjbakkegrd Allé 21, 2630 Taastrup, Denmark
- NARIC, Department of Fruit Science, Park u. 2, H-1225 Budapest, Hungary
- NIAB East Malling Research, New Road, ME19 6BJ East Malling, United Kingdom
- Institute of Biosciences and Bioresources, CNR, Via Amendola 165A, 70126 Bari, Italy
- Swedish University of Agricultural Sciences, Dept. of Plant Breeding, Fjälkestadvägen 459, 29194 Kristianstad, Sweden
- Croatian Agency for Agriculture and Food, Center of Pomology, Gorice 68b, 10000 Zagreb, Croatia
- CREA, Research Centre for Olive, Citrus and Tree Fruit, Via la Canapona 1 bis, 47121 Forlì, Italy

Collaborators

- Marc Lateur, Centre Wallon de Recherches Agronomiques (CRA-W), Department of Life Sciences, Breeding & Biodiversity Unit, Bâtiment Emile Marchal, Rue de Liroux 4, 5030 Gembloux, Belgium

Alignment of SSR data for national cherry collections

SSR data, using ECPGR recommended primers, for cherry from national datasets produced in Germany, Italy, Sweden, the UK, France and Switzerland will be aligned. By selecting additional standard accessions across these collections and genotyping at the site of analysis of the EU.CHERRY dataset, alignment with these international data will also be possible. Loci recommended by EU.CHERRY are listed below.

Locus	Size range (bp)	Partner	Samples
EMPa002	100-132	Germany	100
CPSTC038	185-205	Italy	150
CPCT022	204-228	Sweden	20
BPPCT034	210-255	UK	300
CPCT006	173-202	France	~200
PAV-Rf-SSR	351-361	Switzerland	~400
EMPaS02	124-156	EU.Cherry	324
BPPCT037	117-170		
EMPaS06	226-278		
EMPa004	178-206		
EMPa017	227-250		
EMPa018	95-106		
EMPaS12	100-149		
EMPaS14	170-216		

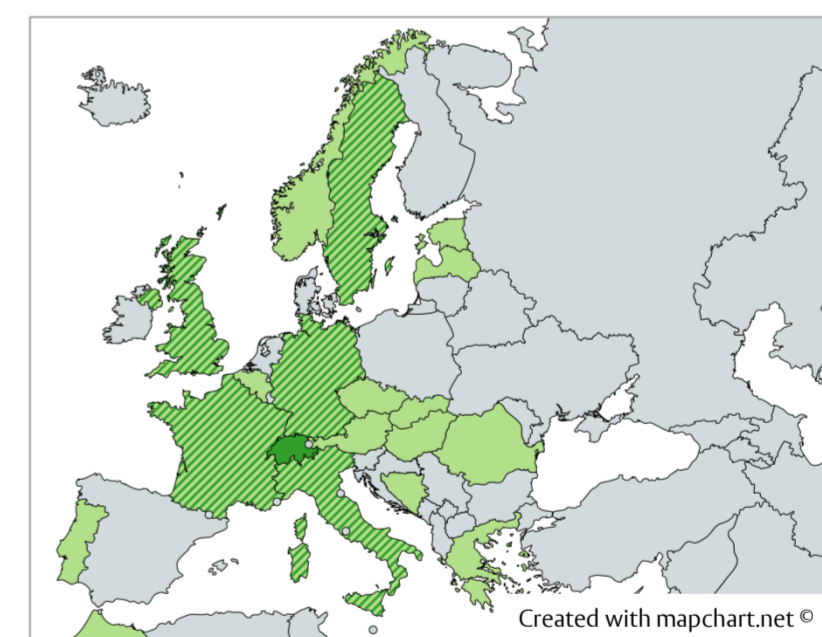


Figure 3. Map showing the origin of analysed accessions. Countries with data supplied from EU.CHERRY (light green), countries with data supplied only from national programs (dark green), and countries with data from both national programs and EU.CHERRY (striped green) are highlighted.

Acknowledgements

- We would like to thank Stephanie Mariette and Markus Kellerhals for collaborating to share French and Swiss national datasets with the project.

Phenotypic descriptor data for plum accessions and all SSR data will be submitted to the ECPGR Prunus database and formatted for future inclusion in EURISCO.

Publications in progress

- Gasi, F.; Sehic, J., et al., Genetic assessment of the pomological classification of plum *Prunus domestica* accessions sampled across Europe (submitted).

References

- Merkouropoulos, G., Ganopoulos, I., et al., (2017) Combination of high resolution melting (HRM) analysis and SSR molecular markers speeds up plum genotyping: case study genotyping the Greek plum GeneBank collection. *Plant Genetic Resources: Characterization and Utilization* 15(4): 366-375.

Acknowledgements

- Financial support for the project was provided by ECPGR under the ECPGR Phase IX Grant Scheme.