



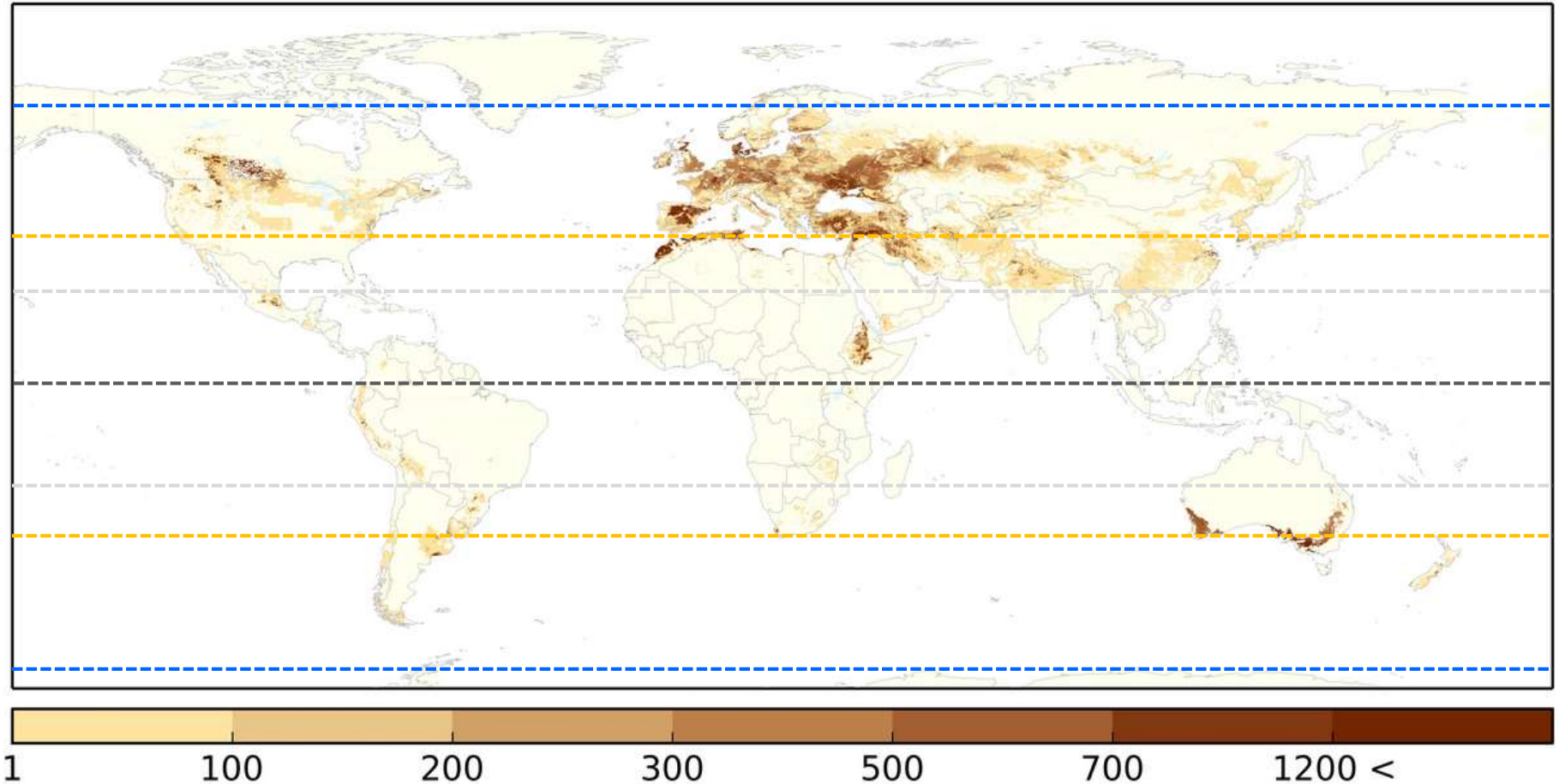
# The BRIDGE project: From 1 – 20,000 barley genomes

Nils Stein

Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben & Georg-August University Göttingen, CiBreed

# Barley – a globally grown crop species

## Barley Total Harvested Area (ha)



You, L., U. Wood-Sichra, S. Fritz, Z. Guo, L. See, and J. Koo. 2014  
Spatial Production Allocation Model (SPAM) 2005 Version 2.0.  
03.10.2015. Available from <http://mapspam.info>

HarvestChoice  
BETTER CHOICES, BETTER LIVES

INTERNATIONAL  
FOOD POLICY  
RESEARCH  
INSTITUTE  
IFPRI

RESEARCH  
PROGRAM ON  
Policies,  
Institutions,  
and Markets  
CGIAR  
Leif Johansson

International Institute for  
Applied Systems Analysis  
IIASA

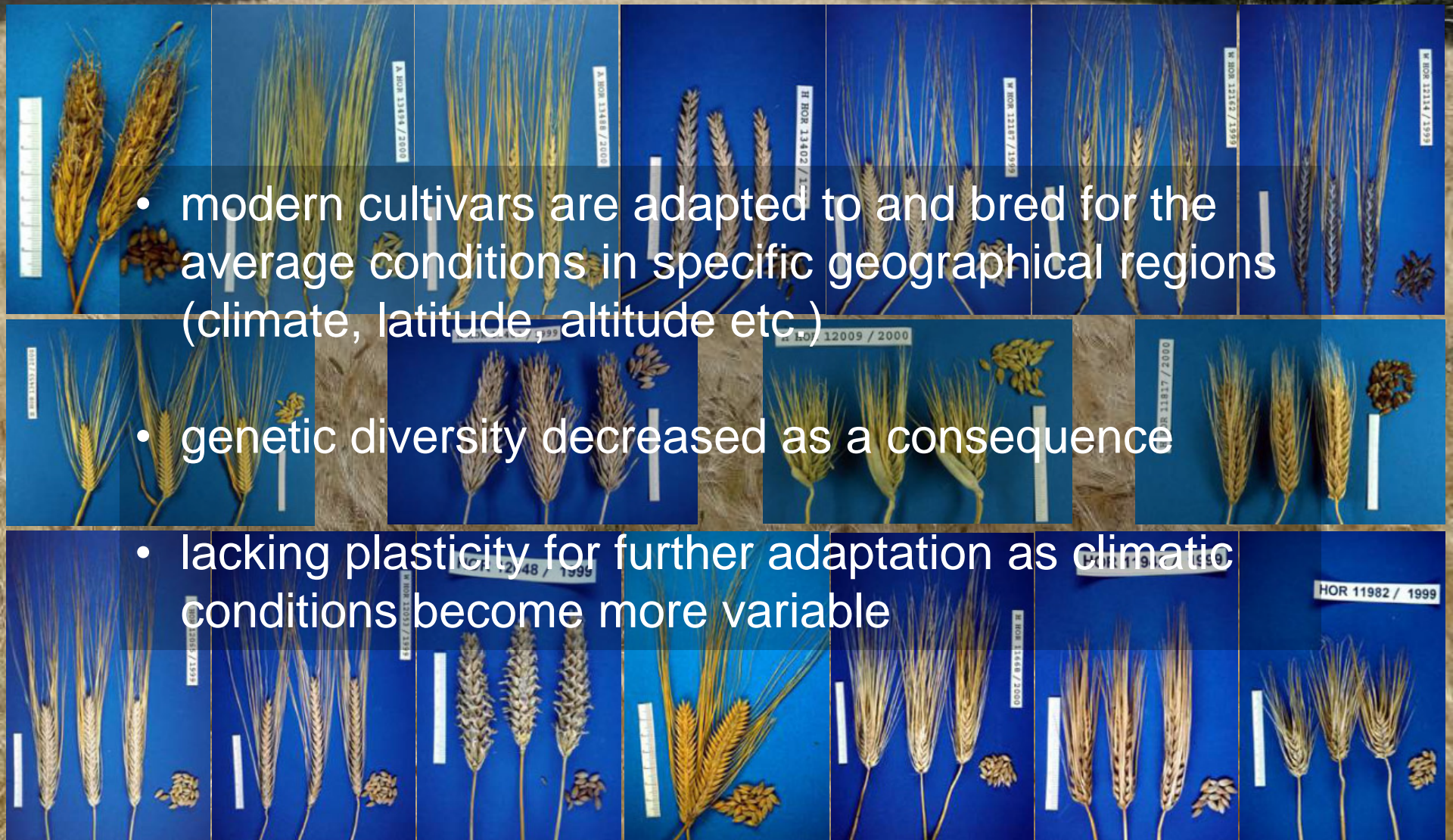
IPK  
GÄTERSLEBEN

75

1943 – 2018

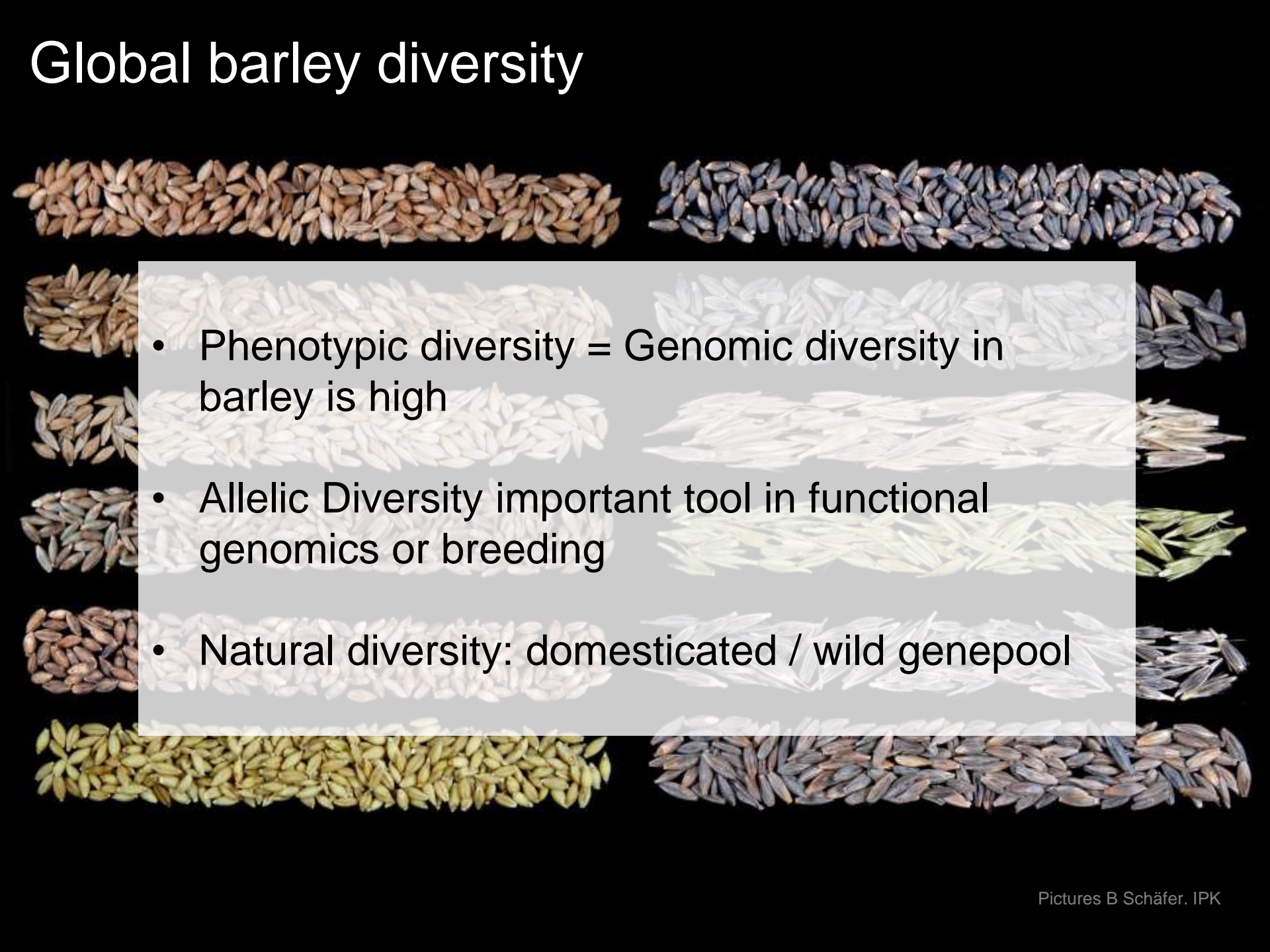


# Barley diversity – modern cultivars vs. genetic resources

- 
- modern cultivars are adapted to and bred for the average conditions in specific geographical regions (climate, latitude, altitude etc.)
  - genetic diversity decreased as a consequence
  - lacking plasticity for further adaptation as climatic conditions become more variable



# Global barley diversity

- 
- Phenotypic diversity = Genomic diversity in barley is high
  - Allelic Diversity important tool in functional genomics or breeding
  - Natural diversity: domesticated / wild genepool

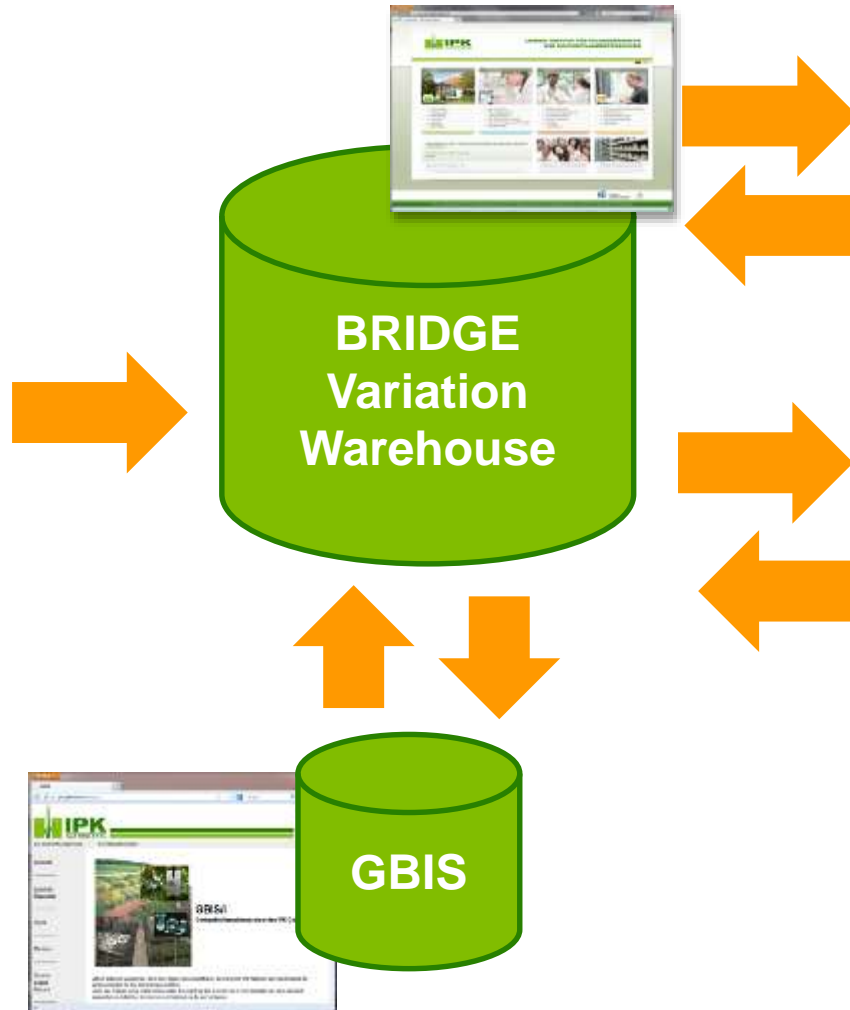
# BRIDGE: Biodiversity infoRmatics to close the gap from genome Information to educated utilization of Diversity hosted in GEnebanks

## Primary data analysis



## Field based phenotyping

## BRIDGE Web Portal

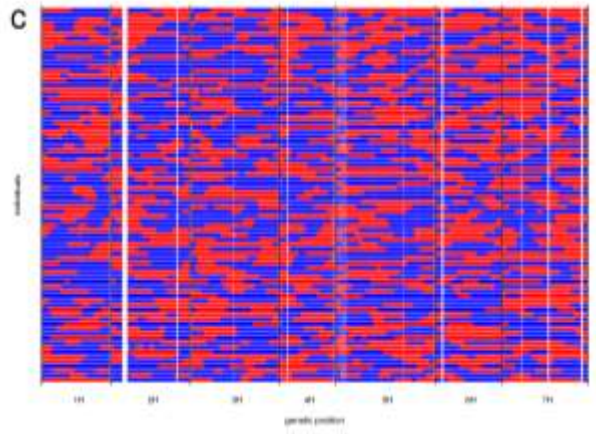
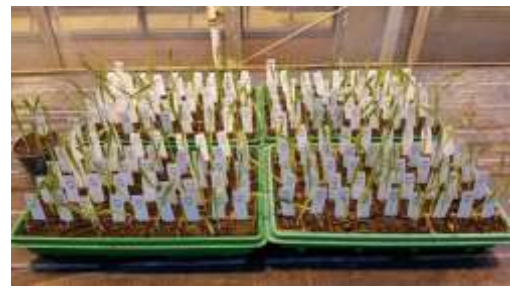
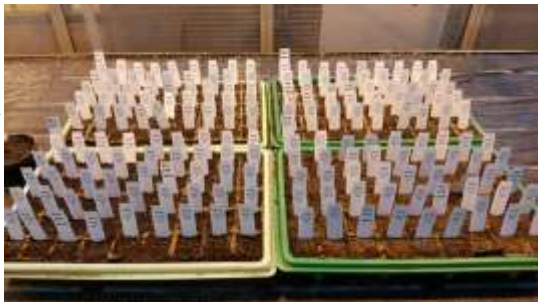


- Interactive haplotype browser
- Comparison to existing marker data to guide pre-breeding

## Interfaces to other systems

- EURISCO
- EDBD
- transPLANT
- de.NBI
- SeedSeq
- Digital Seed Bank
- GENESYS

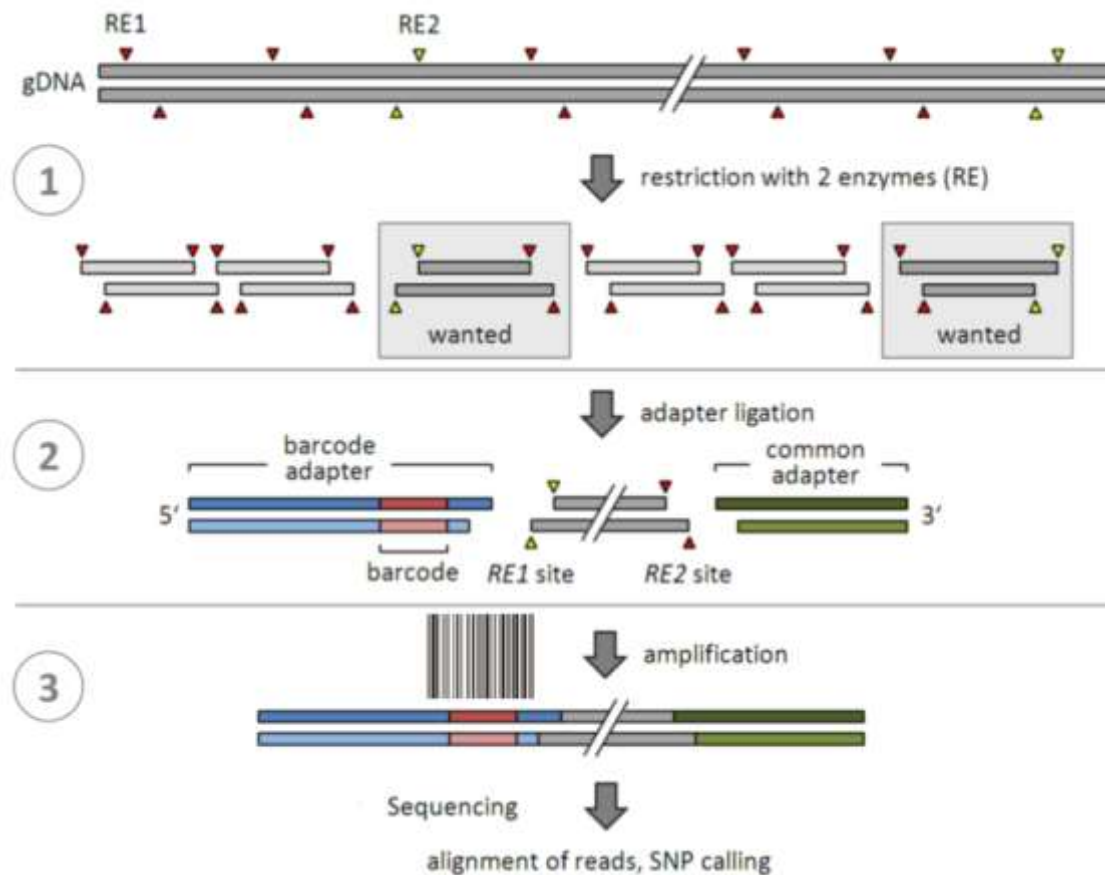
# BRIDGE project: GBS of >20,000 barley accs.



- + WGS / exome capture of selected accessions
- + historic evaluation data (morphologic and agronomic)
- + passport and geo-reference information
- + ear- and seed phenotyping at harvest



# GBS of >20,000 barley accs.



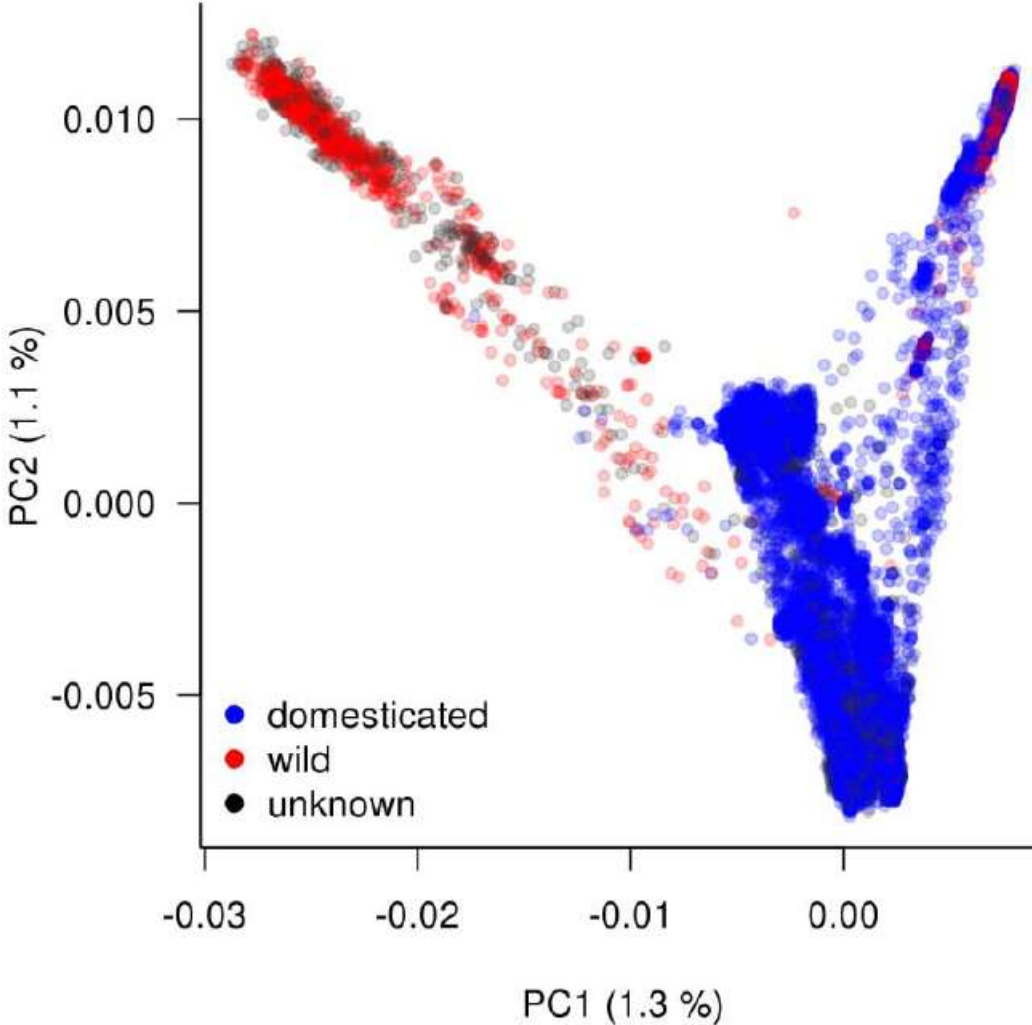
- GBS (PstI/MspI) library preparation (Wendler et al. 2014; >180-plex barcoded )
- Bioinformatics pipeline (Mascher et al. 2013):
  - Minimal read depth per genotype: 2x
  - Maximal fraction of missing calls: 10%
  - Both alleles at least once in homozygous state

# Diversity in barley - whole collection



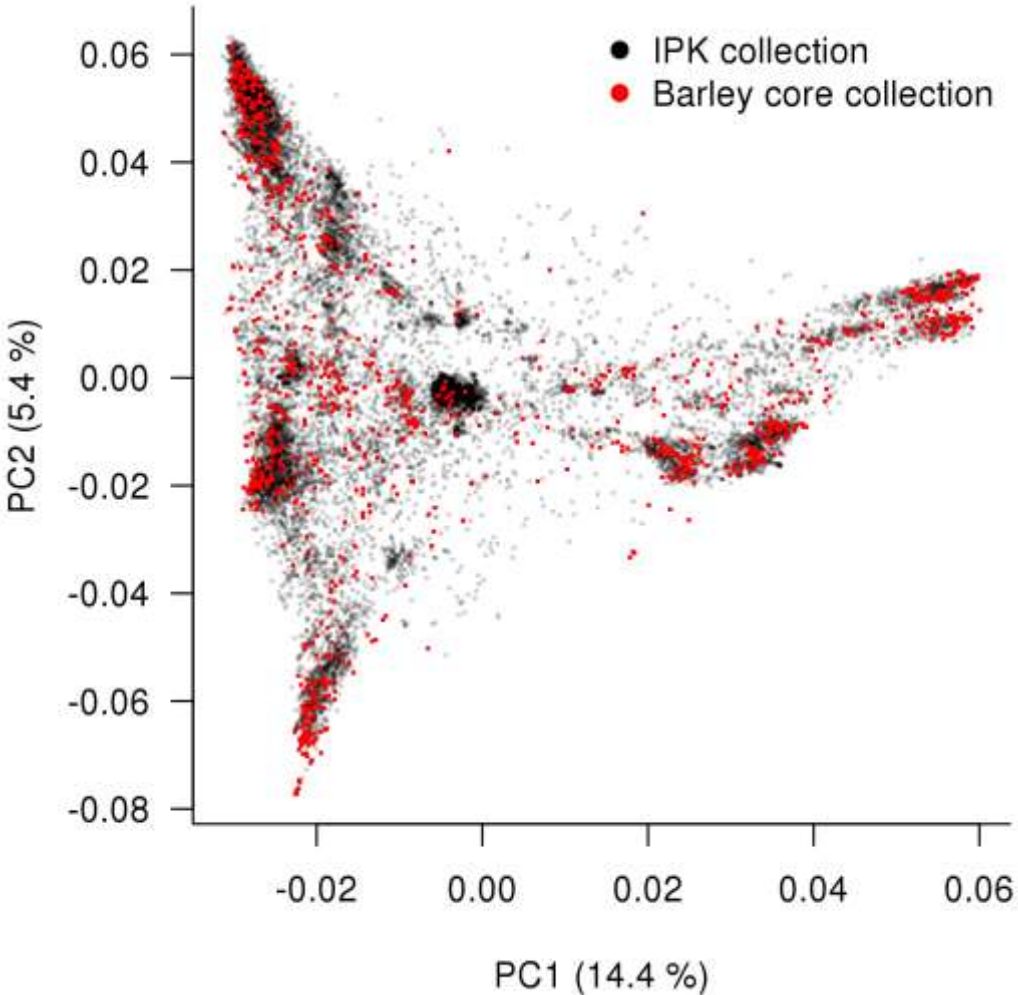
Sara Milner

22,621 samples  
171,263 SNP





# Representativeness of IPK collection

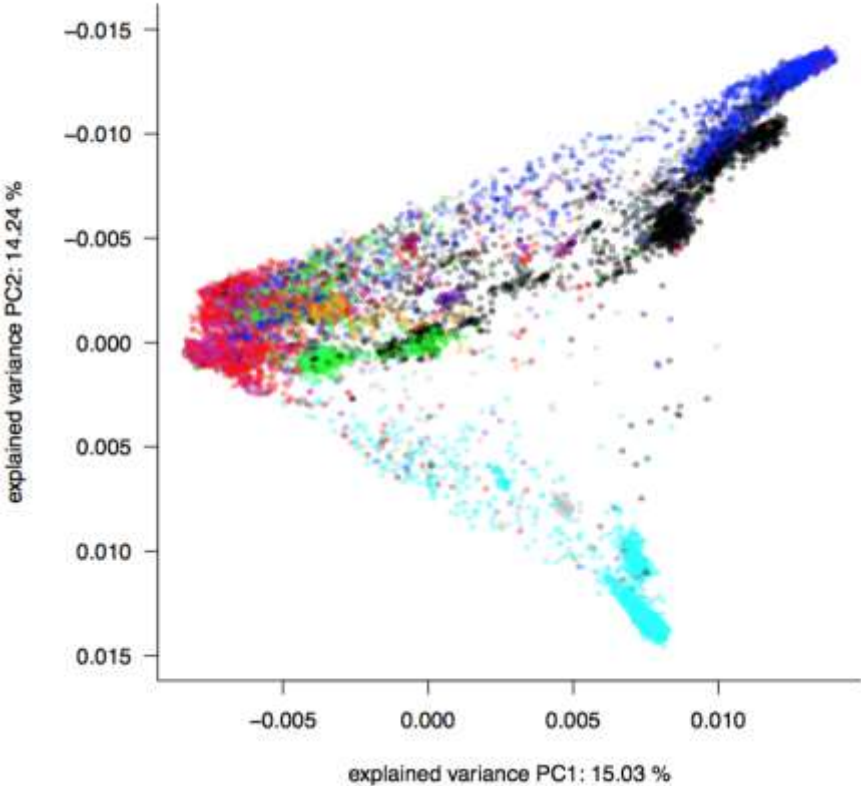


# Diversity in domesticated barley

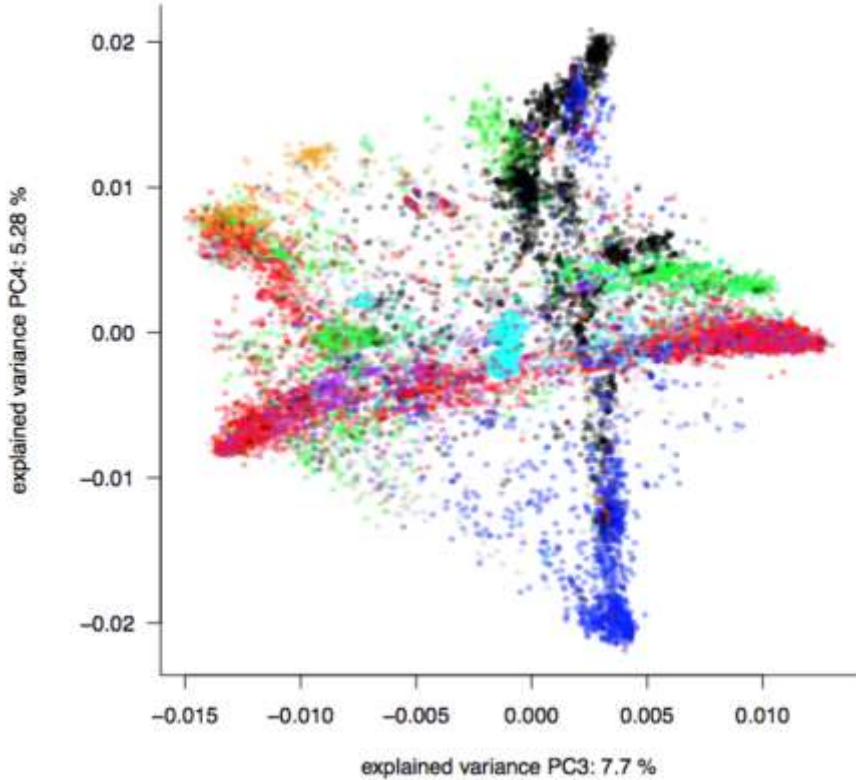


- Far East (N=1669)
- Central Asia (N=2639)
- Near East (N=1619)
- West Eu (N=4338)
- East Eu (N=1477)
- North Africa/Arabic (N=443)
- Ethiopia (N=3920)

PCA (20,267 samples, 76,419 SNPs)



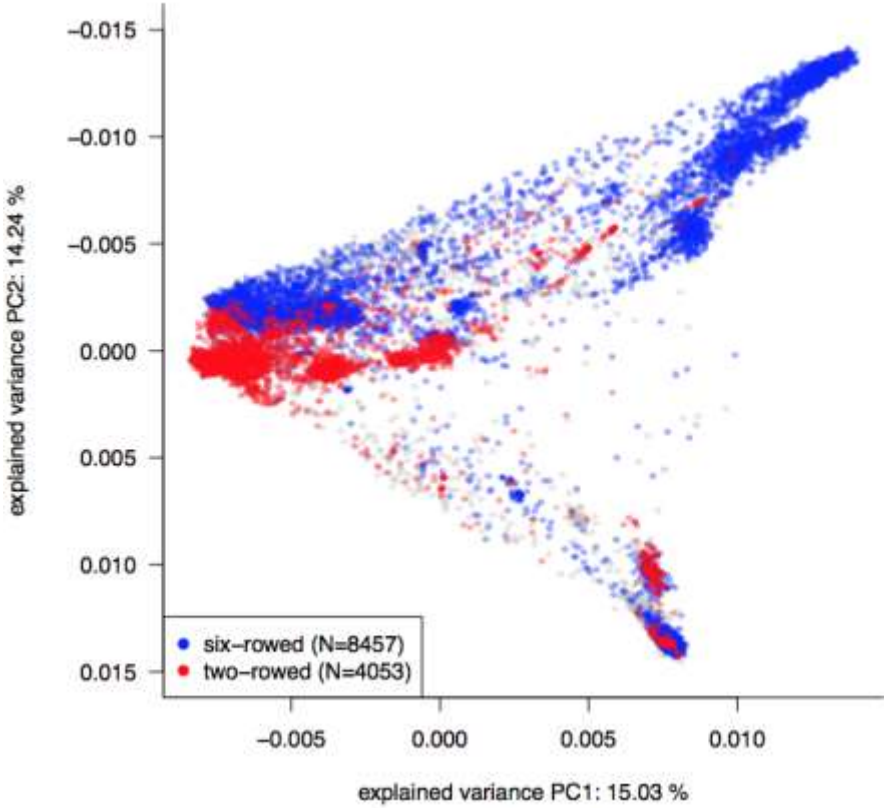
PCA (20,267 samples, 76,419 SNPs)



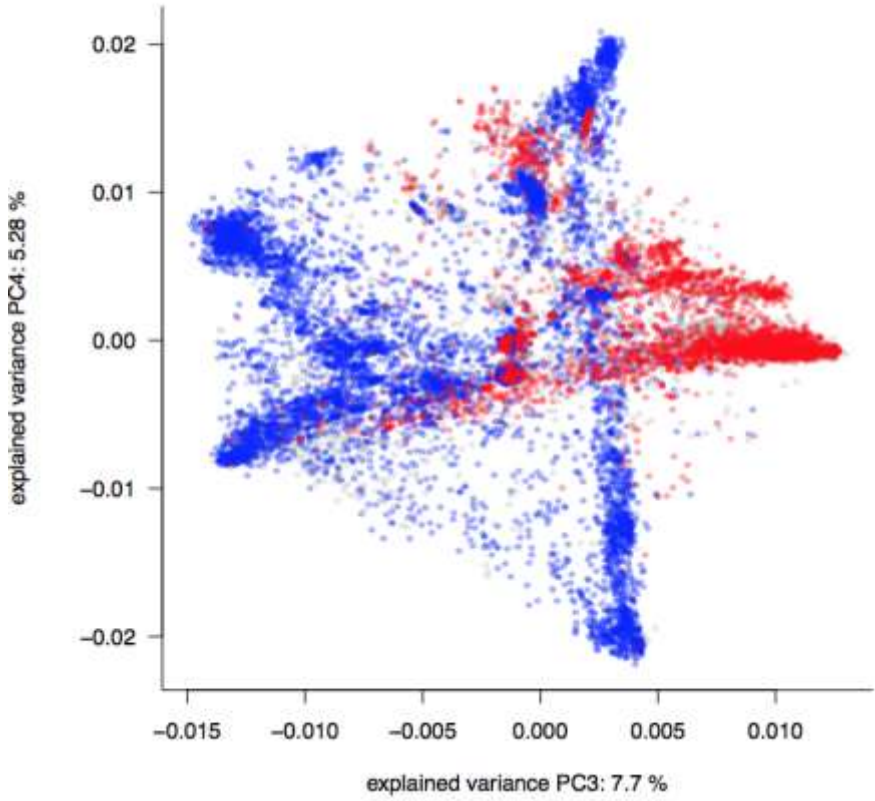
# Diversity in domesticated barley



PCA (20,267 samples, 76,419 SNPs)



PCA (20,267 samples, 76,419 SNPs)

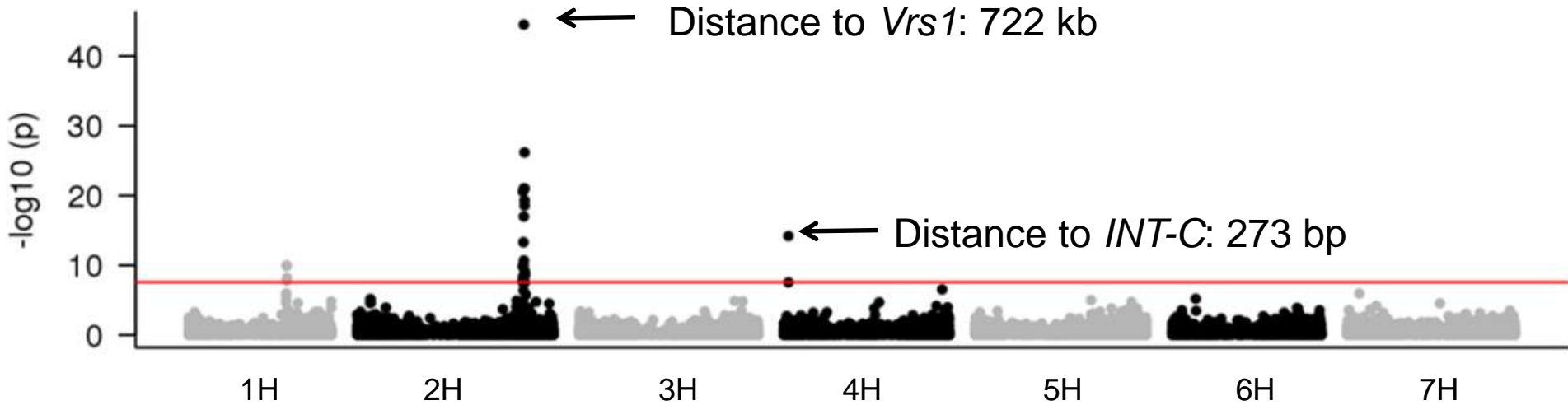




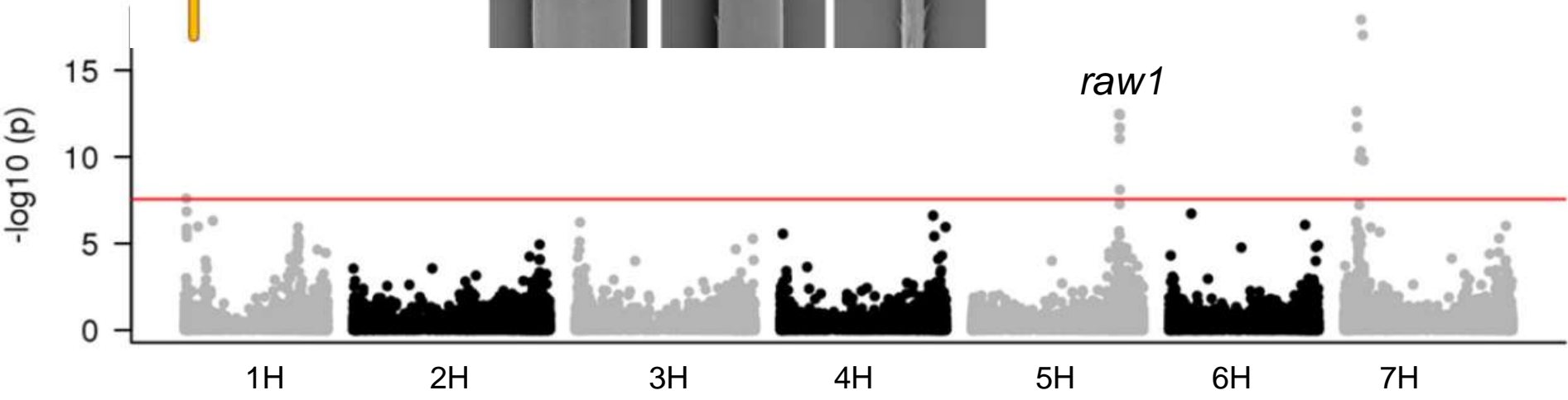
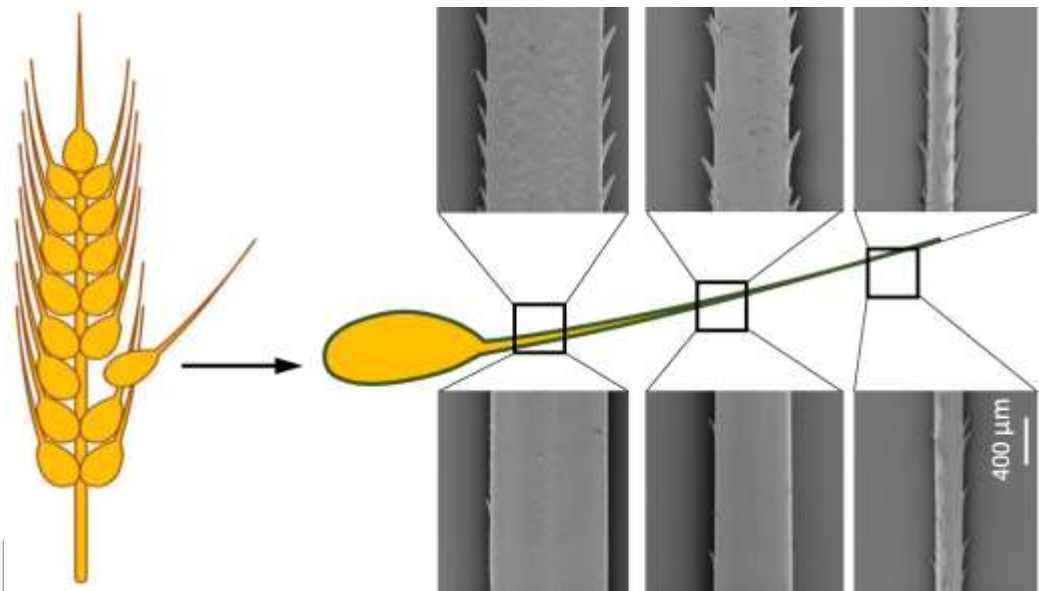
# GWAS for row-type

**Genotypes:** SNPs with a MAF  $\geq 1\%$  (19,507 SNPs).

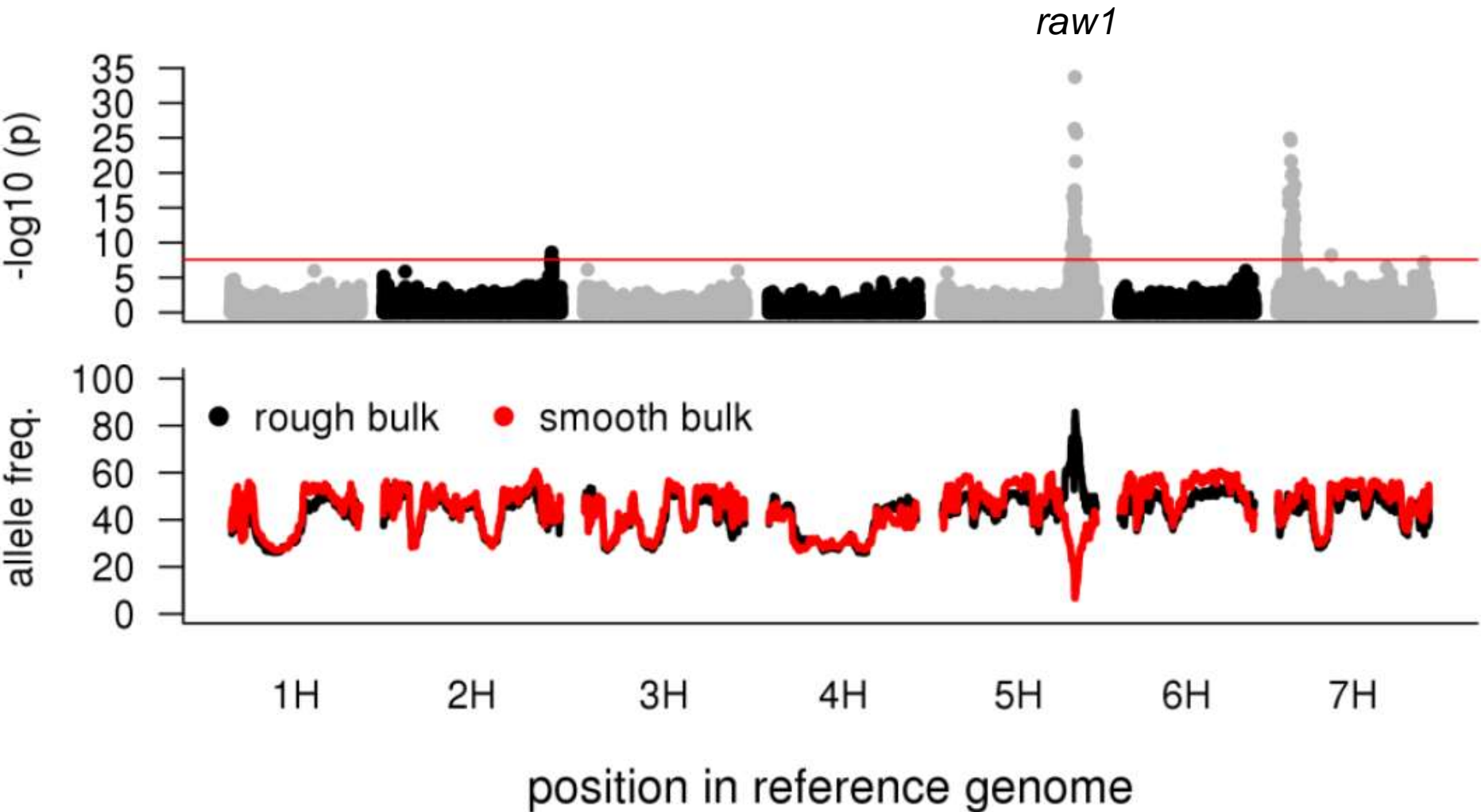
**Software:** GAPIT R package (Lipka et al. 2012), using a mixed linear model, kinship, PC1/2 as covariants



# GWAS for awn roughness

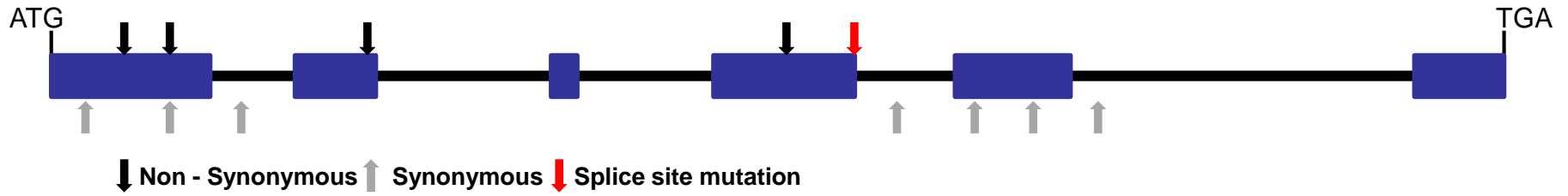


# GWAS vs BSA for awn roughness

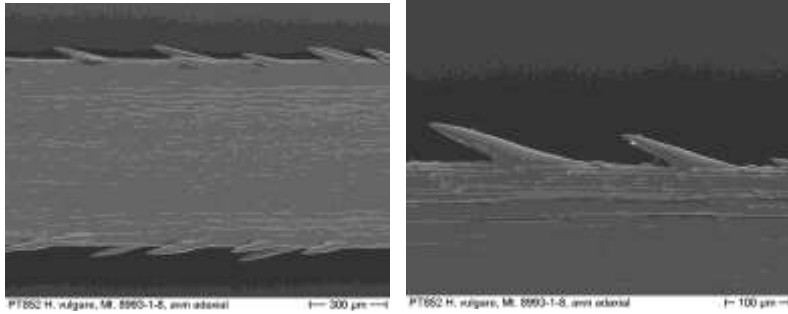




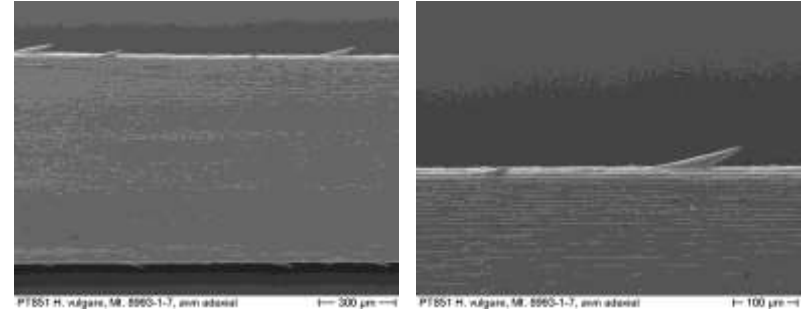
# TILLING to confirm raw1 function



8993-1\_8 → WT/WT



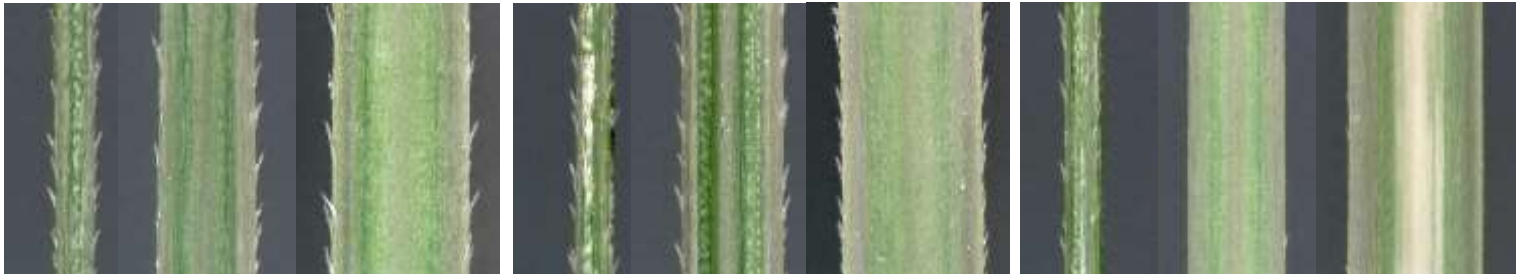
8993-1\_7 → MT/MT



8993-1\_2\_10  
WT/WT

8993-1\_2\_8  
WT/MT

8993-1\_2\_5  
MT/MT



# Genebank genomics

- GWAS for simple traits
- GWAS for more complex and agronomically relevant traits



# how about historical (legacy) data in genebanks?

unbalanced legacy data from  
regeneration cycles



manual quality assessment



- checking sowing date and off-season sowing date
- checking extreme data points



Outlier detection based on re-scaled  
median absolute deviation and Bonferroni-  
Holm test



describing the phenotypic diversity of the  
collection / Estimating heritability and  
BLUEs

examine the data suitability for  
selection of accessions



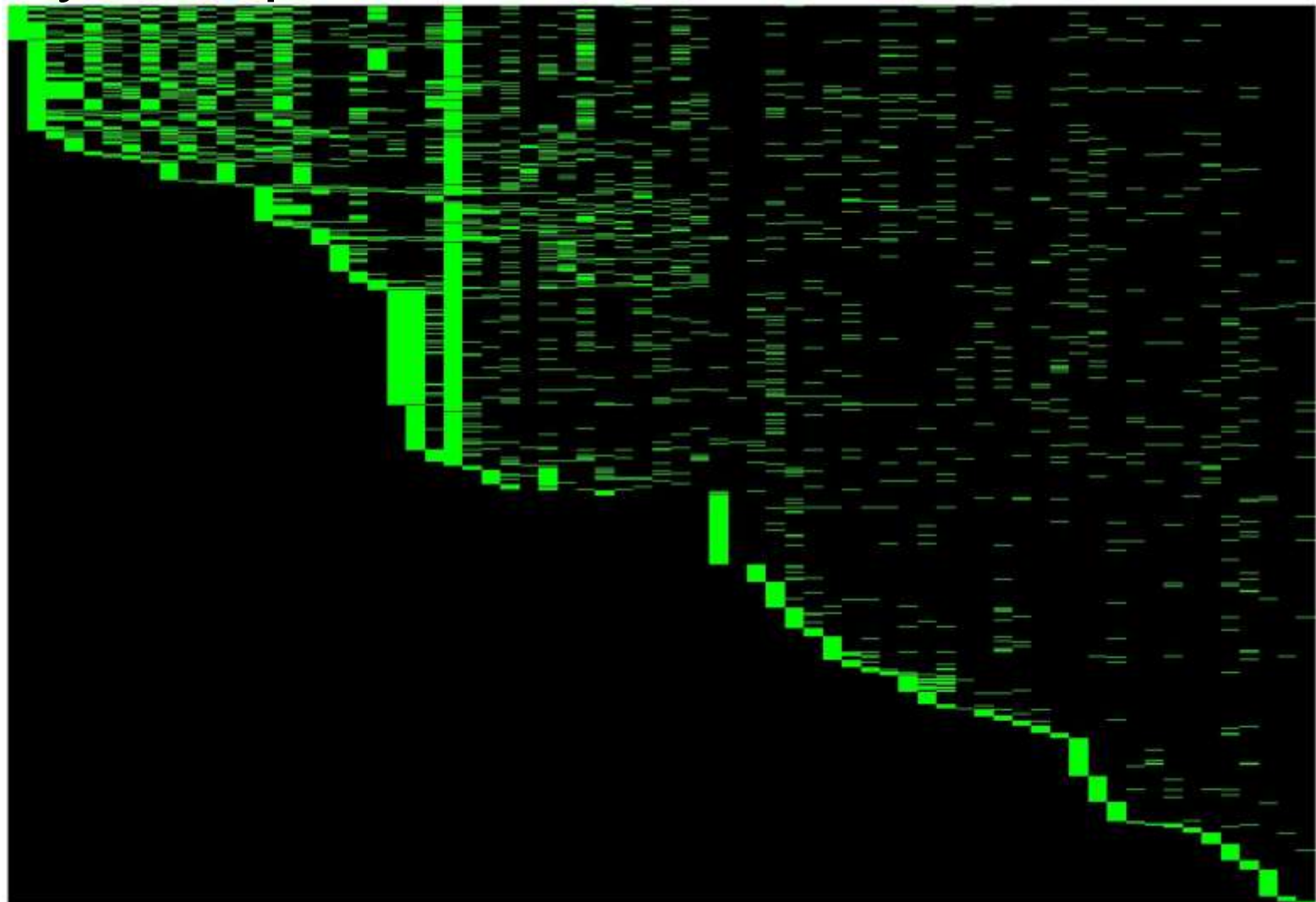
re-sampling study

two-fold cross validation

Maria Y. Gonzalez et al. 2018, TAG 131: 2009-2019

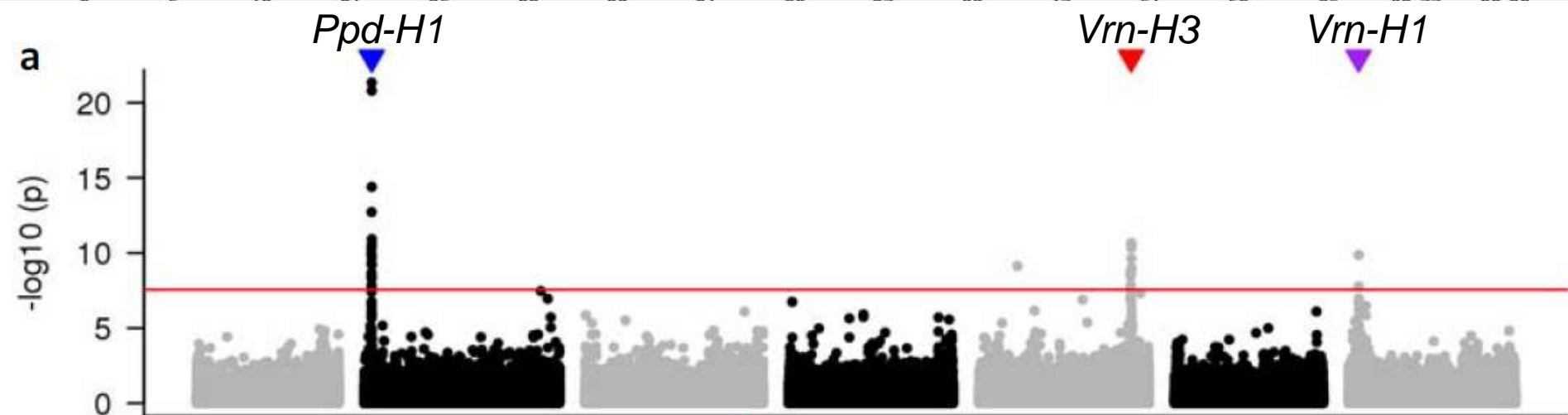
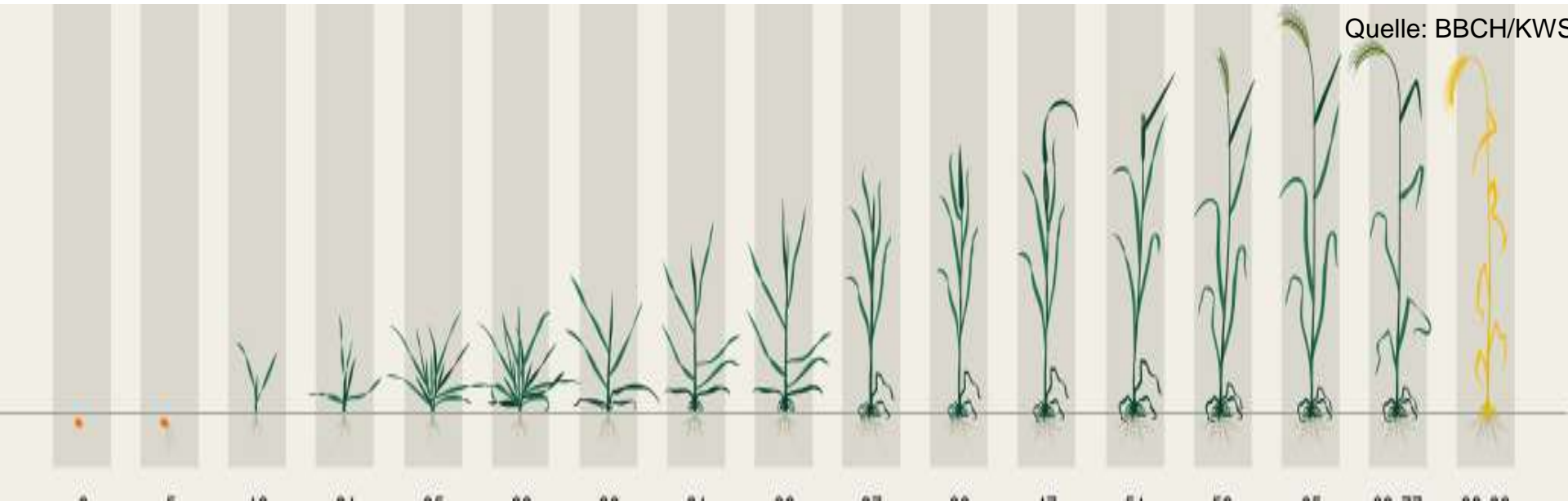


# Barley multiplications at IPK Genebank



1946 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015

# Value of genebank legacy data for GWAS?

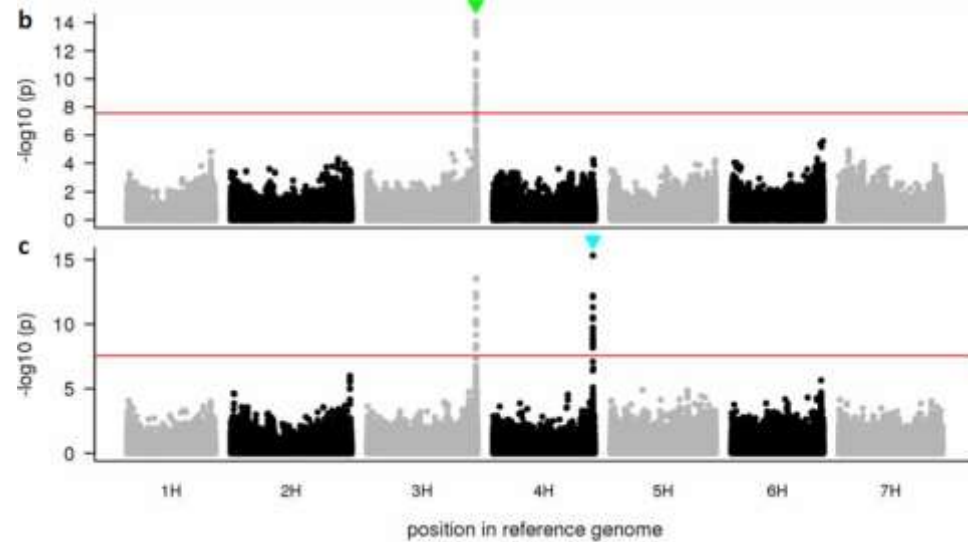


# GWAS for resistance to soil-borne viruses



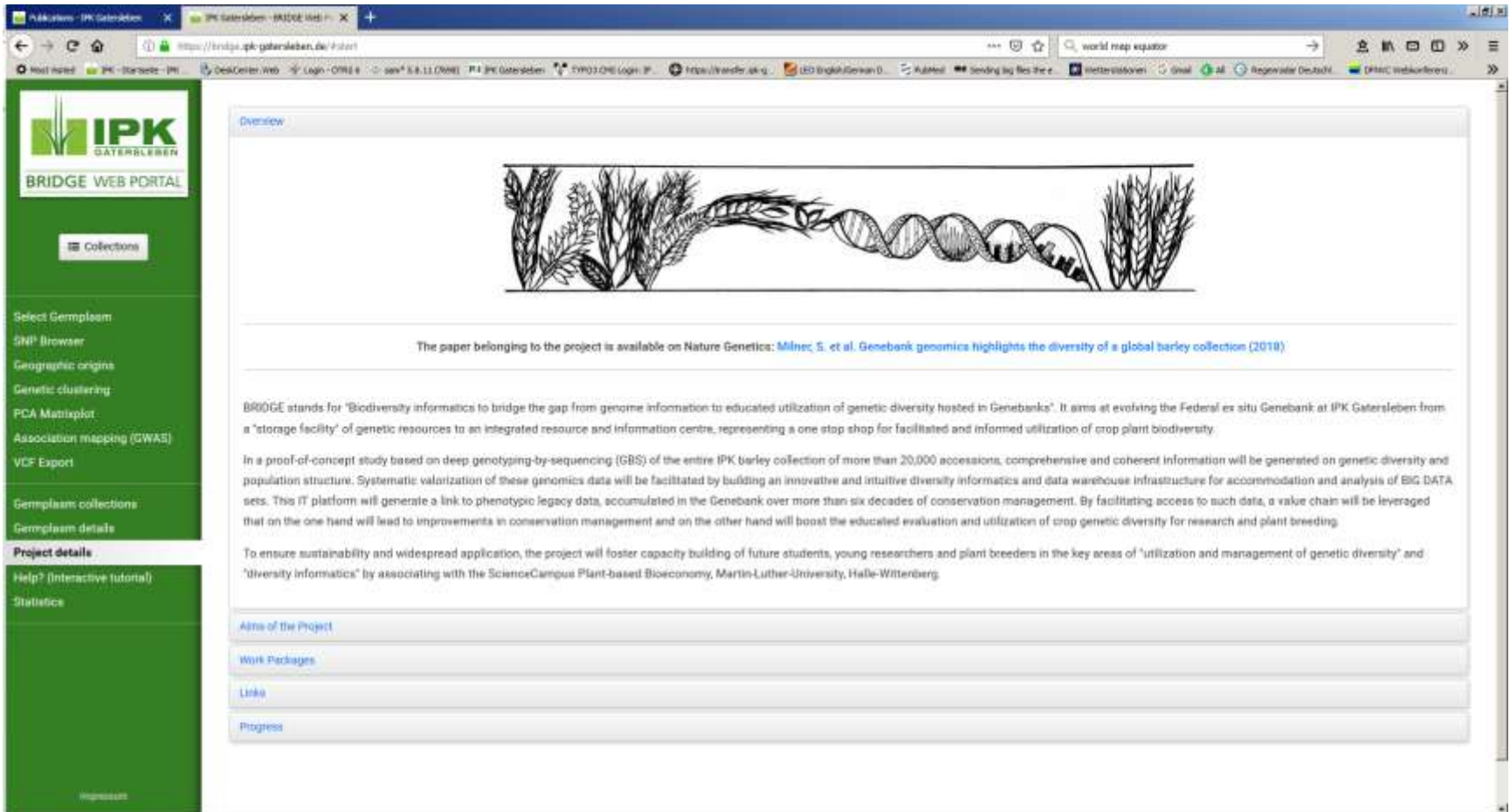
1894 accessions tested

collaboration with JKI QLB, Ordon+Habekuss





# The BRIDGE portal



The screenshot shows the BRIDGE web portal in a browser window. The browser's address bar displays the URL <https://bridge.ipk-gatersleben.de/portal>. The page features a green sidebar on the left with the IPK Gatersleben logo and the text "BRIDGE WEB PORTAL". Below the logo is a "Collectors" button. The sidebar contains several menu items: "Select Germplasm", "SNP Browser", "Geographic origins", "Genetic clustering", "PCA Matriplot", "Association mapping (GWAS)", "VCF Export", "Germplasm collections", "Germplasm details", "Project details", "Help? (Interactive tutorials)", and "Statistics".

The main content area is titled "Overview" and features a central illustration of a DNA double helix flanked by various plant species. Below the illustration, a text box states: "The paper belonging to the project is available on Nature Genetics: [Milne, S. et al. Genebank genomics highlights the diversity of a global barley collection \(2018\)](#)".

The main text describes the BRIDGE project: "BRIDGE stands for 'Biodiversity informatics to bridge the gap from genome information to educated utilization of genetic diversity hosted in Genebanks'. It aims at evolving the Federal ex situ Genebank at IPK Gatersleben from a 'storage facility' of genetic resources to an integrated resource and information centre, representing a one stop shop for facilitated and informed utilization of crop plant biodiversity."

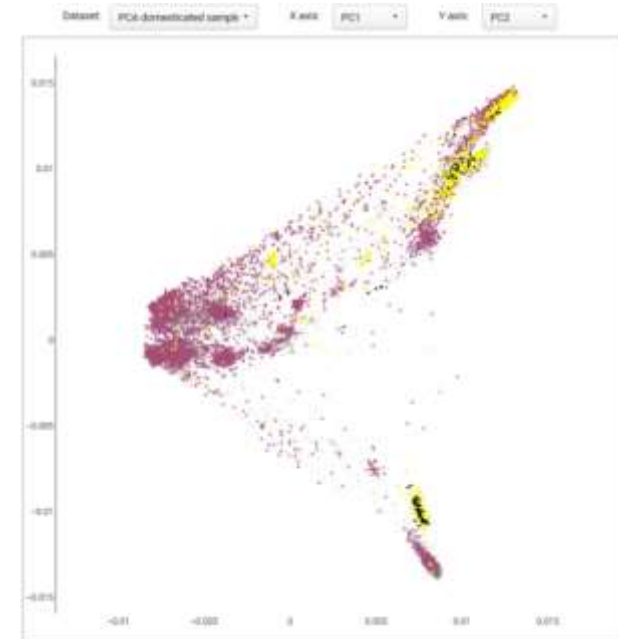
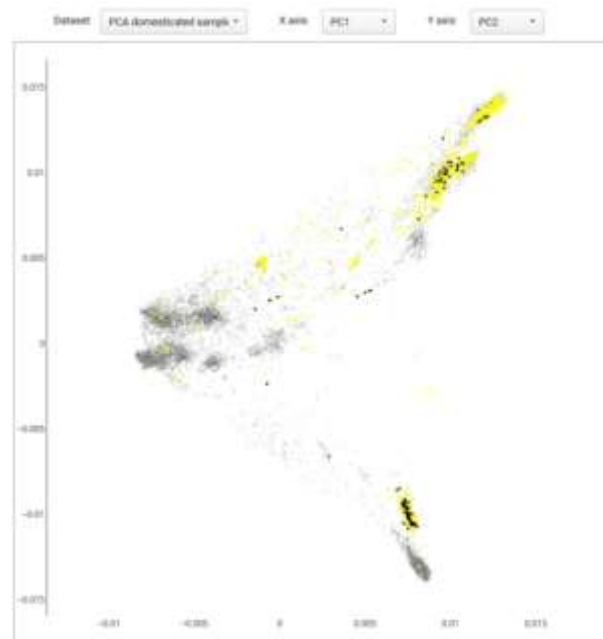
It further explains: "In a proof-of-concept study based on deep genotyping-by-sequencing (GBS) of the entire IPK barley collection of more than 20,000 accessions, comprehensive and coherent information will be generated on genetic diversity and population structure. Systematic valorization of these genomics data will be facilitated by building an innovative and intuitive diversity informatics and data warehouse infrastructure for accommodation and analysis of BIG DATA sets. This IT platform will generate a link to phenotypic legacy data, accumulated in the Genebank over more than six decades of conservation management. By facilitating access to such data, a value chain will be leveraged that on the one hand will lead to improvements in conservation management and on the other hand will boost the educated evaluation and utilization of crop genetic diversity for research and plant breeding."

Finally, it states: "To ensure sustainability and widespread application, the project will foster capacity building of future students, young researchers and plant breeders in the key areas of 'utilization and management of genetic diversity' and 'diversity informatics' by associating with the ScienceCampus Plant-based Bioeconomy, Martin-Luther-University, Halle-Wittenberg."

At the bottom of the main content area, there are four buttons: "Aims of the Project", "Work Packages", "Links", and "Progress".

<https://bridge.ipk-gatersleben.de>

# The BRIDGE portal



<https://bridge.ipk-gatersleben.de>

# Summary

BRIDGE – a complete barley ex situ collection characterized by GBS

- Diversity landscape of the collection – what is the context of global diversity
- GWAS
- Collection management
- Better informed selection of genetic resources in pre-breeding

# Acknowledgements

nature  
genetics

ARTICLES

<https://doi.org/10.1038/s41588-018-0266-x>

## Genebank genomics highlights the diversity of a global barley collection

Sara G. Milner <sup>1,12</sup>, Matthias Jost <sup>1,9,12</sup>, Shin Taketa<sup>2</sup>, Elena Rey Mazón <sup>1</sup>, Axel Himmelbach <sup>1</sup>, Markus Oppermann <sup>1</sup>, Stephan Weise <sup>1</sup>, Helmut Knüpffer <sup>1</sup>, Martín Basterrechea<sup>1</sup>, Patrick König <sup>1</sup>, Danuta Schüler<sup>1</sup>, Rajiv Sharma <sup>1,10</sup>, Raj K. Pasam <sup>1,11</sup>, Twan Rutten <sup>1</sup>, Ganggang Guo <sup>3</sup>, Dongdong Xu<sup>3</sup>, Jing Zhang<sup>3</sup>, Gerhard Herren<sup>4</sup>, Thomas Müller <sup>4</sup>, Simon G. Krattinger <sup>4,5</sup>, Beat Keller <sup>4</sup>, Yong Jiang <sup>1</sup>, Maria Y. González <sup>1</sup>, Yusheng Zhao <sup>1</sup>, Antje Habekuß<sup>6</sup>, Sandra Färber<sup>6</sup>, Frank Ordon <sup>6</sup>, Matthias Lange <sup>1</sup>, Andreas Börner <sup>1</sup>, Andreas Graner <sup>1</sup>, Jochen C. Reif <sup>1</sup>, Uwe Scholz <sup>1</sup>, Martin Mascher <sup>1,7\*</sup> and Nils Stein <sup>1,8\*</sup>

Funding:

SAW Pakt f. Forschung und Innovation

  
Leibniz  
Association

  
IPK  
GÄTERSLEBEN  
75  
1943–2018





Thanks!