GrassLandscape
Genomic markers of climatic adaptation in perennial ryegrass

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INTRODUCTION

Anthropogenic increase in atmospheric greenhouse gases concentration is expected to have a negative impact on the persistency of grassland communities in the medium-long term (2030-2100) due to the raise in temperatures.

Our study focus on perennial ryegrass (*Lolium perenne* L.), which is a major grass species naturally distributed over Europe and surroundings. We will implement the latest developments in Landscape Genomics to discover genetic variability involved in climatic adaptation using high-throughput genotyping in a wide collection of natural populations. Results of this approach will be used in breeding programs (marker-assisted selection) to drive adaptation of perennial ryegrass to future climatic conditions. The ultimate target will be to create new genetic pools for reseeding grasslands that may be degraded by future climatic shifts.

Here we present preliminary results for the first step of the project: The detection of SNPs involved in climatic adaptation.

Climate Change Scenarios

Most optimistic

Less optimistic

MATERIAL AND METHODS

We performed Landscape Genomics analyses to discover genetic variability involved in climatic adaptation. We used a method based on population differentiation (SelEstim, Vitalis *et al.*, 2013) and a method based on environmental associations (LFMM, Frichot *et al.*, 2013). As a prior information required for the LFMM method, we will perform an analysis of population structure (DAPC, Jombart et al., 2010).
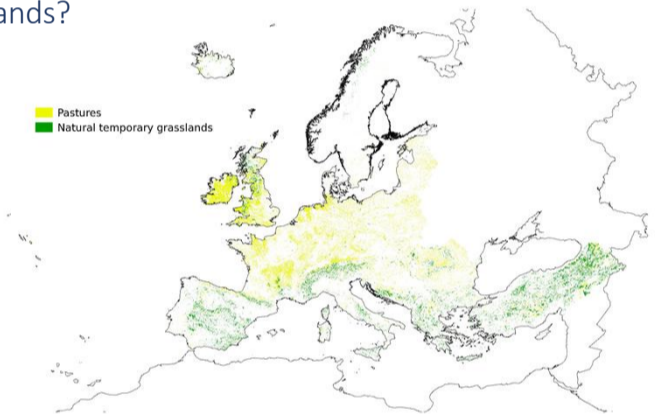
80 environmental and ecophysiological variables:
˝ ETCCDI (Extreme Climate Change Detection Indices) (27)
˝ WorldClim BIOCLIM (indexes used for Species Distribution Modeling (27)
˝ Newly created "Ecophysiological indexes" specially relevant for perennial ryegrass (25)

467 perennial ryegrass populations
˝ 412 from European genebanks and 55 from new In situ sampling

>500 000 SNPs in >70% populations
˝ Genotyping-by-sequencing (GBS) of pools of individuals (Pool-seq)
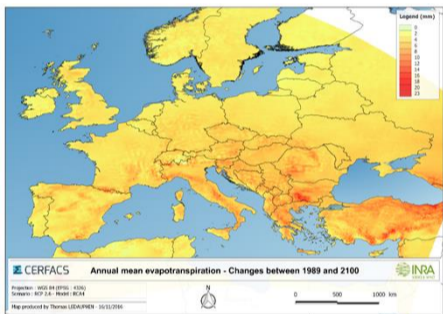→ DNA mixture of 300 individuals used per pool (population)

Why do we study grasslands?

˝ Economical services
↳ 36% of the total utilized agricultural area in the EU.

˝ Ecological services
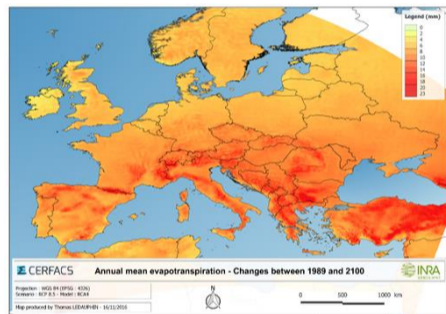↳ Vast territories occupied by natural grasslands producing hábitat for wildlife.

Pastures
Natural temporary grasslands

RESULTS AND DISCUSSION

Genetic structure
˝ The DAPC analysis (Fig. 1) shows a strong geographical structure. Seven clusters were recovered (upper-right inset), with an admixture zone in central Europe mainly between cluster 1 and 6 (admixed individuals shown in upper-left inset).
˝ This suggests that genetic composition of natural populations of perennial ryegrass have been scarcely affected by human-mediated migration derived from domestication practices.
˝ The two main eigenvalues of the DAPC analysis (lower-right inset) represents latitude and longitude. This indicates a strong differentiation in the species along these two spatial dimensions.

Fig. 1

Legend
Cluster1
Cluster2
Cluster3
Cluster4
Cluster5
Cluster6
Cluster7
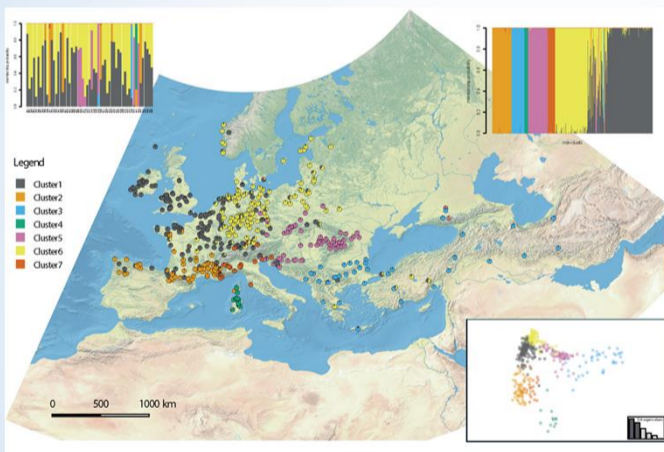
Analyses of selection (from a subset of 50 000 SNPs)
˝ For the SelEstim analysis we used the 95% quantile of the KLD distribution obtained from simulated data (5%-threshold KLD value) (see Vitalis et al., 2013) and we obtained 2395 candidate loci showing high differentiation.
˝ A preliminary LFMM analysis was performed to analyze associations among SNP frequencies and plant evapotranspiration. We obtained 1785 candidate loci with expected FDR = 0.01.
˝ We combined both results and obtained 79 LFMM candidate loci that were also supported by SelEstim (Fig. 2).

Fig. 2

SNPs ~ Evapotranspiration Manhattan plot (FDR = .01)

LFMM
LFMM + SelEstim
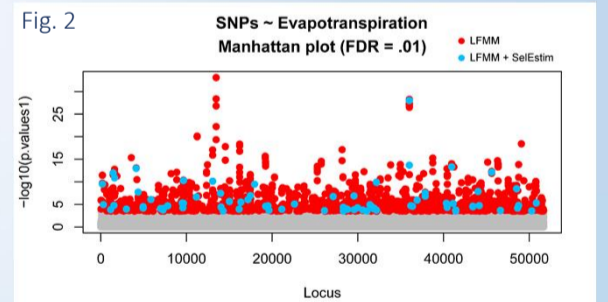
CONCLUSIONS

˝ *Lolium perenne* populations are moderately structured and show low levels of admixture.
˝ Differentiation within *Lolim perenne* is mostly explained by latitudinal and longitudinal gradients. Main drivers of differentiation could have been either (i) isolation-by-distance processes after latitudinal and longitudinal migrations or (ii) latitudinal/longitudinal environmental gradients
˝ 1785 SNPs were found to be associated with plant evapotranspiration with LFMM of which 79 showed high differentiation with SelEstim. It is important to combine results from complementary analyses to avoid false positives and target the best candidate loci for genomic selection.

REFERENCES

˝ Frichot, E., et al. (2013). "Testing for associations between loci and environmental gradients using latent factor mixed models." Molecular Biology and Evolution 30(7): 1687-1699.
˝ Jombart, T., et al. (2010). "Discriminant analysis of principal components: a new method for the analysis of genetically structured populations." BMC genetics 11(1): 1.
˝ Vitalis, R., et al. (2013). "Detecting and measuring selection from gene frequency data." Genetics: genetics. 113.152991.

CONTACT

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