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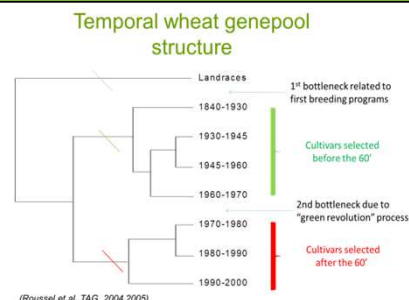
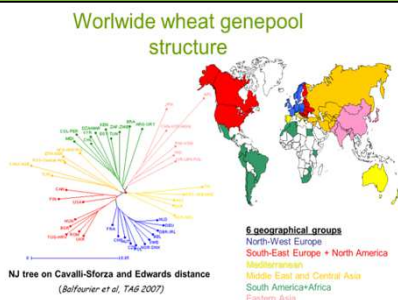
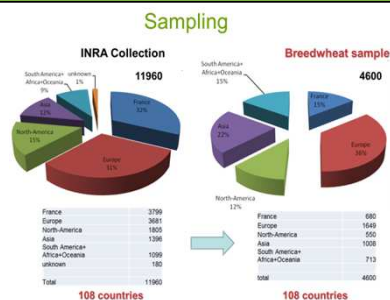
A worldwide bread wheat sample for the French BREEDWHEAT project

François BALFOURIER, Marion DELOCHE, Lionel BARDY and Audrey DIDIER

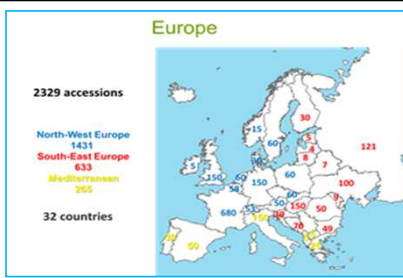
INRA, UMR 1095, Genetics, Diversity and Ecophysiology of Cereals
5 chemin de Beaulieu, F-63039 Clermont-Ferrand, cedex 2, France

Context: BREEDWHEAT is a “genomics to breeding” precompetitive national project built along a chain starting with the establishment of tools, methods and plant material for association genetics and ecophysiological studies of yield and quality components under abiotic and biotic stress, down to the evaluation of new breeding methods and the creation of prebreeding material that will support the selection of improved wheat varieties.

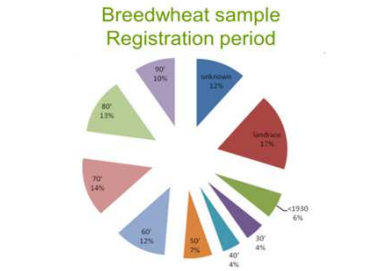
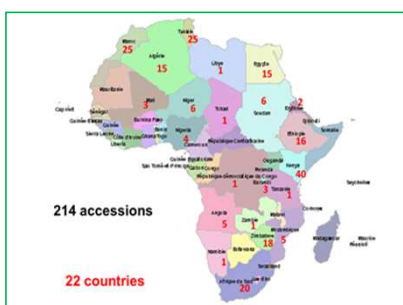
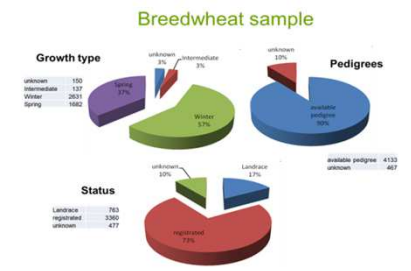
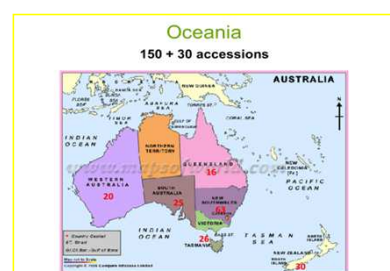
In the framework of this project, a specific task in work-package 3 (WP3) is dedicated to the definition of a worldwide wheat sample of 4600 accessions from the global INRA collection, in order to analyse genetic diversity in wheat germplasm and deliver two panels of ‘easy to use accessions’ for association analyses on biotic and abiotic stress tolerance in other WPs.



The initial INRA bread wheat collection consisted on 11960 accessions originating from 108 different countries. Available data on this collection mainly consist on passport data: geographical origin (country, region, state, department,...), status (landraces, breeding lines, cultivars, elite lines,...) registration period, habit (spring, intermediate or winter type) and pedigrees. Some molecular data, previously obtained on a part of the whole collection, highlighted the importance of both geographical and temporal effects in structuring the genetic diversity of this collection (Balfourier et al. 2007; Roussel et al. 2004, 2005).



The methodology used consists on sampling an optimal worldwide diversity sample mainly based on available passport data. The selected sample of 4600 accessions produces a balanced sample size between countries, regions and registration periods, able to reflect the genetic structure of wheat genepools.



Conclusion: This sample should permit to answer to the objectives of the BREEDWHEAT project. Furthermore, deliverable molecular data of WP1(400.000 SNPs) on this sample of 4600 accessions should allow diverse population genetic analyses, such as multiple comparisons of genetic diversity evolution (between countries, between regions within country, between registration periods, between breeders, ...) and analysis of diversity at different time and eco-geographical scales.