Genome-wide association mapping of yellow rust resistance in Nordic spring wheat collections

Min Lin[1], Ennian Yang[2], Jon Arne Dieseth[3], Muath Alsheikh[3], Morten Lillemo[1]

1 Dep. of Plant Sciences, Norwegian Univ. of Life Sciences, Post Box 5003, NO-1432 ÅS, NORWAY
2 Crop Research Institute, Sichuan Academy of Agricultural Sciences, Chengdu 610066, Sichuan, China
3 Graminor, Hommelstadvegen 60, 2322 Ridabu, Norway

Email: min,lin@nmbu.no

Introduction

Yellow rust (YR), caused by *Puccinia striiformis* f. sp. *tritici*, reemerged as an important wheat disease in Norway with the recent incursion of the new race group in 2014. Thus, little is known about the YR resistance of the current Norwegian wheat materials. In addition, since the race-specific resistance is easily overcome by the rapid pathogen evolution, race non-specific resistance is needed to obtain more sustainable cultivar resistance. In order to assess the field resistance of Norwegian wheat materials, thirteen trials were conducted in seven locations across three European countries and China using a Nordic spring wheat association panel consisting of 300 lines. Another independent Norwegian wheat breeding panel, genotyped by the same 25K SNP chip, was used for validating the haplotype effect caused by the 6A QTL.

Methods and Materials

GWAS analysis: (by R Gapit package): FarmCPU model

Threshold: FDR adjusted P value <0.05

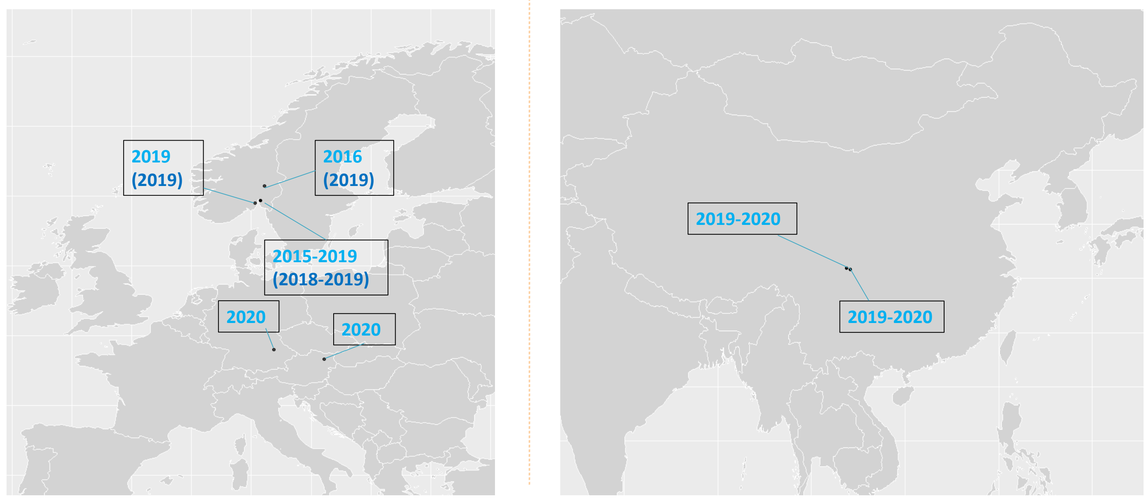
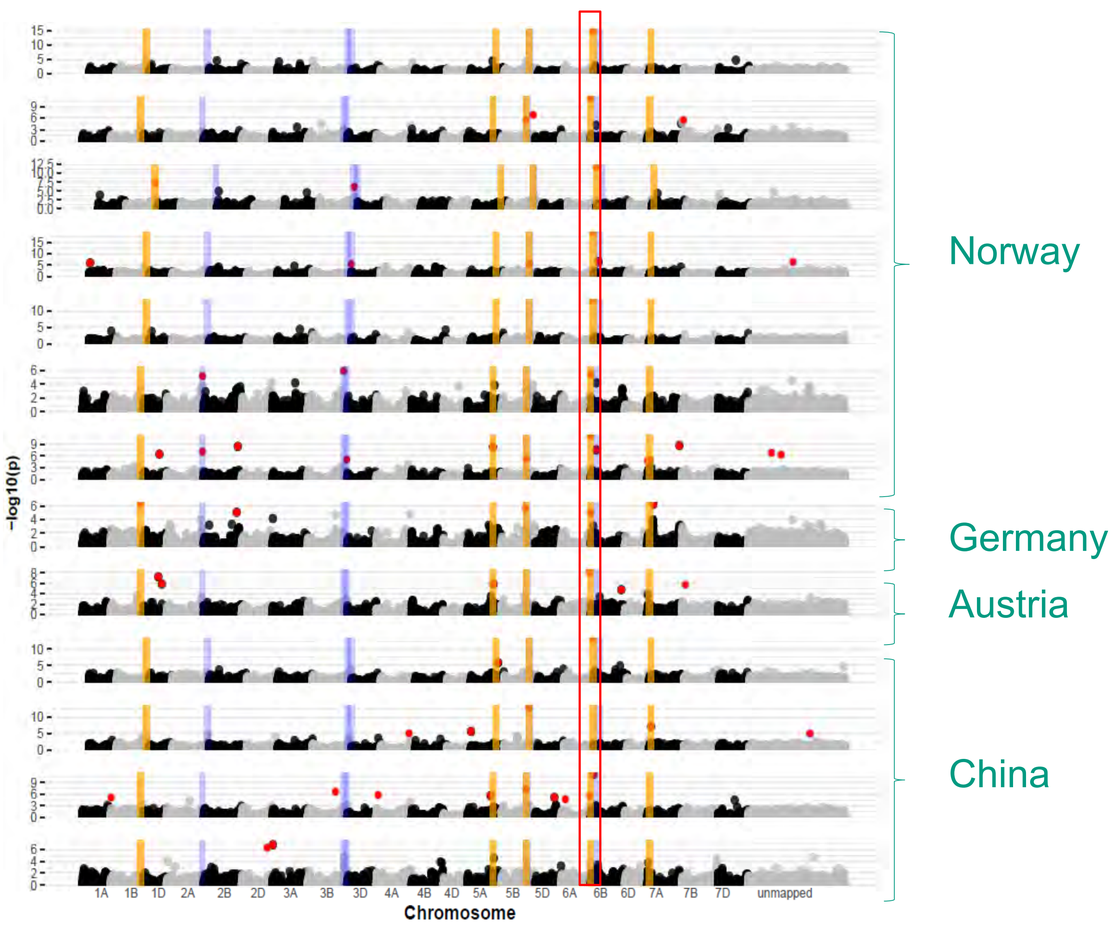


Figure 2: Field trial locations in Norway, Germany, Austria and China. For GWAS panel: the years of field trial conducted were labeled in light blue; for validation panel: the years of field trial conducted were labeled in dark blue with parenthesis.

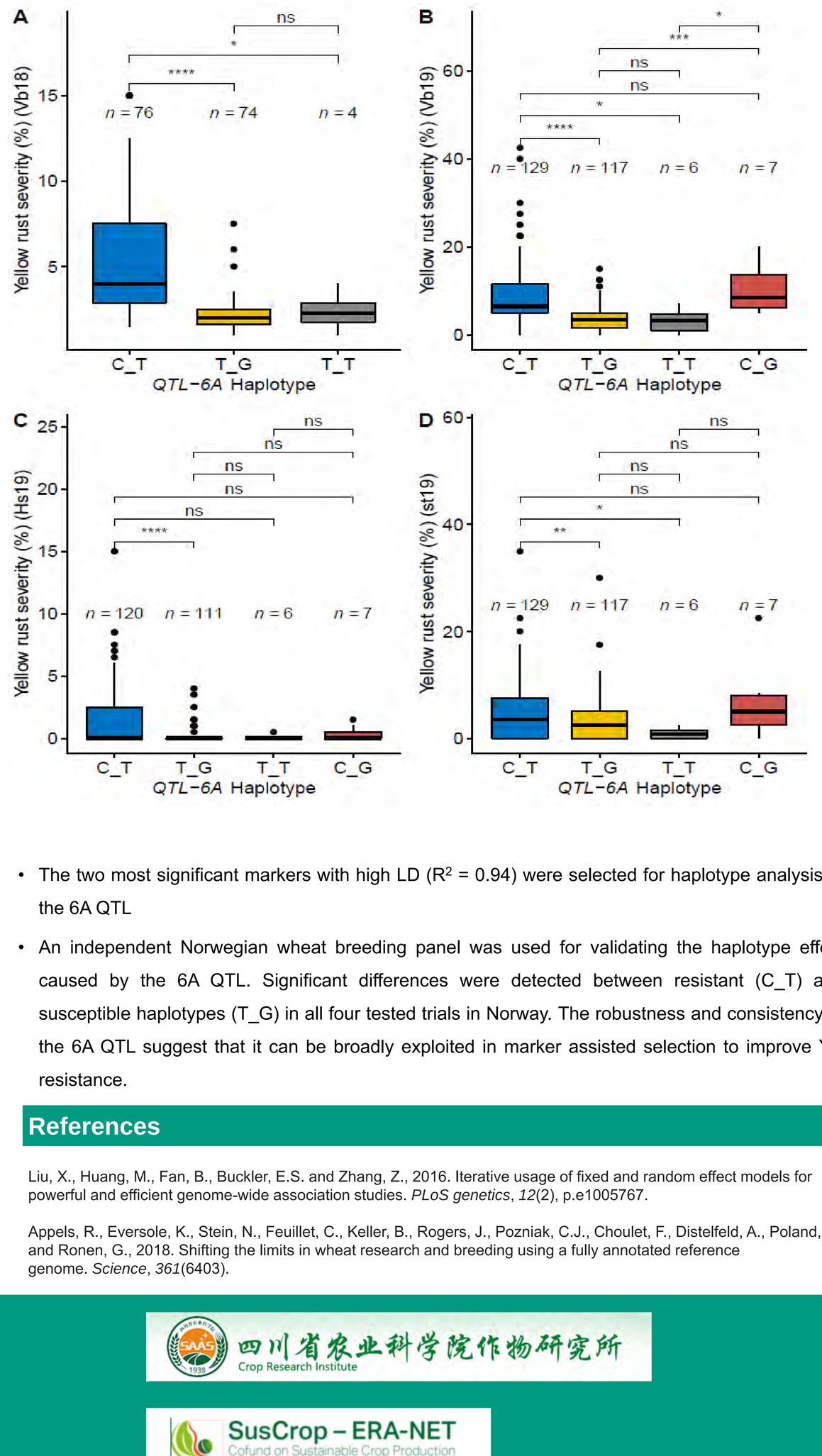
Results and Discussion



- 5 consistent QTL detected across environments (**within country**: **highlighted in blue)** on chromosome 2A, 3B, 5B, 6B
- 5 consistent QTL detected across environments (**across country: highlighted in orange)** on chromosome 1B, 5A, 5B, 6A, 7A
- One robust QTL detected around 610 Mb (Chinese spring RefSeq v1.0) on chromosome 6A (significant in 11 out of the 13 tested environments).
- We hypothesize that the 6A QTL might be driven by a race non-specific gene, because of the consistent detection in all four tested countries.

A B

Figure 1A Yellow rust symptoms; 1B Field scoring in hillplots in Norway
(Photo 1A: Morten Lillemo, Staur, Norway, 2015; Photo 1B: Min Lin, Ås, Norway, 2021)



- The two most significant markers with high LD (R^2 = 0.94) were selected for haplotype analysis of the 6A QTL
- An independent Norwegian wheat breeding panel was used for validating the haplotype effect caused by the 6A QTL. Significant differences were detected between resistant (C_T) and susceptible haplotypes (T_G) in all four tested trials in Norway. The robustness and consistency of the 6A QTL suggest that it can be broadly exploited in marker assisted selection to improve YR resistance.

References

Liu, X., Huang, M., Fan, B., Buckler, E.S. and Zhang, Z., 2016. Iterative usage of fixed and random effect models for powerful and efficient genome-wide association studies. *PLoS genetics*, *12*(2), p.e1005767.

Appels, R., Eversole, K., Stein, N., Feuillet, C., Keller, B., Rogers, J., Pozniak, C.J., Choulet, F., Distelfeld, A., Poland, J. and Ronen, G., 2018. Shifting the limits in wheat research and breeding using a fully annotated reference genome. *Science*, *361*(6403).

Norwegian University of Life Sciences
The Research Council of Norway
Graminor
四川省农业科学院作物研究所 Crop Research Institute
SusCrop – ERA-NET Cofund on Sustainable Crop Production FACCEJPI
WheatSustain