This project has received funding
from the European Union's H2020 Programme
under grant agreement no 633571

www.diversifood.eu

EXEMPLES OF THE DIFFERENT TYPES OF POPULATIONS DEVELOPED WITHIN DIVERSIFOOD

AT FIRST GLANCE

To carry out plant breeding on-farm, farmers use and develop various types of populations and varieties depending on their breeding objectives and on the crop mating system. We illustrate it here with DIVERSIFOOD cases.

Embedding crop diversity and networking for local high quality food systems

A range of populations' types

To carry out on-farm participatory plant breeding (PPB), farmers use and develop various types of populations and varieties depending on their breeding objectives and on the crop mating system. Usually they aim at developing varieties with a certain level of diversity, i.e. population-varieties, which are suited to their specific environmental conditions, farming practices and marketing objectives. After describing the different types of those populations-varieties in IF#2, we illustrate it here with DIVERSIFOOD examples.

Comparison of a bread wheat Mixture and a Composite Cross Population: These two different breeding strategies have been investigated by ITAB, INRA and a group of farmers in western France on bread wheat. A dynamic population (mix of 6 parents) and a Composite Cross Population (mix of the seeds from 2x2 crosses) created with the same six parents have been evaluated in two sites (FM and GS) corresponding to two geographical areas in 2015 and 2016 (see Fig. 1). Each population showed a particular response, which seemed slightly affected by the growing conditions. The structure of phenotypic diversity, studied thanks to monitoring agronomic criteria (vegetative development and spike characterisation), was affected by the interaction between the type of population and the environment. Both populations revealed different pathways of evolution over generations within the two sites. Now, farmers will apply their own selection within both populations and follow the evolution of selected and unselected population in both sites, to observe which kind of initial diversity will better fit to farmers' selection.

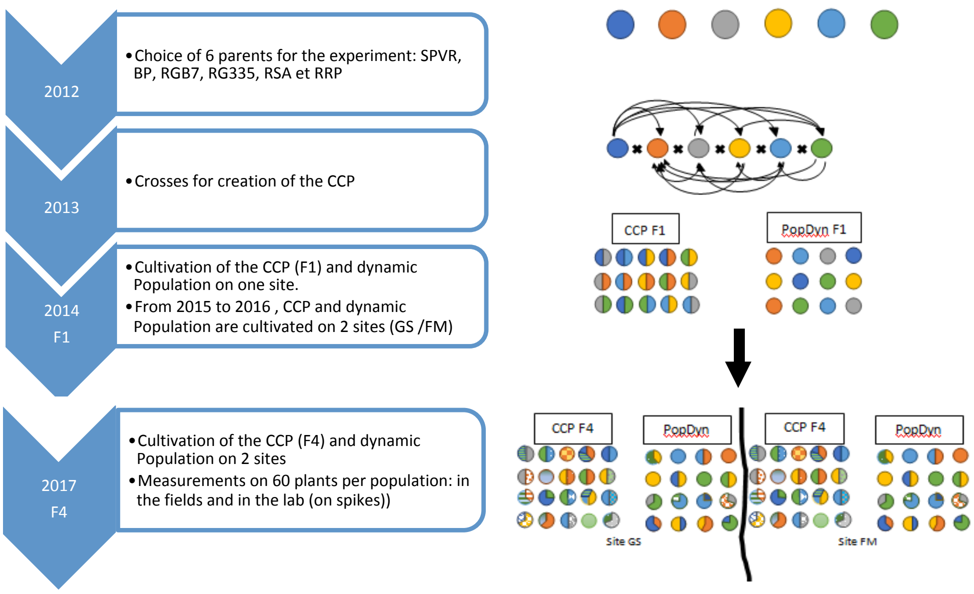

Figure 1: Extract of the evaluation and comparaison of the phenotypic diversity of two bread wheat populations, created with two different breeding strategies (and with the same six parents): a dynamic population and a Composite Cross Population (descent of the crosses 2x2). Diversifood D3.3

This project has received funding from the European Union's H2020 Programme under grant agreement no 633571

High potential of landraces and old varieties bi-parental crosses in bread wheat: In 2006, INRA GQE-Le Moulon and RSP started a participatory breeding project on bread wheat. RSP coordinated the programme with its members, organized in local community seed banks. A large number of crosses have been made using different types of parents: landraces (LR), old varieties (developed before the 60s, OV), modern organic varieties (MV). During the first years of the PPB project, 149 populations have been derived from 25 crosses. They have been evaluated on farm for agronomic behaviour and characterized for genetic diversity using molecular markers. Although crosses including one modern variety (MV) as parent tend to be more productive, there were many crosses based only on landraces (LR) and old varieties (OV) that were as productive, indicating that significant performance can be obtained without resorting to modern varieties. Moreover, the potential of diversification of bi-parental crosses including at least one LR or OV proved to be very high, as shown by the strong differentiation detected among populations derived from a given cross, both at the phenotypic and at the genetic level, and both due to natural and farmers mass selection.

Composite Cross Populations (CCP) to breed for Colletotrichum resistance in white lupin: White lupin cultivars have no sufficient tolerance to *Colletotrichum* for cultivation in Switzerland. Based on a large scale screening of genetic resources, parental lines were selected and crossed in order to increase the genetic diversity available for disease tolerance and to combine different resistance sources, resistance x vigour, resistance x earliness. In 2015, 22 crosses have been made among 14 parents. In 2016, the F1 seeds obtained from 10 different crosses were grown in the field under severe *Colletotrichum* infestation. At the harvest, two CCP populations were created resulted either from (i) bulking equal proportions of all F1 progenies or (ii) bulking progenies according to their number of seeds produced (i.e. resistance level). Strategy (ii) allowed selection of out-crossed healthy plants but made pollination protection necessary to maintain lines or populations. Another CCP has been created from simple and double crosses made in 2016, 2017 and 2018. The aim is to evaluate the potential of CCP methods to create relevant diversity for *Colletotrichum* resistance breeding.

Maize open-pollinated populations: To select genetically contrasted maize accessions with superior quality to create diversified populations through crosses, researchers of ITQB-NOVA and IPC jointly analyzed phenotypic data (quality traits) and genotypic data (molecular markers). Quality of flour and diversity at microsatellite markers were assessed on 32 maize open-pollinated populations (EU-SOLIBAM) and 134 maize inbred lines (FCT-MOXI). Phenotypic information was used to rank the different accessions according to aroma, antioxidants content and rheological ability and the genotypic information was used to calculate genetic distances among them. The rank was used to select maize open-pollinated populations and inbred lines to be used as parents in crossing schemes to increase (tocopherols and total free phenolic acids content) or decrease (overall viscosity values or volatile aldehydes content) particular quality traits. The pairs of accessions that were genetically the most distant were finally selected. The aim of this combined approach is to avoid a drastic reduction of diversity, by crossing only genetically distant plants and to improve specific quality traits by considering those important for the nutritional and technological ability.

This Innovation Factsheet is the result of the collective work of DIVERSIFOOD partners, coordinated by Margaux Kutelmach (INRA), with the support of Isabelle Goldringer (INRA) and Frederic Rey (ITAB).