Bridging landscape genomics and quantitative genetics for a regional adaptation of European grasslands to climate-change

Project 'GrassLandscape' awarded by the 2014 FACCE-JPI ERA-NET+ call 'Climate Smart Agriculture'

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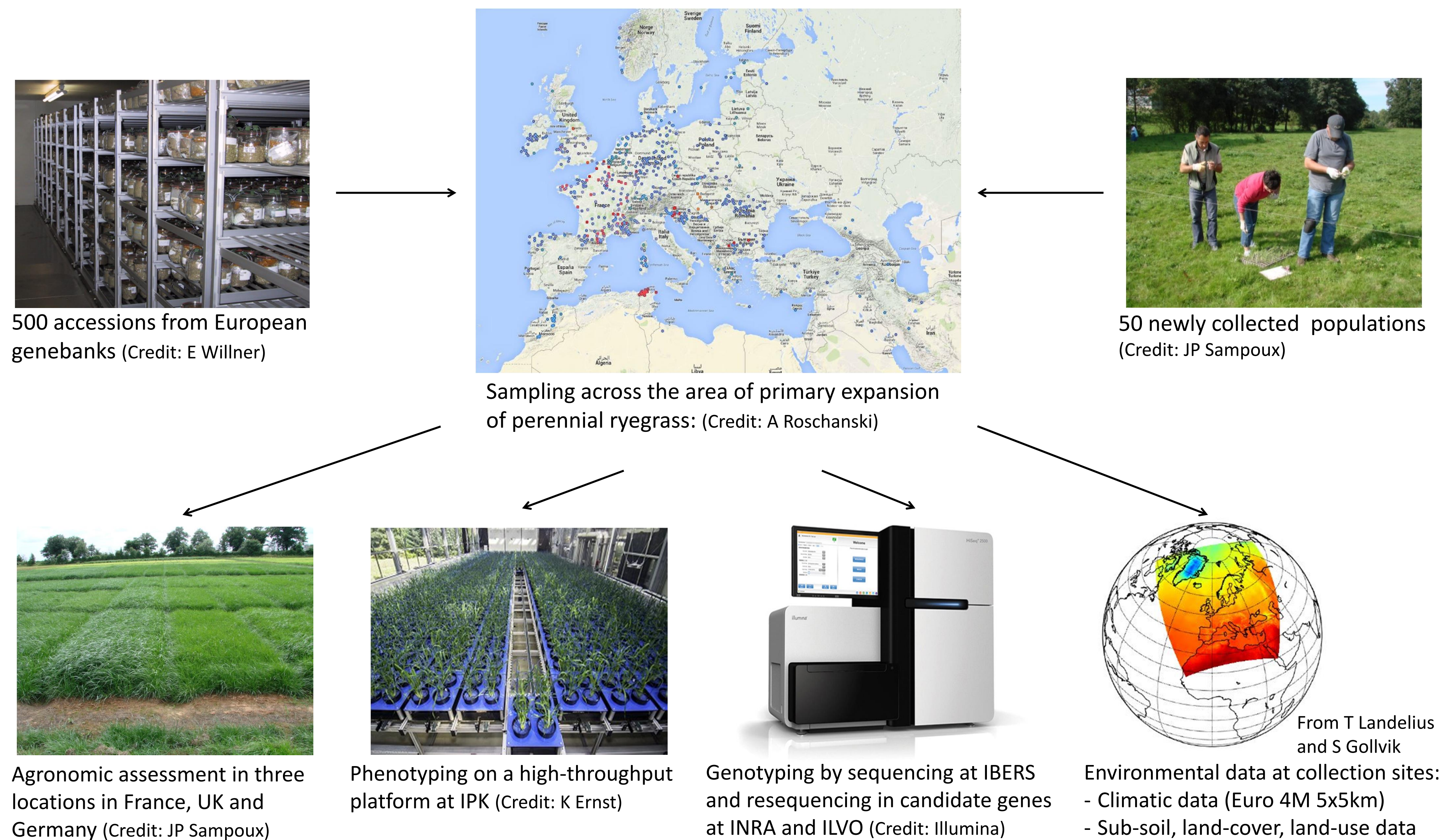
Aims of the project 'GrassLandscape' (2015 – 2017)

In the next decades, grasslands are likely to experience damages and subsequent production losses due to changing climate. However, most grassland species show large ecotype diversity over wide environmental ranges. This large ecotype diversity could be used to recombine natural climatic adaptations and value for services to create improved populations of grassland species adapted to the foreseen future regional climates. The project 'GrassLandscape' aims to implement this strategy to perennial ryegrass (Lolium perenne L.) which is a major grassland species in Europe.
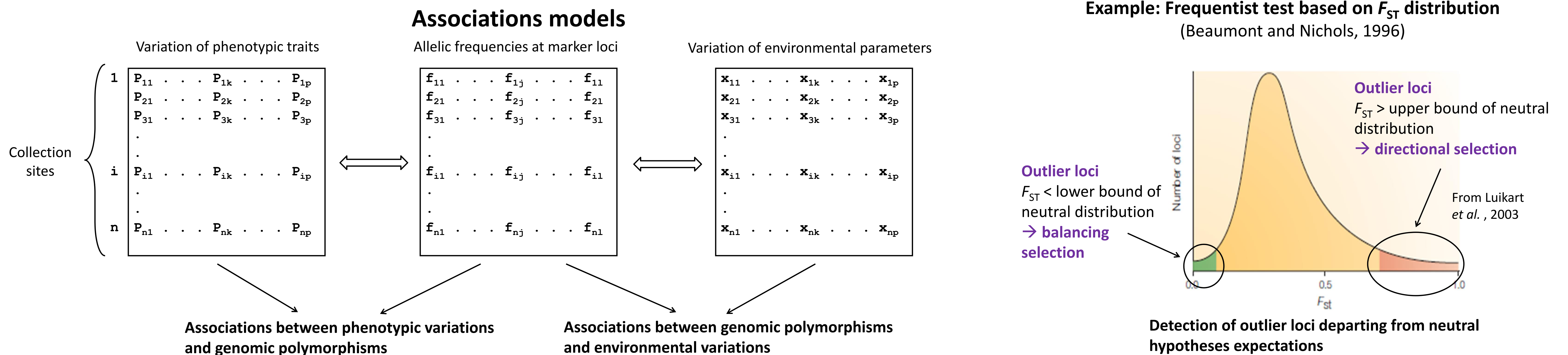
Methods

The project 'GrassLandscape' uses the innovative methodological frame of the Landscape genomics (Manel et al., 2010) to screen the natural diversity of perennial ryegrass in order to discover genomic variability involved in environmental adaptation, and more specifically in climatic adaptation (Sampoux et al., 2013). The landscape genomics approach is based on the combined use of methods correlating genomic polymorphisms and environmental variations at sites of origin of genotypes and of tests of signature of selection. A genotyping method based on a NGS technology (Hegarty et al., 2013) is applied to 550 populations of perennial ryegrass sampled across the area of primary expansion of this species (Europe, Northern Africa, Near East). These populations have been taken out from genebanks of plant research institutes (Nehrlich et al., 2013) or will be collected in situ across Europe. The genotyping protocol is expected to deliver several tens thousands Single Nucleotide Polymorphisms (SNPs) along perennial ryegrass genome. Resequencing in about ten candidate genes is furthermore expected to reveal additional SNPs (Ruttink, 2015). Populations will be furthermore phenotyped in fields and on a high-throughput phenotyping platform to record agronomic and eco-physiological traits.

Study of a sample of 550 populations from the natural diversity of perennial ryegrass

500 accessions from European genebanks (Credit: E Willner)

Sampling across the area of primary expansion of perennial ryegrass: (Credit: A Roschanski)

50 newly collected populations (Credit: JP Sampoux)

Agronomic assessment in three locations in France, UK and Germany (Credit: JP Sampoux)

Phenotyping on a high-throughput platform at IPK (Credit: K Ernst)

Genotyping by sequencing at IBERS and resequencing in candidate genes at INRA and ILVO (Credit: Illumina)

Environmental data at collection sites:
- Climatic data (Euro 4M 5x5km)
- Sub-soil, land-cover, land-use data

From T Landelius and S Gollvik

Strategy for a regional adaptation of perennial ryegrass to climate change

Association models between genomic polymorphisms and environmental variations will be used to map the spatial distribution of genomic markers linked to adaptive diversity in present climatic conditions. Possible shifts in the spatial range fitting these markers will be foreseen in the context of several climate change scenarios based on the four Representative Concentration Pathways of IPCC AR5. Based on these results, the consortium will define allelic profiles of perennial ryegrass expected to provide climatic adaptation at regional scale over Europe under the future climatic conditions foreseen by climate models. Strategies will be proposed to combine climatic adaptation and value for services by genetic recombination. A number of genetic pools will be designed to mix different natural populations. These genetic pools will be the basis to initiate breeding programmes aiming to deliver improved populations adapted to future regional climates. These improved populations will enable to restore grasslands degraded by future climatic disruptions.

References

Hegarty M. et al. (2013) Genotyping by RAD sequencing enables mapping of fatty acid composition traits in perennial ryegrass (Lolium perenne L.). Plant Biotech. J., 11, 572–581.

Manel S. et al. (2010) Perspectives on the use of landscape genetics to detect genetic adaptive variation in the field. Mol. Ecol., 19, 3760-3772.

Nehrlich S. et al. (2013) Characterization and evaluation of genebank accessions as a pre-selection instrument for plant breeding objectives and strategies. In: Barth S. & Milbourne D. (eds.). Springer, Dordrecht, pp. 301-305.

Ruttink T. (2015) Probing genome diversity in wild and breeding populations of Lolium perenne. International Plant & Animal Genome Conference XXIII, 10-14 January 2015, San Diego, USA.

Sampoux J.P. et al. (2013) High-throughput genome-wide genotyping to revive the use of natural diversity in forage and turf breeding. In: Sokolovic D. et al. (eds). Springer, Dordrecht, pp. 313-323.

Associations models

Variation of phenotypic traits

Allelic frequencies at marker loci

Variation of environmental parameters

Collection sites

Associations between phenotypic variations and genomic polymorphisms

Associations between genomic polymorphisms and environmental variations

Multiple-population test of signature of selection

Example: Frequentist test based on F_{ST} distribution
(Beaumont and Nichols, 1996)

Outlier loci
F_{ST} > upper bound of neutral distribution
→ directional selection

Outlier loci
F_{ST} < lower bound of neutral distribution
→ balancing selection

From Luikart et al., 2003

Detection of outlier loci departing from neutral hypotheses expectations

Environmental distribution models of adaptive diversity

Fine-resolution grids of climatic norms for the 1990-2010 period (Euro 4M 5x5km)

Fine-resolution grids of climatic norms for several climate change scenarios at the 2050 and 2100 terms (Eurocordex RCM)

Expected spatial distribution of adaptive diversity in the 1990-2010 period

Foreseen spatial distribution of adaptive diversity at the 2050 and 2100 terms

Models of association phenotype x genomic diversity

Foreseen shifts in the range of suitability of adaptive diversity

Genomic markers of agronomic value

Use of genomic markers of climatic adaptation to drive:
- Assisted migration
- Recombination of climatic adaptations

Recombination of agronomic value and climatic adaptation

- Genetic pools to reseed permanent grasslands
- Introgression of climatic adaptations into elite cultivars

Regional adaptation of perennial ryegrass to climate change across Europe

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