



Genebank genomics - now and the future: a barley example

Nils Stein, IPK Gatersleben & Georg-August-University Göttingen

<https://www.genesys-pgr.org/>

Genesys – single hub to explore the world’s crop diversity conserved in genebanks

Genesys Home Explore About Genesys Documentation My List 0

APPLY FILTERS Reset

Accession browser

Explore passport data of selected accessions

OVERVIEW **ACCESSIONS** MAP IMAGES

About 250.578 accessions Text: Hordeum vulgare Excluding Historic

- 35774** • *Hordeum vulgare* L. • **HORDEUM VULGARE** • Breeding/Research Material • Czechoslovakia, Czechoslovak Socialist Republic
POL003 • Plant Breeding and Acclimatization Institute, Poland • DOI: N/A
- 35773** • *Hordeum vulgare* L. • **HORDEUM VULGARE1** • Breeding/Research Material • Czechoslovakia, Czechoslovak Socialist Republic
POL003 • Plant Breeding and Acclimatization Institute, Poland • DOI: N/A
- 35775** • *Hordeum vulgare* L. var. *nigripallidum* Ser. • **HOREUM VULGARE** • Breeding/Research Material • Czechoslovakia, Czechoslovak Socialist Republic
POL003 • Plant Breeding and Acclimatization Institute, Poland • DOI: N/A
- 35777** • *Hordeum vulgare* L. var. *erectum* Schubl. • **HORDEUM VULGARE (ANATOLIA)** • Breeding/Research Material
POL003 • Plant Breeding and Acclimatization Institute, Poland • DOI: N/A
- AGG402712BARL** • *Hordeum vulgare* • **HORDEUM VULGARE/ELYMUS MOLLIS** • United States of America
AUS165 • Australian Grains Genebank, Department of Economic Development Jobs Transport and Resources, Australia • DOI: N/A

HOLDING INSTITUTE

Institute code

Suggested filters

USA029	36,245
LBN002	31,868
DEU146	22,909
AUS165	18,748
BRA003	18,578
RUS001	17,788
SWE054	16,126
MEX002	15,330
GBR247	10,437
POL003	6,839

Country of holding institute

Barley diversity



>20,000 barley accessions at IPK genebank

How do you know which accession is of importance for your purpose?

Barley diversity



MOBILIZING CROP DIVERSITY

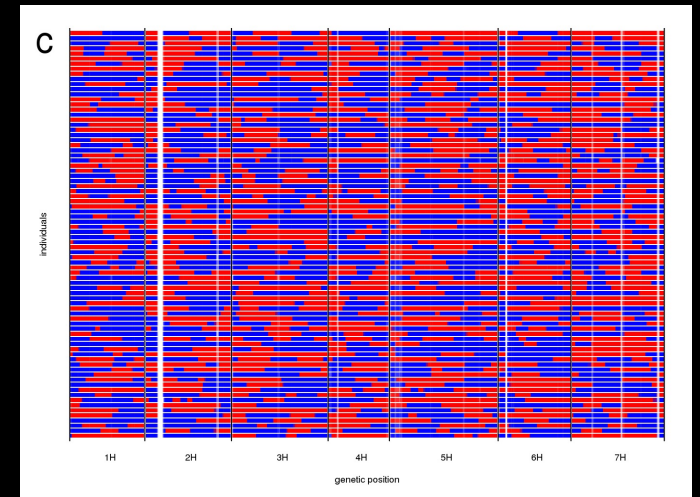
The DivSeek International Network is a global community driven Not-for-Profit organization that aims to facilitate the generation, integration, and sharing of data and information related to plant genetic resources (PGR).

[ABOUT US](#)

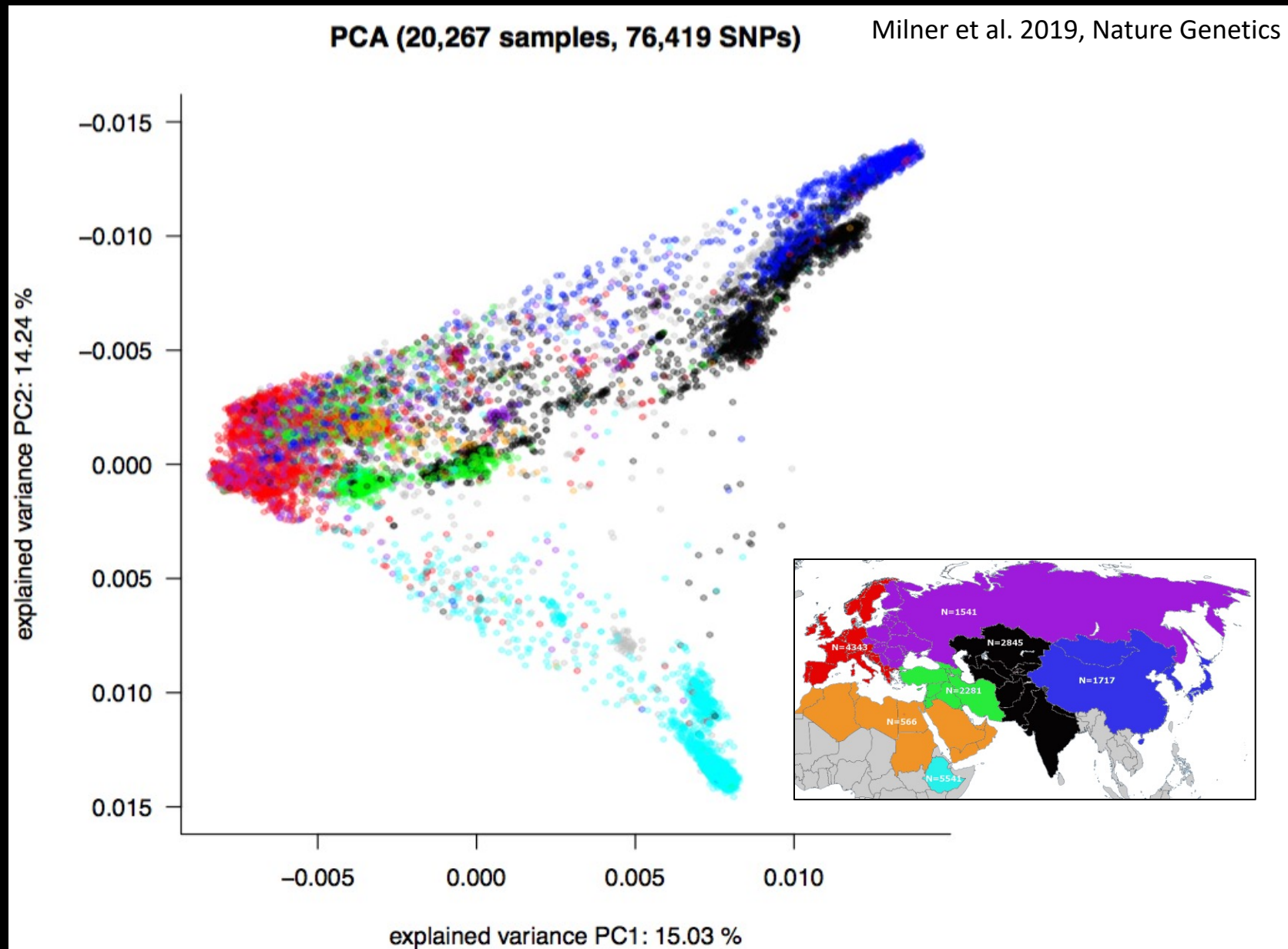
HARNESSING CROP DIVERSITY

DivSeek aims to unlock the potential of crop diversity so that it can be utilized to enhance the productivity, sustainability and resilience of crops and agricultural systems.

barley genebank genomics



barley diversity and geographic origin

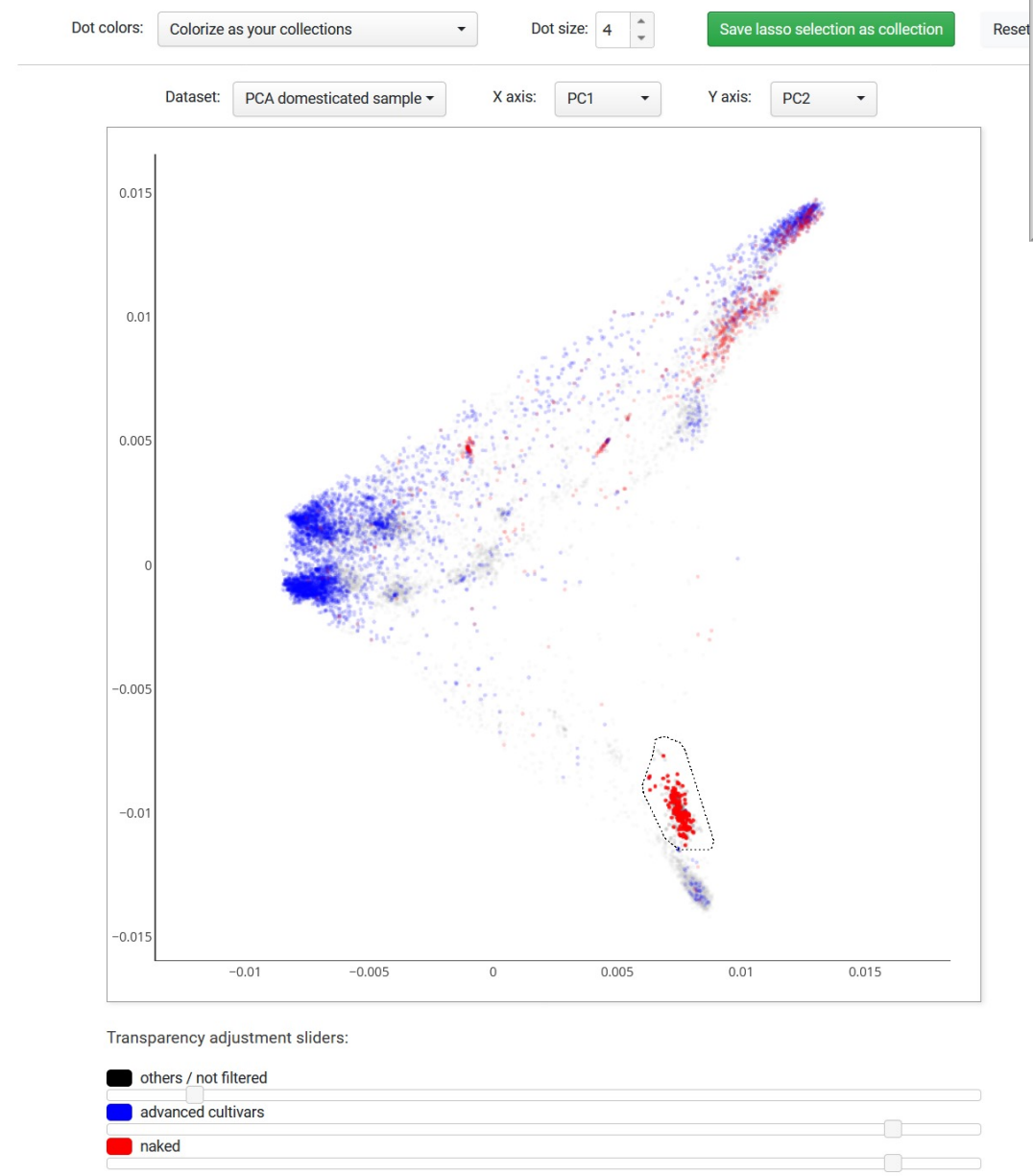


https://bridge.ipk-gatersleben.de/



- ☰ Collections
- Search Germplasm
- SNP Browser
- Geographic Origins
- Genetic Clustering
- PCA Matrixplot
- Association Mapping (GWAS)
- Collection Details
- Phenotypic Data
- VCF Export
- ISA-Tab Export
- Order Germplasm
- Project Details
- Help (Interactive Tutorial)
- Statistics

Impressum



frontiers
in Plant Science

ORIGINAL RESEARCH
published: 11 June 2020
doi: 10.3389/fpls.2020.00701

Check for updates

BRIDGE – A Visual Analytics Web Tool for Barley Genebank Genomics

Patrick König^{1*}, Sebastian Beier¹, Martin Basterrechea¹, Danuta Schüler¹, Daniel Arend¹, Martin Mascher^{1,2}, Nils Stein^{1,3}, Uwe Scholz^{1*} and Matthias Lange¹

A General Filter

Passport attributes

Country of origin: Nothing selected

Row type: Nothing selected

Only germplasm with a photo

B **C**

D Save a collection

Your selected SNPs samples (link) and can now save them as a named collection.

Your collection to save consists of samples that are already present in previously saved collections.

Subselected collection	Description	Include*	Exclude*
Core 1000	2347 your selected SNPs samples are part of 'Core 1000'	<input type="checkbox"/>	<input checked="" type="checkbox"/>
My custom collection		<input checked="" type="checkbox"/>	<input type="checkbox"/>

Marker color: My custom collection Save collection

E Saved germplasm collections

Collection name	Color	Samples	Active	Actions
Core 1000	■	1000	<input checked="" type="checkbox"/>	Delete
My custom collection	■	SNP	<input checked="" type="checkbox"/>	Delete

Predefined collections: [Load 'Core 50' set](#) [Load 'Core 200' set](#) [Load 'Core 1000' set](#)

[Delete all](#) [Load collections from file](#) [Save collections to file](#) [Close](#)

F **G** **H**

I VCF Export of genotypic data

Here you can export genotypic data in gzip-compressed Variant Call Format (VCF) file in version 4.0.

SNP matrix type: unfiltered

Chromosome: 1H

Start position: 34 99320

End position: 3901 3902

Accession number(s) (or comma separated): 42761:KOR:14222:KOR:10226:KOR:43421:KOR:42253:KOR:19915:KOR

[Use one of your collections](#) Submit

J Export of an ISA-Tab archive

Phenotypic data is only available for a subset of 323 samples from your collection of SNPs samples.

A photo is only available for 209 samples.

The ISA-Tab export will contain phenotypic data for 323 samples and 209 photos.

Please choose between the following two download variants.

Variant 'System Included as .PDS File'

The ISA-Tab archive will contain physical .PDS files of the photos of the germplasm samples.

Variant 'System referenced as URL'

The ISA-Tab archive will contain hyperlinks (URLs) to the photos of the germplasm samples.

[Download ISA-Tab archive](#) Close

K Order germplasm

Selected and named collections of germplasm can be ordered online through the IPK germplasm information system (GIS).

Please note: you will receive seeds from the regular stocks of the IPK germplasm accessions but not from progeny of the individual plants that were generated in the BRIDGE project (Müller et al. 2019). Backup of single-seed descent material derived from the genotyped Core 1000 is still underway. Furthermore, you cannot order through this system accessions that are not managed by IPK.

Collection-ID	Color	Samples	Actions
Core 1000	■	1000	Transfer to GIS
My custom collection	■	SNP	Transfer to GIS

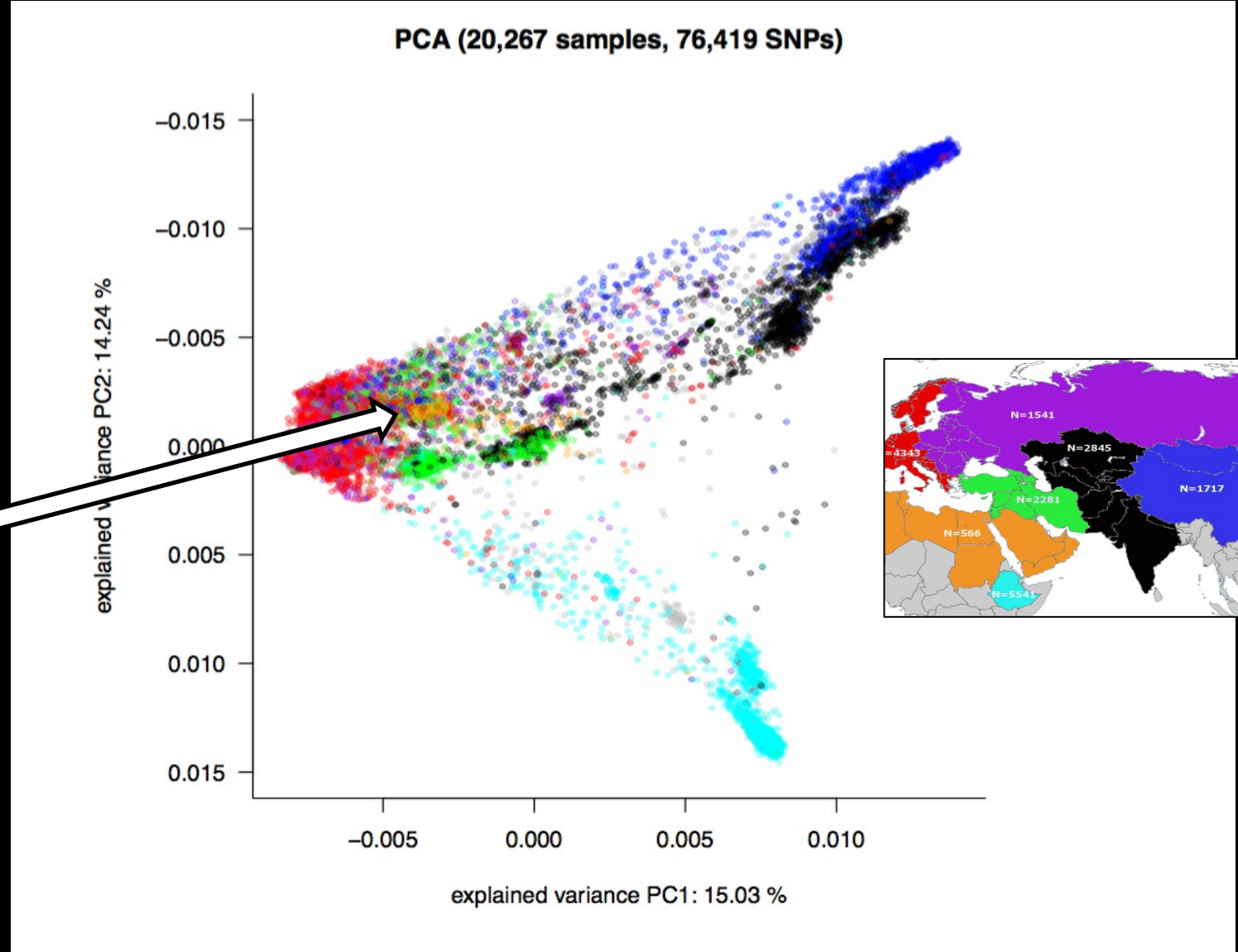
0.18%

It is technically feasible to unlock barley diversity at species' level!

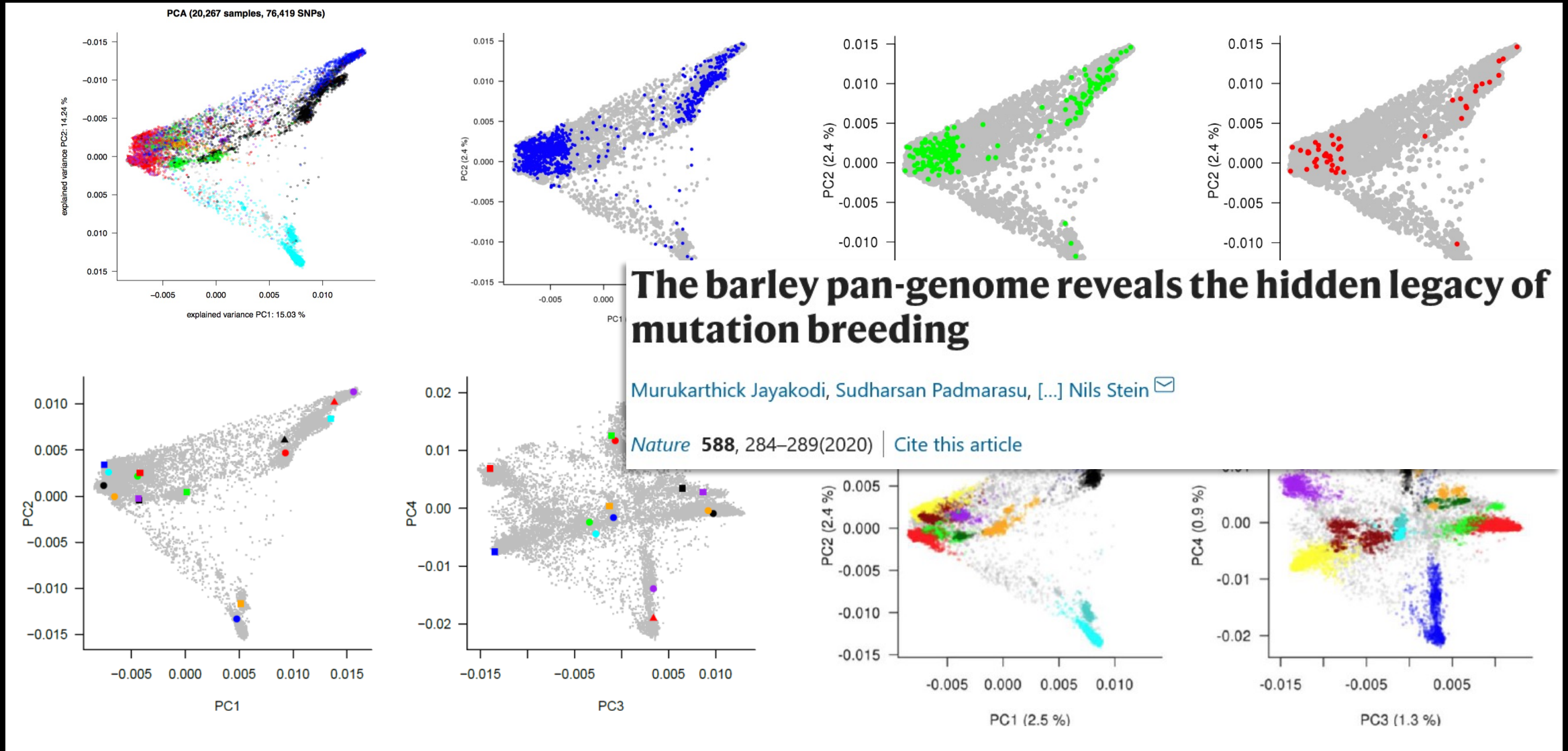
- What is your reference?
- 25K (IPK) or 250K (Genesys) represent global diversity?

How to best capture barley diversity

Barley reference sequence:
cultivar Morex



From gene bank genomics to barley pan-genome



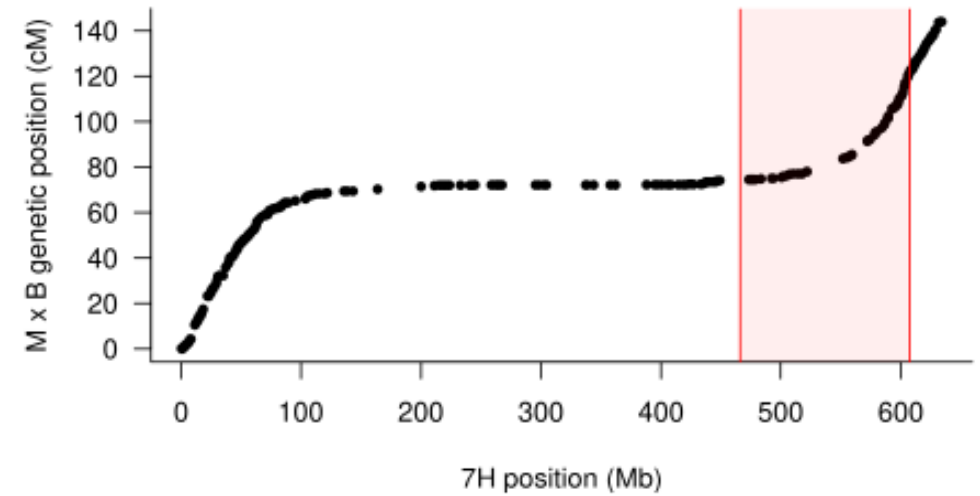
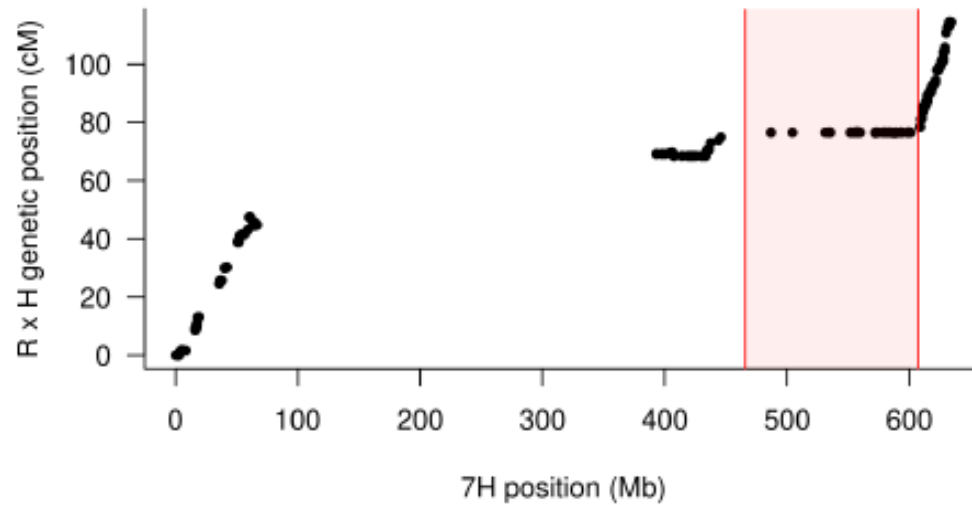
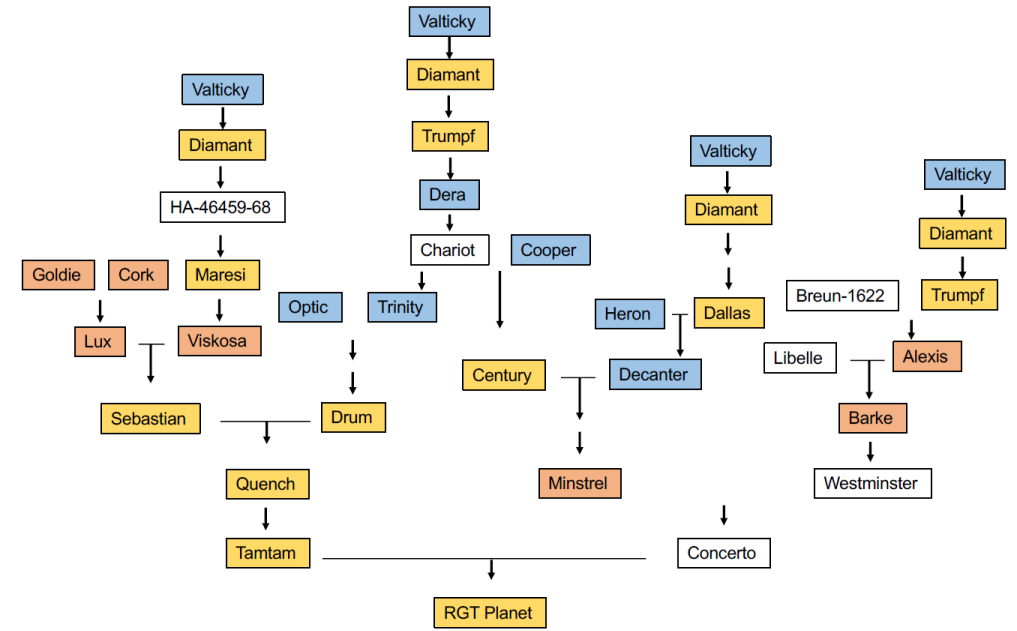
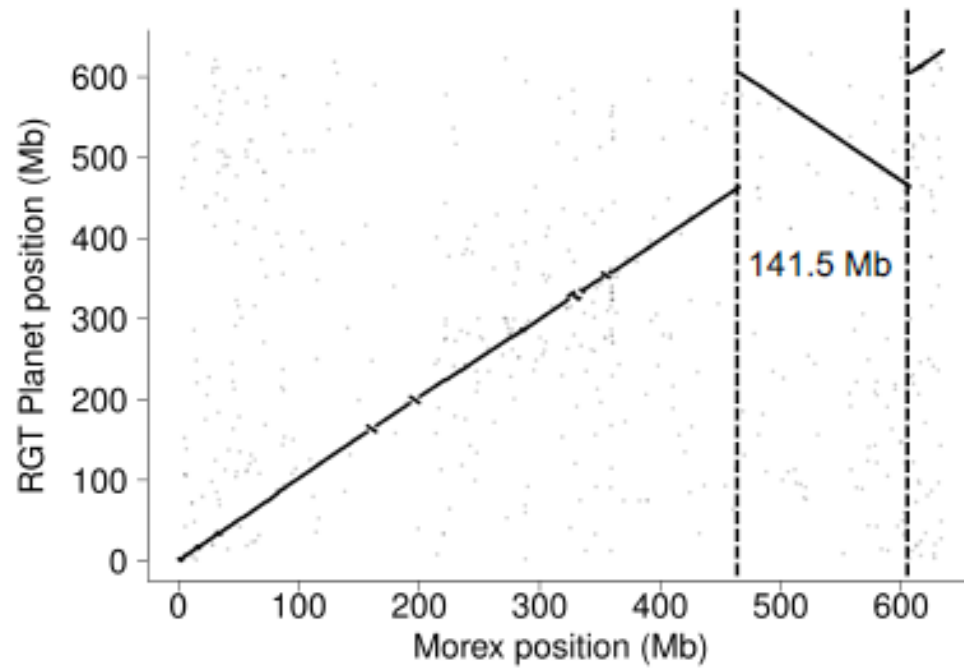
International barley pan-genome consortium



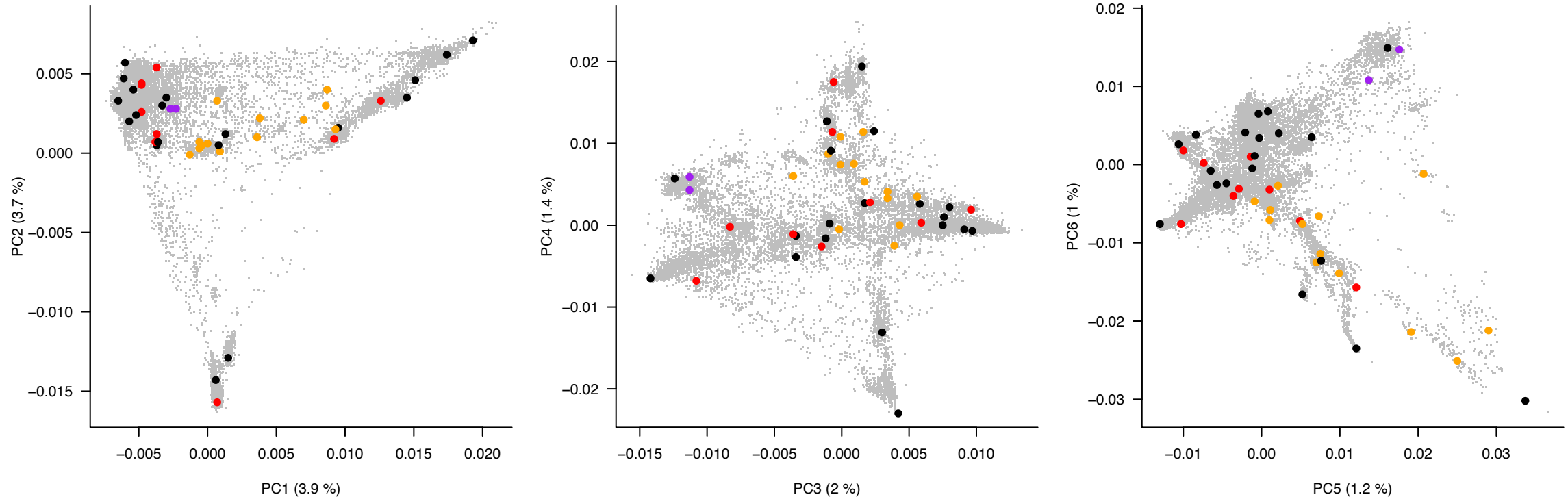
Helmholtz Zentrum münchen
Deutsches Forschungszentrum für Gesundheit und Umwelt



Barley pan-genome alignments



Pan-genome v2 selection in diversity space



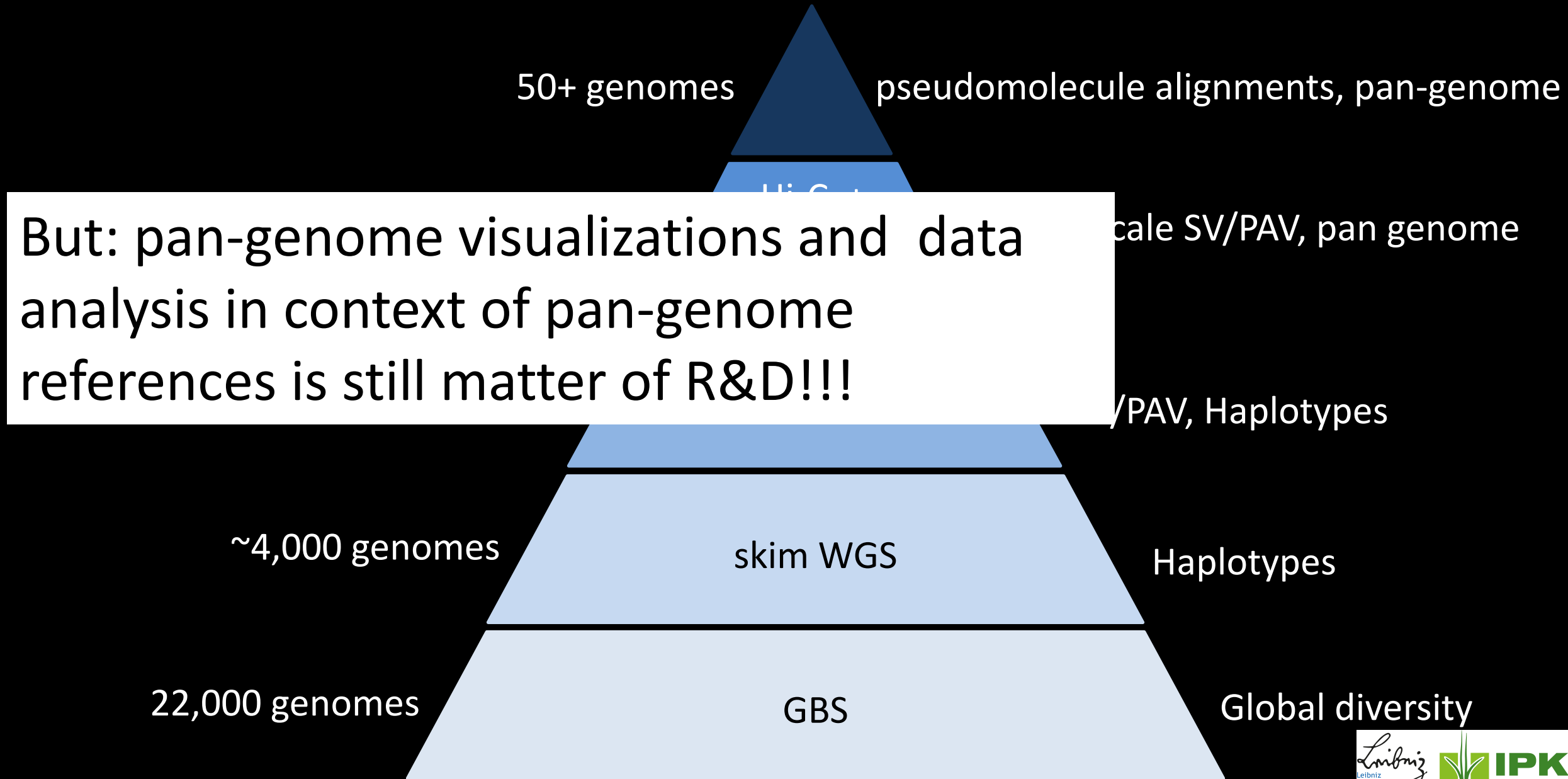
Black: Pangenome V1 (N=20)

Orange: Near Eastern barleys from „orange“ ADMIXTURE group (N=13)

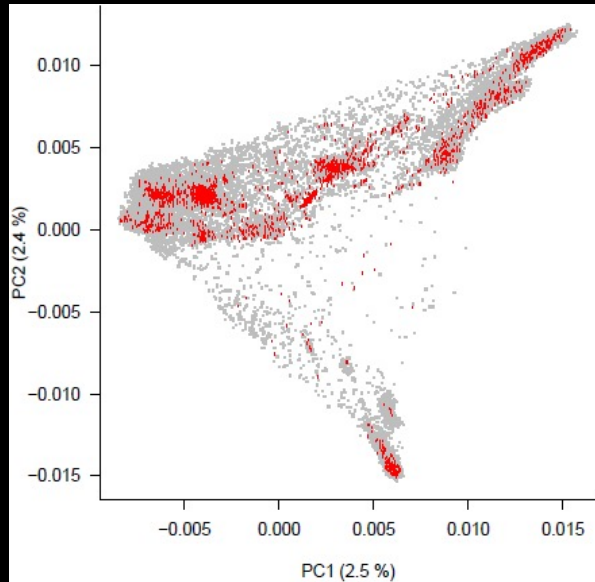
Purple: Mediterranean barleys from „purple“ ADMIXTURE group (N=2)

Red: Hand-picked barleys to cover PCA space / ADMIXTURE groups (all from CORE1000, most CORE50) (N=9)

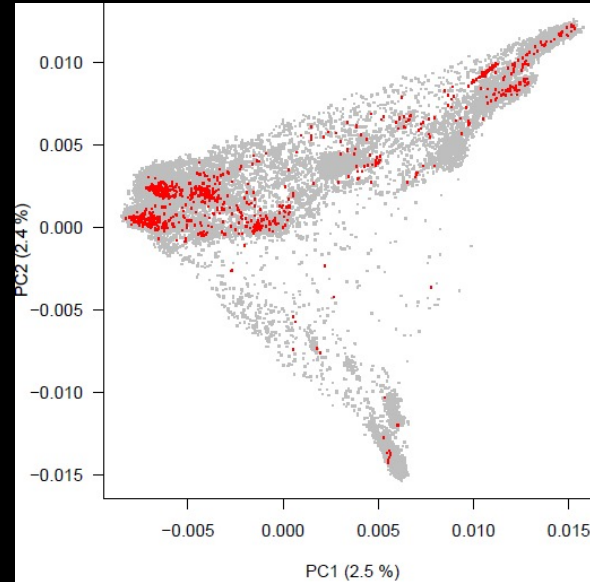
Barley pan-genome – towards barley personal genomics



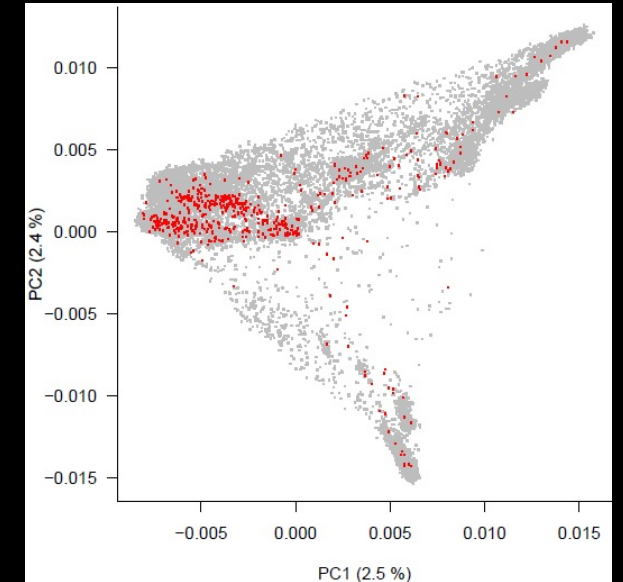
Global barley diversity represented in IPK collection



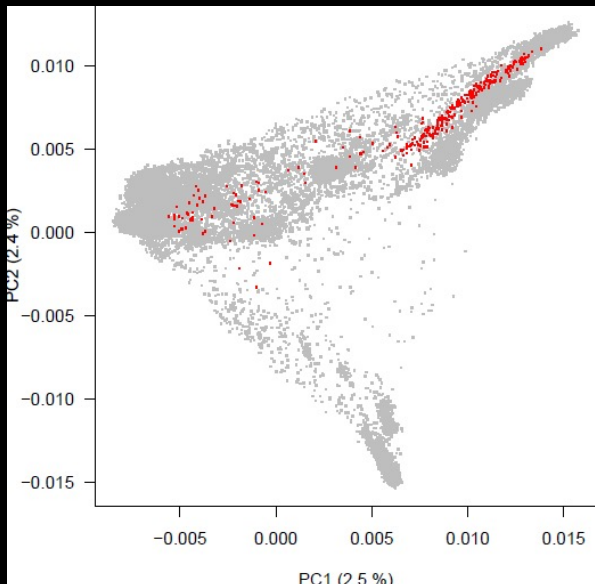
IPK/ICARDA: 2,290



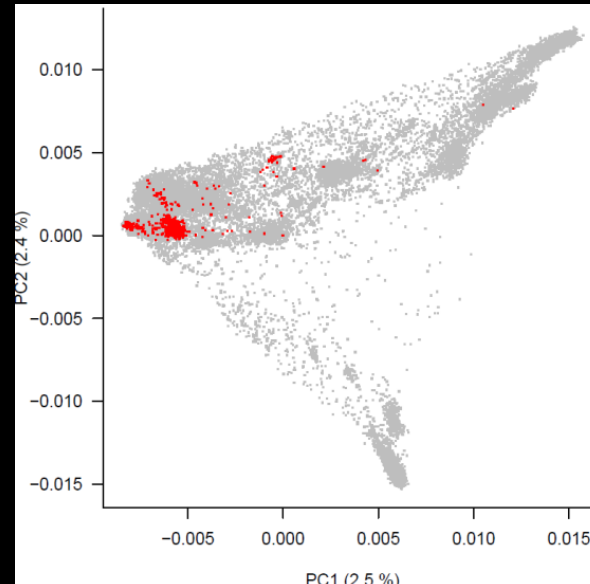
IPK/VIR: 500 (x2)



IPK/WHEALBI: 512



IPK/CAAS: 297



IPK/Swiss Genbank: 684

collaboration with:

ICARDA: A Amri

VIR: E Potokina, I Loskutov, E Grigoreva

WHEALBI: Nat. Genet. 51 (2019) 905-911

CAAS: G Guo

Swiss G.: B Schierscher-Viret, B Keller



Global Access to Plant Genetic Resources

Mega environments

AGENT will analyse data for plant height, flowering time and weight (TKW) across gene banks through:

- trials with checks to understand trait-specific genotype-environment patterns:
50 winter and 50 spring accessions
- bridging genotypes to connect present and historic phenotypic data across gene banks:
75 winter and 75 spring accessions

AGENT will verify and refine the categorisation of regions with similar climatic conditions ('mega environments').

Southern Europe

Western Europe

Northern Europe

(South) Eastern Europe

Training data and genomic prediction



Summary - Discussion

Genotyping: no better access to PGRFA without!

What would you make different? Lessons learned?

- capable of detecting novel variation
- integration of independently generated datasets
- ultimately: sequencing

*To continue unlocking crop
species' genome diversity
for R&D&B:*

*DSI has to be and remain
FAIR, Open Access and a
public common good*

Ploidy, zygoty, homogeneity, self-compatibility, sexual reproduction

„in for a penny, in for a pound“

- genotyped material becomes the higher value accessions
- it requires to implement QC/QM for tracking, cost recovery
- There will be errors – no reason to wait

Basis for integrated efforts of data generation, e.g. genomic prediction

Acknowledgements



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Guoping Zhang
Tanja Gerjets

GEFÖRDERT VOM



Bundesministerium
für Bildung
und Forschung

SAW Pakt f. Forschung und Innovation



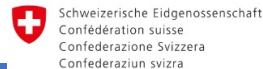
Acknowledgements



Activated GEnebank NeTwork



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