

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

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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]

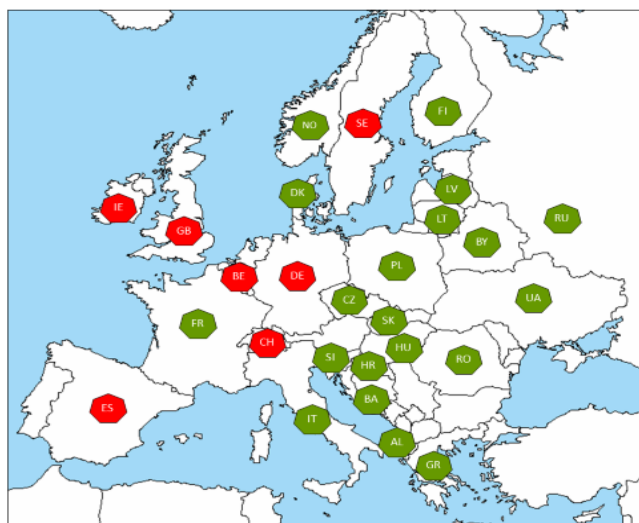
MultiPlex	Marker	LG	Dye	ECPGR set
GP_MP01	EMPc11	11	FAM	x
	CH01f07a	10	NED	x
	CH02b10	2	VIC	x
	CH01h01	17	NED	
GP_MP02	CH05f06	5	PET	
	CH05c06	16	NED	x
	GD147	13	PET	x
	CH01f03b	9	FAM	
GP_MP03	CH02c11	10	NED	
	CH01h10	8	VIC	
	CH03d12	6	NED	x
	EMPc117	7	PET	x
GP_MP04	CH01d08	15	VIC	x
	GD142	9	FAM	
	CH-Vf1	1	VIC	
	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

## 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.

**References:** [1] <http://www.ecpgr.cgiar.org/working-groups/maluspyrus/pomefruit-ce/> // [2] Evans et al. (2009) Harmonising fingerprinting protocols to allow comparisons between germplasm collections - *Malus / Pyrus*. *Acta Hort* // [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 Hort* // [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] Urrestazu 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>



Country	Institut Acronym	Nb acc.	Country	Institut Acronym	Nb acc.
AL	ABG	10	GR	NAGREF	10
BA	UNSA	34	HR	HCPHS	10
	UNIBL-GRI	17	HU	NARIC	8
BE	CRA-W	152	IE	ISSA	25
BY		9	IT	UNIBO	56
CH	Fructus	179			CREA-OFA RM
CZ	RBIPH	20	LT	LAMMC	20
DE	JKI	122	LV	LLU	60
DK	UCPH	28	NO	NNU	8
ES	UPNA	156	PL	InHort	10
FI	LUKE	29	RO	RIFG	32
FR	INRA	1,067	RU	NCRRIHV	48
	UPF	1,035			VNIISPK
GB	UoR	549	SI	UNI-LJ	9
	FruitID	743	SK	VURV	6
	HHLBT	312	SW	SLU	136
			UA	IH NAAS	11

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

## Next step

- Analysis of genetic structure
- Analysis of relationship inferences