



**Seventh framework programme
Food, Agriculture and Fisheries, and Biotechnology**

Specific International Co-operation Actions
Small or medium scale focused research project



Sweet Sorghum an alternative energy Crop

Grant Agreement n° 227422

Deliverable 1.13:

*QTLs for cold tolerance developed and
successfully applied for trait pyramiding*

Composition of the consortium

CIRAD
ICRISAT
EMBRAPA
KWS
IFEU
UniBO
UCSC
ARC-GCI
UANL
WIP



This deliverable is not achieved as it was a too ambitious regarding the project duration.

Identification of QTLs requires first to identify parental lines with a contrasted response to low temperatures tolerance at germination and plant establishment stages. These parents are then crossed to create one or several populations of Recombined Inbred Lines (at least 200 RILs per population) that must be advanced to F6 generation. These RILs are then genotyped and phenotyped in field for their response to low temperatures at germination/plant establishment as well as related agronomic traits. Then the analysis of both genotyping and phenotyping data will allow to identify QTLs linked to cold tolerance and other traits.

During Sweetfuel, we defined first a working collection for WP1 coming from the partners. This collection was genetically analyzed with 360 SNP markers (see figure 1).

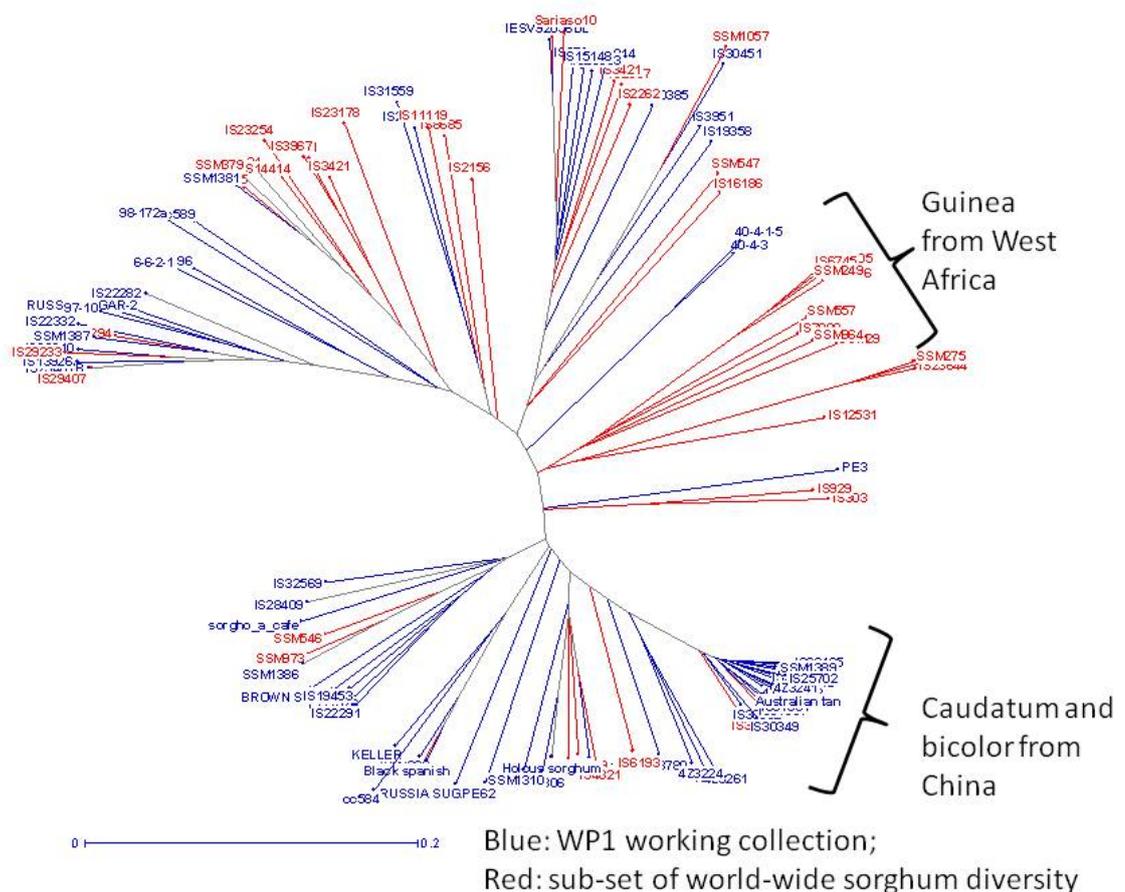


Figure 1: Dendrogram of the genetic diversity of the 70 lines included in the WP1 working collection, compared to a sub-set of 48 accessions representing the world-wide cultivated sorghum diversity

We concluded that this working collection represented fairly well the world-wide cultivated sorghum diversity.

During the cropping season 2010, this working collection was evaluated in Germany, Italy and France, that allowed to identify contrasted genotypes regarding the tolerance to low temperatures.

But at that time of the project, it was already too late for achieving this deliverable before the end of the project. Even by doing 2 cycles per year as KWS carries out a winter nursery in Chili and Puerto Rico, in the best case, we could have been able to get the F6 lines in October 2014, which means the complete data (genotyping + phenotyping) in the best case by end of 2015.

We choose to postpone this investigation in order to focus on the WP1 activities for finalizing other deliverables (e.g. 1.8, 1.9 and 1.11).

But the RILs populations will be anyway developed in the frame of other projects.