Grains Research & Development Corporation

THE UNIVERSITY OF ADELAIDE AUSTRALIA

Trait Discovery in Wild Barley

Monday, March 17, 2014

Tim March

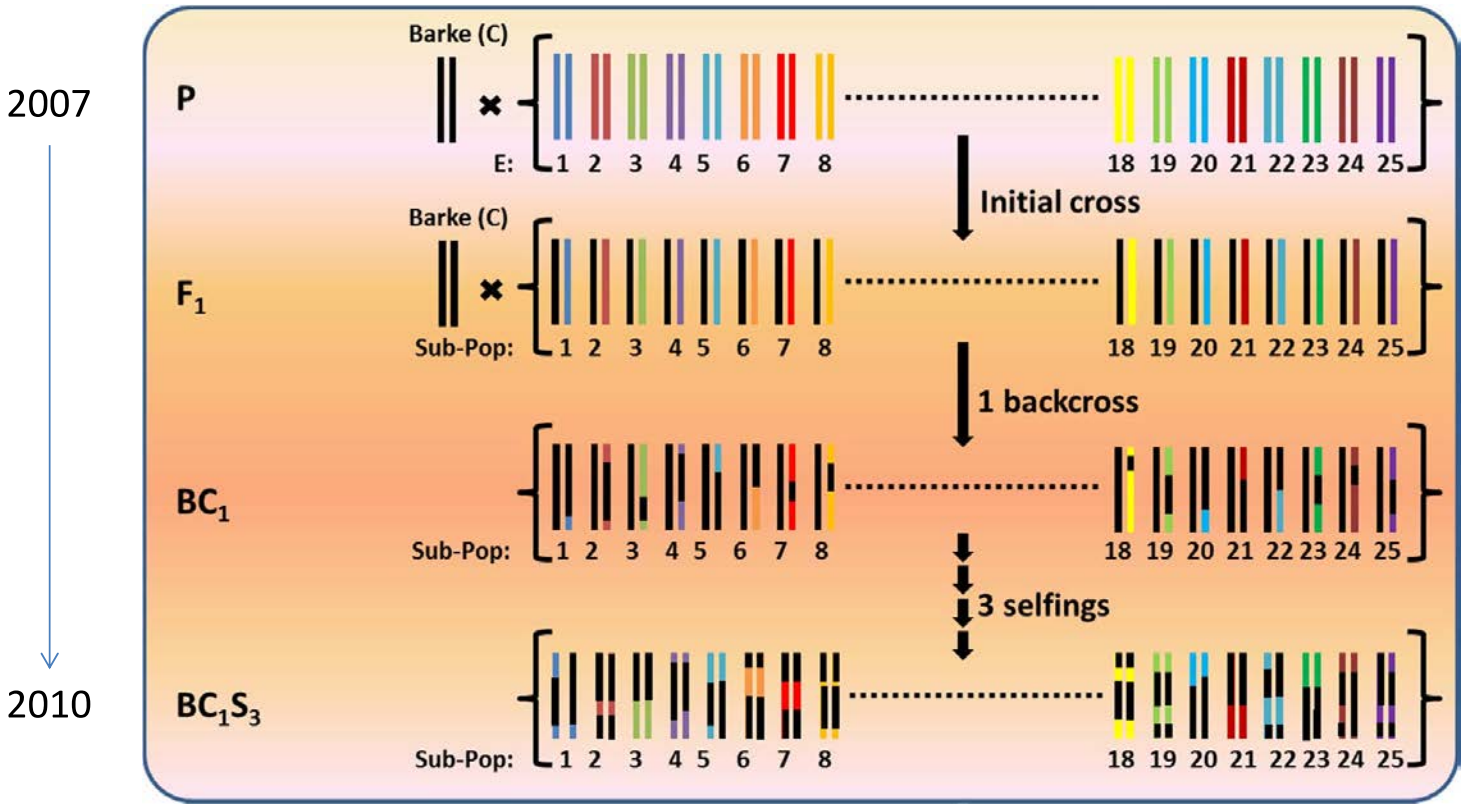
Life Impact The University of Adelaide

Development of the NAM population HEB-25

Klaus Pillen, Martin Luther University, Halle, Germany

- 25 highly divergent wild barley accessions, used as donors
- German spring barley elite cv. Barke used as recipient

Badr et al. (2000)



HEB-25 (*Halle exotic barley)* = 25 families with 1.500 NAM lines in BC1S3
Segregation: 72%:6%:22%, already genotyped with 7,800 iSELECT SNPs

Propject 1

Allele mining of wild barley resistance genes using a nested association mapping (NAM) approach

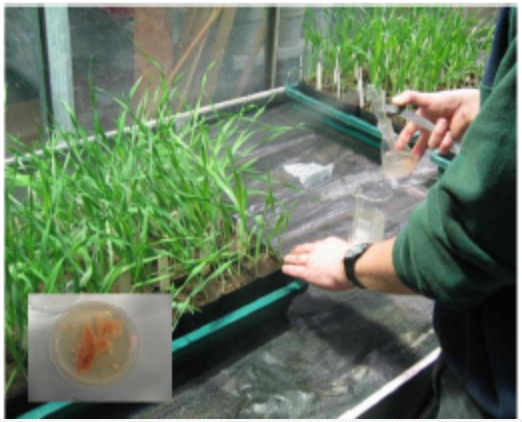
Participants:

- **Vera Draba & Klaus Pillen,** Martin-Luther University Halle-Wittenberg
- **Doris Kopahnke & Frank Ordon**, Julius Kühn-Institute (JKI)
- **Bianca Büttner & Günther Schweizer,** Bavarian State Research Center for Agriculture (LfL)

Support:

Traits:

- **Leaf rust (*Puccinia hordei*)**
- **Net blotch (*Pyrenophora teres*)**
- **Leaf blotch/scald (*Rhynchosporium secalis*)**
- **Brittelness & threshability**



Propject 2

Allele mining in wild barley: finding new exotic genes which control flowering time in the barley nested association mapping (NAM) population HEB-25

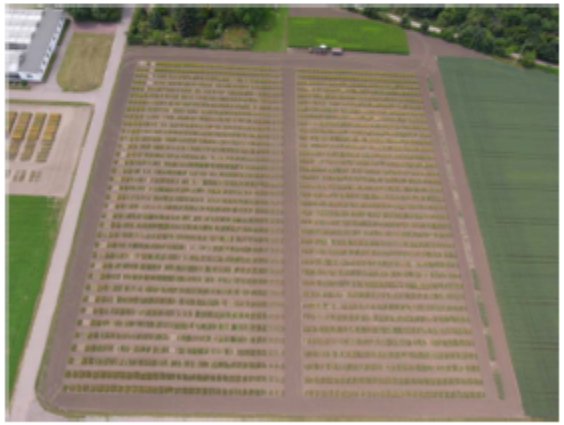
Participants:

- Andreas Maurer & Klaus Pillen

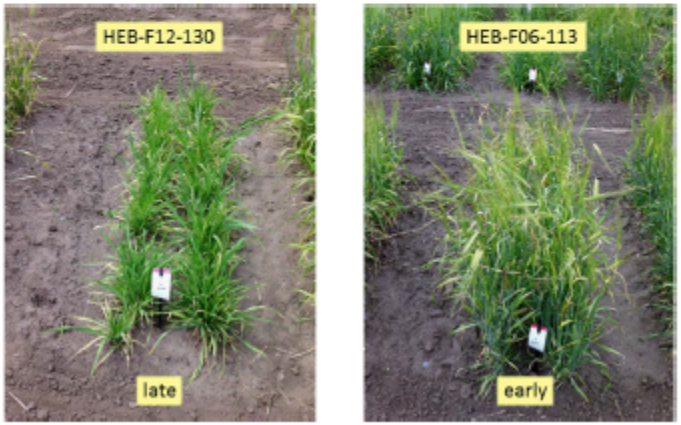
Traits:

- Life history traits (shooting, flowering, maturity)

Support:
DFG SPP1530,
Flowering Time Control

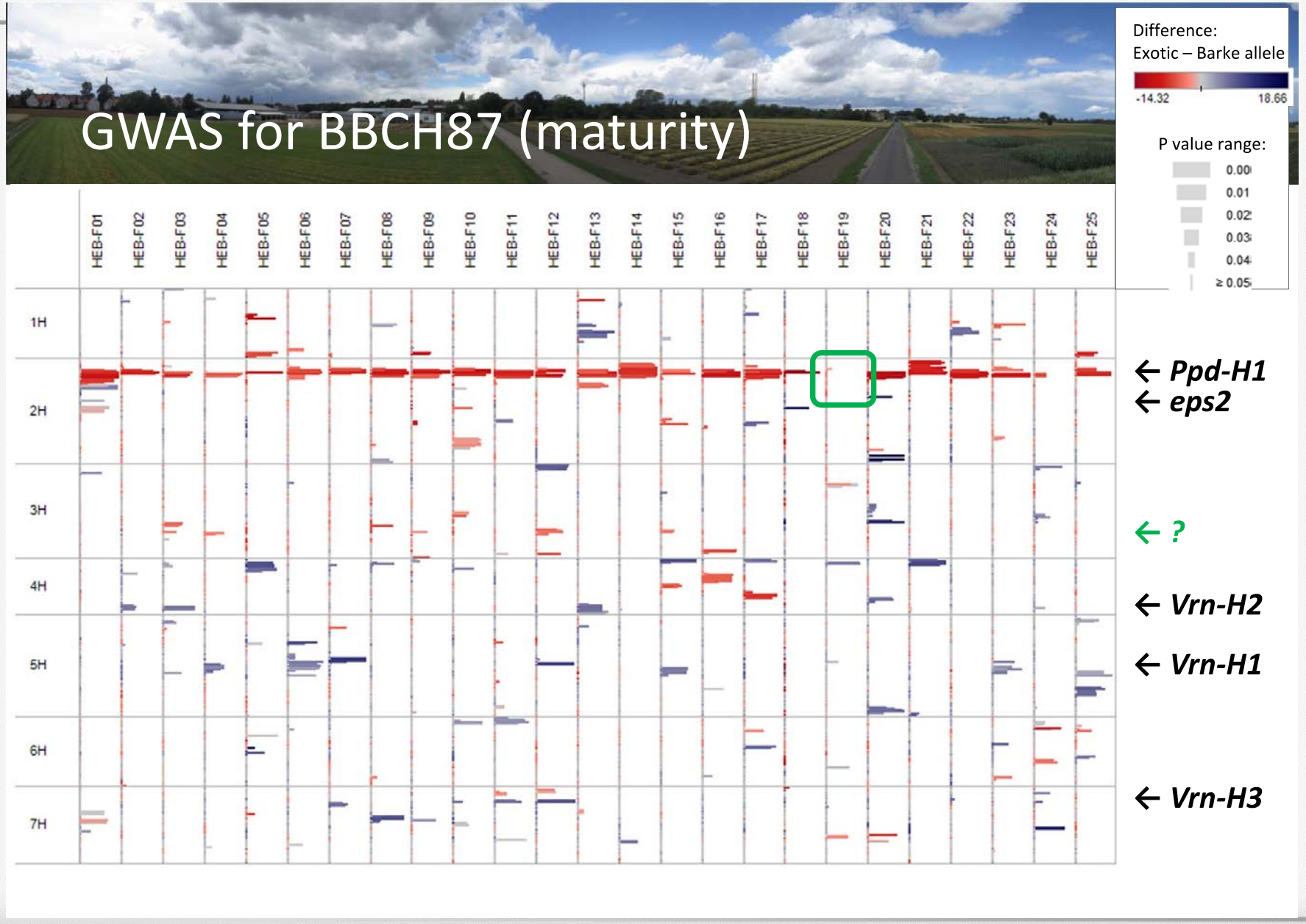


Field Trial Halle 2012



Differentiation of Flowering Time

GWAS for BBCH87 (maturity)



GRDC Project Outline – Starting 2014

Quarantine

- 500 HEB-25 lines released annually (3 years)
- Drought stress screen in the Plant Accelerator

Phenotyping

- Field phenology and disease scoring
- Disease nurseries

Genetic analysis

- Nested association mapping to identify QTL and markers
- Data stored centrally and publically available

Output

- QTL for target traits backcrossed into 3x Australian barley varieties and provided to all Australian barley breeding organisations