GENETIC DIVERSITY STUDIES IN SWEET CHERRY

COST-Cherry 114
WG 1 – Genetic Resources and Breeding, Genetics and Genomics
« Use of Molecular Markers for Diversity Studies » Meeting

TERESA BARRENECHE

03 – 05 March 2014 Budapest
Structure of the Presentation

- Presentation of the *Prunus* Genetic Resources Center (GRC)
- Genetic diversity studies
The Prunus Genetic Resources Center of Bordeaux

The Prunus GRC belongs to INRA’s network of GRC

**Objectives:**
- to collect
- to preserve
- to evaluate
- to distribute the GR of *Prunus* species

**What kind of GR ?**
- accessions of the cultivated species
- accessions of wild or related species to the cultivated ones
- « scientific GR »

The *Prunus* GRC counts with 1429 *Prunus* accessions, among them:
- 581 cherry accessions
  - 144 sweet cherries, 30 sour cherries and 9 *Prunus x gondouinii* accessions of the French National Cherry Collection

![Graph showing distribution of accessions by type](image-url)
The Prunus GRC of Bordeaux

Conservation in insect proof greenhouses:

For grafting at the introduction

For maintaining and delivery virus-free plant material

Conservation in orchards in 2 sites

Quality Management System

Methodology used: Process approach

Make easier:

Plant and information exchange

Long term preservation

Biological Resources Center (OECD)
The Prunus GRC of Bordeaux

Aim: reach a common management process by using the same database

Access public and private

✓ Passport data
✓ Phenotypic data
✓ Genotypic data (restricted access)
✓ Queries for material (2 shoots/accession)

http://urgi.versailles.inra.fr/siregal/siregal/

The Prunus GRC collections are integrated in the French and in the ECPGR conservation networks.
Our aim:

to evaluate the phenotypic variability and genetic diversity available in our collections

- to verify the identity of the accessions
- to identify redundancies
- to define « core collections »  ➡ AGS and GWAS
- to define a strategy of national collections improvement
Study of the phenotypic variability of the collection is underway

Based on 20 phenotypic traits: flowering date, maturity date, weight of fruit, sugar content, etc.

380 accessions among them 160 accessions of the French National Collection

Large variability for flowering and maturity dates (60 days flowering, 50 days for ripening dates)
Diversity of cherry collections

Genetic structure analysis

- 207 cultivated accessions: 141 landraces and 66 modern varieties
- 211 French wild individuals

26 SSR and SI locus

Mariette et al, 2010

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Genetic structure analysis

Structure
(Pritchard et al, 2000)

K=3

Identification of three clusters:

- Wild populations
- Cultivars
- Landraces

Figure 2 Structure bar plot results obtained on the whole set of data at K = 3. 1 is population identification for modern varieties, 2 is population identification for landraces and 3 is population identification for wild cherries.

Mariette et al, 2010

Important admixture in Cultivars and in Landraces populations
**Genetic structure analysis**

Structure

(Pritchard et al, 2000)

K=3

Identification of three clusters:

- Wild populations
- Cultivars
- Landraces

**Modern varieties**

**Landraces**

**Wild cherries**

Mariette et al, 2010

Important admixture in Cultivars and in Landraces populations

Important structure in the collection
Diversity of cherry collections

148 accessions: landraces and modern varieties

6K SNP array RosBRRED project
(Peace et al, 2012)

Nearly 2000 SNP were polymorph

18 groups of synonyms

30 accessions redundant

Largest group = 6 accessions

Several groups of 2 accessions

Unweighted NJ tree
Genetic structure analysis

148 accessions: landraces and modern varieties

6K SNP array RosBRRED project (Peace et al, 2012)

K=2

Structure of collections has to be considered for AGS.

Study of DL: rapid decay (Mariette et al, 2012), promising for future association genetics studies
Diversity of cherry collections

Links with the breeding programme:

- QTL detection and CG mapping studies conducted on three mapping progenies on numerous traits related to phenology and fruit quality

- Validation of CG through AG

- GWAS with SNP markers (6K SNP chip- RosBREED) and through resequencing

Ex: QTL for flowering date and chilling requirement

Castède & Campoy et al, 2014
THANKS

Jean Claude Barbot
Hélène Christmann
José Antonio Campoy Corbalán
Emilie Lerigoleur
José Quero Garcia
Sandra Robert