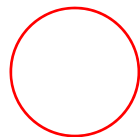


Comparing genetic diversity within a crop and its wild progenitor: a case study for barley

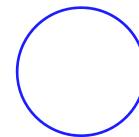
Benjamin Kilian

kilian@ipk-gatersleben.de

SEVERAL OPINIONS ON BARLEY DOMESTICATION HISTORY



„Core Area“ of plant domestication in the Fertile Crescent



Possible areas of barley domestication in the Fertile Crescent

BARLEY

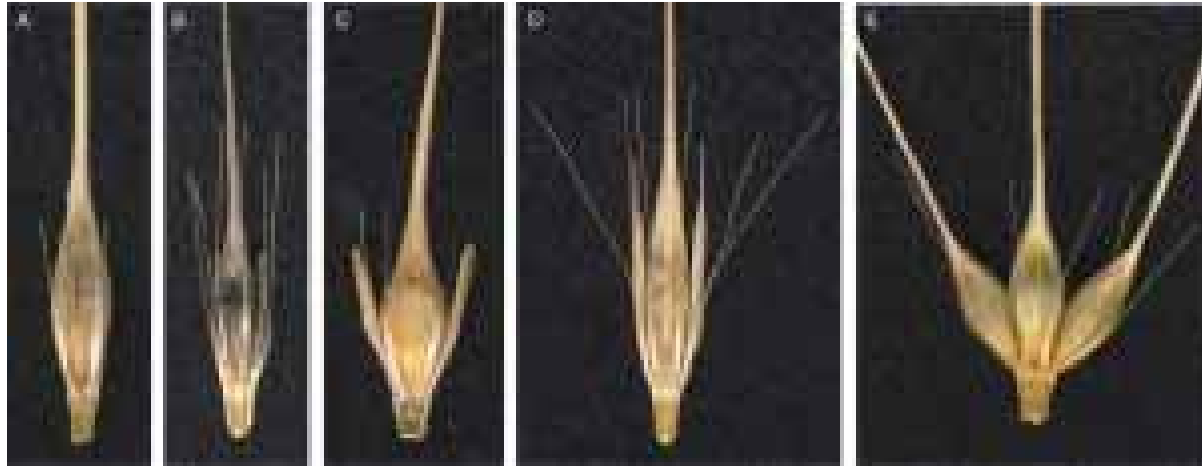


Hordeum spontaneum



Hordeum vulgare

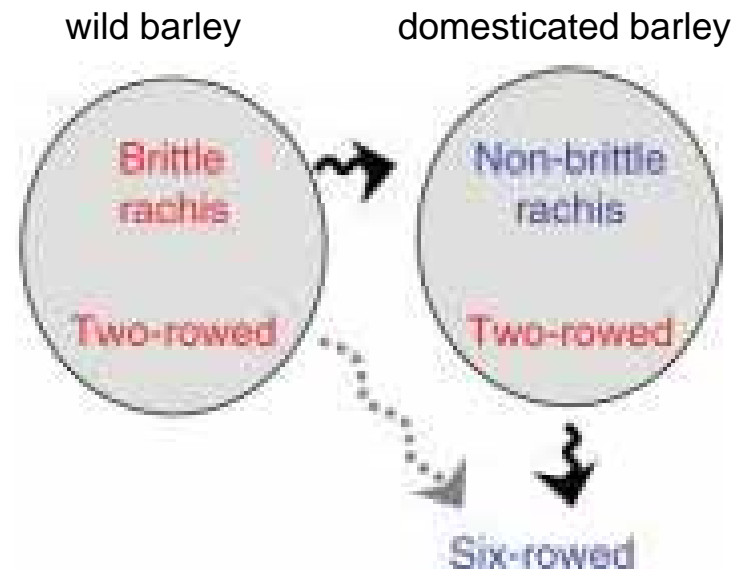
BARLEY DOMESTICATION



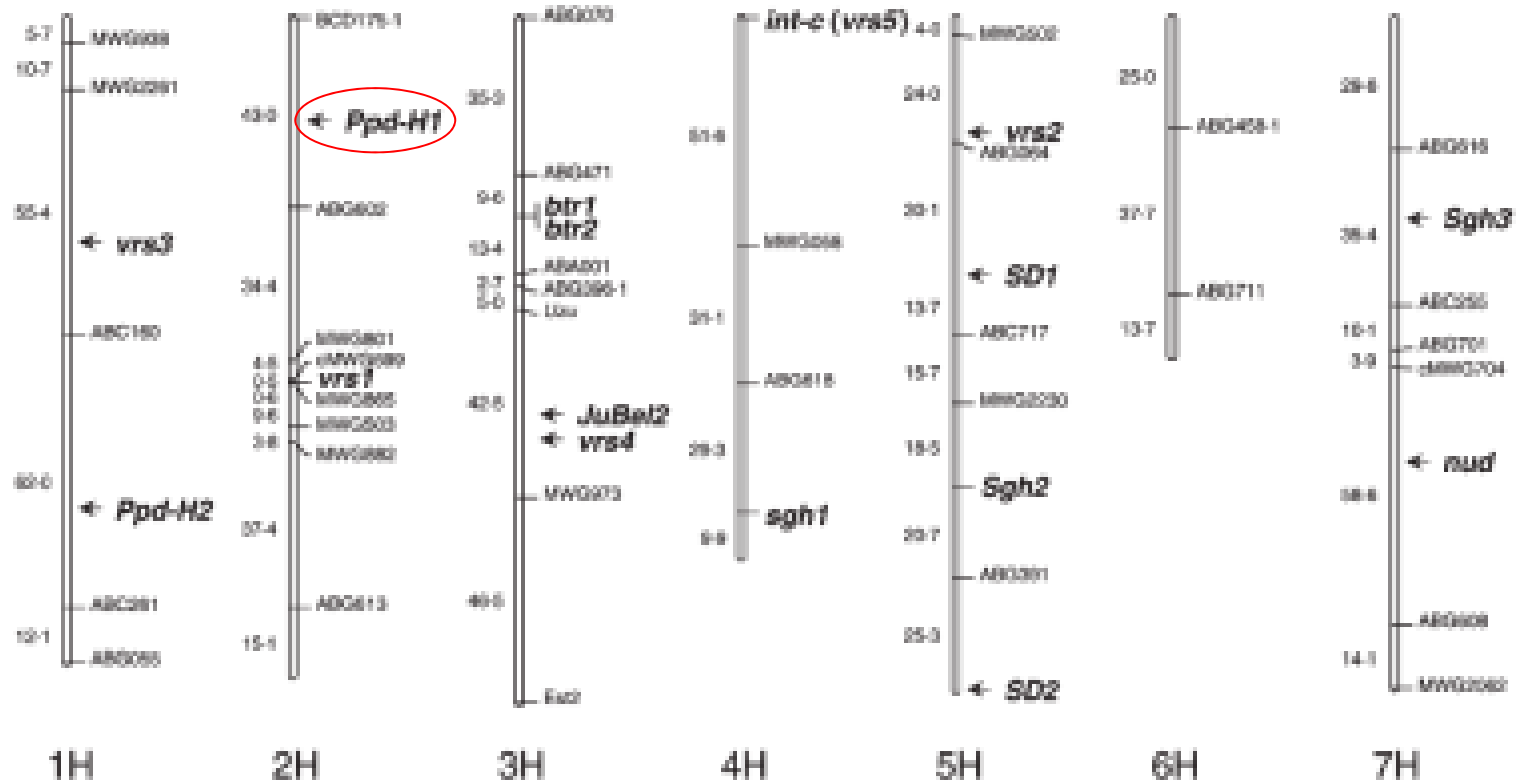
wild

2-rowed

6-rowed



CONSENSUS MAP OF BARLEY DOMESTICATION-RELATED GENES



DEVELOPMENT AND USE OF THE BARLEY CORE REFERENCE SET **BR816**

Diverse core collections considered:

- MPIZ922, B1K, BCC



Max. genetic and phenotypic diversity



Core Reference Set **BR816** (from 65 countries):

- **579** wild *H. spontaneum* (whole natural distribution range)
- 109 *H. vulgare*, landraces
- 128 *H. vulgare*, cultivars

Phenotypic Data available

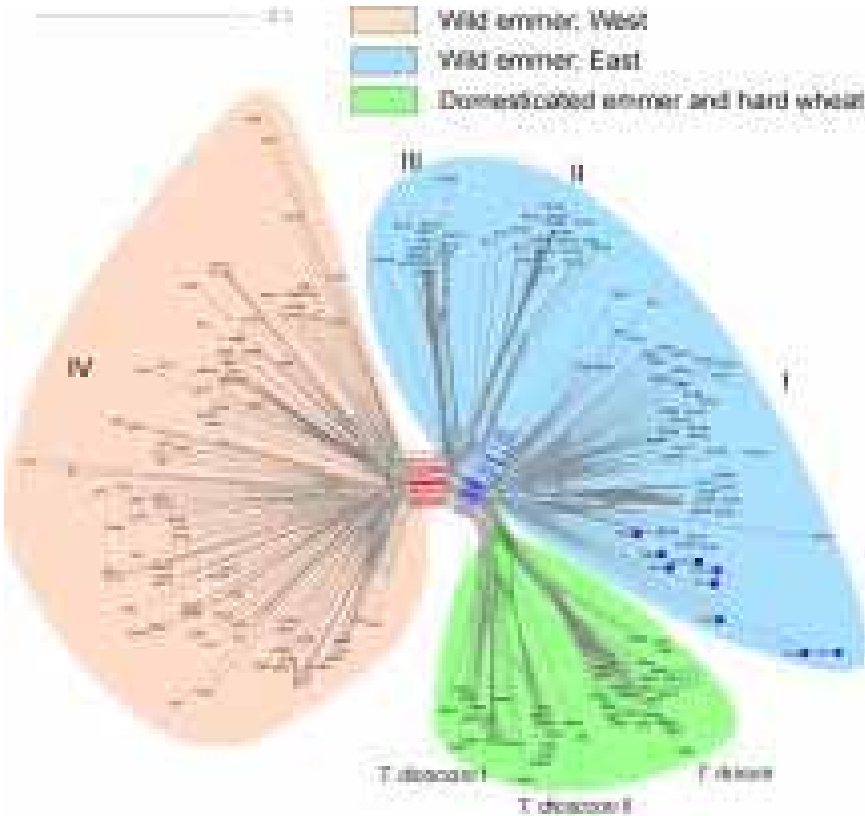
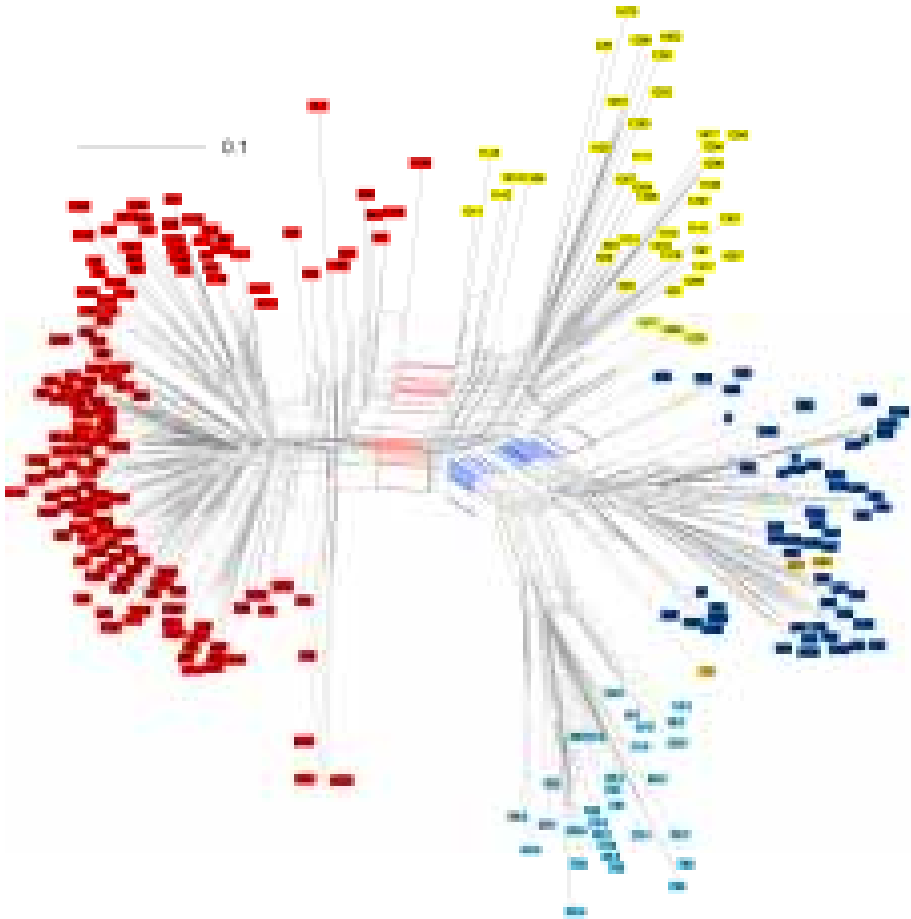
Several traits over several years

Genotypic Data available

300 retrotransposon-based polymorphic SSAP markers
400 AFLP marker
400 SSR markers
1536 BOPA1 marker
20 candidate genes have been re-sequenced; more in progress

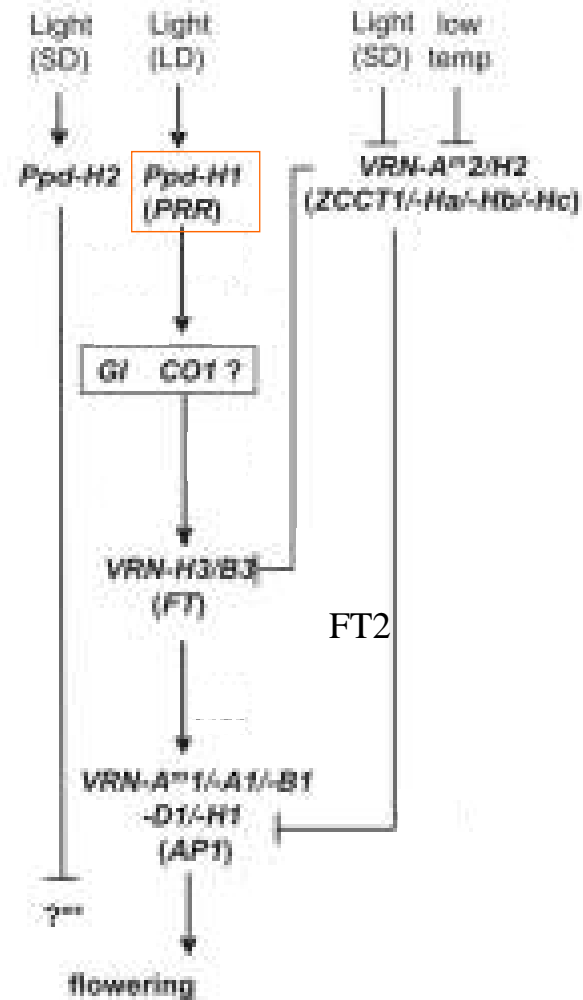
GENETIC DIVERSITY AMONG EINKORN AND EMMER WHEAT

haplotypes (SNPs) at 17 loci (267/452 lines)



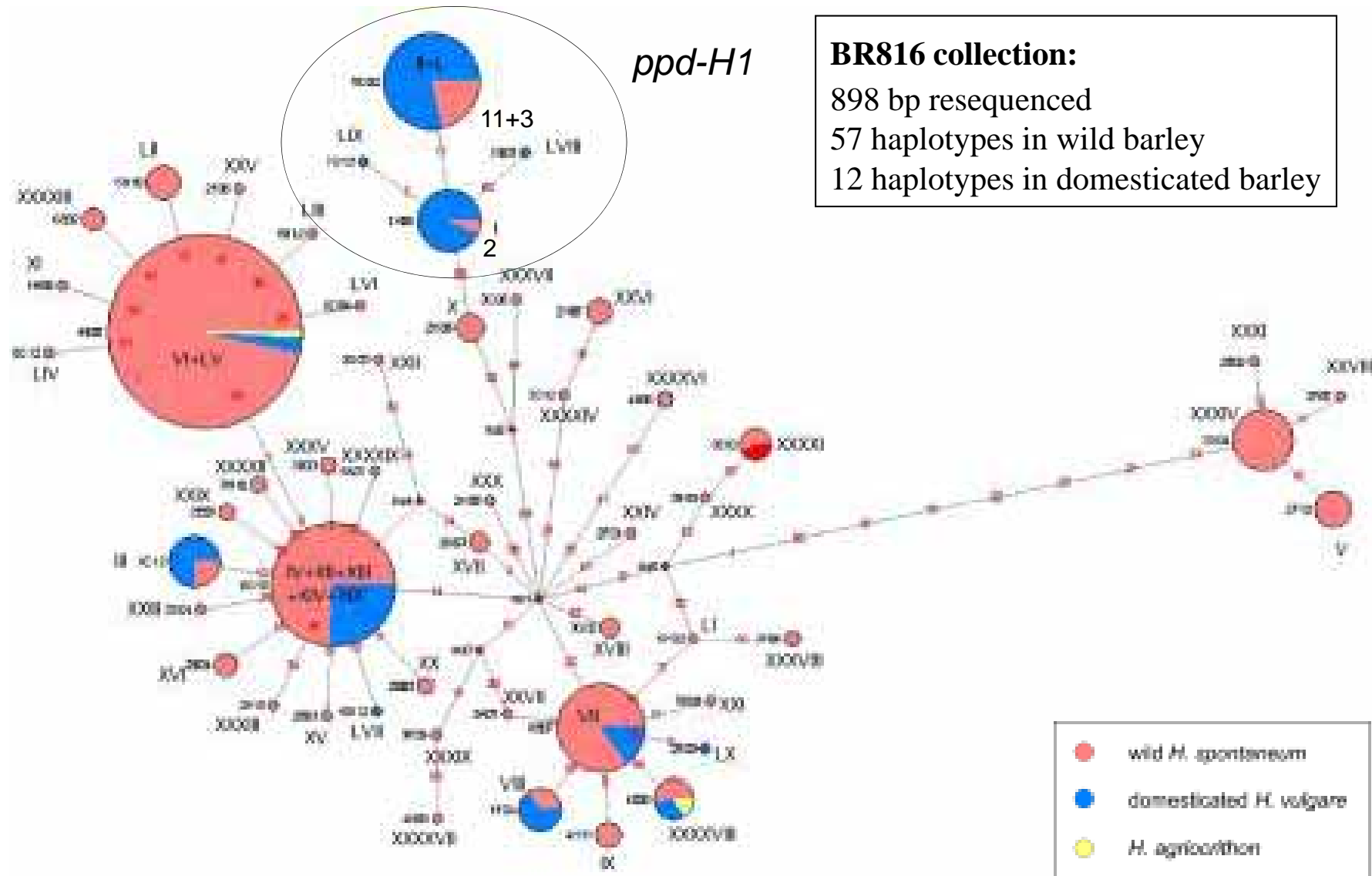
BR816 AS RESOURCE FOR ALLELE MINING

GENETIC DIVERSITY AT MAJOR FLOWERING PATHWAY GENES IN BARLEY



adapted from Cockram et al. 2007

PpdH1-haplotypes in BR816:
LOSS OF GENETIC DIVERSITY IN CULTIVATED BARLEY



PHENOTYPING OF **BR816** (2009)

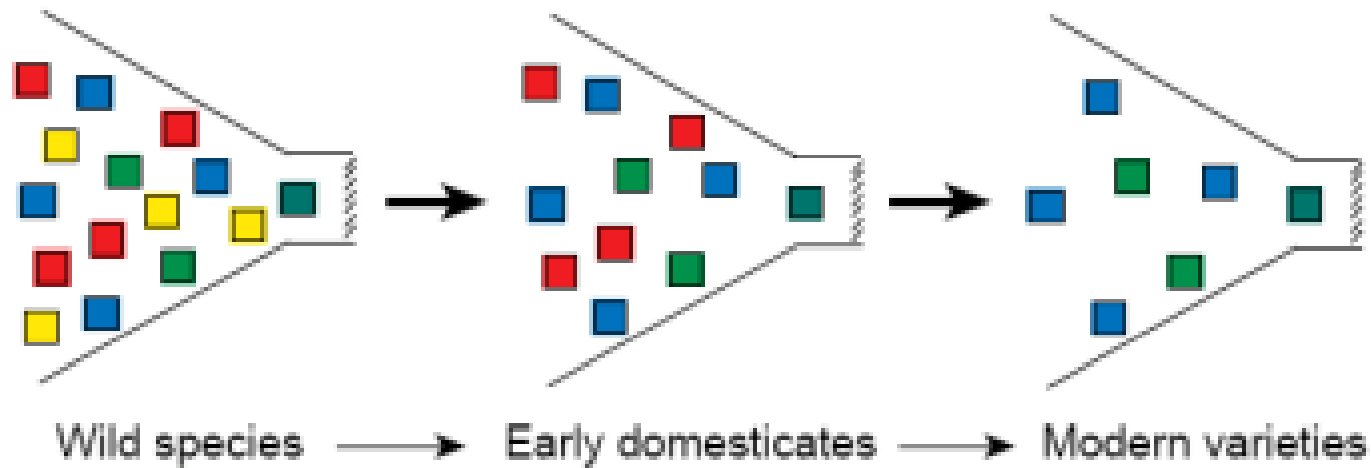


ASSESSING GENETIC DIVERSITY FOR CROP IMPROVEMENT:

Ongoing work and future research tactics for crop plants and their wild progenitors:

- High-throughput genotyping
- High-throughput phenotyping
- Whole-genome association studies*
- generating new resources*
- Re-sequencing of candidate genes in large collections*
- next-generation sequencing*
- *in situ* conservation and collection trips
- Interdisciplinary cooperation

WHOLE-GENOME ASSOCIATION STUDIES IN DIFFERENT BARLEY COLLECTIONS



Linkage Disequilibrium level

HSC < LRC < HVCC
H. spontaneum < *H. vulgare* landraces < *H. vulgare* cultivars

EXAMPLE: EXBARDIV – EUROPEAN CONSORTIUM FOR ASSOCIATION MAPPING IN BARLEY

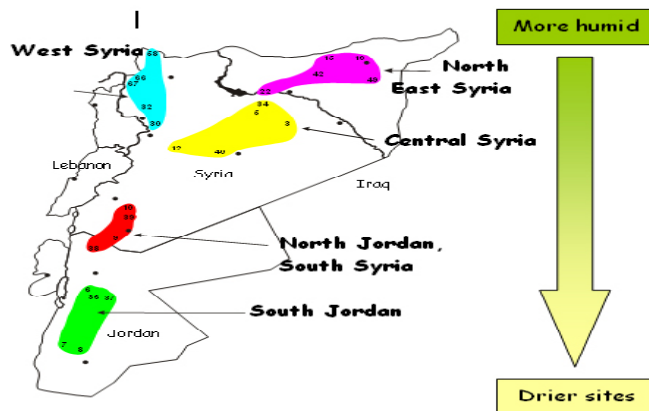


Hordeum vulgare **Cultivar** Collection

451 lines

128* Winter lines

323* Spring lines



Hordeum vulgare **Landrace** Collection

480 lines

obtained from Stefania Grandi, ICARDA

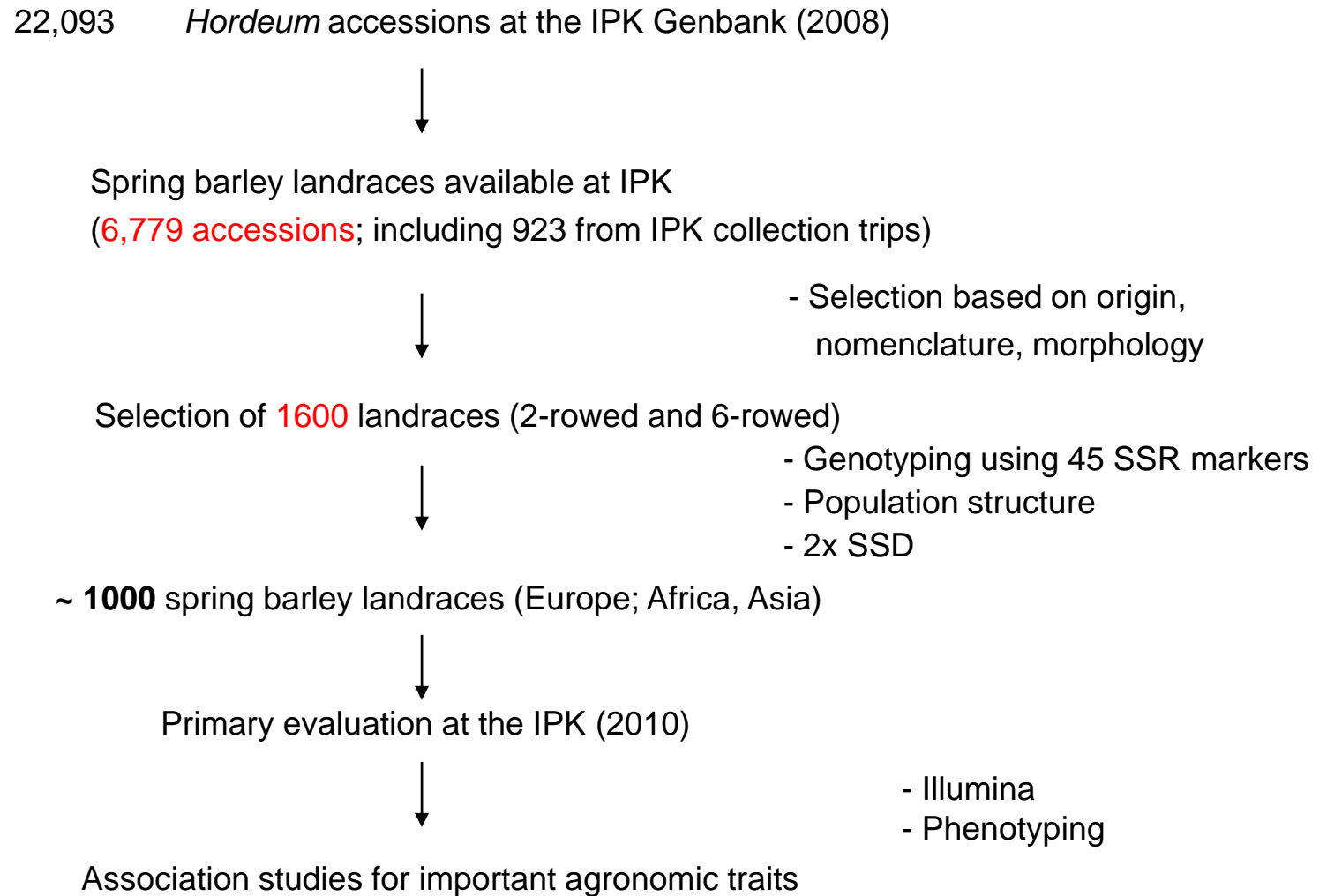


H. spontaneum Collection

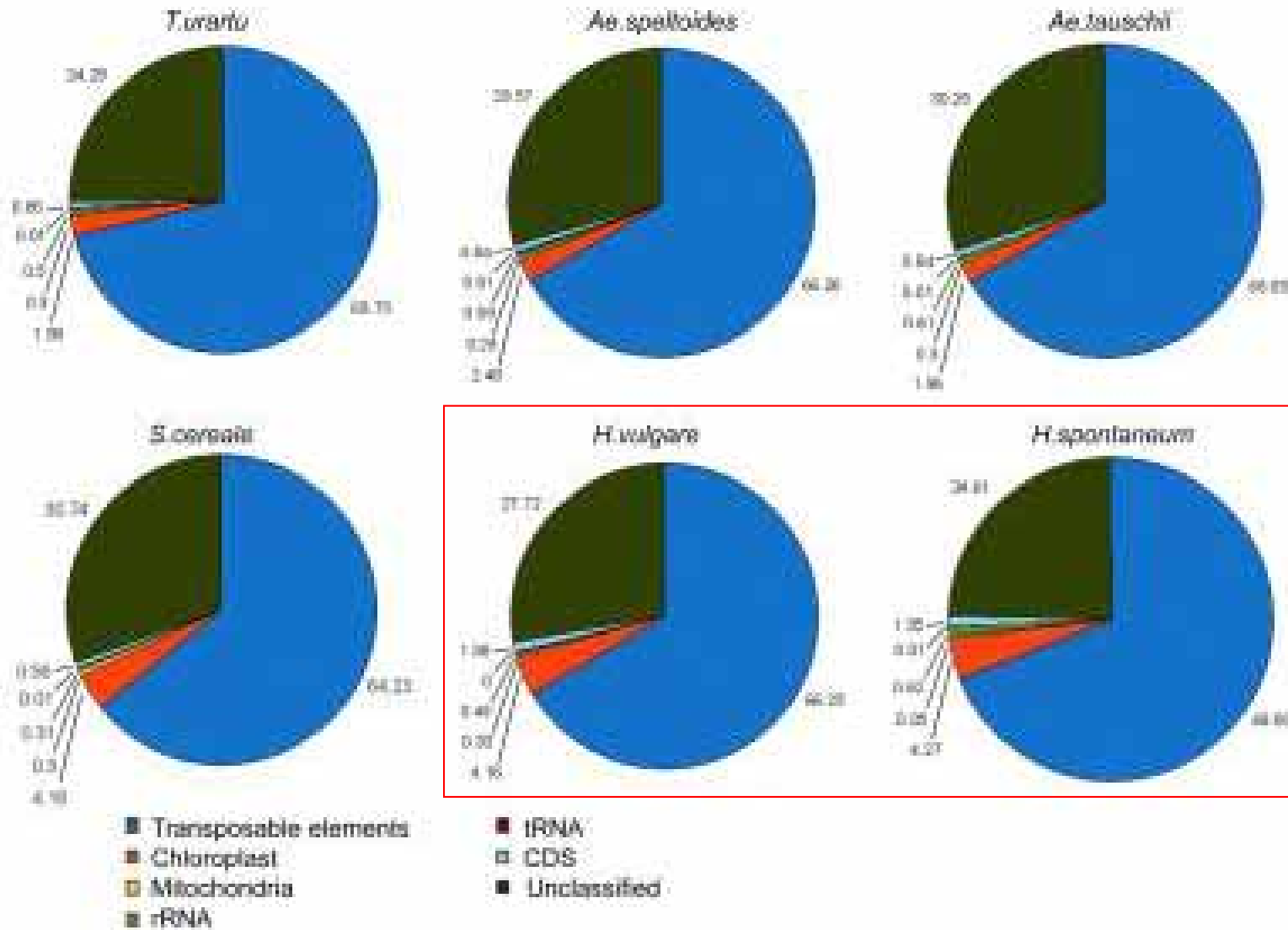
218 lines

obtained from Eyal Fridman, Jerusalem

DEVELOPMENT OF RESOURCES: LANDRACE COLLECTION FOR HIGH-RESOLUTION LD-MAPPING



MORE PROGRESS: NEXT-GENERATION SEQUENCING



ACKNOWLEDGEMENTS

IPK Gatersleben, Germany

Andreas Graner, Nils Stein, Sabine Jakob,
Jürgen Marlow, Peter Schreiber, Raj K. Pasam,
Rajiv Sharma, Patrick Schweizer *and many others*

MPIPZ Cologne, Germany

George Coupland, Maria von Korff, Maarten Koornneef,
Sigi Effgen, Jutta Schütze, Charlotte Bulich,

University of Cukurova, Turkey

Hakan Özkan

University Jerusalem, Israel

Eyal Fridman

University Haifa, Israel

Sariel Hübner

University Göteborg, Sweden

Alexander Walther

UZH Zürich, Switzerland

Thomas Wicker

Vavilov Institute of General Genetics, Moscow, Russia

Fedor A. Konovalov

University Halle, Germany

Klaus Pillen

University of Tehran, Iran

Salar Shaaf

DAI Berlin, Germany

Klaus Schmidt, Reinder Neef

Archéorient CNRS UMR Lyon, France

George Willcox

University Düsseldorf, Germany

William Martin

Parco Tecnologico Padano, Lodi, Italy

Francesco Salamini

Financial Support

Deutsche Forschungsgemeinschaft
Alexander von Humboldt Foundation
IPK Gatersleben

