An Roinn Talmhaíochta,
Bia agus Mara
Department of Agriculture,
Food and the Marine

2017EN104 Knowledge-driven genomic predictions for sustainable disease resistance in wheat

Final Report

This project was funded under the Department of Agriculture, Food and the Marine Competitive Funding Programme.

SUMMARY

WheatSustain established a close collaboration among world leading experts on genomic prediction modelling, bioinformatics, wheat genomics and leaders in the field of plant pathology and genetics of stripe rust and FHB resistance in wheat. Research groups from Norway, Ireland, Germany, Austria, Mexico, USA and Canada have worked in close collaboration with public and private wheat breeding programs. Plant breeders have taken active part in the research by providing germplasm, conducted field trials, and validated molecular markers and genomic prediction models in their breeding programs. To facilitate seamless exchange of data among the partners, a common database was established. We also merged project data with previously existing data and public repositories, using a new data harmonization approach that we published. We also developed methodology for the optimal design of training populations, which is a crucial question for the application of GS in plant breeding. The R- package TrainSel was developed for this purpose and published open source. Computer simulations were done to compare alternative approaches to applying GS for disease resistance. Common winter wheat and spring wheat training populations were tested for FHB and stripe rust resistance in field trials across the partner countries using standardized field scoring protocols. Moreover, seedling assays were conducted for stripe rust. Genome-wide association studies (GWAS) yielded new knowledge and insight into the genetics of the resistance to these two important diseases in the most relevant winter wheat and spring wheat germplasm. Markers for the most important QTL as well as genomic prediction models were further validated on new breeding lines and are now being used as selection tools by the collaborating breeding companies. In summary, the project has fostered a very fruitful transnational collaboration between academic research institutes and breeding companies and led to practical application of project results in variety development..

KEYWORDS

wheat, genomic prediction, training optimisation

ACRONYM	WheatSustain
PROJECT COORDINATOR, INSTITUTION	Kevin McDonnell, University College Dublin
EMAIL	kevin.mcdonnell@ucd.ie

COLLABORATORS

Name	Institution
Morten Lillemo	Norwegian University of Life Sciences
Hermann Buerstmayr	University of Natural Resources and Life Sciences Vienna
Lorenz Hartl	Bavarian State Research Center for Agriculture
Maria Antonia Henriquez	Agriculture and Agri-Food Canada Morden Research and Development Centre
Josef Holzapfel	SECOBRA Saatzucht GmbH
Anja Hanemann	Saatzucht Josef Breun GmbH & Co. KG
Deniz Akdemir	StatGen Consulting
Muath Alsheikh	Graminor AS
Jose Crossa	International Maize and Wheat Improvement Center (CIMMYT)
Johann Birschitzky	Saatzucht Donau GesmbH & CoKG

PUBLICATION DATE 22/05/2023

Section 1 - Research Approach & Results

Start Date

01 June 2019

End Date

31 May 2022

Research Programme

Research Stimulus Fund

TRL Scale

TRL 6: Technology demonstrated in relevant environment

NRPE Priority area

Sustainable Food Production and Processing

Total DAFM Award

€173,915.15

Total Project Expenditure

€121,958.90

Rationale for undertaking the Research

We are faced by an increasing population relying on a limited area of arable land, a more erratic climate and crop losses due to plant diseases. To meet the Grand Societal Challenges, we need a sustainable intensification of agricultural production, improving both yield and quality. Sustainability includes optimized plant health to lower the risk of crop losses from plant diseases and to reduce the dependency on pesticides, which is a key element of the 2009/128/EC directive. New cultivars are needed with reduced environmental impact that combine excellent disease resistance with productivity and end-use quality.

Wheat is the most cultivated cereal crop in Europe, and among the top three cereals globally with a total production of 749 million tones in 2016 (FAOSTAT). As proof-of-concept cases, we are targeting stripe rust and Fusarium head blight (FHB), which are among the most threatening wheat diseases in Europe and North America. Stripe rust is infamous for its ability to quickly evolve new pathogen races that overcome resistances in widely grown cultivars. FHB epidemics regularly causes both yield and quality losses in major wheat growing region and is of serious concern for human and animal nutrition due to the production of mycotoxins.

WheatSustain with European and Canadian wheat breeders innovate new genomic selection methodologies that can greatly enhance the breeding of new cultivars with improved stripe rust and FHB resistance.

.**Methodology**

Genomic selection (GS) allows for a faster and more effective breeding of new cultivars by utilizing high-density marker data to predict breeding values of progeny lines. Much room exists to improve the genomic prediction of complex disease resistances such as stripe rust and Fusarium Head Blight (FHB) in wheat. The core idea behind WheatSustain was to make use of biologically relevant data, known trait correlations, environmental effects and quantitative trait loci (QTL) to build more robust GS models. In the long run, this will enable breeders to develop new cultivars with improved disease resistance, which will suffer less yield and quality losses and can be cultivated with less use of fungicides.

WheatSustain established a close collaboration among world leading experts on genomic prediction modeling, bioinformatics, wheat genomics and leaders in the field of plant pathology and genetics of stripe rust and FHB resistance in wheat. Research groups from Norway, Ireland, Germany, Austria, Mexico, USA and Canada have worked in close collaboration with public and private wheat breeding programs. Plant breeders have taken active part in the research by providing germplasm, conducted field trials, and validated molecular markers and genomic prediction models in their breeding programs.

Project Results

The WheatSustain project has tested and implemented new concepts in genomic prediction modeling to tackle some of the major challenges of applying genomic selection as a cost-saving breeding methodology for disease resistance. With the work on stripe rust we have addressed challenges related to the non-durable nature of race-specific resistance, while the work on Fusarium head blight (FHB) has advanced the science on using multi-trait prediction. Our concepts can easily be transferred and adapted to other disease resistance traits and crop species.

Through very fruitful collaboration across all the partners in the consortium, our main goals have been achieved and the developed breeding tools such as markers and genomic selection methods are actively being used by the collaborating plant breeding companies. The project has achieved the main goals that were set at the proposal stage. It has fostered a very fruitful transnational collaboration between academic research institutes and breeding companies and led to practical application of project results in variety development. Some of the issues addressed in WheatSustain can be still be considered “work in progress”, and will be followed up in other ongoing research projects by the national partners.

Section 2 - Research Outputs

Summary of Project Findings

A common database was established using pre-existing data from the partners and public repositories, and extended during the project as new genotypic and phenotypic information was generated by the consortium.
- A package for training population was developed.
- A computer simulation model to predict multi-trait genomic selection accuracy and selection responses was implemented, which can use either existing genotype data or simulated genotypes.
- GWAS identified a total of thirteen consistent QTL for FHB resistance across all seven field trials. Haplotype analysis revealed a highly significant QTL on 7A, which was validated on an independent set of breeding lines. The GWAS results were further used as the basis for modeling genomic selection for FHB resistance in WP2, and to train genomic prediction models using the significant GWAS markers as fixed effects
- or the NMBU spring wheat panel, GWAS on stripe rust data from a total of seventeen field trials across nine locations identified ten consistent QTL. Among those, the QTL on chromosome 6A was the most significant and coincided with the 6A QTL detected in winter wheat. Haplotype analysis showed that the resistant allele has increased in frequency in modern spring wheat cultivars. Further work to trace the origin of the resistant allele and compare it with the winter wheat QTL is currently carried out in the ongoing HVETERUST project at NMBU.
- Significant haplotype effects were detected for all three FHB-associated traits: visual head blight, DON content and anther extrusion, highlighting the importance of this QTL as a source in resistance breeding. Validated KASP marker were published as part of the study and can be used as selection tools in breeding.

Summary of Staff Outputs

Research Output	Male	Female	Total Number
Post Doctorates	1		2

Summary of Academic Outputs

Research Output	Total Number	Details
Publications in Peer Reviewed Scientific Journals	5	Journal Article; Akdemir,Deniz, Knox,Ron, Isidro y Sánchez,Julio, Combining Partially Overlapping Multi-Omics Data in Databases Using Relationship Matrices. Frontiers in Plant Science, 2020, 11:p.947 DOI:10.3389/fpls.2020.00947. Journal Article; Akdemir,Deniz, Rio,Simon, Isidro y Sánchez,Julio, TrainSel: An R Package for Selection of Training Populations. Frontiers in Genetics, 2021, 12 : p.655287 DOI: 10.3389/fgene.2021.655287. Journal Article; Garcia-Abadillo, J., Morales, Laura, Buerstmayr, Hermann, Michel, Sebastian, Lillemo, Morten, Holzapfel, J., Hartl, Lorenz, Akdemir, Deniz, Carvalho, H. F., Isidro-Sánchez, Julio, Alternative scoring methods of Fusarium Head Blight resistance for genomic assisted breeding. Submitted mansucript, 2022, Journal Article; Isidro y Sánchez,Julio, Akdemir,Deniz, Training Set Optimization for Sparse Phenotyping in Genomic Selection: A Conceptual Overview. Frontiers in Plant Science, 2021, 12 : p. 715910 DOI:10.3389/fpls.2021.715910.

Intellectual Property

N/A

Summary of other Project Outputs

N/A

Potential Impact related to Policy, Practice and Other Impacts

Impact	Details
Environmental Sustainability	Yellow rust is an important disease in many regions worldwide. Effective yellow rust resistance was identified in spring and winter wheat. Molecular markers for selection and improvement of resistance were developed. The usage of the genes in newly developed cultivars increases resistance. Yellow rust often appears at early stages in spring and causes the need of early application of fungicides avoiding severe yield loss. Resistant cultivars will often reduce the need of fungicides at early stages. This provides both ecologically and economically friendly solutions for food production. Improved resistance to yellow rust improves food security by avoiding severe yield losses in organic farming without the possibility of using fungicides. At conventional conditions resistance minimizes the risk of overlooking starting diseases and following yield losses. Food security is improved. Resistance to fusarium head blight (FHB) were confirmed to be quantitatively inherited. The developed genomic selection models including associated traits like plant height, flowering time and anther extrusion as well as environmental covariables provide better accuracy and improved selection intensity. Cultivars combining resistance against several pathogens and other productivity traits will be fostered by genomic selection tools. DON mycotoxin contamination is a problem at several wheat growing regions. Improved resistance will provide cereal products with lower risk of contamination of mycotoxins which avoid the rejection of the harvest for human consumption and improves food safety and security. Improved resistance results in healthier plants and avoids yield reductions or the application costs of fungicides. The economic returns will be enhanced, and affordability of food will be preserved. This will improve the competitiveness of the European farmers and breeder as partners in the supply chain. Improved resistance against FHB and yellow rust through genomic selection reduces the need of fungicide application at two different growing stages of wheat. At several growing regions wheat production without fungicides will be possible, which an optimal ecological and economical solution for food production. This lowers the application of chemical products in the natural environment and improves the sustainability of agriculture.

Dissemination Activities

Activity	Details
Other	An important success factor for the WheatSustain project has been the close interaction with the collaborating breeding companies, who contributed valuable germplasm and took a major part in disease evaluation and validation of the molecular markers and genomic prediction models developed in the project. This setup ensured a streamlined dissemination and uptake of project results for the target user group of the project. As a result, the validated markers and prediction models we developed in collaboration are now being applied in practical breeding. Field days have been arranged by the national partners, and the WheatSustain project has been highly visible at international conferences resulting in a total of 14 conference presentations. So far, 14 research papers have been published. Many more are in the pipeline, either under review, or as manuscripts that are expected to be submitted by the end of the year as the project is being wrapped up. A final dissemination workshop with breeders is planned to be held at the end of November 2022.

Knowledge Transfer Activities

Identify knowledge outputs generated during this project.	The integration of heterogeneous and large omics data constitutes a challenge in plant research today, but also offers big advantages for re- use of data across studies. The data harmonization tool provided by WheatSustain enables cross-national and international comparative research, facilitating the extraction of new scientific knowledge. WheatSustain addressed the complex issue of combining high dimensional and unbalanced omics data, and proposed a new methodology for combining partial datasets in the genotype to phenotype spectrum. This data harmonization methodology allows merging of datasets to make available information across gene-banks, data repositories, or other data resources. Also, the WheatSustain project established common disease scoring protocols for stripe rust and Fusarium head blight resistance related traits in field trials, which facilitated harmonized use of data from all partners in the project and eased the downstream data analyses.
Identify any knowledge transfer activities executed within the project.	To our great satisfaction, the collaborating breeding companies in the project are already making actively use of the developed breeding tools such as validated marker assays and genomic prediction models that have resulted from the project. By open access publication of the results, we can enable use of the project results and modeling concepts beyond the consortium. Several of the studies have already been published, and the remaining are either already submitted or at the manuscript stage and will be completed over the next few months.
List any impacts resulting from the knowledge transferred during the project.	To make impact beyond the project, the modeling concepts validated in our project, should be further tested on other disease and crop species. We can hope that our conference presentations and open access publications will facilitate uptake of the methodologies by other scientists and breeders working on relevant diseases and crops. The dissemination workshop for breeders that we are planning in November 2022 is targeted for this purpose. All partners in the WheatSustain consortium have expressed interest in continuing the collaboration in one way or another, and we are currently looking for relevant funding opportunities to achieve that.

Section 3 - Leveraging, Future Strategies & Reference

Leveraging Metrics

N/A

Future Strategies

Within this project, genomic selection was used as a tool to allow for potentially more effective breeding of new cultivars that demonstrate required disease resistance. This project - WheatSustain was able to test new concepts in genomic predication modelling for looking at disease resistance breeding methods. Whilst the lead researcher is now working in Spain, it is planned that other team members will use the learning outcomes to see if the same methodology can be applied to an Oat breeding project. Hence we are looking at a collaboration project between our temporary hire (Dr Cathal McCabe) and the School of Biology (Prof Doohan) to help further develop this work but this is likely to be in oats rather than wheat which was the focus of this project. There are some outcomes of this project that Dr McCabe is hoping to use to grow his breeding expertise and hence to support further opportunities.

Project Publications

1. Journal Article; Akdemir,Deniz, Knox,Ron, Isidro y Sánchez,Julio, Combining Partially Overlapping Multi-Omics Data in Databases Using Relationship Matrices. Frontiers in Plant Science, 2020, 11 : p. 947 DOI: 10.3389/fpls.2020.00947.
2. Journal Article; Akdemir,Deniz, Rio,Simon, Isidro y Sánchez,Julio, TrainSel: An R Package for Selection of Training Populations. Frontiers in Genetics, 2021, 12 : p. 655287 DOI: 10.3389/fgene.2021.655287.
3. Conference Paper; Garcia-Abadillo, J., Morales, Laura, Buerstmayr, Hermann, Michel,Sebastian, Lillemo, Morten, Holzapfel, J., Akdemir, Deniz, Isidro-Sánchez, Julio, Evaluation of Fusarium head blight resistance by alternative methods for genomics assisted breeding, in XVIIIth Eucarpia Biometrics in Plant Breeding Conference . 2022. Gif-sur- Yvette, France.
4. Journal Article; Garcia-Abadillo, J., Morales, Laura, Buerstmayr, Hermann, Michel, Sebastian, Lillemo, Morten, Holzapfel, J., Hartl, Lorenz, Akdemir, Deniz, Carvalho, H. F., Isidro-Sánchez, Julio, Alternative scoring methods of Fusarium Head Blight resistance for genomic assisted breeding. Submitted mansucript, 2022,
5. Journal Article; Isidro y Sánchez,Julio, Akdemir,Deniz, Training Set Optimization for Sparse Phenotyping in Genomic Selection: A Conceptual Overview. Frontiers in Plant Science, 2021, 12 : p. 715910 DOI:10.3389/fpls.2021.715910.
6. Conference Paper; Isidro-Sánchez, Julio, Enabling comparative research through multi-omics data harmonization (invited speaker), in XVIIIth Eucarpia Biometrics in Plant Breeding Conference. 2022. Gif-sur-Yvette, France.
7. Conference Paper; Lin, Min, Crossa, Jose, Lillemo, Morten, Comparison of genomic prediction methods for yellow rust resistance in wheat, in XVIIIth Eucarpia Biometrics in Plant Breeding Conference. 2022.Gif-sur-Yvette, France.
8. Conference Paper; Lin, Min, Dieseth, Jon Arne, Alsheikh, Muath, Yang, Ennian, Holzapfel, J., Schürmann, F., Morales, Laura, Michel, Sebastian, Buerstmayr, Hermann, Bhavani, S., Lillemo, Morten, Genome-wide association mapping across multiple field environments identifies a stable QTL for yellow rust resistance on chromosome 6A, in 16th International Cereal Rusts and Powdery Mildew conference. 2022. Cambridge, UK.
9. Conference Paper; Lin, Min, Dieseth, Jon Arne, Alsheikh, Muath, Yang, Ennian, Holzapfel, J., Schürmann, F., Morales, Laura, Michel, Sebastian, Buerstmayr, Hermann, Lillemo, Morten, A major QTL for yellow rust resistance on chromosome 6A shows increased frequency in recent Norwegian spring wheat cultivars and breeding lines, in 72nd Conference of the Austrian Plant Breeding Association. 2021. Online.
10. Conference Paper; Lin, Min, Yang, Ennian, Dieseth, Jon Arne, Alsheikh, Muath, Lillemo, Morten, Genome-wide association mapping of yellow rust resistance in Nordic spring wheat collections, in BGRI 2021 Virtual Technical Workshop. 2021. Online.
11. Journal Article; Lopez-Cruz, Marco, Dreisigacker, Susanne, Crespo-Herrera, Leonardo, Bentley, Alison R, Singh, Ravi, Poland, Jesse, Shrestha, Sandesh, Huerta-Espino, Julio, Govindan, Velu, Juliana, Philomin, Mondal, Suchismita, Pérez-Rodríguez, Paulino, Crossa, Jose, Sparse kernel models provide optimization of training set design for genomic prediction in multiyear wheat breeding data. The Plant Genome, 2022, p.e20254 DOI: https://doi.org/10.1002/tpg2.20254.
12. Journal Article; Montesinos López,Osval Antonio, Mosqueda González,Brandon Alejandro, Palafox González,Abel, Montesinos López,Abelardo, Crossa,José, A General-Purpose Machine Learning R Library for Sparse Kernels Methods With an Application for Genome-Based Prediction. Frontiers in Genetics, 2022, 13: p. 887643 DOI: 10.3389/fgene.2022.887643.
13. Journal Article; Montesinos-López, Osval Antonio, Gonzalez, Henry Nicole, Montesinos- López, Abelardo, Daza-Torres, María, Lillemo, Morten, Montesinos-López, José Cricelio, Crossa, José, Comparing gradient boosting machine and Bayesian threshold BLUP for genome-based prediction of categorical traits in wheat breeding. The Plant Genome, 2022, 15 (3): p. e20214 DOI: https://doi.org/10.1002/tpg2.20214
14. Journal Article; Montesinos-López, Osval A., Montesinos-López, Abelardo, Cano-Paez, Bernabe, Hernández-Suárez, Carlos Moisés, Santana-Mancilla, Pedro C., Crossa, José, A Comparison of Three Machine Learning Methods for Multivariate Genomic Prediction Using the Sparse Kernels Method (SKM) Library. Genes, 2022,13 (8): p. 1494
15. Journal Article; Montesinos-López,Osval A., Montesinos-López,Abelardo, Mosqueda- González,Brandon A., Bentley,Alison R., Lillemo,Morten, Varshney,Rajeev K., Crossa,José, A New Deep Learning Calibration Method Enhances Genome-Based Prediction of Continuous Crop Traits. Frontiers in Genetics, 2021, 12 : p.798840 DOI: 10.3389/fgene.2021.798840.
16. Conference Paper; Morales, Laura, Akdemir, Deniz, Girard, A. L., Holzapfel, J., Isidro y Sánchez, Julio, Kempf, H., Lillemo, Morten, Löschenberger, Franziska, Michel, Sebastian, Nannuru, Vinay Kumar Reddy, Stadlmeier, M., Steiner, B., Buerstmayr, Hermann, Genomic prediction of Fusarium head blight resistance in the WheatSustain winter wheat training set, in 72nd Conference of the Austrian Plant Breeding Association. 2021. Online.
17. Journal Article; Morales, Laura, Michel, Sebastian, Ametz, Christian, Dallinger, Hermann Gregor, Löschenberger, Franziska, Neumayer, Anton, Zimmerl, Simone, Buerstmayr, Hermann, Genomic signatures of selection for resistance to stripe rust in Austrian winter wheat. Theoretical and Applied Genetics, 2021, 134 (9): p. 3111-3121 DOI: 10.1007/s00122-021-03882-3.
18. Conference Paper; Morales, Laura, Michel, Sebastian, Ametz, Christian, Dallinger, Hermann Gregor, Löschenberger, Franziska, Neumayer, Anton, Zimmerl, Simone, Buerstmayr, Hermann, Genomic and pedigree-based prediction of resistance to stripe rust in Austrian winter wheat, in 2nd International Wheat Congress. 2022. Beijing, China.

19. Conference Paper; Morales, Laura, Michel, Sebastian, Lillemo, Morten, Hartl, Lorenz, Isidro y Sánchez, Julio, McCartney, Curt, Holzapfel, J., Hanemann, Anja, Akdemir, Deniz, Alsheikh, Muath, Crossa, Jose, Löschenberger, Franziska, Buerstmayr, Hermann, Preliminary findings from ERA-Net WheatSustain: Knowledge-driven genomic predictions for sustainable disease resistance in wheat, in 71st Conference of the Austrian Plant Breeding Association. 2020. Online.

20. Journal Article; Nannuru, Vinay Kumar Reddy, Dieseth, Jon Arne, Alsheikh, Muath, Dong, Yanhong, McCartney, Curt, Henriques, Maria Antonia, Buerstmayr, Hermann, Michel, Sebastian, Meuwissen, Theodorus H. E., Crossa, Jose, Lillemo, Morten, Effect on prediction ability of single-trait and multi-trait genomic prediction models byincorporating genome-wide association study results to improve fusarium disease resistance. Submitted mansucript, 2022,

21. Conference Paper; Nannuru, Vinay Kumar Reddy, Dieseth, Jon Arne, Alsheikh, Muath, Dong, Yanhong, McCartney, Curt, Henriques, Maria Antonia, Buerstmayr, Hermann, Michel, Sebastian, Meuwissen, Theodorus H. E., Crossa, Jose, Lillemo, Morten, Effect on prediction ability of single-trait and multi-trait genomic prediction models by incorporating genome-wide association study results to improve fusarium disease resistance, in XVIIIth Eucarpia Biometrics in Plant Breeding Conference . 2022. Gif-sur-Yvette, France.

22. Conference Paper; Nannuru, Vinay Kumar Reddy, Windju, Susanne S., Belova, Tatiana, Dieseth, Jon Arne, Alsheikh, Muath, Dong, Yanhong, McCartney, Curt, Henriques, Maria Antonia, Buerstmayr, Hermann, Michel, Sebastian, Meuwissen, Theodorus H. E., Genetic architecture of fusarium head blight disease resistance and associated traits in Nordic spring wheat, in 72nd Conference of the Austrian Plant Breeding Association . 2021. Online.

23. Conference Paper; Nannuru, Vinay Kumar Reddy, Windju, Susanne S., Belova, Tatiana, Dieseth, Jon Arne, Alsheikh, Muath, Dong, Yanhong, McCartney, Curt, Henriques, Maria Antonia, Buerstmayr, Hermann, Michel, Sebastian, Meuwissen, Theodorus H. E., Genetic architecture of fusarium head blight disease resistance and associated traits in Nordic spring wheat, in The SPPS conference 2022. 2022. Svalbard, Norway.

24. Journal Article; Nannuru, Vinay Kumar Reddy, Windju, Susanne S., Belova, Tatiana, Dieseth, Jon Arne, Alsheikh, Muath, Dong, Yanhong, McCartney, Curt A., Henriques, Maria Antonia, Buerstmayr, Hermann, Michel, Sebastian, Meuwissen, Theodorus H. E., Lillemo, Morten, Genetic architecture of fusarium head blight disease resistance and associated traits in Nordic spring wheat. Theoretical and Applied Genetics, 2022, 135 (7): p. 2247-2263 DOI: 10.1007/s00122-022-04109-9.

25. Conference Paper; Shahinnia, Fahimeh, Genome wide association mapping for resistance to stripe rust in Central European winter wheat, in 72nd Conference of the Austrian Plant Breeding Association. 2021. Online.

26. Conference Paper; Shahinnia, Fahimeh, Geyer, Manuel, Mohler, Volker, Isidro-Sánchez, Julio, Buerstmayr, Hermann, Lillemo, Morten, Hartl, Lorenz, Genome-wide association study and genomic prediction for resistance to stripe rust in Central and Northern European winter wheat germplasm, in 2nd International Wheat Congress. 2022. Beijing, China.

27. Journal Article; Shahinnia, Fahimeh, Geyer, Manuel, Schürmann, Friederike, Rudolphi, Sabine, Holzapfel, Josef, Kempf, Hubert, Stadlmeier, Melanie, Löschenberger, Franziska, Morales, Laura, Buerstmayr, Hermann, Sánchez, Julio Isidro y, Akdemir, Deniz, Mohler, Volker, Lillemo, Morten, Hartl, Lorenz, Genome-wide association study and genomic prediction of resistance to stripe rust in current Central and Northern European winter wheat germplasm. Theoretical and Applied Genetics, 2022, DOI:10.1007/s00122-022-04202-z.

28. Journal Article; Shahinnia, Fahimeh, Mohler, Volker, Hartl, Lorenz, Genome-Wide Association Mapping of Resistance to Warrior (-) Yellow Rust Race at the Seedling Stage in Current Central and Northern European Winter Wheat Germplasm. Preprints, 2022, 2022: p.2022090301 DOI:10.20944/preprints202209.0301.v1.