

BARLEY-NAM – Locating exotic genes that control agronomic traits under stress in a wild barley Nested Association Mapping (NAM) population

ERA-CAPS Meeting, May 7-8 2015, Lisbon



ERA-NET for Coordinating
Action in Plant Sciences

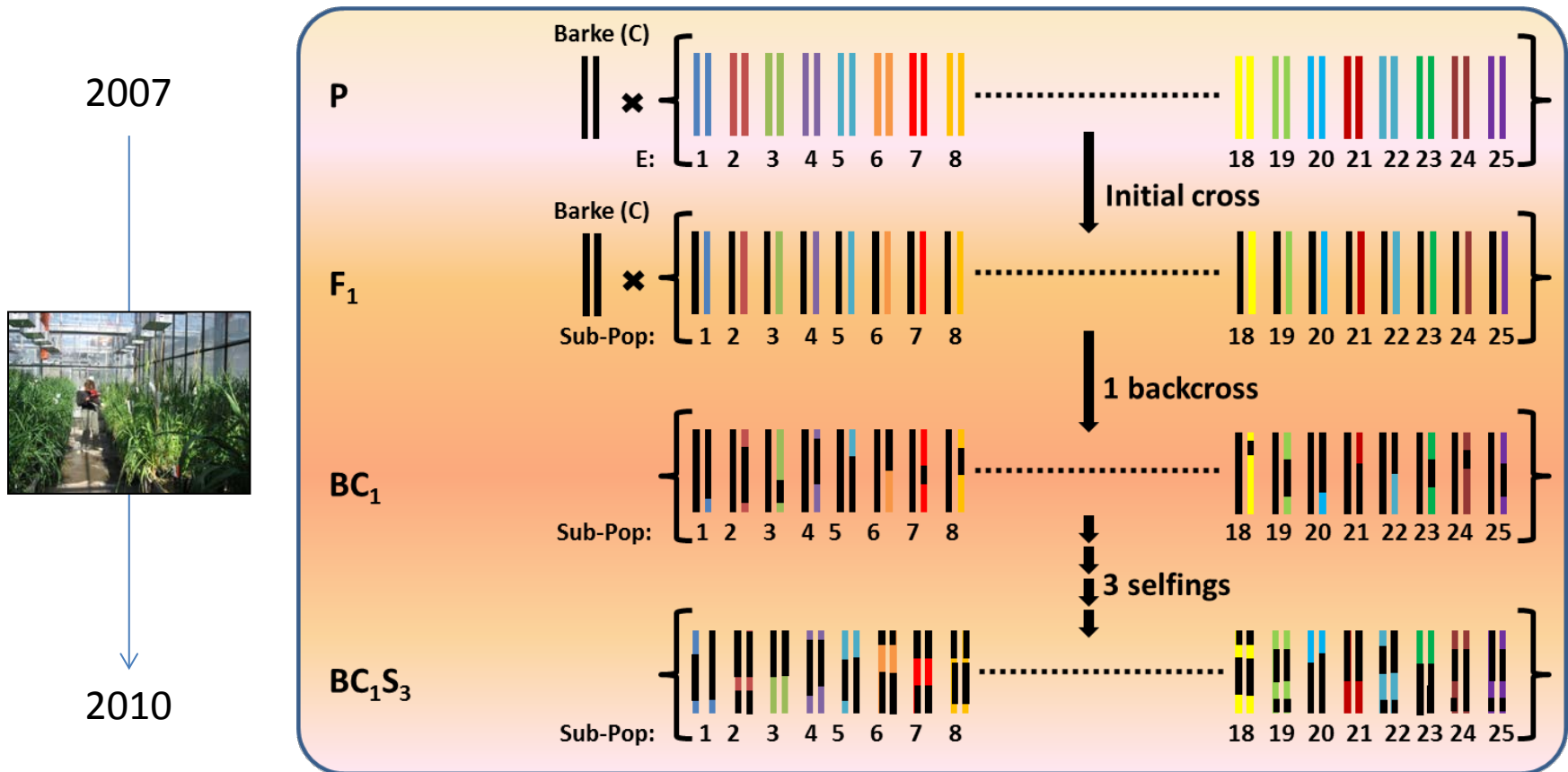


Partners

- **Klaus Pillen, Andreas Maurer, Paul Herzig**
MLU, Martin Luther University Halle, Halle, **Germany**
- **Andy Flavell, Rajiv Sharma, Fulvia Draicchio**
DUN, University of Dundee, Dundee, **UK**
- **Bill Thomas, Hazel Bull**
JHI, James Hutton Institute, Invergowrie, **UK**
- **Eyal Fridman, David Bonfil, Efrat Laiba**
ARO, Agricultural Research Organization, Gilat, **Israel**
- **Frank Ordon, Doris Kopahnke, Thomas Vatter**
JKI, Julius Kühn Institute, Federal Research Centre for Cultivated Plants, Quedlinburg, **Germany**



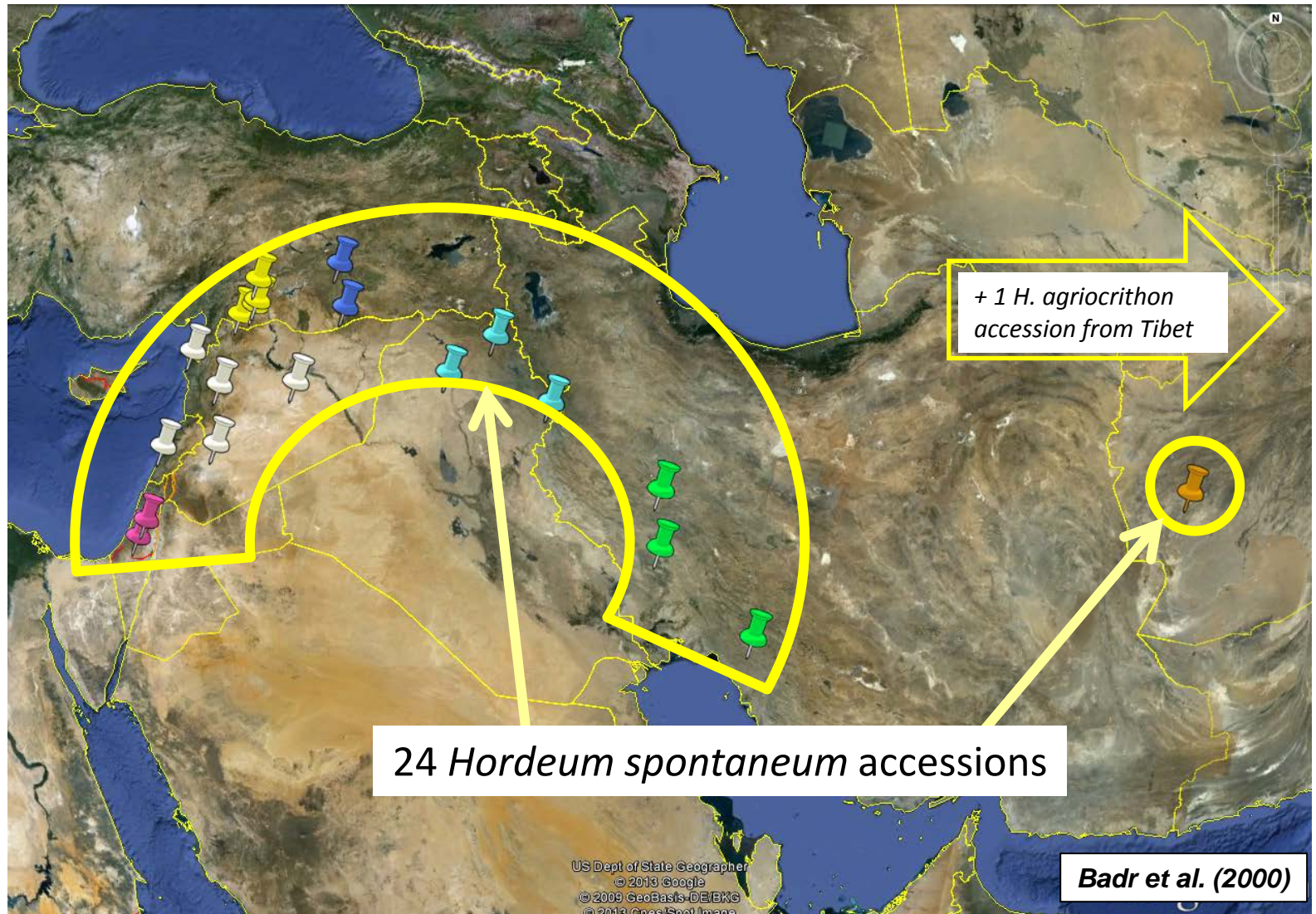
The Nested Association Mapping population HEB-25 – studying allelic variation among 25 wild barley lines in parallel



HEB-25 (*Halle exotic barley*) = 25 families of roughly 60 lines each = ~ 1,420 lines

Each family derived from a cross between cultivar Barke and a different wild barley parent

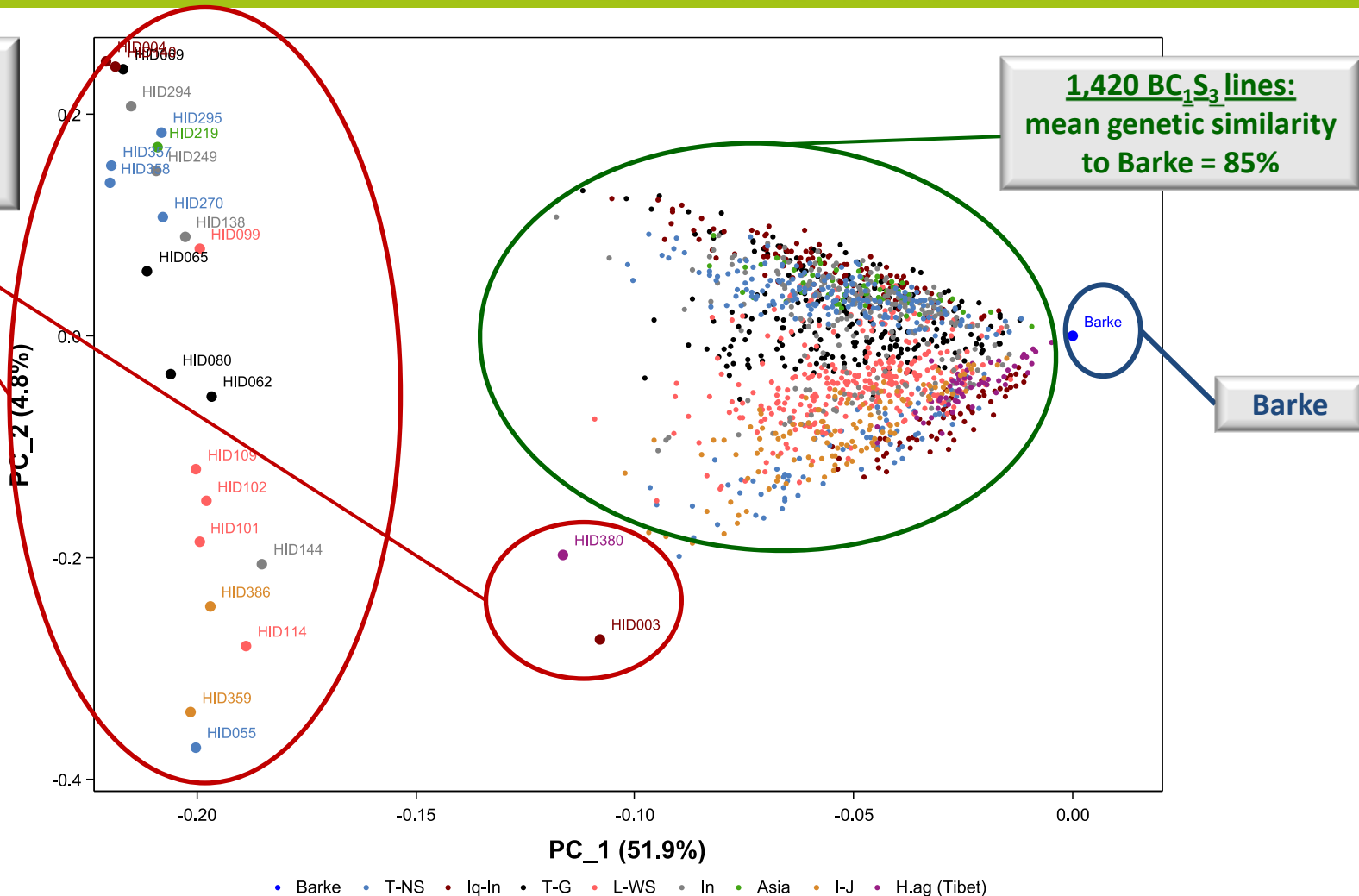
Origin of the 25 wild HEB donors



Genetic Diversity among HEB lines and their parental wild and Barke parents

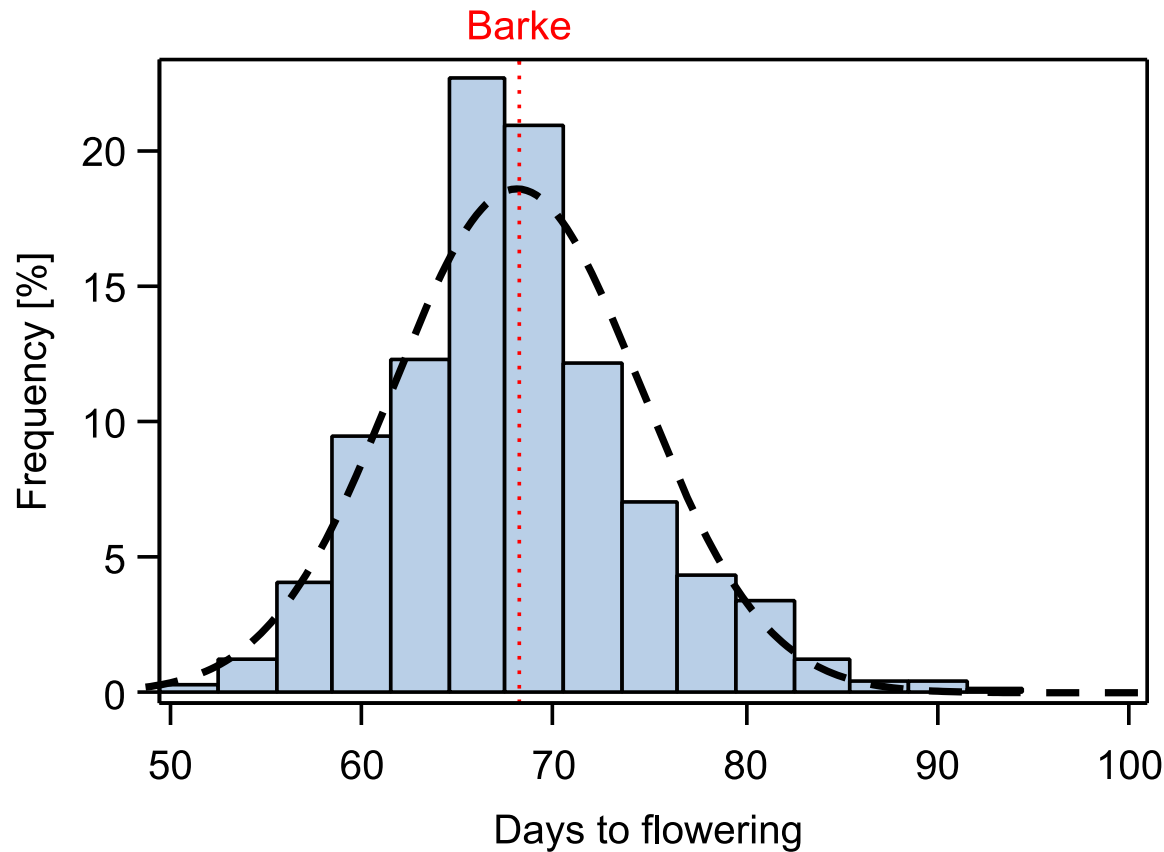
25 exotic donors:
mean genetic
similarity
to Barke = 43%

1,420 BC₁S₃ lines:
mean genetic similarity
to Barke = 85%



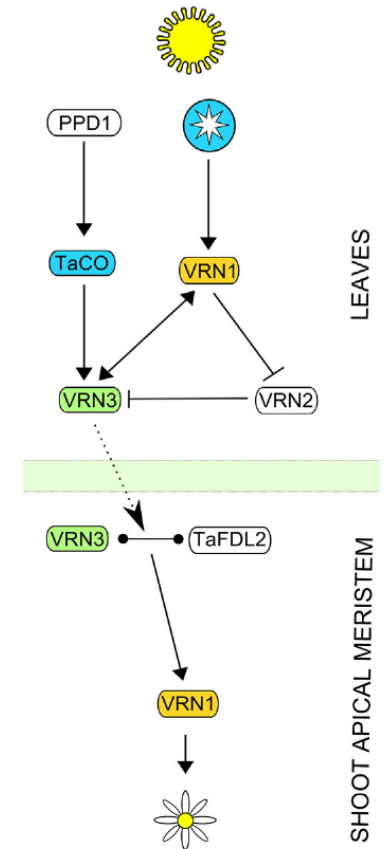
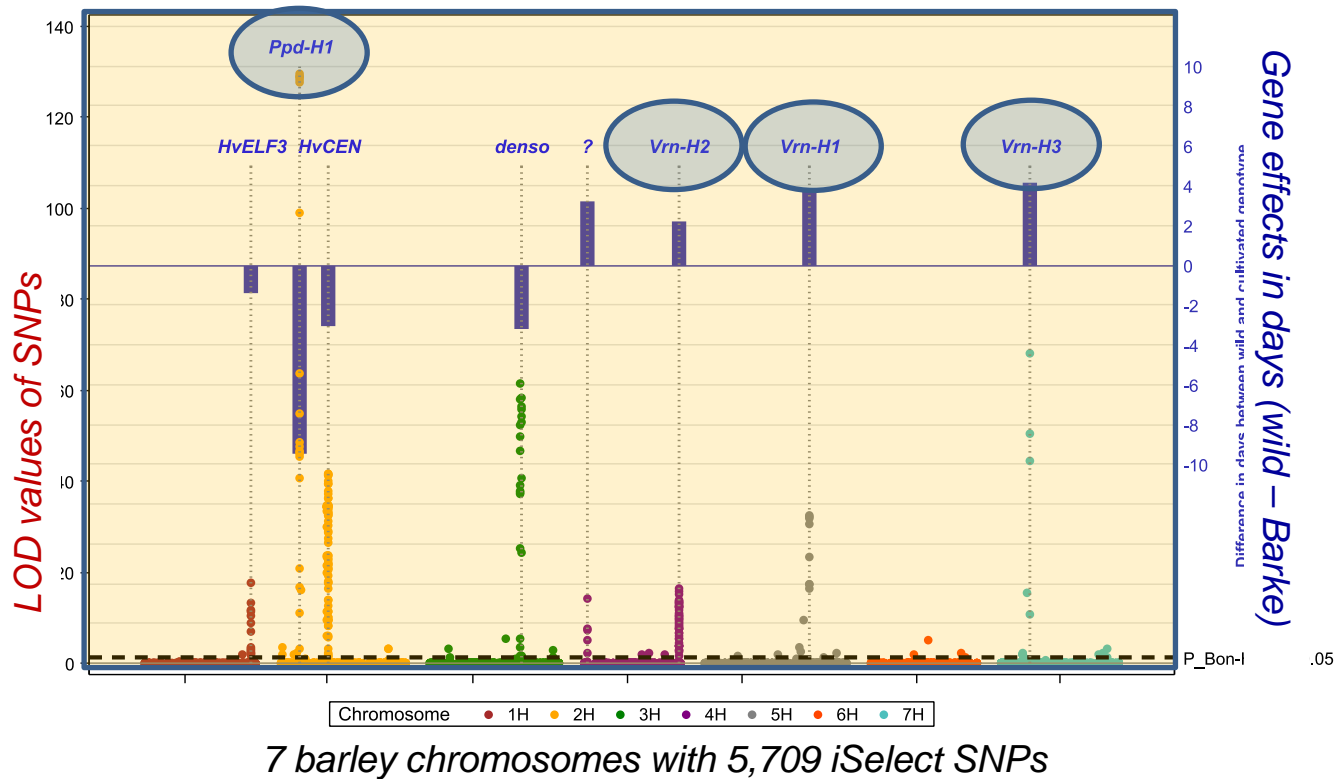
Data based on 5,709 iSelect SNPs

Variation in flowering time in HEB-25



*Data averaged across
3 years and 5 field trial
replications*

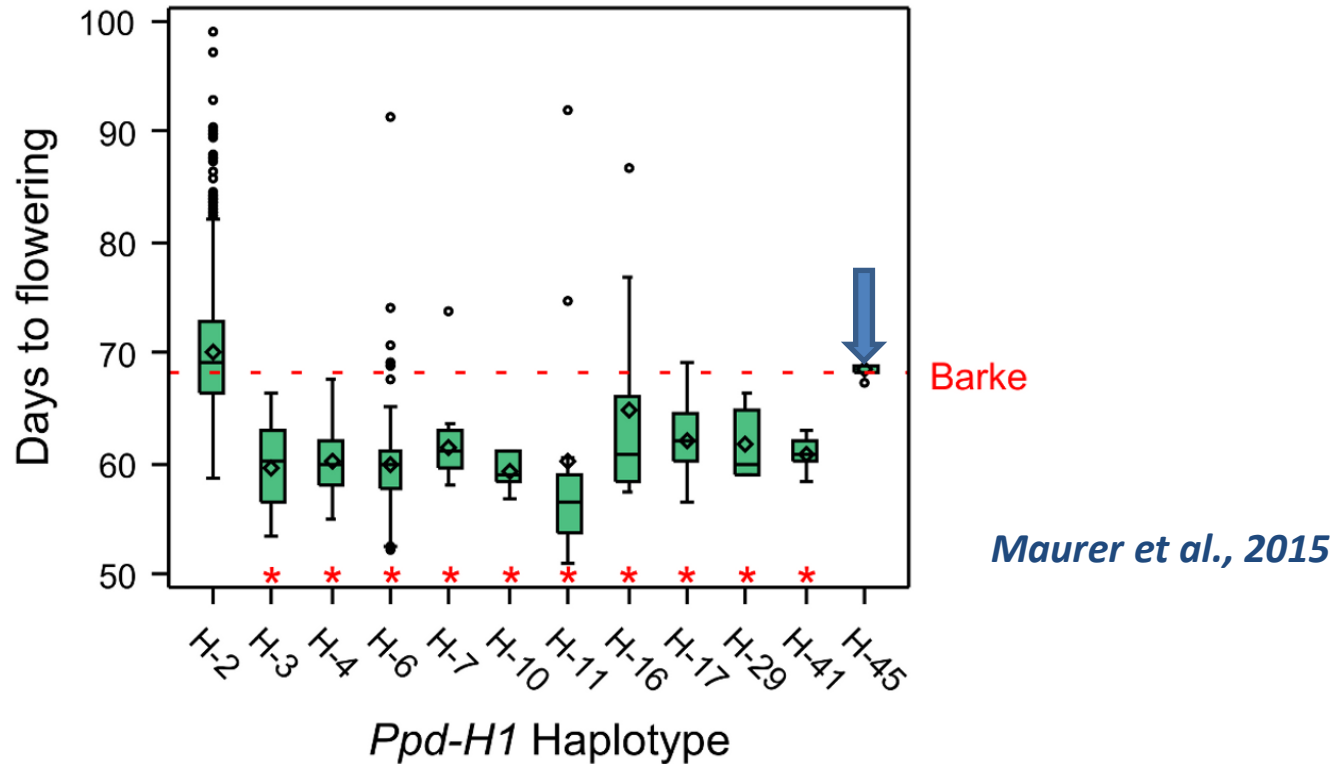
GWAS for flowering time in HEB-25



QTL analysis: Multiple linear regression with step-wise selection of co-factors (X)

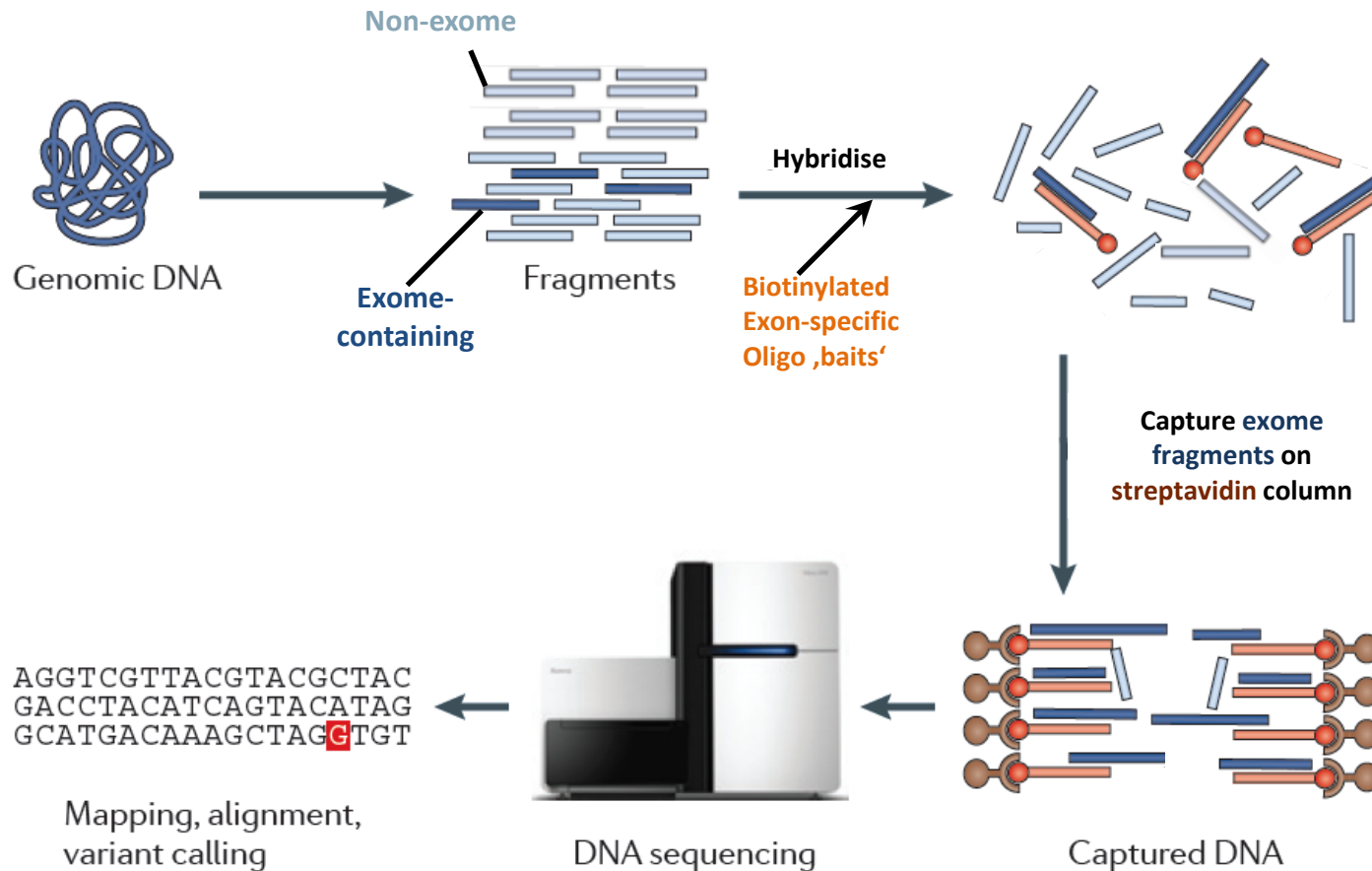
Model: $Y = \beta_0 + \text{HEB family} + \alpha \text{ SNP} + \sum (\beta_i X_i) + \varepsilon$

Allelic variation at *Ppd-H1* in HEB-25 - Effect on flowering time



→ Optimizing QTL definition and estimation of wild effect through definition of haplotypes

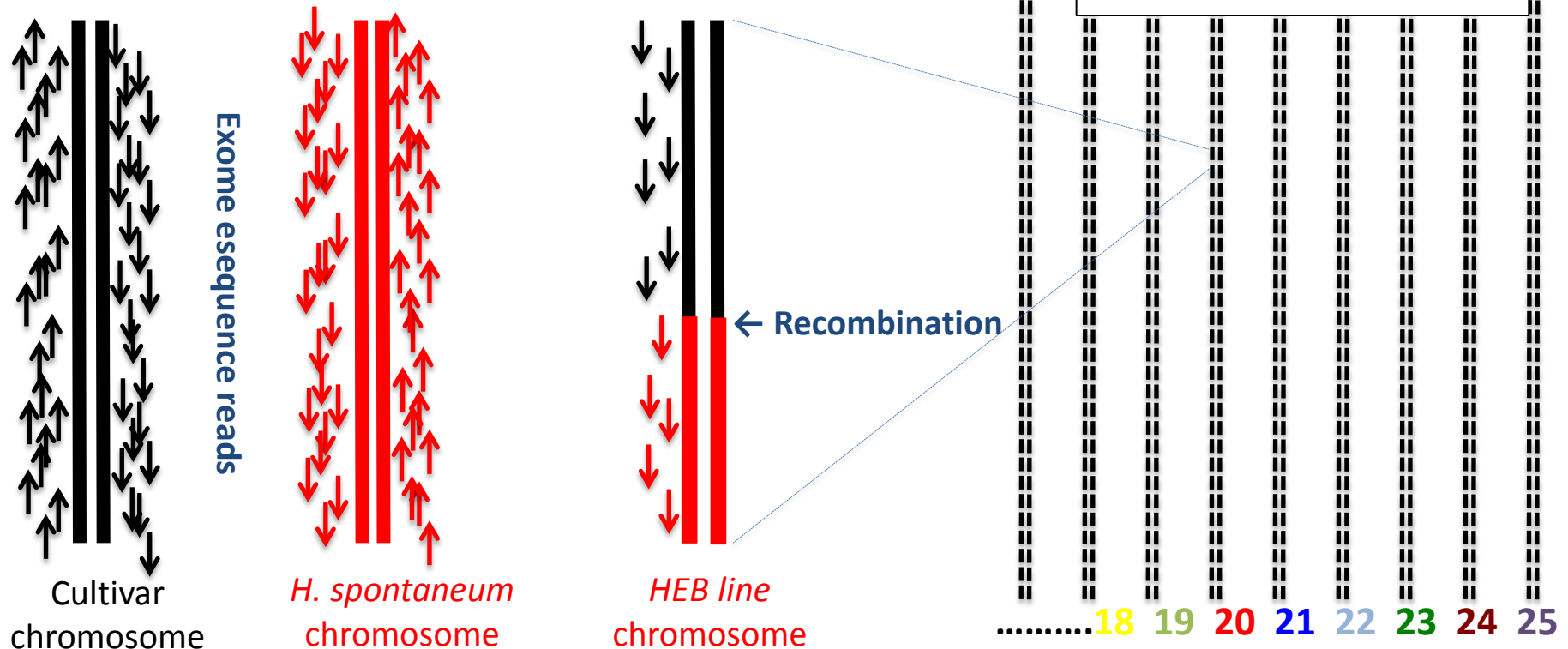
Task #1: Genotyping the HEB-25 population by exome Capture Sequencing (DUN)



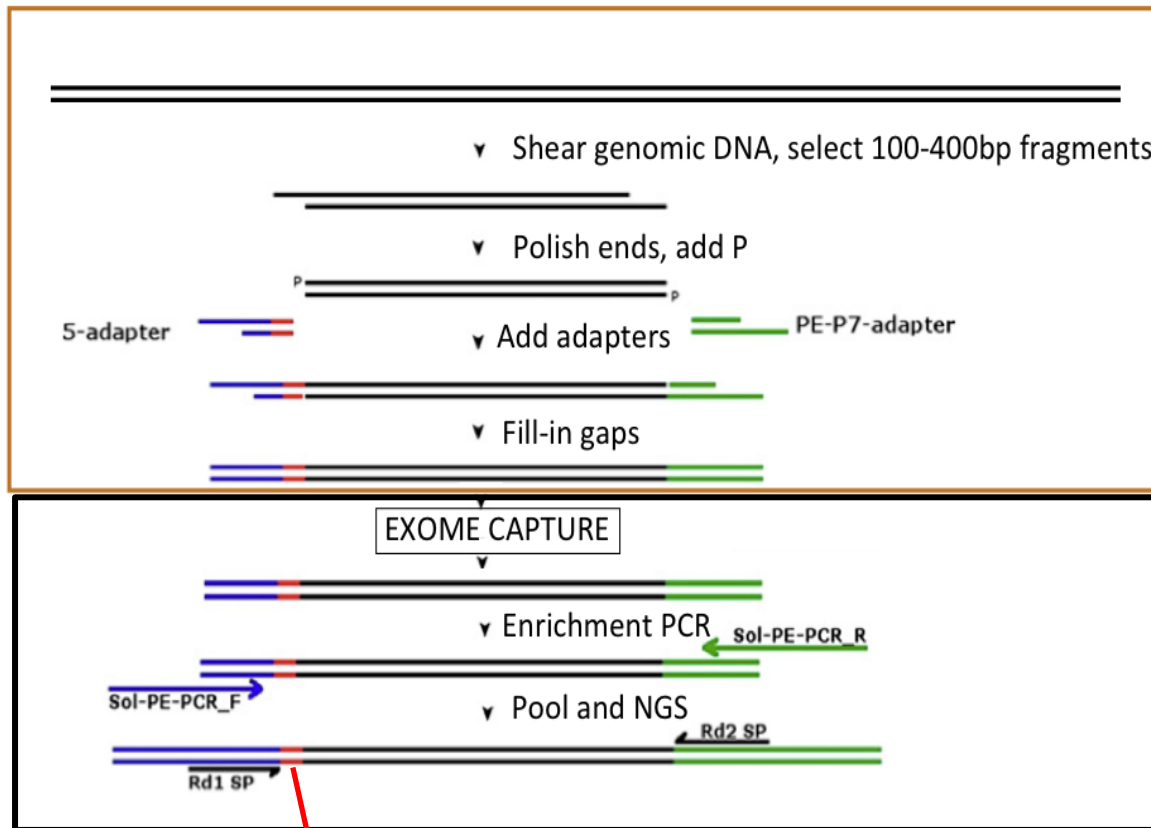
**Sequencing only the exons means you sequence
~ all the genes but only 1% of the genome**

Task #1: Genotyping the HEB-25 population by exome Capture Sequencing (DUN)

1. Sequence parental exomes at high coverage (20x)
2. Sequence exomes of HEB lines at low coverage (4x)
3. Align exome sequences of each HEB line against its 2 parental lines to define the recombination breakpoints at ~ gene level



Task #1: Genotyping the HEB-25 population by exome Capture Sequencing (DUN)



**Illumina library
construction
(X 1400!)**

**Exome capture-NGS*
(@ TGAC, Norwich)**

* 84 Exome captures of 16 samples each -> 28 Illumina sequencing lanes @ 48 samples/lane

Task #1: Genotyping the HEB-25 population by exome Capture Sequencing (DUN)

Progress

DNAs have been prepared and sheared into ~400bp fragments for all HEB-25 lines

A high-throughput Illumina library protocol has been developed and optimised*

*** A commercial kit would cost more than we can afford!**

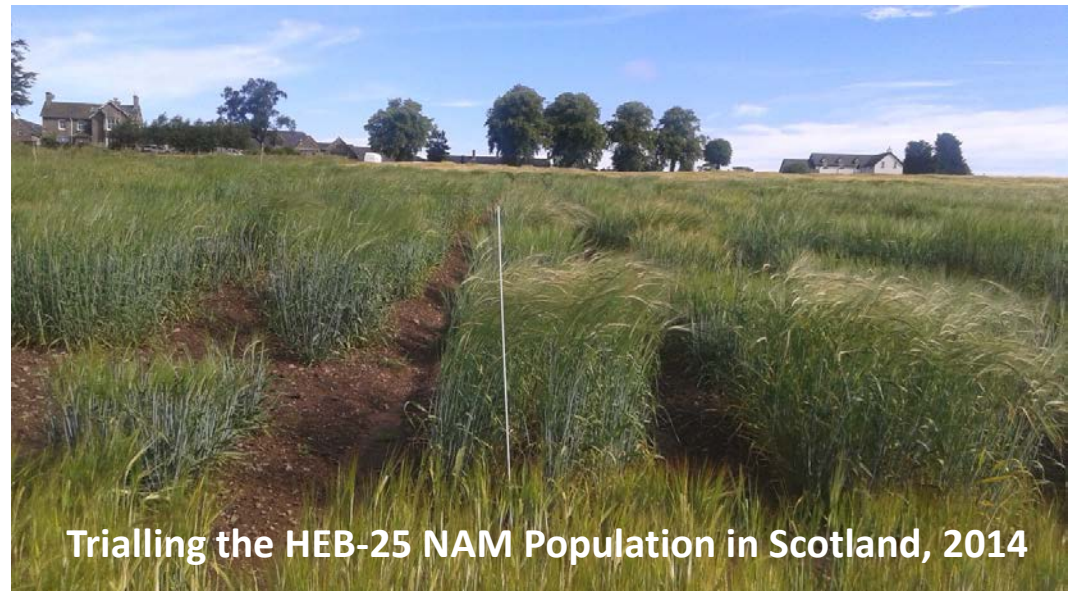
Task #2: Studying HEB-25 under abiotic stress

Field trialling HEB-25 (2014 and 2015)

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

Traits scored

- Life history
- Yield & its components
- Nutrient content
- Stress response



Task #2: Studying pathogen resistance (JKI Quedlinburg)

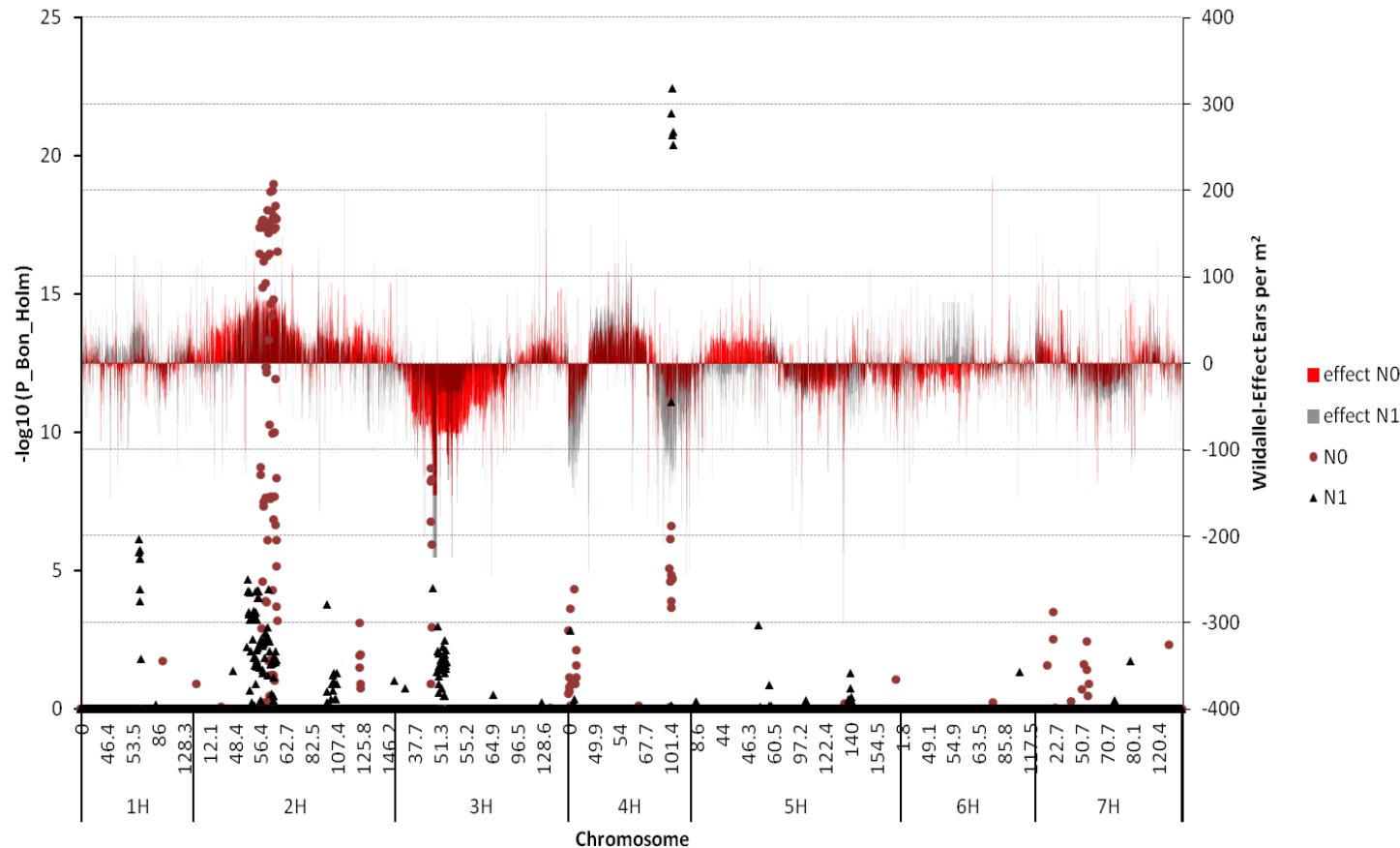
- Testing HEB-25 vs 3 fungal pathogens responsible for severe yield loss

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



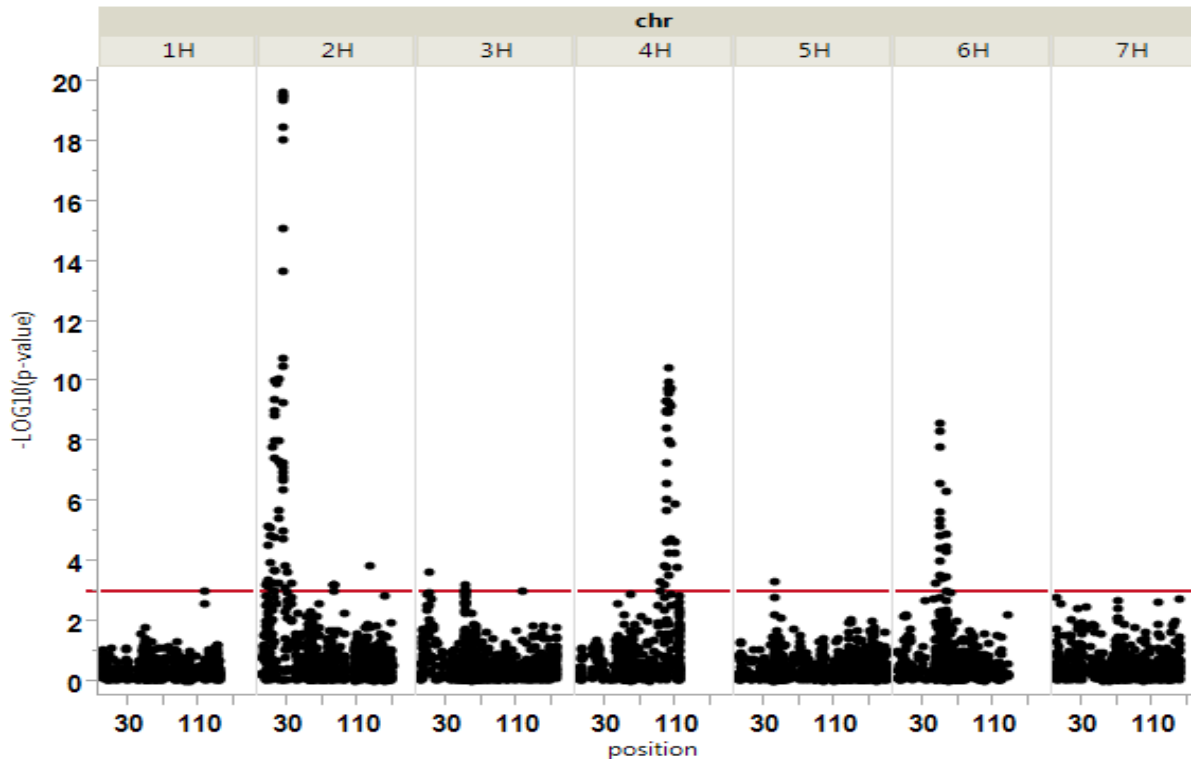
- Nested association mapping (NAM) to identify exotic resistance genes

Task #4: SNP-trait association



Ears per square meter; low vs normal Nitrogen

Task #4: SNP-trait association

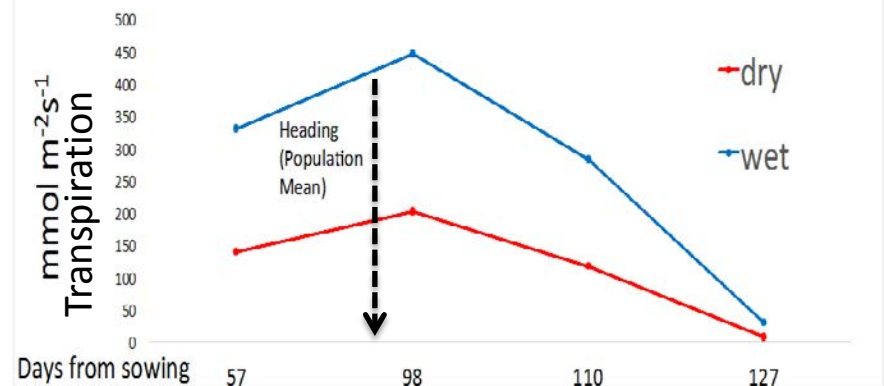


Net blotch
resistance,

Task #3: Studying HEB 25 under water deficit

- Testing HEB-25 under optimal and chronic water deficit

- Apply nested association mapping (NAM) to identify and utilize exotic alleles mediating drought-resistance
- Compare between association for trait per-se to its index
 $1 - (\text{TRAIT}^{\text{wet}} / \text{TRAIT}^{\text{dry}})$
- Incorporate remote sensing in field to estimate drought response

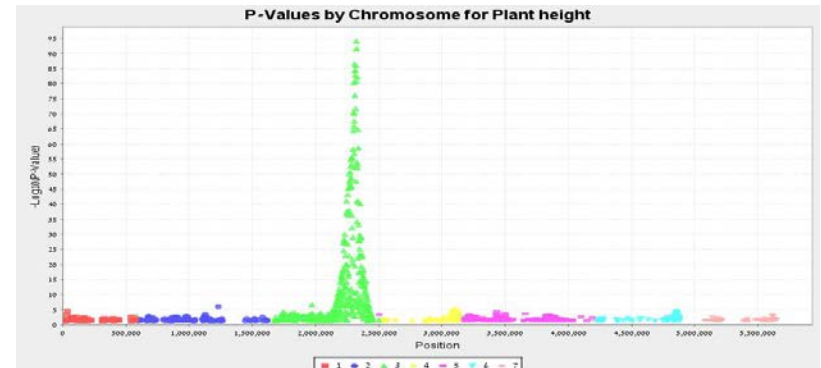
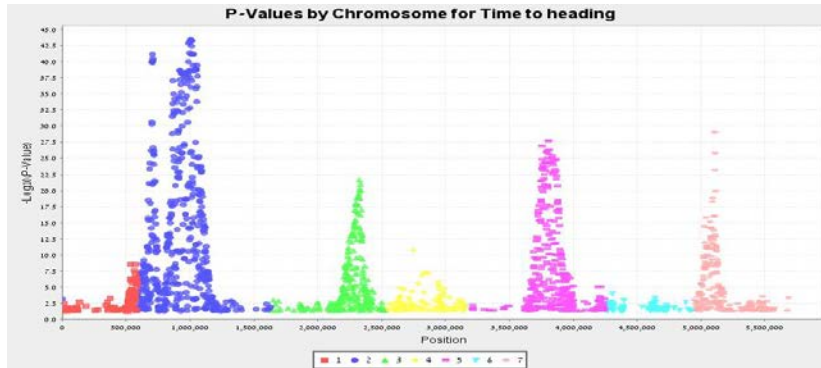


Task #3: Studying HEB 25 under water deficit

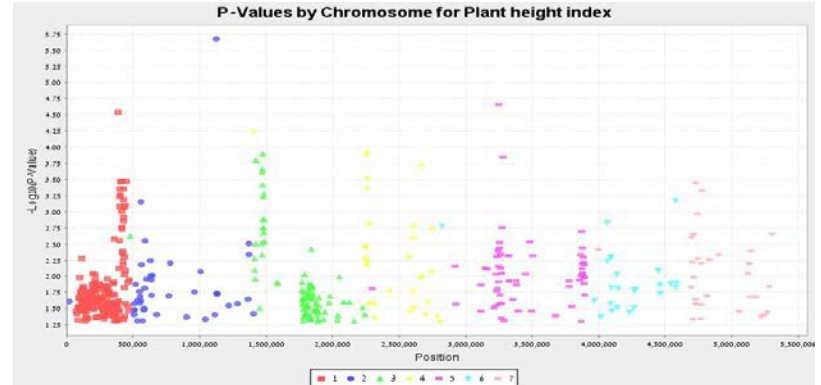
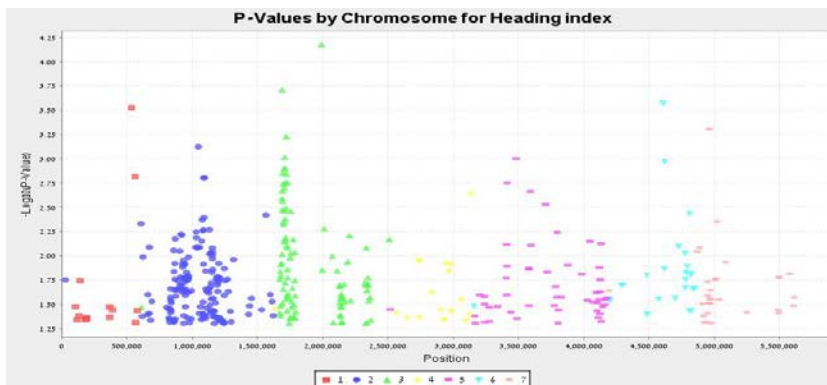
Trait per-se

Days to heading

Height



Trait Index



>>> Genetic architecture not necessarily overlapping, i.e. novel alleles for drought resistance?



Klaus Pillen
Andreas Maurer
Paul Herzig
Vera Draba



Frank Ordon
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Thomas Vatter



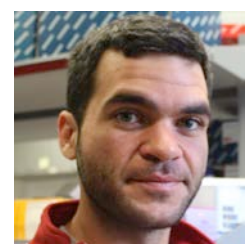
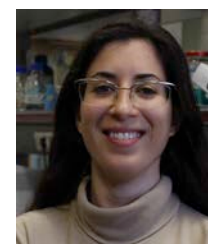
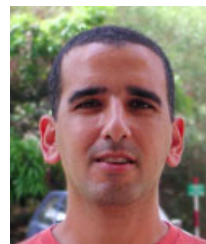
Bill Thomas
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Andy Flavell
Rajiv Sharma
Fulvia Draicchio



Eyal Fridman
David Bonfil
Efrat Laiba
Roi Silberman



Thanks for your attention!



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