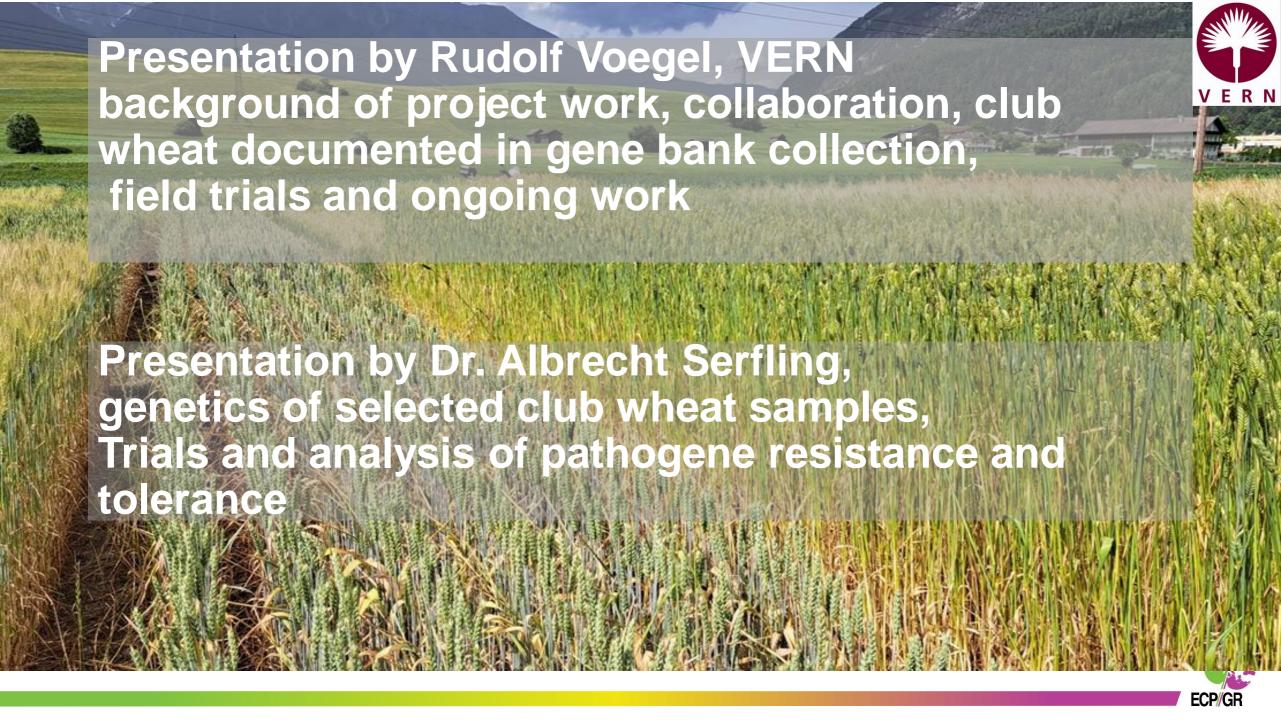


CHANCES FOR THE CONSERVATION
AND RE-CULTIVATION OF CENTRAL
EUROPEAN CLUB WHEAT (BINKEL)
THROUGH A NUTRITIONAL AND GENETIC
DIFFERENTIATION TOWARDS OTHER
WHEAT SPECIES (BIDIFFERENT)

Rudolf Voegel, VERN Albrecht Serfling, JKI



September 18, 2025





Club wheat // Triticum compactum ssp.

- eneglected,
- ·underutilized,
- extincted...



- a forgotten wheat species of history....
- out of formal interest of seed policies and breeding



Historic migration of club wheat







Black line: 10,000-4,000 BCE. Movement of hexaploid wheat from Turkey throughout Central Asia and into Europe.

Red line: 4,000 BCE-1800. Wheat is tracked across Europe at archaeological sites in Romania, Catalonia, Iberia and the Black Sea to Budapest and through Spain to Portugal, then on to South America and Mexico.

Green line: 1800-1900. Shipping routes from Chile to California expedite wheat's progress to North America. By the 1830s, wheat finds its home in the Pacific Northwest.

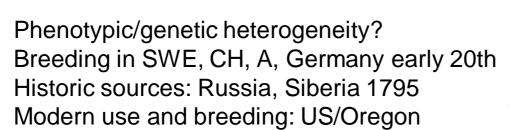


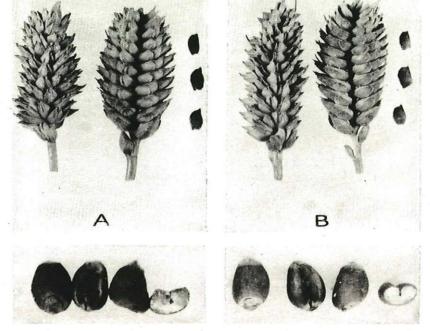






PLATE 39





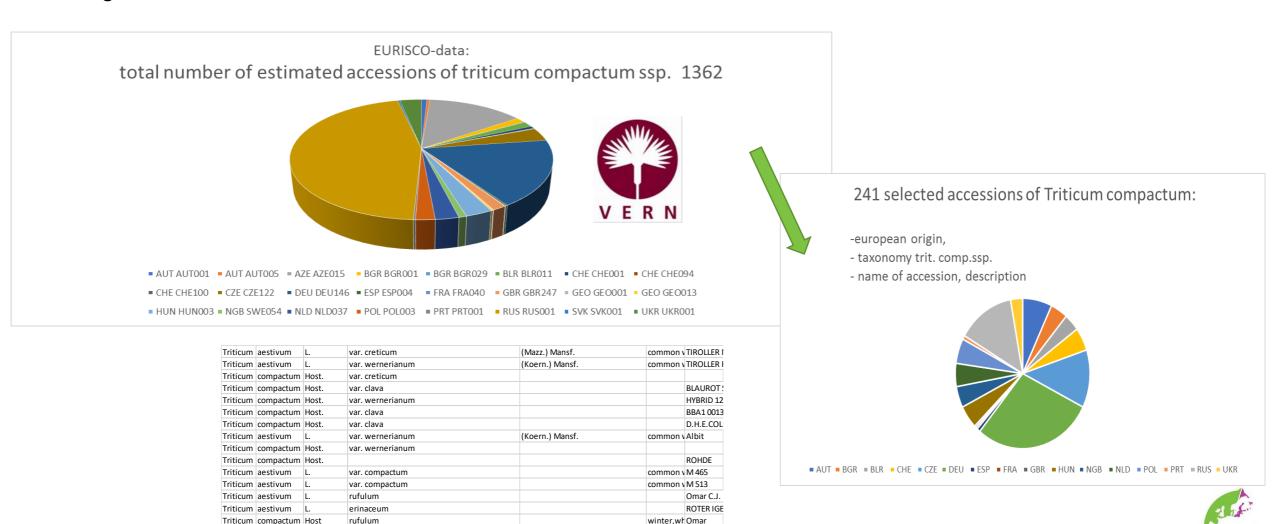
A. Hybrid 128 and B. Albit wheats: Spikes and glumes natural size; kernels imes 3.



Group of triticum compactum var. Part of Triticum collection:



Binkel/Igelweizen, Herisson, mocho, Kubbweisen, Teremok, club wheat



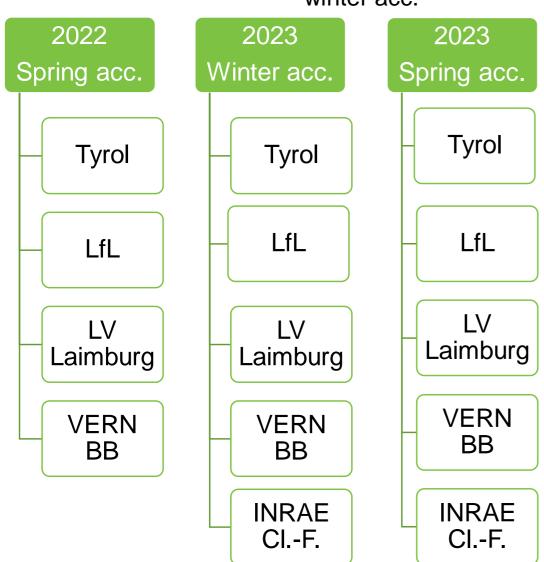


Proposal	Tasks	Timetable	Responsible
3	baking tests and experiments, quality analysis 9 acc. spring, 2022 29 acc. winter acc. 2023	2022-2024	VERN VERN
3	disposal to interested farmers, bakers, groups	2023-2024	VERN, all, Slow Food
3	transformation, seed multiplying, establishing on farm conservation, Information and public	2023	VERN, all, Slow Food



Field survey 2022/2023 2022 4 locations, spring acc. 2023 5 locations, spring (second time) 2023 5 locations, winter acc.





Parameters...

- Yield
- Agronomics
- Tolerance/resistence
- Cultivation value
- Phenotype description

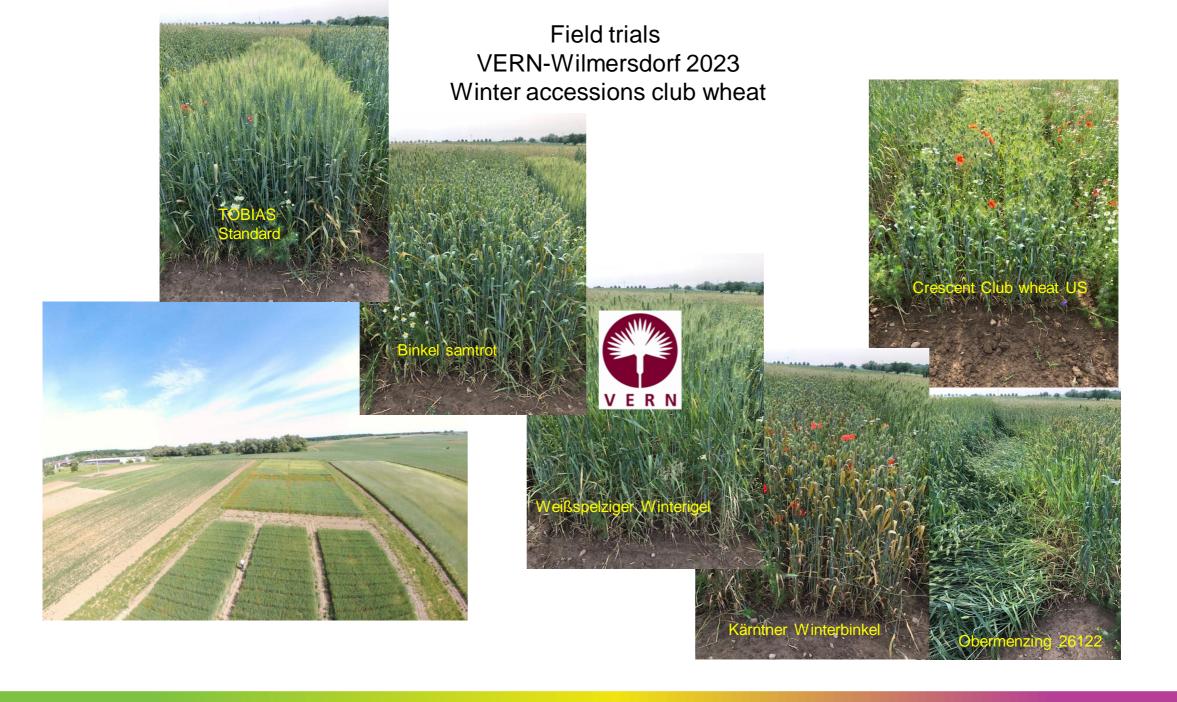
Total:

field plots/5 locations

- ~10 acc. spring (2x), ~15 acc. Winter
- Additional ~15 acc.

small plots by INRAE

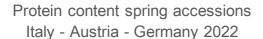


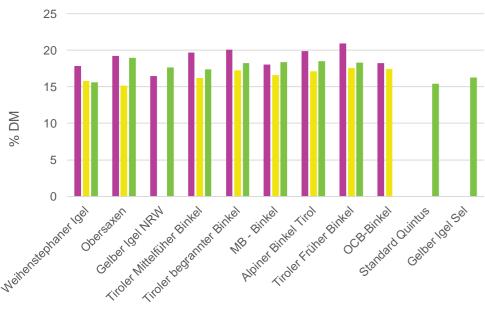












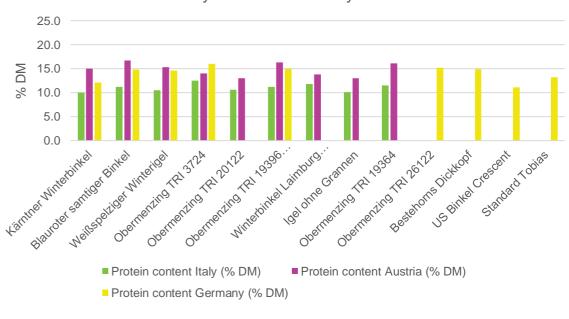
■Protein content Italy (% DM)

Protein content Austria (% DM)

■ Protein content Germany (% DM)



Protein content winter accessions Italy - Austria - Germany 2023

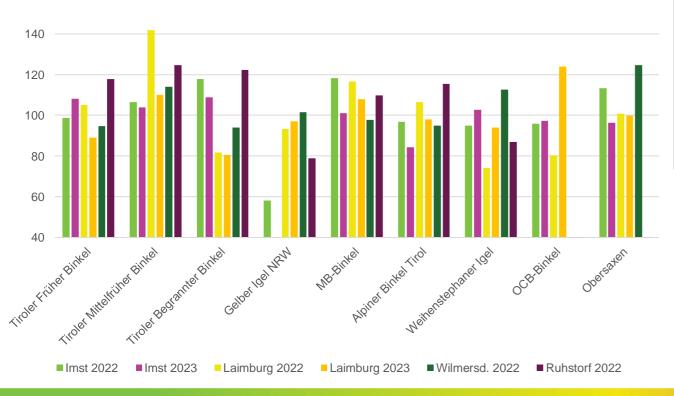


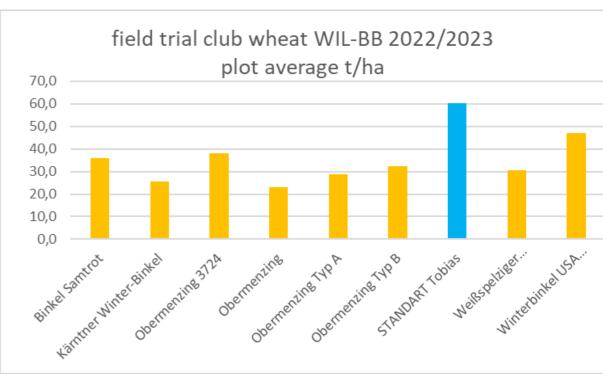














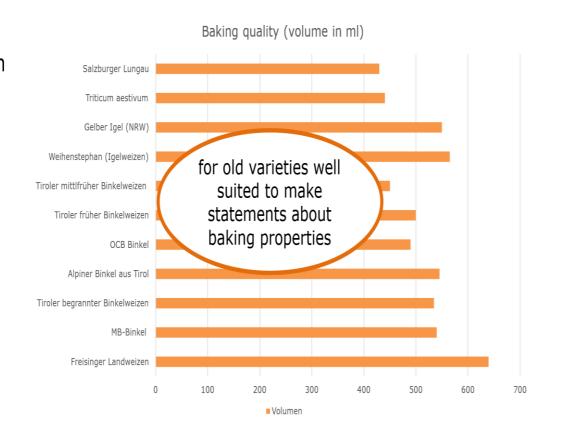
Baking quality of club wheat

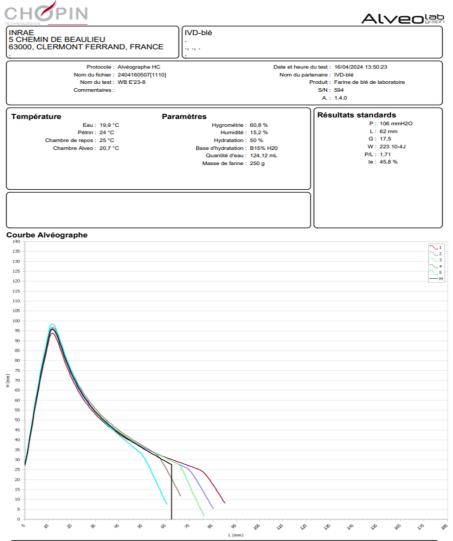


analysis-baking laboratory

Checked parameters:

- Water absorption
- Sedimentation
- Ash
- Falling number
- Crude protein
- Wet glue
- Gluten index
- Crumb elasticity
- Dough elasticity
- Dough surface
- Volume







v: 1.1.2.4

1/1

BiDifferent- Genetic differentiation of Binkel accessions and identification of possible resistances



Albrecht Serfling
JKI- Institute for Resistance Research and Stress Tolerance





BiDifferent- Genetic differentiation of Binkel accessions and identification of possible resistances



Albrecht Serfling
JKI- Institute for Resistance Research and Stress Tolerance





Are there genetic differences between binkel and common wheat?

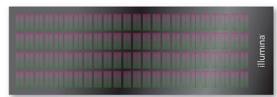


Analysis of genotypic variability in previous projects

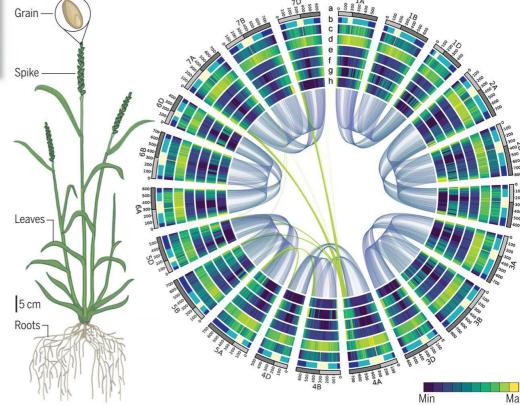
Julius Kühn-Institut
Federal Research Centre for Cultivated Plants

- Material: 2458 wheat genotypes
 - ✓ Winter wheat (Germany)
 - ✓ Winter wheat, F, RUS, SVK
 - ✓ Spring wheat, D
 - ✓ Spring wheat CIMMYT
 - ✓ Watkins core collection
 - ✓ PGR (LfL, GRIN)
 - ✓ Landraces (VERN e.V.)
 - ✓ Club wheat accessions (IPK genebank):
 - 1 TRI 28234 Alpiner Binkel Tirol
 - 2 TRI 853/TRI 24327 Gelber Igel Germany
 - 3 TRI 9237 Landrace Austria before 1930
 - 4 TRI 8857 Landrace Austria before 1930
 - 5 TRI 7769 Tiroler Mittelfrüher Binkel
 -Landrace before 1930







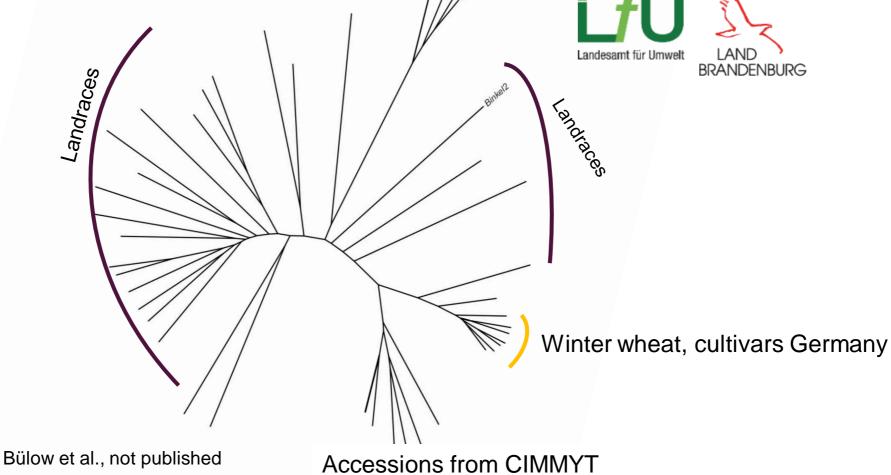




Preliminary results- Differentiation of wheat accessions

Binkel





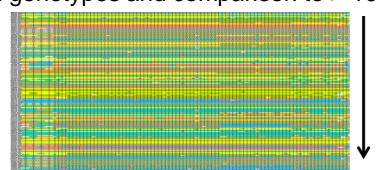
accessions

BiDifferent-Detection of Binkel by genotyping



Analysis of 227 Binkel genotypes and comparison to > 100 wheat accesions using 25k chip (>24,000 markers)

Filtering and selection of SNP-markers



Identification of polymorphic markers

Reference genomes of wheat available!

Mapping of SNP-markers (Wang et al. 2014, Wen et al. 2017, Sun et al. 2022)

Identification of Binkel specific introgressions/ translocations/ SNPs

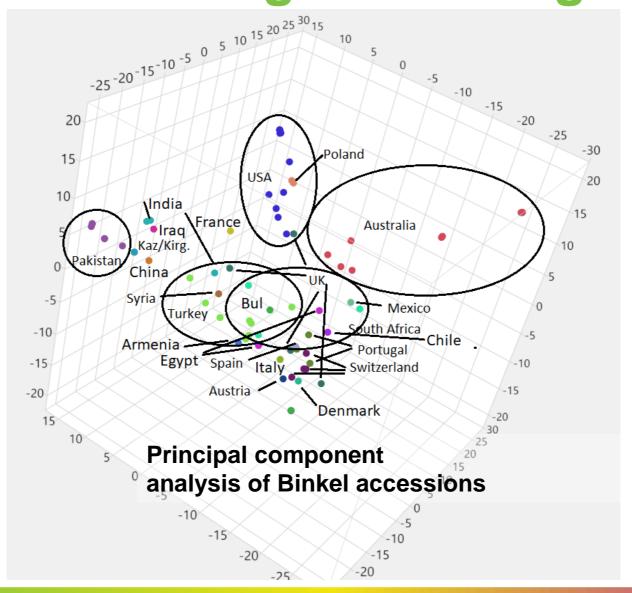
Comparison of polymorphic SNP markers with wheat accessions

Blast to publicly available databases and derivation of KASP-markers for differentiation of Binkel accessions/ varieties and comparison to common wheat cultivars



Allocation of the regions of origin of

Binkel

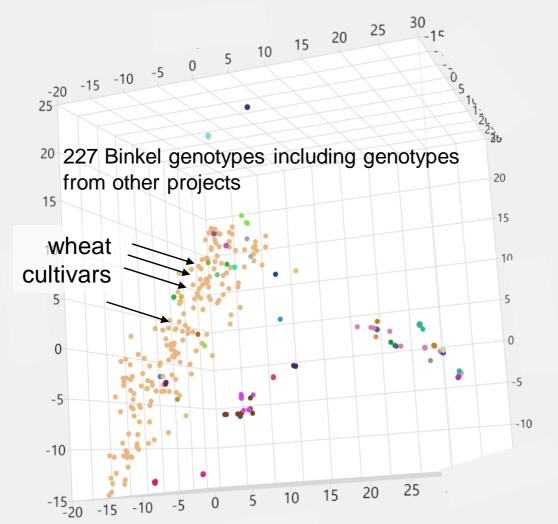






Comparison of Binkel and winter wheat

accessions by principal component analysis



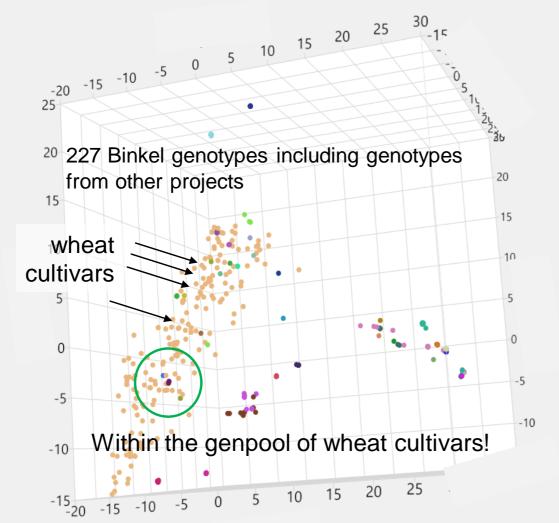
- Alpiner Binkel
- aus Weihenstephan
- Bin_Tri_853/Bin_Tri_24327
- Bin Tri 7769
- Bin Tri 8857
- Bin_Tri_9237
- Bin_Tri_28234
- Binkel Suigez
- Binkelweizen Nr.1
- Blauroter samtiger Winterbinkel
- Canuto
- CP. clavatum
- CP. crebicum
- CP. erinaceum
- CP. icterinum
- Gelber Igel
- Gruyere
- Herisson Brun
- Igel ohne Grannen
- Jailya Bugda
- Kaerntner Winterbinkel
- Kubbweizen
- Landrasse
- LTA001
- LTAe001
- LTAe002
- MB Binkel
- Nendaz
- Obermenzina
- Obermenzing Spelze behaart
- Obermenzing Spelze glatt
- Obersaxener
- Rouge de la Gruyere
- T. aestivum creticum
- T.aestivum lutescenscompactoides
- Tiroler begrannter Dinkel
- tiroler Binkel
- Tiroler früher Binkel
- Tiroler mittelfrüher Binkel
- Tiroler Mittelfrüher Binkelweizen
- Typ A Obermenzing
- Typ B Obermenzing
- von Obersaxen
- VRIN 195C
- Weihenstephaner Igelweizen weissspelziger Winterigel





Comparison of Binkel and winter wheat

accessions by principal component analysis



- Alpiner Binkel
- aus Weihenstephan
- Bin_Tri_853/Bin_Tri_24327
- Bin_Tri_7769
- Bin_Tri_8857
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- Typ B Obermenzing
- von Obersaxen
 VRIN 195C
- Weihenstephaner Igelweizen
- weissspelziger Winterigel

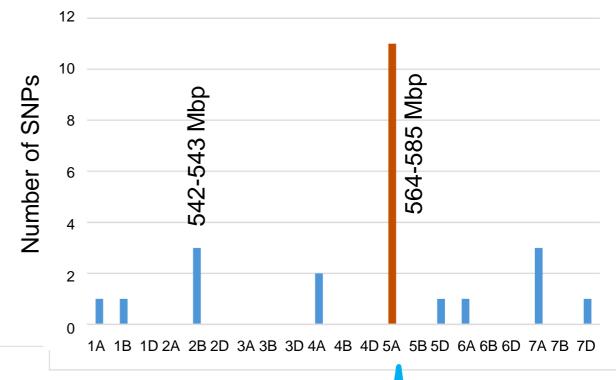




How to differentiate wheat phenotypes genetically?

Chromosome	Markers	Lowest	Highest (bp)
1A	609	7184499	593550661
1B	531	1203935	689000691
1D	219	216813	493936055
2A	654	259213	780714971
2B	799	1251459	801253577
2D	238	5086803	749278574
3A	520	1306410	749278574
3B	647	337188	827042743
3D	125	773182	614367136
4A	352	2791040	744515299
4B	297	537211	670438383
4D	52	1242201	509666790
5A	636	13858	708442531
5B	662	6648543	712905690
5D	157	1613079	563854980
6A	646	287373	617689725
6B	549	164066	720952203
6D	110	1415350	472890118
7A	358	653444	736690246
7B	240	114913	750604135
7D	60	378699	630528147





Federal Research Centre for Cultivated Plants

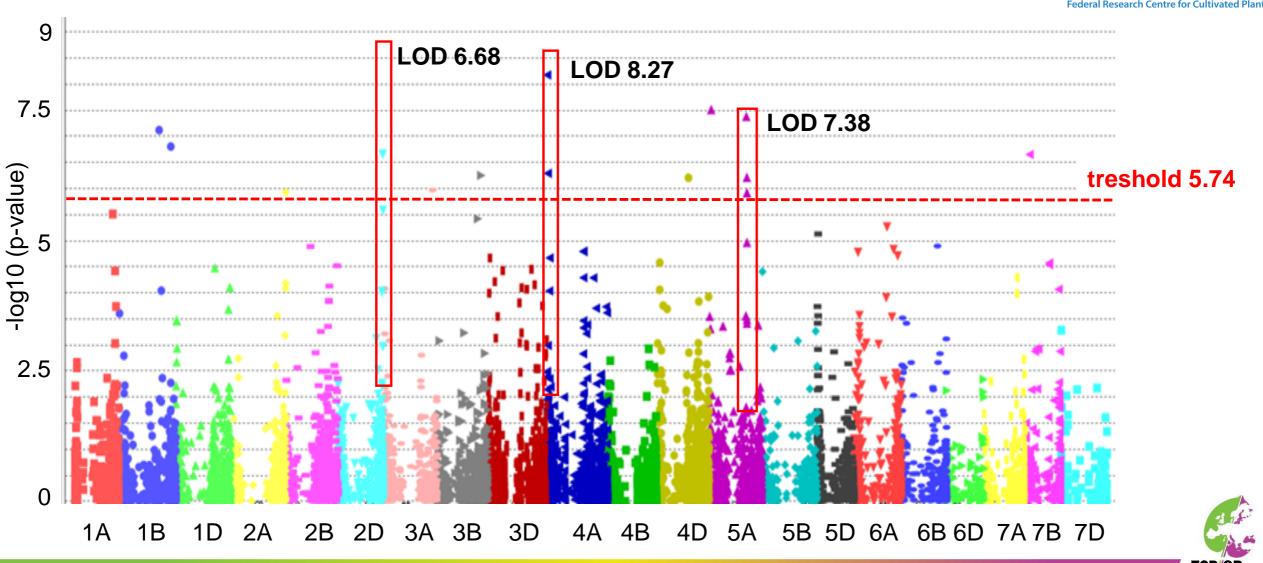
Chromosome 5A

10

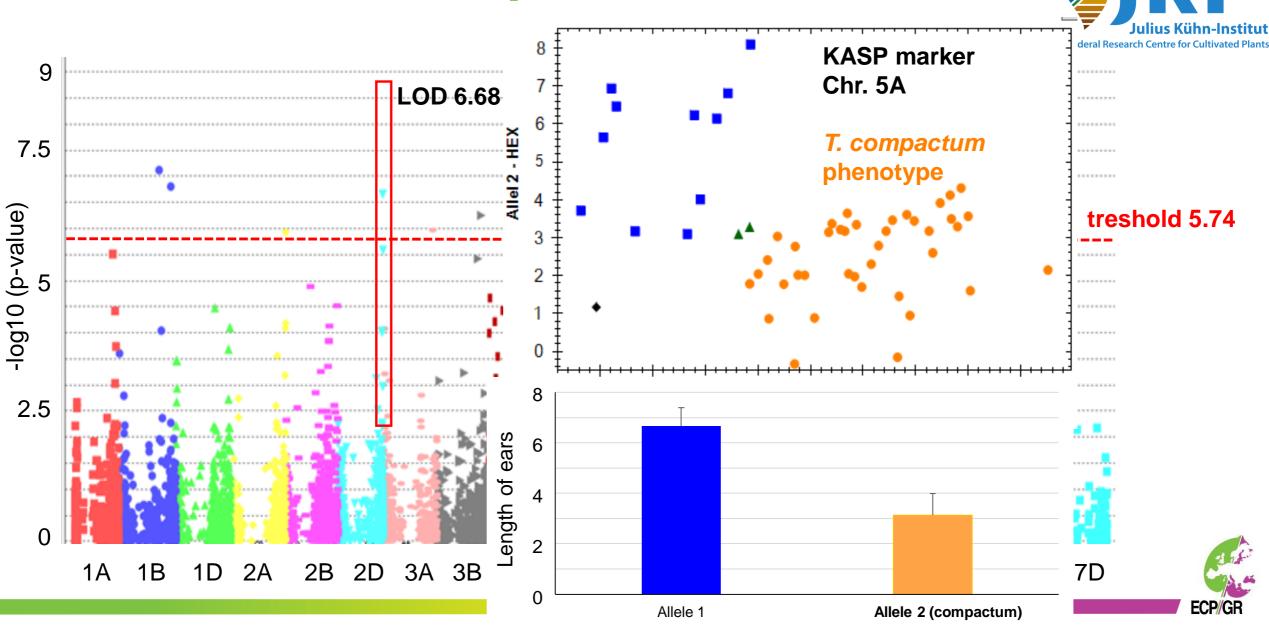
0 30 60 90 120 150 180 210 240 270 300 330 360 390 420 450 480 510 540 570 600 630 660 690

Detection of *T. compactum* alleles





Detection of *T. compactum* alleles



What is known about QTL, associated with a compactum phenotype?



- "It was evident that the loci affecting compact spikes in *T. aestivum* mutants were located on chromosome **5AL** distal from *Q* locus."-Kosuge et al. 2011
- "In hexaploid wheat, spike morphology is regulated by three major genes, namely Q, C (Compactum), and S (Sphaerococcum) located on chromosomes 5A, 2D, and 3D, respectively"- Fan et al. 2019
- "Other QTL that were significantly associated with spike morphology-related traits, in at least one environment, were localized on chromosomes 2B, 3A, 3D, 4D, and 5A."_—Jantasuriyarat et al. 2009



Resistance to rusts



Wheat rusts, a plague that accompanies the cultivation of wheat



Stripe rust (Puccinia striiformis)

Yield losses up to 60%

Races "Warrior" overcome important resistances

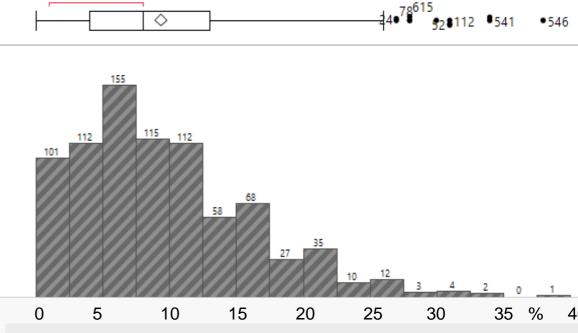


Leaf rust (*Puccinia* triticina)

Yield losses up to 40%

High diversity of races with different virulences

overcome important resistances, e.g. *Lr*37

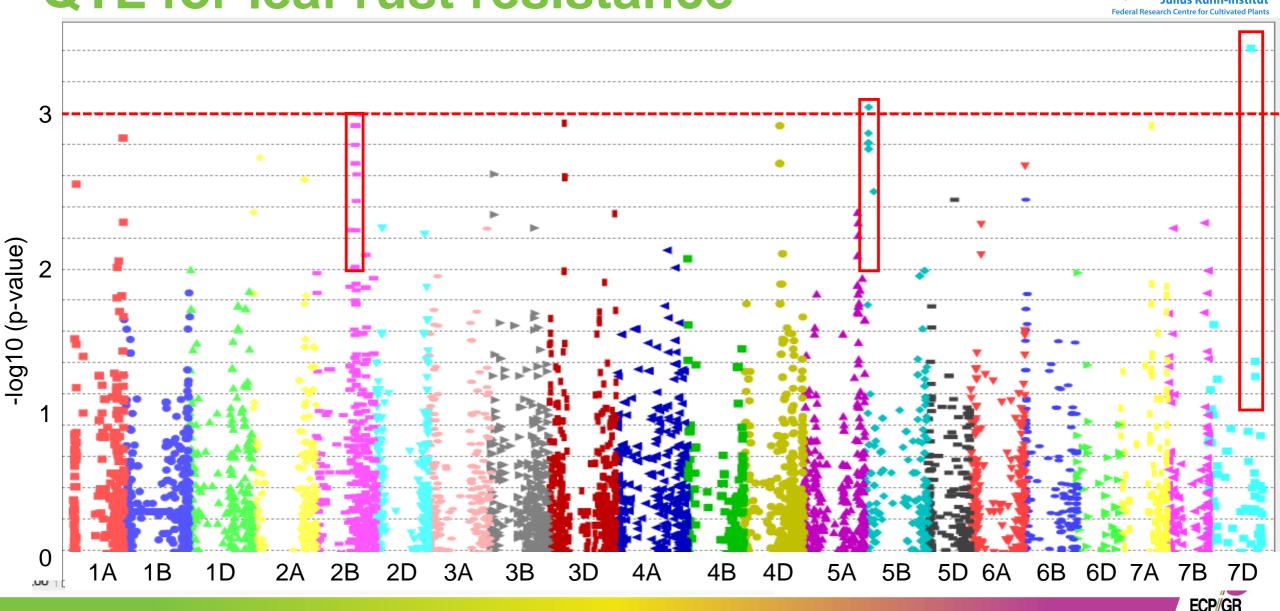


Analysis of variance (trait leaf rust)

Source	dF	SQ	AQ	F value	F (sign.)
Genotypes Error Sum		6646.65 27007.78 33654.43	_	5.00256	0.0001*

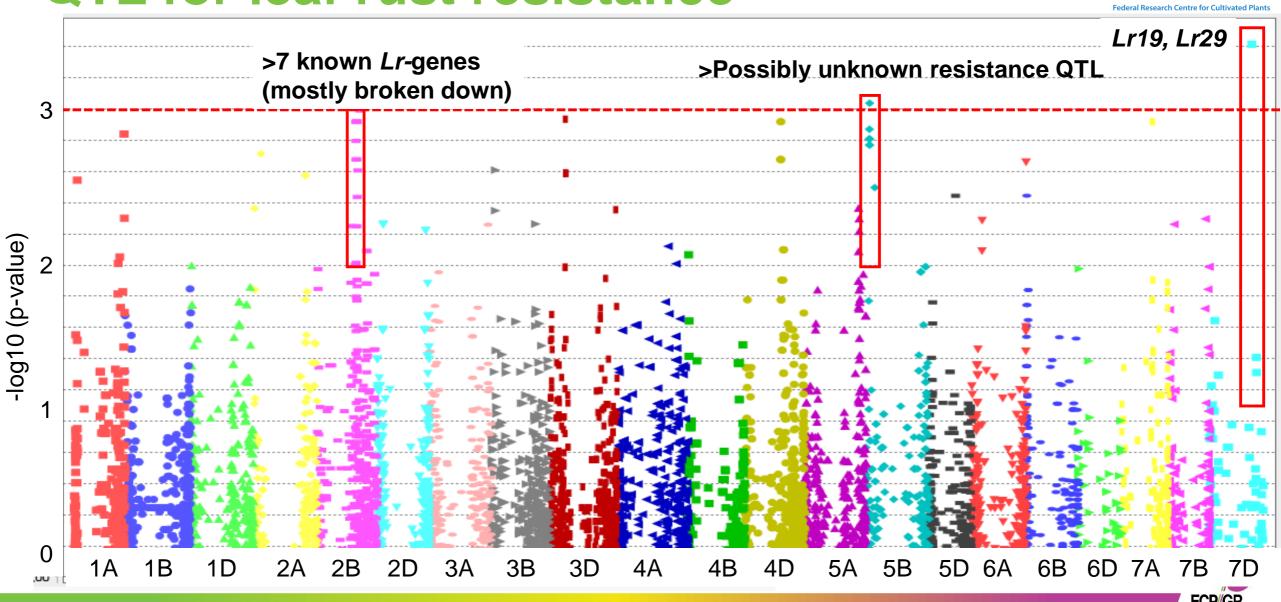
QTL for leaf rust resistance





QTL for leaf rust resistance







Summary

- Differentiation between *T. compactum* accessions and common wheat is possible by using molecular markers
- Origins and relations of *T. compactum* accessions could be identified by PCA
- Leaf rust resistant *T. compactum* accesions could be identified
- One QTL on chromosome 5B could be an unknown resistance to leaf rust
- Genotype data for many *T. compactum* genebank accessions are now avaible and can be used for GWAS after phenotyping of further traits





Thank you for your attention

Special thanks for the project collaboration to Clement Debiton, INRAE, Chr. Partl, Innsbruck, M. Pramsohler, Laimburg Italy, H. Steiner, Slowfood, Klaus Fleissner, U. Konradl LfL and all farmers, bakers and external collegues involved...



Selection of SNP-markers

Markers excluded

- >10% missing data
- <10% minor allele frequency
- >5% heterocygosity
- More than one hit to the reference genome of wheat

8461 from more than 24,000 SNP markers selected



