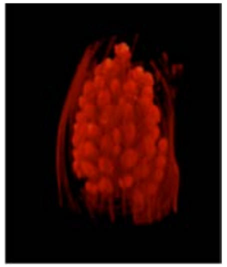
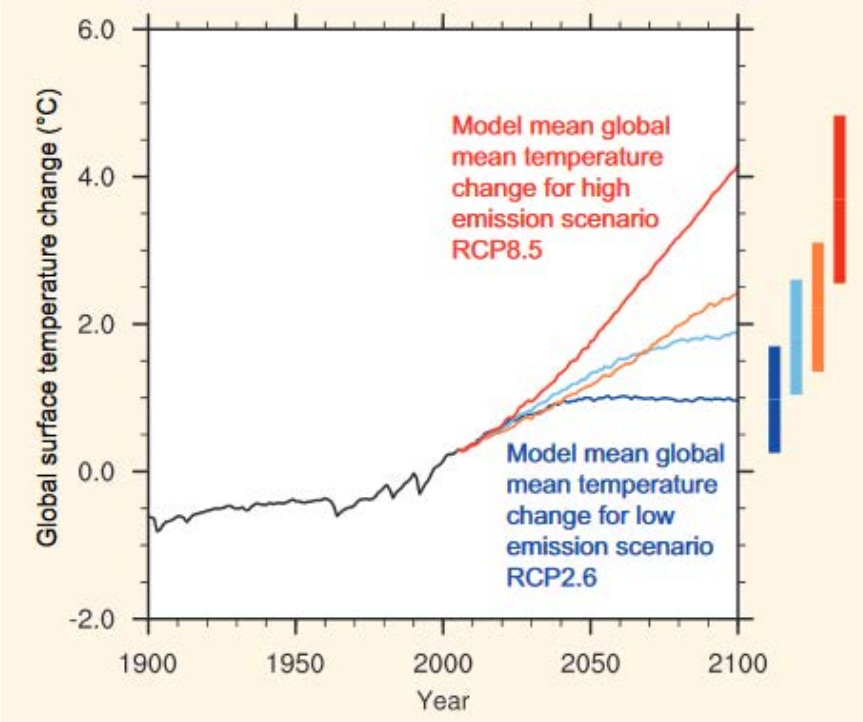
   

Example of application of adaptative genomics and genetic offset

Yves Vigouroux & Philippe Cubry
Bénédicte Rhoné

Institut de Recherche pour le Développement FRANCE
UNIVERSITÉ DE MONTPELLIER
cirad LA RECHERCHE AGRONOMIQUE POUR LE DÉVELOPPEMENT
diade



Source :IPCC report, AR5, 2014

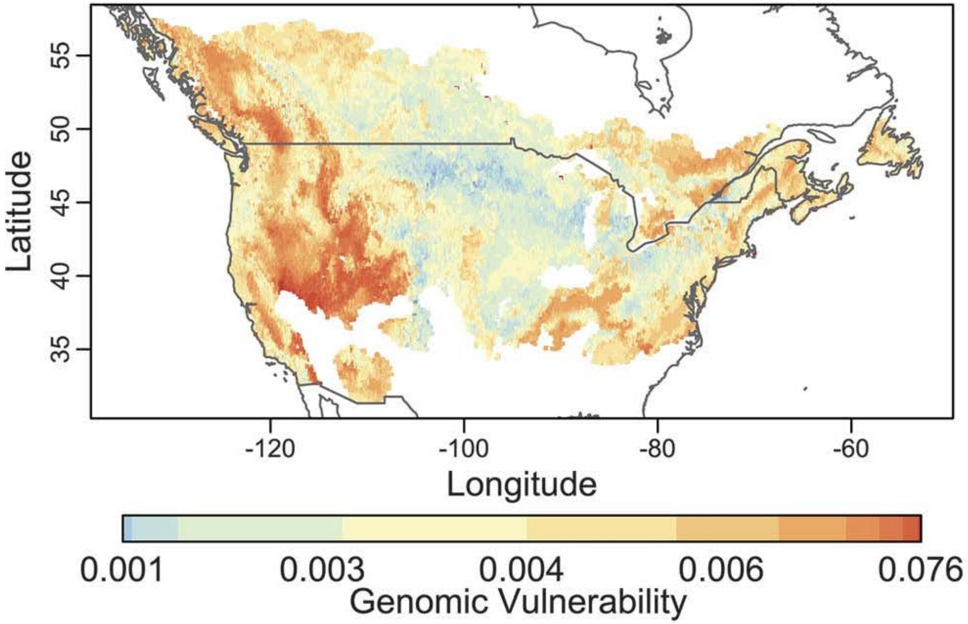
- Consequence of future climate on population adaptation?

- How to assess plant/crop adaptation/maladaption in future climate?

Ecological studies

« risk of mal-adaptation », « genetic-offset », « Genomic vulnerability », « genetic gap » try to predicts the genomic mal-adaptation to future climate

Setophaga petechia Wikipedia



Ellis et al. 2012

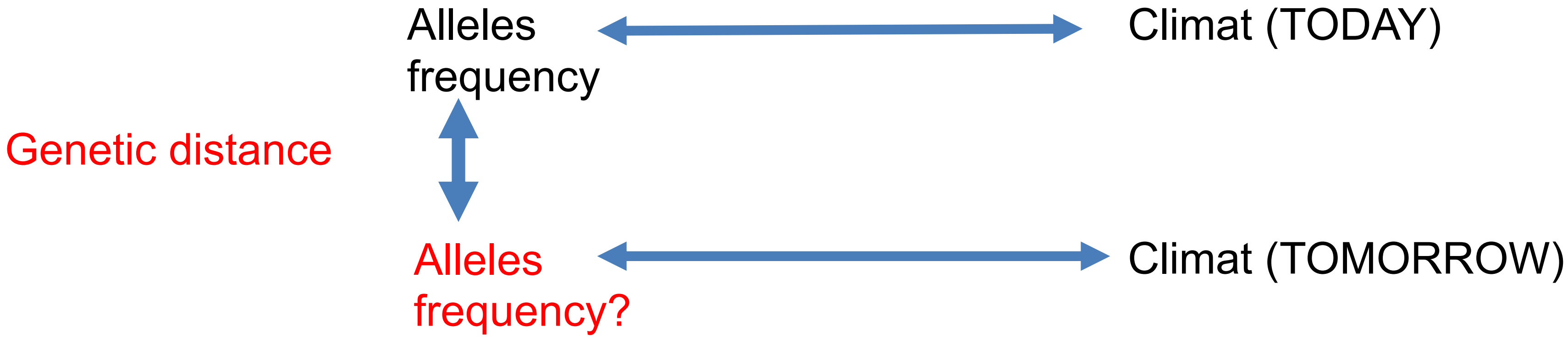
Fitzpatrick & Keller 2015

Bay et al. 2018

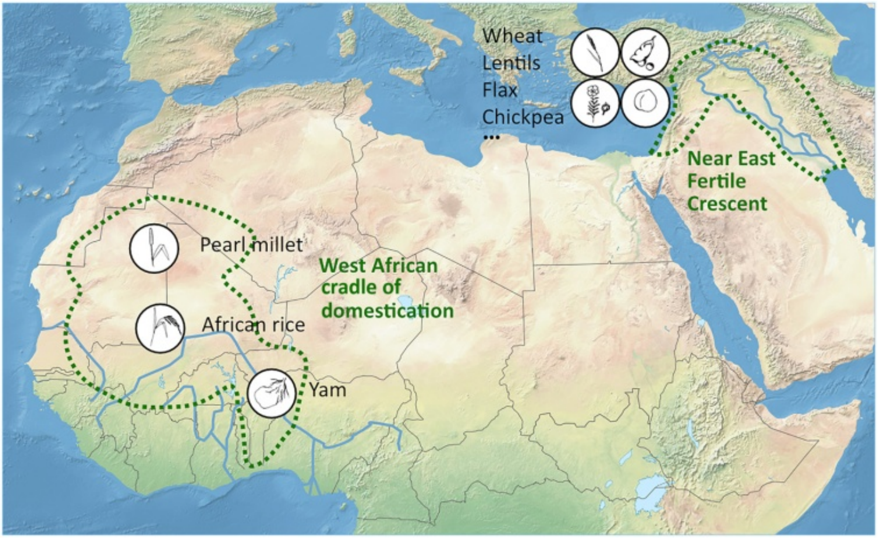
ECOLOGICAL GENOMICS

Genomic signals of selection predict climate-driven population declines in a migratory bird

Rachael A. Bay,[1,2*] Ryan J. Harrigan,[1] Vinh Le Underwood,[1] H. Lisle Gibbs,[3] Thomas B. Smith,[1,4] Kristen Ruegg[1,5]


Alleles frequency
Climat (TODAY)
Genetic distance
Alleles frequency?
Climat (TOMORROW)

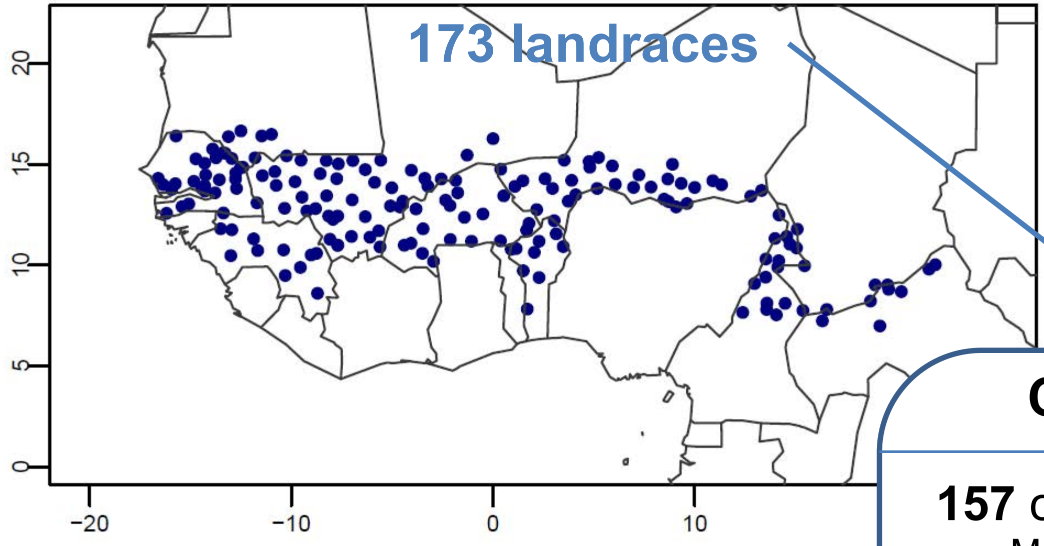
Pearl millet (*Pennisetum glaucum*)
- Cultivated in arid and low-fertility soils
- Traditional varieties



~1.8 Gb draft whole genome sequence
Varshney et al. 2017

•Domesticated 5000 y. ago in West Africa

Burgarella et al. 2018 Nat Ecol Evol
Scarcelli et al. 2019 Science Adv



Climate data

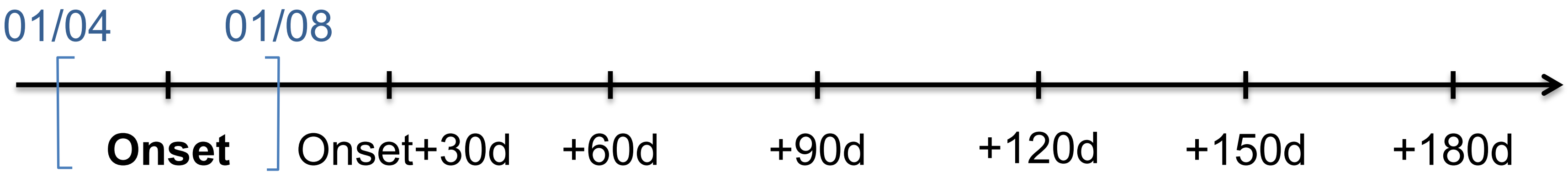
157 climate metrics

Monsoon onset, temperature, precipitation, radiation

Climate data

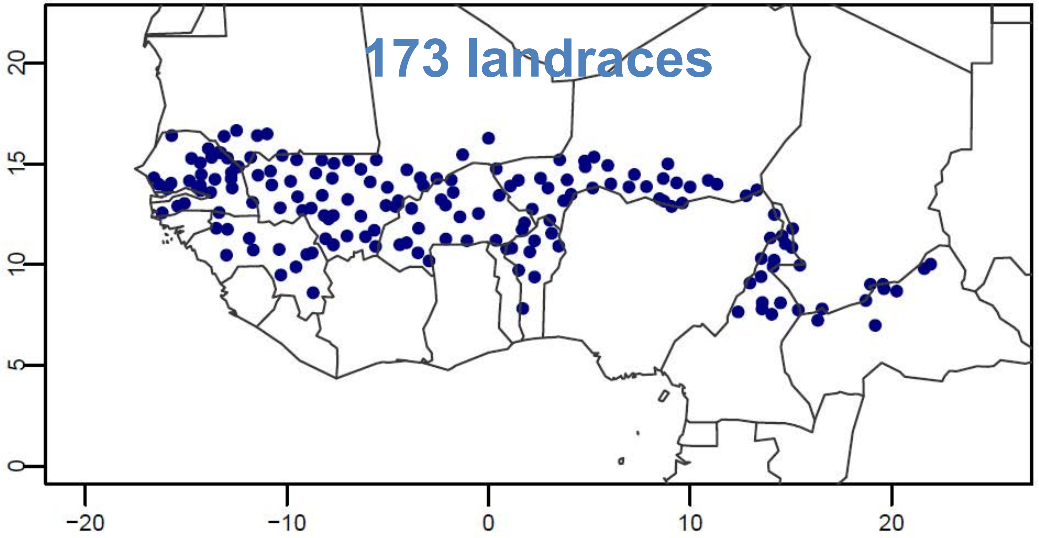
What make the more sense?

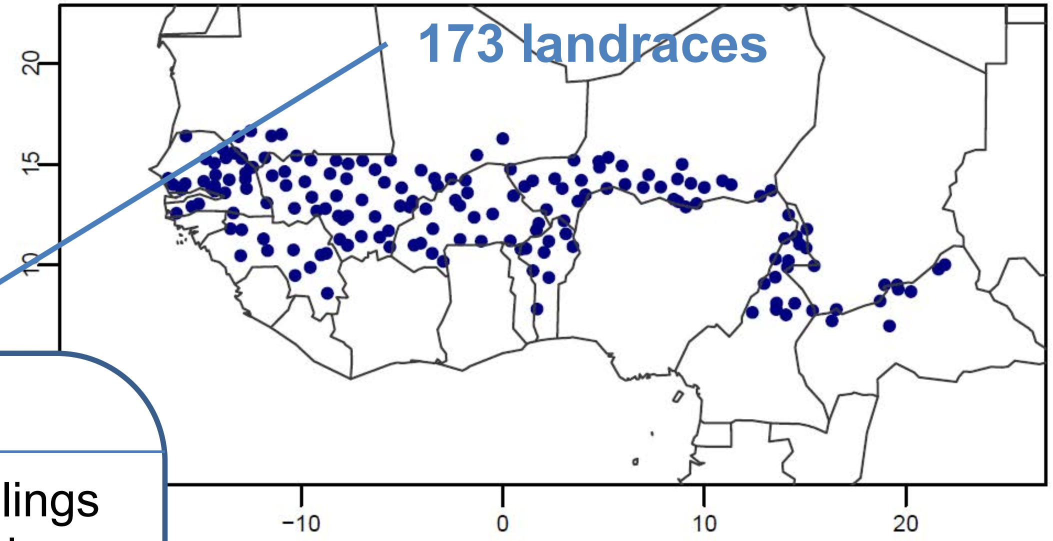
Collaboration with climatologist
Annual plant
Experience climate (seed, seedling, adult)



Mooson onset calculated based on historical & future climate
variable in term of geography & time

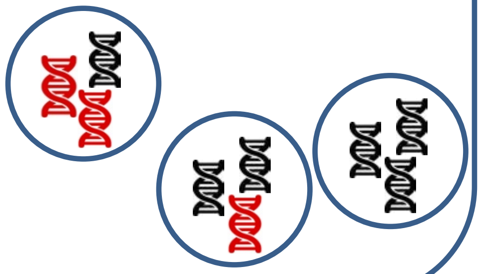
Temperature related variables (min, max, mean, nb of days T>30°C/T>40°C)
Rainfall related variables (aggregate, wetspell, dryspell, intensity, number of rainy days (>30mm, >50mm).
Radiation (in MJ.time^{-1} : aggregate, min, max)

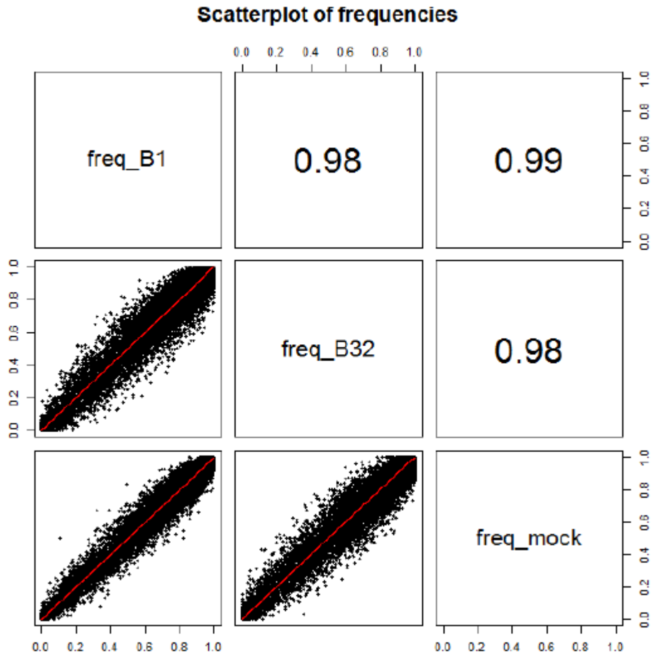

173 landraces
20
15
10
5
0
−20
−10
0
10
20



Genomic data

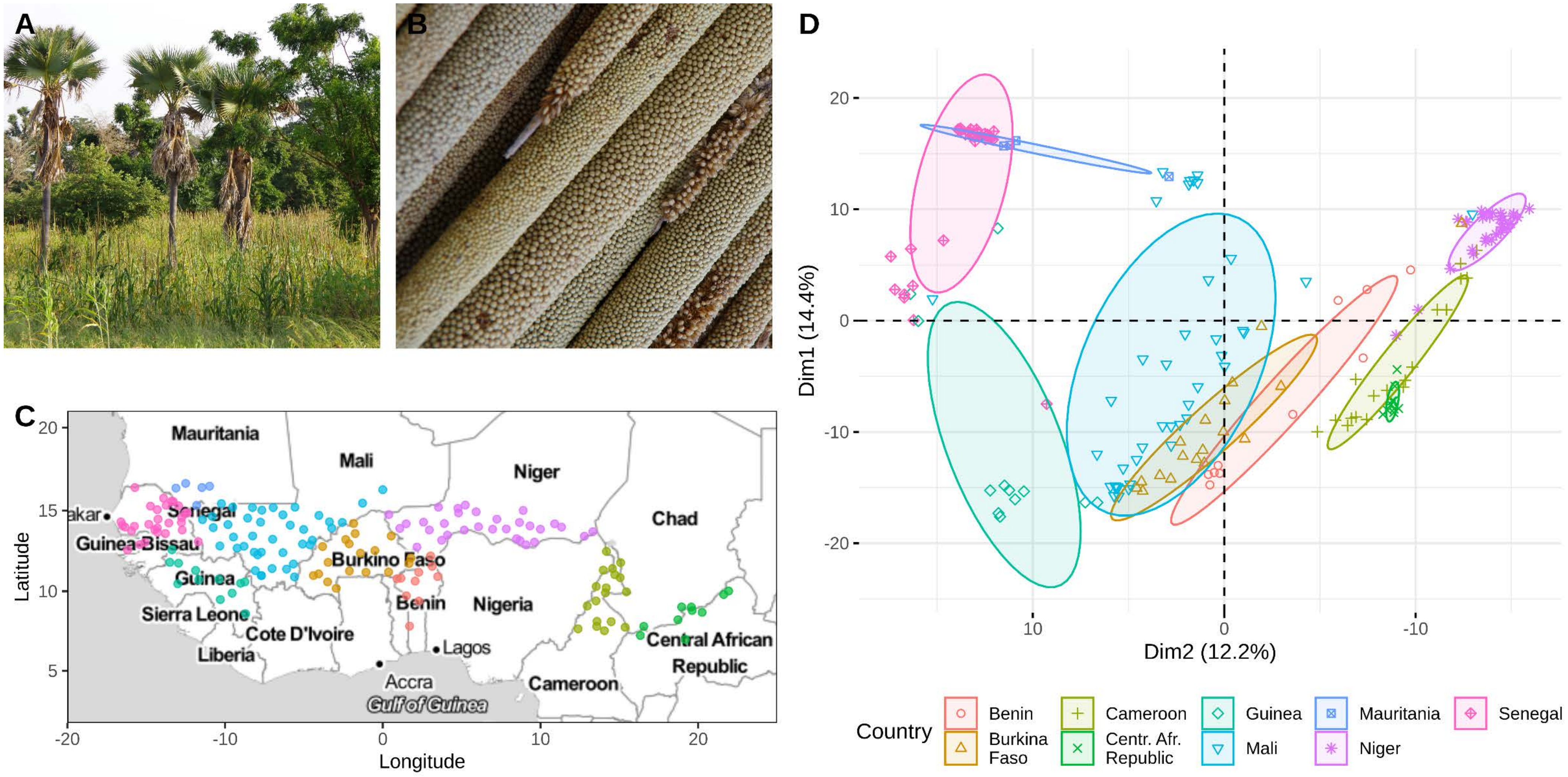
Poolseq: 17300 seedlings
100 individuals/173 landraces
Capture whole exomes
Allele frequencies 139k SNPs

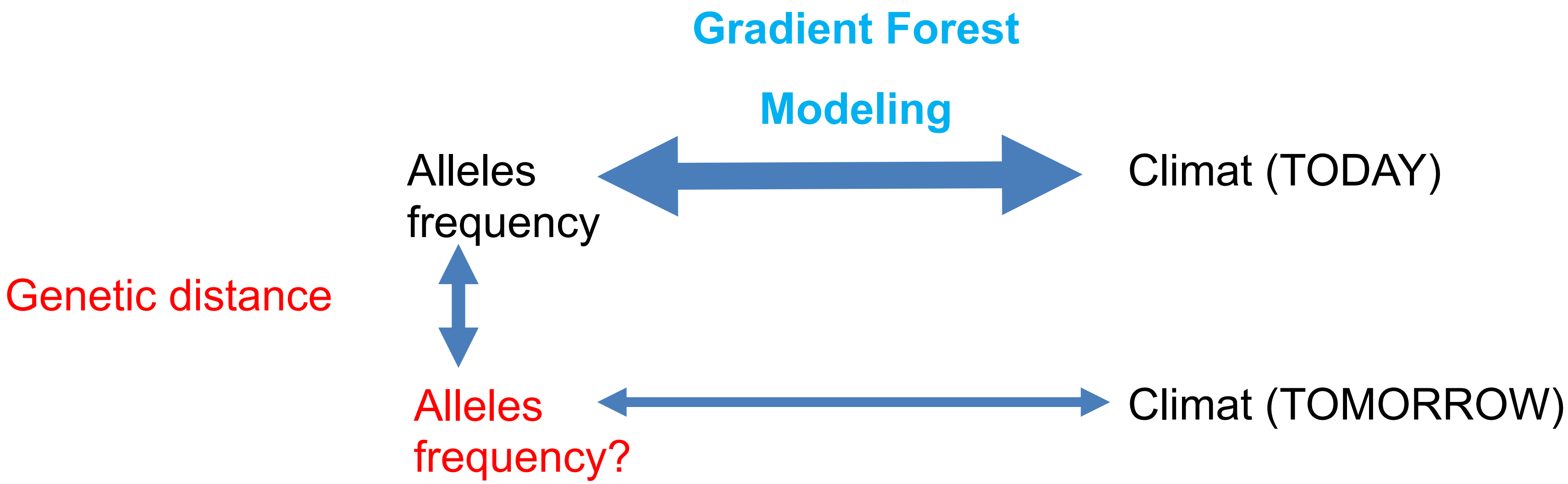


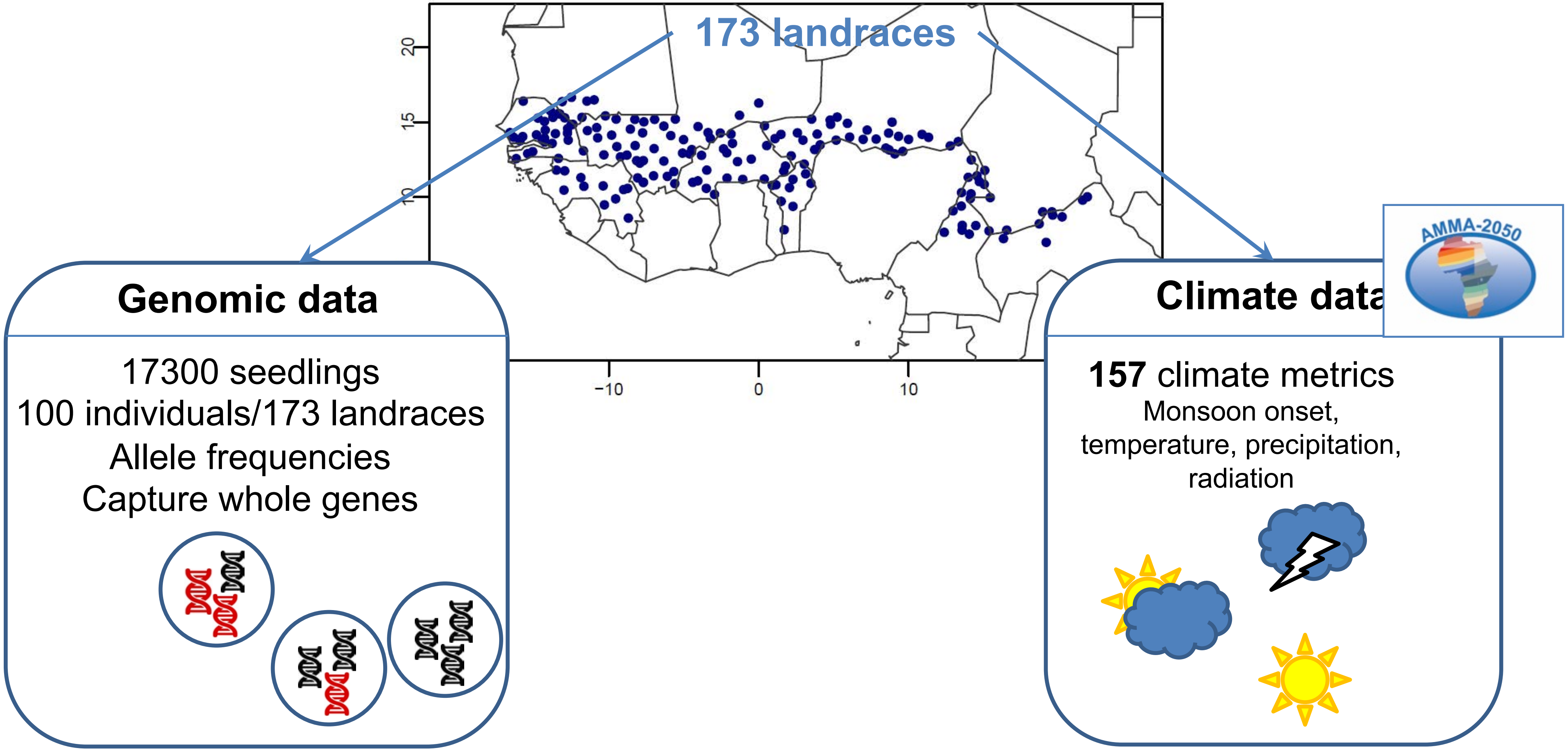


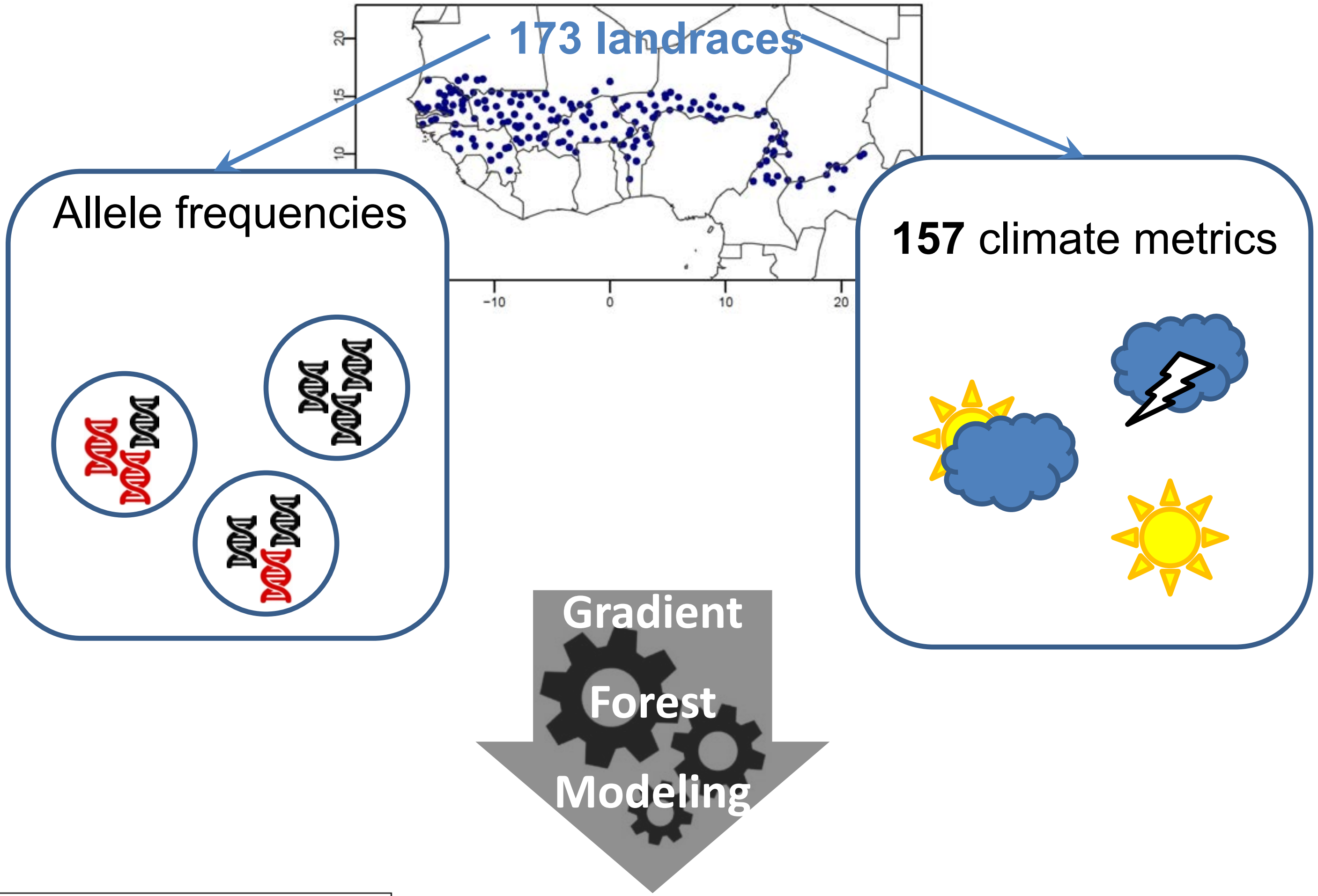
Mariac et al. 2022. Bioxirv.

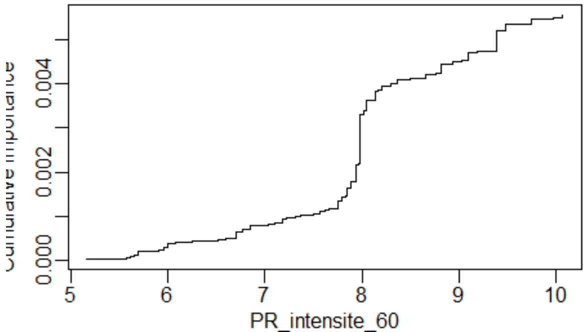
STRUCTURATION reflects geography




Gradient Forest
Modeling
Alleles frequency
Climat (TODAY)
Genetic distance
Alleles frequency?
Climat (TOMORROW)


173 landraces
20
15
10
-10
0
10
Genomic data
17300 seedlings
100 individuals/173 landraces
Allele frequencies
Capture whole genes
Climate data
AMMA-2050
157 climate metrics
Monsoon onset,
temperature, precipitation,
radiation



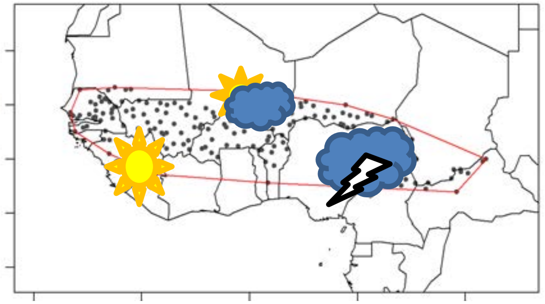


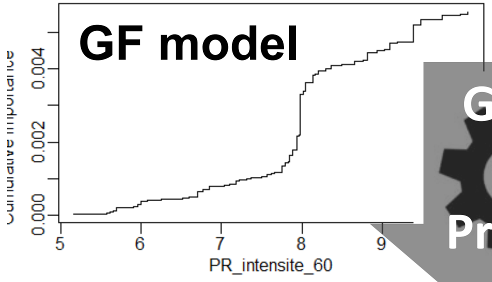
Model allele frequencies change along multiple environmental gradients

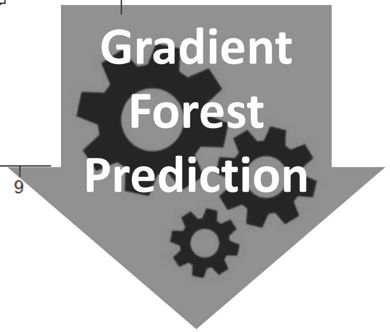
Ellis et al. 2012
Fitzpatrick & Keller 2015

Gradient forest predictions

157 climate metrics

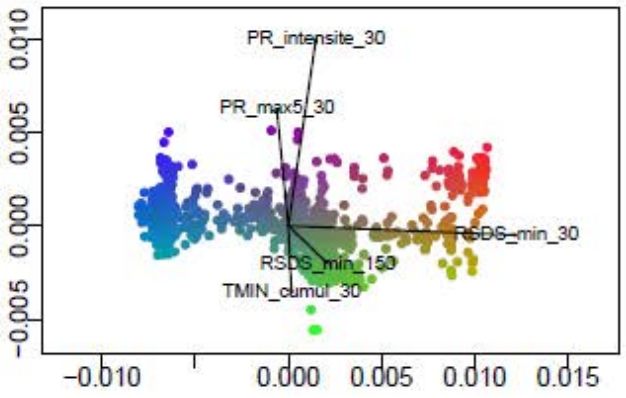


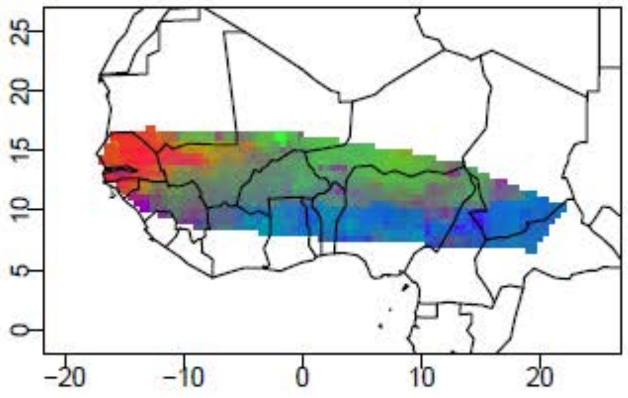




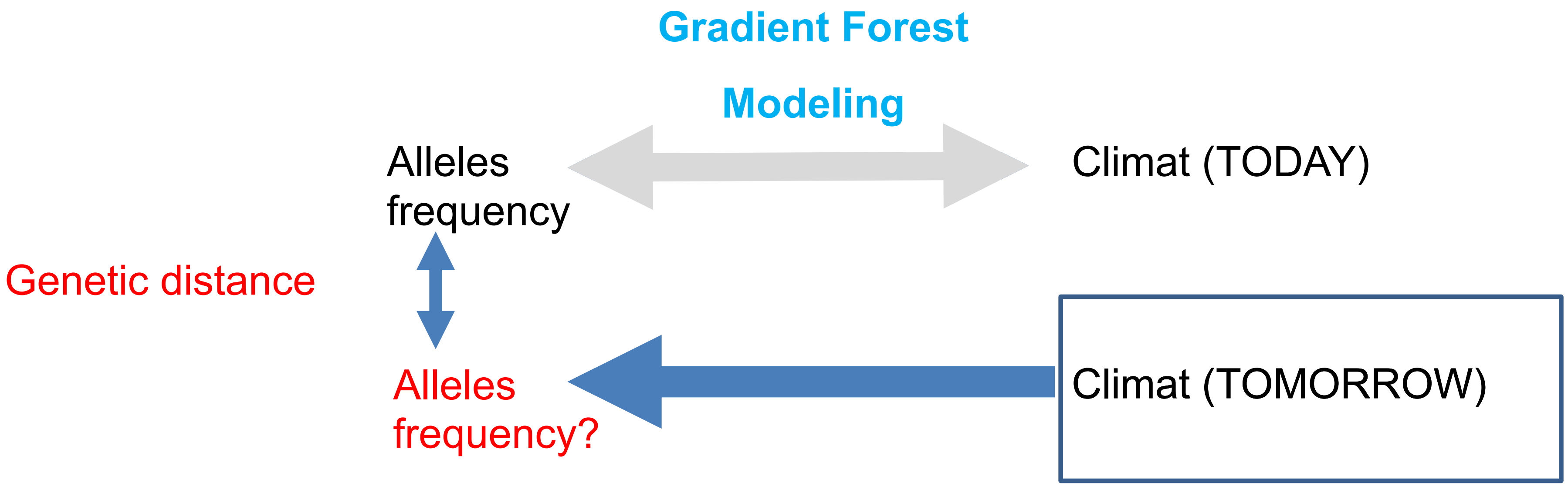
Predict genomic composition at spatial scale

PCA on climate data





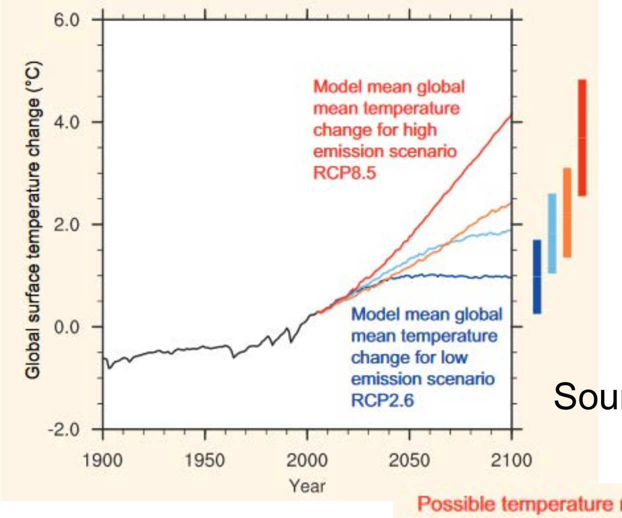
Similar colors should reflect similar allele frequencies at climate-associate loci


Gradient Forest
Modeling
Alleles frequency
Climat (TODAY)
Genetic distance
Alleles frequency?
Climat (TOMORROW)

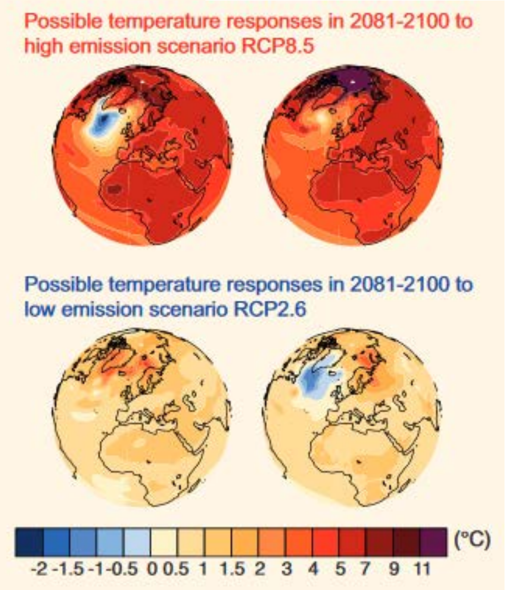
17 climate models 2050

Modelling centre (or group)	CMIP5 Models
Commonwealth Scientific and Industrial Research Organization (CSIRO) and Bureau of Meteorology (BOM), Australia	ACCESS1-0 ACCESS1-3
Beijing Climate Center, China Meteorological Administration	bcc-csm1-1 bcc-csm1-1-m
College of Global Change and Earth System Science, Beijing Normal University	BNU-ESM
Canadian Centre for Climate Modelling and Analysis	CanESM2
Centro Euro-Mediterraneo per I Cambiamenti Climatici	CMCC-CESM CMCC-CM CMCC-CMS
Centre National de Recherches Météorologiques/Centre Européen de Recherche et Formation Avancée en Calcul Scientifique	CNRM-CM5
Commonwealth Scientific and Industrial Research Organization in collaboration with Queens land Climate Change Centre of Excellence	CSIRO-Mk3-6-0
NOAA Geophysical Fluid Dynamics Laboratory	GFDL-CM3 GFDL-ESM2G GFDL-ESM2M
Met Office Hadley Centre (additional HadGEM2-ES realizations contributed by Instituto Nacional de Pesquisas Espaciais)	HadGEM2-AO HadGEM2-CC HadGEM2-ES
Institute for Numerical Mathematics	Inmcm4
Institut Pierre-Simon Laplace	IPSL-CM5A-LR IPSL-CM5A-MR IPSL-CM5B-LR
Atmosphere and Ocean Research Institute (University of Tokyo), National Institute for Environmental Studies, and Japan Agency for Marine-Earth Science and Technology	MIROC5
Japan Agency for Marine-Earth Science and Technology, Atmosphere and Ocean Research Institute (University of Tokyo), and National Institute for Environmental Studies	MIROC-ESM MIROC-ESM-CHEM
Max-Planck-Institut für Meteorologie (Max Planck Institute for Meteorology)	MPI-ESM-LR MPI-ESM-MR
Meteorological Research Institute	MRI-CGCM3 MRI-ESM1

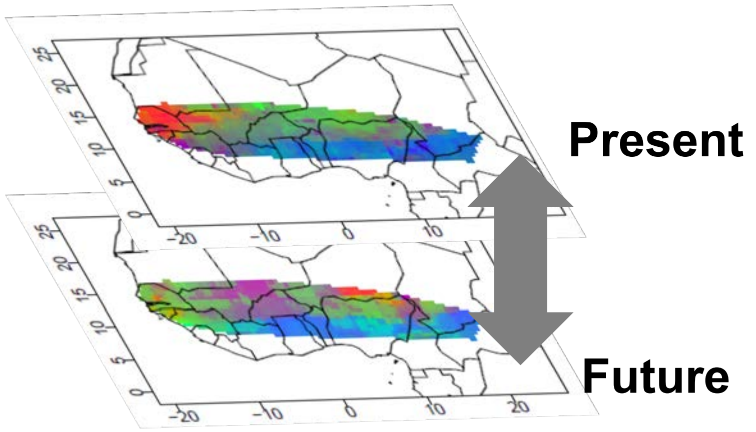
Climate scenario:

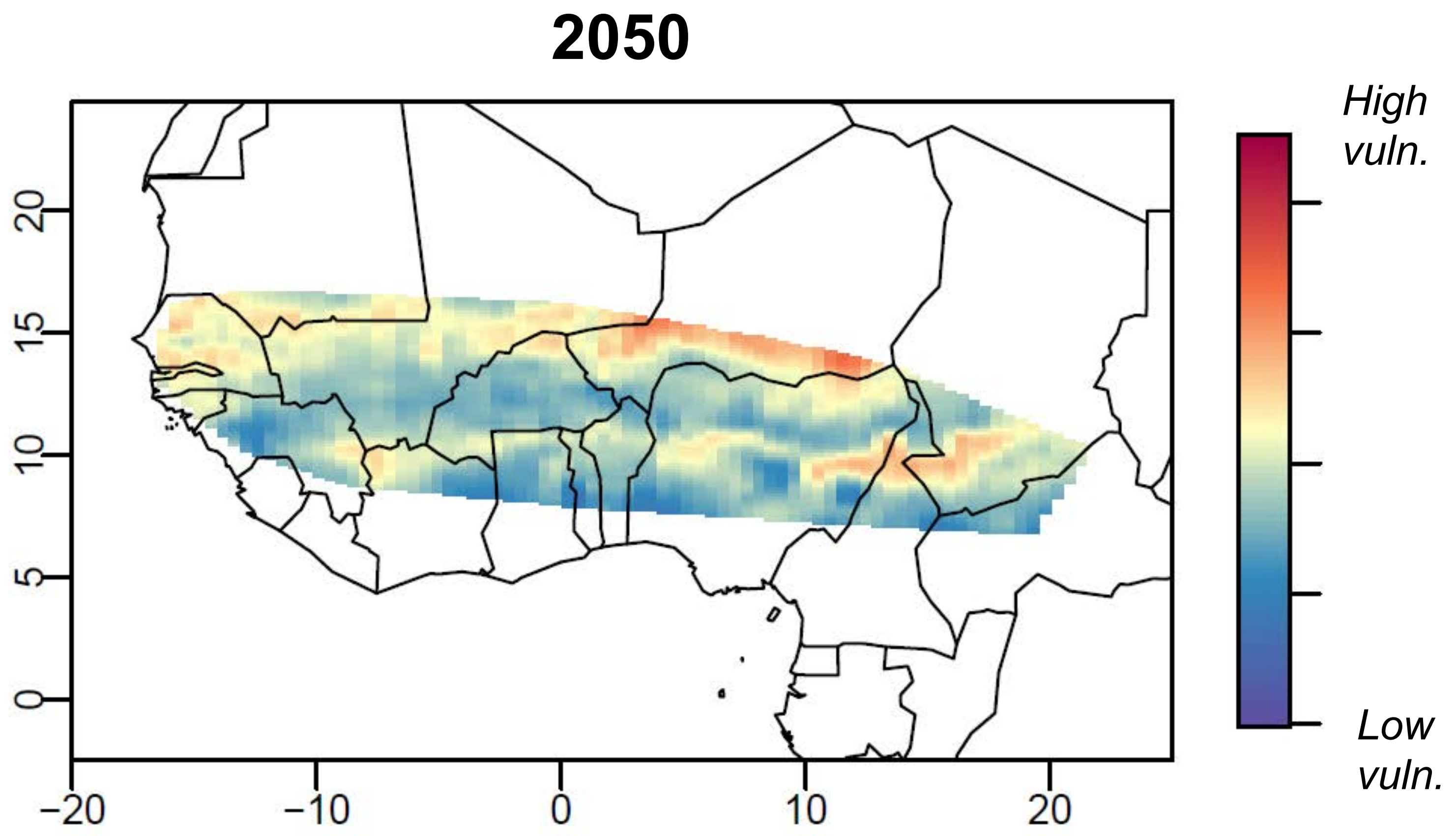


Source :IPCC report, AR5, 2014



RCP8.5, **Mean of 17 climate models**



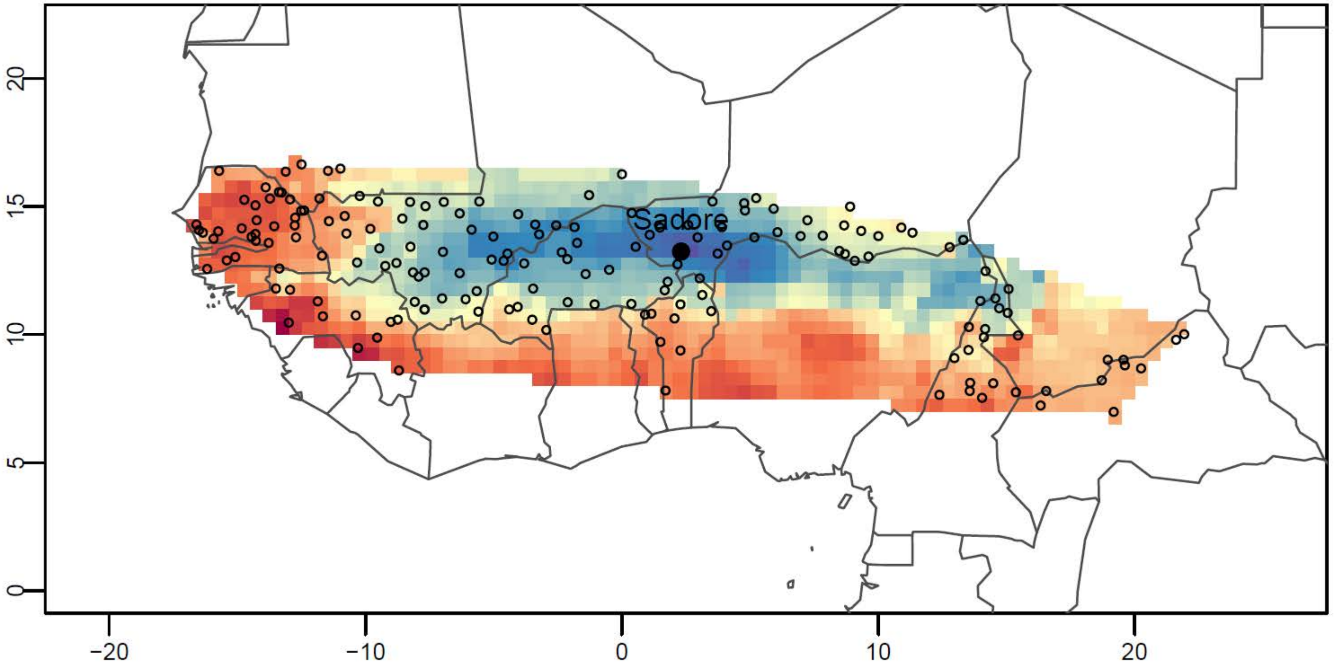


Rhoné et al. 2020

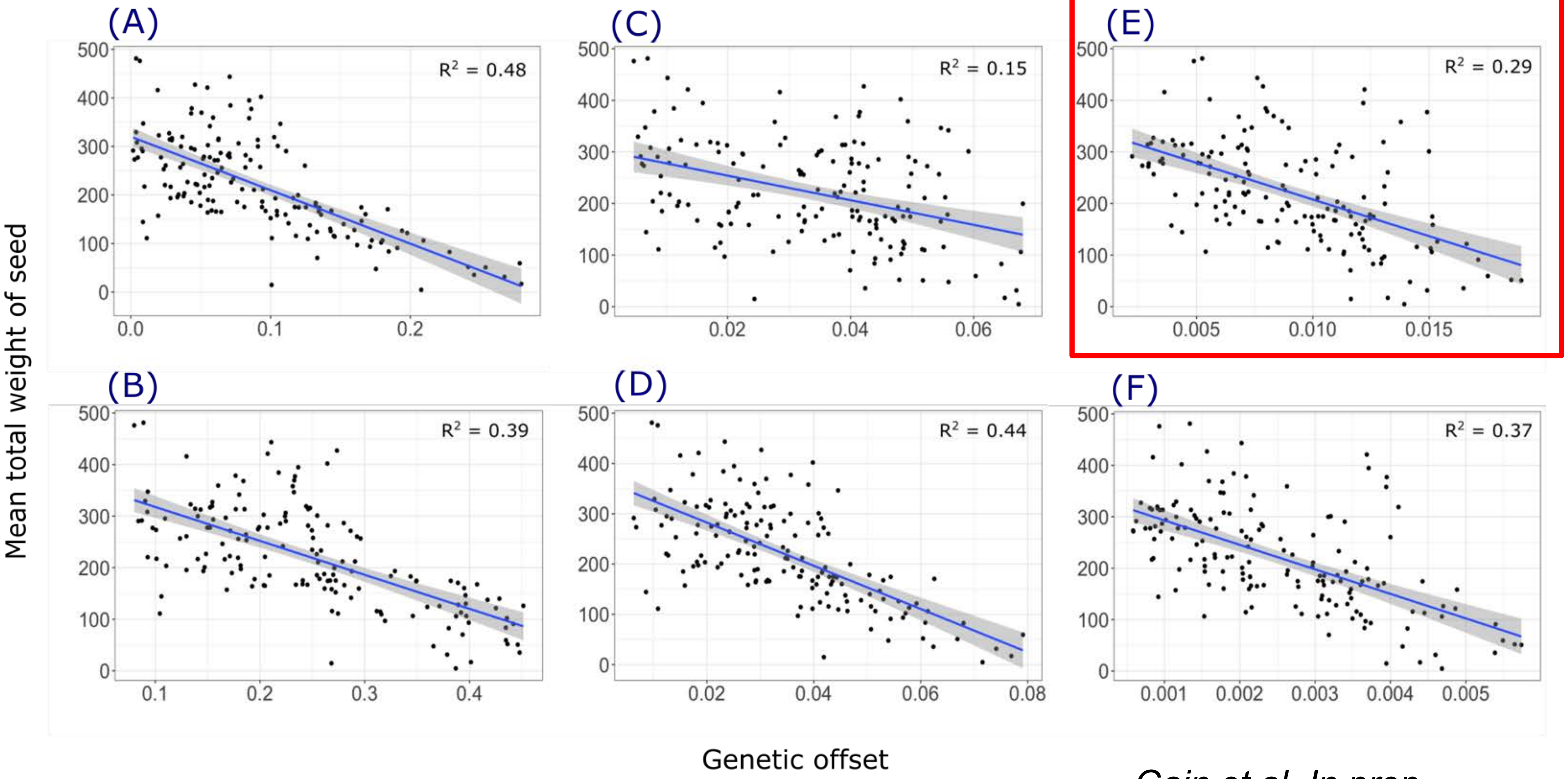
Relation to fitness based on experimental spatial contrast

Common garden 7 fields trails over 2 years
1730 plants in each field trials / 12110 plants

Spatial contrat to experimental site

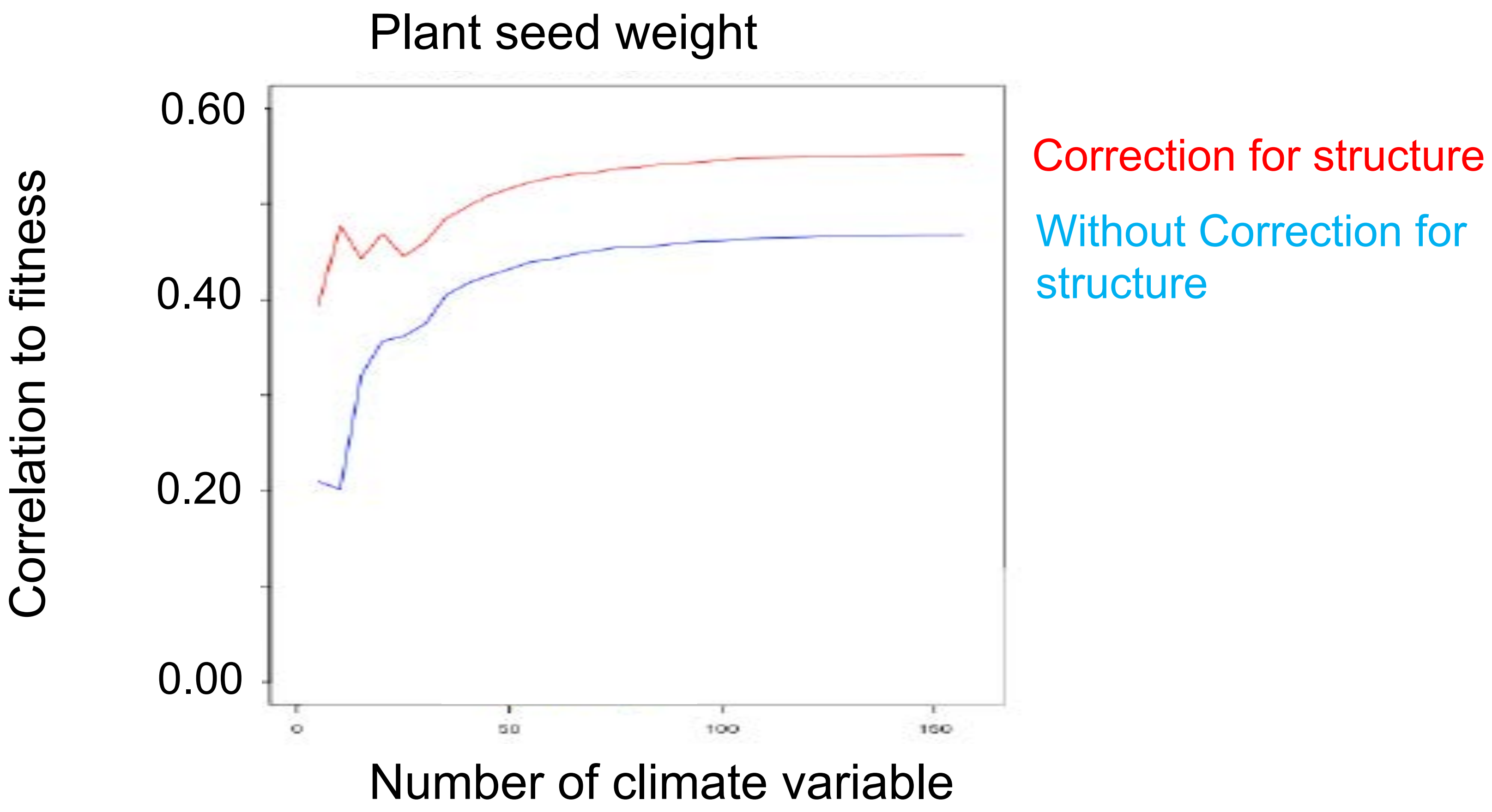


Correlation with fitness and spatial contrast

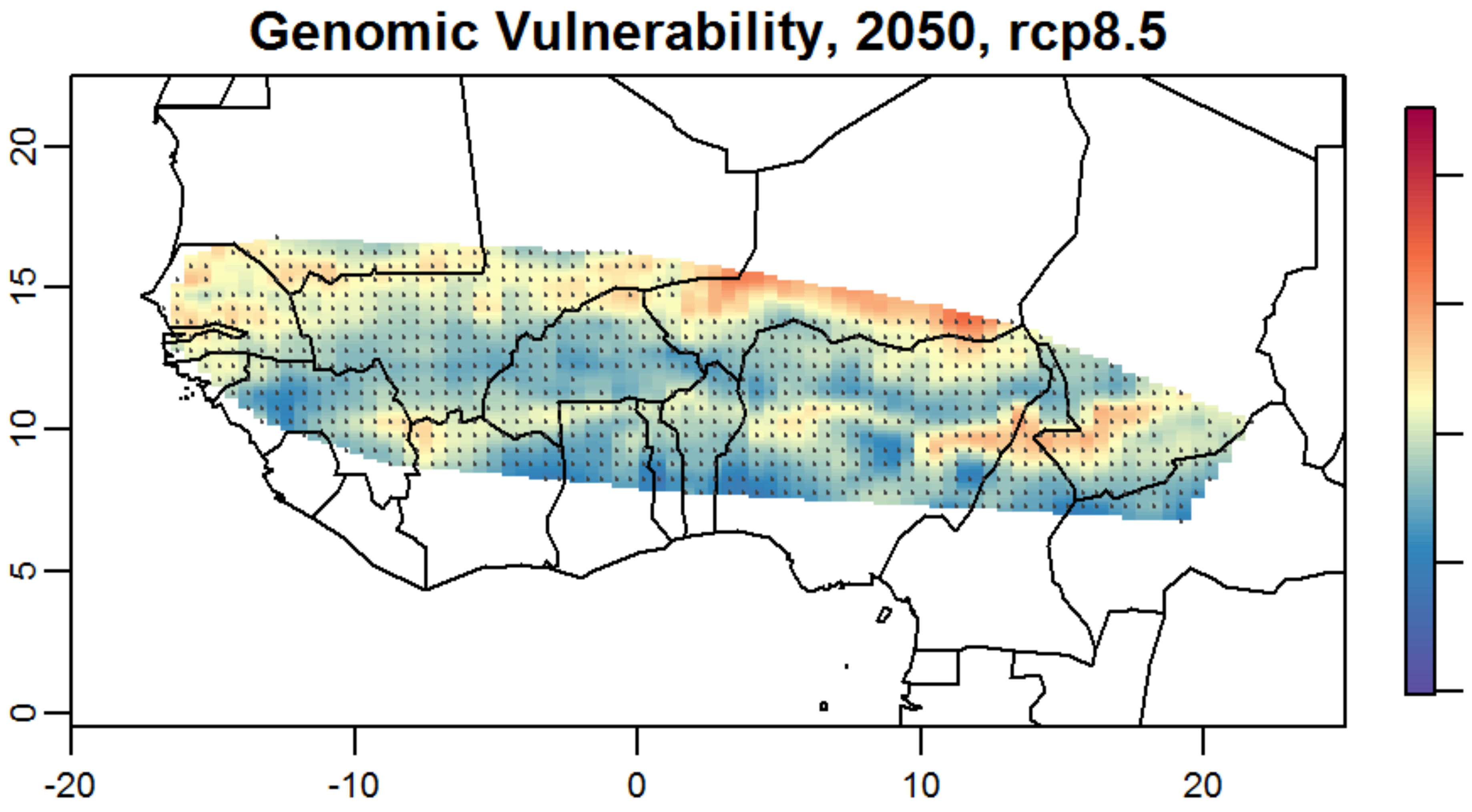


Gain et al. In prep.

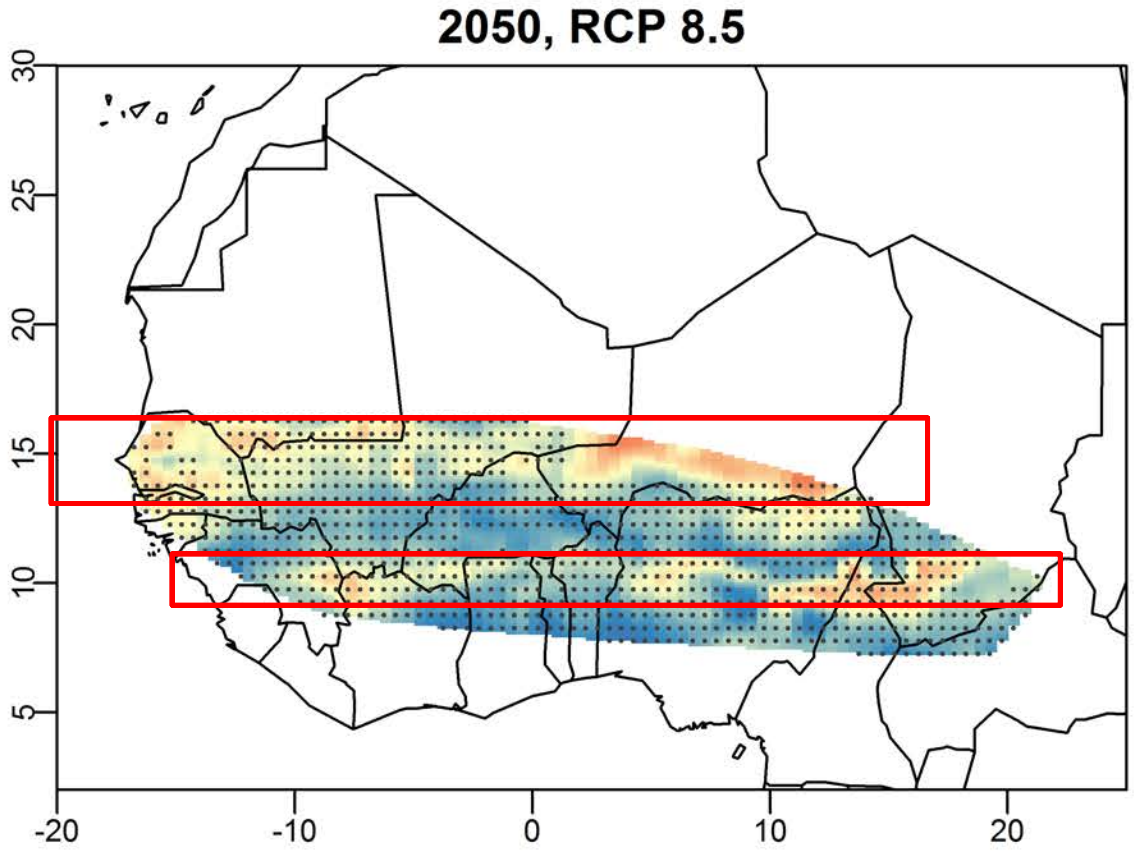
How about structure and number of climate variables ?



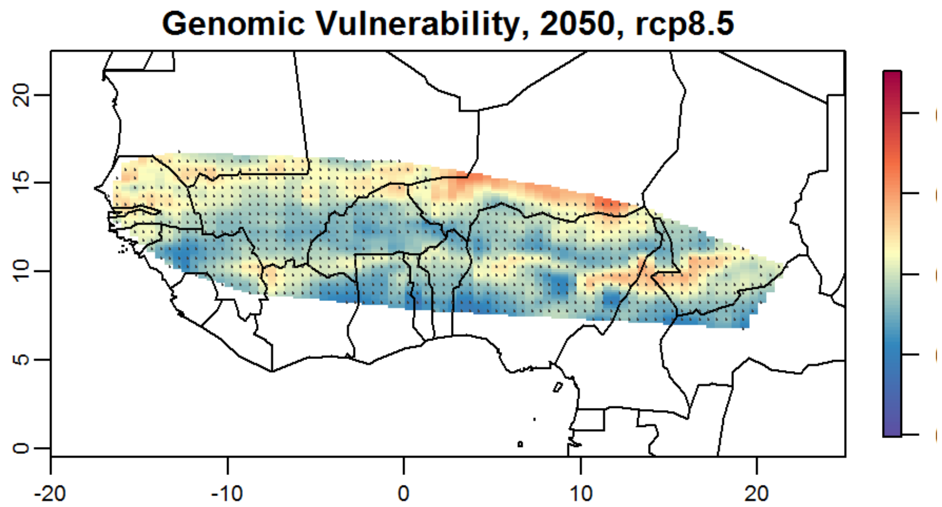
Convergence across 17 climate models

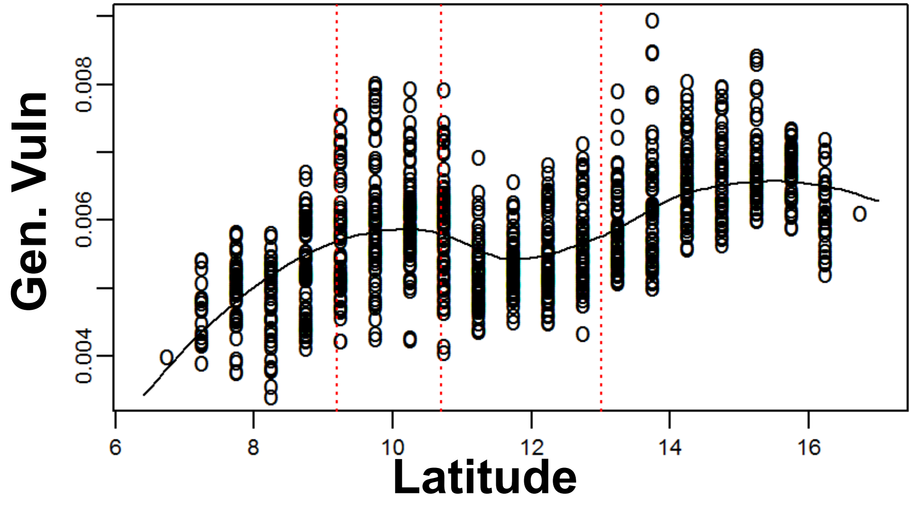


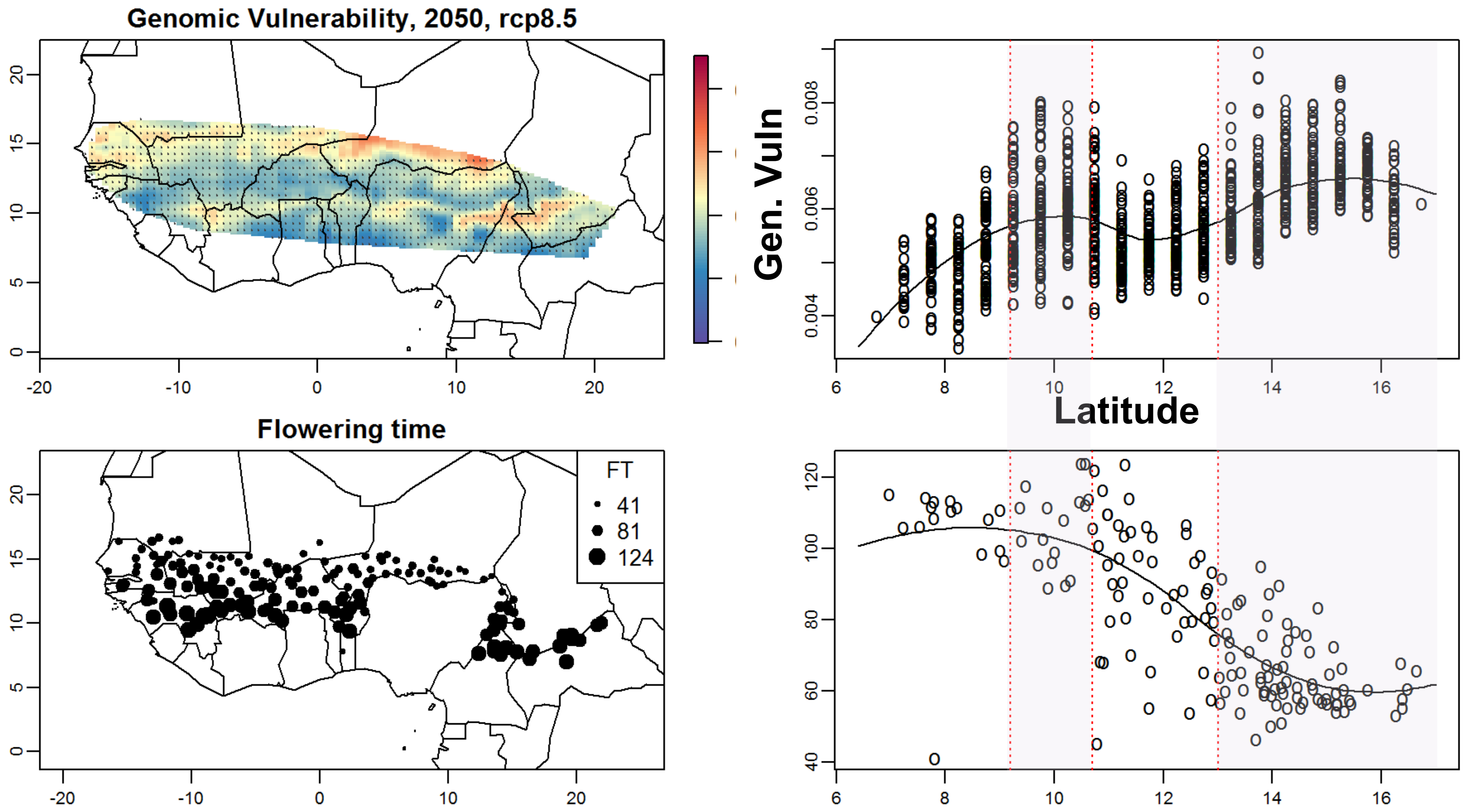
How to make sense of the result ?



Genomic vulnerability and flowering time



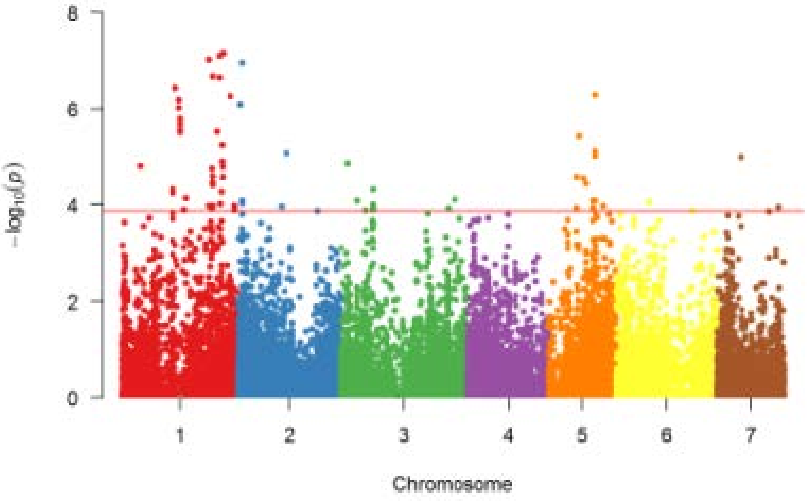




➔ Cycle length is a key component in millet adaptation to climate ?

Could we assess if flowering time SNPs are over-represented in the model, have stronger effect?

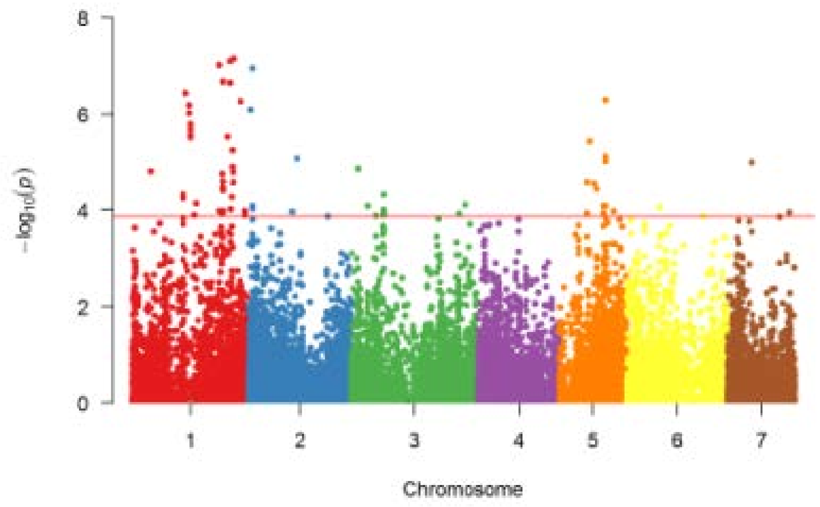
Association study (GWAS) for flowering time



Association corrected for covariance with population structure : 103 SNPs

Contribution to the gradient forest model : higher?

Association study for flowering time



Average correlation in the gradient forest model:

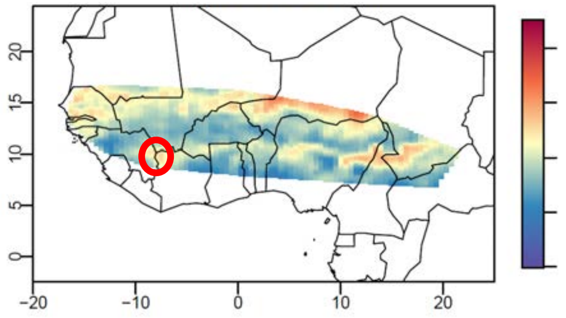
103 SNPs: mean(R^2)= **0.53**

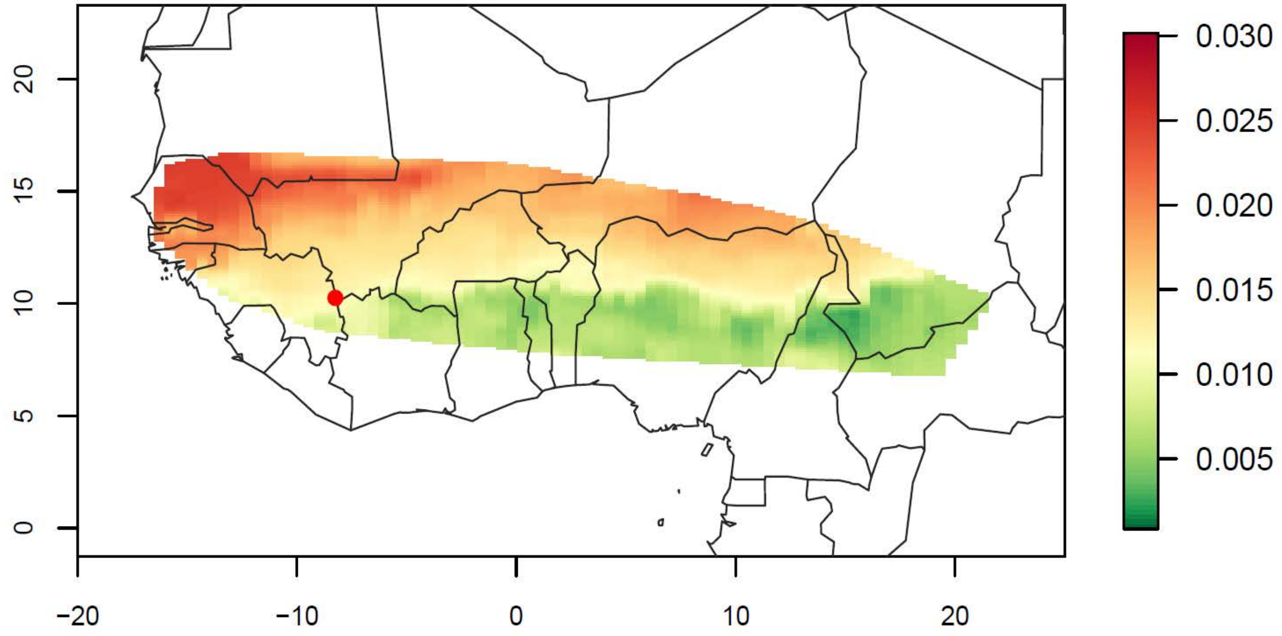
All significant SNPs: mean(R^2)= 0.28

Yes, flowering time QTLs contribute strongly to the model (2 times more)

Can we found already adapted population to future climate projections ?

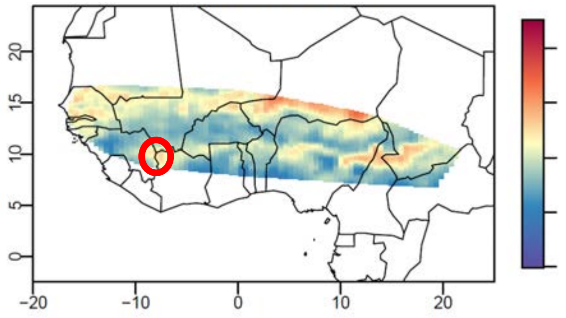
➔Model-based optimal scenario of migration



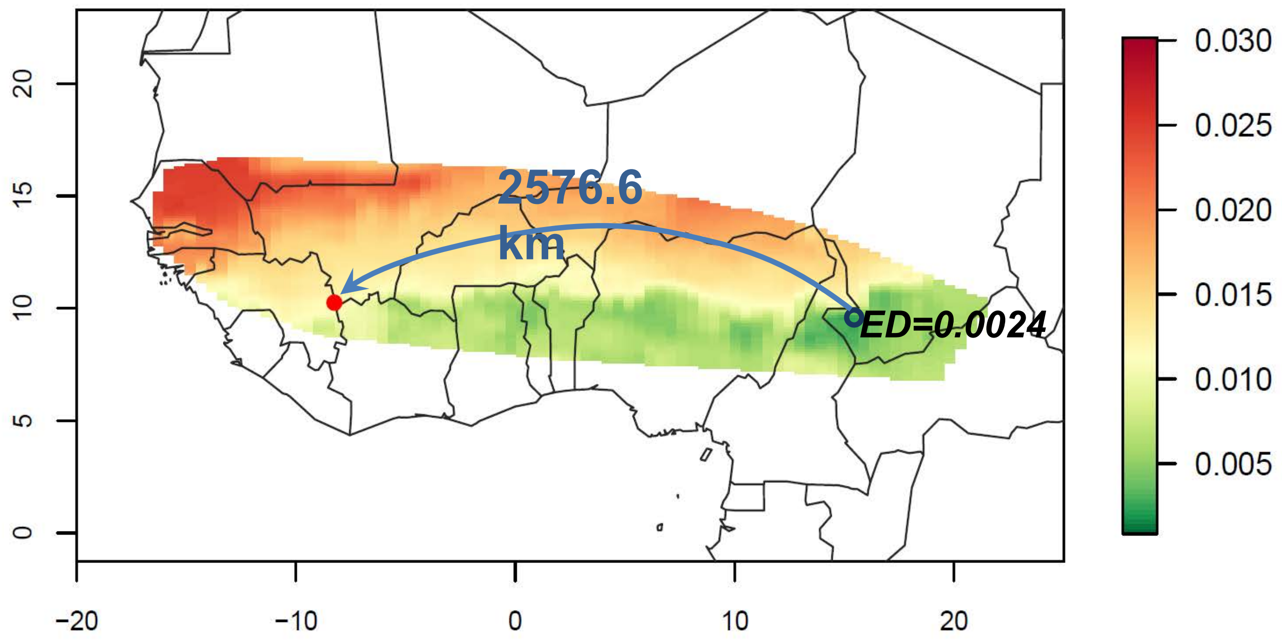


➔ Projection of the mal-adaptation of current landraces to future climate condition forecast at the vulnerable area

Gougerthy et al. 2021
Rhoné et al. 2020

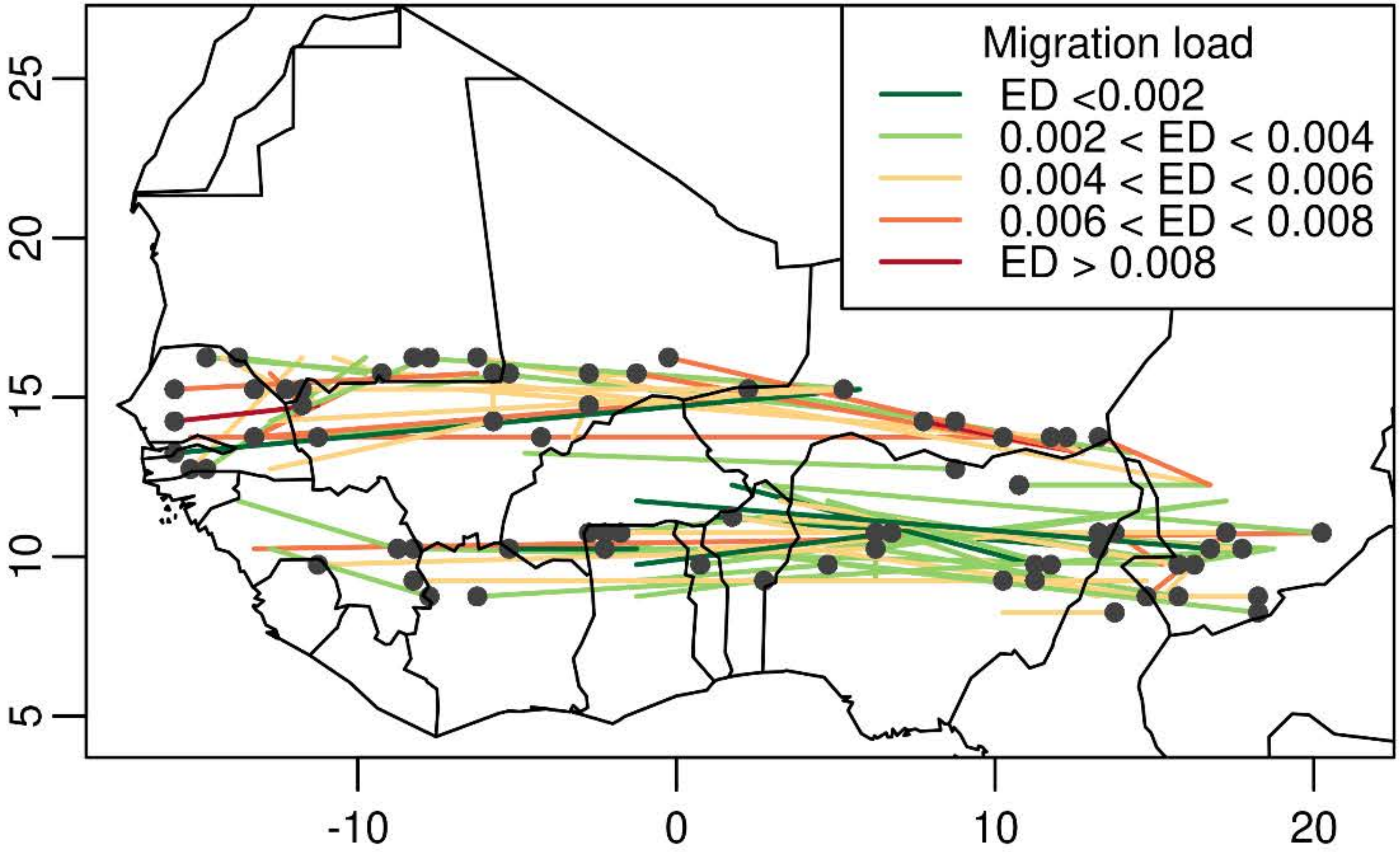


→Model-based optimal scenario of migration



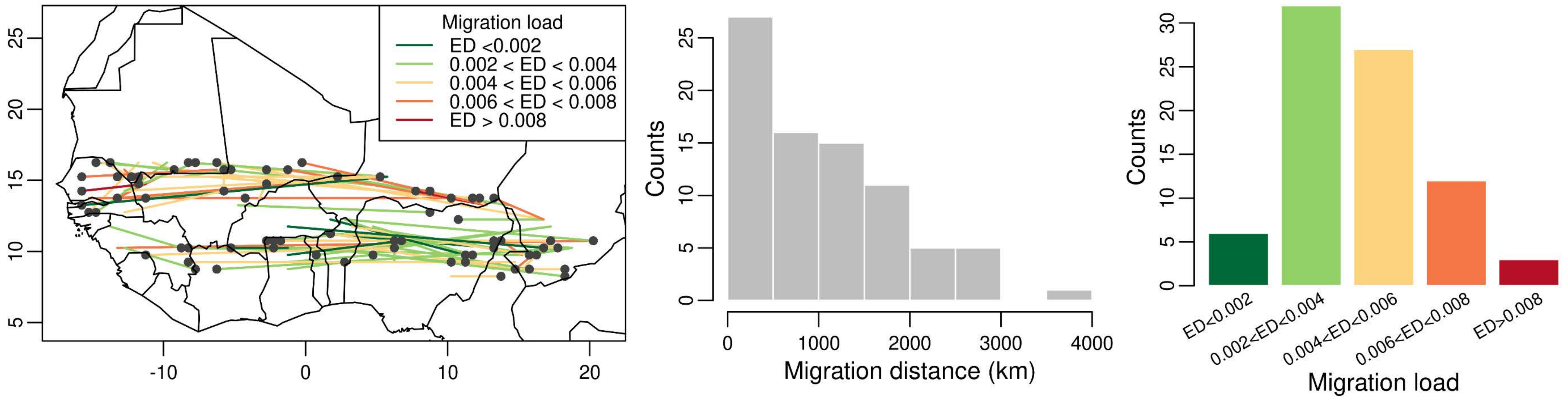
North Cameroon could be used to mitigate genomic vulnerability to future climate in East Guinea

Potential scenario of assisted migration



Rhoné et al. 2020

Potential scenario of assisted migration



➔ Mean distance of migration = **1060 km**

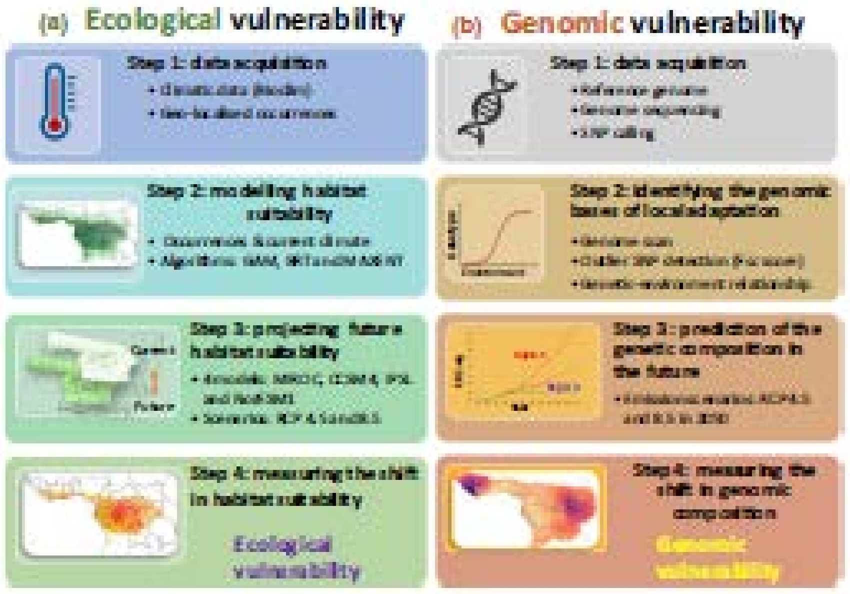
➔ **86%** of trans-boundary migrations

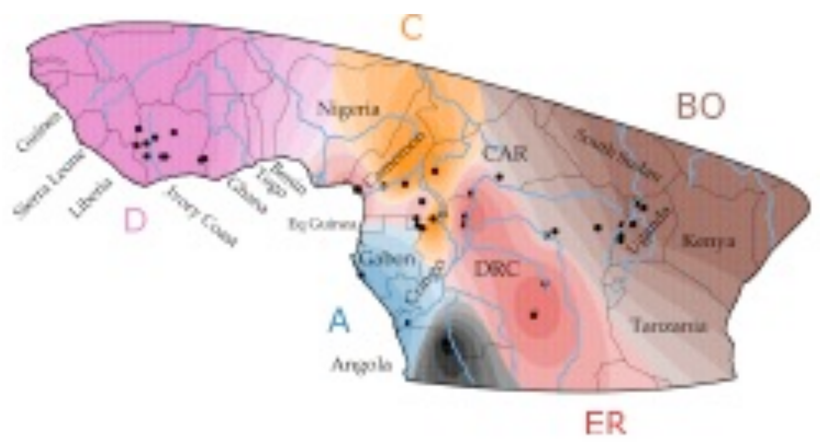
Rhoné et al. 2020

Summary

- Build genomic map of risk of maladaptation to future climate
- Link to some key phenotypic traits
- Using common garden experiment also demonstrate using spatial climate contrast relationship between GO-GV ~ fitness
- Potential scenario of migration (could be test today using spatial contrast)

Comparing niche modeling and genetic offset





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DOI: 10.1111/gcb.16191

Global Change Biology WILEY

RESEARCH ARTICLE

Ecological and genomic vulnerability to climate change across native populations of Robusta coffee (*Coffea canephora*)

Rémi Tournebize[1,2] | Leyli Borner[3,4] | Stéphanie Manel[5] | Christine N. Meynard[5] | Yves Vigouroux[1] | Dominique Crouzillat[6] | Coralie Fournier[7,8] | Mohamed Kassam[7,9] | Patrick Descombes[7] | Christine Tranchant-Dubreuil[1] | Hugues Parrinello[10,11] | Catherine Kiwuka[12] | Ucu Sumirat[13] | Hyacinthe Legnate[14] | Jean-Léon Kambale[15] | Bonaventure Sonké[16] | Jose Cassule Mahinga[17] | Pascal Musoli[12] | Steven B. Janssens[18,19] | Piet Stoffelen[18] | Alexandre de Kochko[1] | Valérie Poncet[1]

Received: 26 April 2021 | Revised: 12 November 2021 | Accepted: 6 January 2022
DOI: 10.1111/mec.16360

MOLECULAR ECOLOGY WILEY

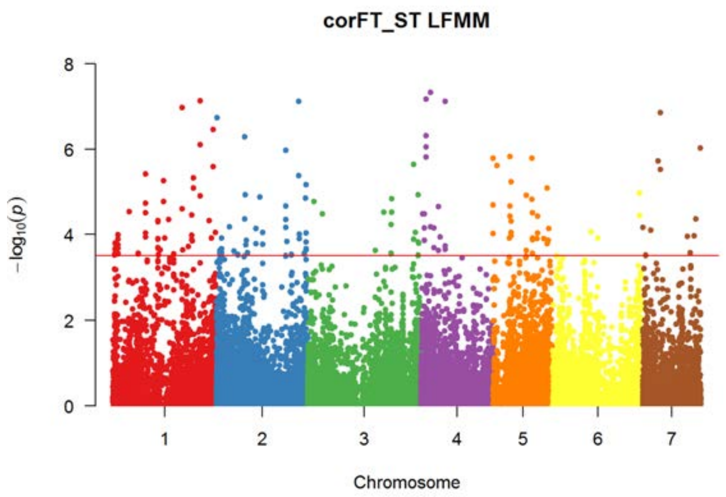
ORIGINAL ARTICLE

Adaptive potential of *Coffea canephora* from Uganda in response to climate change

Sinara Oliveira de Aquino[1,2] | Catherine Kiwuka[3,4] | Rémi Tournebize[1] | Clément Gain[5,6] | Pierre Marraccini[1] | Cédric Mariac[1] | Kévin Bethune[1] | Marie Couderc[1] | Philippe Cubry[1] | Alan C. Andrade[7] | Maud Lepelley[8] | Olivier Darracq[8] | Dominique Crouzillat[8] | Niels Anten[4] | Pascal Musoli[3] | Yves Vigouroux[1] | Alexandre de Kochko[1] | Stéphanie Manel[9] | Olivier François[5,6] | Valérie Poncet[1]

Perspective

- Include more than climate in model
- Analysis across several species (and wild relatives)
- Role of genetic determined plasticity in model?
- Temporal analysis



Thanks !

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Anaïs Dequincey
Cédric Mariac
Leila Zekraoui
Nora Scarcelli
Valérie Poncet

UG
Olivier François
C Gain

CEERAS-ISRA (Sénégal)
Ndjido Kane

UAM (Niger) - IRD
Aichatou Assoumane
Moussa Tidjani
Djibo Moussa

Climate data
Benjamin Sultan
Dimitri DeFrance

Funding:

Thanks