

BARLEY-NAM – Locating exotic genes that control agronomic traits under stress in a wild barley nested association mapping (NAM) population

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ERA-NET for Coordinating
Action in Plant Sciences



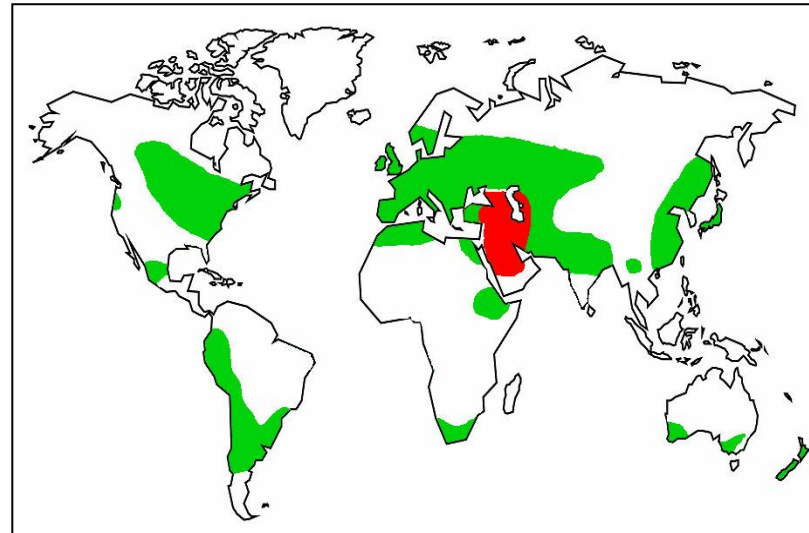
Origin and distribution of barley



Wild barley

Hordeum vulgare
ssp. spontaneum
(Hsp)

Domestication
→
appr. 10,000 years ago



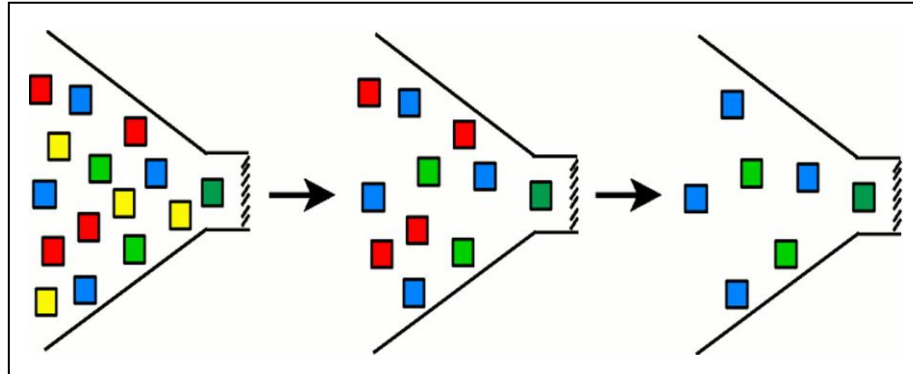
Elite barley

Hordeum vulgare
ssp. vulgare
(Hv)

■ Origin of cultivated barley
■ Distribution of elite barley

FAOSTAT: 132 Mio. tonnes barley ~ 26.4 billion € in 2012

Allele erosion occurred during and after domestication



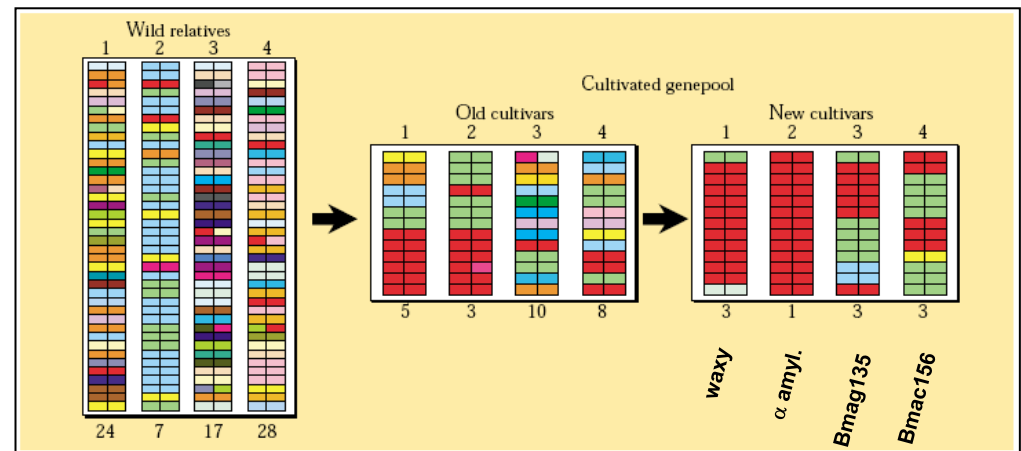
Wild species (10,000 yrs. ago) → Land races (100 yrs. ago) → Modern elite cultivars (today)

Alleles lost after domestication
(Tanksley & McCouch, 1997)

Utilization of wild barley

1. Pathogen resistance
2. Stress tolerance
3. Quality improvement
4. Yield stability

(Ellis et al. 2000)



Breeding level: Wild barley

Land races

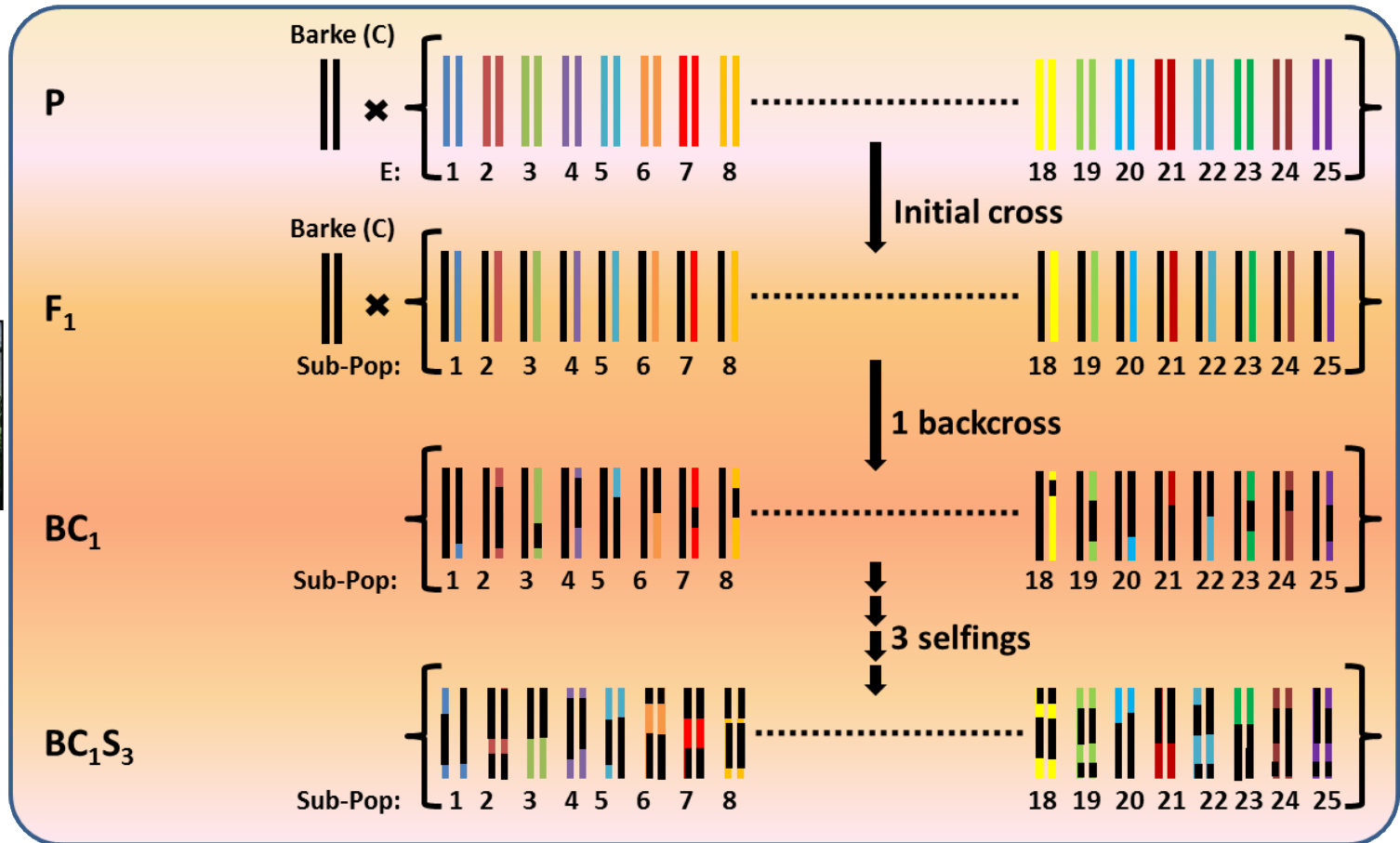
Modern elite barleys

The nested association mapping population HEB-25 – studying allelic variation among 25 wild barley accessions in parallel



2007

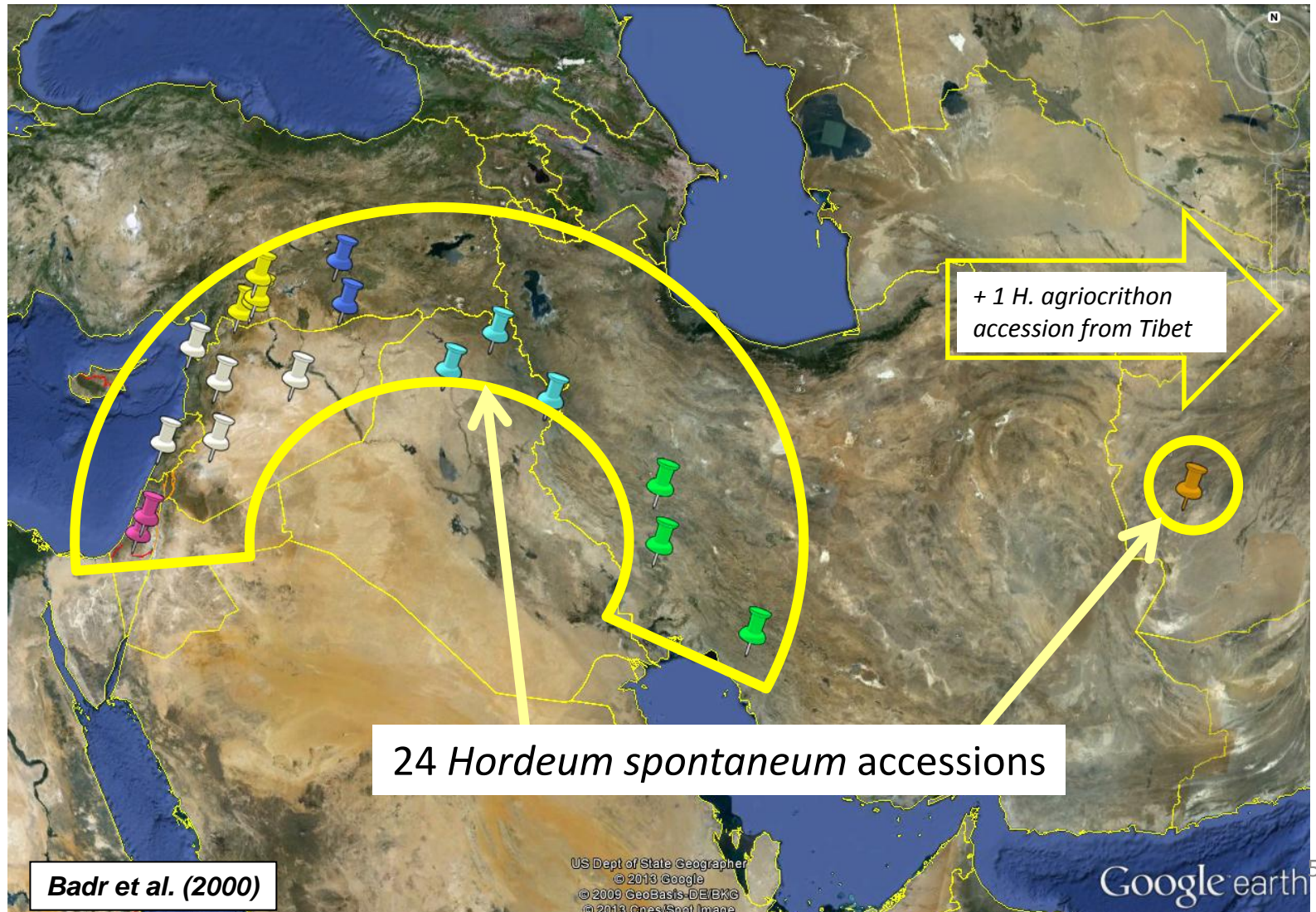
2010



HEB-25 (*Halle exotic barley*) = 25 families with 1,420 NAM lines in BC₁S₃

Expected segregation per locus: 72% : 6% : 22% (Hv:het:Hsp)

Origin of the 25 exotic HEB donors



SNP genotyping of HEB-25

Single nucleotide polymorphism (SNP)

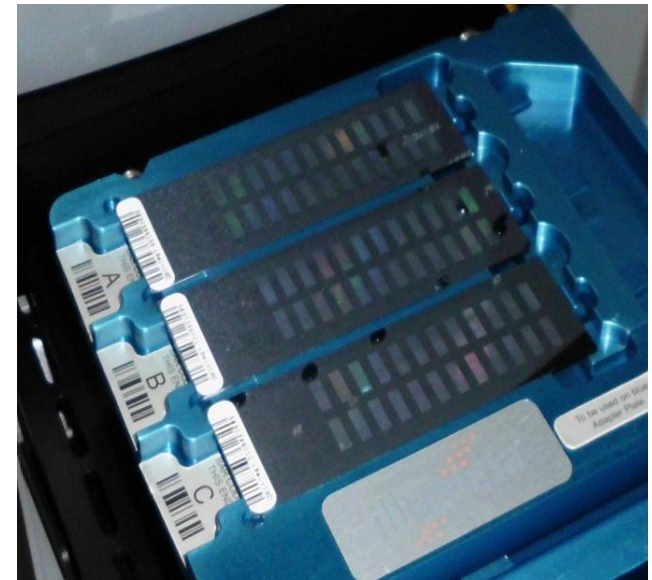


Barke: ...ACGT**A**CAGTCA...

Exote: ...ACGT**G**CAGTCA...

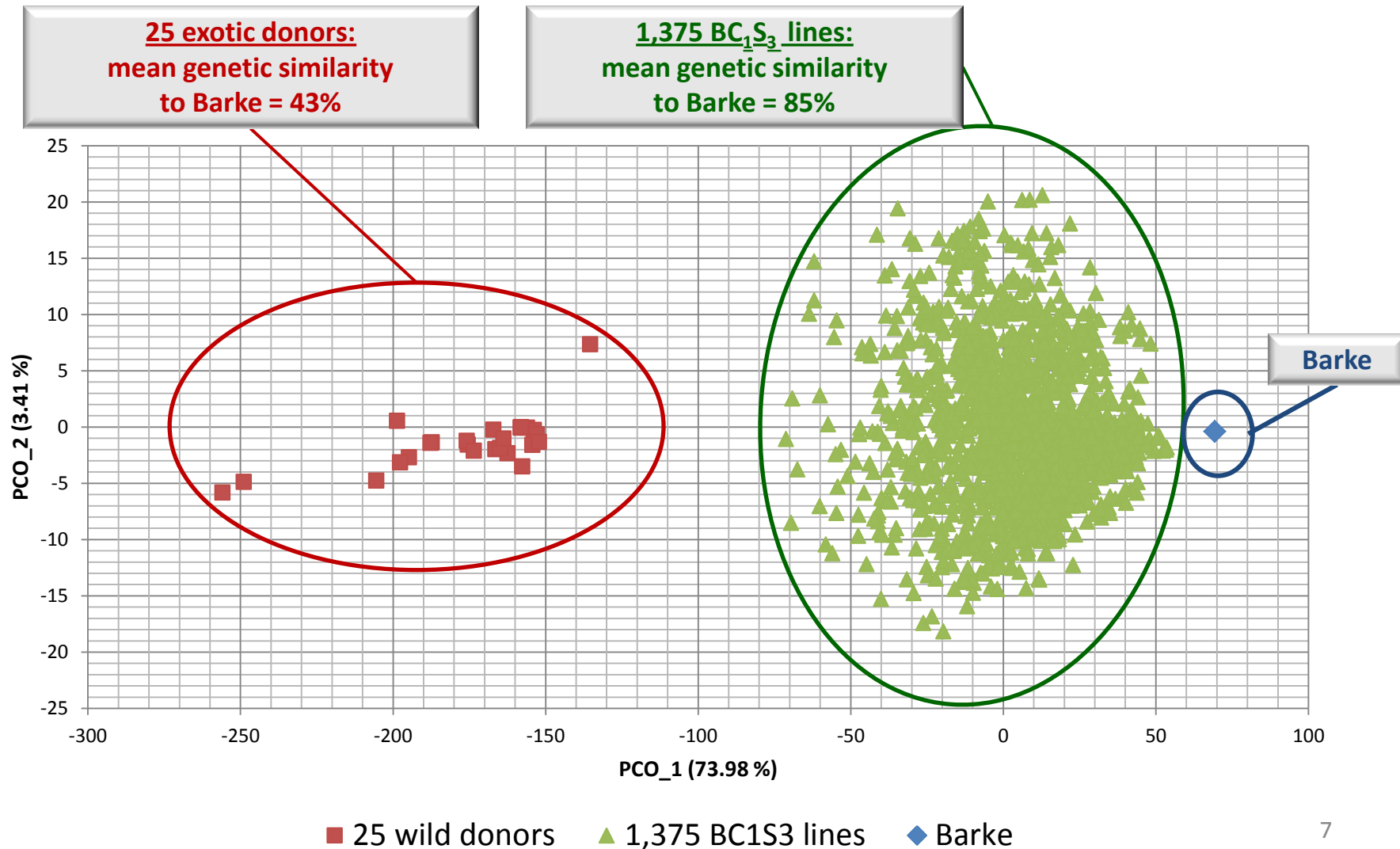


- Infinium iSelect 9k barley chip at **TraitGenetics**, Gatersleben, with 7,864 SNPs
- **5,727 SNPs** are informativ in HEB-25
- Estimation of **genetic similarity (GS)** between lines with DICE
- Calculation of **genetic diversity** with principle component analysis (PCA)

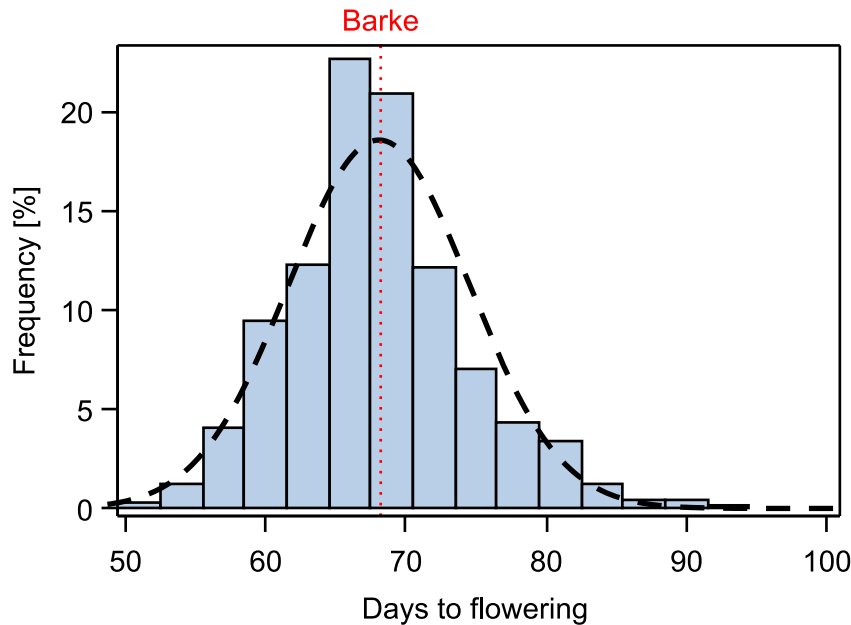


3 chips in Illumina BeadStation 500G

Genetic Diversity among 1,375 HEB lines, 25 HEB donors and Barke



Variation in flowering time



Days until flowering, averaged across 3 years and 5 replications at Julius-Kühnfeld, Halle

HEB-F06-113



Barke



HEB-F12-130



GWAS mapping of 8 QTLs/candidate genes, controlling flowering time

QTL analysis: Step-wise multiple regression,
with selection of co-factors (X)

Model: $Y = \beta_0 + \alpha \text{ SNP} + \sum(\beta_i X_i) + \varepsilon$

X axis:

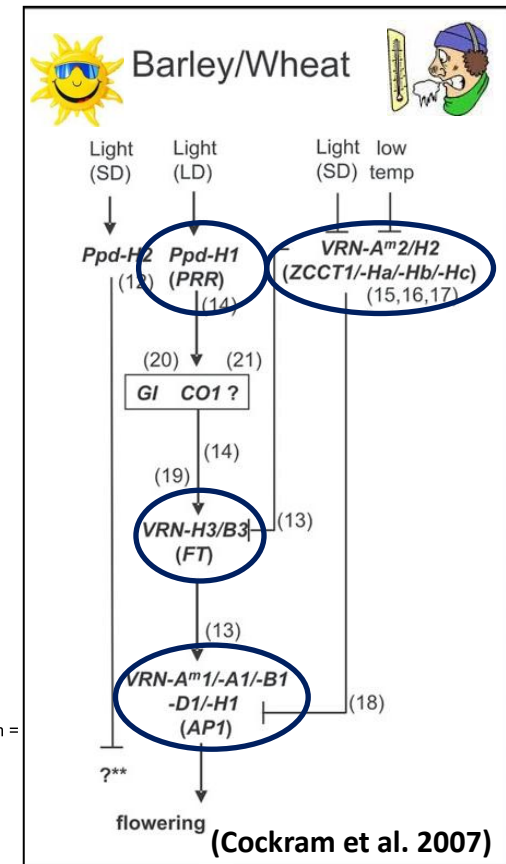
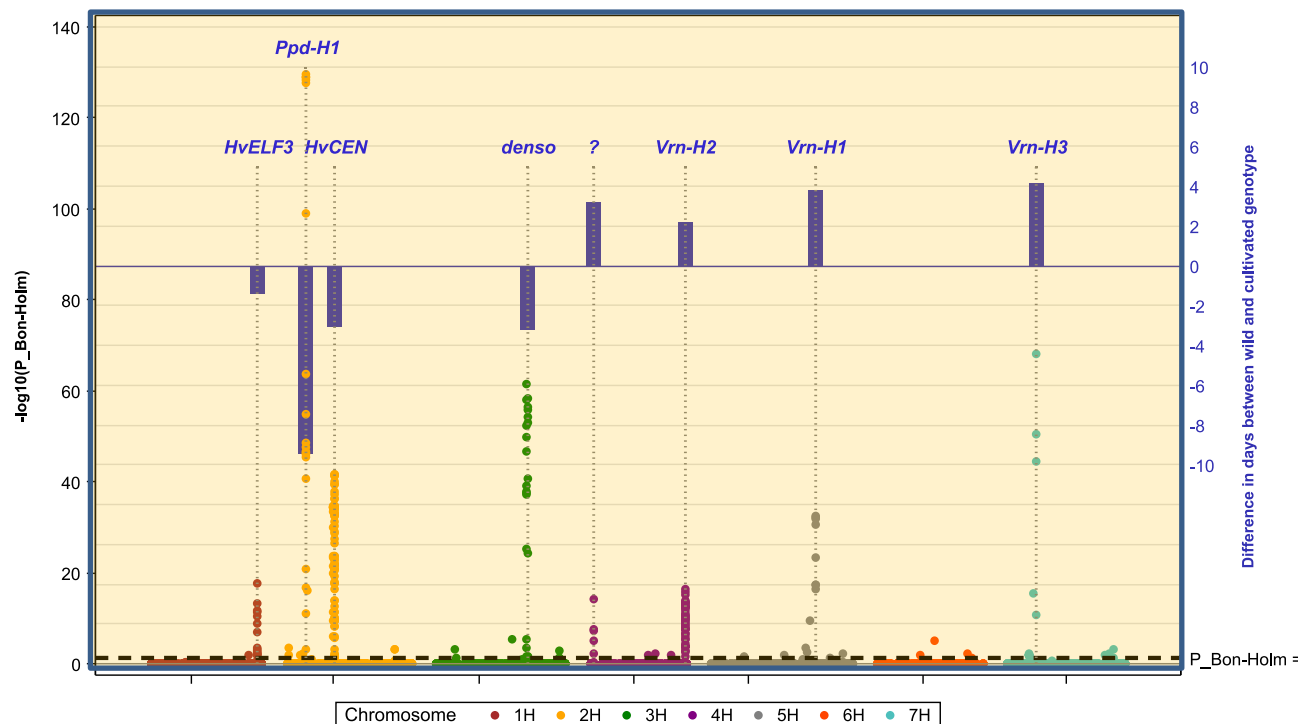
SNPs on 7 barley chromosomes

Colored dots:

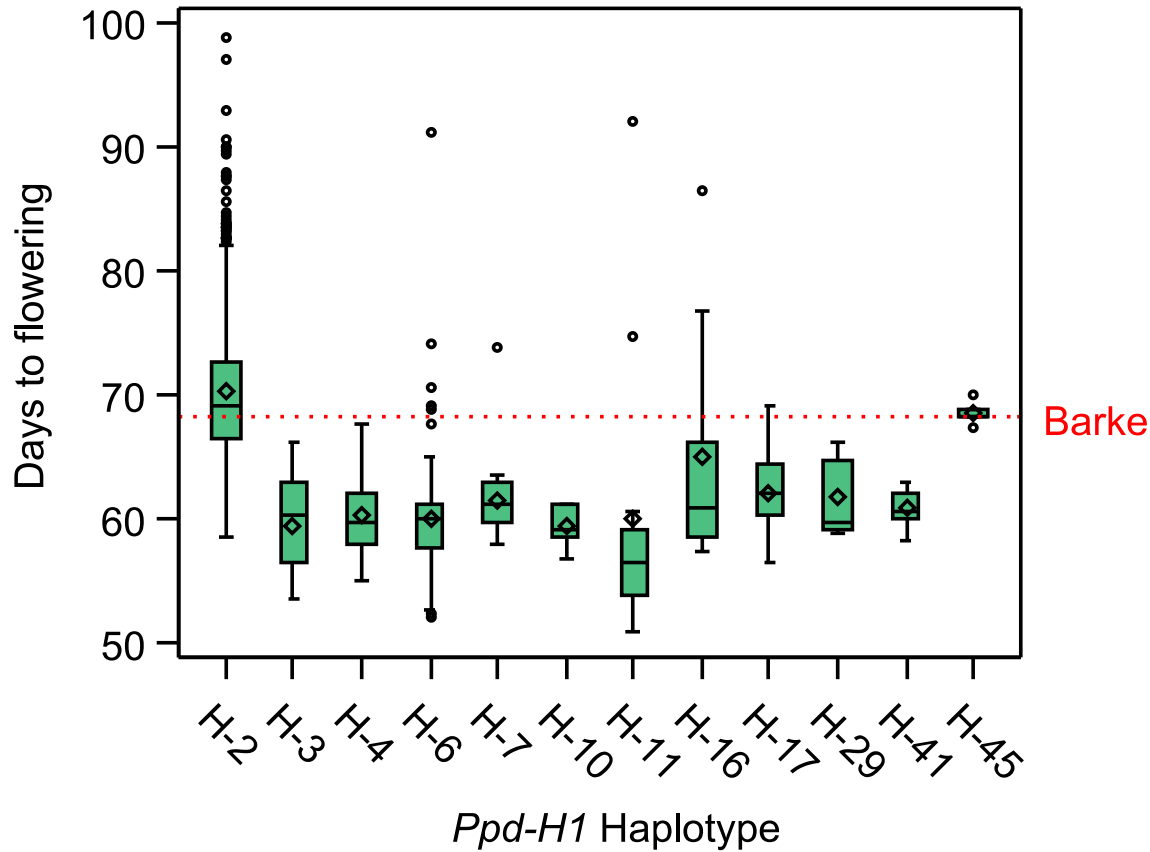
P values of SNPs (scale on left Y axis)

Blue columns:

Gene effects (scale on right Y axis)



Allelic variation of flowering time at the *Ppd-H1* locus



The BARLEY NAM project

EU ERA-CAPS:
BARLEY-NAM

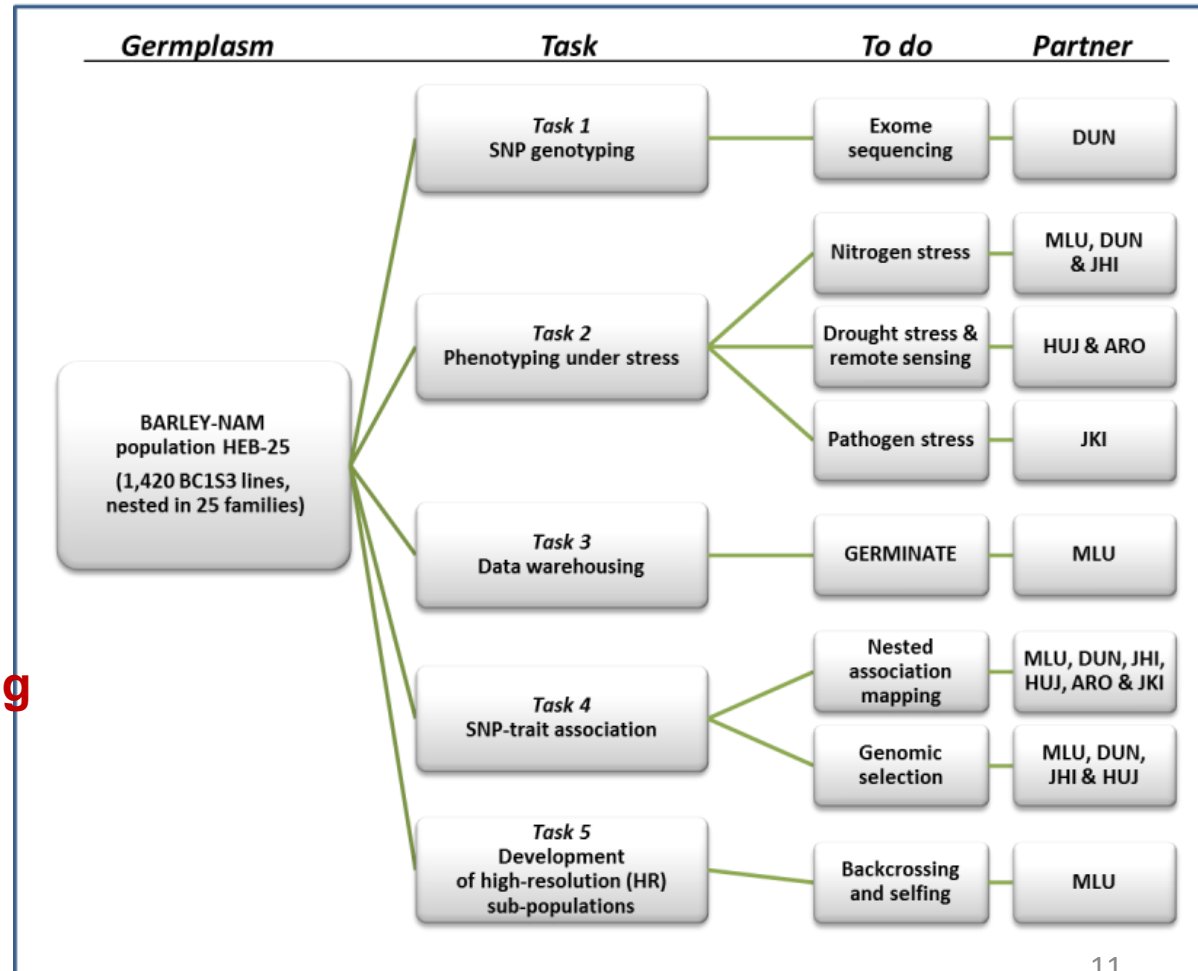
Partners: HAL, DUN, JHI,
HUJ, ARO, JKI

► **Testing HEB-25 under stress**

- N deficiency,
- drought and
- pathogen resistance

► **Exome capture sequencing of 1,420 HEB lines**

<http://www.eraCaps.org/>



Partners

- **Pillen, Klaus**
Martin-Luther-University Halle (MLU), Halle, **Germany**
- **Flavell, Andy**
University of Dundee (DUN), Dundee, **UK**
- **Thomas, William**
James Hutton Institute (JHI), Invergowrie, **UK**
- **Fridman, Eyal**
The Hebrew University of Jerusalem (HUJ), Rehovot, **Israel**
- **Bonfil, David**
Agricultural Research Organization (ARO), Gilat, **Israel**
- **Ordon, Frank**
Julius Kühn-Institute (JKI), Federal Research Centre for Cultivated Plants, Quedlinburg, **Germany**

BARLEY NAM Goals

1. Applying new breeding approaches including new population types

- ▶ First nested association mapping population in barley.

2. Characterization, evaluation and use of wild barley biodiversity

- ▶ Testing wild barley genes to locate new favourable alleles for trait complexes life history, yield, grain quality and pathogen resistance.

3. Development of genetic and genomic (pre-) breeding tools

- ▶ NAM population strategy, exome capture sequencing, mixed model association mapping and genomic selection will be applied.

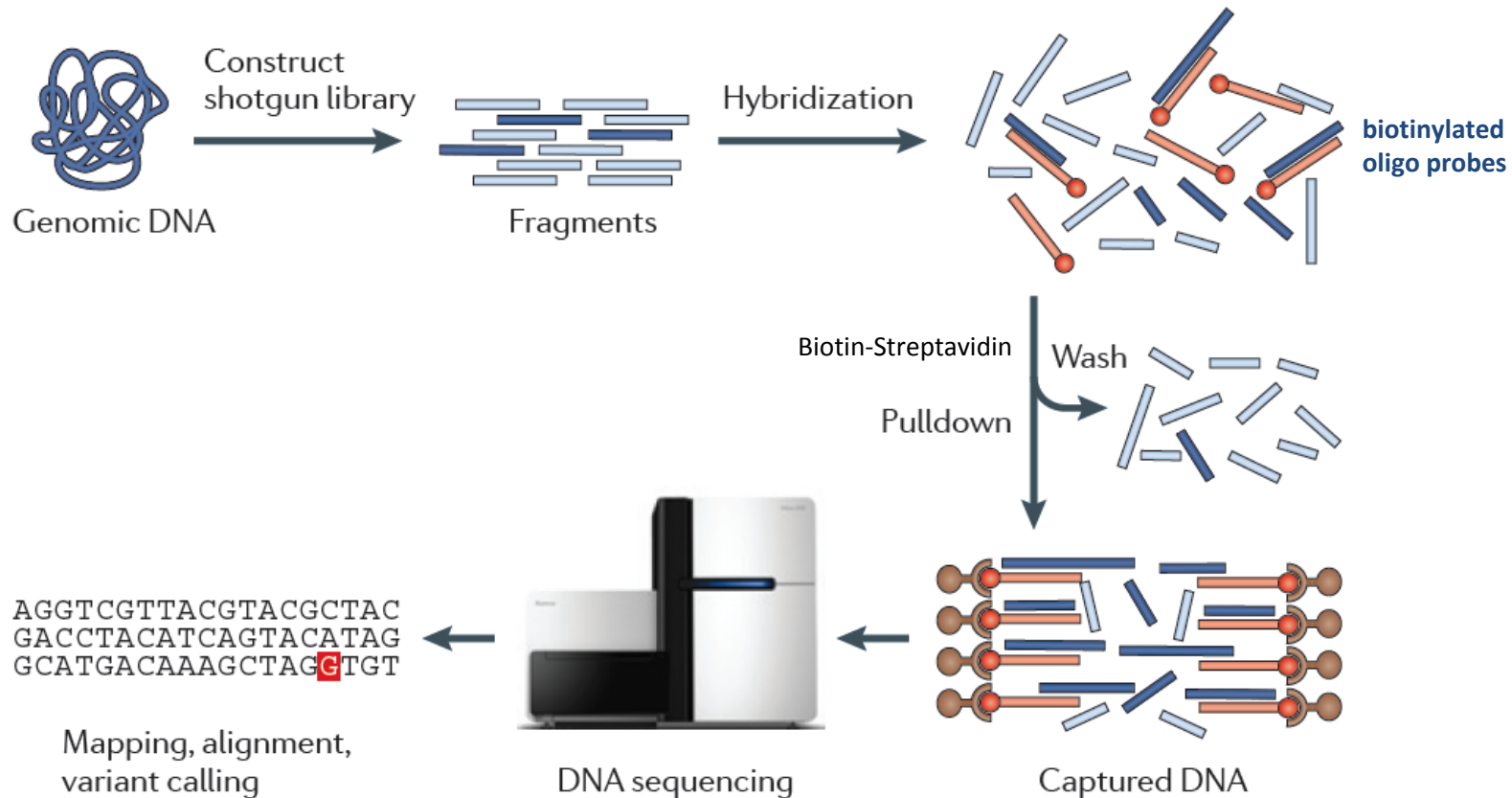
4. Biofortification of crop plants

- ▶ Improving grain quality by increasing nutrient contents (e.g. iron, or zinc)

5. Development of remote sensing tools for phenotyping

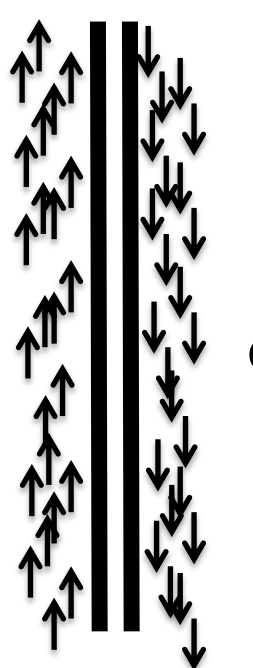
- ▶ Using state-of-the-art sensors to map and use new exotic alleles that improve stress tolerance.

Exome Capture Sequencing at University of Dundee



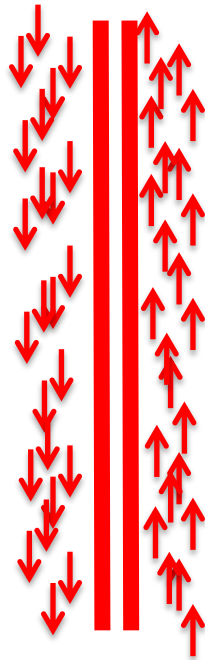
Exome Capture Sequencing of 1,420 HEB lines at University of Dundee

1. Sequence the parental exomes at **high coverage**
2. Sequence exoms of HEB lines at **low coverage**
3. Aligning the exome sequences against the two parental exomes will provide sufficient sequence information to define **recombinations** at roughly **single gene level**

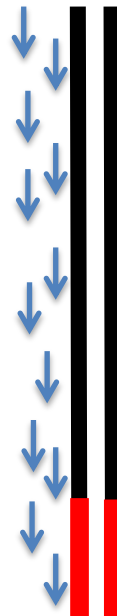


Cultivar
chromosome

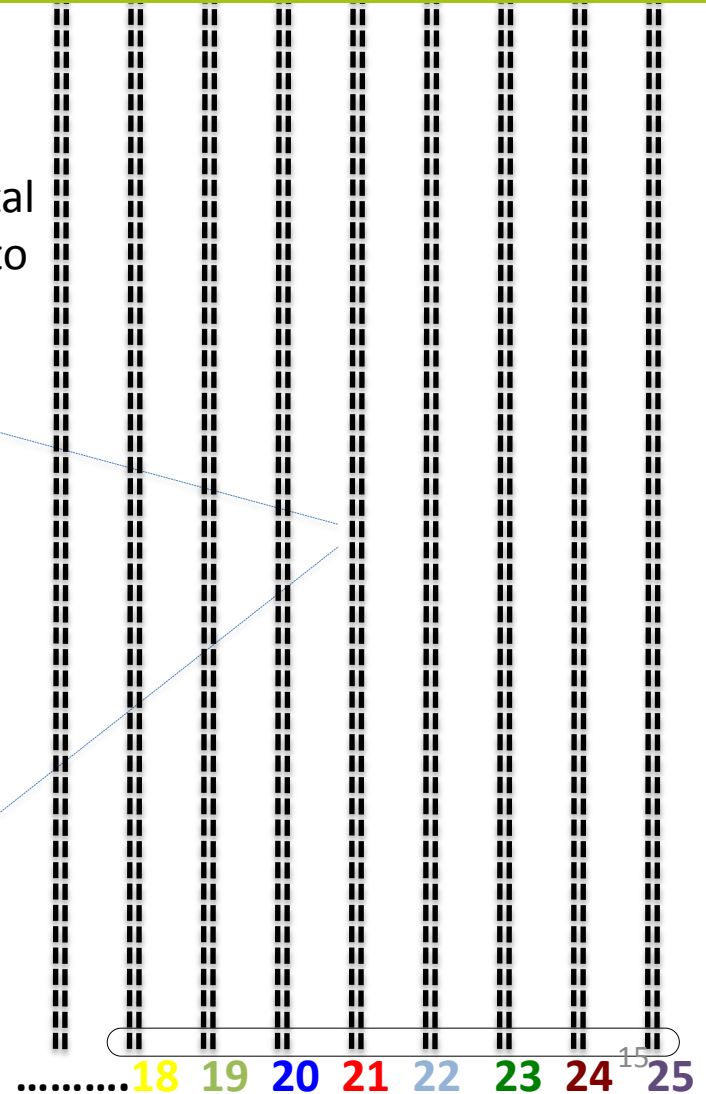
&



H. spontaneum
chromosome



HEB line
chromosome



Studying HEB-25 under abiotic stress

Testing HEB-25 during 2014 and 2015 at

- Dundee & Halle (N deficiency)
- Rehovot & Gilat (drought stress)

Traits

- Life history
- Yield
- Nutrient content
- Stress response

Nested Association Mapping

- Locate trait-improving exotic QTLs
with exome sequences down to single genes

Studying pathogen resistance at JKI, Quedlinburg

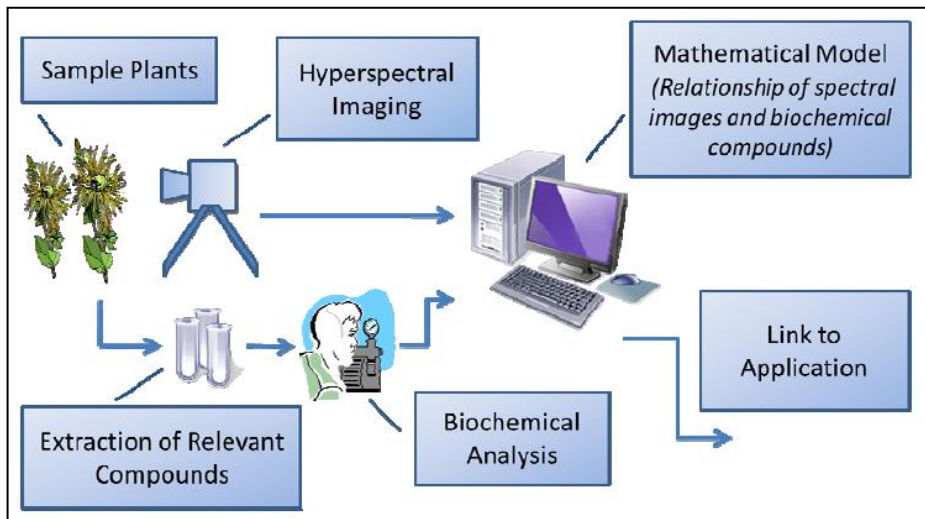
- Testing HEB-25 for 3 fungal pathogens responsible for severe yield losses of up to 50%

- **Stripe rust** (*Puccinia striiformis*)
- **Leaf rust** (*Puccinia hordei*)
- **Net blotch** (*Pyrenophora teres*)



- Apply nested association mapping (NAM) to identify and utilize exotic resistance genes

Two additional studies with HEB-25



(1) BMBF-IPAS: BARLEY-BIODIVERSITY
Partners: HAL, IFF, IPK, BREUN

► None-invasive **hyperspectral imaging** of HEB-25 lines to measure **growth and nutrient content**



(2) DFG-SPP1530: Flowering regulation
Partners: MLU, IPK, DUN, JHI, ICARDA, KAUST, ADELAIDE

► World-wide testing of **HEB-25 lines** under **abiotic stress** (N deficiency, drought, heat, salt)

Martin-Luther-Universität Halle, Professur für Pflanzenzüchtung

- Klaus Pillen
- Erika Schumann
- Jeannette Lex



- Andreas Maurer
- Vera Draba
- Stefanie Pencs
- Wiebke Weißgerber
- Doreen Neumeister
- Pavlina Nedelkou
- Sebastian Förster
- Nora Honsdorf
- Behnaz Soleimani
- Astrid Hoffmann
- Florian Schnaithmann



Finacial Support

- EU (ERA-CAPS)
- EU (ERA-NET PG)
- DFG (SPP 1530)
- IZN, Halle
- BMBF (PLANT 2030)

- F. Ordon & D. Kopahnke

- P. Schweizer, B. Kilian,
N. Stein, A. Graner, H.P. Mock
J. Kumlehn & G. Hensel

- J. Léon & A. Naz

- G. Schweizer & B. Büttner

- A. Flavell, W.T. Thomas,
J. Russell & R. Waugh

- E. Fridman

- D. Bonfil

- T. March, J. Eglinton,
G. Fincher & R. Burton

- M. Tester & B. Berger

- M. von Korff & I. Schmalenbach

- L. Cattivelli & A. Tondelli

- A. Schulman

- S. Rasmussen

- M. Ganal

