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RCA
Yield under Abiotic
Challenges

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Keywords

Brassica napus
Seed Yield
Seed Quality

Quantitative Trait Loci (QTL)
Genotype by Environment
Interaction



Identification of the genetic and molecular determinants controlling seed yield and quality in oilseed rape



Social-economic context

A major challenge in plant breeding is to ensure an optimized and stable production under fluctuating environments while reducing the environmental impacts of agriculture. Thus the new rapeseed varieties should be tolerant to many stresses (water, temperature, pests ...) while maintaining a high level of yield and seed quality in low input systems. Understanding the 'genotype x environment' interaction determinants is needed to built ideotype adapted to multiple stresses combination occurring in the field.

Scientific context

Genetic analyses of the yield were conducted on a winter oilseed rape population with a wide genetic basis on 20 experiments (different N regime, fully protected). We are interested in identifying the genomic regions controlling seed yield and seed quality under a wide range of environmental conditions. Previous genetic analyses based on multi-local trials revealed that numerous loci are involved in seed yield and seed quality control and strong Genotype by Environment (GxE) interaction effects (10%) led to a high environment-specificity of the QTL.

Objectives

- Identify the critical QTL for seed yield and seed quality that are stable between the different environment by GWAS.
- Decipher environmental effect and GxE interaction by elaborating a set of abiotic descriptors to identify the limiting environmental stresses on a field network and cluster environment based on this results.
- Prioritize QTL depending on the environmental specificity pattern and investigate the genomic organization in the light of the polyploidy and duplicated nature of the rapeseed genome

Results

- Analysis of the variance for different traits showed an important contribution of the environment (~30%) and the genotype by environment interaction (~10%) in the global variation of the traits.
- A numerous QTL for seed yield (**Fig 1**) and for seed quality have been detected and some QTL presented an environmental specificity.
- To understand these specificities, 84 pedoclimatic indicators were designed according to main abiotic stress that could occurred during the crop cycle (**Fig 2**).
- 10 pedoclimatic indicators were identified as limiting factor for seed yield and clustering of the environments was done according to these limiting factors
- 5 clusters for 20 environments were identified and showed seed yield differences

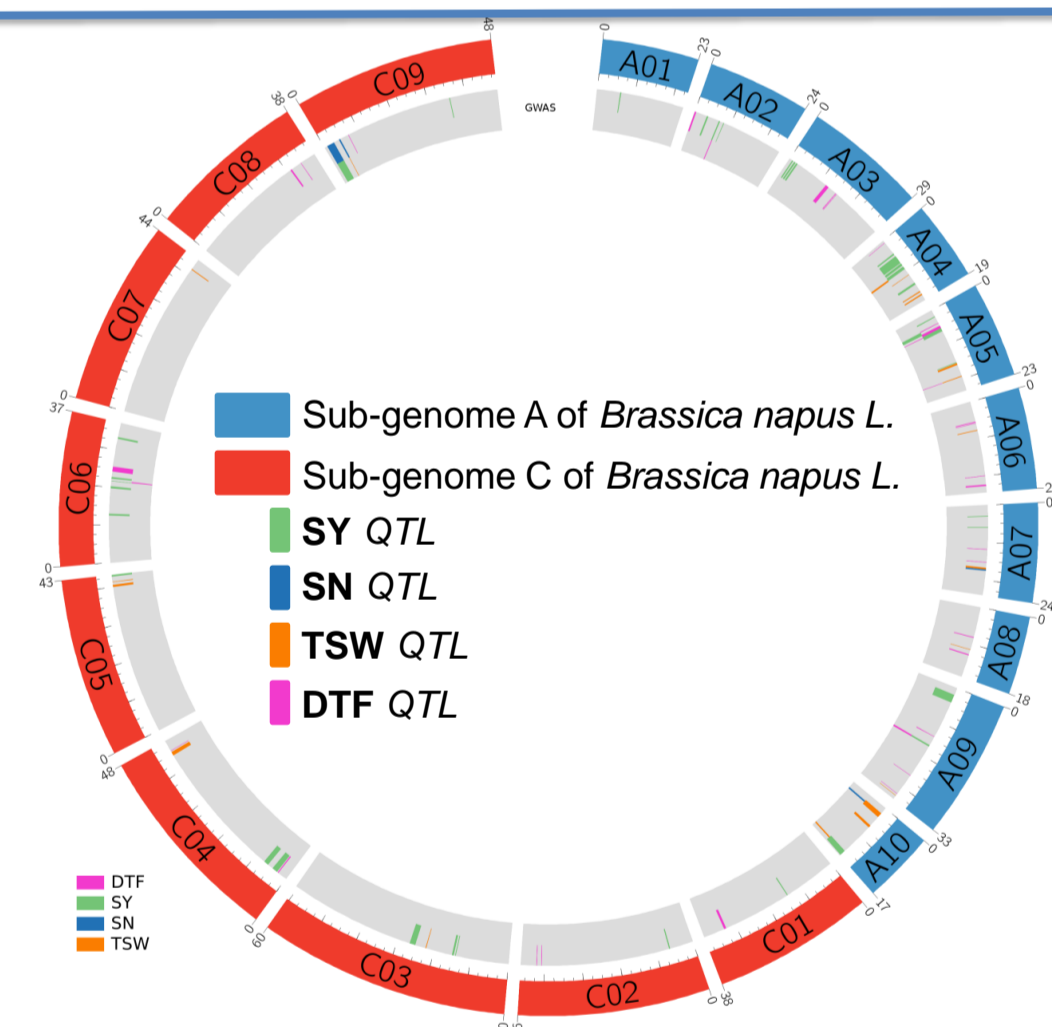
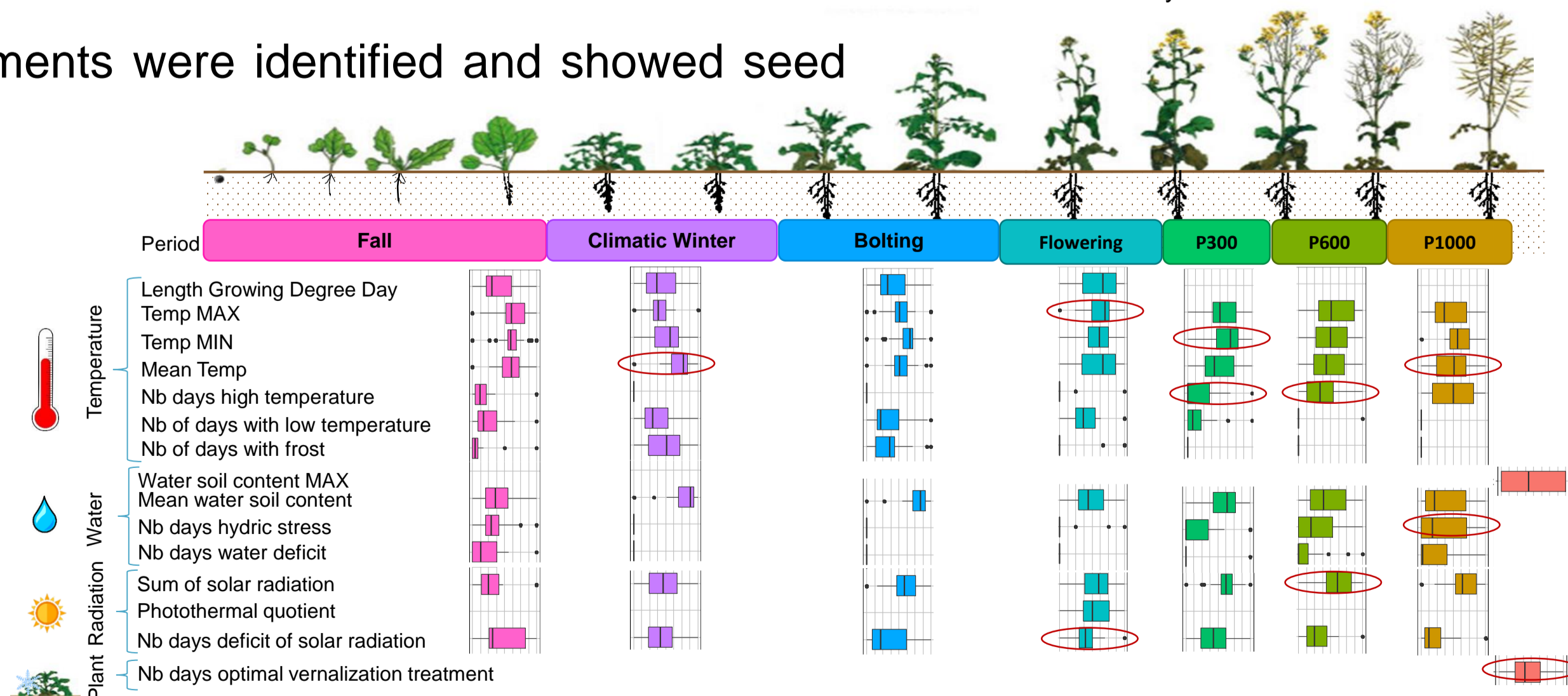


Fig 1: Circos diagram showing the mapping of seed yield, seed number, thousand seed weight and days to flower QTL obtained by GWAS

Fig 2: Elaboration of a pedo-climatic indicator set according to the developmental stage of WOSR. The P300/600/1000 periods corresponded to Flowering + 300/600/1000 growing degree days respectively. Each indicator is represented by a 0-10 scale. The red ellipses highlighted the limiting factors for seed yield.



Perspectives

- Identify QTL profile in relation with cluster to access QTLxE interaction
- Investigate the interaction between QTL and limiting factors
- Transfer to breeding with an optimization for MAS
- Test application in genomic selection (Calibration per clusters)

