

Pomefruit – C&E

SHORT PROGRES REPORT – 2017 Period

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Appropriate characterization and evaluation (C&E) of agronomic traits in fruit collections is fundamental to improved management and utilization of our genetic resources. Agreed methods, protocols and tools need to be continuously adapted to such objectives.

Objective 1: “ECPGR Methods and descriptor lists for the Characterization and Evaluation of apple and pear genetic resources” finalized, approved and widely disseminated through ECPGR and partners channels.

During the expert meeting in April 2017 at Gembloux a common characterization and evaluation test has been planned for studying the applicability/reproducibility of commonly defined first priority descriptors across a range of reference (and/or proposed reference) cultivars during this 2017 season.

A final work document adopted with specific extracts from the full descriptor lists which focus only on the descriptors agreed to be scored was sent to all partners during summer 2017.

A summary of the agreed recommendations on gathering standard photographs was also made available to all.

For **pear**, a total of 12 traits (5 for characterization and 7 for evaluation) and 18 descriptors need to be applied in each collection on a common set of 9 reference cultivars – if one or another was missing it was agreed that each collection should propose a replacement one (**Table 1**).

For **apple**, the same exercise also needs to be applied on 14 traits (5 for characterization and 9 for evaluation) with 20 descriptors on 11 reference cultivars (**Table 1**).

All data are not yet collected but with the atypical 2017 season with high frost conditions during the flowering period, on many collections, it has not been possible to perform a lot of observations. A common template still needs to be circulated in order to encode the data from each partner.

This exercise is planned to be carried out in the coming 2018 season.

Table 1. First priority descriptors for apple and pear to be applied in each collection on a common set of reference cultivars

PEAR First Priority Descriptors decided to be used in implementation test trial on 9 different common reference cultivars			
Type	TRAITS		# Descriptors
C	1.1	Flowering phenology	2
C	1.2	Time of fruit ripening for eating (harvest maturity)	2
C	1.3	Fruit shape	4
E	1.4	Relative fruit size	1
C	1.5	Depth of fruit stalk cavity	1
E	1.6	Average amount of over colour on fruit skin	1
E	1.7	Over colour of the fully mature fruit skin	1
E	1.8	Amount of russet on fruit skin - global estimated russet coverage on the skin, mostly the cheeks	1
E	1.9	Evaluation of the optimal fruit eating maturity stage	1
E	1.10	Global ratio between acidity and sweetness sensory perception	1
E	1.11	Overall global fruit quality appreciation	1
C	1.12	Standardized fruit pictures <i>in situ</i> and <i>ex situ</i>	2
			18
APPLE First Priority Descriptors decided to be used in implementation test trial on 11 different common reference cultivars			
Type	TRAITS		# Descriptors
C	1.1	Flowering phenology	2
C	1.2	Time of fruit ripening for eating (harvest maturity)	2
C	1.3	Fruit shape	4
E	1.4	Relative fruit size	1
C	1.5	Depth of fruit stalk cavity	1
E	1.6	Average amount of over colour on fruit skin	1
E	1.7	Over colour of the fully mature fruit skin	1
E	1.8	Amount of russet on fruit skin - global estimated russet coverage on the skin, mostly the cheeks	1
E	1.9	Fruit firmness sensory analysis	1
E	1.10	Global ratio between acidity and sweetness sensory perception	1
E	1.11	Flesh juiciness	1
E	1.12	Overall aroma sensory detection	1
E	1.13	Overall global fruit quality appreciation	1
C	1.14	Standardized fruit pictures <i>in situ</i> and <i>ex situ</i>	2

Objective 2: Harmonization and adjustment of SSR allele sizes over the various sources of data

- *Sharing of SSR data.*

On **Pear (Table 2)**: following active communication between partners, 10 institutes or associations decided to share their already historical available SSR data with an email bilateral scientific informal partnership agreement that commonly (1) protect data that are not yet published and (2) offer open access for all other data. An open access to such large diversity of data is a big achievement with added value for all but is only feasible thanks to the huge work of alignment and harmonization of data developed by the project.

A total of **4766** accessions – representing 11 collections from 8 countries - are potentially already shared with SSR data with at least 12 common ECPGR SSR marker set. This high number of already collected data is a good surprise because it is much higher than what we foresaw when writing the project.

Concerning the alignment basic step of the harmonization action, it was necessary to ask to eight partners to send to Angers new leaves of specific accessions in order to be newly genotyped – work is ongoing.

Analysis of already harmonized data started for seven collections with the view to track putative synonyms, duplicates and/or errors.

On **Apple (Table 2)**: the project makes advantage of starting with a big apple harmonized SSR database (2436 accessions) built by INRA in the framework of the EU *FruitBreedomics* project. Nevertheless, already three important new collections decided to share their data (1446 accessions) under the same partnership agreement decided for pear. Preliminary work of new genotyping of representative sample of accessions from those new collections was necessary to make the alignment possible in order to harmonize all data. Duplicates tracking is already achieved for the German collection and is still ongoing for the two others.

Table 2 - Global overview of the tasks achieved and planned concerning SSR data collection, alignment, harmonization and duplicates identification

Pear							
Country	Contact	Institute	SSR Data previously available (SSR in common with the 19 SSR PomeFruit Set)	Numbers of Accessions	Alignment thanks to new genotyping	Genotyping with PomeFruit SSR Set	Duplicates research
BEL	Dominique Mingeot, Marc Lateur	CRA-W	12 (11)	152	yes		in progress
GBR	Matthew Ordidge	NFC	12 (11)	548	yes		in progress
GBR	Peter Laws	responsible for FruitID.com	12 (11)	122	in progress		in progress
GBR	Jim Chapman	Hartpury Historic Land & Buildings Trust	12 (11)	297	in progress		in progress
ESP	Jorge Urrestarazu	University Navarra	25 (15)	156	yes		in progress
DEU	Henryk Flachowsky	JKI	11 (10)	122	in progress		in progress
SWE	Hilde Nybom	SLU	12 (11)	147	yes		in progress
CZE	Jiri Sedlak	RBIPH	no	20	-	yes	yes
LTU	Vidmentas Bendokas	LAMMC	no	20	-	yes	yes
DNK	Bjarne Larsen	University Copenhagen	no	28	-	yes	yes
HRV	Daniel Cicek	HCPHS	no	10	-	yes	yes
LVA	Gunars Lacis	Institute of Horticulture	no	15	-	yes	yes
ITA	Petra Engel	CREA	no	24	-	yes	yes
ITA	Luca Dondini	UNIBO	no	56	-	no	no
ITA	Thomas Letschka	Laimbourg	no	1	-	yes	yes
CHE	Markus Kellerhals	Agroscope/Fructus	16 (15)	1481	to be started in 2018		no
BIH	Fuad Gasi	University Sarajevo	11 (9)	64	in progress		no
FRA	Arnaud Guyader, Laurence Feugey	INRA	19 (19)	966	-	yes	yes
FRA	Denis Retournard	Union Pomologique de France	19 (19)	711	-	yes	yes
			Total	4940			
			Yes	4766	96.5%		
			No	174			
Apple							
Country	Contact	Institute	SSR Data previously available (SSR in common with the 16 PomeFruit SSR Set)	Numbers of Accessions	Alignment thanks to new genotyping	Genotyping with PomeFruit SSR Set	Duplicates research
FruitBreedomics	Caroline Denance & Charles-Eric Durel	INRA	16 (16)	2436		yes	yes
DNK	Bjarne Larsen	University Copenhagen	15 (15)	491	yes		in progress
DEU	Henryk Flachowsky	JKI	17 (12)	955	yes		yes
IRL	Pat	ISSA Orchard	12 (12)	436	yes		in progress
GBR	Matthew Ordidge	NFC	12 (12)	2163	yes		yes
			Total	6481			

Contacts were established with Nahla Bassil from the USDA Pear National Clonal Germplasm Repository at Corvallis for developing collaboration on SSR analysis. First data exchanged show many difficulties related to the capacity to compare data. It should be noted that INRA received aliquots of pear DNAs for ca. 600 accessions from Corvallis. On apple, data have been received from Gayle Volk (USDA Apple National Clonal Germplasm Repository at Geneva) and were analysed by INRA but unfortunately the number of common SSR being low, the common alignment is subject to caution.

- *The harmonized set of SSR marker data of apple and pear genetic resources will be made openly available and included in EURISCO.*

This deliverable is a key goal of this action. It is a dream that EURISCO could become the European open window for such important sharing of harmonized data, helpful firstly for the implementation of the EURISCO concept – helping to point out most unique material and most appropriate accessions, but also helpful for a large diversity of **users** such as curators, NGOs, scientists, students, breeders, nurseries, ECPGR National Coordinators,...

Active dialogue and interaction need to take place with Stephan Weise, EURISCO Coordinator, to organize such transfer of data to be hosted in EURISCO.