Envirotyping within a multi-environment trial allowed identifying genetic determinants of WOSR yield plasticity

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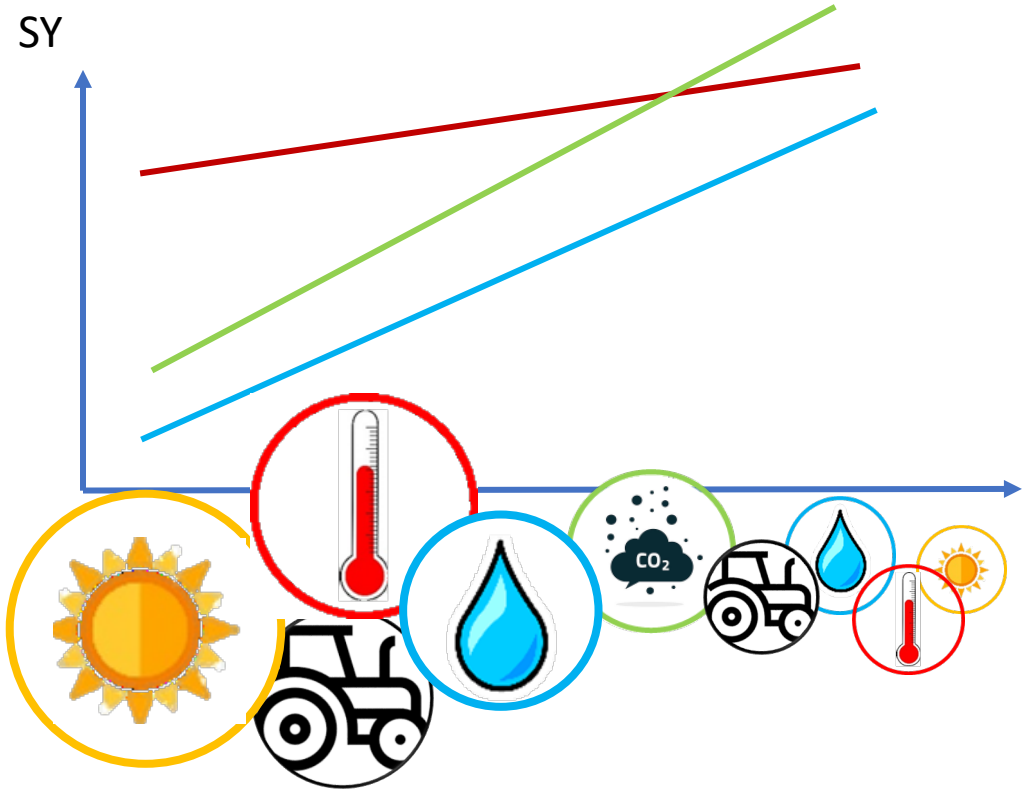
Research questions

Which are the genetic determinants of Seed Yield GxE ?

How to interpret them in the light of environmental characteristics ?

Cultivar Seed Yield Plasticity



Adaptation to a wide range of conditions

vs

Local adaptation

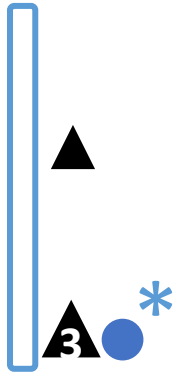
driven by GxE

Research questions and main result

Which are the genetic determinants of Seed Yield GxE ?

How to interpret them in the light of environmental characteristics ?

A SY- QTL on A07 specifically detected for stressed environments (mean SY of 1.85 t.ha^{-1})



A07

- Bad vernalisation conditions
- Lower T°C and radiation at flowering and beyond
- N limitation

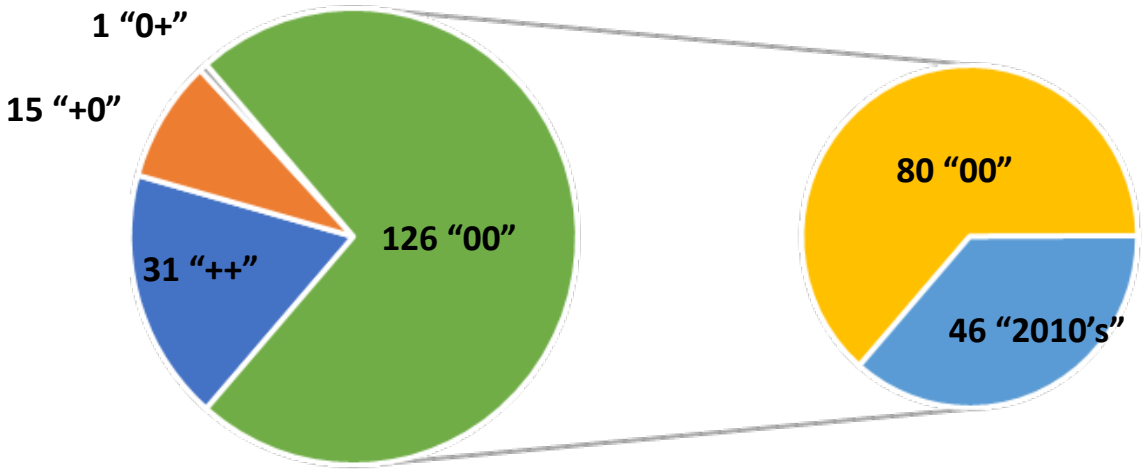
The favorable allele is more frequent in '++' than in '00' germplasm

How did we get there ?

Genetic Material and Multi-Environment Trial (MET)

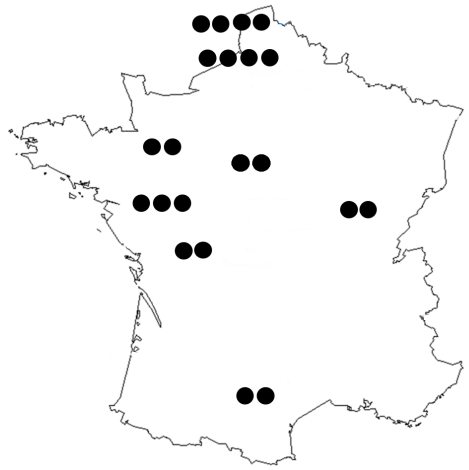
Genetic material

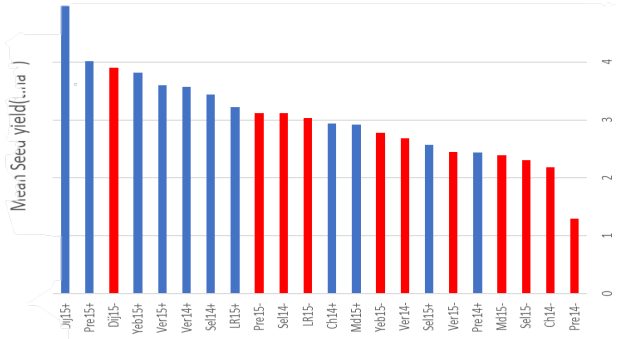
- 173 WOSR (including ++ and 00)
- 217,805 SNP from a whole exome sequence capture



Multi-Environmental Trial (MET)

- 22 environments (2Y, 8 Loc)
- 2 N conditions N+ (3.5 t.ha^{-1}) ; N- (2.0 t.ha^{-1})
- No biotic constraints
- Seed Yield (SY) estimation

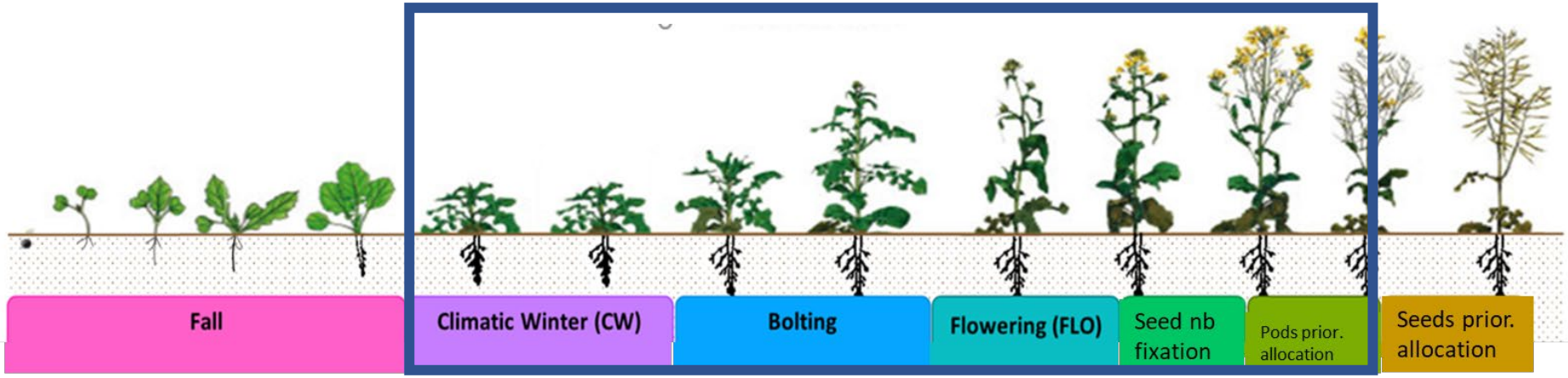


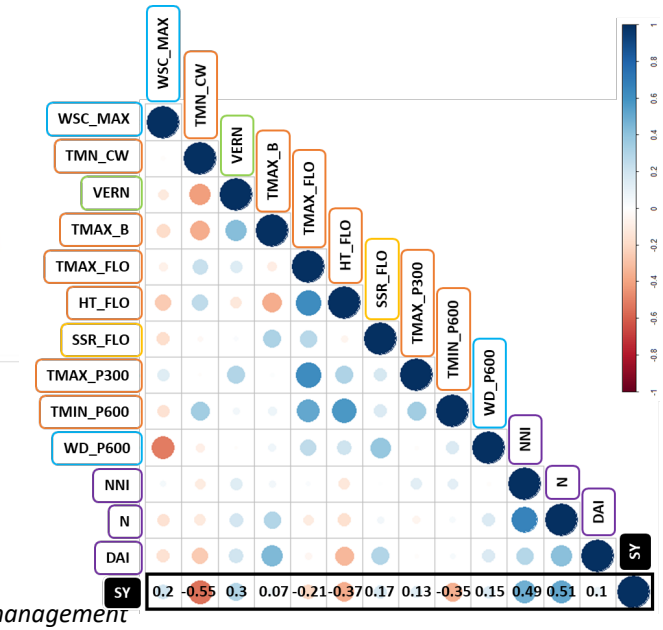


N was not the unique SY limiting factor

=> Need for a comprehensive environmental characterization to understand genotype plasticity

Step 1 : identification of the 13 environmental factors (out of 79) that impacted SY





Plant

Nb of days with optimal vernalization treatment (NBD_VERN_OPTI)

Solar

Sum of solar radiation (SSR)

Phototermal quotient (QPT)

Nb of days lacking of solar radiation (NBD_LSR)

Nitrogen management

Nitrogen Nutrition Index (NNI)

Plant Aerial Biomass at bolting (ADB)

Plant aerial nitrogen quantity at bolting (AN)

Amount of mineral N supplied (Ntot)

Nb of days without rainfall preceding fertilisation (DRI)

Nb of days without rainfall over 10 days after fertilisation (DAI)

Rainfalls over 10 days after N fertilisation (RF)

Nb of days of leaching (RO)

Mean water soil content at fertilisation (WSC_I)

Temperature

Length Growing Degree Day (LGDD)

Temp MAX TMAX TMAX TMAX

Temp MIN TMIN TMIN

Mean Temp (TMN)

Nb of days with high temperature (**NBD_HT**)

Nb of days with low temperature (NBD_LT)

Nb of days with frost (NBD_FR)

Water

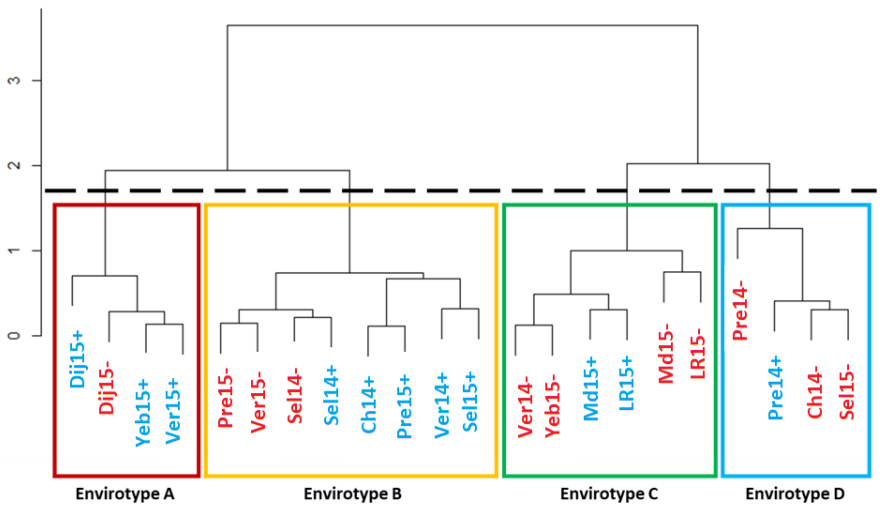
Water soil content MAX (WSC_MAX)

Mean Water content (WSC_MN)

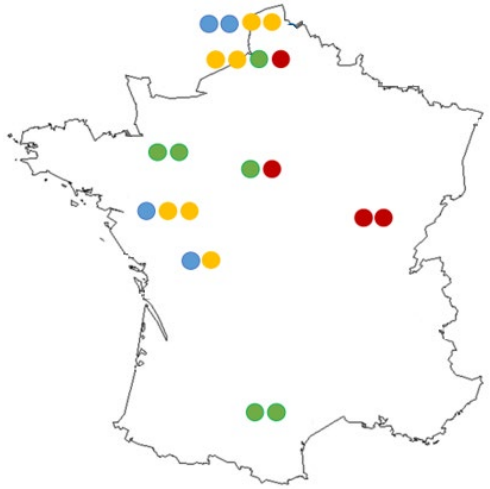
Nb of days with water moderate stress (NBD_WS)

Nb of days with water intense water stress (NBD_WD)

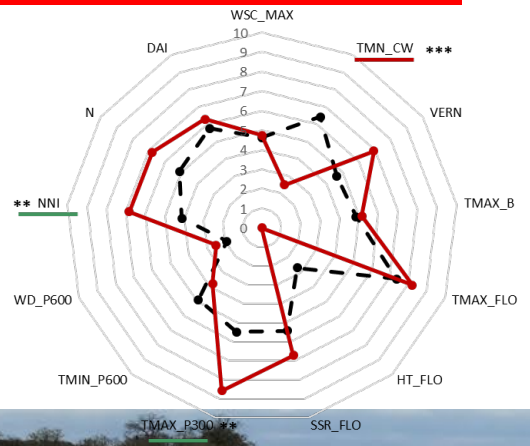
Step 2 : clustering of The MET into 4 envirotypes



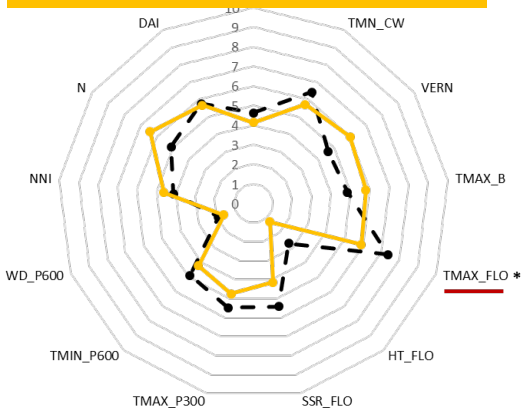
SY	3.04	3.76	2.84	2.72	1.85
NNI	1.06	1.29	1.22	0.92	0.91



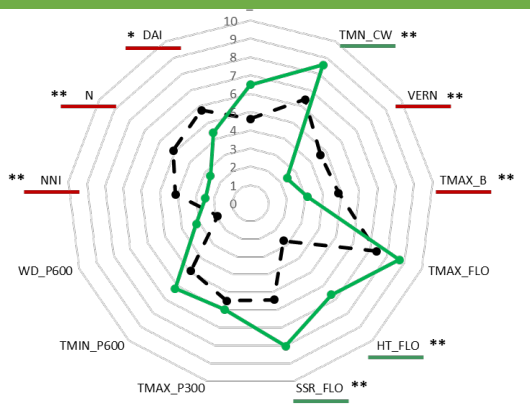
Low T°C / winter
High T°C post-flowering
High N



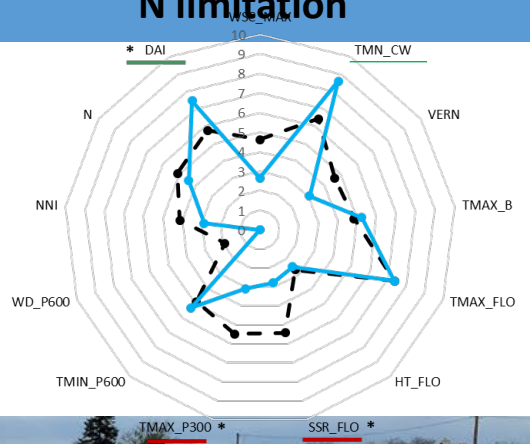
Similar to the mean MET



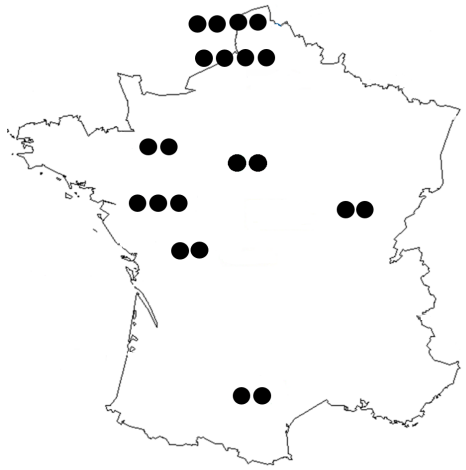
High T°C and radiation at flowering
Bad vernalisation conditions
N stress

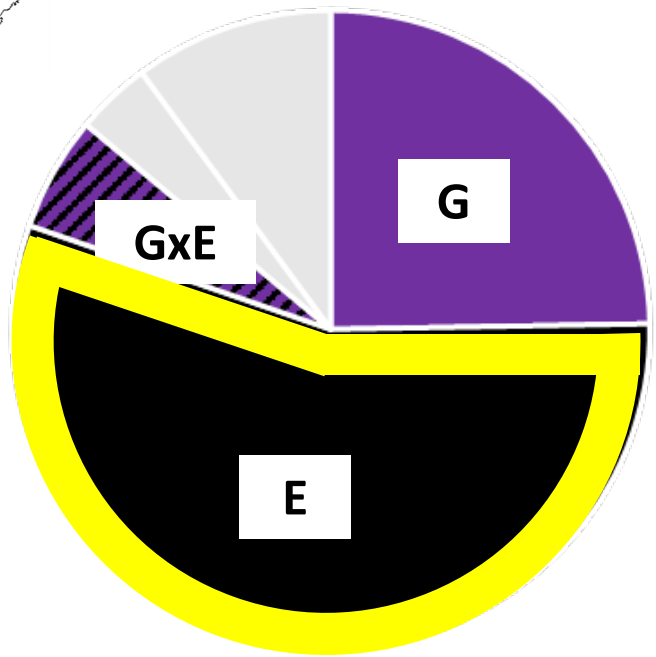


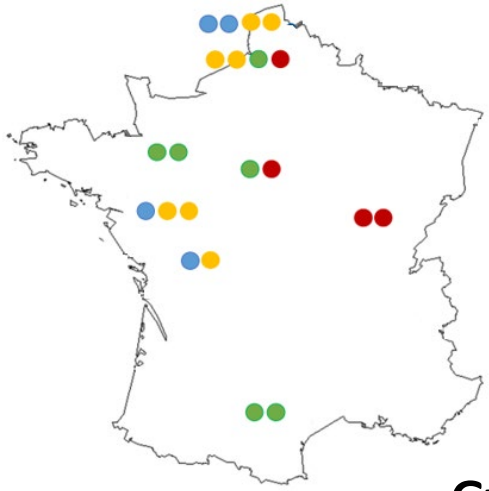
Bad vernalisation conditions
Lower T°C and radiation at flowering and beyond
N limitation

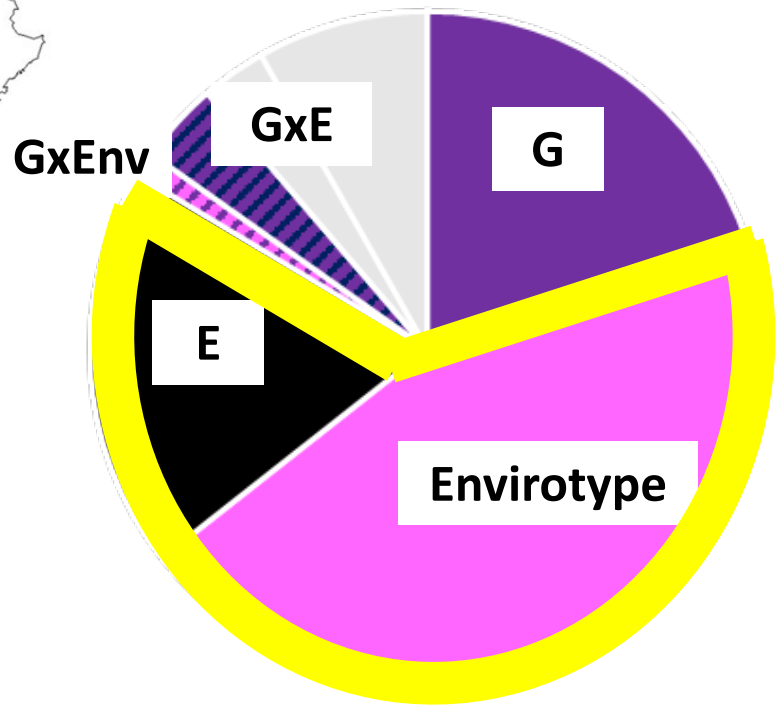


Envirotyping captured 70% of Environmental effect and 24% of GxE

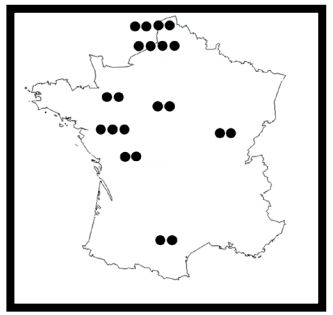


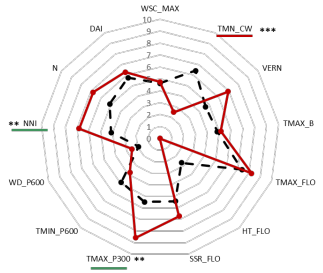


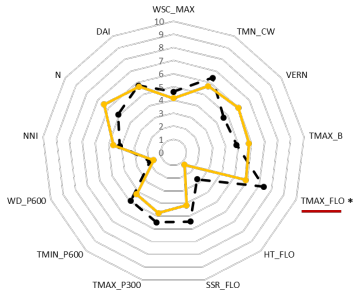


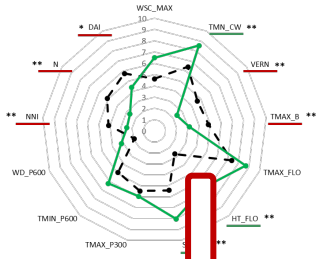


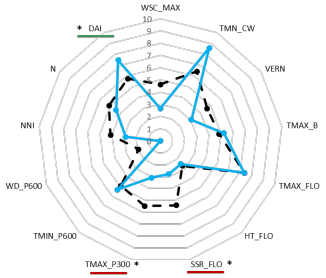
Step 3 : GWAS per envirotype allowed identifiyng QTL involved in GxE

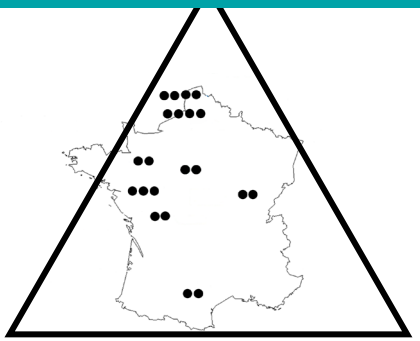








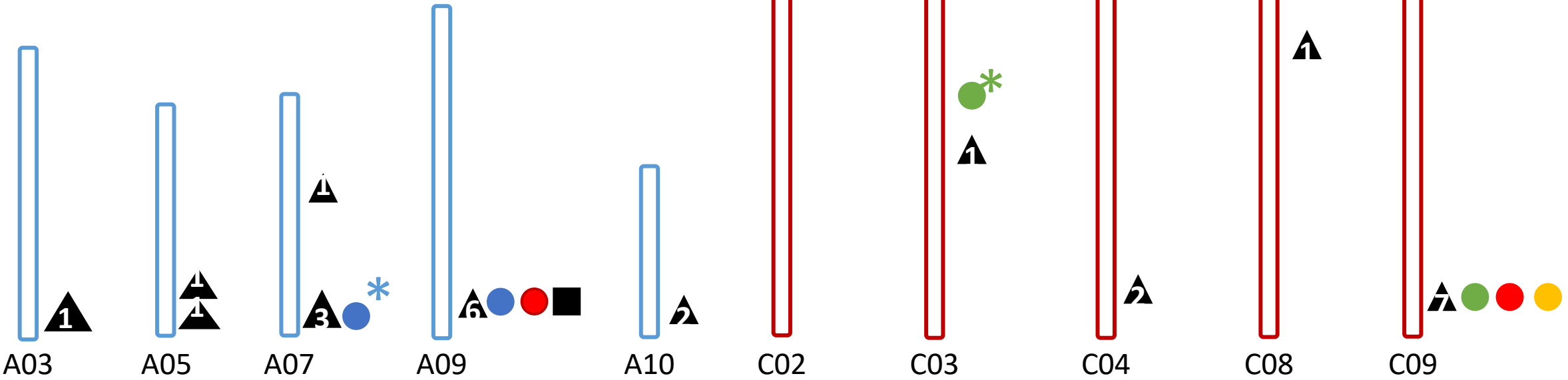




■ MET : 1

● Envirotype : 7

▲ Essai : 29



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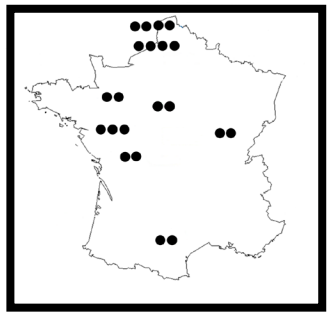
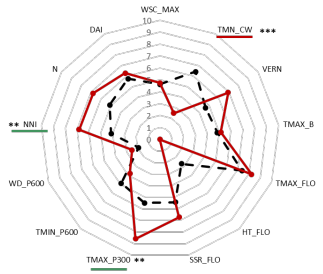
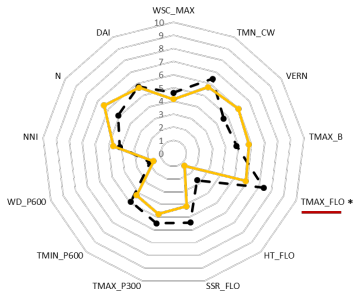
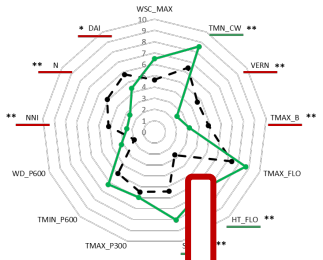
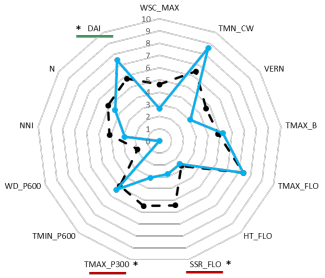
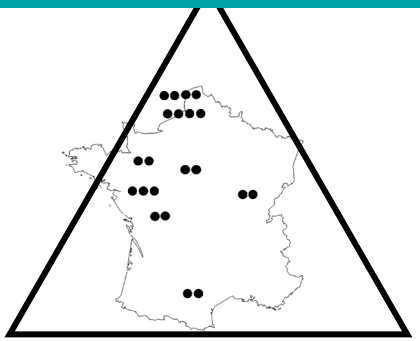












■ Réseau : 1

● Envirotype : 7

▲ Essai : 29

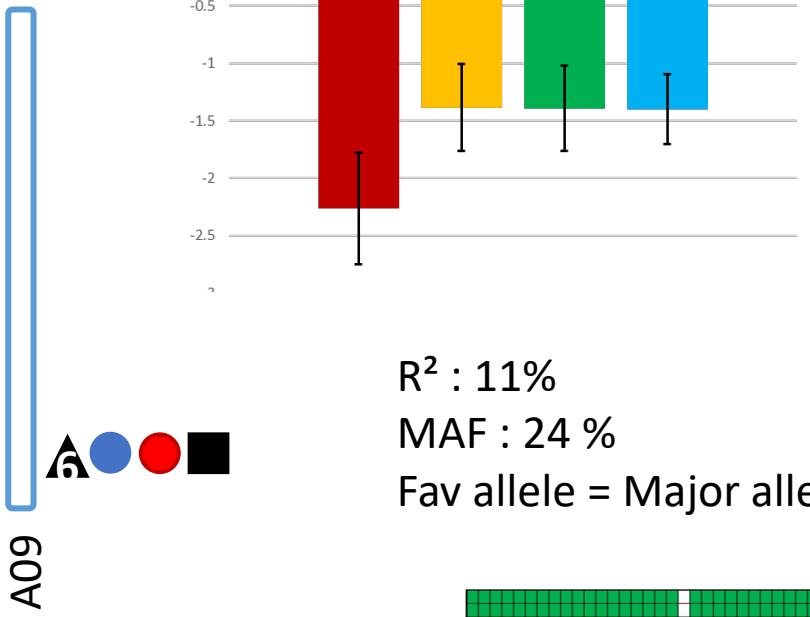
INTERACTIVE

STABLE

STABLE

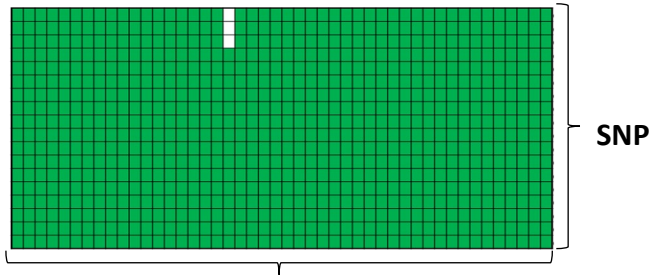
A03 A05 A07 A09 A10 C02 C03 C04 C08 C09

A09/C09 a couple of homeologous stable QTL

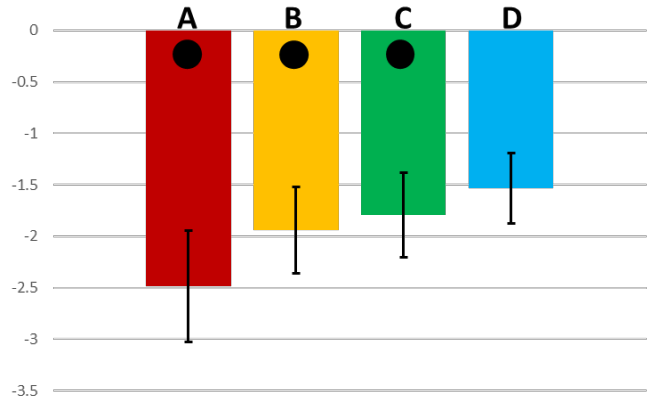


A09

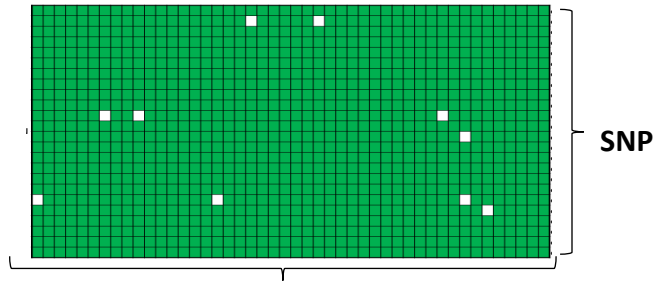
R^2 : 11%
MAF : 24 %
Fav allele = Major allele



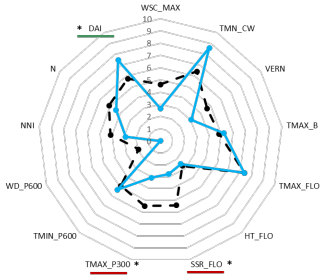
C09

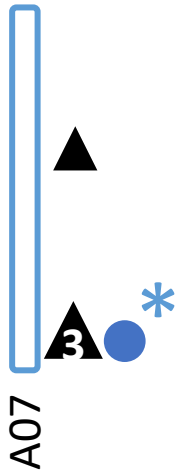


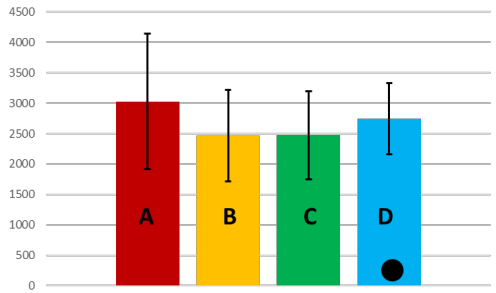
R^2 : 11%
MAF : 23.1%
Fav Allele: Major allele



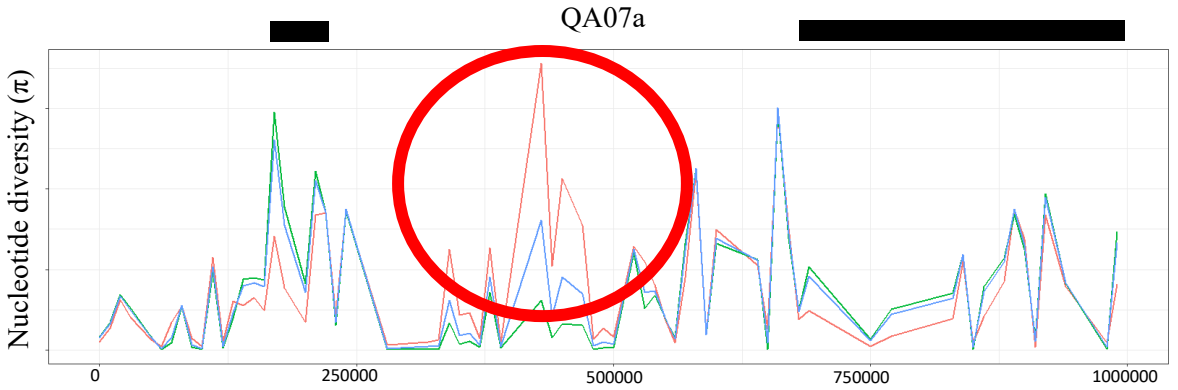
A QTL on A07 specifically detected for the most stressed envirotype



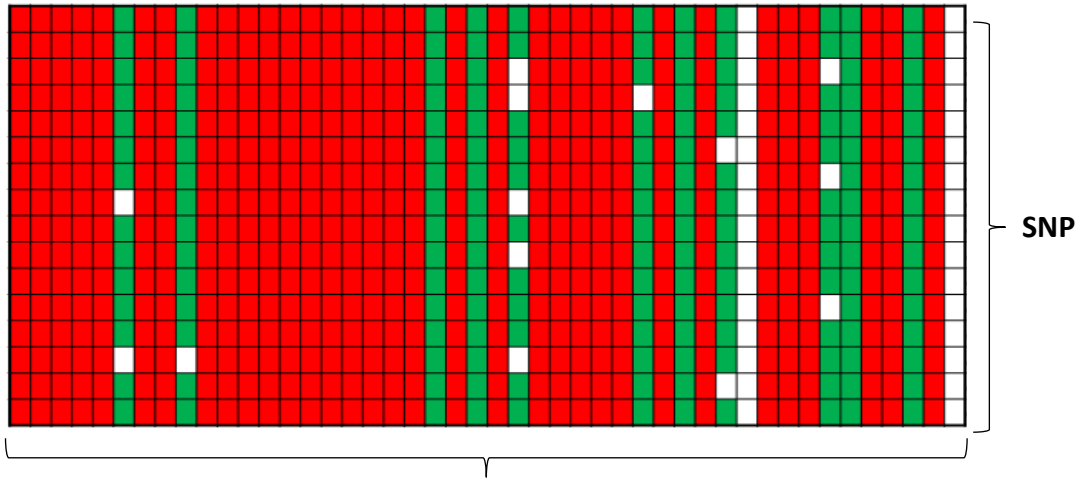




R^2 : 19%
MAF : 18.7%
Fav. Allele = minor all



‘++’ ’00’ 173 G



‘++’ WOSR consist in a valuable resource for improving SY in stressed environments

Perspectives

Deeper characterization of the genetic diversity at the QTL A07.
Which repartition of the favorable variant within WOSR germplasm ?

Complete GWAS by « Genomic Prediction by envirotype » approaches
Catch the polygenic effect involved in WOSR plasticity and adaptation

Enlarge the MET to include biotic stresses (disease and flea beetle,….)

Help proposing new cultivars :

- adapted to limiting environments
- That stabilize Seed Yield
- Adapted to agriculture transition

Conventional agriculture

Low input agriculture

Agroecological practices + Climate Change

Acknowledgements

Optimisation of the **RAP**e**S**eed **O**il content an**D** **Y**ield under low **N**itrogen input: improving breeding of adapted varieties using genetics and genomics (ANR 2012-2020)

Thank you for your attention !!!