

## Summary of the expected outputs from ECPGR project ‘Prunus Align’

Data expected to be generated or aligned as part of the project are highlighted in green or pale green respectively below:

### Objectives 1/2 – Plum SSR Genotyping and F/SPD Characterization

**Background** - The following set of material was identified and characterized within the ECPGR PRUNDOC Project:

85 PRUNDOC accessions characterized with FPD				
Already genotyped within PRUNDOC*		Not Genotyped within Prundoc		
Held by Prunus Alignment Partner	Held by Non-Partner	Held by Prunus Alignment Partner	Held by Non-Partner	Genotyped previously
20	8	39	13	5

\*Note – 10 further accessions were genotyped in PRUNDOC but these were either not phenotyped or data were not available at the time of the project report (and 6 of these were from a non-partner in ‘Prunus Alignment’). 38 accessions were genotyped in total.

**Prunus Alignment Outputs** - The planned outputs from the current proposal are therefore:

	Further analysis of PRUNDOC material (categories as above)					48 new accessions held by Partners 7-10 (12 per partner)	Total
First Priority Descriptors	-	-	-	-	-	48	48
Second Priority Descriptors	18**	-	37**	-	-	-	55
Genotyping by SSR	-	-	39	-	-	20	59

\*\*Note – due to regeneration activity Partner 6 is unable to carry out further morphological characterization.

### Objective 3 – HRM Assessment on a Subset of Plum

The following number of accessions are planned to be included in the HRM testing and analysis:

Partner	Test samples (replicated by each partner)	Analysis only	Total
5	24	36	60
1	24	-	
2	24	-	
8	24	-	
12	24	-	

#### Objective 4 – Cherry SSR Genotyping for Alignment (of Existing National Datasets)

**Background** - The following set of accessions was genotyped within/alongside the ECPGR EU.CHERRY project:

	Samples supplied by 10 partner countries as part of EU.CHERRY	Samples supplied by 9 partner countries through COST FA1104	Total
Accessions genotyped	212	112	324

**Prunus Alignment Outputs** - The planned genotyping within the current proposal is therefore:

Partner/Collaborator	Accessions to be genotyped for alignment	Number of accessions already genotyped for which data can be made available (following alignment)
1	<b>140 accessions distributed between partners to allow the alignment of datasets</b>	~150
4		~100
8		~300
13		~20
INRA (FR)		~200
Agroscope (CH)		n/a (national dataset)