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A genetic investigation of yellow rust resistance in Norwegian wheat

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Genetic study of resistance to yellow rust in Norwegian wheat

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Abstract

This thesis is a preliminary study of the genetic basis for resistance to the fungal disease yellow rust caused by *Piccinia striiformis* Westend f.sp *tritici, (Pst*) in MASBASIS, a core collection of spring and winter wheat lines representing the Norwegian breeding material and important cultivars in Norwegian wheat production. Yellow rust has not been an important disease in Norway until new aggressive races of the pathogen have emerged and spread across Europe. Warrior, Warrior(-) and Kranich are some of the new races that broke the resistance present in the cultivars grown in Europe which have been sampled in Norwegian wheat fields since 2014, Warrior(-) now is the prevailing race in all of western Europe as well as in Norway. There is a need for development of cultivars with high level of durable resistance, as this is the most sustainable method of controlling yellow rust.

In this study 301 spring wheat and 104 winter wheat lines were evaluated for response to *Pst* under field conditions in Norway and China. MASBASIS have previously been genotyped with the Affymetrix 35k SNP chip which was used with phenotype data and population structure to perform a Genome Wide Association study (GWAS). Five significant QTL were detected in both spring and winter wheat, in addition to those significant in one or more of the experimental environments.

This study has produced knowledge and data that can be investigated in an upcoming Norwegian study on yellow rust resistance.

Abbreviations

GWAS – genome wide association study

SNP – single nucleotide polymorphism

MAS – marker assisted selection

MTA – marker trait association

YR – yellow rust

Pst – *Piccinia striiformis* Westend f.sp *tritici*

SNB - Septoria/Stagonospora nodorum blotch

ASR - All stage resistance

APR – adult plant resistance

HTAP - High-Temperature Adult-Plant (Resistance)

PR – partial resistance

PCA – principal component analysis

PC – principal component

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Introduction

Wheat and wheat production

Globally wheat (*Triticum* spp.) is the most important food grain source, accounting for about 20% of the available calories for humans (FAO 2019b). More land area is used for wheat production than any other grains, and according to Food and Agriculture Organization of the United Nations the global production was approximately 771 million tons in 2017 (FAO 2019a).

Wheat has many characteristics that make it one of the most important staple foods in the world. The grain has high nutritional value, containing high amounts of carbohydrates providing energy and starch, protein, dietary fiber as well as being a source of vitamins, lipids and minerals (Shewry & Hey 2015). In addition to high nutritional value, the grain is easy to store and prosses into flour and can be used to produce many types of food. It is used to produce different types of baked products, like pastry, biscuits and such, but most notably raised bread loafs which is possible due to the elastic gluten proteins which is special for wheat compared to other grains (Curtis 2002; Gustafson et al. 2009).

The wheat genus *Triticum* consists of many species with different levels of ploidy, from di-, tetra- and hexapodids, and consists of both wild species are domesticated crop species. The most economically important is the common bread wheat *Triticum aestivum*, while the second most important is durum wheat, *T. turgidum* ssp. *durum* (Sleper & Poehlman 2006). Bread wheat is an allohexaploid (AABBDD, 2n = 6x = 42), with three diploid genomes acquired through a series of hybridization events (Marcussen et al. 2014). The D genome being derived from *Aegilops tauschii*, the A genome being derived from *Triticum urartu*, and the B genome being derived from close relative of *Aegilops speltoides* (Petersen et al. 2006). The first hybridization, between wild einkorn *Triticum urartu* (AA, 2n = 2x = 14) and *Aegilops speltoides* (BB, 2n = 2x = 14), formed the allotetraploid wheat *Triticum turgidum*, AABB, 2n = 4x = 28. The second polyploidization event occurred during the domestication, around 9 000 and 12 000 years ago, between *T. turgidum* and the Tausch's goatgrass *Aegilops tauschii* (DD, 2n = 2x = 14) (Salamini et al. 2002). This resulted in the hexaploid bread wheat *Triticum aestivum* ((Marcussen et al. 2014; Sleper & Poehlman 2006).

Common bread wheat is generally classified as spring or winter wheat. In Norway spring wheat is planted in spring and harvested in autumn the same season, while winter wheat is planted in late summer or early autumn. It will germinate and develop into a young plant that will remain in vegetative phase until it has experienced a period of cold temperatures during winter, and resume growth the following spring. Given that the cold temperature requirement has been met it will then be able to move on to reproductive phase and is harvested in late summer (Curtis 2002).

Bread wheat is adapted to a wide range of growing conditions from temperate to hot areas with dry to humid and rain fed environments (Dupont & Altenbach 2003), and is currently grown from 67ºN, in Norway, Finland, and Russia, to 45ºS, in Argentina and Chile (Gustafson et al. 2009). The optimum growing temperature is considered to be between 15°C and 25 °C (Dupont & Altenbach 2003), with 3–4 °C as minimum and 30–32 °C as maximum growth temperatures.

Wheat in Norway

Production

Norway is a Scandinavian country situated between latitudes 57°58' and 71°10' N with a total distance of 1,752 km from south to north. The country has a land area of 324,000 km2, of which only about 3% is arable land. The climate is greatly influenced by the warm currents transported along the coast by the Gulfstream, creating a milder climate than usual this far north (Lillemo & Dieseth 2011). Most of the arable land is found in the south-eastern part, but also other areas like Jæren on the west coast, and Sør- and Nord-Trøndelag are important areas for agriculture. Figure 1 show the distribution of agricultural land and how much is used for wheat production in Norway. Because of the high latitude Norway must be considered as a marginal area for wheat production.

In 2017, Norway utilized approximately 45 480 and 30 280 hectares for production of spring- and winter wheat respectively, 75 750 hectares in total, yielding 400,5 K tons of wheat, with an average yield of 5290 kg/ha. In 2018 an estimated 58 400 hectares was utilized for wheat, but severe drought lead to a 50% reduction in yield compared to the previous year's according to Statistics Norway (2019). Most of the wheat is produced in the south-eastern part, but there is also some production of wheat in the above-mentioned areas, but cultivation in these parts are modest compared to the south-east.

It is a political aim that Norway produces as much food as possible for its population, and the wheat varieties grown in Norway have potential to be used for baking and production is aimed at human consumption. In good years 75% of the wheat needed for food is produced nationally, but between 1997-2017 the average was 57%.

Topography and size of farms and fields, together with high cost level are challenges to Norwegian wheat production. A short growing season also pose a challenge, and early maturing cultivars are essential to farmers if they are going to be able to produce wheat of high quality every year. If the spring is warm and dry the soil dries up well after the snow melting, planting can be done with relatively little risk of soil compaction. Unfortunately, in some years there is lot of rainfall in early spring and sowing can be delayed and the effective growth season will be even shorter. At the time of harvest in August and September there is a peak in the rainfall, which is critical as it can lead to delayed harvest and lodging which in turn lead to problems with preharvest sprouting (Lillemo & Dieseth 2011). This can cause large variations in both yield and quality, which in turn affects how much of the Norwegian wheat can be used as food, and how much needs to be imported. If the wheat meets the quality requirements of the milling and baking industry a premium is payed, if not it is downgraded to be used as feed, without the premium prize. Challenges with heavy rain fall in critical periods is predicted to worsen with climate changes, and already we are experiencing shorter periods of dry weather in these periods. Growing season has already become longer in both ends due to higher temperatures but taking advantage of this in wheat production when there is also an increase in rain fall in these critical periods can be challenging (Lillemo & Dieseth 2011; Seehusen et al. 2016).

Diseases and pests pose a threat to the wheat crop in Norway like everywhere it is grown. Farmers are obligated by law to practice integrated pest management. This mean that the farmer must consider all possible methods to manage weeds, pests and diseases (NIBIO). Aphids are only chemically controlled in in cases of severe attacks, but this is not necessary in most years (Lillemo & Dieseth 2011). The major diseases that most commonly threaten the wheat crop are Powdery mildew (*Blumeria graminis* f.sp. *tritici*) (Pm), septoria leaf blotch (SNB) and fusarium head blight (FHB) (Lillemo & Dieseth 2011). Three rust pathogens cause infections in Norwegian wheat production, but generally two of them, leaf rust *(Puccinia recondita*) and stem rust (*P. graminis*) do not pose a serious threat to the crop (Ficke et al. 2018). This was also the case with yellow rust until 2014 when there were cases of severe infections and yield loss in Norway for the first time in over 20 years (Abrahamsen et al. 2017; Ficke et al. 2018). Climate change, with warmer and wetter climate, and milder, shorter winters, will have effects on what type of weeds, pests and diseases will threaten wheat and other crops in the future, but it is difficult predict how the situation will develop.

Wheat breeding

According to Lillemo and Dieseth (2011) the first steps towards improving wheat in Norway was systematic evaluation of landraces of spring wheat at the Agricultural university in Ås by Bastian Larsen in 1898. By the beginning of the 20th century similar work was also carried out in regional research stations in different parts of the country. The Norwegian landraces were tested against Swedish lines and found to be superior to these, and earliness was found to be the main characteristic contributing to local adaptation. This resulted in the recommendation of two landraces, Børsum and Østby, for widespread cultivation. Winter wheat cultivation was not common in Norway at this time, but some landraces were tested and the Swedish landrace Upplandsk hvete, as well as two Norwegian landraces, Thorsø and Evenrød, performed well and had better winter hardiness than some of the higher yielding lines. Knut Vik continued the pioneering work started by Bastian Larsen. In 1913 Vik started doing targeted crosses to combine complementary traits found in the Norwegian material and those of improved cultivars. Up to today spring wheat breeding has been based on Norwegian material with local adaptation, crossed to various improved foreign material with desirable traits most notably from Russia, Finland, Sweden and North America. Since the mid 1960's semi-dwarf spring wheat lines from CIMMYT had been used quite extensively for crossing at Ås.

From the start yield potential, earliness and resistance to powdery mildew were important traits in the spring wheat breeding. These traits were also important in winter wheat breeding, in addition winter hardiness has been a particularly important part of local adaptation to Norwegian growing conditions. Today, like in most breeding programs, high yield potential, good quality, good agronomic performance and resistance to important diseases are the main breeding goals in the Norwegian wheat breeding program. Due to some of the climatic challenges specific to Norwegian wheat production, cultivars should have relatively short and stiff straw that is resistance to lodging.

Disease resistance is given given high priority in breeding. As before mentioned, powdery mildew, fusarium head blight, septoria and yellow rust are some of the most important diseases cultivars need to have resistance against. Breeding for disease resistance is done partly with the use of marker assisted breeding, and partly by indirect selection based on strong screening for grain plumpness and high test-weight, as this is not attained in lines heavily infected by diseases in the field. Cultivating wheat of high bread baking quality in the Norwegian climate there are certain requirements for cultivars to be released. Stable and high falling number, i.e. resistance to preharvest sprouting is of great importance to achieve excellent starch quality. To ensure good baking quality and nutritional value it is important that cultivars have high amounts of protein of good quality. Most modern cultivars and breeding lines in the Norwegian breeding material possess the necessary genetics to produce the desired gluten quality that the milling and baking industry require.

Since the beginning of Norwegian wheat breeding there have been several rounds of reorganization. The government funded cereal breeding programs were commercialized in 1993, and that same year the breeding company Norsk Kornforedling AS was established. Statkorn was the majority shareholder together with Felleskjøpet, and the Svalöf-connected breeding program at Bjørke was incorporated into the new company. The company later changed name to Graminor AS and got the responsibilities of all plant breeding in Norway which is the current situation. The wheat breeding program activities of the Agricultural University were moved to the Graminor headquarters at Bjørke research farm, about 120 km north of Oslo, in 2001. Today most of the field work, including selection in segregating generations, is carried out at the nearby Staur experimental farm. An additional location about 70 km south of Oslo is used for early testing of promising lines. Late testing is done at 8-10 locations representatively distributed over the wheat cultivation area, including both experimental farms and farmers' fields. Wheat breeding related research is still being conducted at the university campus, in close collaboration with Graminor. The most relevant research institutions are The Department of Plant Sciences, the Norwegian University of Life Sciences, Nofima Mat (the former Norwegian Food Research Institute, MATFORSK); The division of Biotechnology and Plant Health, Norwegian Institute of Bioeconomy Research (NIBIO)

There is an independent breeding program for spring wheat, with about 100 crosses are made per year and about 150 new lines are tested in replicated yield trials. As Graminor also represents other relevant plant breeders in Europe. 50-100 new spring wheat lines from foreign breeders are tested each year together with the lines developed within the program. More than 80 % of the foreign lines come from Lantmännen SW Seed in Sweden, with which Graminor has a close collaboration. There is not an independent breeding program for winter wheat, but there is a close cooperation with the Swedish winter wheat program of Läntmannen SW Seeds. Planning of crosses and the creation of common segregating populations for final selection in Norway is done in collaboration between the Norwegian and Swedish breeders. A comparable number of Swedish and other foreign winter wheat lines are tested within the breeding program each year. (Lillemo & Dieseth 2011)

Yellow rust on wheat

Yellow rust caused by *Puccinia striiformis* West. f. sp. *tritici* (*Pst*), stem rust caused by *P. graminis* and leaf rust caused by *P. triticina* are all economically important pathogens, causing yield loss in wheat on a global scale (Singh et al. 2016) According to a review by Wellings (2011) it was concluded that *Pst* continues to be a major limiting factor in world wheat production. *Pst* has

previously been considered to be a low-temperature disease, frequently occurring in temperate areas with cool and moist weather (Chen et al. 2014), but the threat has been reported to be increasing and the pathogen have been causing severe epidemics in warmer areas where the disease was rare or absent before (Hovmøller et al. 2010). Cuddy et al. (2015) estimated that the expansion of Pst into new and warmer areas has increased global yield losses from on average at least 0.88 million tons per year to an estimated 5.47 million tons annually.

Since 2011, several new races of Pst have appeared and largely replaced the original pathogen population in Europe (Hovmøller et al. 2016). These new races, termed '*Triticale aggressive/2015'* (first discovered in 2006), *'Warrior'* and '*Kranich'* both discovered in 2011, was virulent to many previously resistant wheat cultivars, but less so in some other previously susceptible varieties, as well as being more aggressive than the races typically found in Europe up to 2010. *Triticale 2015* have caused substantial yield loss in triticale in Scandinavia but can also cause severe infection in wheat. After 25 years without significant outbreaks of *Pst* in Norwegian wheat, there was some severe outbreaks again in 2014 and 2015 and to a lesser degree in 2016.

Samples collected from Norwegian fields in 2015 and 2016 was analyzed at "Global Rust Reference Center" (GRRC) in Århus, Denmark. The analyzes showed presence of Warrior, Kranich, Triticale 2015 and a fourth race termed Warrior(-) in 2015, and in 2016 Warrior(-), Triticale 2015 and a new race temporarily termed Pst New, as well as some samples with a mixture of races was found (Abrahamsen et al. 2017)(GRRC reports). The 2015 samples were dominated by Warrior (64%), Triticale 2015 (22%), Warrior (-) (7%) and Kranich (7%). In 2016 Warrior (-) (43%) and Triticale (36%) dominated, followed by mixed samples (14%) and PstNew (7%). Since 2017 Warrior (-) have become the most prevalent race in western Europe and Norway.

A limited number of samples of infected plant material have been collected in Norway in later years. These have been analyzed at GRRC in Århus, Denmark. Although sampling of *Pst* have not been done systematically over the whole wheat growing area in Norway, the limited sampling that have been carried out show a picture of the pathogen population present in Norwegian fields since 2015, which is very similar that of the rest of Europe. This is expected as most if not all primary inoculum is transported from each season. The Isolate used were derived from a 2017 field sample, tests showed it belonged to the PstS10 a.k.a *Warrior(-)* race, like 17 out of 21 samples that were collected in Norway and analyzed at GRRC in 2017. Two of the other samples belonged to the old PstS7 a.k.a *Warrior* race, and the last two were categorized as "other". Even if sampling in Norway were not systematic and collected from the whole wheat growing area, it is likely that Warrior(-) race were the most prevalent race in Norway in 2017 also, like it was in the rest of western Europe that year. According to the 2018 yellow rust report from GRRC his trend seem to continue in 2018 and also in the 2019 season as well (personal communication with Andrea Ficke, NIBIO, march 9.)

The pathogen and its effect on wheat

The pathogen causing yellow rust, also known as stripe rust, is *Puccinia striiformis* Westend. (Ps), in the genus *Puccinia*, belonging to the family *Pucciniaceae*, order *Pucciniales*, class *Pucciniomycete*, division *Basidiomycota* of the Fungi kingdom (Chen & Kang 2017). The Ps fungi is subdivided into formae speciales based on specialization on different genera and species of host plants in its life cycle (Chen 2005), with Pst being responsible for infections in wheat and triticale. Rust fungi are biotrophic obligate plant parasites, which depend on live plant tissues of its host to survive and reproduce. The alternative host of *P.striiformis* was unknown for a long time and it was not even clear if an alternate host even existed for this rust fungi until Jin et al. (2010) was able to prove that *Berberis* spp. is in fact an alternative host for *P. striiformis* f. sp. *tritici*.

Both yellow- or stripe rust are names descriptive of disease symptoms, as infection of *Pst* on leaves of susceptible plants appear as a mass of yellow to orange urediniospores developing from pustules that are generally arranged as long, narrow stripes between veins of the leaves (Chen et al. 2014). Infection on less susceptible or resistant host plants can produce various infection types (IT) ranging from no visible symptoms to small hypersensitivity flecks to uredinia restricted by surrounding chlorosis or necrosis. Even if symptoms are most easily recognized on infected leaves, all parts above ground can be infected.

According to Chen and Kang (2017) the effect of yellow rust on wheat will vary depending on environmental factors, developmental stage of the host at time of infection and pathogen-host compatibility. As a parasitic biotroph, Pst utilizes water and nutrients from the host plant. Furthermore pathogen-host interactions also lead to changes in the infected tissues that have adverse effects on the host and its development, like reduced photosynthesis and symptoms of water shortage. If infection occur in susceptible plants early in the season it will lead to reduced number of tillers, short plants and poor development of kernels, resulting in low test weight, and reduced grain quality.

Traditionally the European pathogen population have been clonal, and changes in pathogen variation have been driven by mutation, somatic recombination, parasexuality. The new races that have come to dominate the current pathogen population seem to have originated from sexual recombination. It has been established that the Himalaya region is a hot spot for sexual reproduction of *Pst*, and new races are being transported by wind in several legs where new wheat plants are infected and urediniospores are produced and transported further.

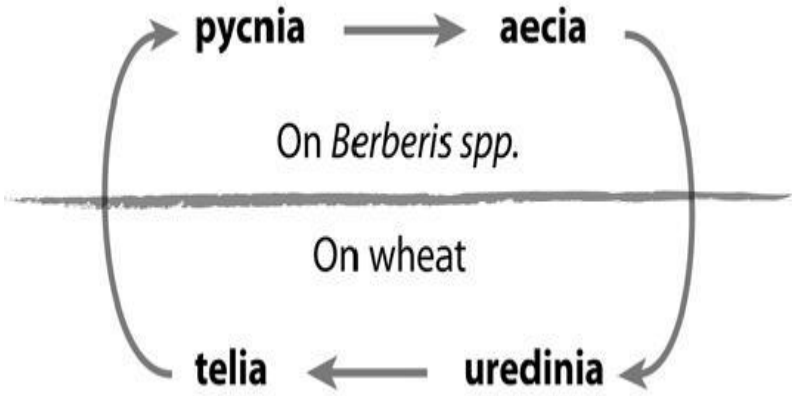


Figure 1 Lifesycle of Pst showing uredinial and telial stages on the primary host wheat and pycnidial and aecia stages on Berberis spp. (Jin et al. 2010)

Pst life cycle and infection process
Pst is a heteroecious macrocyclic rust pathogen that have a complex lifecycle, with five known spore stages and the need for two different hosts to complete its lifecycle. Urediniospores are generally dikaryotic (n+n) and is the dominant asexual stage of the pathogen population on the primary host. Urediniospores have the capacity for long distance wind dispersal, and are responsible for the wide-scale yellow rust epedemics reported on cereal crops (Chen et al. 2014). Jin et al. (2010) identified *Berberis* spp. (*B. chinensis, B. holstii, B. koreana, B. vulgaris*) as alternate hosts supporting pycniospores and aeciospores of *Pst*. Later Wang and Chen (2013) reported that also Oregon grape (*Mahonia aquifolium*) is a host for the sexual phase of *Pst*. It is not certain how important the alternate host and sexual recombination are for producing variability in the pathogen population or in overwintering and as a source of new inoculum that infect the wheat host. As the dominant asexual stage of the primary host, and as primary source of new inoculum the uredinial stage is most interesting in the context of this thesis. It is not known if *Pst* is able to overwinter in Norway, but in any case, urediniospores transported by wind from Denmark and southern parts of Sweden is the most important source of primary inoculum and infection in wheat Norwegian fields. This is possibly the explanation for why there is usually not severe infections starting early in the season in Norway, as it takes some time before there is sufficient inoculum transported by wind and further inoculum is produced so that infection

take place on a large scale in Norwegian fields. As mentioned before, the severity of infection and yield loss is greatly influenced by how early the host is infected.

Infection can occur at temperatures between 0-26 °C, but optimal temperature for urediniospore germination is between 7-12 °C. Germination and infection by urediniaspores requires at least 3 hours of free moisture on the leaf surface. Optimum temperature in latent period is 13-16 °C. First symptoms that are visible with the naked eye can be observed from 6-8 days after infection in the form of chlorotic spots. Chlorosis can be the result of other types of stress, so under field conditions it is not a reliable symptom to determine if there is infection by *Pst.* Sporulation can occur from 12-14 days after infection, producing the characteristic yellow to orange urediniospores typically but not exclusively seen on leaves but can appear on any above the ground parts of the plant.

Management

Yellow rust is usually controlled chemically, and there are not any other agricultural practices or measures that can effectively control *Pst* epidemics. In field experiments with the variety Bjarne, an increase in yield of up 80% was found in fields treated with fungicides compared to untreated fields. However it should be mentioned that the observed reduction in yield was likely due to presence of both leaf blotch diseases in combination with yellow rust rather than yellow rust alone (Abrahamsen et al. 2017).

Treating the crop with fungicides provides an effective protection against *Pst*, but it has an economic cost, as well as being time consuming for the farmer. Fungicides also have adverse effects on the environment and their repeated use over decades has disrupted natural biological systems, and in some cases resulted in development of reduced sensitivity or resistance to fungicides in the pathogen. Furthermore fungicides can have undesirable effects on non-target organisms, and fostered environmental and human health concerns (Yoon et al. 2013). The use of cultivars with efficient and durable resistance to Pst, and indeed other diseases, is a more economically and environmentally sustainable method of crop protection than chemical control (Chen 2005).

Yellow rust resistance

So far eighty *Yr* genes (*Yr1–Yr80*) have been formally named, and more than 100 temporarily named *Pst* resistance genes were reported (Liu, R. et al. 2020). In addition, Rosewarne et al. (2013) reported that 150 resistance QTLs have been mapped on 21 wheat chromosomes (McIntosh 2017). According to Chen and Kang (2017) resistance to *Pst* can be characterized as wheat reducing and/or avoiding damage from *Pst*, hampering the infection and growth of the fungus and/or development of rust. Different types of resistance can be sorted based on various criteria, like plant development and environment, degree of resistance, genetics and plant-pathogen interaction.

Race-specific resistance is monogenic, and resistance or susceptibility in the host depends on the interaction and compatibility of a single gene in both host and pathogen. This type of resistance provides complete protection against specific races of the pathogen, and resistance is generally expressed at all stages of plant development (all stage resistance, ASR). The ease of working with resistance traits controlled by only one gene, as well as the high level of protection provided against specific races has led to widespread use of this type of resistance genes. Unfortunately, due to the simple gene for gene action, race-specific resistance has proven to be easily overcome by the pathogen. Furthermore, as a result of complete or near complete protection provided by this type of resistance, there will be a strong selection for new virulent genotypes in the pathogen population when resistance is broken. Due to these factors race-specific resistance will usually be circumvented by the pathogen within few years after the release of cultivars with that resistance (Line & Chen 1995), and is therefore considered non-durable (Chen & Kang 2017). Plants with adult-plant resistance

(APR) or High-temperature-adult-plant resistance (HTAP) will be susceptible at the seedling stage but express increasing resistance as it grows older and in the case of HTAP as temperature rises. Both APR and HATP resistance is usually race non-specific, but *Yr11*, *Yr12*, *Yr13* and *Yr14* are examples of race-specific APR genes (Chen & Kang 2017). Some of the HTAP genes are more dependent on developmental stage, while others are more dependent on temperature. Both APR and HTAP are usually quantitatively inherited, and resistance is controlled by more than one quantitative trait loci (QTL). Quantitative resistance will be under the control of several QTL, with each QTL having small to intermediate effects. The additive effects of each QTL contribute to the overall resistance, and level of protection provided depends on particular QTL and number of QTL. Because of the complexity of quantitative resistance this type of resistance is usually durable and can potentially provide high levels of resistance (Chen & Kang 2017; Singh et al. 2016). Some genes, like *Lr34*/*Yr18*/*Sr57*/*Pm38* and *Lr67*/*Yr46*/*Sr55*/*Pm46* are known to have pleiotropic effects, conferring multipathogen resistance to leaf-, yellow-, and stem rust and powdery mildew. (Lagudah et al. 2009; Moore et al. 2015). Pleiotropic resistance is not only durable but are great opportunities to improve resistance to several important fungal diseases with fewer genes/QTL, saving resources and potentially reduce the time it takes to develop cultivars with improved disease resistance.

Genotyping

Genotyping is important and the key in research of genes and gene variants associated with phenotypic traits. It can define biological populations by use of molecular tools, but does not involve defining the genes of an individual, it just define a small fraction of DNA. Due to current technological limitations, almost all genotyping is partial. That is, only a small fraction of an individual's genotype is determined. Therefore, genotype process is used to determine differences in the genome of an individual by sequencing the individual's DNA using biological assays (markers) and comparing it to another individual's sequence or a reference sequence such as Chinese spring wheat reference genome (IWGSC 2018a).

Current methods of genotyping include molecular markers (genetic marker) that is the fragment of DNA linked with a specific location DNA sequence on a chromosome within the genome. Molecular markers can identify deference at the DNA level like nucleotide changes due to deletion, inversion or insertion. Markers can include a short DNA sequence such as Single Sequence Repeats (SSR), or a single base-pair change of nucleotides as Single Nucleotide Polymorphism (SNP).

Single Nucleotide Polymorphism (SNP) is a single nucleotide (A,T,G,C) at specific position on the genome that has been substituted with another nucleotide. Theoretically, any of the four alleles can be present at each nucleotide position because of four existing nucleotide types, but in practice, only two allelic variants occur (Syvånen et al. 1999)

Association mapping

Is one of the methods used to detect quantitative trait loci (QTL), QTL is a region (locus) of DNA which is associated with variation of a quantitative trait in the phenotype. Salvi and Tuberosa (2005) defined QTL as the genetic locus where functionally different alleles segregate that cause significant effects on a quantitative trait. The number of QTL can vary for the various traits, i.e. some QTL may indicate that the resistance to a disease is controlled by many genes with a small effect, or a few genes with large effect, or combination of genes with varying effects.

Genome Wide Association Study (GWAS) is a method that identify markers that are associated with a disease or other traits, but this type of study cannot specify which genes are causal of a trait. However, it requires extensive information of the markers within the genome of the organism of interest. (Gupta et al. 2014). Thanks to the release of the sequenced genome of hexaploid spring

wheat cultivar ‘Chinese spring’ in 2018 (IWGSC 2018b) GWAS can easily be applied in the research of this species.

Aims of study

Because Pst had not been a problem in Norwegian wheat production for decades it has not been a priority for research or breeding efforts. As a result of these new races of the pathogen being present and posing a real threat to wheat production also in Norway, there is now a need to gain a better understanding of the genetic basis for resistance and susceptibility to Pst in important cultivars and in breeding material used in Norway.

This study aims to identify the genetic basis yellow rust resistance with emphasis race-nonspecific resistance in a core collection of so and so many WW and SW accessions representing the genetic variation in the breeding material used in the Norwegian spring- and winter wheat breeding programs. GWAS (genome wide association study) will hopefully make it possible to identify loci significantly associated with yellow rust infections. Interesting Markers and QTL can then be investigated further to be validated and characterized. Suitable QTL identified can then be used in MAS or GS when they have been sufficiently researched, as well as detection of specific lines with beneficial combinations of QTL’s giving particularly effective partial resistance to be used as donor parent of these QTL’s in a breeding program with this goal.

Getting a better understanding of the genetic basis for yellow rust resistance harbored in the breeding material will hopefully help the development of new varieties with high levels of durable resistance to yellow rust, thereby contributing to enhance yields and reducing the use of fungicides in the production, making a positive impact on the sustainability of the Norwegian wheat production in the future.

The study will result in a 60 study points thesis describing and documenting the work that has been done and the results there of.

Materials and methods

Plant material

MASBASIS is a core collection of advanced breeding lines, as well as historically and currently important cultivars to represent most of the genetic variation in the plant material used within the national spring- and winter wheat breeding programs. The collection consists of 301 spring wheat lines and 104 winter wheat lines. Some of the lines were added to MASBASIS since 2015, hence all lines have not been scored in all environments and disease severity (Yr SEV) data are missing for 2015 and 2016 for the lines that were added later. Full lists of MASBASIS spring- and winter wheat lines are attached in Appendix table 1 and 2. These lines include important sources of quality traits and disease resistance, crossing parents and advanced breeding lines from Graminor (Norwegian plant breeding company). MASBASIS have been used in several genetic studies investigating resistance to different diseases like powdery mildew (Agha 2019), fusarium head blight (Jansen 2015; Sørensen 2016) and Parastagnosporum nodorum blotch (SNB) (Ruud et al. 2018). The panel has been genotyped with SNP markers (Affymetrix 35K wheat array)(Allen et al. 2017) as part of

ongoing collaborative wheat research projects between Graminor and NMBU (Norwegian University of Life Sciences). Additionally, previously tested SSR and KASP markers were also added to the data set.

Experimental design and field orientation

The hill plot method was adopted for this project using alpha lattice block design (12 plots per blocks) with at least two replications for each cultivar/line at each location, except from the trials in China which did not have any replications. For the spring wheat trials, Avocet (susceptible) was used as a border and Bastian (moderately susceptible) was used as a barrier between the susceptible border the trial plots. For the winter wheat trials, Kanzler (susceptible) and Bjørke (moderately susceptible) were used as borders and barriers in a similar fashion. Each trial was planted with 50 cm between plots and 40 cm between each row

MASBASIS spring wheat lines were scored for Yr SEV in eight field experiments at three locations in eastern Norway. Trials were performed at Vollebekk (Vb) research farm at the Norwegian University of Life Sciences (NMBU), Ås (59°N, 90 m above sea level) in 2015-19; Staur (St) research farm close to Hamar (60°N, 153 m above sea level) in 2015-16; and Bringaker field close to Holmenstrand (Hs) (59°N, 123 m above sea level) in Vestfold in 2019. Through collaboration between my supervisor Morten Lillemo and Dr. Yang Ennian at Sichuan Academy of Agricultural sciences, MASBASIS spring wheat lines were scored for yellow rust at two locations in China, Xindu (XD) (30°N, 104°E) and Pixian (PX) (31°N, 104°E) in the 2019 cropping season. All winter wheat data used in this study have been collected from experimental fields at Vollebekk research farm at NMBU in Ås between 2015 and 2019.

Trails depended only on naturally occurring *Pst* in 2015-17. To ensure sufficient disease levels, wheat plants infected with an isolate from *Pst* 'Warrior(-)' were planted in borders and spreader rows, one plant per two meters, in spring- and winter wheat experimental fields in Vollebekk and at Staur in 2018 (spring and winter ehrat) and 2019 (winter wheat). Susceptible cultivars used for this purpose was Cartago in 2018 and Cartago and Anja in 2019. To promote sporulation and secondary infections and spreading throughout the field, both spring and winter wheat fields at Vb were mist irrigated for 15 minutes per hour between 19.00-22.00 in the evenings a few days after planting out the inoculum. When inoculum was planted in Vb, St in 2019 mist irrigation were not used.

Phenotypic evaluation

Disease severity was scored on leaves as the percentage of leaf area infected, using a modified Cobb scale (0 to 100% infected leaf area) (Peterson et al., 1948) as close to the time when the susceptible checks (Avocet and Kanzler for spring and winter wheat, respectively) obtained their maximum disease level. Plots have been scored twice when possible, but in Vb18 spring wheat fields were scored only once. Chinese fields experienced relatively high disease pressure of naturally occurring *Pst*, and according to Mr. Ennian there were different races of *Pst* present in the two locations.

I collected field data for Yr SEV in both spring- and winter wheat plots at Vollebekk in the 2018 growing season but only winter wheat data were used, and spring wheat data from Vb18 were collected by Dr. Morten Lillemo and Mr. Khaled Murad Agha. The remaining phenotypic data that were used in this study have been collected for projects supervised by Dr. Morten Lillemo and granted by him to be used in this project.

Production and maintenance of Yr inoculum

The isolate used for field inoculations in 2018 and 2019 came from to the Global Rust Reference Center (GRRC) in Århus. This isolate was sampled from a Norwegian wheat field in 2017. The sample were tested and found to belong to the Pst race Warrior (-), the most prevalent race in Europe that season. Isolates were returned to us by GRRC on request by my co-supervisor in NIBIO, Andrea Ficke to be used in this and other projects.

In April 2018 production of inoculum started, and the first batch of 90 pots were planted with eight seeds of susceptible cultivar Cartago (seeds received from GRRC). 9 cm pots (OS Plastic A/S Denmark) with peat based potting compost P–Jord (L.O.G AS, Oslo, Norway) were used throughout the project period.

When planting was done pots were placed in plant trays with a capillary mat covering the bottom of the tray and placed in a greenhouse chamber until inoculation. Daylength was 16 hours and day temperature were set to 18 °C during the day and 13.5 °C during the night. Because there was no cooling in the chamber the day temperatures exceeded 18 °C during sunny days, and temperatures were certainly higher during the season while inoculum were maintained in the greenhouse.

Shortly after receiving the isolates of '*Pst* Warrior(-)' from GRRC, the first batch of seedlings at 1-3 leaf stage (10-16 says after planting) were inoculated with urediniaspores. Plant trays were moved to a workstation and prepared for inoculation by carefully sliding leaves firm but gently between the fingers to remove some of the epicuticular wax and make the leaf surface less hydrophobic. Uredinia spores (all we had) were blended with approximately 250 ml 3M™ Novec™ 7100 Engineered Fluid to produce a suspension. A handheld spray bottle with adjustable nozzle were used to distribute the spore suspension evenly on all plants. After inoculation trays were covered with plastic bags. To ensure that there would be moisture on the leaf surface plants were misted with pure water using the same type of bottle as were used to apply the spore suspension before the bags were closed. Inoculated plants were then incubated for 24 hours in climate chambers holding a temperature of 10 °C. After incubation period plants were moved out of the chamber and covers were removed before plants were placed back into the greenhouse chamber again. Light chlorotic spots could generally be observed after about seven days after inoculation. four to seven days later uredinial pustules would start to appear on the leaf surfaces. Spores were collected when it was enough of it to inoculate the next batch with. Different methods were used for collecting the urediniospores. The first batches were harvested by cutting of leaves with sporulating pustules, and spores were scraped on to a waxed paper and then used directly to inoculate as previously described. A vacuum pump with a spore collection device based on a small metal pipe attached to a 1,5ml Eppendorf tube that used negative pressure was used to harvest the spores from the leaf surfaces were also used when dealing with large batches of plants. Alternatively, when only a few plants were inoculated the same general procedure was followed, but instead of harvesting spores and inoculate with spray bottle infected leaves were cut off and rubbed directly on to the leaves of the seedlings to be inoculated. Seeds of Cartago, Anja or GN12737 were planted in 3-90 posts every 7-14 days and inoculation was done every or every other week to maintain production of inoculum until May 2019. The number of plants that were grown and inoculated varied depending on the availability of spores and the need for plants to transfer to experimental fields in addition to those needed to maintain production of inoculum.

Statistical analysis

Genotyping

The MASBASIS spring- and winter wheat lines were genotyped with the Affymetrix 35k SNP chip (Allen et al. 2017). A total of 14136 polymorphic markers for spring wheat and 14089 for winter wheat were chosen to be used in further analyses (Branchereau 2018). Markers consisted of a combination of SNP markers, with some additional SSR and KASP markers.

Population structure

The evolutionary forces such as mutations, genetic drift, isolation, (natural) selection and recombination will over time lead to the formation of population structure producing subpopulations based on how genotypes relate to each other. These subpopulations will have systematic difference in allele frequency between them. In this study the population structure provided and described by Camille Branchereau in her master thesis (2018):

"The population structure was calculated with a subset of 938 single nucleotide polymorphism (SNP) markers for both winter and spring wheat populations and estimated with STRUCTURE v2.3.4 with a Bayesian clustering method (Pritchard et al. 2000). The analysis was performed for K from 1 to 10, 5 000 burnin length, 50 000 repetitions (numbers of Markov chain Monte Carlo, MCMC) and 3 iterations per run. Output results are then analyzed using Structure Harvester (http://taylor0.biology.ucla.edu/structureHarvester/). This program processes STRUCTURE results and, by using the Evanno method (provided there is at least 3 replicates (Evanno et al. 2005), detects the number of K groups that best fit the dataset (Earl 2012). With these results, R-Studio was then used to perform principal component analyses (PCA), often used in population genetics (Engelhardt & Stephens, 2010; Patterson et al., 2006)."

Branchereau (2018) described that the population stratification could be explained by the origin of the lines. The 103 winter wheat set (population) was divided in two subpopulations; the first subpopulation consisted of 66 lines originating mainly from Germany, UK and other European counties, while the second subpopulation with 37 lines were composed of lines that originates mostly from Norway and Sweden. The 299 spring wheat panel was likewise divided in two subpopulations; the first subpopulation with 235 lines from the northern European countries (Norway, Sweden, Germany and Finland and others), whereas the second subpopulation with 64 lines originating from the international maize and wheat improvement centre (CIMMYT), China, Australia, China and USA along with a few lines originating from other countries.

Phenotype data

Least Squares Means (lsm) can be defined as a linear combination (sum) of the estimated effects from a linear model. These means are based on the used model. Lsm are preferred because they reflect the model that is being fit to the data and will adjust according to the field variability between blocks in alpha-lattice models. For this reason, PROC MIXED was used to statistically analyze the disease severity to estimate lsm. Each lsm is computed as $\mathbf{L}\widehat{\boldsymbol{\beta}}$, where $\mathbf{L}$ is the coefficient matrix associated with the least squares mean and $\widehat{\boldsymbol{\beta}}$ is the estimate of the fixed-effects parameter vector.

The raw data for of yellow rust severity (Yr SEV) of each line in each environment (location/year) were used to estimate lsm in SAS statistical package (SAS 9.4) and mixed linear model PROC MIXED with lines as fixed effects, replicates and blocks within replicates, as random factors. Because there were no replications in Chinese trials the phenotypic data from each of the scorings

were treated as individual environments and lsm of Yr SEV in China were estimated with lines as fixed effect and environments as random effects.

Lsm of disease severity (SEV) for each line over all environments, and over environments with high and low disease pressure (HDP and LDP) were estimated for both spring- and winter wheat lines in SAS statistical package (SAS 9.4) and mixed linear model PROC MIXED was used with lines as fixed effects and environments as random effects.
Principal Component Analyses (PCA) of the phenotypic data were done with Unscrambler X.

Association mapping – GWAS

This project utilized association mapping/Genome-Wide Association Study (GWAS) to identify marker-trait associations for yellow rust response in MASBASIS. Markers that associated with yellow rust were identified using mixed linear model (MLM) in TASSEL v.5.2.7 (Bradbury et al. 2007) with regression model: MLM + kinship matrix (K) + population structure. SNP markers were filtered for minor allele frequencies less than 0.05 and heterozygotes were treated as missing data. A p-value was calculated for each marker based on MLM that has the form $y = Xb + Qv + u + e$, where y is the vector of the phenotypic values (best linear unbiased predictors), X is the vector of SNP marker genotypes, b is the vector of marker fixed effects to be estimated, Q is the population structure matrix derived from structure analysis, v is a vector of fixed effects due to population structure, u is the vector of random effects, and e is the vector of residuals. By using MLM which includes both population structure and kinship which reduces type I error resulting from relatedness and population structure.
Previously described genotype data, phenotype data from field trials (incl. PC1 and 2) and population structure results from STRUCTURE v. 2.3.4 together with a kinship matrix constructed in TASSEL from genotype data and population structure were used as input in MLM. Markers with minor allele frequency >=5% were filtered out and heterozygote markers were treated as missing data.
To check if there could be G x E interactions which could potentially produce false positives due to association with earliness in Chinese environments, phenotypic data for days to heading (DH) previously collected at the same locations in China was run in TASSEL.

Significance Threshold

To study partial resistance which is a polygenic and quantitative trait expressed in the phenotype as an effect of several QTL with varying effects, some have major effect on the trait while many can have minor effects and will be difficult to identify in GWAS. With approximately 14 000 markers in this dataset Bonferroni correction with $\alpha = 0.05$ will give a threshold of $-\log10\ (0.05/14136) = 5.451$ for the spring and almost the same for winter wheat $-\log10\ (0.05/14097) = 5.541$. By adopting such a high significance threshold, it would only be possible to detect QTL with major effects and strong association to the trait, while excluding all minor QTL. Applying a significance threshold that would allow for QTL with minor effects on yellow rust resistance to be detected without greatly increasing the risk of false positive MTA's would better serve the purpose of this project. For this reason, arbitrary significance threshold of $-\log10(p) = 3.5$ and 3.7 were chosen for spring- and winter wheat respectively.

QTL analysis

Only markers with -log10 (P) for PC1 higher than 2.5 were used in QTL analysis. Markers which were significant for PC1 (in Norway) were considered as QTL. Markers not significant for PC1, but significant in one or more environments were considered as interesting markers Significant or interesting markers located within a proximity of 10 Mbp to a significant marker, or 5 cM if

physical position is not available, were considered as part of the same QTL. Markers significant for PC1 In Chinese environments were only considered as a QTL if there were at least one significant MTA in Norwegian environments also. The marker with highest PC1-value were chosen as peak marker of the QTL. If a QTL were significant in tree or more environments it was considered to be stable.

Allele-stacking and haplotype analysis

The effects of number of QTL in the genotypes were analyzed by analyzing TASSEL outputs in R Studio (R studio 1.2.1335) with 'Tidyverse' package for allele stacking. To examine the effect of accumulated resistance alleles in cultivars/lines, they were assigned to groups according to the number of resistance alleles they carry. The resistant allele was detected from TASSEL results based on the predicted effect of significant markers associated with the QTL. Significant differences between groups were determined by a Tukey's HSD test. Peak markers used for allele-stacking: spring wheat: AX-94811682, AX-94669191, AX-95145565, AX-94802487 and AX-95182345; Winter wheat: AX-95069984, AX-94401034, AX-94798864, AX-94760077 and AX-94810594.

R studio was also used with 'MultcompView' package for haplotype analysis, and a Tukey's HSD test were performed to determine if there were significant difference between haplotypes. Haplotype analysis were performed for two QTL from each of the groups. In both groups the most significant and stable QTL were analyzed, located in chromosomal region 5AL at 488 Mbp and 384 Mbp in spring and winter wheat respectively. In addition, one interesting QTL located at 680 Mbp in the region of 5AL were analyzed. Haplotype analysis of this QTL were performed using the same three markers for both spring and winter wheat and included the two markers in with significant MTA in spring and winter wheat and a third marker also located at 680 Mbp (Highest PC1 were -log10(P)=2.2 in winter wheat).
QTL and markers used for haplotype analysis: Spring wheat: 5AL_488/83: AX-94450199, AX-94669191, AX-94919900; 5AL_680/48: AX-94577164, AX-94526834, AX-94502901; winter wheat: 5AL_384/72: AX-94403748, AX-94401034, AX-94498038; 5AL_680/43: AX-94577164, AX-94526834, AX-94502901.

Comparing QTL with previously reported Yr genes and QTL

All significant interesting SNP markers which were considered in this study association were assigned to chromosomes with the accurate physical position from a comparison of SNP sequences with the Chinese spring reference genome RefSeq 1.0 (IWGSC 2018b). If the physical position in RefSeq could not be obtained, primer sequences were obtained from the digital platform GrainGenes (https://wheat.pw.usda.gov/cgi-bin/GG3/browse.cgi) that serves small grains research communities. The sequences were blasted (public BLASn, https://urgi.versailles.inra.fr/blast/?dbgroup=wheat_iwgsc_refseq_v1_chromosomes&program=blastn) against RefSeq1.0 to get the physical position.

Several recent studies on *Pst* resistance have used physical positions (Liu, L. et al. 2020; Liu et al. 2019; Tehseen et al. 2020) rather than genetic distances (cM) according to consensus maps (Bulli et al. 2016; Cavanagh et al. 2013; Somers et al. 2004; Weie et al. 2017). For practical reasons studies that have used physical positions have been given most focus when comparing to findings in this study.

Results

Phenotypic evaluation of yellow rust response under field conditions

Least square means (lsm) for disease severity (SEV) over all environments and environments with high and low disease pressure (HDP and LDP) were estimated in SAS. SAS outputs with covariance parameter estimates and type 3 test for fixed effects are shown in Table 1 and 2 respectively. There were significant differences between environments in Norwegian spring wheat data but not in the Chinese or in winter wheat data (Table 1). Type 3 tests of fixed effects (Table 2) show that line effects were significant, demonstrating that the data is useful for association mapping.

Distribution of disease severity (SEV) for MASBASIS spring wheat lines over all eight Norwegian environments (all E NO), both environments in China (CH), and for MASBASIS winter wheat over all environments (all E) are shown in Figure 1. From these figures it is apparent that most spring and winter wheat lines in MASBASIS have some resistance against yellow rust as only a few lines of both growth habits have very high SEV. In Norwegian environments only 22 out of 303 spring wheat lines have SEV-score higher than 15%, the highest being 60 %, and 172 lines had a SEV-score between 0-3 %. In Chinese environments there were a larger variation and higher SEV, 11 lines had SEV over 60%, the highest was 90%, and only 20 lines had SEV between 0-3 %. Two lines had missing data in Chinese environments. Winter wheat lines seem to generally have quite good resistance and 40 out of 104 lines had SEV of 0-3%, only 7 lines having SEV over 15 % and the highest score was 55 %.

Table 1. Covariance parameter estimates from proc mixed preformed in SAS for all spring wheat experimental environments in Norway (a) and two (two registrations at two locations) in China (b), and all winter wheat experimental environments (NO) with original data (c) and transformed data (d) respectively.

a) Covariance Parameter Estimates

Cov Parm	Estimate	Standard Error	Z Value	Pr > Z
Environment	10.5991	5.7223	1.85	0.032
Residual	31.8479	1.0295	30.94	<.0001

b) Covariance Parameter Estimates

Cov Parm	Estimate	Standard Error	Z Value	Pr > Z
Environment	15.5453	13.0515	1.19	0.1168
Residual	132.26	6.2416	21.19	<.0001

c) Covariance Parameter Estimates

Cov Parm	Estimate	Standard Error	Z Value	Pr > Z
Environment	24.6669	17.6373	1.4	0.081
Residual	30.2224	2.1868	13.82	<.0001

d) Covariance Parameter Estimates

Cov Parm	Estimate	Standard Error	Z Value	Pr > Z
Environment	0.001961	0.009161	0.21	0.4152
Residual	0.4636	0.06492	7.14	<.0001

Table 2. Results from type 3 tests of fixed effects for all spring wheat experimental environments in Norway (a) and China (b), and all winter wheat experimental environments with original data (c) and transformed data (d).

a) Type 3 Tests of Fixed Effects

Effect	Num DF	Den DF	F Value	Pr > F
MASBASIS	302	1914	10.94	<.0001

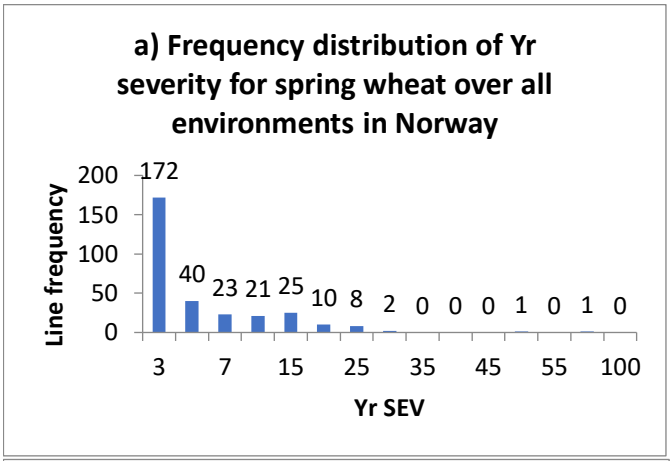
b) Type 3 Tests of Fixed Effects

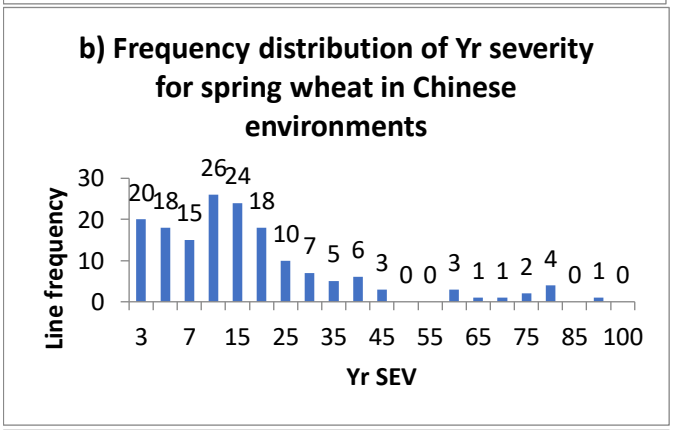
Effect	Num DF	Den DF	F Value	Pr > F
MASBASIS	300	898	10.67	<.0001

c) Type 3 Tests of Fixed Effects

Effect	Num DF	Den DF	F Value	Pr > F
MASBASIS	103	382	7.15	<.0001

QTL with small effects can be difficult to detect in GWAS, but effects of such minor QTL are expected to be more pronounced in environments with high disease pressure (HDP) compared to environments with relatively low disease pressure (LDP). To elucidate such effects lsm was estimated for phenotypic data from environments with high or low disease pressure (HDP and LDP) in Norwegian environments for both spring and winter wheat lines in MASBASIS, these data was also analyzed in GWAS. Grouping of environments as either H/LDP was done arbitrarily as there was not a single parameter could be used to determine what constituted high or low disease pressure environments. Firstly, SEV-score of the most susceptible lines was considered, indicating the potential for infection in each environment. Secondly average SEV of all lines in each environment and over all environments was also considered.





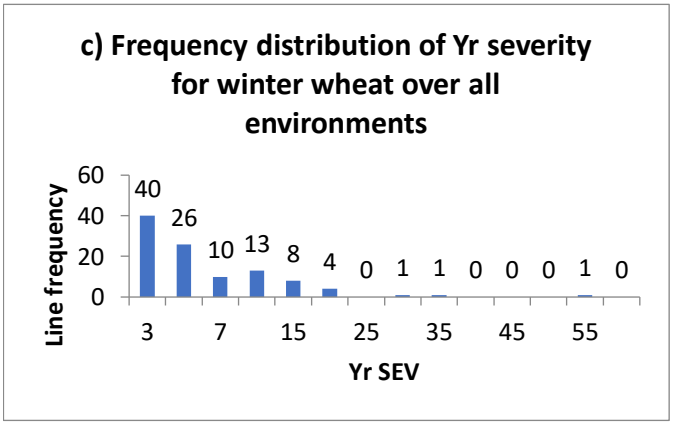
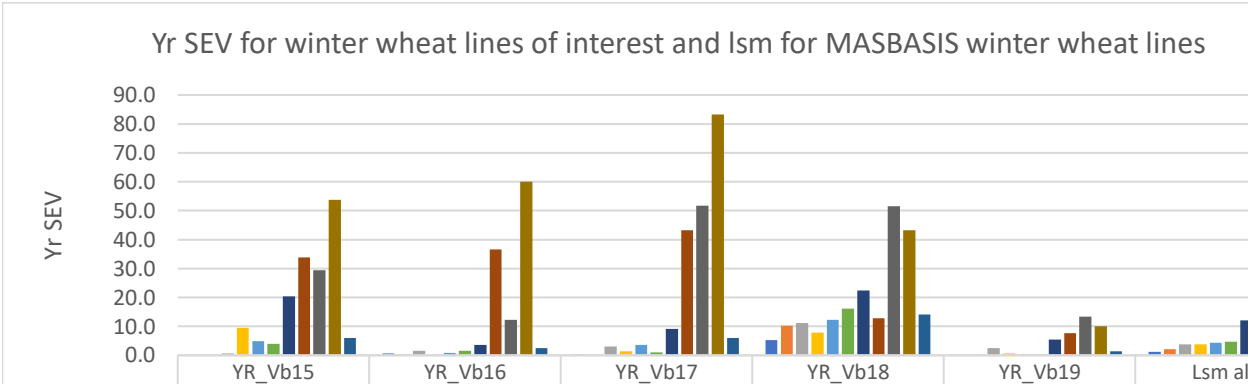


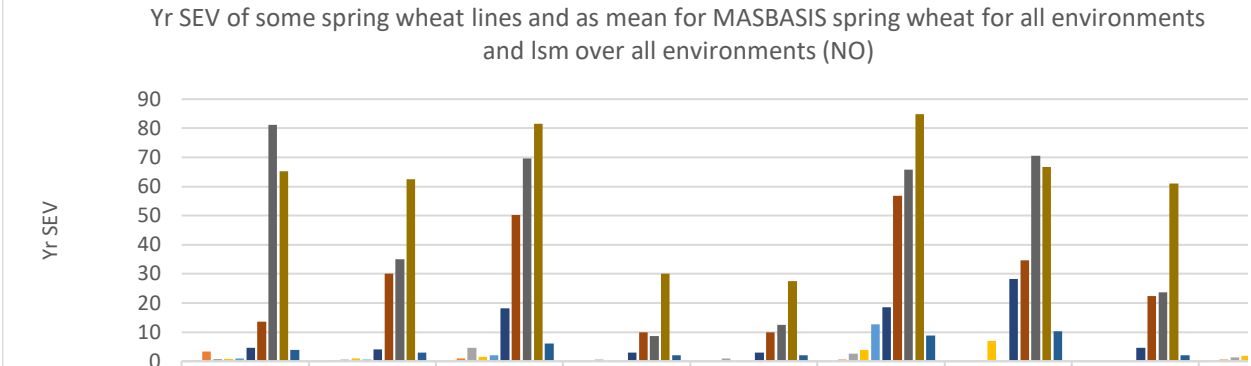
Figure 2. Histograms showing the frequency distribution of yellow rust severity in MASBASIS spring wheat lines over all experimental environments in Norway (a), China (b) and winter wheat lines over all experimental environments (c). Most MASBASIS lines seem to have some resistance, and particularly in Norwegian environments few lines have SEV of more than 20 %. For spring wheat, the spread in disease severity were much greater in Chinese environments than what was observed in Norwegian environments, and more lines had higher disease severity in China relative to Norway. Winter wheat lines seem to generally have quite good resistance, with only few lines having disease severity over 15-20 %.

Disease severity for some MASBASIS spring wheat lines of interest, and lsm for all spring wheat lines in MASBASIS are shown in Figure . Susceptible cultivar Avocet YrA have the highest lsm SEV-score over all environments followed by GN12737 and Bjarne. Mirakel, the most important spring wheat cultivar grown in Norway, have the lowest score among the lines shown in this figure. Average SEV for all spring wheat lines over all environments was 5 %. Avocet YrA had lsm SEV of 60 %, over all environments with lowest SEV-scores, 30 % and 28 % in Vollebekk (Vb) 2016 and 2017 respectively. In Holmestrand (Hs) 2019 Avocet YrA had SEV-score of 61 %, but susceptible GN12737 and moderately susceptible Bjarne both had relatively low scores compared to Avocet YrA. The mean SEV of



	YR_Vb15	YR_Vb16	YR_Vb17	YR_Vb18	YR_Vb19	Lsm al
KWS-Ozon	0.0	0.7	0.3	5.2	0.0	1.2
Ellvis	0.0	0.3	0.0	10.3	0.2	2.2
Kuban	0.6	1.6	3.0	11.1	2.5	3.8
Olivin	9.5	0.0	1.3	7.9	0.7	3.9
Magnifik	5.0	0.9	3.7	12.2	0.3	4.4
Jantarka	4.1	1.6	1.0	16.1	0.3	4.6
Bjørke	20.3	3.5	9.2	22.4	5.4	12.2
Rida	33.9	36.6	43.3	12.9	7.7	26.9
USG3209	29.4	12.4	51.7	51.5	13.3	31.7
Massey	53.7	60.0	83.3	43.3	10.1	50.1
MASBASIS	6.0	2.5	5.9	14.1	1.4	6.0

Figure 3. Disease severity for some lines of interest and lsm SEV for all winter wheat lines in MASBASIS, in all five environments and as lsm over all environments. KWS-Ozon, Ellvis, Kuban, Olivin; Magnific, Jantarka and Bjørke are all cultivars grown in Norway.



	YR_St15	YR_St16	YR_Vb15	YR_Vb16	YR_Vb17	YR_Vb18	YR_Vb19	YR_Hs19	All
Mirakel	0	0	0	0	0	0	0	0	
Caress	3	0	1	0	0	1	0	0	
Saar	1	1	5	1	1	3	0	0	
Seniorita	1	1	2	0	0	4	7	0	
Krabat	1	1	2	0	0	13	0	0	
Zebra	5	4	18	3	3	18	28	5	
Bjarne	14	30	50	10	10	57	35	22	
GN12737	81	35	70	9	13	66	71	24	
Avocet YrA	65	63	81	30	28	85	67	61	
MASBASIS	4	3	6	2	2	9	10	2	

Figure 4. Disease severity on some lines of interest as well as the lsm for all spring wheat lines in MASBASIS over the five environments, and important spring wheat cultivars (Mirakel, Caress, Seniorita, Krabat, Zebra and Bjarne), Saar have known partial resistance

MASBASIS for this environment was 2, the same as in Vb16 and Vb17. Based on this Vb16, Vb17 and Hs19 was considered as low disease pressure environments, while Staur St15 and St16, Vb15, Vb18 and Vb19 was considered as high disease pressure environments.

Disease severity of some MASBASIS winter wheat lines of interest and lsm SEV for all MASBASIS winter wheat lines is shown in figure 3. The most susceptible line with lsm SEV of 50 % over all environments was Massey, followed by Rida and USG3209. In Vollebekk (Vb) 2015-17 Massey had higher SEV-scores than its mean, while SEV-scores of Vb18 and particularly Vb19 was lower than the mean. In Vb18 most of the winter wheat lines, except from Rida and Massey had higher than average SEV. In Vb16 Massey and Rida had a relatively high SEV-score, while USG3209 followed the general trend for this environment, with relatively low SEV well under 6 which is the mean SEV over all environments for MASBASIS winter wheat lines. On this basis Vb16 and Vb19 was considered as LDP environments while Vb15, Vb17 and Vb18 was considered as HDP environments for MASBASIS winter wheat lines.

Principal component analysis

Principal component analysis (PCA) was performed in Unscrambler X with phenotypic data for 297 spring wheat lines in Norwegian (2015-19) and Chinese environments (2019) and for 104 winter lines in the five environments (2015-19). Results are shown as bi-plots for principal component (PC) 1 against PC2 in figure X1-3. PC1 representing the genetic component of the variance between lines could explain 81 % and 83 % of the phenotypic variance for spring wheat lines in Norwegian and Chinese environments respectively, and 79 % in winter wheat. This shows that PC1 captures well the variance between lines and it was therefore chosen as the main trait to analyze in association mapping in Tassel.

GWAS spring wheat

Genome-Wide Association Study (GWAS) was performed twice for spring wheat, as data from Norwegian (2015-2019) and Chinese environments (2019) were run separately in TASSEL. As previously described PC1 was chosen as the main trait analyzed. In addition to scores for PC1 and 2, phenotypic data from all eight environments (location x year) in Norway, lsm for all environments, and lsm for environments with high and low disease pressure were also analyzed. The Chinese data that was run in TASSEL included phenotypic data as lsm of SEV for each of the two environments, but only PC1 was used further due to small dataset with no replications. The marker with highest -log10(p) for PC1 in China was *PpdDD001*, a gene-specific KASP marker for the photoperiod sensitivity gene *Ppd-D1*. This marker was not among the considered (-log10 (p-value) <2,5) markers in the Norwegian dataset. GWAS were also performed with phenotypic data for days to heading (DH) previously collected at the same locations in China was run in TASSEL. Four of the markers: *PpdDD001, Ppd.D1_D002, AX-94500296, AX-94458060* showed significant association to DH and was excluded from further QTL analysis since the purpose was to detect QTL associated with stripe rust resistance and not earliness. Manhattan plots Figur from GWAS in TASSEL show the significant markers on all chromosomes in Norway and China, and the complete lists of all considered markers with -log10 (p-value) higher than 2.5 and 2 in NO and CH respectively can be found in table X1 and X2 in appendix.

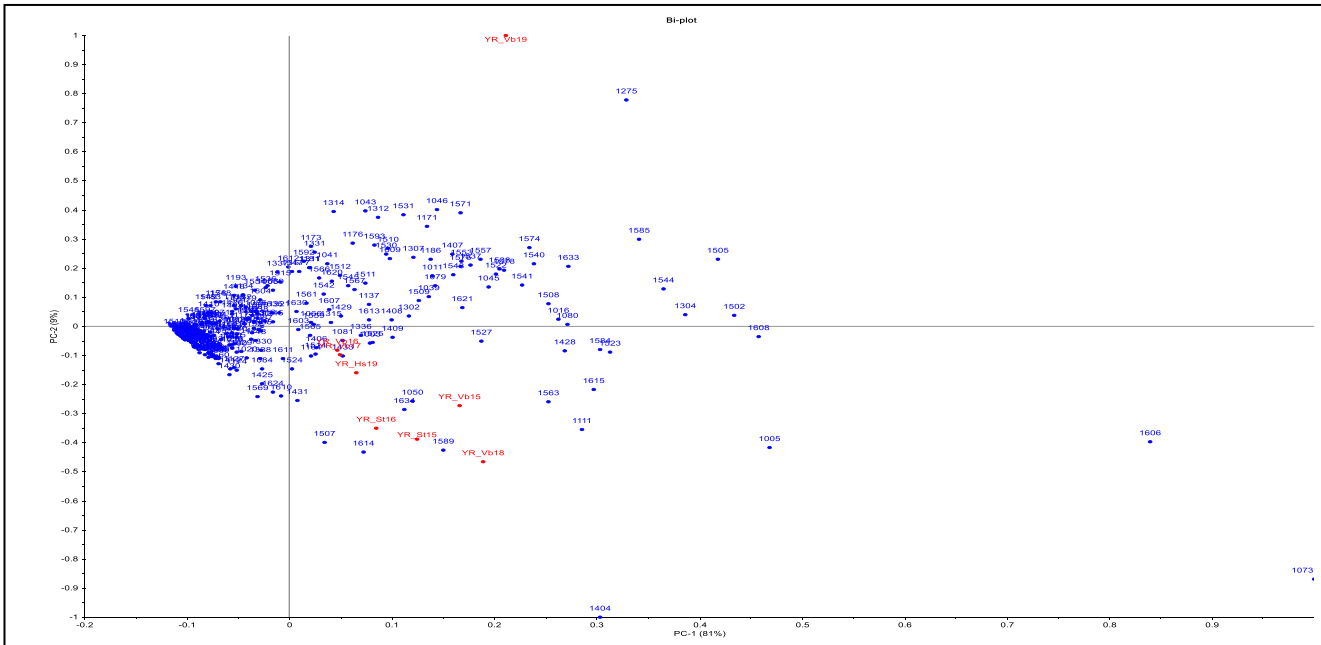


Figure 5. Bi plot for principal component 1 (PC1) and 2 (PC2) of yellow rust in Norwegian spring wheat environments. PC1 and PC2 accounts for 81 % and 9 % of the phenotypic variance respectively. This indicates that PC1 captures well the genetic variance in Yr resistance in these environments, and therefore would be suitable as main trait to analyze in association mapping.

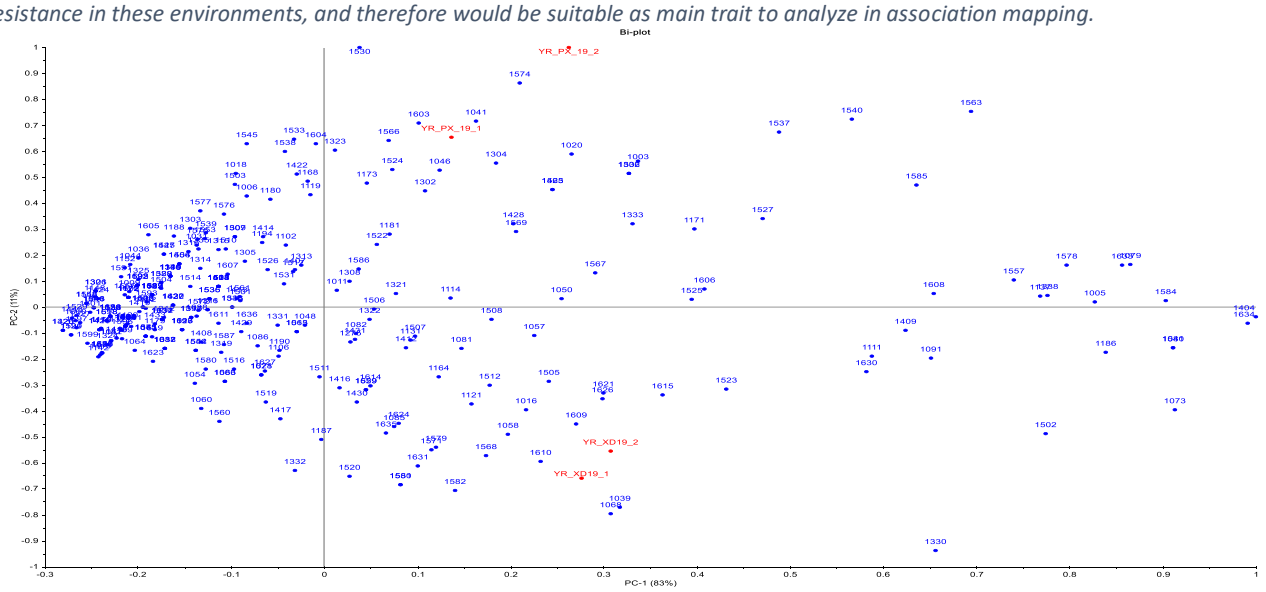


Figure 6 Bi-plot for PC1 and PC2 from PCA of phenotypic data in Chinese spring wheat environments. PC1 and PC2 accounts for 83 % and 11 % of the phenotypic variance respectively. This indicate that PC1 captures well the genetic variance in resistance level in these environments and can be a useful trait to analyze in association mapping.

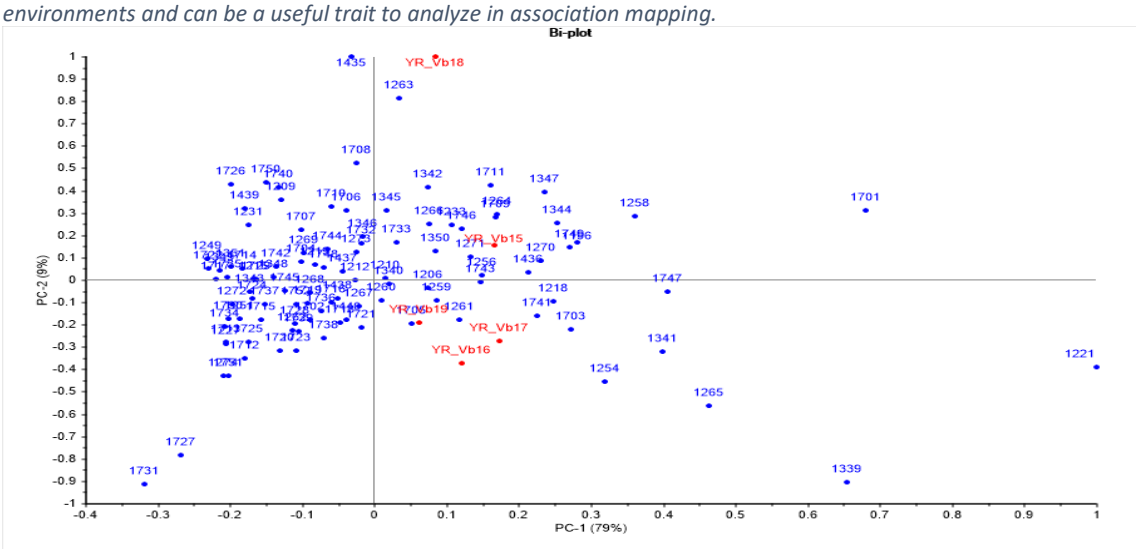


Figure 4. Bi-plot with PC1 and PC2 from principal component analysis (PCA) of phenotypic data in Norwegian winter wheat lines over five different environments. PC-1 and 2 account for 79 % and 9 % of the phenotypic variance respectively. This shows that PC1 captures well the differences in resistance level and is therefore suitable to use as main trait to analyze in association mapping.

Quantile-Quantile plot (QQ-plot) generated in Tassel compares the distributions of expected and

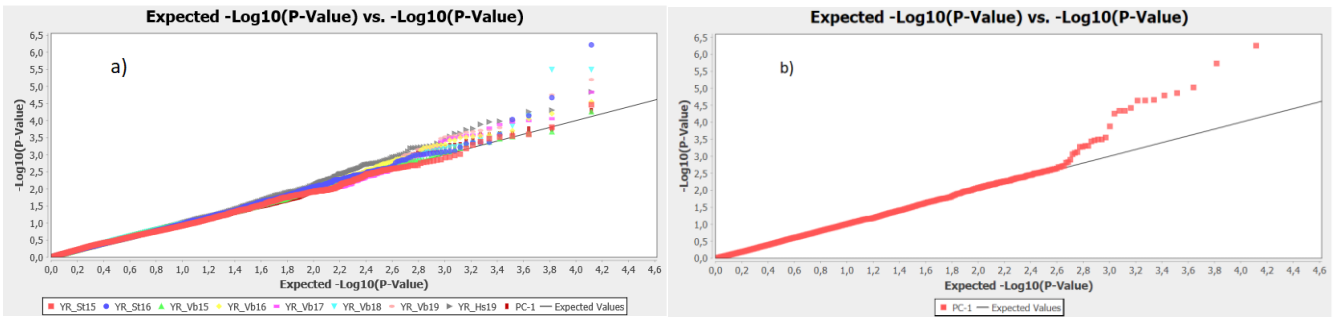


Figure 7. QQ-plot comparing the distribution of expected and observed -Log10(P-value) in for spring wheat experiments. For the Norwegian experiments (a) show results for PC1 and all environments in Norway. Only PC1 are shown for the Chinese experiments as this is the only trait used further in this study.

observed -Log10 (P-values). This is a useful tool to compare the distribution of observed probability (P-value) with reference probability under null hypothesis (no association). Where the P-values match the expected distribution of expected P-values it is an indication of good management of false positives (Type I error), while deviations from the trend line for the markers with the lowest P-values indicate that there is an association between the phenotype and genetic markers. The QQ-plot in figure 7a illustrates that observed P-values for Norwegian spring wheat experiments match the expected values quite well up to -Log10 (P-value) 3.3 before they deviate and show inflation for observed -Log10 (P-values), indicating that the mixed linear model did not sufficiently correct for kinship and population structure in this dataset. Figure 7b show QQ-plot for PC1 in Chinese environments where observed -Log10 (P-value) match the expected up to 2,6 and becomes increasingly inflated after 3.0. A significance threshold of -Log10 (P-value) 3,5 (P=0.000316) was chosen for spring wheat to avoid false positive MTA's.

QTL-analysis

GWAS of yellow rust response in MASBASIS spring wheat lines under Norwegian field conditions identified seven markers with significant MTA's for PC1 Manhattan-plot. Additionally, 17 markers significant in at least one of the eight environments but not significant for PC1 were considered

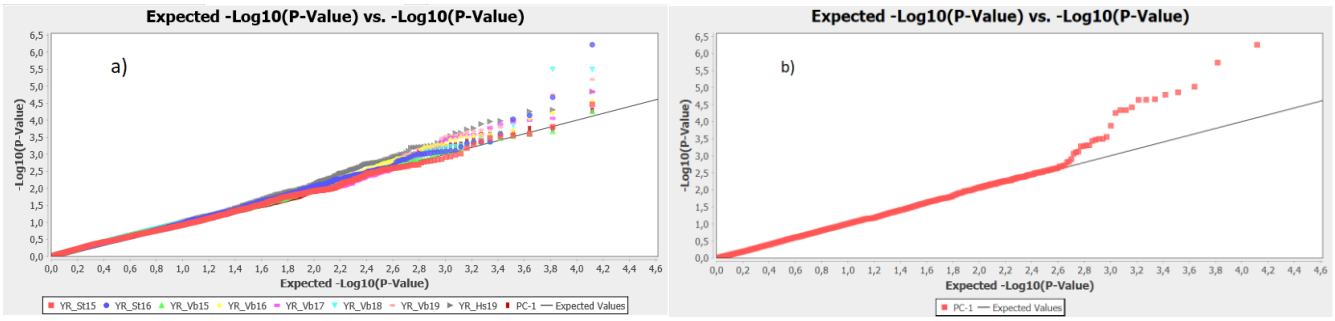


Figure 8. QQ-plot comparing the distribution of expected and observed -Log10(P-value) in for spring wheat experiments. For the Norwegian experiments (a) show results for PC1 and all environments in Norway. Only PC1 are shown for the Chinese experiments as this is the only trait used further in this study.

interesting. Significant markers were discovered in chromosome regions 3BL (1), 5AL (1), 5BL (2) and 6AL (3), and interesting markers were located in chromosome regions 1AL, 1BS, 1D, 3BS, 3BL, 5AL, 5BS, 5BL, 6AL, 6BS, 7AS and 7AL.

GWAS of yellow rust response in MASBASIS spring wheat under Chinese field conditions identified 17 markers with significant MTA's in chromosome regions 2B (5), 3B (4),5A (2), 5B (3) and 22 unknown (2). 36 interesting markers were detected in chromosomal regions 1A, 1B, 1D, 2A, 2B, 3A,3B, 4B, 4d, 5A and 7B.

The QTL-analysis resulted in the detection of five significant QTL and an additional nine interesting QTL with significant MTA in one or two environments. Only two of the QTL were stable, the one on 3AL were significant in three environments while the QTL on 5AL were significant in four environments as well as having significant PC1 in both Norway and China. The QTL on 5BL were not stable, but where significant for PC1 in both counties as well. The addition of PC1 for Chinese environments detected one QTL not significant in Norwegian trials.

Chr	QTL range (Mbp/cM)	Numb. of markers	Number of sign. E	Highest E	Peak marker	Mbp	PC1 NO	PC1 CH	Notes
3BL	705-707/102	3	3	4.8	AX-94811682	705 817 255	3.6	2.2	as
5AL	488/83	3	4	4.1	AX-94669191	488 892 073	4.3	5.7	as, h
5BL	482-484/119	2	1	5.5	AX-94802487	482 424 256	3.6	4.3	as
5BS	45-47/45	2	2	3.7	AX-95145565	45 237 699	3.0	4.8	as,
6AL	609-614/218-222	7	2	5.2	AX-95182345	611 661 167	3.8	1.7	as, p
1AL	493/74	1	1	4.2	AX-94679138	493 820 038	3.1	3.1	
1BS	146/25	1	1	3.6	AX-95194736	146 794 456	3.4	1.7	w+s 1
1D	168/96	1	1	3.5	AX-94425541	168 486 223	3.1	2.6	
3BS	6/1	2	1	3.6	AX-94479164	6 220 123	3.2	1.1	
5AL	680/48	1	1	4.6	AX-94502901	680 880 090	3.2	0.8	h, w+s 2
5BL	544/190	1	1	3.7	AX-95258242	544 608 954	3.3	1.4	
6BS	6/2	1	1	4.0	AX-94689593	6 009 087	3.2	0.8	
7AL	674/110	1	2	3.6	AX-95173991	674 114 920	3.3	2.0	
7AS	40/25	1	1	4.3	AX-94709247	40 189 943	3.1	1.8	

as: used for allele-stacking

h: used in haplotype-analysis

p: possibly pleiotrofic, significant MTA for powdery mildew discovered at 609 Mbp in MASBASIS (Agha 2019)

w+s 1: Yr QTL found at 184 mbp in winter wheat.

w+s 2: QTL in ww

QTL above bold line are significant for PC1, QTL below line have PC1 2,5 or higher and minimum one significant environment

GWAS for Yr SEV in Chinese environments detected two KASP-markers located on chromosome 2D, Ppd.D1_D002 (-log10(P)PC1=3.3, -log10(P)DH=9.3) and PpdDD001 (-log10(P)PC1=6.3, -log10(P)DH=23.1), both gene-specific to photoperiod response gene *Ppd-D1*. GWAS with data for days to heading in the Chinese locations in 2018 (provided by M.L) and Chinese yellow rust data (2019) confirmed that these two markers were significantly associated also for the trait DH (Ppd.D1_D002 -log10(P)DH=9.3, PpdDD001 -log10(P)DH=23.1). Additionally, two markers, AX-94458060 (-log10(P)PC1=2.9, DH=5.2) and AX-94500296 (-log10(P) PC1=2.2 DH=6.06383826) located on chromosome 2B, also showed significant associations with DH. These markers were excluded from further analysis.

Allele-stacking and haplotype analysis

Results from allele-stacking with all significant spring wheat QTL as box-plot (figure) show that there is no significant effect on Yr SEV between genotypes having only one compared to none of these QTL (a), but there were significant effect of having two to four (b) and five (c) QTL. Only 10 lines have zero or one of the significant QTL, and the largest group (n=104) have three and 241 lines have three or more QTL.

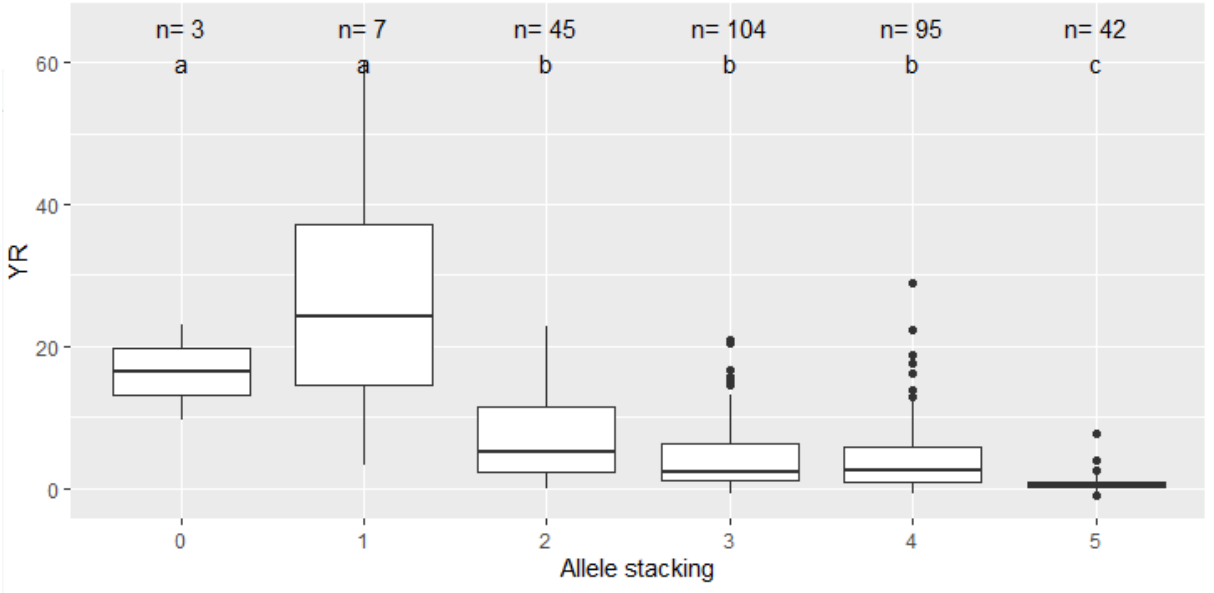


Figure 9 Box-plot of allele-stacking spring wheat showing effects of different numbers of QTL . The different letters on top indicates groups which groups are significantly different with regard to Yr resistanse. There is a significant effect of having

Haplotype analysis of 5AL_488 show that there are five different haplotypes where the majority of lines (245/286) have the 100 haplotype, which did not differ significantly from the 000 (n=24) or 101 (n=1) or 111 (n=7) haplotypes indicated by the letters a and b. This result is not conclusive, and it is difficult to identify the resistance alleles of this QTL based on this boxplot, but the first marker does not seem to have much effect on SEV.

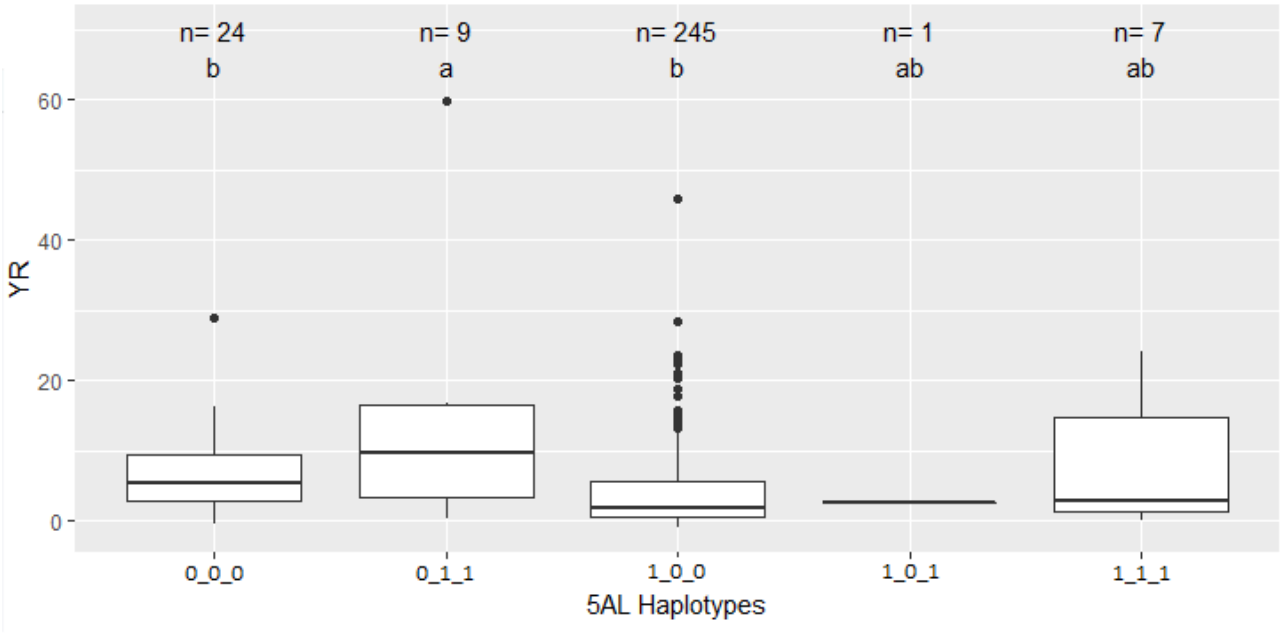


Figure 10. Boxplot showing effect of 5AL_488 haplotypes on Yr SEV. Number of lines in each haplogroup are indicated by n= on top, while the letter underneath indicates result of Tukey's test, groups with SEV significantly different from each other have different letters.

Analysis of 5AL_680 haplotypes detected no significant differences between the different haplogroups (all a's). The most common haplotype was 000 (n=135)

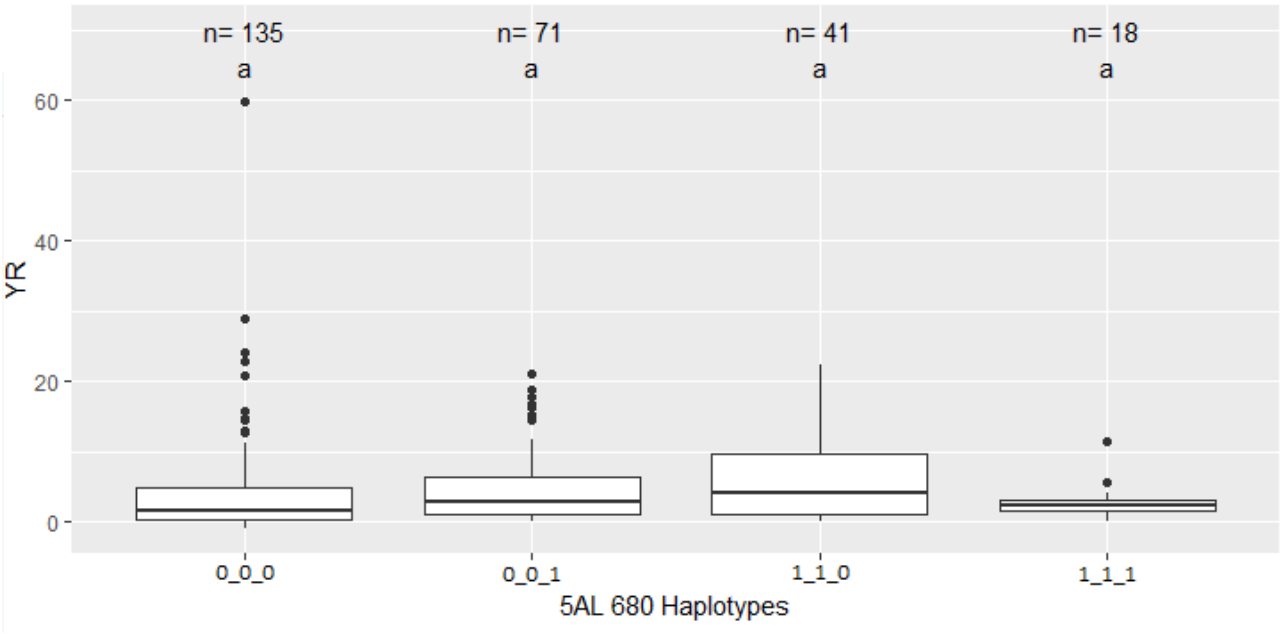


Figure5. Boxplot showing results of 5AL_680 haplotype analysis. Number of lines in each haplogroup are indicated by n= on top, while the letter underneath indicates result of Tukey's test, groups with SEV significantly different from each other have different letters.

Table 3 belongs a table showing how many and which resistance alleles are present in some relevant lines (Many QTL high /low SEV, Few QTL high/low SEV) SEV all E, H/LDP, CH.

QTL		5AL_488/83			5AL_680/48		
Line	Lsm SEV	AX-94450199	AX-94669191	AX-94919900	AX-94577164	AX-94526834	AX-94502901
Mirakel	0	+	+	+	+	+	-
Caress	1	-	+	+	+	+	-
Saar	1	+	+	+	+	+	-
Seniorita	2	+	+	+	+	+	-
Krabat	2	+	+	+	-	-	-
GN13618	5	+	+	+	+	+	-
Zebra	11	+	+	+	+	+	-
Bjarne	28	+	+	+	-	N	-
GN12737	46	+	+	+	-	N	-
Avocet YrA	60	-	-	-	+	+	-

GWAS winter wheat

Genome-Wide Association Study (GWAS) of Yr response in winter wheat were performed for PC1 and PC2 lsm Yr SEV over all five environments (Vb15-19), for each environment and H/LDP environments. Figure … shows two QQ-plots, a) from GWAS with out transforming the data and b) from GWAS with squared data. This demonstrated how transformation made the data more normally distributed and better fit the model. In 11.b the -log10(P-value) follow the expected -log10(P-value) well up to 2,6, when values for PC1 and others become inflated. At about 3.6 there is another increase in -log10(P-value) and the significance threshold were set at 3.7 (P=0.000104)

QTL-analysis

GWAS of yellow rust response in MASBASIS winter wheat lines detected 14 markers significant for PC1 Manhattan-plot. Additionally, six markers were significant in at least one of the five environments but not significant for PC1 were considered interesting. Significant markers were discovered in chromosome regions 1AS (2), 3AL (7) and 5AL (5), and interesting markers were located in chromosome regions 1B, 3AL, 3DL, 5AL and 6 DL. List of significant and interesting markers can be found in table .. in appendix . QTL analysis (table..) resulted in five significant and five interesting with significant MTA's in at least one environment. The most significant QTL, 1AL (-log10(P)=4.0) and both on 5AL (-log10(P)=4.8 and 5.0) were significant in three environments and were considered stable.

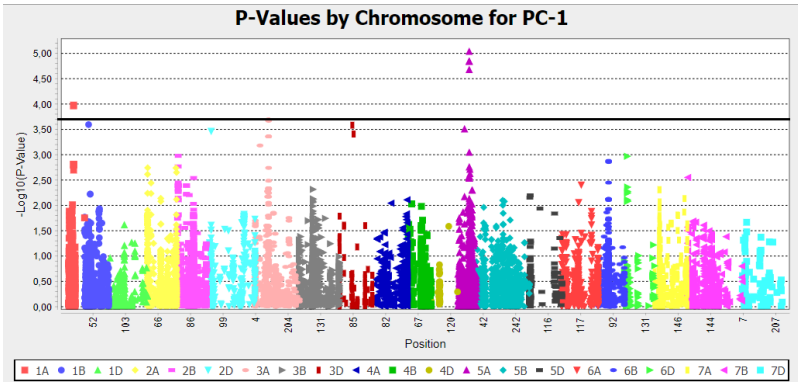


Figure 11. Manhattan-plot showing markers with significant association to PC1 in winter wheat. Thirty one markers were significant (-Log10 (P-value) 3.5 or higher on chromosomes 1A (3), 1B (1), 2B (2), 2D (1), 3A (12), 3D (3), 5A (7), 5B (1) and 6D (1).

Table 4

Chr	QTL range (Mbp/cM)	Number of markers	Number of sign. E	Highest E	Peak marker	Pos (Mbp)	PC1	Notes
1AL	520-522/80-81	2	3	4.4	AX-94810594	522 190 843	4.0	as
3AL	510-519/84	6	2	3.9	AX-94798864	516 790 678	3.7	as
3AL	526-528/84	4	1	3.9	AX-94760077	526 863 990	3.7	as
5AL	269/72	1	3	4.8	AX-95069984	269 319 007	4.8	as
5AL	384/72	4	3	5.1	AX-94401034	384 352 260	5.0	As, h
1B	184/25	1	1	4.0	AX-94576991	184 823 751	3.6	s+w 1
3DL	511/80	1	1	4.8	AX-94534307	511 295 461	3.6	
5AL	451/76	1	1	3.9	AX-94907998	451 886 294	2.7	
5AL	680/43	1	1	4.4	AX-94526834	680 503 211	3.5	h, s+w 2
6DL	498/17	1	1	3.7	AX-95206791	468 907 723	3.0	

as: used for allele-stacking

h: used in haplotype-analysis

w+s 1: Yr QTL found at 184 mbp in winter wheat.

w+s 2: QTL in ww

QTL above bold line are significant for PC1, QTL below line have -Log10 (p-value) of 2,5 or higher for PC1 and minimum one significant environment

Allele-stacking and haplotype analysis

Results from allele-stacking (Table 4) of all significant winter wheat QTL show that most lines have all five QTL (80/103), and none have only one QTL. There were significant differences

between groups with zero QTL and those with two or more. Groups with two to four QTL were not significantly different, but those with five QTL were significantly different from the groups with two or three QTL.

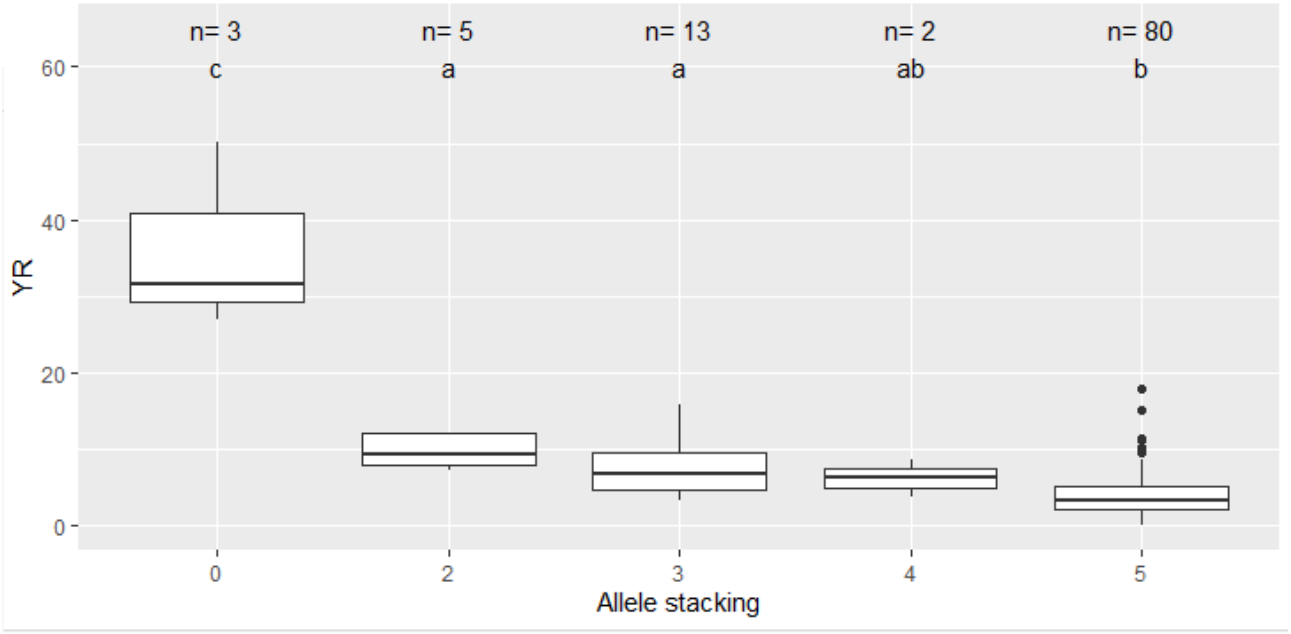
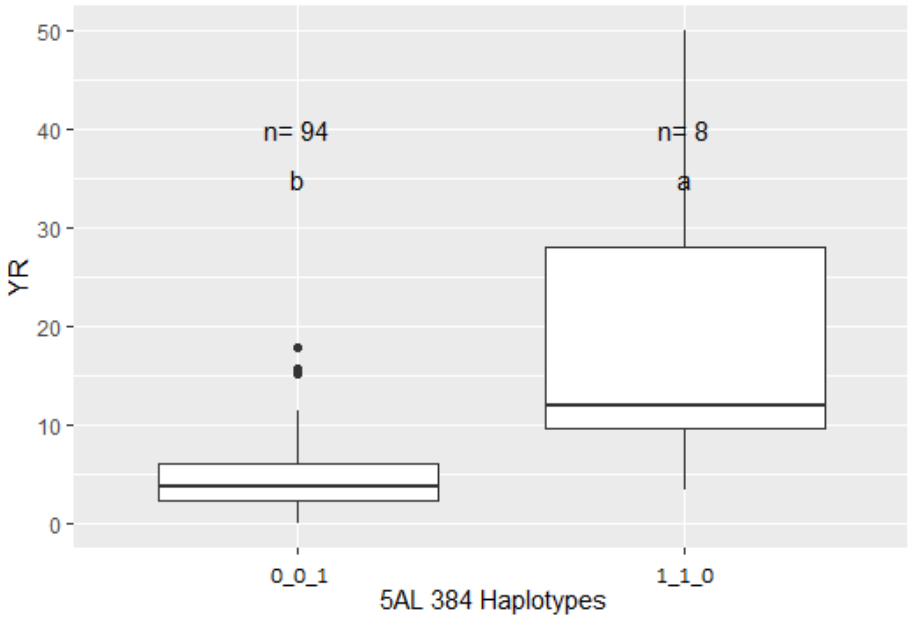


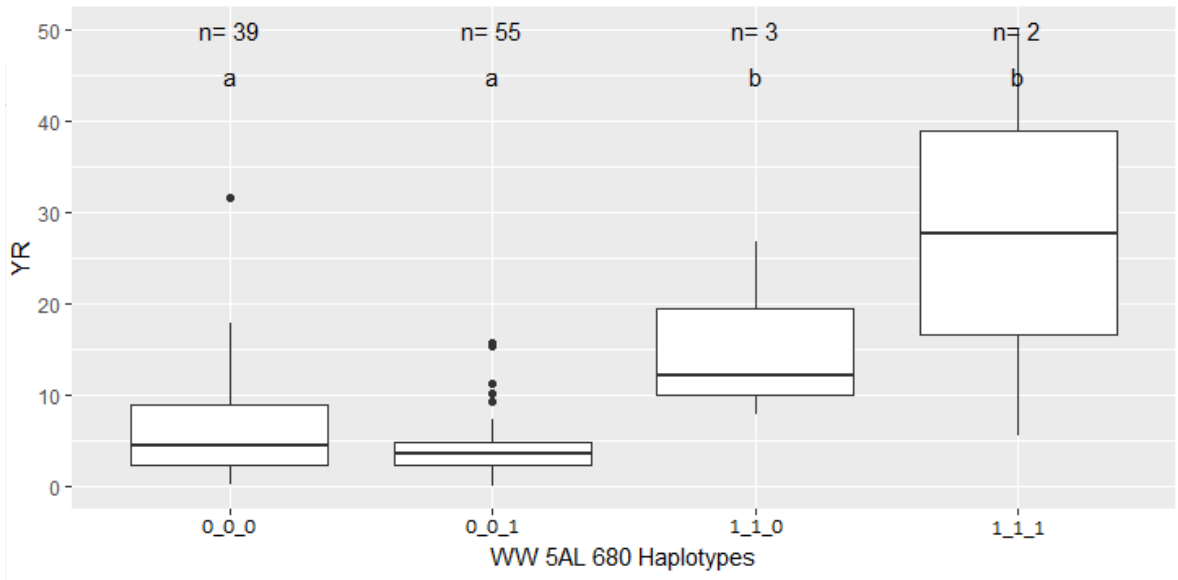
Figure 12 Boxplot showing Allelstacking with significant QTL in springwheat.

Table 5

QTL		3BL_705-707	5AL_488	5BS_45-47	5BL_482-483	6AL_609-614	Sum
Line	Lsm SEV	AX-94811682	AX-94669191	AX-95145565	AX-94802487	AX-95182345	
Mirakel	0	+	+	-	+	+	4
Caress	1	+	+	+	+	+	5
Saar	1	-	+	+	+	-	3
Seniorita	2	+	+	+	+	-	4
Krabat	2	+	+	-	+	-	3
GN13618	5	+	+	+	+	-	4
Zebra	11	+	+	+	+	-	4
Bjarne	28	-	+	N	-	-	1
GN12737	46	-	+	-	-	-	1
Avocet YrA	60	-	-	-	+	-	1

Haplotype analysis of QTL 5AL_384 show that there are only two haplotypes for this QTL in MASBASIS winter wheat lines, 001 (n=94) and 110 (n=8). There were significant differences in SEV between the two haplogroups and 001 had lower SEV than 110.





There were four 5AL_680 haplotypes, 000 and 001 were not different from each other, and the same goes for 110 and 111, but these pairs were different from each other. Again, most lines have the 000 or 001, and only 5 lines have 110 or 111.

QTL		5AL_384/72			5AL_680/43		
Line	Lsm SEV	AX-94403748	AX-94401034	AX-94498038	AX-94577164	AX-94526834	AX-94502901
KWS-Ozon	1	+	+	+	+	+	+
Ellvis	2	+	+	+	+	+	-
Kuban	4	+	+	+	+	+	+
Olivin	4	+	+	+	+	+	+
Magnifik	4	+	+	+	+	+	+
Jantarka	5	+	+	+	+	+	+
Bjørke	12	-	-	-	-	-	-
Rida	27	-	-	-	-	-	-
USG3209	32	-	-	-	+	+	-
Massey	50	-	-	-	-	-	+

Discussion

Most of the research on yellow rust in European wheat have been focused on winter wheat. This can be explained by the fact that winter wheat is a more important crop than spring wheat in most of Europe. The situation is different in Norway where the spring wheat area is much greater than that of winter wheat. The importance of spring wheat compared to winter wheat in Norway is also reflected in the MASBASIS collection, where the number of spring wheat is almost threefold the number of winter wheat lines. Furthermore, the effort of breeders to develop of spring wheat material with adaptation to the distinct growing conditions of Norway have created cultivars and breeding lines that genetically cluster together and is distinctly different from most cultivars developed in the neighboring countries. The Norwegian spring wheat material also have greater genetic diversity than cultivars from surrounding countries, which is likely adue to introduction of North American spring wheat genetics and extensive use of CIMMYT material since the 1960s (Lillemo & Dieseth 2011). For winter wheat on the other hand there is no independent breeding program and cultivars grown in Norway have been developed mostly in other countries or from Swedish or Danish material selected in Norway. These differences are evident from the population structure of MASPASIS spring- and winter wheat groups (Branchereau 2018) which confirms the differences in the genetic makeup of the populations they represent as a core collection. Both groups were divided into two subpopulations where the largest cluster within the spring wheat panel, 235 out of 299 lines, were acomprised of 183 lines originating from Norway, and the rest from Sweden AND other European countries, while subpopulation 2 were comprised of 64 lines comprised mostly of CIMMYT lines and other exotic material as well as 3 Norwegian lines. Winter wheat subpopulations were both comprised of lines from northern and eastern Europe, with 7 and 20 lines of Norwegian origin clustered to subpopulation 1 aand 2 respectively. In both spring and winter wheat the Norwegian material mostly cluster together, but the fraction of lines originating from Norway is much greater in the spring wheat panel than it is in the winter wheat panel. Because of the uneven focus between spring and winter wheat in previous research and the divergent gene pool of the Norwegian spring wheat material it seems more likely that novel QTL will be discovered spring wheat than in winter wheat in this study.

Production and maintenance of Yr inoculum

Production of inoculum for field experiments in Vollebekk and Staur in 2018-19, and maintenance of inoculum between the seasons were successful in the sense that we managed to inoculate the fields as planned, and relatively high disease levels were observed. There were several challenges with the maintenance of the inoculum in the green house, particularly during the hot summer months of 2018. Plants seemed to not thrive, partly due to the high temperatures, and partly because the high humidity in the greenhouse were producing ideal conditions for powdery mildew, which caused some severe infections in

some of the batches. To avoid this problem the MASBASIS spring wheat line GN12737 which is susceptible to yellow rust but resistant against powdery mildew was tested alongside Cartago and Anja. Unfortunately, GN12737 were noticeably smaller in size and leaves were very narrow compared to Cartago and Anja at the same age, and this line did even worse than the other two in the greenhouse. There were no problems with PM when the weather cooled down in the autumn. Except from issues with powdery mildew infections, among the three lines we used Cartago would be the preferred choice due to it having broad leaves which makes it easier to harvest spores from and inoculate if it is done by rubbing with infected leaves of other manual methods.

Phenotypic evaluation of Yr response under field conditions

Aagainst yellow rust as only a few lines of both growth habits have very high SEV, these were generally the susceptible checks along with a few other susceptible lines or cultivars. The relatively low Yr SEV in MASBASIS spring wheat l could also be due to low disease pressure, as the distribution of Yr SEV is more evenly distributed, with increased Yr SEV on many lines and higher Yr SEV on Avocet YrA in Chinese environments … si mer om disse...

A limited number of samples of infected plant material have been collected in Norway in later years. These have been analyzed at GRRC in Århus, Denmark. Although sampling of *Pst* have not been done systematically over the whole wheat growing area in Norway, the limited sampling that have been carried out show a picture of the pathogen population present in Norwegian fields since 2015, which is very similar that of the rest of Europe. This is expected as most if not all primary inoculum is transported from each season. The Isolate used were derived from a 2017 field sample, tests showed it belonged to the **PstS10 a.k.a** *Warrior(-)* race, like 17 out of 21 samples that were collected in Norway and analyzed at GRRC in 2017. Two of the other samples belonged to the old **PstS7** a.k.a *Warrior* race, and the last two were categorized as "other". Even if sampling in Norway were not systematic and collected from the whole wheat growing area, it is likely that Warrior(-) race were the most prevalent race in Norway in 2017 also, like it was in the rest of western Europe that year. According to the 2018 yellow rust report from GRRC

known if *Pst* is capable of overwintering under Norwegian conditions, but it is believed that winters are too cold for the pathogen to survive. It is well known that urediniospores of *Pst* can be transported over long distances by wind, and the main source of primary inoculum of *Pst* responsible Yr epidemics in Norwegian wheat are spores transported from neighboring countries, southern Sweden, Denmark and UK, where milder climate and larger areas with winter wheat production, allow for overwintering of the pathogen population on the standing crop Several factors determine how severe and damaging the yellow rust epidemics will get in any given season; the amount of inoculum and timing, i.e. how early in the season the pathogen is present; availability of susceptible hosts to infect, which will decrease as plants get older if they have APR; *Pst* infection and spread is greatly affected by environmental conditions, more so than other rusts attacking wheat *(Chen 2005),* warm dry conditions are not favorable for *Pst* infection; characteristics of the pathogen population like aggressiveness and ability to reproduce on its host under the prevailing conditions. If inoculum arrives in Norwegian fields where young plants of susceptible wheat cultivars are grown at a period when conditions are ideal for infection, wet and relatively cold temperatures and some winds could lead to severe epidemics, while unfavorable conditions and few susceptible hosts can lead to a potential Yr epidemic burning out before it have begun with little or no crop damage. In 2018, experimental fields at Vollebekk and Staur were inoculated with *Pst* race *Warrior(-).* Locations experienced relatively high temperatures and little precipitation during most of the summer. Yellow rust was observed both in St18 and Vb18, but only a few pustules were found on the most susceptible lines in St18 while Vb18 was considered as a HDP environment. The contrasting disease level in these environments can most likely be accredited to a period with somewhat cooler temperatures shortly after inoculated plants were transplanted in Vb18 combined with mist irrigation, which seems to have produced good conditions for *Pst* infection and spread.

Both high temperatures and dry conditions reduce the rate of *Pst* infection, and the low infection levels seen in Staur reflect the general situation for Yr in Norwegian wheat in 2018.

"MASBASIS bare ble testet på Staur i 2015 og 2016. vi har jo testet MASBASIS der hvert år men jeg sjekket dataene nå, og ser at det bare var brukbare gulrustdata fra 2015 og 2016 så da er det riktig. Det kunne evt være et moment å nevne i diskusjonen at det er vanskelig å oppnå data i alle år når man ikke har tilgang til inokulum og dusjvanning."

Chinese datasets provided useful information about expressed Yr resistance of MASBASIS lines under field conditions in different environments than eastern Norway where all the other Yr data for MASBASIS have been collected so far. Because of the small dataset only the PC1 from Chinese trails were used in GWAS in this project. PC1 could explain 83 % of the variation in Yr SEV in the Chinese environments, and therefore considered to be a good trait to analyze as a supplement to the Norwegian data set.

principal component analysis show that PC1 could explain large parts of the phenotypic variation within both MASBASIS spring and winter wheat panels. Because line is the fixed effect we are investigating, we assume that PC1 represents the variation in resistance level of different genotypes, making this an ideal trait to analyze in GWAS.

QTL analysis spring wheat

GWAS of yellow rust response in MASBASIS spring wheat lines under Norwegian field conditions identified seven markers with significant MTA's for PC1. Additionally, 17 markers significant in at least one of the eight environments but not significant for PC1 were considered interesting. Significant markers were discovered in chromosome regions 3BL (1), 5AL (1), 5BL (2) and 6AL (3), and interesting markers were located in chromosome regions 1AL, 1BS, 1D, 3BS, 3BL, 5AL, 5BS, 5BL, 6AL, 6BS, 7AS and 7AL.

GWAS of yellow rust response in MASBASIS spring wheat under Chinese field conditions identified 17 markers with significant MTA's in chromosome regions 2B (5), 3B (4),5A (2), 5B (3) and 22 unknown (2). 36 interesting markers were detected in chromosomal regions 1A, 1B, 1D, 2A, 2B, 3A,3B, 4B, 4d, 5A and 7B.

Many of the Nordic spring wheat lines in MASBASIS are photoperiod sensitive and require long days to flower, and as much as 14 days delay have been observed when MASBASIS spring wheat lines are grown in these same Chinese locations. This will affect Yr SEV on the photosensitive lines at the time of scoring, as the new leaves of these later developing plants will not have been exposed to Yr inoculum for as long as the lines that flower at an earlier time. These markers were not used further in this study.

The QQ-plot in figure 7a illustrates that observed P-values for Norwegian spring wheat experiments match the expected values quite well up to -Log10 (P-value) 3.3 before they deviate and show inflation for observed -Log10 (P-values)

Comparison between significant QTL and previous research

Chr	QTL range (Mbp/cM)	Numb. of markers	Number of sign. E	Highest E	Peak marker	Mbp	PC1 NO	PC1 CH	Notes
3BL	705-707/102	3	3	4.8	AX-94811682	705 817 255	3.6	2.2	as
5AL	488/83	3	4	4.1	AX-94669191	488 892 073	4.3	5.7	as, h
5BL	482-484/119	2	1	5.5	AX-94802487	482 424 256	3.6	4.3	as
5BS	45-47/45	2	2	3.7	AX-95145565	45 237 699	3.0	4.8	as,
6AL	609-614/218-222	7	2	5.2	AX-95182345	611 661 167	3.8	1.7	as, p

QTL on 3BL

The current study detected a QTL covered by three markers located between 705-707 Mbp in this region. Only the peak marker *AX-94811682* were significant for PC1 (-log10 (P) = 3.6). The QTL were significant in St16, Vb16, Vb18 and Hs19, and were therefore considered to be stable. Two of the markers in this QTL were significant in LDP environments (-log10(P) = 5.0) but not in HDP environments (-log10(P) =3.3).

Several QTL and Yr genes have been reported on chromosome 3B, but most are located on the short arm (Rosewarne et al. 2013). For previously reported QTL for which physical position in the reference genome was obtained none of the QTL mapped in close proximity of the QTL found in this study. Yr82 Two KASP markers, *sunKASP_300* and *sunKASP_301*, with strong association to Yr82, developed by Pakeerathan et al. (2019) have a primers located at 741 and 742 Mbp respectively, about 36-36 Mbp from the studied QTL. Another QTL linked to field based Yr resistance was located at 579 Mbp in a study by Tehseen et al. (2020). this QTL was mapped with two previously reported QTL, QYr.cim-3B_Pastor (Rosewarne et al. 2012). Due to the relatively long distances between the studied and previously reported QTL it is impossible to know if this is a novel QTL or can be mapped together with some of the other QTL if the physical positions are obtained for these to compare.

This QTL could be highly recommended for further research and use in MAS because it were significant for PC1 in Norway and

QTL on 5AL

This QTL located at 488 Mbp by three markers (peak marker *AX-94669191*), were the strongest QTL found in spring wheat and were significantly associated with PC1 in both Norwegian and Chinese environments (-log10 (P) NO=4.3 and CH=5.7) as well being significant in Vb16, Vb17, Vb18 and Hs19 with -log10 (P) = 4.1 in Vb18 as highest value in a single environment. Markers in this QTL behaved quite differently in different environments. The peak marker was significant in HDP environments (-log10(P)=4.3) but were not significant in LDP. The one marker which were not significant for PC1 were significant in LDP (-log10(P)=4.3).

At least three adult-plant resistance QTL have been reported in this chromosomal region. Two of them are *QYr.caas-5AL.2* (Ren et al. 2012) derived from wheat line Shanghai 3/Catbird, in the marker interval between *XwPt-1903-5AL* and *Xwmc727-5AL*, and *QYr.caas-5AL* reported by Lan et al. (2010). As physical positions for these SSR markers were not obtaioned, and it was not possible to determine if these are linked to the QTL detected in this study or not. Hou et al. (2015) detected a stable QTL associated with HTAP resistance in recombinant inbred line (RIL) population from cross Druchamp × Michigan Amber. This QTL, *QYrdr.wgp-5AL* (SNP marker *IWA2558)* located at 708 Mbp, could explain 2.27–17.22% of the variation in this population. Considering the close proximity of only 1 Mbp between *QYrdr.wgp-5AL* and the QTL I the current study, and both were stable over several environments in both studies, these QTL are likely the same QTL.

QTL on 5BS

This QTL were flanked by two markers (peak marker *AX-95145565*) located at 45-47 Mbp in this region. This QTL were not significant for PC1 in Norway (-log10 (P) =3.0) but the peak marker had a -log10(P) for PC1 of 4.8 in China. This QTL was not considered stable because it was only significant in two environments, Vb16 (-log10 (P) =3.7) and Hs19, (-log10 (P) =3.6), and none of them were significant for high or low DP environments.

Yr47 (Bansal et al. 2011), *QYr.*uga-*5B_AGS2000* (small effect QTL) (Hao et al. 2011), *QYr.PI192252-5BS*, reported to have a small but significant effect om HTAP resistance (Lu et al. 2014) Have all been mapped to the short arm of 5B, but physical positions were not obtained for any of these so it is impossible to know if QTL in the present study are different from previously mapped Yr resistance QTL and genes in this region.

Seedling resistance gene *Yr47* have also been mapped close to *Lr52(Bansal et al. 2011)*. Tehseen et al. (2020) also reported a marker *SNP1090007* at 9 Mbp with significant association to seedling resistance against *Warrior* race. *SNP1090007* and *Yr47* both confer seedling resistance and are likely to be linked. This could be an interesting QTL to investigate further as it would be interesting to know if it is linked to Yr47 and if Lr52 is also present. Tests for seedling resistance in greenhouse experiments could also confirm if the QTL in this study confer ASR or APR

QTL on 5BL

This QTL were flanked by two markers (peak marker *AX-94802487*) located at 482-484 Mbp in this region. The QTL were not significant for PC1 in Norway (-log10 (P) =3.6) but had a -log10 (P) PC1 of 4.3 in China. It was only significant in Hs19 (-log10 (P) = 5.5) in that environment. Yrswp-5B.2 ASR 5B 546 827 149–546 849 099 IWB3660

IWA7815 positioned at 528 Mbp corresponds to the race-specific gene YrExp2 (Lin & Chen 2008)(Bulli et al. 2016) 528 Mbp

Tehseen et al. (2020) found the marker 4991320 at 506 Mbp to be associated with field-based Yr resistance This marker was also mapped with QYr-5B_Oligoculm

QTL on 6AL

This QTL were covered by seven markers, three of them were significant for PC1 in Norway (-log10 (P) =3.8), but none were significant In China. The remaining four markers were significant in one or more environments, and this whole QTL were significant in two different environments. In a GWAS of powdery mildew resistance in MASBASIS Agha (2019) found a significant QTL between …-609 in this region. *Bulli et al. (2016) IWA8595* (*QYr.wsu-6A*) 609 Mbp, APR have also been reported in the cultivars Stephens (Vazquez *et al.* 2012) and 'Avocet' (William *et al.* 2006). The same region of *IWA8595* has also been associated with resistance to powdery mildew in the cultivar 'Saar' (Lillemo *et al.* 2008). :

IWA7894, 611 Mbp, overlaps with *QYrpl.orr-6AL* in Stephens (Vazquez *et al.* 2012),

Comparison of interesting QTL to previous research

Chr	QTL range (Mbp/cM)	Numb. of markers	Number of sign. E	Highest E	Peak marker	Mbp	PC1 NO	PC1 CH	Notes
1AL	493/74	1	1	4.2	AX-94679138	493 820 038	3.1	3.1	
1BS	146/25	1	1	3.6	AX-95194736	146 794 456	3.4	1.7	w+s1
1D	168/96	1	1	3.5	AX-94425541	168 486 223	3.1	2.6	
3BS	6/1	2	1	3.6	AX-94479164	6 220 123	3.2	1.1	
5AL	680/48	1	1	4.6	AX-94502901	680 880 090	3.2	0.8	h, w+s2
5BL	544/190	1	1	3.7	AX-95258242	544 608 954	3.3	1.4	

6BS	6/2	1	1	4.0	AX-94689593	6 009 087	3.2	0.8
7AL	674/110	1	2	3.6	AX-95173991	674 114 920	3.3	2.0
7AS	40/25	1	1	4.3	AX-94709247	40 189 943	3.1	1.8

QTL on 1AL

H/LDP: 2.8/1.0

IWA5505, 556 Mbp ,*IWA3215* (*QYr.wsu-1A.2*)(Bulli et al. 2016) *QYr.tam-1AL (*Basnet *et al.* 2014), 593 Mbp

QTL on 1BS

Tehseen et al. (2020) found a SNP marker significantly associated with seedling resistance against Warrior race in a set of bread wheat landraces. This marker, 1110537 was located at 135 Mbp based on IWGSC RefSeq 1.0, which is 11 Mbp from the marker AX-95194736 located at 146 Mbp. This QTL was not significant in the current study, but with -Log10(p) of 3.4 for PC1 it is very close to the significant threshold. H/LDP: 3.2

QTL on 1DS

One marker, AX-94425541 at 168 Mbp, was significant in Vb16 (-log10(P)= 3.5). This marker had -log10(P)= 3.1 and 2.6 for PC1 in Norwegian and Chinese environments respectively. H/LDP: 2.9/3.1

QTL on 3BS

Two markers positioned at 6 Mbp in this region were significant Vb19, the most significant marker was AX-94479164 with -log10(P)=3.6 and -log10(P)=3.2 and 1.1 for PC1 in Norway and China respectively. HDP: 3.3/3.2 LDP: 1.4/1.8

Lui? Found an QTL conveying ASR linked to the SNP- marker IWB35950 at 3 Mbp … This is only a 3 Mbp distance from the two markers with significant MTA's in Vb19 in this study. ASR, race-specific? Same races as in the study? Same races in previous years and fields in Vb18-19 were inoculated with *Warrior(-)* both

QTL on 5AL

One marker AX-94502901 positioned at 680 Mbp in this region was significant (-log10(P)= 4.6) in Vb16. -log10(P) for PC1 were 3.2 in Norwegian and 0.8 in Chinese environments respectively. This marker had a -log10(P) = 3.1 in LDP environments but was highly significant in HDP environments 4.8. This could indicate that this QTL may convey partial resistance which will tends to have larger effects in HDP environments compared to LDP

One marker, AX-94526834 at 680 Mbp in this region, was interesting in winter wheat with significant MTA in … (-Log10 (p) = 4.4) but were not significant for not PC1 (-log10(P)= 3.5). Because both markers are located very close to each other in the reference genome this could be a chromosome region with common resistance traits against.

Haplotype analysis of this QTL with the peak markers in spring and winter wheat and one additional marker not significant in either, show that the variance between the different haplotypes in spring wheat were not significant. In winter wheat the variance was found to be significant between haplotypes AAA, AAT and

TTA, TTT. This is a surprising result because the peak marker in spring wheat had higher PC1-score than the one in winter wheat, so the expectation was that there would be more effect of the haplotypes with the resistant allele in spring wheat compared to winter wheat where PC1 was lower. This analysis show that it is challenging to see clear effects of different QTL when the lines in this collection generally have good resistance. that the resistant allele of AX-94526834 could have an effect of other Yr resistance QTL/genes present in winter wheat material. The majority of winter wheat lines have the haplotypes AAA (39) or AAT (55), and the majority of lines also have relatively good resistance against Yr. This MTA can

Bulli et al. (2016) ? QTL *IWA5002* (*QYr.wsu-5A*) located at 688 Mbp described by .

Another QTL 13 Mbp from the marker 1184257 located at 693 Mbp, which were associated to APR against Yr in the study by Tehseen et al. (2020) overlaps with positions of the APR QTL identified on the 5AL arm of the Chinese landrace Pingyuan 50 (Lan *et al.* 2010), hard red spring wheat PI 610750 (Lowe *et al.* 2011), and the spring wheat line 'SHA3/CBRD' (Ren *et al.* 2012).

(*Yr48,* QYr.ucw-5A.1, QYr.ucw- 5AL_PI610750. Yr48 698 Mbp

QTL on 5BL

AX-95258242 at 544 Mbp significant in Vb19 (-log10(P)= 3.7), -log10(P) for PC1 was 3.3 in Norwegian and 1.4 in Chinese environments respectively. H/LDP: 3.3/2.3

Yrswp-5B.1 ASR 520 886 418–539 293 256 IWA5478

IWA7815, which corresponds to the race-specific gene YrExp2 (Lin and Chen 2008). 528 Mbp (Bulli et al. 2016) 528 Mbp

Yrswp-5B.2 ASR 5B 90.3 546 827 149–546 849 099 IWB3660

QTL on 6BS

AX-94689593 6/2, Hs19 -log10(P) = 4.0. -log10(P) for PC1 was 3.2 and 0.8, H/LDP 3.0/3.3

Closes investigated QTL was QYrswp-6B (*IWA4010*) APR 30 Mbp, likely not the same

QTL on 7AS

AX-94709247 40, Vb15 (-log10(P) =4.3)). -log10(P) for PC1 was 3.1 and 1.8 in Norway and China respectively. H/LDP: 2.9/1.4

QTL on 7AL

7AL AX-95173991 at 674 Mbp, significant MTA's in Vb18 (-log10(P) =3.6) and Hs19 (-log10(P) =3.5). -log10(P) for PC1 was 3.3 and 2.0 in Norway and China respectively. H/LDP: 3.2/3.0

Closest QTL QYrswp-7A APR 636 889 961 *IWA6004*

Evaluation of new QTL

QTL on 3BL

The current study detected a QTL covered by three markers (peak marker AX-94811682) located between 705-707 Mbp in this region. This QTL was significant for PC1 in Norway (-log10 (P) = 3.6) but not in in China, and were significant in three environments, and were therefore considered to be stable. No Known QTL reside close to

QTL Summary

Spring wheat QTL: 3BL can be recommended as it is significant for PC1 in Norway and were also significant in three environments, indicating that this QTL is stable and therefore useful in breeding for Yr resistance. The QTL on 5AL were highly significant for PC1 both Norwegian and Chinese trials. In Chinese trials this QTL had a -log10(p)=5.7 and is the only MTA that were over the Bonferroni correction threshold of 5.451. Moreover, this QTL were significant in 4 environments, more than any other QTL detected in this study. The QTL on 5BL were also significant for PC1 in Norway and China, but were only significant in one environment. This QTL were not located close to any QTL with known position in RefSeq, but several QTL have been mapped in this region and it seems likely that this QTL could reside together with known QTL in this region. BS were only significant for PC1 in China but were significant in two environments in Norway. Few other Yr QTL have been detected in this region, but *Yr47* conferring seedling resistance and incompletely linked to Lr52, and some minor QTL associated with APR and HTAP resistance are all located IN 5BS and could overlap with the QTL in the current study. The QTL on 6AL were only significant for PC1 in Norway, as well as being significant in two environments. Agha (2019) detected a significant QTL with one flanking marker also at 609 Mbp associated with powdery mildew, which makes this an interesting QTL to research further to establish if this region contains pleiotropic QTL that can be used to develop cultivars with high levels of durable resistance against several important dioseases. The QTL detected in 1AL were significant for PC1 an stable over three environments. Two QTL were significant in 5AL, both were highly significant for PC1 and significant in three environments, and otherwise behaving very similar across environments and had the same genetic position of 72 cM. It is there for likely that these QTL are one, LD could determine if these markers are linked. This seems to be an important region for Yr resistance, as the most significant QTL in spring wheat were located 100 Mbp from the closest QTL in spring wheat. Likewise, the two QTL in 3AL are located at 84 cM and 7 Mbp apart, and likely are the same QTL. These QTL were not stable, but further research could reveal the effects and their usefulness in resistance breeding.

Conclusion

This thesis does not reflect very well all the information that have been acquired in this project, but this is all available to be used in further research on yellow rust resistance.

The aim of this study was to do a preliminary study of resistance to yellow rust in MASBASIS. Many significant and interesting QTL were detected in both spring and winter wheat populations. These QTL were detected in chromosome regions 1AL, 3AL, 3BL, 3BS, 5AL and 6AL, five of these QTL were stable. Some could be mapped together with previously reported QTL, but physical positions were not found for many of the QTL and Yr resistance genes in the literature and aligning them with QTL detected in this study could not be done with any certainty.

GWAS have confirmed that the winter wheat material grown in Norway generally have a high level of resistance against yellow rust, and the majority of lines had all the significant QTL detected in winter wheat in this study. Further research may give a more nuanced understanding of the effects of these different QTL, which was very difficult to do in this study because the level of resistance combined with many of the studied QTL being present in most lines makes it difficult to distinguish effects of different QTL.

The knowledge, experiences and data generated in this study should be of value to the upcoming Norwegian study on yellow rust resistance at NMBU.

References

Abrahamsen, U., Ficke, A., Brodal, G., Lillemo, M., Dieseth, J. A. & Kim, M. O. (2017). Gulrust i hvete. In vol. 3 *Jord- og Plantekultur 2017. Forsøk i korn, olje- og proteinvekster, engfrøavl og potet 2016*, pp. 109-118. Ås, Norway: Norsk institutt for bioøkonomi (NIBIO).

Agha, K. M. (2019). *The genetic basis of partial resistance to powdery mildew in Norwegian wheat*. Genetic study. 60 stp. NMBU, Ås: Norwegian University of Life Sciences.

Allen, A. M., Winfield, M. O., Burridge, A. J., Downie, R. C., Benbow, H. R., Barker, G. L. A., Wilkinson, P. A., Coghill, J., Waterfall, C., Davassi, A., et al. (2017). Characterization of a Wheat Breeders' Array suitable for high-throughput SNP genotyping of global accessions of hexaploid bread wheat (Triticum aestivum). *Plant Biotechnology Journal*, 15 (3): 390-401. doi: 10.1111/pbi.12635.

Bansal, U., Forrest, K., Hayden, M., Miah, H., Singh, D. & Bariana, H. (2011). Characterisation of a new stripe rust resistance gene Yr47 and its genetic association with the leaf rust resistance gene Lr52. *Theoretical and applied genetics*, 122 (8): 1461-1466.

Bradbury, P. J., Zhang, Z., Kroon, D. E., Casstevens, T. M., Ramdoss, Y. & Buckler, E. S. (2007). TASSEL: software for association mapping of complex traits in diverse samples. *Bioinformatics*, 23 (19): 2633-2635.

Branchereau, C. (2018). *Genome-wide association mapping of three agronomic traits and resistance to Parastagonospora nodorum in spring and winter wheat*: NMBU, Norwegian University of Life Sciences, PO Box 5003, NO-1432 Ås, Norway.

Bulli, P., Zhang, J., Chao, S., Chen, X. & Pumphrey, M. (2016). Genetic Architecture of Resistance to Stripe Rust in a Global Winter Wheat Germplasm Collection. *G3: Genes, Genomes, Genetics*, 6 (8): 2237-2253. doi: 10.1534/g3.116.028407.

Cavanagh, C. R., Chao, S., Wang, S., Huang, B. E., Stephen, S., Kiani, S., Forrest, K., Saintenac, C., Brown-Guedira, G. L., Akhunova, A., et al. (2013). Genome-wide comparative diversity uncovers multiple targets of selection for improvement in hexaploid wheat landraces and cultivars. *Proceedings of the National Academy of Sciences*, 110 (20): 8057-8062. doi: 10.1073/pnas.1217133110.

Chen, W., Wellings, C., Chen, X., Kang, Z. & Liu, T. (2014). Wheat stripe (yellow) rust caused by P uccinia striiformis f. sp. tritici. *Molecular plant pathology*, 15 (5): 433-446.

Chen, X. & Kang, Z. (2017). *Stripe rust*: Springer.

Chen, X. M. (2005). Epidemiology and control of stripe rust [Puccinia striiformis f. sp. tritici] on wheat. *Canadian Journal of Plant Pathology*, 27 (3): 314-337. doi: 10.1080/07060660509507230.

Cuddy, W., Beddow, J., Pardey, P., Chai, Y., Hurley, T., Kriticos, D., Braun, H.-J., Park, R. & Yonow, T. (2015). Research investment implications of shifts in the global geography of wheat stripe rust. *Nature Plants*, 1. doi: 10.1038/nplants.2015.132.

Curtis, B. C. (2002). *BREAD WHEAT, Improvement and Production*

Curtis, B. C., Rajaram, S. & Gómez Macpherson, H. (eds). FAO Plant Production and Protection Series, 30. Rome: FOOD AND AGRICULTURE ORGANIZATION OF THE UNITED NATIONS.

Dupont, F. M. & Altenbach, S. B. (2003). *Molecular and biochemical impacts of environmental factors on wheat grain development and protein synthesis*, 38. pp. 133-146.

Earl, D. A. (2012). STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method. *Conservation genetics resources*, 4 (2): 359-361.

Evanno, G., Regnaut, S. & Goudet, J. (2005). Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Molecular ecology*, 14 (8): 2611-2620.

FAO. (2019a). *Crops*. FAOSTAT: Food and Agriculture Oranization of the United Nations. Available at: http://www.fao.org/faostat/en/#data/QC (accessed: 11.09).

FAO. (2019b). *Wheat - the largest primary commodity*: Food and Agricultural Organization of the United Nations. Available at: http://www.fao.org/resources/infographics/infographics-details/en/c/240943/ (accessed: 11.09.2019).

Ficke, A., Dieseth, J. A., Kim, M. O. & Lillemo, M. (2018). Bladsjukdommer i norsk hvete. Forekomst, betydning og tiltak. In vol. 4 *Jord- og Plantekultur 2018. Forsøk i korn, olje- og proteinvekster, engfrøavl og potet 2017*, pp. 108-116. Ås, Norway: Norsk institutt for bioøkonomi (NIBIO).

Gupta, P. K., Kulwal, P. L. & Jaiswal, V. (2014). Association mapping in crop plants: opportunities and challenges. In vol. 85 *Advances in genetics*, pp. 109-147: Elsevier.

Gustafson, P., Raskina, O., Ma, X. & Nevo, E. (2009). Wheat evolution, domestication, and improvement. *Wheat: science and trade. Wiley, Danvers*: 5-30.

Hao, Y., Chen, Z., Wang, Y., Bland, D., Buck, J., Brown-Guedira, G. & Johnson, J. (2011). Characterization of a major QTL for adult plant resistance to stripe rust in US soft red winter wheat. *Theoretical and applied genetics*, 123 (8): 1401-1411.

Hou, L., Chen, X., Wang, M., See, D. R., Chao, S., Bulli, P. & Jing, J. (2015). Mapping a large number of QTL for durable resistance to stripe rust in winter wheat Druchamp using SSR and SNP markers. *PLoS One*, 10 (5).

Hovmøller, M. S., Walter, S. & Justesen, A. F. (2010). Escalating Threat of Wheat Rusts. *Science*, 329 (5990): 369. doi: 10.1126/science.1194925.

Hovmøller, M. S., Walter, S., Bayles, R. A., Hubbard, A., Flath, K., Sommerfeldt, N., Leconte, M., Czembor, P., Rodriguez-Algaba, J. & Thach, T. (2016). Replacement of the European wheat yellow rust population by new races from the centre of diversity in the near-Himalayan region. *Plant Pathology*, 65 (3): 402-411.

IWGSC. (2018a). "International Wheat Genome Sequencing Consortium". Shifting the limits in wheat research and breeding using a fully annotated reference genome. *Science*, 361 (6403): eaar7191.

IWGSC. (2018b). Shifting the limits in wheat research and breeding using a fully annotated reference genome. *Science*, 361 (6403): eaar7191.

Jansen, S. C. K. (2015). *Genome-wide association mapping of Fusarium head blight resistance in Norwegian spring and winter wheat lines*: Norwegian University of Life Sciences, Ås.

Jin, Y., Szabo, L. J. & Carson, M. (2010). Century-Old Mystery of Puccinia striiformis Life History Solved with the Identification of Berberis as an Alternate Host. *Phytopathology™*, 100 (5): 432-435. doi: 10.1094/phyto-100-5-0432.

Lagudah, E. S., Krattinger, S. G., Herrera-Foessel, S., Singh, R. P., Huerta-Espino, J., Spielmeyer, W., Brown-Guedira, G., Selter, L. L. & Keller, B. (2009). Gene-specific markers for the wheat gene Lr34/Yr18/Pm38 which confers resistance to multiple fungal pathogens. *Theoretical and Applied Genetics*, 119 (5): 889-898.

Lan, C., Liang, S., Zhou, X., Zhou, G., Lu, Q., Xia, X. & He, Z. (2010). Identification of genomic regions controlling adult-plant stripe rust resistance in Chinese landrace Pingyuan 50 through bulked segregant analysis. *Phytopathology*, 100 (4): 313-318.

Lillemo, M. & Dieseth, J. A. (2011). Wheat breeding in Norway. In Bonjean, A., Angus, W. & van Ginkel, M. (eds) vol. 2 *The World Wheat Book A history of wheat breeding*, pp. 45-79. Paris, France: Lavoisier Publishing.

Lin, F. & Chen, X. M. (2008). Quantitative trait loci for non-race-specific, high-temperature adult-plant resistance to stripe rust in wheat cultivar Express. *Theoretical and Applied Genetics*, 118 (4): 631. doi: 10.1007/s00122-008-0894-0.

Line, R. F. & Chen, X. (1995). Successes in breeding for and managing durable resistance to wheat rusts. *Plant Disease*, 79 (12): 1254-1255.

Liu, L., Wang, M., Zhang, Z., See, D. R. & Chen, X. (2020). Identification of Stripe Rust Resistance Loci in U.S. Spring Wheat Cultivars and Breeding Lines Using Genome-wide Association Mapping and Yr Gene Markers. *Plant Disease*, 0 (ja): null. doi: 10.1094/pdis-11-19-2402-re.

Liu, R., Lu, J., Zhou, M., Zheng, S., Liu, Z., Zhang, C., Du, M., Wang, M., Li, Y., Wu, Y., et al. (2020). Developing stripe rust resistant wheat (Triticum aestivum L.) lines with gene pyramiding strategy and marker-assisted selection. *Genetic Resources and Crop Evolution*, 67 (2): 381-391. doi: 10.1007/s10722-019-00868-5.

Liu, W., Kolmer, J., Rynearson, S., Chen, X., Gao, L., Anderson, J. A., Turner, M. K. & Pumphrey, M. (2019). Identifying Loci Conferring Resistance to Leaf and Stripe Rusts in a Spring Wheat Population (Triticum aestivum) via Genome-Wide Association Mapping. *Phytopathology*, 109 (11): 1932-1940. doi: 10.1094/phyto-04-19-0143-r.

Lu, Y., Wang, M., Chen, X., See, D., Chao, S. & Jing, J. (2014). Mapping of Yr62 and a small-effect QTL for high-temperature adult-plant resistance to stripe rust in spring wheat PI 192252. *Theoretical and Applied Genetics*, 127 (6): 1449-1459. doi: 10.1007/s00122-014-2312-0.

Marcussen, T., Sandve, S. R., Heier, L., Spannagl, M., Pfeifer, M., Jakobsen, K. S., Wulff, B. B., Steuernagel, B., Mayer, K. F. & Olsen, O.-A. (2014). Ancient hybridizations among the ancestral genomes of bread wheat. *science*, 345 (6194): 1250092.

McIntosh, R. A., Dubcovsky, J., Rogers, W. J., Morris, C., Appels, R., and Xia, X. C. (2017). *Catalogue of gene symbols for wheat: 2017 supplement.* KOMUGI (ed.). https://shigen.nig.ac.jp/wheat/komugi/genes/macgene/supplement2017.pdf: KOMUGI.

Moore, J. W., Herrera-Foessel, S., Lan, C., Schnippenkoetter, W., Ayliffe, M., Huerta-Espino, J., Lillemo, M., Viccars, L., Milne, R. & Periyannan, S. (2015). A recently evolved hexose transporter variant confers resistance to multiple pathogens in wheat. *Nature genetics*, 47 (12): 1494-1498.

NIBIO. *Integrert plantevern IPV*. Ås, Norge: NIBIO. Available at: https://www.nibio.no/tema/plantehelse/integrert-plantevern (accessed: 01.15).

Pakeerathan, K., Bariana, H., Qureshi, N., Wong, D., Hayden, M. & Bansal, U. (2019). Identification of a new source of stripe rust resistance Yr82 in wheat. *Theoretical and Applied Genetics*, 132 (11): 3169-3176. doi: 10.1007/s00122-019-03416-y.

Petersen, G., Seberg, O., Yde, M. & Berthelsen, K. (2006). Phylogenetic relationships of Triticum and Aegilops and evidence for the origin of the A, B, and D genomes of common wheat (Triticum aestivum). *Molecular phylogenetics and evolution*, 39 (1): 70-82.

Pritchard, J. K., Stephens, M. & Donnelly, P. (2000). Inference of population structure using multilocus genotype data. *Genetics*, 155 (2): 945-959.

Ren, Y., He, Z., Li, J., Lillemo, M., Wu, L., Bai, B., Lu, Q., Zhu, H., Zhou, G. & Du, J. (2012). QTL mapping of adult-plant resistance to stripe rust in a population derived from common wheat cultivars Naxos and Shanghai 3/Catbird. *Theoretical and applied genetics*, 125 (6): 1211-1221.

Rosewarne, G. M., Singh, R. P., Huerta-Espino, J., Herrera-Foessel, S. A., Forrest, K. L., Hayden, M. J. & Rebetzke, G. J. (2012). Analysis of leaf and stripe rust severities reveals pathotype changes and multiple minor QTLs associated with resistance in an Avocet × Pastor wheat population. *Theoretical and Applied Genetics*, 124 (7): 1283-1294. doi: 10.1007/s00122-012-1786-x.

Rosewarne, G. M., Herrera-Foessel, S. A., Singh, R. P., Huerta-Espino, J., Lan, C. X. & He, Z. H. (2013). Quantitative trait loci of stripe rust resistance in wheat. *Theoretical and Applied Genetics*, 126 (10): 2427-2449. doi: 10.1007/s00122-013-2159-9.

Ruud, A. K., Dieseth, J. A. & Lillemo, M. (2018). Effects of three Parastagonospora nodorum necrotrophic effectors on spring wheat under Norwegian field conditions. *Crop Science*, 58 (1): 159-168.

Salamini, F., Özkan, H., Brandolini, A., Schäfer-Pregl, R. & Martin, W. (2002). Genetics and geography of wild cereal domestication in the near east. *Nature Reviews Genetics*, 3 (6): 429-441. doi: 10.1038/nrg817.

Salvi, S. & Tuberosa, R. (2005). To clone or not to clone plant QTLs: present and future challenges. *Trends in Plant Science*, 10 (6): 297-304. doi: https://doi.org/10.1016/j.tplants.2005.04.008.

Seehusen, T., Waalen, W., Hoel, B., Uhlen, A. K., Persson, T. & Strand, E. (2016). Endret klima- effekter og behov for tilpasninger i norsk kornproduksjon. In vol. 1 *Jord- og Plantekultur 2016. Forsøk i korn, olje- og proteinvekster, engfrøavl og potet 2015*, pp. 14-17. Ås, Norway: Norsk institutt for bioøkonomi (NIBIO).

Shewry, P. R. & Hey, S. J. (2015). The contribution of wheat to human diet and health. *Food and energy security*, 4 (3): 178-202. doi: 10.1002/fes3.64.

Singh, R. P., Singh, P. K., Rutkoski, J., Hodson, D. P., He, X., Jørgensen, L. N., Hovmøller, M. S. & Huerta-Espino, J. (2016). Disease impact on wheat yield potential and prospects of genetic control. *Annual review of phytopathology*, 54: 303-322.

Sleper, D. A. & Poehlman, J. M. (2006). *Breeding field crops*: Blackwell publishing.

Somers, D. J., Isaac, P. & Edwards, K. (2004). A high-density microsatellite consensus map for bread wheat (Triticum aestivum L.). *Theoretical and Applied Genetics*, 109 (6): 1105-1114. doi: 10.1007/s00122-004-1740-7.

Statistics Norway. (2019). *Cereals and oil seeds, area and yields*: Statistics Norway. Available at: https://www.ssb.no/en/jord-skog-jakt-og-fiskeri/statistikker/korn (accessed: 11.22.2019).

Syvånen, A.-C., Landegren, U., Isaksson, A., Gyllensten, U. & Brookes, A. (1999). First International SNP Meeting at Skokloster, Sweden, August 1998. Enthusiasm mixed with scepticism about single-nucleotide polymorphism markers for dissecting complex disorders. *European Journal of Human Genetics*, 7 (1): 98-101.

Sørensen, E. S. (2016). *Identification and validation of SNP markers for Fusarium head blight resistance in wheat*: Norwegian University of Life Sciences, Ås.

Tehseen, M. M., Tonk, F. A., Tosun, M., Amri, A., Sansaloni, C. P., Kurtulus, E., Yazbek, M., Al-Sham'aa, K., Ozseven, I., Safdar, L. B., et al. (2020). Genome Wide Association Study of Resistance to PstS2 and Warrior Races of Stripe (Yellow) Rust in Bread Wheat Landraces. *bioRxiv*: 2020.02.09.940775. doi: 10.1101/2020.02.09.940775.

Wang, M. N. & Chen, X. M. (2013). First Report of Oregon Grape (Mahonia aquifolium) as an Alternate Host for the Wheat Stripe Rust Pathogen (Puccinia striiformis f. sp. tritici) Under Artificial Inoculation. *Plant Disease*, 97 (6): 839-839. doi: 10.1094/pdis-09-12-0864-pdn.

Weie, W., Zhonghu, H., Fengmei, G., Jindong, L., Hui, J., Shengnan, Z., Yanying, Q. & Xianchun, X. (2017). A High-Density Consensus Map of Common Wheat Integrating Four Mapping Populations Scanned by the 90K SNP Array. *Frontiers in Plant Science*, 8. doi: 10.3389/fpls.2017.01389.

Wellings, C. R. (2011). Global status of stripe rust: a review of historical and current threats. *Euphytica*, 179 (1): 129-141. doi: 10.1007/s10681-011-0360-y.

Yoon, M.-Y., Cha, B. & Kim, J.-C. (2013). Recent trends in studies on botanical fungicides in agriculture. *The plant pathology journal*, 29 (1): 1.

Appendix

Appendix

Table 6 Spring MASBASIS lines with lsmeans for disease severity in each environment, over all environments, over all high disease pressure environments, over all low disease pressure environments and PC1

Name	St 15	St 16	Vb 15	Vb 16	Vb 17	Vb 18	Vb 19	Hs 19	PX 19	XD 19	All env.	HDP	LDP	PC1
Bastian	3.0	2.0	5.0	0.5	0.5	29.7	15.0	3.5	47.5	35.0	7.4	10.9	1.5	45.9
Bjarne	13.5	30.1	50.2	9.9	10.0	56.8	34.6	22.4	65.0	85.0	28.4	37.0	14.1	112.7
Tjalve	1.0	1.5	2.3	0.5	0.0	5.7	13.8	0.0	25.0	5.5	3.1	4.9	0.2	-11.3
Avle	1.5	0.0	0.0	0.0	0.0	0.5	0.0	0.0	10.0	3.0	0.3	0.4	0.0	-28.6
Zebra	4.6	4.0	18.1	3.0	3.0	18.5	28.2	4.7	20.0	20.0	10.5	14.7	3.6	1.8
Berserk	25.0	3.0	15.5	5.0	4.0	37.8	34.7	4.2	20.0	45.0	16.2	23.2	4.4	29.6
Brakar	0.0	1.0	1.8	0.0	0.5	6.6	5.4	0.0	27.5	3.0	1.9	3.0	0.2	-12.9
Runar	1.5	2.4	3.8	0.5	1.5	8.7	2.5	2.9	50.0	30.0	3.0	3.8	1.6	36.2

T2038	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	7.5	10.0	0.0	0.0	0.0	-20.7
T9040	0.0	0.0	0.0	0.0	0.5	1.9	0.0	0.0	10.0	5.0	0.3	0.4	0.2	-25.1
T9040 (1995)	2.5	0.5	2.8	0.5	0.0	3.4	0.0	0.0	17.5	5.0	1.2	1.8	0.2	-18.6
T10014	0.0	0.0	0.0	0.5	0.0	3.5	0.0	0.0	5.0	5.0	0.5	0.7	0.2	-29.1
NK93602 (1995)	0.0	0.0	1.0	0.0	0.5	0.5	2.9	0.0	12.5	1.0	0.6	0.9	0.2	-27.1
MS 273-150	1.9	2.0	4.0	1.0	1.3	4.9	8.7	2.4	9.0	10.0	3.3	4.3	1.6	-18.7
DH 49-18 Bastian/Adder	10.0	5.0	20.3	4.0	2.0	15.4	25.4	2.4	15.0	60.0	10.6	15.2	2.8	43.2
Naxos (x3)	3.8	3.0	6.5	4.1	2.5	6.5	21.7	1.7	50.0	20.0	6.2	8.3	2.8	22.3
Paros	1.5	2.5	2.8	2.6	1.0	11.9	32.0	1.9	5.0	1.0	7.0	10.1	1.8	-33.7
Paros/NK93602	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	12.5	1.0	0.1	0.2	0.0	-28.4
Paros/T9040	8.5	4.9	20.8	4.0	7.5	25.0	31.6	4.0	5.0	7.5	13.3	18.2	5.2	-26.0
T9040/Paros	10.0	5.0	12.4	3.9	4.0	9.7	38.2	3.2	40.0	20.0	10.8	15.1	3.7	16.9
Saar	0.8	0.5	4.5	0.5	1.0	2.6	0.0	0.0	15.0	20.0	1.2	1.7	0.5	-2.7
Filin	4.0	22.5	15.3	4.0	3.5	24.6	12.0	5.1	35.0	40.0	11.4	15.7	4.2	34.7
Milan	0.0	0.0	0.0	0.5	0.0	3.7	4.2	0.0	3.0	5.0	1.1	1.6	0.2	-31.1
Pfau/Milan	1.5	0.8	2.3	0.5	1.0	1.3	1.5	1.1	2.5	15.0	1.3	1.5	0.9	-18.9
Bau/Milan -2	2.0	2.5	4.2	1.0	3.0	2.1	4.0	0.0	27.5	40.0	2.4	3.0	1.3	30.6
Dulus	2.0	2.6	5.0	1.0	2.0	3.6	2.5	0.0	15.0	45.0	2.3	3.1	1.0	26.9

Gondo -1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	17.5	0.0	0.0	0.0	-18.0
Catbird -2	2.9	3.0	3.8	0.5	1.0	0.0	1.0	0.0	15.0	20.0	1.5	2.1	0.5	-4.0
Croc_1/Ae.squarrosa (205)//Kauz	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.5	7.5	0.0	0.0	0.0	-27.7
Altar84/Ae.squarrosa(219)// 2*Seri	0.9	0.6	2.8	1.0	0.5	19.6	12.6	0.5	5.0	17.5	4.8	7.3	0.7	-14.6
Altar84/Ae.sq(219)//2*Seri/3/ Avle	0.0	2.2	1.8	1.0	1.0	4.9	0.0	0.0	15.0	60.0	1.4	1.8	0.7	41.9
Kariega	1.0	0.0	1.0	0.5	0.0	3.0	5.0	0.0	7.5	20.0	1.3	2.0	0.2	-9.3
Avocet YrA	65.2	62.5	81.5	30.0	27.5	84.9	66.7	61.0	60.0	100.0	59.9	72.2	39.5	124.4
NK93604	0.0	0.0	0.5	0.0	0.0	1.3	0.0	0.0	70.0	85.0	0.2	0.4	0.0	#N/A
CJ9306	4.0	4.0	15.1	3.0	4.0	23.5	27.4	3.0	65.0	95.0	10.5	14.8	3.3	117.8
CJ9403	12.5	12.5	20.2	4.0	6.0	40.3	34.5	4.0	22.5	35.0	16.8	24.0	4.7	124.2
512-21	0.5	4.0	2.8	3.5	2.5	25.5	13.2	2.1	17.5	25.0	6.8	9.2	2.7	20.0
512-50	1.5	1.0	0.0	1.0	0.0	5.8	5.6	2.7	0.0	0.0	2.2	2.8	1.2	4.6
512-54	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	NA
512-70	1.5	1.5	1.0	1.9	1.0	16.8	2.5	0.0	10.0	35.0	3.3	4.7	1.0	NA
512-87	2.0	0.5	1.0	0.0	0.5	4.4	0.0	0.0	10.0	17.5	1.1	1.6	0.2	10.2
SHA3/CBRD	3.5	1.0	1.8	1.5	1.0	4.6	9.5	2.3	5.0	10.0	3.2	4.1	1.6	-9.7
Soru #1	0.5	0.0	2.8	1.9	2.0	10.0	7.8	1.5	47.5	75.0	3.3	4.2	1.8	-23.3
Sumai 3 (18.)	1.5	1.2	2.8	0.0	0.5	4.2	4.6	1.9	22.5	12.5	2.1	2.9	0.8	88.7
Nobeokabouzu (Mhazy)	1.5	5.0	2.3	1.0	1.0	3.5	8.3	1.5	10.0	20.0	3.0	4.1	1.2	-5.6
Frontana (95)	0.5	0.0	1.8	0.5	0.5	3.3	8.2	0.0	45.0	70.0	1.9	2.8	0.3	-6.7
Nanjing 7840 - Pl.4	40.0	24.9	16.0	14.9	7.5	30.5	24.8	9.2	25.0	30.0	21.0	27.2	10.5	80.1

Ning 8343 - Pl.4	0.5	0.5	0.5	0.5	1.0	6.1	4.0	0.9	2.5	3.0	1.8	2.3	0.8	18.4
Vinjett	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	25.0	10.0	0.0	0.0	0.0	-32.6
DH20070	1.5	0.0	0.0	1.0	0.0	3.8	0.0	0.0	5.0	5.0	0.8	1.1	0.3	-2.0
DH20097	0.0	0.8	0.5	0.0	0.5	1.3	3.7	0.0	17.5	40.0	0.9	1.3	0.2	-28.8
GONDO	2.0	2.5	5.0	3.5	2.5	4.5	6.9	0.0	0.5	1.0	3.4	4.2	2.0	21.6
MILAN/SHA7	0.0	0.0	0.5	0.0	0.0	1.3	3.8	1.2	10.0	5.0	0.9	1.1	0.4	-37.1
CBRD/KAUZ	5.0	2.5	7.5	1.5	2.0	2.7	0.0	0.0	20.0	30.0	2.7	3.5	1.2	-25.1
R37/GHL121//KAL/BB/3/JUP/MUS/4/2 *YMI #6/5/CBRD	0.0	2.6	5.8	1.0	1.0	3.6	2.5	0.0	7.5	7.5	2.1	2.9	0.7	12.7
GUAM92//PSN/BOW	1.0	0.9	3.1	0.0	2.0	1.0	10.4	1.1	62.5	80.0	2.4	3.3	1.0	-23.8
NG8675/CBRD	6.5	4.0	12.3	4.1	4.0	12.3	19.6	5.3	3.0	5.0	8.5	10.9	4.5	104.7
ALTAR 84/AE.SQUARROSA (224)//ESDA	0.0	0.0	0.0	0.0	0.0	0.0	2.5	1.1	0.0	5.0	0.5	0.5	0.4	-31.1
BCN*2//CROC_1/AE.SQUARROSA (886)	1.5	1.8	2.7	1.5	2.0	0.0	0.0	0.0	12.5	5.0	1.2	1.2	1.2	-33.0
MAYOOR//TK SN1081/ AE.SQUARROSA (222)	6.5	4.0	4.5	1.5	1.0	4.1	9.9	1.5	5.0	0.0	4.1	5.8	1.3	-22.6
AC Somerset	2.5	1.3	4.0	1.0	1.0	7.9	5.5	2.0	10.0	0.5	3.2	4.2	1.3	-33.6
Sport	4.9	1.0	4.7	1.0	0.5	4.6	6.2	0.5	5.0	0.0	2.9	4.3	0.7	-29.1
CD87	0.0	0.4	1.0	0.5	0.0	2.9	0.0	0.0	5.0	5.0	0.6	0.9	0.2	-34.8
Chara	2.9	2.9	4.1	1.0	1.5	3.2	3.1	0.0	17.5	35.0	2.3	3.2	0.8	-29.1
Kukri	1.5	0.9	5.0	3.0	2.0	20.4	8.0	3.7	5.0	5.0	5.6	7.2	2.9	16.8

Naxos/2*Saar	3.0	2.0	2.8	1.5	1.5	2.1	0.0	1.1	32.5	10.0	1.8	2.0	1.4	-29.1
ONPMSYDER-05	1.5	1.5	5.0	1.5	2.0	3.6	8.4	0.5	2.5	3.0	3.0	4.0	1.3	-2.3
BAJASS-5	3.0	1.1	2.3	0.0	1.0	2.2	0.0	0.0	45.0	45.0	1.2	1.7	0.3	-32.6
NK00521	2.5	4.8	10.6	4.0	3.0	16.6	34.9	5.2	7.5	3.0	10.2	13.9	4.1	54.2
NK01513	2.0	0.7	0.0	0.0	0.0	6.5	0.0	0.0	35.0	15.0	1.2	1.8	0.0	-28.7
Demonstrant	3.4	0.9	5.4	0.5	1.3	4.0	22.6	1.9	12.5	5.0	5.0	7.3	1.2	6.3
Krabat	1.0	0.6	2.0	0.0	0.0	12.6	0.0	0.0	7.5	3.0	2.0	3.2	0.0	-22.6
GN03531	0.0	0.0	0.0	0.0	0.0	0.0	0.0	NA	10.0	10.5	-0.4	0.0	0.0	-28.7
GN04537	1.5	3.5	6.0	4.0	3.0	9.8	26.5	3.0	7.5	3.0	7.2	9.5	3.3	-17.0
GN05507	1.5	1.5	2.8	1.0	2.0	5.2	6.8	0.0	5.0	3.0	2.6	3.6	1.0	-28.7
Laban	0.5	0.0	0.5	0.0	0.0	0.0	7.2	0.5	5.0	7.5	1.1	1.6	0.2	-31.2
Breeding line1	0.5	0.0	0.0	0.0	0.0	0.5	0.0	0.0	25.0	7.5	0.1	0.2	0.0	-24.8
Breeding line2	2.0	1.0	4.9	1.9	2.0	3.4	4.2	0.8	27.5	20.0	2.5	3.1	1.6	-7.9
GN03597	4.0	3.9	6.6	1.5	4.8	2.8	19.6	1.3	7.5	5.4	5.6	7.4	2.5	9.5
GN04528	1.5	0.5	0.5	1.0	0.0	4.8	9.1	0.0	0.0	0.0	2.2	3.3	0.3	-26.0
GN05580	0.0	0.0	0.0	0.0	0.0	0.5	6.3	0.0	62.5	90.0	0.9	1.4	0.0	#N/A
GN06557	7.0	8.6	15.5	8.6	3.5	13.1	30.9	2.1	5.0	30.0	11.2	15.0	4.7	114.3
GN06573	2.5	1.5	1.0	2.5	0.8	0.5	2.5	1.1	20.0	3.0	1.6	1.6	1.5	-0.4

Breeding line3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.1	2.5	5.5	0.1	0.0	0.4	-21.9
Amulett	1.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	12.5	20.0	0.2	0.2	0.2	-29.6
Bombona	5.0	2.5	4.7	1.5	2.5	2.3	2.5	1.8	5.0	1.0	2.9	3.4	1.9	-6.6
QUARNA	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	10.0	3.0	0.1	0.1	0.0	-33.7
GN03529	1.0	0.5	5.1	0.0	0.0	1.0	0.0	0.0	7.5	10.0	1.0	1.5	0.0	-27.3
Breeding line4	1.5	0.0	0.5	0.0	0.5	1.1	11.1	0.5	20.0	10.0	1.9	2.8	0.3	-20.7
GN04526	2.5	0.5	2.7	0.5	2.5	2.6	0.0	0.0	15.0	25.0	1.4	1.7	1.0	-9.1
J03	4.0	4.1	12.5	6.0	5.0	34.6	68.4	7.9	7.5	0.0	17.8	24.7	6.3	3.9
NK01565	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	35.0	20.0	0.0	0.0	0.0	-33.5
GN03503	2.9	6.0	19.8	3.5	3.5	19.3	20.9	1.5	17.5	3.0	9.7	13.8	2.8	14.8
GN05551	1.5	1.5	4.4	1.5	0.5	3.9	0.0	0.0	47.5	25.0	1.7	2.3	0.7	-19.6
GN05589	15.0	10.0	30.5	7.4	7.0	47.7	44.9	19.8	17.5	10.0	22.8	29.6	11.4	25.1
GN06578	2.5	2.4	7.7	2.5	2.5	4.0	7.0	0.0	45.0	35.0	3.6	4.7	1.7	-11.6
GN07581	1.5	2.0	2.3	1.0	0.0	5.2	5.7	0.0	20.0	7.5	2.2	3.3	0.3	44.5
GN08504	4.0	2.4	11.1	2.9	3.0	19.1	29.5	3.8	20.0	20.0	9.5	13.2	3.2	-13.0
GN08531	2.0	2.0	1.0	0.0	0.0	5.2	0.0	1.9	12.5	5.0	1.5	2.0	0.6	3.7
GN08533	1.0	0.5	1.0	0.0	0.5	0.0	2.9	0.0	12.5	5.0	0.7	1.1	0.2	-22.6
GN08534	4.0	4.0	5.4	4.0	2.0	2.9	7.4	0.5	10.0	10.5	3.8	4.7	2.2	-22.6

GN08541	2.0	3.5	1.8	1.5	1.0	8.4	20.1	3.8	7.5	7.5	5.3	7.2	2.1	-17.0
GN08554	4.9	3.0	5.6	3.1	1.8	10.8	32.3	0.0	20.0	15.0	7.7	11.3	1.6	-23.5
GN08557	2.0	4.0	2.9	1.5	0.5	5.0	8.1	0.7	17.5	7.5	3.1	4.4	0.9	-3.3
GN08564	4.5	0.5	6.6	1.0	2.8	1.0	28.9	3.3	20.0	7.5	6.1	8.3	2.4	-18.1
GN08568	5.0	3.1	17.6	4.0	4.0	6.5	13.3	0.0	17.5	5.0	6.7	9.1	2.7	-15.5
GN08588	6.5	1.0	5.6	1.5	1.8	2.4	8.8	3.1	10.0	10.0	3.8	4.9	2.1	-19.9
GN08595	1.0	0.0	0.0	0.0	0.5	1.0	0.0	0.0	5.0	10.0	0.3	0.4	0.2	-19.4
GN08596	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	7.5	15.0	0.1	0.1	0.0	-23.3
GN08597	2.5	1.1	2.8	0.5	0.5	2.7	9.2	1.2	0.5	0.0	2.6	3.7	0.7	-15.0
GN08647	0.0	0.6	1.0	0.0	0.0	2.9	0.0	0.0	22.5	25.0	0.6	0.9	0.0	-38.2
TJALVE/Purpur seed	4.0	5.1	4.2	1.0	1.5	5.6	11.6	1.0	20.0	25.0	4.3	6.1	1.2	10.4
Sabin	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0	37.5	10.0	0.2	0.3	0.0	6.6
Breeding line5	2.0	2.0	8.1	1.0	0.5	2.4	7.5	0.0	2.5	5.0	2.9	4.4	0.5	1.6
Breeding line6	0.5	0.0	0.0	0.0	0.0	1.0	3.4	0.0	12.5	3.0	0.6	1.0	0.0	-31.6
Breeding line7	2.5	0.5	0.0	0.0	0.0	0.0	0.0	0.0	7.5	0.0	0.4	0.6	0.0	-27.2
Breeding line8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.0	1.0	0.0	0.0	0.0	-33.5
Breeding line9	1.5	0.0	0.5	0.0	0.0	0.0	0.0	0.0	5.5	5.0	0.3	0.4	0.0	-35.7

Breeding line10	1.5	0.0	1.0	0.0	1.0	0.5	0.0	0.7	12.5	5.0	0.6	0.6	0.6	-29.8
Granary	1.0	1.5	1.8	1.0	1.0	0.9	2.9	0.0	30.0	90.0	1.3	1.6	0.7	-23.8
Tom	0.5	1.4	2.3	0.5	1.8	13.0	4.8	2.4	12.5	17.5	3.3	4.4	1.6	89.4
RB07	3.5	1.5	4.6	2.0	2.0	3.5	22.2	7.0	0.0	30.0	5.8	7.1	3.7	-6.8
C80.1/3*QT4522//2*ATTILA	0.5	0.0	0.0	0.0	0.0	0.0	2.5	0.0	45.0	40.0	0.4	0.6	0.0	-4.3
C80.1/3*QT4522//2*PASTOR	2.0	2.0	3.7	1.5	2.0	3.2	0.0	1.0	5.0	3.0	1.9	2.2	1.5	45.0
Møystad	2.0	0.0	0.5	0.0	0.0	1.3	4.1	0.0	15.0	5.0	1.0	1.6	0.0	-31.2
Rollo	2.5	2.0	2.8	2.0	0.5	3.6	0.0	0.5	12.5	12.5	1.7	2.2	1.0	-18.4
Norrøna	3.0	4.0	17.0	7.5	4.0	13.7	14.3	4.0	7.5	7.5	8.4	10.4	5.2	-13.5
Fram II	1.5	1.5	1.8	1.0	2.0	3.8	16.5	4.2	60.0	80.0	4.0	5.0	2.4	-23.8
Sumai #3-1 (12SRSN)	0.0	2.8	5.1	2.2	0.0	11.1	3.4	3.4	5.0	5.0	3.5	4.5	1.9	105.8
Mirakel	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	5.0	5.0	0.0	0.1	0.0	-29.1
Rabagast	1.0	0.0	0.0	0.0	0.5	0.5	0.0	0.0	15.0	10.0	0.3	0.3	0.2	-29.1
Seniorita	0.8	1.0	1.5	0.0	0.0	3.9	7.1	0.0	75.0	100.0	1.8	2.9	0.0	-15.5
GN07548	20.0	35.0	30.4	15.0	25.0	55.8	0.0	7.0	7.5	5.0	23.5	28.2	15.7	136.2
GN07560	2.0	0.0	1.0	0.5	0.5	0.5	0.0	0.0	15.0	5.0	0.6	0.7	0.3	-26.5
GN07525	3.0	3.0	7.1	3.5	1.5	16.6	9.6	2.9	20.0	15.0	5.9	7.9	2.6	-21.2
GN08530	2.0	7.0	17.4	3.5	6.0	19.1	33.0	5.2	7.5	12.5	11.7	15.7	4.9	-4.3

GN09572	2.0	1.0	6.3	1.5	1.0	31.7	19.7	0.0	45.0	70.0	7.9	12.1	0.8	-18.0
GN08581	4.9	4.1	15.1	2.6	2.5	21.7	17.1	4.8	0.0	5.0	9.1	12.6	3.3	85.0
GN10510	0.5	0.0	0.0	0.0	0.5	0.5	5.3	0.8	2.5	3.0	1.0	1.3	0.4	-32.7
Willy	0.5	0.0	0.5	0.0	0.5	4.2	0.0	0.0	17.5	30.0	0.7	1.0	0.2	-32.8
GN10524	6.5	4.0	5.1	0.5	3.0	1.9	0.0	NA	15.0	12.5	2.6	3.5	1.8	11.9
Berlock	1.9	0.5	2.0	1.0	0.0	2.1	0.0	0.0	22.5	10.0	0.9	1.3	0.3	-12.8
Arabella	2.3	0.5	3.2	1.0	0.0	4.7	0.0	0.0	2.5	5.0	1.5	2.1	0.3	-9.0
Breeding line11	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	12.5	15.3	0.1	0.1	0.0	-30.4
GN07580	3.5	1.9	1.8	2.9	0.8	1.7	0.0	0.0	5.0	25.0	1.6	1.8	1.2	2.3
GN09584	2.5	0.0	2.3	0.0	0.5	2.0	0.0	0.5	5.0	5.0	1.0	1.4	0.3	-6.4
GN10512	0.0	0.7	0.0	0.0	0.0	3.4	9.7	0.0	6.5	5.0	1.7	2.8	0.0	-29.1
Polkka	0.0	0.5	1.0	1.9	1.0	9.1	2.5	0.5	2.5	3.0	2.1	2.6	1.1	-27.0
Avans	1.5	2.0	1.8	2.4	1.0	1.4	7.4	0.0	0.5	5.0	2.2	2.8	1.1	-32.8
BJY/COC//CLMS/GEN	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	27.5	7.5	0.0	0.0	0.0	-32.5
HAHN/PRL//AUS1408	1.0	3.0	3.3	1.0	0.0	3.6	0.0	0.9	40.0	30.0	1.6	2.2	0.6	-4.0
TUI/RL4137	0.0	0.6	0.5	0.0	0.5	0.9	0.0	0.0	5.0	0.5	0.3	0.4	0.2	33.3
T7347	0.5	0.6	0.0	0.0	0.0	0.5	0.0	0.0	15.0	3.0	0.2	0.3	0.0	-33.0
Reno	0.0	0.0	5.7	0.5	0.0	17.6	0.0	0.5	0.5	0.0	3.0	4.7	0.3	-23.4

Bjarne/LW91W86	0.0	0.0	0.0	0.0	0.0	1.6	0.0	0.0	10.0	7.5	0.2	0.3	0.0	-38.2
Anniina	NA	2.0	NA	0.5	0.5	7.5	5.6	1.5	37.5	30.0	3.0	4.2	0.8	-22.1
Aino	2.5	3.0	21.1	3.9	4.0	54.7	29.4	6.7	10.0	15.0	15.7	22.1	4.9	27.6
Kruunu	2.5	3.0	4.0	1.5	2.5	19.8	16.2	3.5	10.0	30.0	6.6	9.1	2.5	-12.1
Marble	NA	5.0	NA	4.0	3.5	6.0	0.0	2.3	15.0	25.0	3.6	2.9	3.3	4.8
Wanamo	NA	2.5	NA	3.0	3.5	19.4	2.5	0.0	10.0	7.5	5.3	7.3	2.2	4.5
Wellamo	NA	1.0	NA	0.0	0.5	3.8	0.0	0.5	7.5	7.5	1.1	0.8	0.3	-22.1
Scirocco	4.0	3.1	9.6	4.0	2.0	20.0	10.7	3.5	5.0	5.0	7.1	9.5	3.2	-24.7
Dragon	0.5	0.0	0.0	0.0	0.0	0.5	0.0	0.0	5.0	5.5	0.1	0.2	0.0	-29.1
Sirius	3.0	3.4	1.8	0.0	0.5	4.2	8.1	1.5	3.0	0.0	2.8	4.1	0.7	-28.2
Cadenza	0.0	1.0	0.0	0.0	0.0	0.0	0.5	0.0	12.5	12.5	1.8	2.3	0.8	-36.9
GN11591	NA	1.0	NA	1.5	1.5	2.3	7.6	0.5	45.0	90.0	0.2	0.3	0.0	-12.2
GN11569	NA	10.0	NA	10.0	12.5	47.7	48.8	8.4	32.5	5.0	1.8	2.0	1.3	105.5
GN11572	NA	1.0	NA	1.0	0.0	2.1	2.5	0.0	10.0	5.0	2.5	2.8	1.2	-13.1
GN10607	NA	1.0	NA	0.5	0.5	2.3	4.4	0.5	25.0	45.0	23.0	34.7	10.3	-23.9
GN10613	NA	24.9	NA	19.0	8.5	29.9	55.0	7.0	22.5	25.0	1.2	1.1	0.3	32.9
GN12639	NA	2.0	NA	1.5	0.5	4.3	0.0	0.5	20.0	30.0	1.6	1.8	0.5	7.3
GN12640	NA	2.0	NA	1.9	2.5	28.3	0.0	1.1	25.0	35.0	24.2	35.8	11.5	13.3

GN12700	NA	4.9	NA	6.0	5.5	29.9	34.4	10.2	20.0	7.5	1.6	1.3	0.8	24.5
GN12733	NA	8.4	NA	6.0	2.8	15.5	24.4	4.1	17.5	7.5	6.1	9.3	1.8	-13.0
GN12699	NA	2.5	NA	2.4	3.0	9.8	27.2	2.9	10.0	25.0	15.3	22.3	7.2	-14.4
Breeding line12	NA	NA	NA	NA	14.8	7.3	21.0	3.0	20.0	40.0	10.3	15.3	4.3	-0.6
GN11505	NA	5.0	NA	3.1	4.5	6.2	20.4	2.0	15.0	10.0	8.1	12.4	2.8	24.1
GN11537	NA	2.5	NA	4.0	2.8	3.5	0.0	1.0	12.5	7.5	10.6	11.2	8.9	-15.5
GN11604	NA	4.0	NA	6.0	5.0	13.4	9.3	1.1	15.0	20.0	7.0	9.7	3.2	-19.5
GN11634	NA	1.0	NA	1.5	0.0	4.2	14.4	1.0	7.5	17.5	2.4	1.2	2.6	-4.0
Breeding line13	NA	NA	NA	NA	0.0	0.0	0.0	0.0	20.0	15.0	6.6	8.1	4.0	-13.2
Breeding line14	NA	NA	NA	NA	0.0	4.2	2.9	0.0	15.0	10.0	3.8	5.7	0.8	-4.6
Breeding line15	NA	NA	NA	NA	0.5	0.5	0.0	0.0	5.0	22.5	-1.0	-3.0	0.0	-15.5
Breeding line16	NA	NA	NA	NA	0.0	0.5	0.0	0.0	2.5	35.0	0.8	0.6	0.0	-8.5
GN12722	NA	0.0	NA	0.5	1.2	0.0	0.0	0.5	15.0	10.0	-0.7	-2.7	0.3	3.7
GN11527	NA	1.5	NA	0.5	0.5	2.7	2.5	0.0	27.5	20.0	-0.8	-2.7	0.0	-15.5
GN11551	NA	8.6	NA	5.0	10.2	16.3	33.6	12.9	32.5	60.0	0.5	-0.8	0.7	7.7
GN10680	NA	15.0	NA	5.0	4.0	39.1	35.0	7.2	32.5	15.0	1.4	1.4	0.3	58.8
GN11516	NA	2.5	NA	2.6	2.0	14.5	5.7	2.3	37.5	50.0	14.5	18.7	9.4	9.9
GN10547	NA	3.5	NA	2.5	2.0	20.2	15.4	1.3	17.5	12.5	17.7	28.9	5.4	53.7
GN10603	NA	1.0	NA	0.0	0.0	1.3	0.0	0.0	50.0	50.0	5.0	6.8	2.3	-8.3

GN11574	NA	8.6	NA	4.0	3.5	26.9	25.0	7.3	7.5	5.0	7.6	12.2	1.9	64.1
GN11646	NA	0.5	NA	0.5	0.0	0.0	0.0	0.0	2.5	0.0	0.5	0.0	0.0	-26.5
GN12606	NA	0.0	NA	0.0	0.0	0.5	0.0	0.0	52.5	5.0	12.7	19.4	4.9	-36.1
GN12625	NA	5.0	NA	7.0	4.0	7.2	26.5	4.4	17.5	15.0	0.3	-0.6	0.2	5.1
GN12628	NA	2.0	NA	2.5	2.5	8.1	32.2	2.3	45.0	35.0	0.2	-0.6	0.0	-5.9
GN12634	NA	2.5	NA	1.5	2.0	3.7	5.0	3.2	32.5	5.0	9.1	12.1	5.1	44.5
GN12635	NA	1.0	NA	1.0	1.0	0.0	2.5	0.9	5.0	5.0	8.4	13.3	2.4	-4.4
GN12641	NA	0.0	NA	0.0	0.0	1.0	0.0	0.0	12.5	10.0	3.1	2.9	2.2	-29.1
GN04603	NA	2.5	NA	3.6	2.0	5.3	10.3	1.5	12.5	10.0	1.2	0.4	1.0	-16.8
GN11592	NA	2.0	NA	0.5	1.0	2.4	12.7	1.9	60.0	45.0	0.3	-0.5	0.0	-16.8
GN11514	NA	10.0	NA	2.0	5.2	15.7	32.8	5.9	30.0	5.0	4.3	5.2	2.4	66.6
GN12750	NA	5.9	NA	4.0	4.0	22.2	34.4	4.3	20.0	5.0	3.5	4.9	1.1	-5.7
GN12626	NA	3.0	NA	2.0	1.2	2.4	13.0	2.8	65.0	50.0	12.0	18.7	4.4	-17.3
GN12656	NA	12.5	NA	6.0	8.5	19.9	38.3	5.1	65.0	95.0	12.6	20.0	4.1	77.2
GN12658	NA	12.5	NA	3.9	7.2	21.6	35.0	6.6	7.5	5.0	4.2	5.3	2.0	124.2
GN13542	NA	1.4	NA	3.0	0.0	10.1	16.6	1.2	12.5	12.5	15.2	22.8	6.5	-26.5
GN13576	NA	5.0	NA	2.1	5.2	16.8	29.8	8.7	5.0	12.5	14.6	22.2	5.9	-13.5
GN13577	NA	NA	NA	NA	5.0	36.4	46.1	5.9	37.5	3.0	5.5	8.6	1.4	-18.8
Mandaryna	NA	NA	NA	NA	4.0	9.3	19.5	1.1	5.0	1.0	11.4	16.4	5.3	-11.3

Breeding line17	NA	NA	NA	NA	0.0	0.0	2.5	0.0	15.0	3.0	22.4	38.3	5.5	-33.7
Breeding line18	NA	NA	NA	NA	1.0	3.7	16.1	0.0	5.0	0.0	7.5	11.4	2.6	-23.4
Breeding line19	NA	NA	NA	NA	0.0	1.0	6.9	0.0	5.0	5.0	-0.3	-1.7	0.0	-34.8
GN12727	NA	0.0	NA	0.0	0.0	0.0	5.4	0.0	5.0	40.0	4.2	6.9	0.5	-29.1
GN12721	NA	0.5	NA	0.0	0.5	1.0	0.0	0.0	5.0	7.5	1.0	1.0	0.0	11.1
GN13614	NA	0.4	NA	0.0	0.0	1.0	0.0	0.0	5.0	12.5	1.0	1.0	0.0	-26.0
GN13615	NA	1.5	NA	0.5	0.5	0.5	0.0	0.0	17.5	5.0	0.4	-0.3	0.2	-18.8
Breeding line20	NA	NA	NA	NA	5.0	15.7	31.7	3.8	15.0	5.0	0.3	-0.3	0.0	-17.4
Breeding line21	NA	NA	NA	NA	1.5	2.4	11.0	0.0	7.5	2.5	0.6	-0.1	0.3	-21.2
Breeding line22	NA	NA	NA	NA	0.5	1.1	0.0	0.0	5.0	3.0	13.1	20.7	4.4	-29.2
GN11641	NA	3.0	NA	1.0	0.0	3.8	7.6	2.0	55.0	75.0	2.8	3.7	0.8	-31.2
GN12607	NA	15.0	NA	8.5	4.0	8.2	34.6	17.4	0.5	5.0	-0.6	-2.4	0.3	100.8
GN13528	NA	0.0	NA	0.0	0.0	0.5	0.0	0.0	12.5	30.0	3.0	4.0	1.0	-32.5
GN12681	NA	2.0	NA	2.0	2.5	12.5	12.4	0.0	0.5	20.0	14.7	18.5	10.0	6.1
GN12697	NA	0.5	NA	0.0	0.0	8.5	0.0	0.0	15.0	12.5	0.2	-0.6	0.0	-15.3
GN12759	NA	1.0	NA	1.5	1.5	9.9	14.1	0.0	10.0	5.0	5.3	8.2	1.5	-12.5
GN12701	NA	0.0	NA	0.0	0.0	2.3	3.8	0.0	75.0	60.0	1.6	2.2	0.0	-25.1

GN13505	NA	15.0	NA	7.5	4.5	38.9	24.3	3.5	15.0	10.0	4.8	7.5	1.0	94.6
GN13509	NA	3.9	NA	1.5	0.0	2.4	0.0	0.9	40.0	30.0	1.1	1.2	0.0	-15.5
GN13516	NA	3.0	NA	4.0	4.0	11.6	10.9	1.3	35.0	12.5	15.7	25.3	5.2	33.3
GN13523	NA	0.0	NA	1.5	0.0	8.2	18.0	2.5	35.0	40.0	1.6	1.3	0.8	9.5
GN12741	0.0	3.0	3.9	1.0	1.5	21.1	20.7	2.9	12.5	45.0	5.9	7.7	3.1	39.6
GN13633	NA	0.0	NA	0.5	0.0	1.0	0.0	0.0	32.5	30.0	5.1	7.9	1.3	23.7
GN13641	NA	5.9	NA	3.0	1.0	12.8	0.0	1.0	0.5	5.0	6.8	9.7	1.8	28.0
GN11644	3.8	1.5	1.2	1.5	2.0	0.0	4.0	0.0	10.0	40.0	0.4	-0.5	0.2	-32.5
GN12630	5.5	5.1	17.2	3.5	3.5	14.9	39.1	2.5	10.0	NA	4.1	5.4	1.7	15.6
GN10677	2.0	1.0	2.2	1.0	1.2	8.2	8.4	1.9	5.0	7.5	1.8	2.1	1.2	-18.4
GN11542	0.0	0.4	0.0	0.5	0.0	2.9	0.0	0.0	52.5	20.0	11.4	16.4	3.2	-26.0
GN12687	6.0	4.1	19.7	6.1	5.0	30.8	40.2	3.8	20.0	5.0	3.2	4.4	1.4	28.6
GN12770	1.8	1.5	6.2	1.5	2.0	2.8	3.0	1.4	22.5	5.0	0.5	0.7	0.2	-18.5
GN13578	3.3	7.0	14.7	3.5	7.5	22.9	32.4	6.3	22.5	3.0	14.5	20.2	5.0	-14.7
GN12645	2.0	0.5	5.7	1.0	2.2	5.9	18.1	2.2	67.5	80.0	2.5	3.1	1.6	-18.1
GN13521	6.8	5.0	24.7	8.5	5.5	24.3	34.6	1.4	10.0	40.0	12.2	16.1	5.8	108.6
GN12767	1.8	0.9	1.0	0.5	0.5	1.0	0.0	0.9	5.0	15.0	4.7	6.4	1.8	16.3
GN13560	1.0	0.5	0.0	0.5	0.0	0.0	0.0	0.0	5.0	40.0	13.9	19.1	5.1	-17.3
GN14502	0.5	0.5	0.0	0.0	0.5	1.1	0.0	0.0	7.5	45.0	0.8	0.9	0.6	11.1

GN14512	1.5	0.6	0.0	0.0	0.0	1.1	0.0	0.0	5.0	17.5	0.3	0.3	0.2	19.1
GN14547	3.0	0.0	0.5	0.0	0.0	6.0	3.9	0.5	65.0	90.0	0.3	0.4	0.2	-14.6
GN14634	27.3	15.0	29.7	7.5	10.0	25.8	34.1	13.8	60.0	60.0	0.4	0.6	0.0	123.1
GN14636	17.3	6.1	34.7	7.4	17.5	26.3	49.9	7.5	22.5	20.0	1.7	2.7	0.2	86.6
GN14649	1.5	0.0	1.2	0.0	0.5	5.6	0.0	0.0	10.0	15.0	20.4	26.4	10.4	5.0
Caress	3.3	0.5	1.0	0.0	0.0	0.5	0.0	0.0	12.5	5.0	20.8	26.9	10.8	-14.6
GN10637	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	10.0	5.0	1.1	1.7	0.2	-23.8
Breeding line23	27.9	8.5	29.7	3.5	7.0	17.4	6.9	3.1	0.5	1.0	0.7	1.1	0.0	-25.1
Breeding line24	1.0	0.0	0.0	1.5	0.0	1.3	0.0	0.0	10.0	1.0	0.1	0.2	0.0	-37.1
Breeding line25	1.5	0.4	2.2	0.5	0.5	3.1	4.6	0.0	10.0	3.0	13.0	18.1	4.5	-29.7
GN13618	2.7	1.0	7.2	1.0	1.5	3.4	19.7	2.1	8.5	5.0	0.5	0.5	0.5	-27.3
Breeding line26	2.0	7.5	1.7	3.9	3.5	12.5	28.9	10.7	5.0	5.0	1.6	2.4	0.3	-25.9
Breeding line27	0.5	0.5	0.0	0.0	0.0	0.0	0.0	0.0	10.0	10.0	4.8	6.8	1.5	-29.1
Breeding line28	1.5	0.0	4.7	0.0	0.0	2.6	2.5	0.5	4.0	5.0	8.8	10.5	6.0	-19.4
Breeding line29	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.0	1.0	0.1	0.2	0.0	-29.6
Breeding line30	0.5	0.7	0.0	0.0	0.0	0.5	4.2	0.0	4.0	3.0	1.5	2.3	0.2	-36.3
Breeding line31	1.0	0.0	0.5	0.0	0.0	1.3	0.0	0.0	0.5	3.0	0.1	0.2	0.0	-31.8

Breeding line32	2.0	2.1	3.7	1.9	0.5	5.0	9.3	0.5	3.0	0.5	0.7	1.2	0.0	-34.7
GN13616	0.0	0.6	1.0	0.0	0.0	0.0	0.0	0.0	4.0	1.0	0.4	0.6	0.0	-36.3
GN14539	0.0	0.0	0.0	0.0	0.0	0.0	2.5	0.0	7.5	3.0	3.1	4.4	1.0	-34.2
GN14540	0.5	0.0	0.0	0.0	0.0	1.3	0.0	0.0	45.0	15.0	0.2	0.3	0.0	-28.7
GN14544	2.9	1.0	4.7	2.0	1.5	13.8	10.5	2.2	35.0	7.5	0.3	0.5	0.0	13.8
GN14583	2.2	1.0	3.7	1.0	0.5	4.4	11.2	0.0	15.0	0.0	0.2	0.4	0.0	-1.2
GN12637	0.0	0.5	1.0	0.5	0.0	1.3	0.0	1.2	37.5	50.0	4.8	6.6	1.9	-25.7
GN12737	81.2	35.0	69.7	8.6	12.5	65.8	70.6	23.6	17.5	10.0	3.0	4.5	0.5	55.6
GN12760	4.9	1.0	8.2	1.9	2.0	13.0	15.6	2.3	52.5	70.0	0.6	0.6	0.6	-14.1
GN12661	50.3	12.5	44.7	15.0	30.0	26.1	48.7	4.1	20.0	50.0	45.9	64.5	14.9	89.1
GN14529	6.6	2.5	9.7	2.6	1.5	14.7	27.6	1.6	15.0	50.0	6.1	8.5	2.1	36.9
GN14530	6.9	2.1	12.2	3.0	1.5	10.5	0.0	2.5	10.0	12.5	28.9	36.5	16.4	31.7
GN13527	2.0	2.5	2.2	0.5	1.5	17.4	5.8	1.3	7.5	7.5	8.4	12.2	1.9	-15.4
GN12764	2.2	0.4	4.7	1.5	0.5	4.1	17.8	1.5	10.0	5.0	4.8	6.3	2.3	-23.8
GN13519	4.7	3.1	19.7	3.0	4.5	12.2	16.8	1.1	12.5	30.0	4.2	6.0	1.1	-25.1
GN13606	4.7	7.5	12.2	4.4	4.0	32.2	0.0	4.9	27.5	55.0	4.1	5.8	1.2	6.7
GN13626	19.6	10.0	24.7	7.5	6.0	44.9	27.9	9.8	7.5	10.0	8.1	11.3	2.9	49.4
GN12615	2.2	1.0	1.7	0.5	0.5	4.7	0.0	1.7	0.5	5.0	8.7	11.3	4.4	-20.7

GN13553	1.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	4.0	3.0	18.8	25.4	7.8	-32.5
GN14522	1.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	5.0	8.0	1.5	1.9	0.9	-31.8
GN13595	3.4	0.5	2.2	0.0	0.0	0.0	0.0	0.0	10.0	7.5	0.2	0.3	0.0	-25.2
GN13596	3.3	1.0	7.2	1.5	2.5	11.2	19.5	2.4	25.0	50.0	0.3	0.4	0.0	-22.1
GN12650	6.3	7.6	19.7	12.5	4.5	21.3	26.7	7.3	5.0	3.0	0.8	1.2	0.0	40.8
GN14506	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3.0	10.0	6.1	8.4	2.1	-31.2
GN14511	0.5	0.6	0.5	0.0	0.0	0.0	1.5	0.0	9.0	35.0	13.2	16.3	8.1	-25.1
GN14515	4.7	1.5	8.2	0.5	0.0	14.4	0.0	1.9	10.0	3.0	0.0	0.0	0.0	10.9
GN14516	0.5	0.5	1.7	1.0	0.0	1.2	0.0	0.0	22.5	50.0	0.4	0.6	0.0	-27.3
EMB16/CBRD//CBRD	NA	1.5	NA	2.4	1.0	2.1	0.0	0.0	7.5	20.0	3.9	5.8	0.8	40.7
N894037	NA	0.9	NA	0.0	0.5	2.5	0.0	1.8	7.5	20.0	0.6	0.8	0.3	-8.7
SHA5/WEAVER//80456/YANGMAI 5	NA	0.4	NA	1.0	1.0	0.9	1.5	0.0	12.5	30.0	1.3	0.4	1.1	-9.3
VERDE/3/BCN//DOY1/AE.SQUARROSA (447)	NA	1.5	NA	0.0	1.0	8.7	3.4	0.0	40.0	70.0	1.1	0.3	0.8	6.1
80456/YANGMAI 5//SHA5/WEAVER/3/PRINIA	NA	5.0	NA	4.0	5.0	6.1	12.7	0.0	7.5	40.0	0.9	0.1	0.7	79.3
NG8675/CBRD//SHA5/WEAVER	NA	0.0	NA	0.0	0.0	1.2	1.5	0.0	5.0	10.0	2.5	3.7	0.3	13.7
TRAP#1/BOW//TAIGU DERIVATIVE	NA	2.5	NA	1.5	1.5	1.0	0.0	2.0	72.5	85.0	5.6	7.1	3.0	-23.3
IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/AE.SQUARROSA (190)	NA	10.0	NA	10.0	7.5	24.9	40.7	5.5	75.0	100.0	0.6	0.1	0.0	116.7
GAMENYA	NA	2.5	NA	7.4	1.5	30.6	10.3	5.0	10.0	35.0	1.5	0.4	1.7	135.0
WHEAR/2*KRONSTAD F2004	NA	0.0	NA	0.0	0.0	0.0	0.0	0.0	12.5	15.0	16.5	24.4	7.7	9.0

T.DICOCCON PI94625/AE.SQUARROSA (372)//TUI/CLMS/3/2*PASTOR/4/EXCALIBUR	NA	1.0	NA	0.5	0.0	3.5	0.0	0.0			9.7	13.7	4.6	-11.4

Table 7 Winter MASBASIS lines with lsmeans for disease severity in each environment, over all environments, over all high disease pressure environments, over all low disease pressure environments and PC1.

Name	Vb15	Vb16	Vb17	Vb18	Vb19	All env.	HDP	LDP	PC1
Bjørke	4.5	1.9	3.0	4.7	2.3	3.3	4.1	2.1	3.3
Folke	2.9	1.5	1.6	3.6	1.6	2.3	2.7	1.6	0.9
Mjølner	1.0	0.0	0.8	4.1	0.0	1.2	2.0	0.0	-1.5
Magnifik	2.2	0.9	1.9	3.5	0.6	1.8	2.5	0.8	0.2
Olivin	3.1	0.0	1.2	2.8	0.8	1.6	2.4	0.4	-0.3
Finans	0.0	0.0	1.0	3.3	1.2	1.1	1.4	0.6	-2.0
NK03029	3.3	1.8	4.5	4.1	0.8	2.9	4.0	1.3	2.9
RE714	0.6	0.8	1.7	3.7	0.0	1.4	2.0	0.4	-1.0
Massey	7.3	7.7	9.1	6.6	3.2	6.8	7.7	5.5	11.8
Fenman	0.8	0.0	0.6	1.8	0.0	0.7	1.1	0.0	-2.4
Soissons	0.0	0.0	1.0	3.9	0.0	1.0	1.6	0.0	-2.1
Arina	3.2	1.7	2.1	4.4	0.0	2.3	3.2	0.8	1.3
LW91W89	0.0	0.0	0.0	3.2	0.6	0.8	1.1	0.3	-2.7
Bersee	0.5	1.3	0.0	2.6	0.0	0.9	1.0	0.6	-2.2
Apollo	3.8	2.8	4.3	3.5	2.7	3.4	3.9	2.7	3.8
Spark	3.3	1.2	2.4	4.0	2.2	2.6	3.3	1.7	1.8
Vlasta	4.9	1.7	4.1	5.3	2.3	3.7	4.8	2.0	4.3
Senat	3.3	0.9	2.2	3.2	1.5	2.2	2.9	1.2	1.0
Solist	2.1	1.4	1.3	3.3	1.5	1.9	2.3	1.5	0.1
Ambition	2.7	1.7	2.9	3.4	0.6	2.3	3.0	1.2	1.4
Jenga	0.8	0.6	1.4	2.6	0.6	1.2	1.6	0.6	-1.3
Senta	2.0	0.7	1.4	6.1	0.6	2.2	3.2	0.7	0.4
Mironovskaja 808	2.6	1.7	3.2	5.1	0.8	2.7	3.6	1.2	2.0
Siria	4.5	5.2	5.0	3.9	1.5	4.0	4.5	3.3	5.4
Regina	3.0	1.3	1.4	4.3	1.4	2.3	2.9	1.3	0.9
GN04035	2.4	1.0	1.5	2.8	0.0	1.5	2.3	0.5	-0.3
GN04034	1.6	0.0	1.6	2.8	0.0	1.2	2.0	0.0	-1.0
GN05012	1.1	0.0	1.3	3.5	0.8	1.4	2.0	0.4	-1.1
GN05013	4.6	1.6	2.6	4.2	2.0	3.0	3.8	1.8	2.7
V1004	1.8	1.4	3.4	4.7	1.4	2.5	3.3	1.4	1.6
V9001	0.0	0.0	0.8	2.8	0.8	0.9	1.2	0.4	-2.3
TARSO	1.4	0.0	2.2	3.8	1.2	1.7	2.5	0.6	-0.3
Kamerat	0.0	0.0	1.2	1.7	0.6	0.7	1.0	0.3	-2.5

Rida	5.8	6.1	6.6	3.6	2.8	5.0	5.3	4.4	7.7
Trond	2.0	1.3	1.5	3.7	1.6	2.0	2.4	1.4	0.2
Sigyn II	4.2	3.0	5.3	4.1	2.0	3.7	4.6	2.5	4.7
REDCOAT	3.2	1.3	1.3	4.7	0.6	2.2	3.1	0.9	0.9
Skagen	0.0	0.6	0.6	3.2	1.0	1.1	1.3	0.8	-2.0
Plutos	4.1	1.8	3.3	4.9	1.0	3.0	4.1	1.4	3.0
Akratos	2.8	1.0	1.3	4.2	0.0	1.8	2.7	0.5	0.2
Jantarka	2.0	1.3	1.0	4.0	0.6	1.8	2.3	0.9	-0.2
Akteur	4.2	2.2	2.3	5.3	1.3	3.1	3.9	1.8	2.8
Breeding line33	1.0	0.0	0.8	3.1	0.9	1.2	1.6	0.4	-1.6
Ellvis	0.0	0.6	0.0	3.2	0.4	0.8	1.1	0.5	-2.5
GN08004	1.7	1.0	3.2	4.4	0.8	2.2	3.1	0.9	1.0
Frontal	0.0	0.7	0.0	3.4	0.8	1.0	1.1	0.7	-2.3
Kalle	1.7	0.0	1.0	6.2	0.0	1.8	3.0	0.0	-0.4
Portal	2.5	2.7	3.3	4.8	1.5	3.0	3.6	2.1	2.5
Rudolf	1.1	0.8	1.4	3.7	1.5	1.7	2.1	1.2	-0.5
Kosack	1.6	0.8	1.3	3.1	1.0	1.6	2.0	0.9	-0.6
Granitt	0.0	0.0	0.6	4.1	0.6	1.1	1.6	0.3	-2.1
Kuban	0.8	1.3	1.7	3.3	1.6	1.7	2.0	1.4	-0.5
USG3209	5.4	3.5	7.2	7.2	3.6	5.4	6.6	3.6	8.0
Stava	NA	0.9	1.2	2.8	0.8	1.4	1.7	0.9	-1.1
NK03030	NA	1.6	4.6	3.8	1.7	2.9	3.9	1.7	3.2
GN04041	NA	0.0	1.0	3.5	1.6	1.5	1.9	0.8	-1.2
20121	NA	1.8	2.1	3.3	1.0	2.0	2.4	1.4	0.6
20126	NA	0.8	1.4	4.3	0.0	1.6	2.6	0.4	-0.5
20128	NA	0.0	1.0	3.9	1.1	1.5	2.1	0.6	-1.2
20130	NA	0.4	1.6	4.9	0.0	1.7	3.0	0.2	-0.3
20146	NA	2.1	2.6	5.0	0.9	2.6	3.5	1.5	2.0
20228	NA	1.0	1.0	4.4	0.0	1.6	2.4	0.5	-0.7
Kanzler	3.0	1.4	2.6	5.3	1.1	2.7	3.6	1.3	1.9
Breeding line34	0.7	0.0	1.0	1.9	0.6	0.8	1.2	0.3	-2.1
KWS-Ozon	0.0	0.8	0.6	2.3	0.0	0.7	1.0	0.4	-2.4
Breeding line35	0.0	0.0	0.8	3.3	0.8	1.0	1.4	0.4	-2.2
Breeding line36	0.7	0.6	0.6	2.6	0.8	1.1	1.3	0.7	-1.8
Breeding line37	0.7	0.9	1.4	3.5	2.1	1.7	1.9	1.5	-0.7

Breeding line38	0.0	0.0	0.6	2.9	0.0	0.7	1.2	0.0	-2.6
Prierier	1.4	1.4	1.4	3.0	0.6	1.5	1.9	1.0	-0.6
Sarmund	1.2	0.0	1.7	2.8	0.6	1.3	1.9	0.3	-1.1
Breeding line39	1.0	0.6	1.0	2.2	0.9	1.1	1.4	0.7	-1.5
Breeding line40	0.7	1.2	2.1	3.4	1.9	1.9	2.1	1.6	-0.2
Agil	0.0	0.0	0.0	3.1	0.8	0.8	1.0	0.4	-2.7
Breeding line41	0.0	1.2	1.6	2.8	0.9	1.3	1.5	1.1	-1.3
Breeding line42	0.0	0.7	0.8	3.1	0.6	1.0	1.3	0.6	-2.0
Breeding line43	1.2	0.0	0.6	1.9	0.6	0.9	1.2	0.3	-2.0
Breeding line44	0.0	0.0	0.0	4.4	0.8	1.0	1.5	0.4	-2.3
GN11018	0.0	0.0	0.6	0.4	0.8	0.4	0.3	0.4	-3.1
GN13023	1.0	0.7	1.0	2.7	1.1	1.3	1.6	0.9	-1.3
Ceylon	0.0	0.0	1.5	3.2	0.0	1.0	1.6	0.0	-1.9
Mariboss	0.0	0.0	1.2	2.5	0.0	0.7	1.2	0.0	-2.4
Torp	NA	0.7	0.0	0.0	0.0	0.1	-0.3	0.3	-3.7
Ritmo	NA	0.8	1.9	3.9	0.0	1.6	2.6	0.4	-0.2
KWS Magic	NA	1.1	2.2	4.1	0.0	1.9	2.9	0.6	0.4
BAYP4535 (W01217.4 Me/De)	NA	0.3	0.6	2.3	0.0	0.8	1.1	0.2	-2.4
Julius	NA	0.0	0.0	3.0	1.3	1.1	1.2	0.7	-2.4
Potenzial	NA	0.4	2.0	2.8	0.0	1.3	2.1	0.2	-0.9
Format	NA	0.0	1.0	2.7	0.8	1.1	1.6	0.4	-1.8
FIRL3565(Amigos)	NA	0.8	1.3	2.7	1.6	1.6	1.7	1.2	-0.8
Bussard	NA	0.9	1.2	2.6	0.6	1.3	1.6	0.7	-1.2
Event	NA	0.0	0.8	4.3	0.0	1.3	2.2	0.0	-1.6
SvP72017	NA	NA	4.2	3.8	0.0	2.4	3.7	0.0	2.7
Alchemy	NA	0.6	0.8	3.3	0.0	1.2	1.7	0.3	-1.6
Brompton	NA	1.1	3.4	4.0	1.1	2.4	3.4	1.1	1.7
Claire	NA	1.2	0.8	3.9	0.6	1.6	2.0	0.9	-0.8
Hereward	NA	0.5	1.2	3.0	0.0	1.2	1.8	0.3	-1.5
Rialto	NA	1.3	2.8	4.6	0.8	2.4	3.4	1.1	1.4
Robigus	NA	1.5	5.6	4.7	2.8	3.6	4.8	2.2	4.8
Xi19	NA	1.2	1.2	3.5	0.0	1.4	2.0	0.6	-0.8
Matrix	NA	1.7	4.1	4.8	1.5	3.0	4.2	1.6	3.2
Arktis	NA	0.0	0.6	4.3	0.0	1.2	2.1	0.0	-1.8
Breeding line45	0.0	0.0	1.2	1.8	0.9	0.8	1.0	0.5	-2.4

Janne	1.0	0.6	1.2	2.9	0.6	1.3	1.7	0.6	-1.3

Table 8 Interesting and significant markers in spring wheat supported with chromosome location, physical position (bp), -log10 (p-value) for all environments, high and low disease pressure environments, PC1 for China and PC1 for Norway

Marker	Chrom.	Phys. Pos.	St15	St16	Vb15	Vb16	Vb17	Vb18	Vb19	Hs19	All env.	HDP	LDP	PC1-NO	PC1-CH
AX-94679138	1AL	493,820,038	1.9	1.1	1.3	2.0	1.2	1.8	4.2	0.7	2.4	2.8	1.0	3.1	3.1
AX-95194736	1BS	146,794,456	0.5	3.3	1.0	3.6	1.3	2.5	2.5	2.7	3.2	3.2	3.2	3.4	1.7
AX-94425541	1D	168,486,223	0.5	2.6	0.8	3.5	1.3	1.8	2.6	2.8	2.9	2.9	3.1	3.1	2.6
AX-94479164	3BS	6,220,123	0.8	1.3	0.7	0.9	2.2	2.0	3.5	1.2	2.8	3.3	1.4	3.2	1.1
AX-94595115	3BS	6,241,246	0.8	1.5	0.8	1.0	2.3	1.9	3.6	1.6	2.8	3.2	1.8	3.1	0.9
AX-94820422	3BS	6,677,093	0.5	1.4	0.8	0.5	1.9	2.0	2.8	1.2	2.5	3.0	1.4	2.8	1.0
AX-94717252	3BS	6,250,383	1.3	1.7	1.3	0.6	1.5	2.3	3.0	1.2	2.5	3.1	0.9	2.8	1.2
AX-94811682	3BL	705,817,255	1.1	4.1	2.4	3.6	2.7	3.2	2.5	4.8	3.8	3.3	5.0	3.6	2.2
AX-94501412	3BL	707,414,380	1.0	3.6	1.9	3.3	2.1	2.5	2.5	2.0	3.3	3.1	3.2	3.2	2.6
AX-95681535	3BL	705,817,383	1.2	4.0	2.2	2.1	2.0	3.2	1.4	3.9	3.2	3.0	3.6	3.0	2.4
AX-94907975	3BL	719,922,692	0.8	3.1	1.8	2.3	1.9	3.1	2.1	2.0	2.9	2.9	2.5	2.9	2.5
AX-94716868	3BL	721,070,908	0.8	3.1	1.8	2.2	1.8	3.0	1.9	1.8	2.7	2.7	2.4	2.7	2.3
AX-94684556	3BL	719,086,098	0.8	2.8	1.9	2.0	1.7	2.9	1.9	1.9	2.6	2.6	2.2	2.6	2.1
AX-94851468	3BL	723,032,052	0.9	2.9	1.9	2.8	1.8	2.9	1.7	2.0	2.6	2.5	2.8	2.6	1.6

AX-94502901	5AL	680,880,090	0.6	2.6	1.2	4.6	2.4	2.8	2.0	2.1	3.4	3.1	4.8	3.2	0.8
AX-94669191	5AL	488,892,073	1.0	2.3	1.3	3.0	2.5	4.1	2.7	3.8	4.1	4.3	3.3	4.3	5.7
AX-94919900	5AL	488,634,210	0.9	2.3	1.1	2.7	2.1	3.1	1.8	2.9	3.1	3.1	2.8	3.1	5.0
AX-94450199	5AL	488,410,411	2.6	2.4	2.9	3.6	3.6	1.8	2.6	2.2	3.4	3.0	4.3	3.0	2.6
AX-95145565	5BS	45,237,699	2.2	2.8	2.0	3.7	2.6	2.2	1.7	2.5	3.2	3.0	3.3	3.0	4.8
AX-94464434	5BS	47,584,694	0.7	3.1	1.3	3.2	1.5	2.0	1.9	3.6	2.6	2.3	3.1	2.6	3.3
AX-95075647	5BL	484,735,537	1.2	1.7	2.3	1.1	2.5	5.5	2.3	1.4	3.1	3.3	1.9	3.6	4.3
AX-94802487	5BL	482,424,256	1.2	1.7	2.3	1.1	2.5	5.5	2.3	1.4	3.1	3.3	1.9	3.6	4.3
AX-94758742	5BL	514,852,931	3.0	1.2	2.9	1.1	3.4	3.5	1.9	1.2	2.9	3.1	2.3	2.9	1.2
AX-95258242	5BL	544,608,954	1.7	1.5	1.7	2.1	3.2	2.4	3.7	0.9	3.0	3.3	2.3	3.3	1.4
AX-94787743	5BL	545,403,169	1.9	2.2	1.5	1.5	2.0	2.5	3.0	1.0	2.5	2.8	1.4	2.7	1.3
AX-94411794	6AL	609,453,850	1.5	0.7	2.3	1.7	1.9	2.7	3.8	0.8	3.0	3.3	1.7	3.4	1.2
AX-95144243	6AL	611,660,745	1.1	0.4	2.0	0.9	2.2	2.1	4.0	0.2	2.4	2.8	0.9	3.0	1.0
AX-95182345	6AL	611,661,167	1.3	0.6	2.8	1.6	2.1	2.4	5.2	0.6	3.1	3.5	1.6	3.8	1.7
AX-94876976	6AL	614,669,454	2.1	1.5	3.7	2.0	3.2	2.1	3.7	3.2	3.8	3.6	3.6	3.7	2.4
AX-94436123	6AL	NA	1.9	1.5	3.3	1.9	3.3	1.9	3.7	3.4	3.7	3.6	3.4	3.6	2.0

AX-94963438	6AL	611,563,809	1.1	0.5	2.3	1.1	1.8	2.0	4.8	0.4	2.7	3.1	1.1	3.3	1.1
AX-94582693	6AL	NA	1.4	0.9	2.4	1.3	2.4	1.3	3.6	2.0	2.7	2.7	2.2	2.8	1.7
AX-94689593	6BS	6,009,087	2.3	2.6	2.0	2.9	1.5	2.1	2.8	4.0	3.3	3.0	3.3	3.2	0.8
AX-94946243	6BS	115848;137443	1.7	1.8	2.0	2.2	1.3	2.3	2.1	3.0	2.6	2.4	2.7	2.5	0.8
AX-94709247	7AS	40,189,943	2.9	0.9	4.3	1.1	1.6	3.2	2.6	1.3	2.9	2.9	1.4	3.1	1.8
AX-94514616	7AL	674,272,435	0.8	1.9	1.2	1.3	1.5	3.2	2.0	3.3	2.7	2.7	2.7	2.8	1.7
AX-95173991	7AL	674,114,920	1.1	2.1	1.8	1.6	1.6	3.6	2.5	3.5	3.2	3.2	3.0	3.3	2.0
AX-94512826	7AL	674,277,268	0.8	1.8	1.2	1.3	1.4	3.3	1.9	3.2	2.7	2.7	2.6	2.7	1.6
AX-94430071	7AL	673,783,501	0.8	2.1	1.2	1.5	1.4	3.4	1.8	3.2	2.7	2.7	2.7	2.8	1.8
AX-94440790	7AL	673,013,918	0.8	1.9	1.2	1.3	1.5	3.3	1.9	3.2	2.7	2.7	2.6	2.7	1.8

Table 9 Interesting and significant markers in winter wheat supported with chromosome location, physical position (bp), -log10 (p-value) for all environments, high and low disease pressure environments and PC1

Marker	Chr	Phys. Pos.	Vb15	Vb16	Vb17	Vb18	Vb19	All env.	HDP	LDP	PC1
AX-94949146	1AS	520580077	3.0	3.7	4.1	1.0	3.4	4.0	3.3	4.3	4.0
AX-94810594	1AS	522190843	2.6	4.4	3.5	2.5	2.8	4.2	3.6	4.5	4.0
AX-94576991	1B	184823751	2.1	3.6	4.0	1.5	1.9	3.5	3.3	3.5	3.6
AX-95091069	3AL	516237916	1.5	2.9	3.9	2.5	1.0	3.6	3.7	2.5	3.7
AX-94935938	3AL	516641491	1.5	2.9	3.9	2.5	1.0	3.6	3.7	2.5	3.7
AX-94798864	3AL	516790678	1.5	2.9	3.9	2.5	1.0	3.6	3.7	2.5	3.7
AX-94713349	3AL	517079920	1.7	3.8	3.8	1.5	2.1	3.4	2.9	3.6	3.4
AX-94787893	3AL	517662652	1.7	3.8	3.8	1.5	2.1	3.4	2.9	3.6	3.4
AX-94611522	3AL	519207665	1.7	3.8	3.8	1.5	2.1	3.4	2.9	3.6	3.4
AX-94952900	3AL	526510440	1.3	3.5	3.9	2.0	0.9	3.5	3.5	2.8	3.7
AX-94760077	3AL	526863990	1.5	2.9	3.9	2.5	1.0	3.6	3.7	2.5	3.7
AX-94543296	3AL	528555206	1.5	2.9	3.9	2.5	1.0	3.6	3.7	2.5	3.7
AX-94401862	3AL	528555228	1.5	2.9	3.9	2.5	1.0	3.6	3.7	2.5	3.7
AX-94534307	3DL	511295461	2.2	4.8	2.7	2.3	2.6	3.9	3.1	4.7	3.6
AX-95069984	5AL	269319007	3.0	4.8	4.8	1.0	4.5	5.0	3.9	5.6	4.8

AX-94498038	5AL	384193548	3.0	4.8	4.8	1.0	4.5	5.0	3.9	5.6	4.8
AX-94403748	5AL	384193584	3.0	4.8	4.8	1.0	4.5	5.0	3.9	5.6	4.8
AX-94401034	5AL	384352260	3.1	5.1	5.0	1.1	4.4	5.2	4.1	5.8	5.0
AX-94465072	5AL	384627588	3.0	4.7	4.7	0.9	4.5	4.8	3.7	5.5	4.7
AX-94526834	5AL	680503211	2.4	4.4	3.0	0.9	1.6	3.4	2.9	3.6	3.5
AX-94907998	5AL	451886294	1.9	3.4	2.6	0.5	3.9	2.8	1.9	4.3	2.7
AX-95206791	6DL	468907723	1.9	3.6	3.7	0.5	3.2	3.0	2.2	4.2	3.0

Table 10 Allele stacking Table for studied QTL in all spring wheat cultivars/lines, Yellow rust lsmeans over all spring environments and sum number of resistant alleles for all studied QTL in each line. (T/A are computed letters and do not refer to nucleotide allele, N means the marker is not valid in this line).

Name	**YR-lsmeans**	**AX-94811682**	**AX-94669191**	**AX-95145565**	**AX-94802487**	**AX-95182345**	**Nr of QTL**
Resistant Allele		**T**	**A**	**T**	**T**	**T**	
Bastian	7.4	A	A	T	T	A	3
Bjarne	28.4	A	A	N	A	A	1
Tjalve	3.1	T	A	A	A	A	2
Avle	0.3	T	A	T	T	T	5
Zebra	10.5	T	A	T	T	A	4
Berserk	16.2	T	A	T	T	A	4
Brakar	1.9	T	A	A	T	A	3
Runar	3.0	T	A	A	T	A	3
T2038	0.0	T	A	T	T	A	4
T9040	0.3	T	A	N	T	A	3
T9040 (1995)	1.2	A	A	A	T	A	2
T10014	0.5	T	A	T	A	A	3
NK93602 (1995)	0.6	A	A	T	T	A	3
MS 273-150	3.3	A	A	A	T	A	2
DH 49-18 Bastian/Adder	10.6	T	A	A	T	A	3
Naxos (x3)	6.2	T	A	T	T	A	4
Paros	7.0	A	A	T	T	A	3
Paros/NK93602	0.1	T	A	T	T	A	4
Paros/T9040	13.3	A	A	A	T	A	2
T9040/Paros	10.8	A	A	A	T	A	2
Saar	1.2	A	A	T	T	A	3
Filin	11.4	A	A	T	A	A	2
Milan	1.1	A	A	T	T	A	3
Pfau/Milan	1.3	A	A	T	T	A	3
Bau/Milan -2	2.4	A	A	T	T	A	3
Dulus	2.3	A	A	A	T	A	2
Gondo -1	0.0	A	A	T	T	A	3
Catbird -2	1.5	T	A	T	T	A	4
Croc_1/Ae.squarrosa (205)//Kauz	0.0	T	A	T	T	A	4
Altar84/Ae.squarrosa(219)// 2*Seri	4.8	A	A	A	T	A	2

Altar84/Ae.sq(219)//2*Seri/3/ Avle	1.4	T	A	A	T	A	3
Kariega	1.3	T	T	T	T	A	3
Avocet YrA	59.9	A	T	A	T	A	1
NK93604	0.2	T	A	T	T	A	4
CJ9306	10.5	T	A	T	T	A	4
CJ9403	16.8	T	T	T	T	A	3
512-21	6.8	T	A	A	T	A	3
512-50	2.2	T	A	A	T	A	3
512-54	0.0	T	A	A	T	A	3
512-70	3.3	T	A	A	T	A	3
512-87	1.1	T	A	A	T	A	3
SHA3/CBRD	3.2	T	A	N	T	A	3
Soru #1	3.3	A	T	T	T	A	2
Sumai 3 (18.)	2.1	T	A	T	T	A	4
Nobeokabouzu (Mhazy)	3.0	T	A	T	A	A	3
Frontana (95)	1.9	T	A	T	T	A	4
Nanjing 7840 - Pl.4	21.0	T	A	A	T	A	3
Ning 8343 - Pl.4	1.8	T	A	A	T	A	3
Vinjett	0.0	T	A	T	T	T	5
DH20070	0.8	T	A	A	T	A	3
DH20097	0.9	T	A	T	T	A	4
GONDO	3.4	A	A	T	T	A	3
MILAN/SHA7	0.9	T	A	T	T	A	4
CBRD/KAUZ	2.7	T	A	T	T	A	4
GUAM92//PSN/BOW	2.4	A	A	T	T	A	3
NG8675/CBRD	8.5	T	T	T	A	A	2
ALTAR 84/AE.SQUARROSA (224)//ESDA	0.5	T	A	A	T	A	3
BCN*2//CROC_1/AE.SQUARROSA (886)	1.2	A	A	T	T	A	3
MAYOOR//TK SN1081/ AE.SQUARROSA (222)	4.1	A	A	T	T	A	3
AC Somerset	3.2	A	A	T	T	A	3
Sport	2.9	T	T	T	T	A	3
CD87	0.6	A	A	T	T	A	3
Chara	2.3	A	A	T	T	A	3
Kukri	5.6	A	A	T	A	A	2
Naxos/2*Saar	1.8	A	A	T	T	A	3

ONPMSYDER-05	3.0	T	A	T	T	A	4
BAJASS-5	1.2	T	A	T	T	A	4
NK00521	10.2	T	A	A	T	A	3
NK01513	1.2	T	T	T	T	A	3
Demonstrant	5.0	T	A	T	T	A	4
Krabat	2.0	T	A	A	T	A	3
GN03531	-0.4	T	A	T	T	T	5
GN04537	7.2	T	A	T	T	A	4
GN05507	2.6	A	A	A	T	A	2
Laban	1.1	T	A	T	T	T	5
Breeding line1	0.1	T	A	T	T	T	5
Breeding line2	2.5	T	A	T	T	A	4
GN03597	5.6	T	A	T	T	A	4
GN04528	2.2	A	A	T	T	A	3
GN05580	0.9	T	A	A	T	N	3
GN06557	11.2	T	A	A	T	A	3
GN06573	1.6	T	A	T	T	T	5
Breeding line3	0.1	N	A	T	T	T	4
Amulett	0.2	T	A	T	T	T	5
Bombona	2.9	A	A	T	T	T	4
QUARNA	0.1	A	A	A	T	A	2
GN03529	1.0	T	A	T	T	A	4
Breeding line4	1.9	T	A	T	T	T	5
GN04526	1.4	T	A	T	T	A	4
J03	17.8	A	A	A	T	A	2
NK01565	0.0	T	A	A	T	A	3
GN03503	9.7	T	A	T	T	A	4
GN05551	1.7	T	A	A	T	A	3
GN05589	22.8	A	A	T	A	A	2
GN06578	3.6	T	A	T	T	A	4
GN07581	2.2	A	A	A	T	A	2
GN08504	9.5	T	A	T	T	A	4
GN08531	1.5	T	A	T	T	A	4
GN08533	0.7	T	A	T	T	A	4
GN08534	3.8	T	A	A	T	A	3

GN08541	5.3	A	A	T	A	A	2
GN08554	7.7	T	A	T	T	T	5
GN08557	3.1	A	A	T	T	A	3
GN08564	6.1	T	A	T	T	A	4
GN08568	6.7	T	A	T	T	A	4
GN08588	3.8	T	A	A	T	A	3
GN08595	0.3	T	A	A	T	T	4
GN08596	0.1	T	A	T	T	T	5
GN08597	2.6	T	A	T	T	T	5
GN08647	0.6	T	A	T	T	T	5
TJALVE/Purpur seed	4.3	T	A	T	A	A	3
Sabin	0.2	A	T	T	T	A	2
Breeding line5	2.9	T	A	A	A	A	2
Breeding line6	0.6	T	A	T	T	T	5
Breeding line7	0.4	T	A	A	T	T	4
Breeding line8	0.0	T	A	T	T	N	4
Breeding line9	0.3	A	A	A	A	T	2
Breeding line10	0.6	T	A	T	T	T	5
Granary	1.3	A	T	T	T	A	2
Tom	3.3	A	T	A	T	A	1
RB07	5.8	A	A	A	A	A	1
C80.1/3*QT4522//2*ATTILA	0.4	A	A	T	T	A	3
C80.1/3*QT4522//2*PASTOR	1.9	A	A	T	T	A	3
Møystad	1.0	T	A	A	T	A	3
Rollo	1.7	T	A	A	T	A	3
Norrøna	8.4	A	A	A	T	A	2
Fram II	4.0	A	A	A	T	A	2
Mirakel	0.0	T	A	A	T	T	4
Rabagast	0.3	T	A	T	T	A	4
Seniorita	1.8	T	A	T	T	A	4
GN07548	23.5	A	A	A	A	A	1
GN07560	0.6	T	A	A	T	T	4
GN07525	5.9	T	A	T	T	A	4
GN08530	11.7	A	A	T	T	A	3
GN09572	7.9	T	A	T	A	A	3

GN08581	9.1	A	A	T	T	A	3
GN10510	1.0	T	A	T	T	T	5
Willy	0.7	T	A	A	T	A	3
GN10524	2.6	T	A	A	T	T	4
Berlock	0.9	T	A	T	T	T	5
Arabella	1.5	T	A	A	T	A	3
Breeding line11	0.1	A	A	A	A	T	2
GN07580	1.6	T	A	T	T	A	4
GN09584	1.0	T	A	T	T	T	5
GN10512	1.7	A	A	T	T	N	3
Polkka	2.1	T	A	A	T	A	3
Avans	2.2	T	A	A	T	T	4
BJY/COC//CLMS/GEN	0.0	A	A	T	T	A	3
HAHN/PRL//AUS1408	1.6	A	A	T	T	A	3
TUI/RL4137	0.3	A	A	A	T	A	2
T7347	0.2	A	A	A	T	A	2
Reno	3.0	T	A	T	A	A	3
Bjarne/LW91W86	0.2	T	A	T	A	A	3
Anniina	3.0	A	A	A	T	T	3
Aino	15.7	A	A	T	T	A	3
Kruunu	6.6	A	A	T	T	A	3
Marble	3.6	A	A	A	T	T	3
Wanamo	5.3	T	A	T	A	A	3
Wellamo	1.1	A	A	A	T	A	2
Scirocco	7.1	A	A	T	T	A	3
Dragon	0.1	T	A	T	T	T	5
Sirius	2.8	A	A	T	T	A	3
Cadenza	0.2	A	A	T	A	A	2
GN11591	2.5	A	A	T	T	A	3
GN11569	23.0	A	T	A	A	A	0
GN10607	1.6	T	A	T	T	A	4
GN10613	24.2	A	T	A	T	A	1
GN12639	1.6	T	A	A	T	A	3
GN12640	6.1	T	A	A	T	A	3
GN12700	15.3	T	A	A	T	A	3

GN12733	10.3	A	A	T	T	A	3
GN12699	8.1	A	A	T	T	A	3
Breeding line12	10.6	A	A	T	T	A	3
GN11505	7.0	T	A	T	T	A	4
GN11537	2.4	T	A	T	T	A	4
GN11604	6.6	T	T	A	T	A	2
GN11634	3.8	T	A	T	T	A	4
Breeding line13	-1.0	T	A	T	T	T	5
Breeding line14	0.8	A	A	T	T	A	3
Breeding line15	-0.7	T	A	T	T	A	4
Breeding line16	-0.8	A	A	T	T	A	3
GN12722	0.5	A	A	A	T	T	3
GN11527	1.4	T	A	T	T	A	4
GN11551	14.5	T	A	A	T	A	3
GN10680	17.7	T	A	T	T	A	4
GN11516	5.0	T	A	T	T	A	4
GN10547	7.6	T	A	A	T	A	3
GN10603	0.5	T	A	T	T	T	5
GN11574	12.7	A	T	T	T	A	2
GN11646	0.3	T	N	N	T	N	2
GN12606	0.2	T	A	T	T	A	4
GN12625	9.1	T	A	A	T	A	3
GN12628	8.4	T	A	A	A	A	2
GN12634	3.1	A	A	N	T	A	2
GN12635	1.2	T	A	A	T	A	3
GN12641	0.3	T	A	A	T	A	3
GN04603	4.3	T	A	A	T	A	3
GN11592	3.5	A	A	T	T	A	3
GN11514	12.0	T	A	A	T	A	3
GN12750	12.6	T	A	T	T	A	4
GN12626	4.2	T	A	T	T	A	4
GN12656	15.2	A	A	A	T	A	2
GN12658	14.6	A	A	T	A	A	2
GN13542	5.5	T	A	T	T	A	4
GN13576	11.4	T	A	N	A	A	2

GN13577	22.4	T	A	T	T	A	4
Mandaryna	7.5	T	A	T	T	A	4
Breeding line17	-0.3	A	A	T	T	T	4
Breeding line18	4.2	T	A	T	T	A	4
Breeding line19	1.0	T	A	T	T	T	5
GN12727	1.0	T	A	A	T	T	4
GN12721	0.4	A	A	A	T	T	3
GN13614	0.3	T	A	T	T	T	5
GN13615	0.6	T	A	T	T	T	5
Breeding line21	2.8	T	A	T	T	A	4
Breeding line22	-0.6	A	A	T	T	A	3
GN11641	3.0	T	A	T	T	A	4
GN12607	14.7	A	A	A	T	A	2
GN13528	0.2	T	A	T	T	T	5
GN12681	5.3	A	A	A	T	A	2
GN12697	1.6	T	A	T	T	T	5
GN12759	4.8	T	A	T	T	A	4
GN12701	1.1	A	A	T	T	A	3
GN13505	15.7	A	A	A	T	A	2
GN13509	1.6	T	A	A	T	T	4
GN13516	5.9	A	A	A	T	A	2
GN13523	5.1	T	A	T	T	A	4
GN12741	6.8	T	A	A	A	A	2
GN13633	0.4	T	A	A	T	A	3
GN13641	4.1	T	A	A	T	A	3
GN11644	1.8	A	A	T	T	A	3
GN12630	11.4	T	A	A	A	A	2
GN10677	3.2	T	A	T	T	A	4
GN11542	0.5	T	A	A	T	T	4
GN12687	14.5	T	A	A	T	A	3
GN12770	2.5	T	A	T	T	A	4
GN13578	12.2	T	A	T	T	A	4
GN12645	4.7	T	A	T	T	A	4
GN13521	13.9	T	A	T	T	A	4
GN12767	0.8	T	A	T	T	T	5

GN13560	0.3	T	A	T	T	T	5
GN14502	0.3	T	A	A	T	T	4
GN14512	0.4	T	A	T	T	T	5
GN14547	1.7	T	A	T	T	T	5
GN14634	20.4	T	A	A	T	A	3
GN14636	20.8	T	A	A	A	A	2
GN14649	1.1	T	A	T	T	A	4
Caress	0.7	T	A	T	T	T	5
GN10637	0.1	T	T	T	T	A	3
Breeding line23	13.0	T	A	T	T	A	4
Breeding line24	0.5	T	A	T	T	A	4
Breeding line25	1.6	T	A	A	T	A	3
GN13618	4.8	T	A	T	T	A	4
Breeding line26	8.8	A	A	T	T	T	4
Breeding line27	0.1	T	A	T	T	T	5
Breeding line28	1.5	T	A	T	T	A	4
Breeding line29	0.1	T	A	T	T	T	5
Breeding line30	0.7	T	A	T	T	T	5
Breeding line31	0.4	A	A	T	T	A	3
Breeding line32	3.1	T	A	T	T	A	4
GN13616	0.2	T	A	T	T	T	5
GN14539	0.3	T	A	T	T	T	5
GN14540	0.2	T	A	T	T	T	5
GN14544	4.8	T	A	T	T	A	4
GN14583	3.0	T	A	T	T	A	4
GN12637	0.6	T	A	T	T	A	4
GN12737	45.9	A	A	A	A	A	1
GN12760	6.1	T	A	T	T	A	4
GN12661	28.9	T	A	T	T	A	4
GN14529	8.4	T	A	T	T	A	4
GN14530	4.8	T	A	T	T	A	4
GN13527	4.2	T	A	A	A	A	2
GN12764	4.1	T	A	T	T	A	4
GN13519	8.1	T	A	A	T	A	3
GN13606	8.7	A	A	T	A	A	2

GN13626	18.8	T	A	T	T	A	4
GN12615	1.5	T	A	T	T	A	4
GN13553	0.2	T	A	T	T	T	5
GN14522	0.3	T	A	T	T	T	5
GN13595	0.8	T	A	T	T	T	5
GN13596	6.1	T	A	T	T	A	4
GN12650	13.2	A	A	T	T	A	3
GN14506	0.0	T	A	T	T	T	5
GN14511	0.4	T	A	T	T	T	5
GN14515	3.9	T	A	T	T	T	5
GN14516	0.6	T	A	T	T	A	4
EMB16/CBRD//CBRD	1.3	T	A	T	T	A	4
N894037	1.1	T	A	T	T	A	4
SHA5/WEAVER//80456/YANGMAI 5	0.9	T	A	T	T	A	4
VERDE/3/BCN//DOY1/AE.SQUARROSA (447)	2.5	A	A	T	T	A	3
80456/YANGMAI 5//SHA5/WEAVER/3/PRINIA	5.6	T	A	T	T	A	4
NG8675/CBRD//SHA5/WEAVER	0.6	T	A	T	T	A	4
IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/AE.SQUARROSA (190)	16.5	A	T	A	A	A	0
GAMENYA	9.7	A	T	A	A	A	0
WHEAR/2*KRONSTAD F2004	0.1	A	A	T	T	A	3
T.DICOCCON PI94625/AE.SQUARROSA (372)//TUI/CLMS/3/2*PASTOR/4/EXCALIBUR	0.9	T	A	A	T	A	3

Table 11 Allele stacking Table for studied QTL in all winter wheat cultivars/lines, Yellow rust lsmeans over all winter environments and sum number of resistant alleles in each line. (T/A are computed letters and do not refer to nucleotide allele, N means the marker is not valid in this line).

Name	**YR-lsmeans**	**AX-95069984**	**AX-94401034**	**AX-94798864**	**AX-94760077**	**AX-94810594**	
Resistant allele		**A**	**A**	**A**	**A**	**T**	
Bjørke	12.2	T	T	A	A	A	2
Folke	5.8	A	A	A	A	T	5
Mjølner	3.7	A	A	A	A	T	5
Magnifik	4.4	A	A	A	A	T	5
Olivin	3.9	A	A	A	A	T	5
Finans	2.6	A	A	A	A	T	5
NK03029	10.3	A	A	A	A	T	5

RE714	3.5	A	A	T	T	T	3
Massey	50.1	T	T	T	T	A	0
Fenman	0.9	A	A	A	A	T	5
Soissons	3.2	A	A	T	T	T	3
Arina	7.3	A	A	A	A	T	5
LW91W89	2.1	A	A	A	A	T	5
Bersee	1.7	A	A	A	A	T	5
Apollo	12.0	T	T	A	A	N	2
Spark	7.9	T	N	A	A	N	2
Vlasta	15.4	A	A	T	T	T	3
Senat	5.8	A	A	A	A	T	5
Solist	4.4	A	A	A	A	T	5
Ambition	6.2	A	A	A	A	T	5
Jenga	2.0	A	A	A	A	T	5
Senta	8.7	A	A	A	A	A	4
Mironovskaja 808	9.3	A	A	T	T	A	2
Siria	17.9	A	A	A	A	T	5
Regina	6.7	A	A	A	A	T	5
GN04035	3.4	T	T	A	A	T	3
GN04034	2.6	A	A	A	A	T	5
GN05012	3.2	A	A	A	A	T	5
GN05013	10.3	T	T	A	A	T	3
V1004	8.1	T	T	A	A	T	3
V9001	1.8	A	A	A	A	T	5
TARSO	4.6	A	A	A	A	T	5
Kamerat	0.9	A	A	A	A	T	5
Rida	26.9	T	T	T	T	A	0
Trond	4.8	A	A	A	A	T	5
Sigyn II	15.1	A	A	A	A	T	5
REDCOAT	7.2	A	A	T	T	N	2
Skagen	2.4	A	A	A	A	T	5
Plutos	11.2	A	A	A	A	T	5
Akratos	5.5	A	A	A	A	T	5
Jantarka	4.6	A	A	A	A	T	5
Akteur	11.5	A	A	A	A	T	5

Breeding line33	2.4	A	A	A	A	T	5
Ellvis	2.2	A	A	A	A	T	5
GN08004	6.8	A	A	A	A	T	5
Frontal	2.5	A	A	A	A	T	5
Kalle	8.5	A	A	A	A	T	5
Portal	10.0	A	A	A	A	T	5
Rudolf	4.0	A	A	A	A	T	5
Kosack	3.1	A	A	A	A	T	5
Granitt	3.5	A	A	A	A	T	5
Kuban	3.8	A	A	A	A	T	5
USG3209	31.7	T	T	T	T	A	0
Stava	2.6	A	A	A	A	T	5
NK03030	10.1	A	A	A	A	T	5
GN04041	3.9	A	A	A	A	T	5
20121	4.7	A	A	T	T	T	3
20126	5.3	A	A	T	T	T	3
20128	4.2	A	A	A	A	T	5
20130	6.6	A	A	T	T	T	3
20146	9.1	A	A	T	T	T	3
20228	5.2	A	A	T	T	T	3
Kanzler	9.4	A	A	A	A	T	5
Breeding line34	1.0	A	A	A	A	T	5
KWS-Ozon	1.2	A	A	A	A	T	5
Breeding line35	2.5	A	A	A	A	T	5
Breeding line36	1.7	A	A	A	A	T	5
Breeding line37	3.9	A	A	A	A	T	5
Breeding line38	1.8	A	A	A	A	T	5
Prierier	3.0	A	A	A	A	T	5
Sarmund	2.6	A	A	A	A	T	5
Breeding line39	1.6	A	A	A	A	T	5
Breeding line40	4.3	A	A	A	A	T	5
Agil	2.1	A	A	A	A	T	5
Breeding line41	2.6	A	A	A	A	T	5
Breeding line42	2.2	A	A	A	A	T	5
Breeding line43	1.2	A	A	A	A	T	5

Breeding line44	4.0	A	A	A	A	T	5
GN11018	0.2	A	A	A	A	T	5
GN13023	2.2	A	A	A	A	T	5
Ceylon	2.5	A	A	A	A	T	5
Mariboss	1.5	A	A	A	A	T	5
Torp	0.0	A	A	A	A	T	5
Ritmo	4.9	A	A	A	A	T	5
KWS Magic	5.7	A	A	A	A	T	5
BAYP4535 (W01217.4 Me/De)	1.4	A	A	A	A	T	5
Julius	2.7	A	A	A	A	T	5
Potenzial	3.0	A	A	A	A	T	5
Format	2.2	A	A	A	A	T	5
FIRL3565(Amigos)	2.9	A	A	A	A	T	5
Bussard	2.2	A	A	A	A	T	5
Event	4.6	A	A	A	A	T	5
SvP72017	9.6	A	A	T	T	T	3
Alchemy	2.9	A	A	A	A	T	5
Brompton	7.4	A	A	A	A	T	5
Claire	4.3	A	A	A	A	T	5
Hereward	2.6	A	A	A	A	T	5
Rialto	7.7	A	A	A	A	T	5
Robigus	15.8	A	A	T	T	T	3
Xi19	3.8	A	A	A	A	N	4
Matrix	11.3	A	A	A	A	T	5
Arktis	4.6	A	A	A	A	T	5
Breeding line45	1.1	A	A	A	A	T	5

Table 12 Dataset for haplotypes analysing on 5AL chromosome for all spring wheat cultivars/lines, Yellow rust lsmeans over all spring environments. (T/A are computed letters and do not refer to nucleotide allele, N means the marker is not valid in this line).

		QTL (5AL_488/83)			**QTL (5AL_680/48)**		
Line	**YR-lsmeans**	**AX-94450199**	**AX-94669191**	**AX-94919900**	**AX-94577164**	**AX-94526834**	**AX-94502901**
Resistance allele		**T**	**A**	**A**	**A**	**A**	**T**
Bastian	7.4	T	A	A	T	T	A
Bjarne	28.4	T	A	A	T	N	A
Tjalve	3.1	T	A	A	A	A	T
Avle	0.3	T	A	A	A	A	A
Zebra	10.5	T	A	A	A	A	A
Berserk	16.2	A	A	A	A	A	T
Brakar	1.9	T	A	A	T	N	A
Runar	3.0	T	A	A	T	N	A
T2038	0.0	T	A	A	T	N	A
T9040	0.3	T	A	A	T	T	A
T9040 (1995)	1.2	T	A	A	T	T	A
T10014	0.5	T	A	A	T	T	A
NK93602 (1995)	0.6	T	A	A	T	T	T
MS 273-150	3.3	T	A	A	T	T	A
DH 49-18 Bastian/Adder	10.6	T	A	A	A	A	A
Naxos (x3)	6.2	A	A	A	A	A	T
Paros	7.0	A	A	A	A	A	A
Paros/NK93602	0.1	T	A	A	T	N	T
Paros/T9040	13.3	T	A	A	T	T	A
T9040/Paros	10.8	T	A	A	T	N	A
Saar	1.2	T	A	A	A	A	A
Filin	11.4	T	A	A	T	T	T
Milan	1.1	T	A	A	T	N	T
Pfau/Milan	1.3	T	A	A	T	N	T
Bau/Milan -2	2.4	T	A	A	T	T	T
Dulus	2.3	T	A	A	T	T	T
Gondo -1	0.0	T	A	A	T	T	A
Catbird -2	1.5	T	A	A	T	T	T

Croc_1/Ae.squarrosa (205)//Kauz	0.0	T	A	A	A	A	T
Altar84/Ae.squarrosa(219)// 2*Seri	4.8	T	A	A	A	A	A
Altar84/Ae.sq(219)//2*Seri/3/ Avle	1.4	T	A	A	T	N	A
Kariega	1.3	A	T	T	A	A	A
Avocet YrA	59.9	A	T	T	A	A	A
NK93604	0.2	T	A	A	T	T	A
CJ9306	10.5	T	A	A	A	A	T
CJ9403	16.8	A	T	T	A	A	T
512-21	6.8	T	A	A	T	N	A
512-50	2.2	T	A	A	T	N	A
512-54	0.0	T	A	A	T	T	A
512-70	3.3	T	A	A	T	T	A
512-87	1.1	T	A	A	T	T	A
SHA3/CBRD	3.2	T	A	A	T	T	T
Soru #1	3.3	A	T	T	A	A	T
Sumai 3 (18.)	2.1	T	A	A	A	A	T
Nobeokabouzu (Mhazy)	3.0	T	A	A	T	T	T
Frontana (95)	1.9	T	A	A	T	T	T
Nanjing 7840 - Pl.4	21.0	T	A	A	A	A	T
Ning 8343 - Pl.4	1.8	T	A	A	A	A	T
Vinjett	0.0	T	A	A	A	A	A
DH20070	0.8	T	A	A	A	A	T
DH20097	0.9	T	A	A	T	T	A
GONDO	3.4	T	A	A	T	T	T
MILAN/SHA7	0.9	T	A	A	T	T	T
CBRD/KAUZ	2.7	T	A	A	T	T	T
GUAM92//PSN/BOW	2.4	T	A	A	A	A	T
NG8675/CBRD	8.5	A	T	T	A	A	T
ALTAR 84/AE.SQUARROSA (224)//ESDA	0.5	T	A	A	A	A	A
BCN*2//CROC_1/AE.SQUARROSA (886)	1.2	T	A	A	A	A	T
MAYOOR//TK SN1081/ AE.SQUARROSA (222)	4.1	T	A	A	T	T	T
AC Somerset	3.2	T	A	A	T	T	A
Sport	2.9	T	T	T	A	A	T
CD87	0.6	T	A	A	A	A	T
Chara	2.3	T	A	A	A	A	T

Kukri	5.6	T	A	A	T	T	A
Naxos/2*Saar	1.8	T	A	A	A	A	A
ONPMSYDER-05	3.0	T	A	A	T	T	T
BAJASS-5	1.2	T	A	A	A	A	T
NK00521	10.2	T	A	A	A	A	A
NK01513	1.2	T	T	T	A	A	T
Demonstrant	5.0	T	A	A	T	T	A
Krabat	2.0	T	A	A	T	T	A
GN03531	-0.4	T	A	A	A	A	A
GN04537	7.2	T	A	A	A	A	A
GN05507	2.6	T	A	A	T	T	A
Laban	1.1	T	A	A	A	A	A
Breeding line1	0.1	T	A	A	N	N	A
Breeding line2	2.5	T	A	A	A	A	A
GN03597	5.6	T	A	A	A	A	A
GN04528	2.2	T	A	A	T	N	A
GN05580	0.9	T	A	A	T	N	A
GN06557	11.2	T	A	A	A	A	A
GN06573	1.6	T	A	A	A	A	A
Breeding line3	0.1	T	A	A	A	A	A
Amulett	0.2	T	A	A	A	A	A
Bombona	2.9	T	A	A	A	A	A
QUARNA	0.1	T	A	A	A	A	A
GN03529	1.0	T	A	A	A	A	A
Breeding line4	1.9	T	A	A	A	A	A
GN04526	1.4	T	A	A	A	A	A
J03	17.8	T	A	A	T	N	A
NK01565	0.0	T	A	A	A	A	A
GN03503	9.7	T	A	A	A	A	A
GN05551	1.7	T	A	A	T	T	A
GN05589	22.8	T	A	A	A	A	A
GN06578	3.6	A	A	A	A	A	T
GN07581	2.2	T	A	A	A	A	T
GN08504	9.5	T	A	A	A	A	T
GN08531	1.5	T	A	A	A	A	T

GN08533	0.7	N	A	A	A	A	T
GN08534	3.8	T	A	A	A	A	A
GN08541	5.3	T	A	A	A	A	A
GN08554	7.7	T	A	A	T	N	A
GN08557	3.1	T	A	A	A	A	T
GN08564	6.1	T	A	A	A	A	A
GN08568	6.7	A	A	A	A	A	T
GN08588	3.8	T	A	A	A	A	A
GN08595	0.3	T	A	A	A	A	A
GN08596	0.1	T	A	A	A	A	A
GN08597	2.6	T	A	A	A	A	A
GN08647	0.6	T	A	A	A	A	T
TJALVE/Purpur seed	4.3	T	A	A	A	A	T
Sabin	0.2	A	T	T	T	T	T
Breeding line5	2.9	T	A	A	A	A	A
Breeding line6	0.6	T	A	A	A	A	A
Breeding line7	0.4	A	A	A	A	A	A
Breeding line8	0.0	T	A	A	A	A	A
Breeding line9	0.3	T	A	A	A	A	A
Breeding line10	0.6	T	A	A	A	A	A
Granary	1.3	T	T	T	A	A	A
Tom	3.3	N	T	T	T	N	T
RB07	5.8	T	A	A	A	A	T
C80.1/3*QT4522//2*ATTILA	0.4	T	A	A	A	A	A
C80.1/3*QT4522//2*PASTOR	1.9	T	A	A	T	T	T
Møystad	1.0	T	A	A	T	T	A
Rollo	1.7	T	A	A	T	N	A
Norrøna	8.4	T	A	A	T	N	A
Fram II	4.0	T	A	A	T	T	A
Mirakel	0.0	T	A	A	A	A	A
Rabagast	0.3	T	A	A	A	A	A
Seniorita	1.8	T	A	A	A	A	A
GN07548	23.5	T	A	A	T	N	A
GN07560	0.6	T	A	N	A	A	T
GN07525	5.9	T	A	A	A	A	A

GN08530	11.7	T	A	A	A	A	T
GN09572	7.9	T	A	A	T	T	A
GN08581	9.1	T	A	A	A	A	A
GN10510	1.0	T	A	A	T	T	A
Willy	0.7	T	A	A	A	A	T
GN10524	2.6	T	A	A	A	A	A
Berlock	0.9	T	A	A	A	A	A
Arabella	1.5	T	A	A	A	A	A
Breeding line11	0.1	T	A	A	A	A	A
GN07580	1.6	T	A	A	A	A	A
GN09584	1.0	T	A	A	A	A	A
GN10512	1.7	T	A	A	A	A	A
Polkka	2.1	T	A	A	N	N	A
Avans	2.2	T	A	A	A	A	A
BJY/COC//CLMS/GEN	0.0	T	A	A	A	A	T
HAHN/PRL//AUS1408	1.6	T	A	A	A	A	A
TUI/RL4137	0.3	T	A	A	A	A	A
T7347	0.2	T	A	A	T	T	A
Reno	3.0	T	A	A	A	A	A
Bjarne/LW91W86	0.2	T	A	A	T	N	A
Anniina	3.0	T	A	A	A	A	A
Aino	15.7	T	A	A	A	A	A
Kruunu	6.6	T	A	A	A	A	A
Marble	3.6	T	A	A	A	A	A
Wanamo	5.3	T	A	A	A	A	A
Wellamo	1.1	T	A	A	A	A	A
Scirocco	7.1	T	A	A	A	A	A
Dragon	0.1	T	A	A	A	A	A
Sirius	2.8	T	A	A	A	A	A
Cadenza	0.2	T	A	A	A	A	A
GN11591	2.5	T	A	A	T	N	A
GN11569	23.0	T	T	T	T	N	A
GN10607	1.6	T	A	A	A	A	T
GN10613	24.2	T	T	T	A	A	A
GN12639	1.6	T	A	A	A	A	T

GN12640	6.1	T	A	A	A	A	T
GN12700	15.3	T	A	A	A	A	T
GN12733	10.3	T	A	A	A	A	A
GN12699	8.1	T	A	A	A	A	T
Breeding line12	10.6	A	A	A	A	A	A
GN11505	7.0	T	A	A	T	T	A
GN11537	2.4	N	A	A	A	A	A
GN11604	6.6	T	T	T	A	A	T
GN11634	3.8	T	A	A	A	A	A
Breeding line13	-1.0	T	A	A	A	A	A
Breeding line14	0.8	T	A	A	A	A	A
Breeding line15	-0.7	T	A	A	A	A	A
Breeding line16	-0.8	N	A	T	A	A	A
GN12722	0.5	T	A	A	A	A	T
GN11527	1.4	T	A	A	A	A	T
GN11551	14.5	T	A	A	A	A	T
GN10680	17.7	T	A	A	A	A	T
GN11516	5.0	T	A	A	A	A	A
GN10547	7.6	T	A	A	A	A	A
GN10603	0.5	T	A	A	A	A	A
GN11574	12.7	A	T	T	T	N	A
GN11646	0.3	T	N	A	N	N	A
GN12606	0.2	T	A	A	A	A	T
GN12625	9.1	A	A	A	A	A	A
GN12628	8.4	T	A	A	A	A	T
GN12634	3.1	T	A	A	A	A	T
GN12635	1.2	T	A	A	T	T	A
GN12641	0.3	T	A	A	A	A	A
GN04603	4.3	T	A	A	A	A	A
GN11592	3.5	T	A	A	T	T	A
GN11514	12.0	T	A	A	T	T	A
GN12750	12.6	T	A	A	A	A	A
GN12626	4.2	N	A	A	A	A	A
GN12656	15.2	T	A	A	T	T	A
GN12658	14.6	T	A	A	A	A	A

GN13542	5.5	T	A	A	A	A	T
GN13576	11.4	T	A	N	T	T	A
GN13577	22.4	T	A	A	T	T	A
Mandaryna	7.5	A	A	A	A	A	A
Breeding line17	-0.3	T	A	A	A	A	A
Breeding line18	4.2	A	A	A	A	A	A
Breeding line19	1.0	T	A	A	A	A	A
GN12727	1.0	A	A	A	A	A	T
GN12721	0.4	T	A	A	A	A	T
GN13614	0.3	T	A	A	A	A	A
GN13615	0.6	T	A	A	A	A	A
Breeding line21	2.8	T	A	A	A	A	A
Breeding line22	-0.6	A	A	A	A	A	A
GN11641	3.0	T	A	A	A	A	T
GN12607	14.7	A	A	A	A	A	A
GN13528	0.2	T	A	A	A	A	A
GN12681	5.3	A	A	A	A	A	T
GN12697	1.6	A	A	A	A	A	T
GN12759	4.8	T	A	N	A	A	A
GN12701	1.1	T	A	A	A	A	A
GN13505	15.7	T	A	A	T	T	A
GN13509	1.6	T	A	A	A	A	A
GN13516	5.9	T	A	A	A	A	T
GN13523	5.1	A	A	A	A	A	T
GN12741	6.8	T	A	A	T	T	A
GN13633	0.4	T	A	A	A	A	T
GN13641	4.1	A	A	A	A	A	A
GN11644	1.8	T	A	A	A	A	T
GN12630	11.4	T	A	A	A	A	T
GN10677	3.2	T	A	A	A	A	T
GN11542	0.5	T	A	A	A	A	N
GN12687	14.5	A	A	A	A	A	T
GN12770	2.5	T	A	T	T	T	T
GN13578	12.2	T	A	A	T	T	A
GN12645	4.7	T	A	A	A	A	T

GN13521	13.9	T	A	A	T	T	A
GN12767	0.8	T	A	A	A	A	A
GN13560	0.3	T	A	A	A	A	A
GN14502	0.3	T	A	A	A	A	A
GN14512	0.4	T	A	A	A	A	A
GN14547	1.7	A	A	A	A	A	T
GN14634	20.4	T	A	A	T	T	A
GN14636	20.8	T	A	A	A	A	A
GN14649	1.1	T	A	A	A	A	T
Caress	0.7	A	A	A	A	A	A
GN10637	0.1	T	T	T	A	A	T
Breeding line23	13.0	T	A	A	A	A	A
Breeding line24	0.5	T	A	A	A	A	T
Breeding line25	1.6	T	A	A	A	A	A
GN13618	4.8	T	A	A	A	A	A
Breeding line26	8.8	T	A	N	A	A	A
Breeding line27	0.1	T	A	A	A	A	A
Breeding line28	1.5	T	A	A	A	A	A
Breeding line29	0.1	T	A	A	A	A	A
Breeding line30	0.7	T	A	A	A	A	A
Breeding line31	0.4	T	A	A	T	N	A
Breeding line32	3.1	A	A	A	A	A	A
GN13616	0.2	T	A	A	A	A	A
GN14539	0.3	T	A	A	A	A	A
GN14540	0.2	T	A	A	A	A	A
GN14544	4.8	T	A	A	A	A	A
GN14583	3.0	T	A	A	A	A	A
GN12637	0.6	T	A	A	A	A	T
GN12737	45.9	T	A	A	T	N	A
GN12760	6.1	T	A	A	A	A	A
GN12661	28.9	A	A	A	A	A	A
GN14529	8.4	T	A	A	A	A	T
GN14530	4.8	T	A	A	A	A	T
GN13527	4.2	T	A	A	T	T	A
GN12764	4.1	A	A	A	A	A	A

GN13519	8.1	T	A	A	T	T	A
GN13606	8.7	T	A	A	T	T	A
GN13626	18.8	T	A	A	A	A	T
GN12615	1.5	T	A	A	A	A	A
GN13553	0.2	T	A	A	A	A	A
GN14522	0.3	T	A	A	A	A	A
GN13595	0.8	T	A	A	A	A	A
GN13596	6.1	T	A	A	A	A	A
GN12650	13.2	A	A	A	T	T	A
GN14506	0.0	T	A	A	A	A	A
GN14511	0.4	T	A	A	A	A	A
GN14515	3.9	T	A	A	A	A	A
GN14516	0.6	T	A	A	T	T	A
EMB16/CBRD//CBRD	1.3	T	A	A	T	N	T
N894037	1.1	T	A	A	A	A	T
SHA5/WEAVER//80456/YANGMAI 5	0.9	T	A	A	A	A	T
VERDE/3/BCN//DOY1/AE.SQUARROSA (447)	2.5	T	A	A	A	A	A
80456/YANGMAI 5//SHA5/WEAVER/3/PRINIA	5.6	T	A	A	T	T	T
NG8675/CBRD//SHA5/WEAVER	0.6	T	A	A	A	A	T
IVAN/6/SABUF/5/BCN/4/RABI//GS/CRA/3/AE.SQUARROSA (190)	16.5	A	T	T	T	N	T
GAMENYA	9.7	A	T	T	T	T	A
WHEAR/2*KRONSTAD F2004	0.1	T	A	A	T	T	T
T.DICOCCON PI94625/AE.SQUARROSA (372)//TUI/CLMS/3/2*PASTOR/4/EXCALIBUR	0.9	T	A	A	A	A	A
					1636		

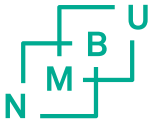
Table 13 Dataset for haplotypes analysing on 5AL chromosome for all winter wheat cultivars/lines, Yellow rust lsmeans over all spring environments. (T/A are computed letters and do not refer to nucleotide allele, N means the marker is not valid in this line).

		QTL (5AL_384/72)			**QTL (5AL_680/43)**		
Name	**YR-Lsmeans**	**AX-94403748**	**AX-94401034**	**AX-94498038**	**AX-94577164**	**AX-94526834**	**AX-94502901**
Resistance allele		**A**	**A**	**T**	**A**	**A**	**T**
Bjørke	12.2	T	T	A	T	T	A
Folke	5.8	A	A	T	A	A	T
Mjølner	3.7	A	A	T	A	A	T
Magnifik	4.4	A	A	T	A	A	T
Olivin	3.9	A	A	T	A	A	T
Finans	2.6	A	A	T	A	A	A
NK03029	10.3	A	A	T	A	A	A
RE714	3.5	A	A	T	A	A	T
Massey	50.1	T	T	A	T	T	T
Fenman	0.9	A	A	T	A	A	T
Soissons	3.2	A	A	T	A	A	T
Arina	7.3	A	A	T	A	A	T
LW91W89	2.1	A	A	T	A	A	T
Bersee	1.7	A	A	T	A	A	T
Apollo	12.0	T	T	A	T	N	A
Spark	7.9	T	N	A	T	T	A
Vlasta	15.4	A	A	T	A	A	T
Senat	5.8	A	A	T	A	A	T
Solist	4.4	A	A	T	A	A	T
Ambition	6.2	A	A	T	A	A	T
Jenga	2.0	A	A	T	A	A	T
Senta	8.7	A	A	T	A	A	A
Mironovskaja 808	9.3	A	A	T	A	A	T
Siria	17.9	A	A	T	A	A	A
Regina	6.7	A	A	T	A	A	A
GN04035	3.4	T	T	A	A	A	T
GN04034	2.6	A	A	T	A	A	A
GN05012	3.2	A	A	T	A	A	A
GN05013	10.3	T	T	A	A	A	T

V1004	8.1	T	T	A	A	A	A
V9001	1.8	A	A	T	A	A	A
TARSO	4.6	A	A	T	A	A	A
Kamerat	0.9	A	A	T	A	A	A
Rida	26.9	T	T	A	T	T	A
Trond	4.8	A	A	T	A	A	T
Sigyn II	15.1	A	A	T	A	A	A
REDCOAT	7.2	A	A	T	A	A	A
Skagen	2.4	A	A	T	A	A	T
Plutos	11.2	A	A	T	A	A	T
Akratos	5.5	A	A	T	T	T	T
Jantarka	4.6	A	A	T	A	A	T
Akteur	11.5	A	A	T	A	A	A
Breeding line33	2.4	A	A	T	A	A	T
Ellvis	2.2	A	A	T	A	A	A
GN08004	6.8	A	A	T	A	A	A
Frontal	2.5	A	A	T	A	A	T
Kalle	8.5	A	A	T	T	W	A
Portal	10.0	A	A	T	A	A	A
Rudolf	4.0	A	A	T	A	A	A
Kosack	3.1	A	A	T	A	A	T
Granitt	3.5	A	A	T	A	A	T
Kuban	3.8	A	A	T	A	A	T
USG3209	31.7	T	T	A	A	A	A
Stava	2.6	A	A	T	A	A	T
NK03030	10.1	A	A	T	A	A	A
GN04041	3.9	A	A	T	A	A	T
20121	4.7	A	A	T	A	A	A
20126	5.3	A	A	T	A	A	T
20128	4.2	A	A	T	N	W	A
20130	6.6	A	A	T	A	A	T
20146	9.1	A	A	T	A	A	A
20228	5.2	A	A	T	A	A	A
Kanzler	9.4	A	A	T	A	A	A
Breeding line34	1.0	A	A	T	A	A	T

KWS-Ozon	1.2	A	A	T	A	A	T
Breeding line35	2.5	A	A	T	A	A	T
Breeding line36	1.7	A	A	T	A	A	A
Breeding line37	3.9	A	A	T	A	A	A
Breeding line38	1.8	A	A	T	A	A	A
Prierier	3.0	A	A	T	A	A	T
Sarmund	2.6	A	A	T	A	A	T
Breeding line39	1.6	A	A	T	A	A	A
Breeding line40	4.3	A	A	T	A	A	T
Agil	2.1	A	A	T	A	A	A
Breeding line41	2.6	A	A	T	A	A	T
Breeding line42	2.2	A	A	T	A	A	A
Breeding line43	1.2	A	A	T	T	W	T
Breeding line44	4.0	A	A	T	A	A	T
GN11018	0.2	A	A	T	A	A	A
GN13023	2.2	A	A	T	A	A	T
Ceylon	2.5	A	A	T	A	A	A
Mariboss	1.5	A	A	T	A	A	T
Torp	0.0	A	A	T	A	A	T
Ritmo	4.9	A	A	T	A	A	T
KWS Magic	5.7	A	A	T	A	A	A
BAYP4535 (W01217.4 Me/De)	1.4	A	A	T	A	A	T
Julius	2.7	A	A	T	A	A	A
Potenzial	3.0	A	A	T	A	A	T
Format	2.2	A	A	T	A	A	T
FIRL3565(Amigos)	2.9	A	A	T	A	A	A
Bussard	2.2	A	A	T	A	A	A
Event	4.6	A	A	T	A	A	T
SvP72017	9.6	A	A	T	A	A	A
Alchemy	2.9	A	A	T	A	A	T
Brompton	7.4	A	A	T	A	A	T
Claire	4.3	A	A	T	A	A	T
Hereward	2.6	A	A	T	A	A	T
Rialto	7.7	A	A	T	A	A	A
Robigus	15.8	A	A	T	A	A	T

Xi19	3.8	A	A	T	A	A	A
Matrix	11.3	A	A	T	A	A	T
Arktis	4.6	A	A	T	A	A	T
Breeding line45	1.1	A	A	T	A	A	T



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