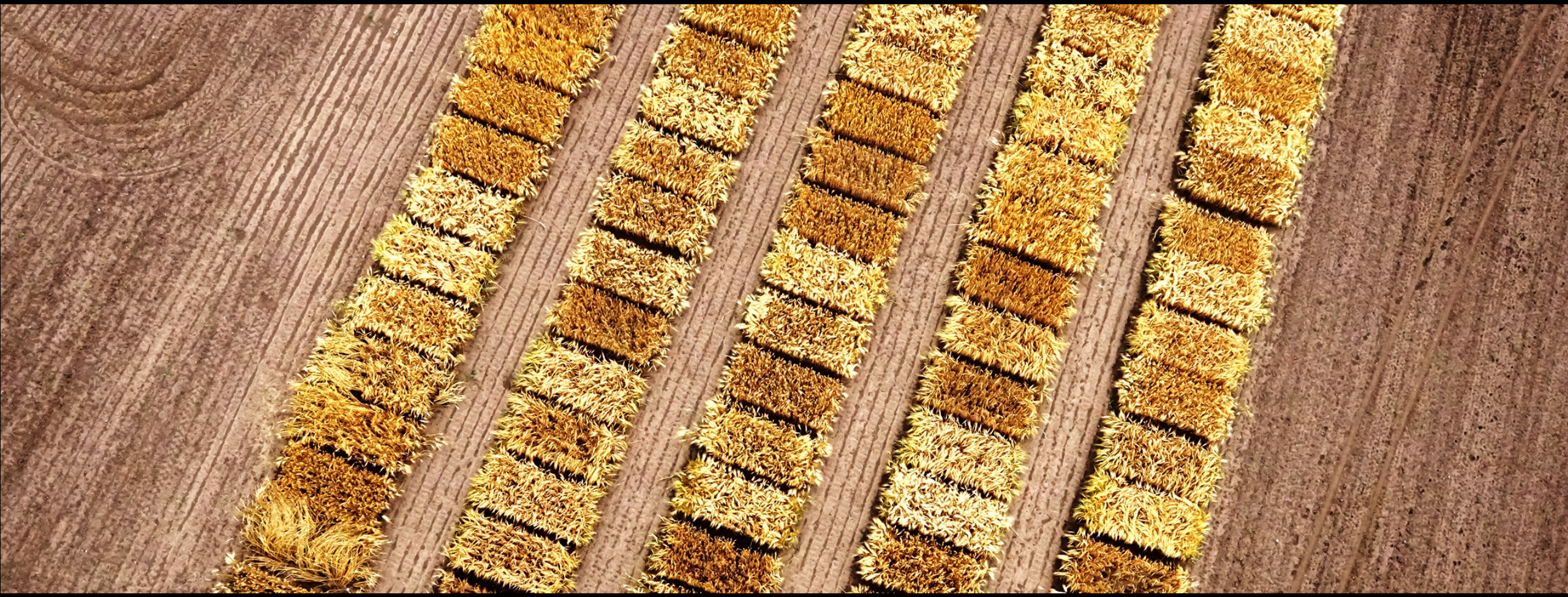
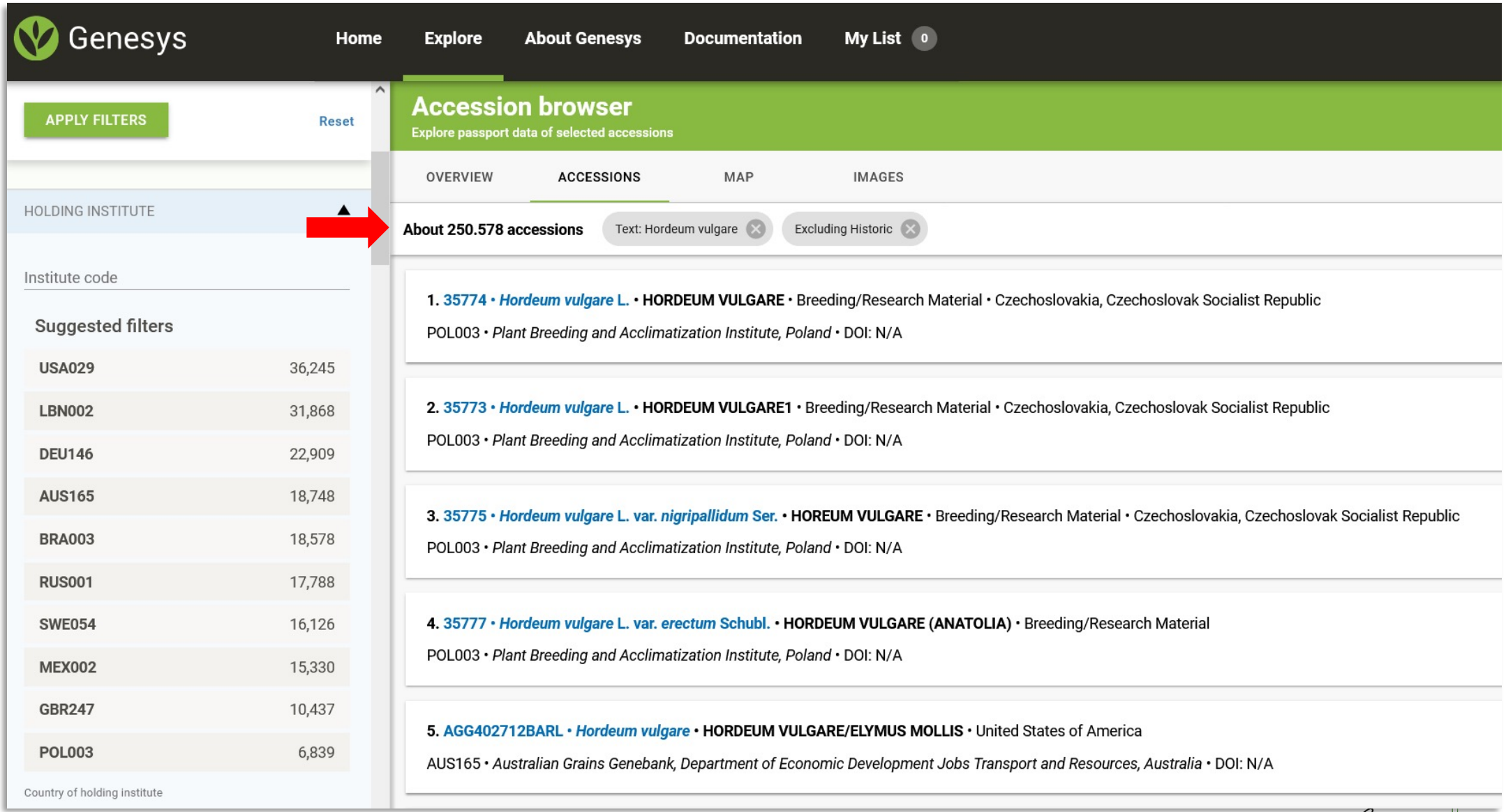


Genebank genomics - now and the future: a barley example

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



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Barley diversity

>20,000 barley accessions at IPK genebank

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

Barley diversity

Leibniz Association

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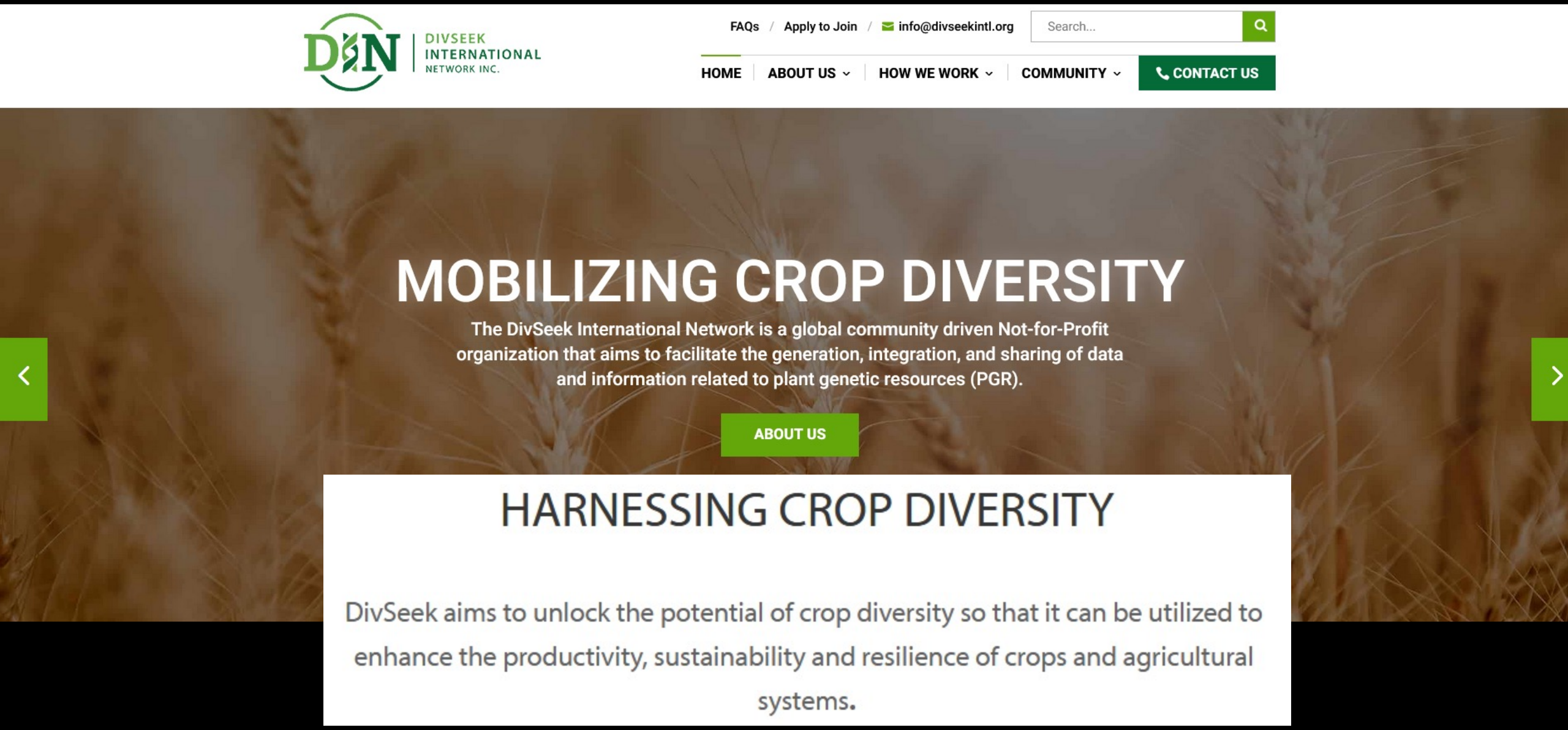
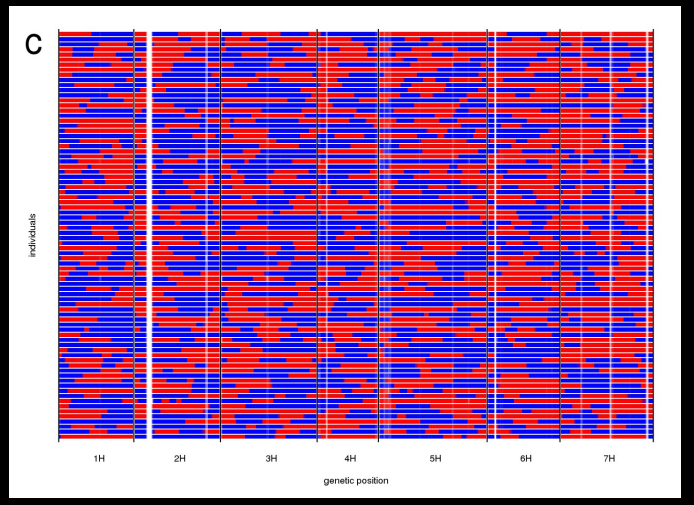


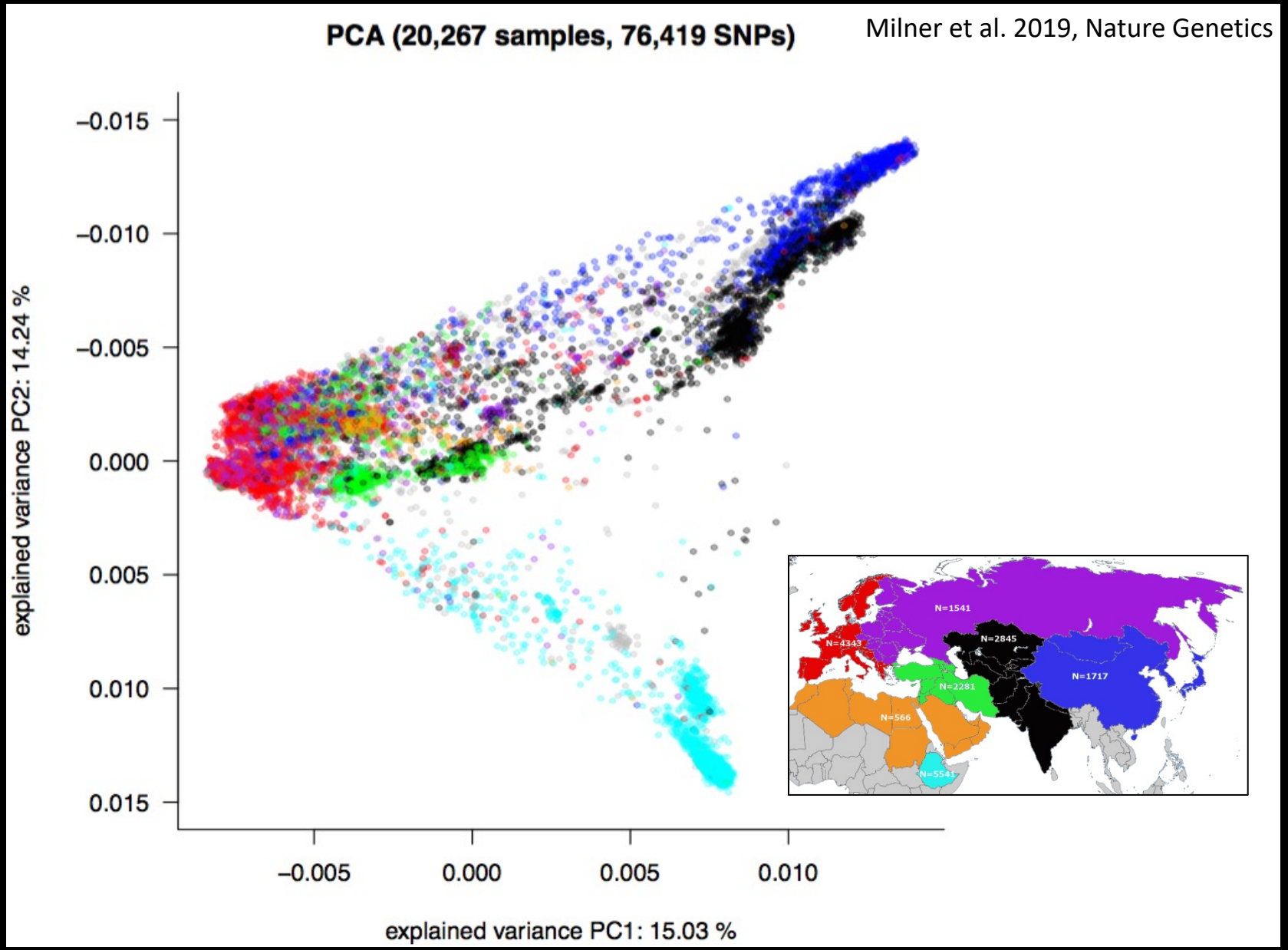
http://divseekintl.org/

barley genebank genomics

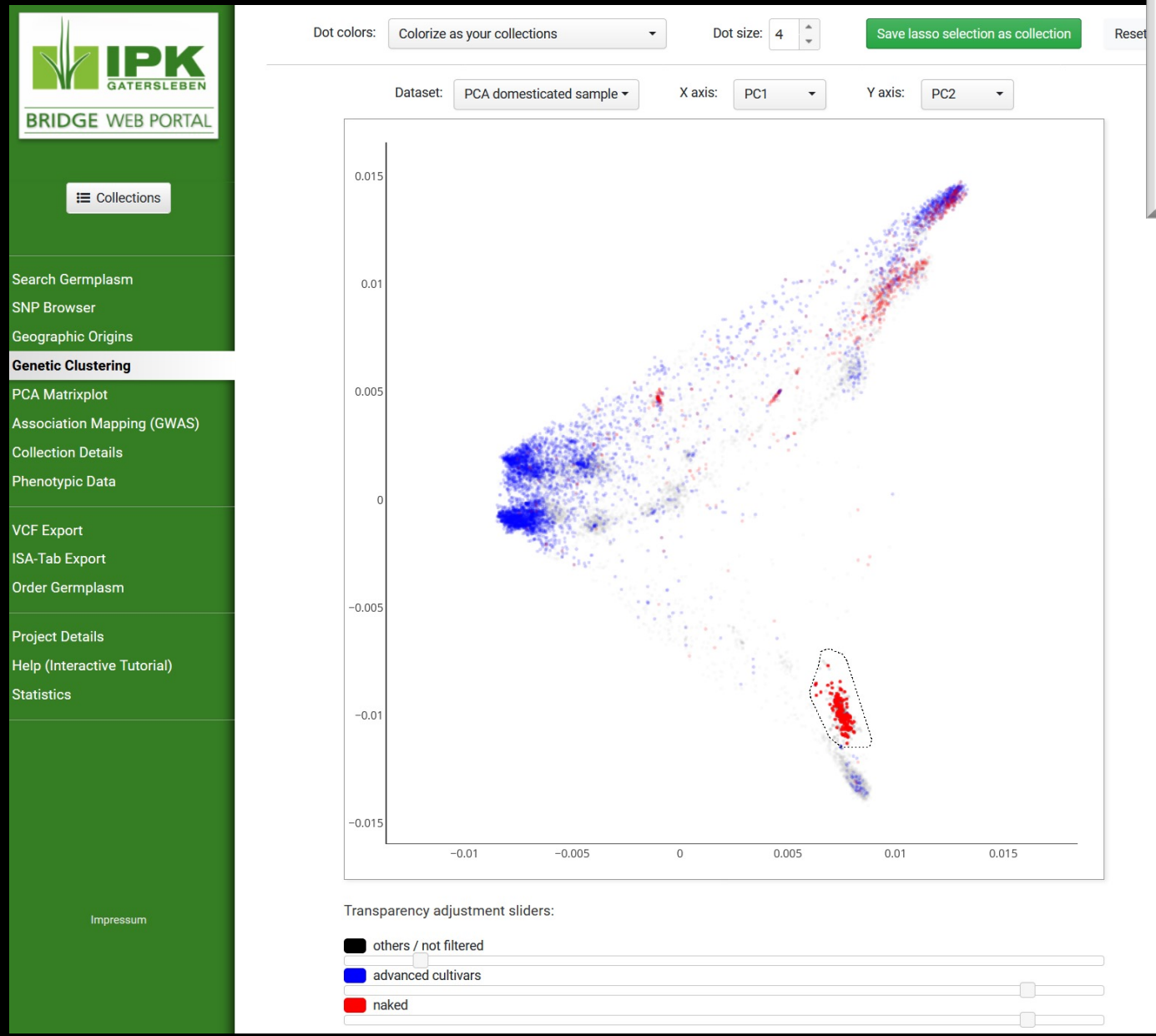


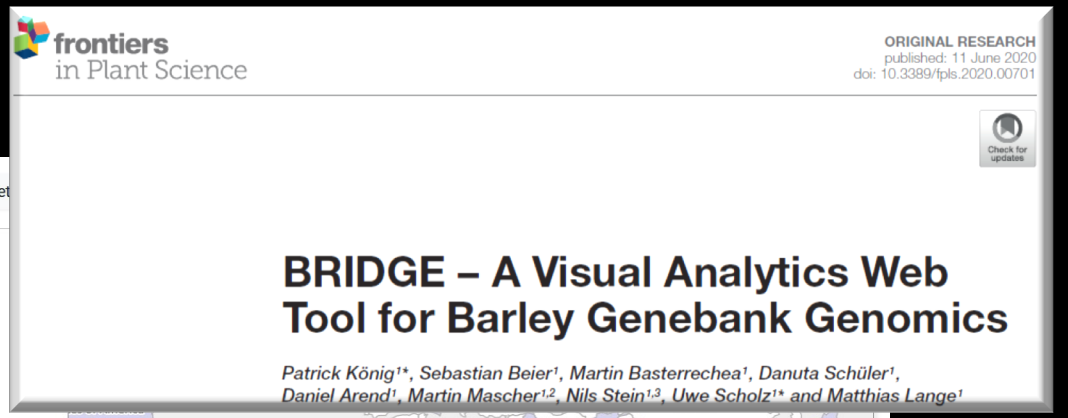
IPK GATERSLEBEN

barley diversity and geographic origin

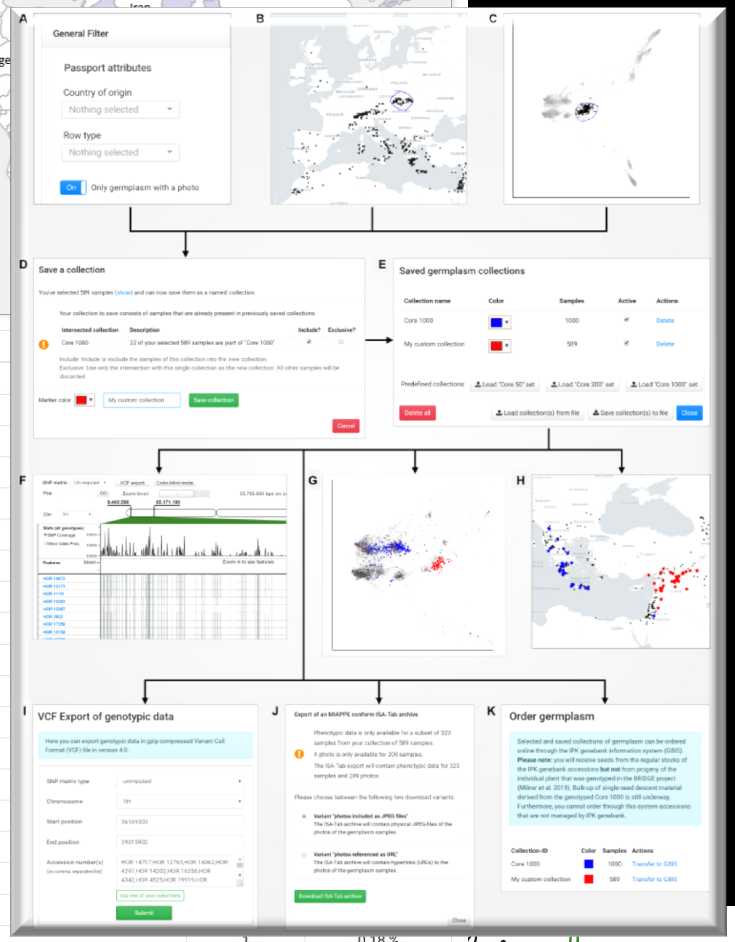


https://bridge.ipk-gatersleben.de/





Country
Ethiopia
Unknown (not in passport data)
Italy
United States of America
Germany
Iraq
Nepal
Czechoslovakia (formerly)
France
India
UdSSR (now: Russian Federation)
Russian Federation
Japan
Germany
Afghanistan
Denmark
Morocco
Austria
Sudan

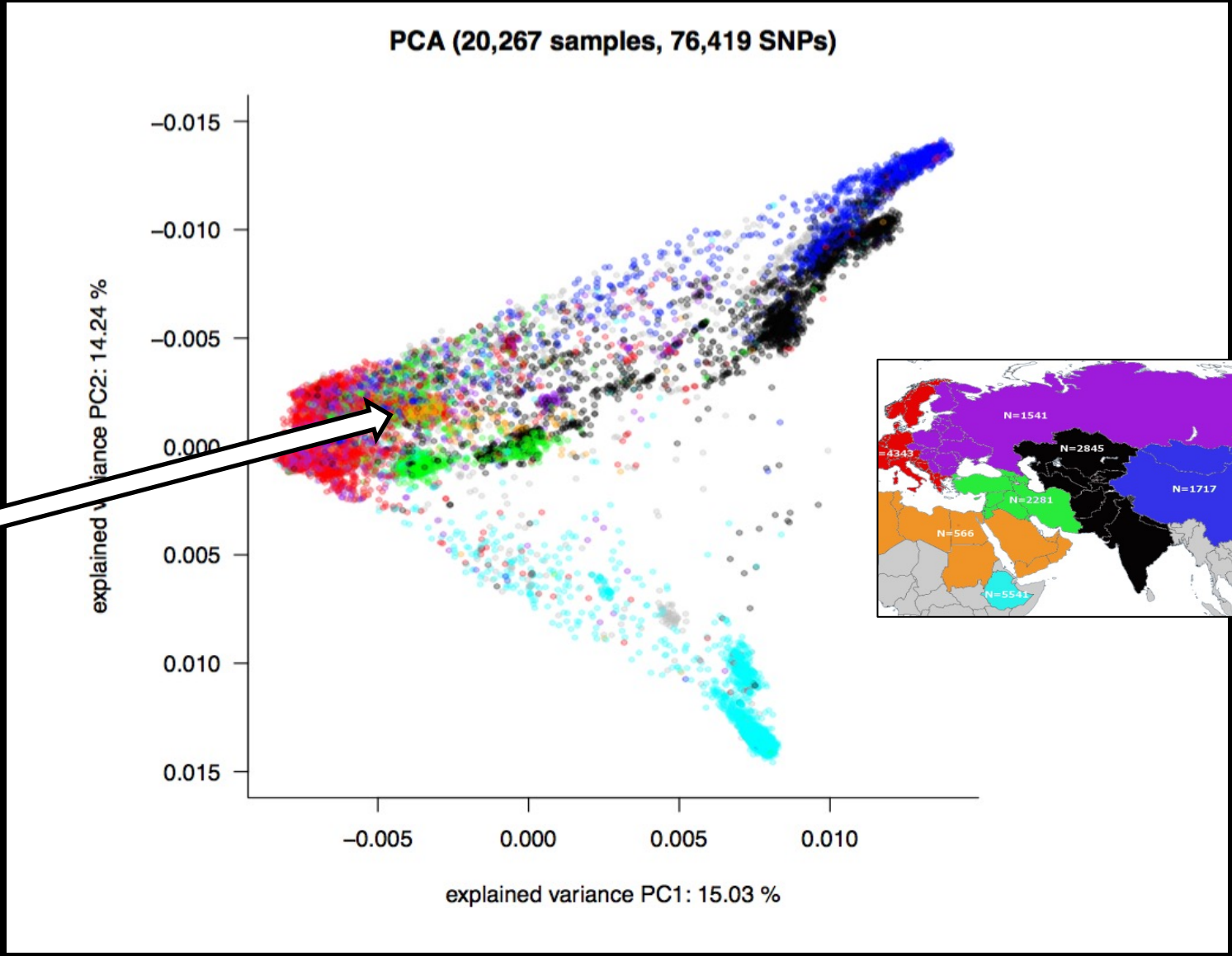


It is technically feasible to unlock barley diversity at species‘ level!

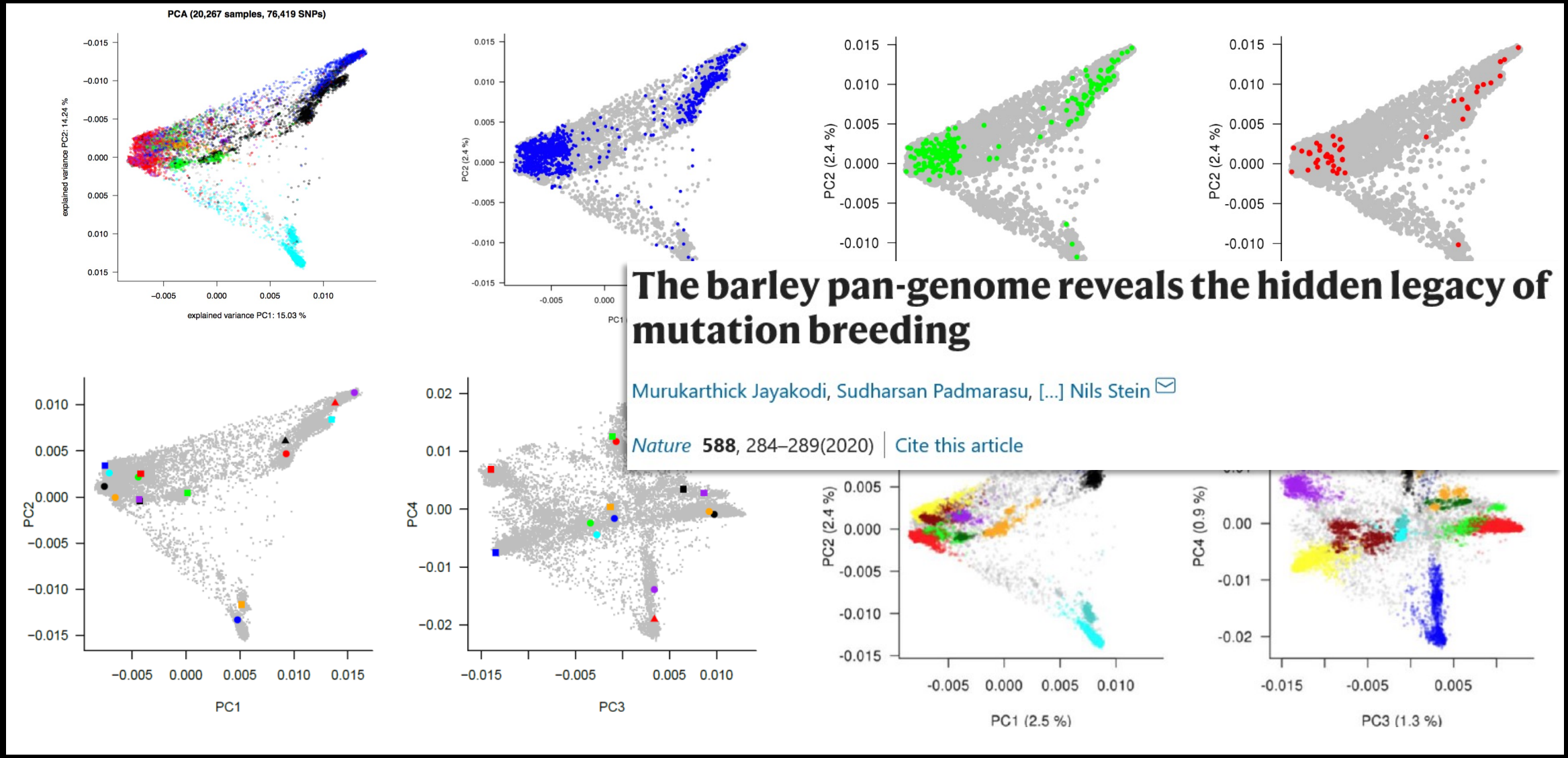
- What is your reference?
- 25K (IPK) or 250K (Genesys) represent global diversity?

How to best capture barley diversity

Barley reference sequence:
cultivar Morex



From gene bank genomics to barley pan-genome



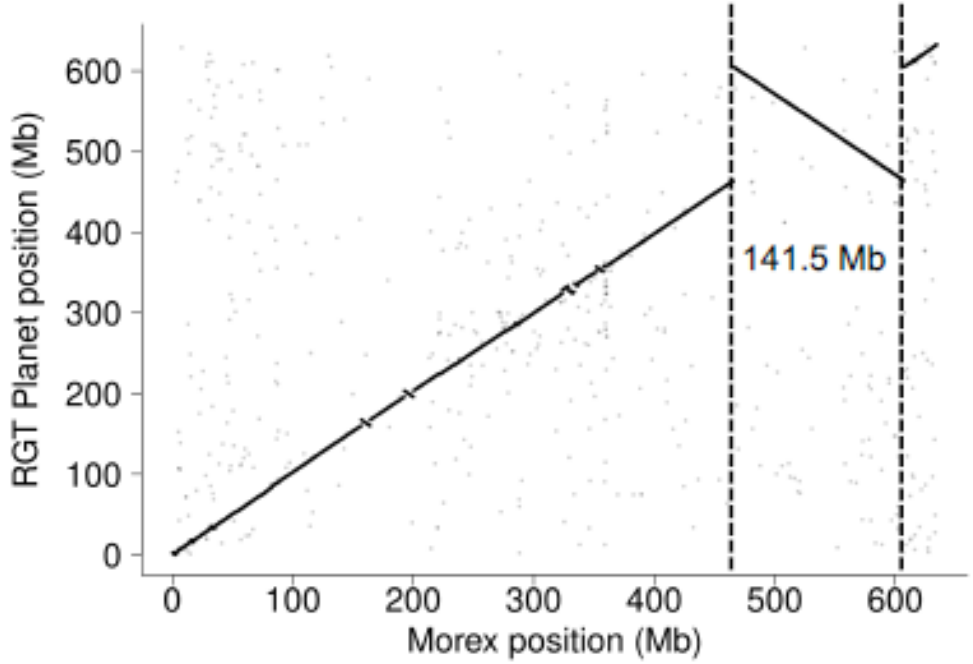
The barley pan-genome reveals the hidden legacy of mutation breeding

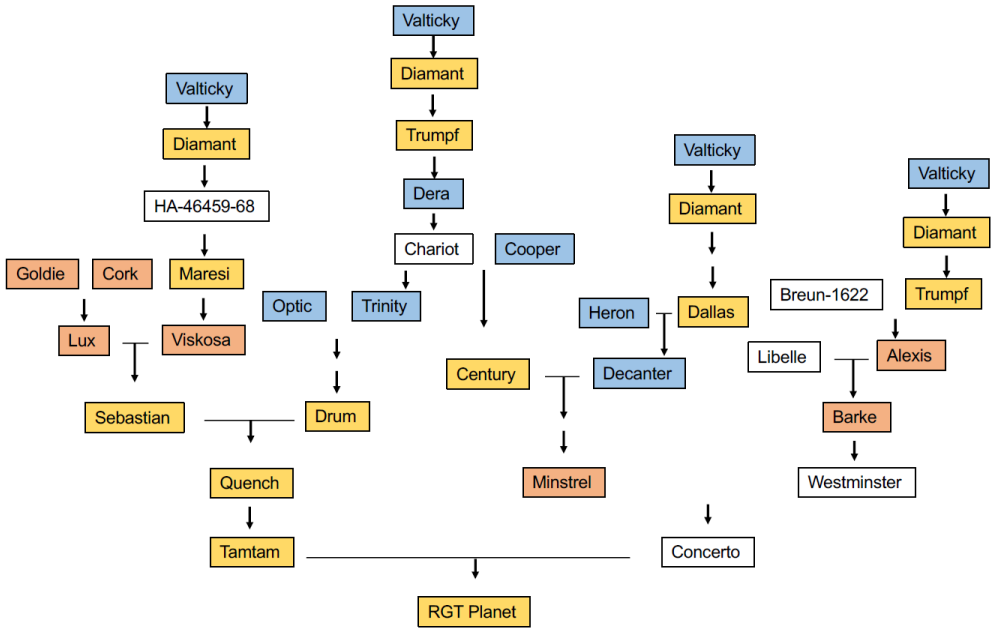
Murukarthick Jayakodi, Sudharsan Padmarasu, [...] Nils Stein

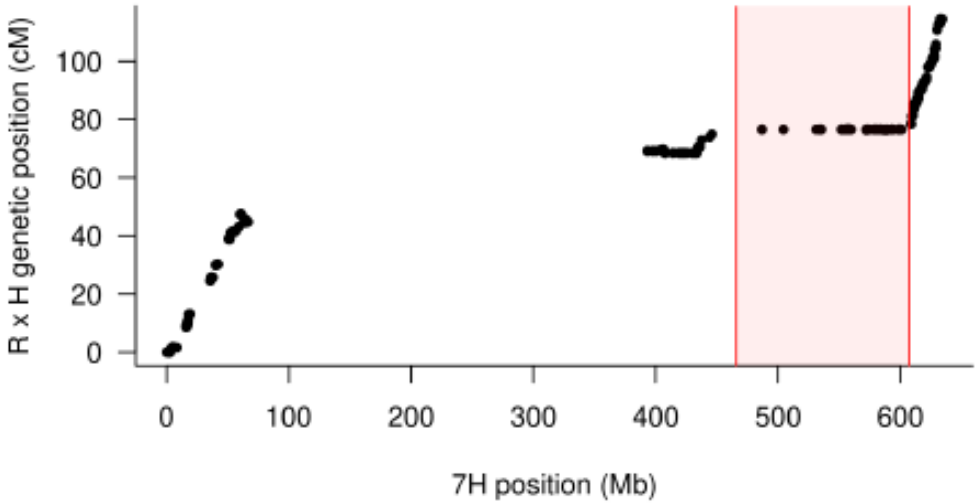
Nature **588**, 284–289(2020) | Cite this article

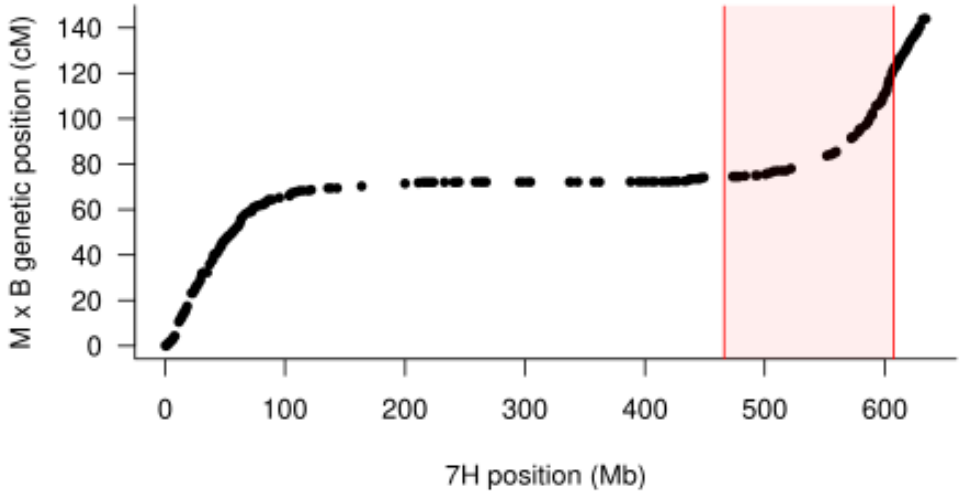
International barley pan-genome consortium

Barley pan-genome alignments

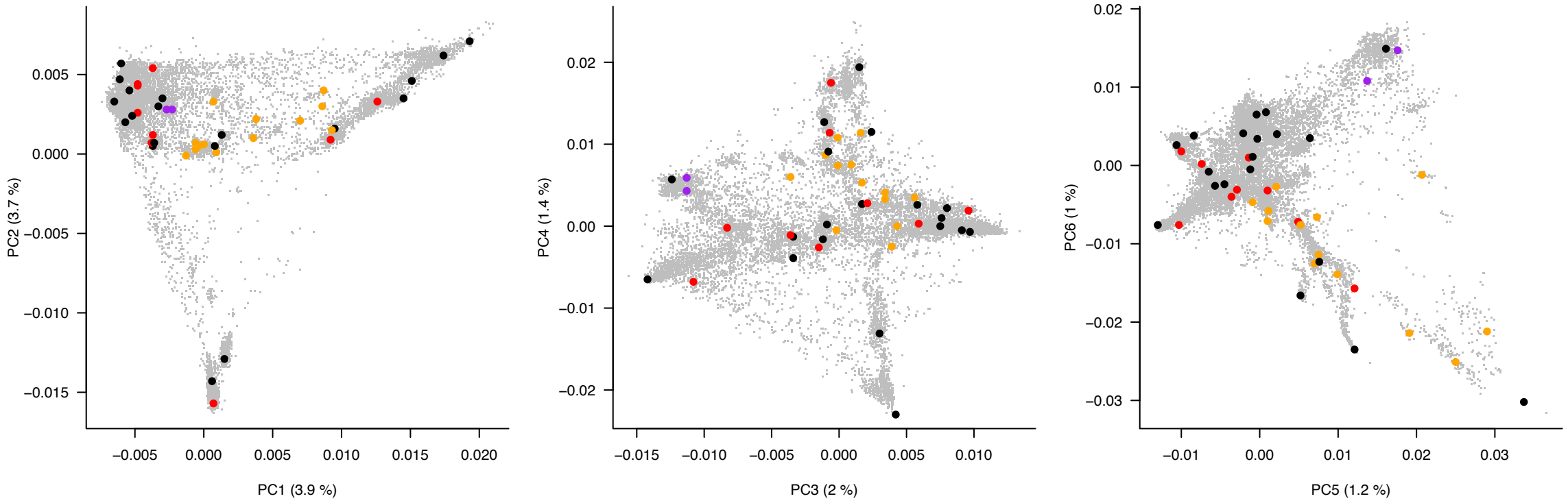






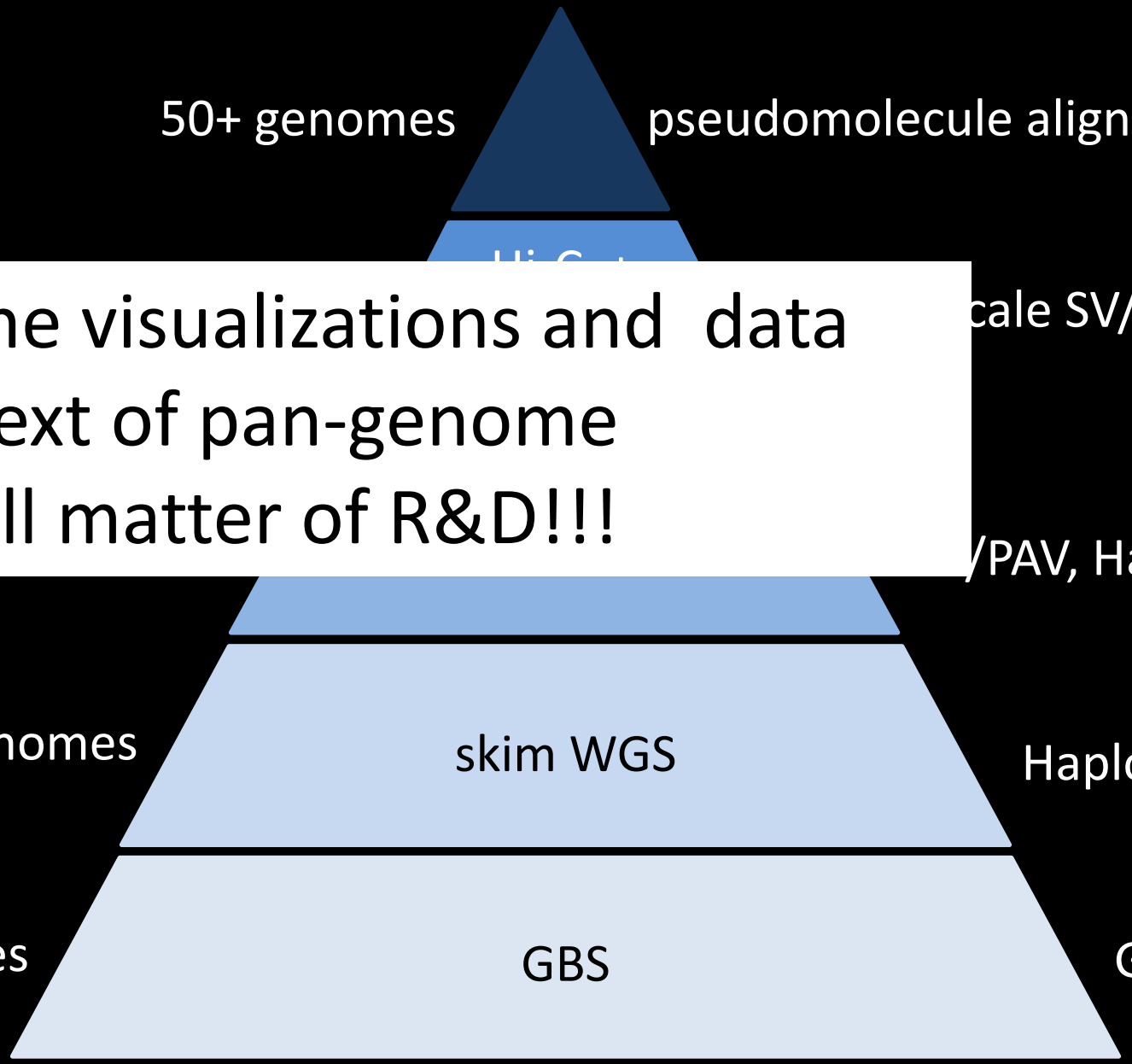


Pan-genome v2 selection in diversity space



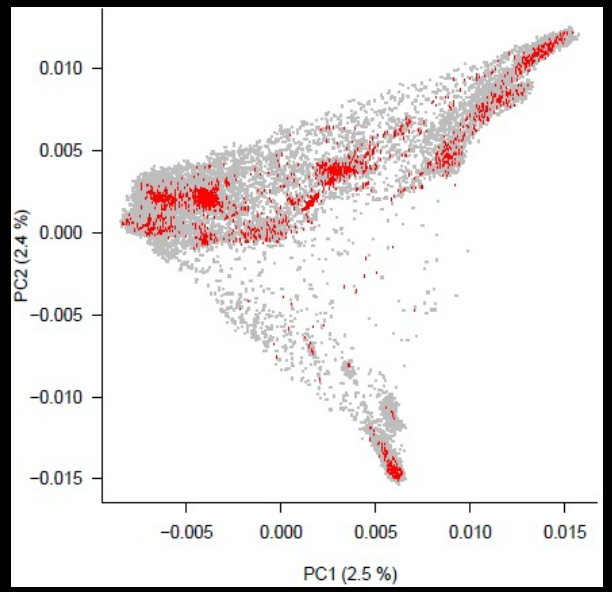
Black: Pangenome V1 (N=20)
Orange: Near Eastern barleys from „orange“ ADMIXTURE group (N=13)
Purple: Mediterranean barleys from „purple“ ADMIXTURE group (N=2)
Red: Hand-picked barleys to cover PCA space / ADMIXTURE groups (all from CORE1000, most CORE50) (N=9)

Barley pan-genome – towards barley personal genomics

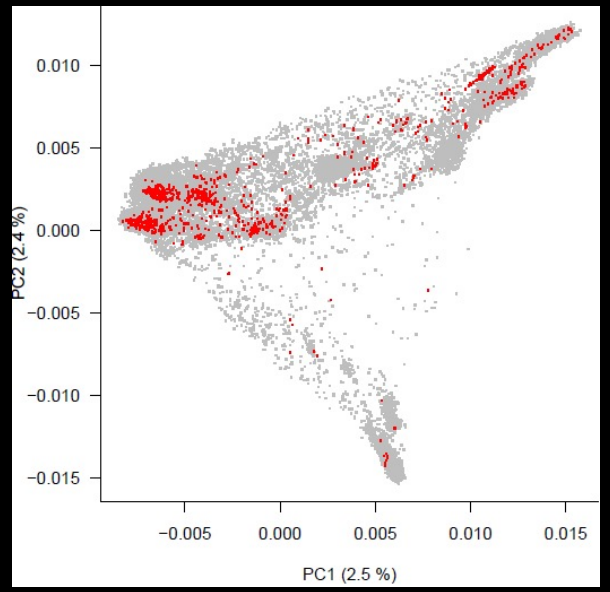


But: pan-genome visualizations and data analysis in context of pan-genome references is still matter of R&D!!!

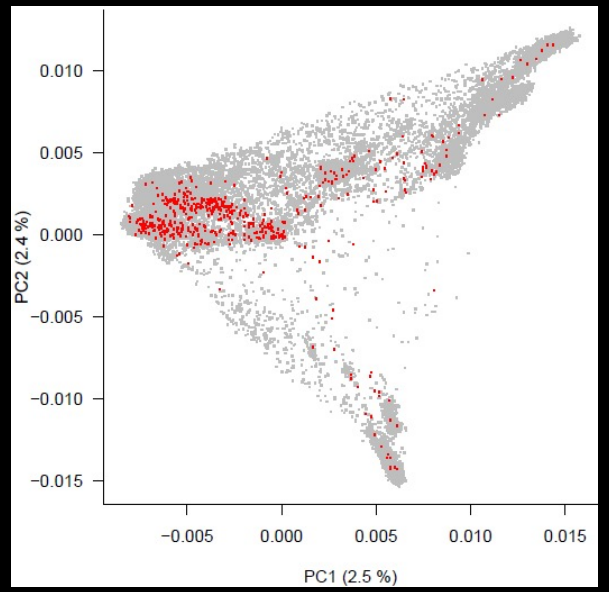
Global barley diversity represented in IPK collection



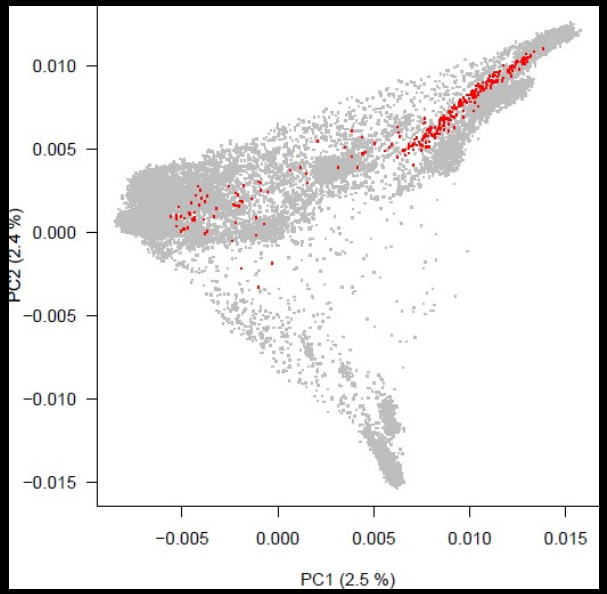
IPK/ICARDA: 2,290



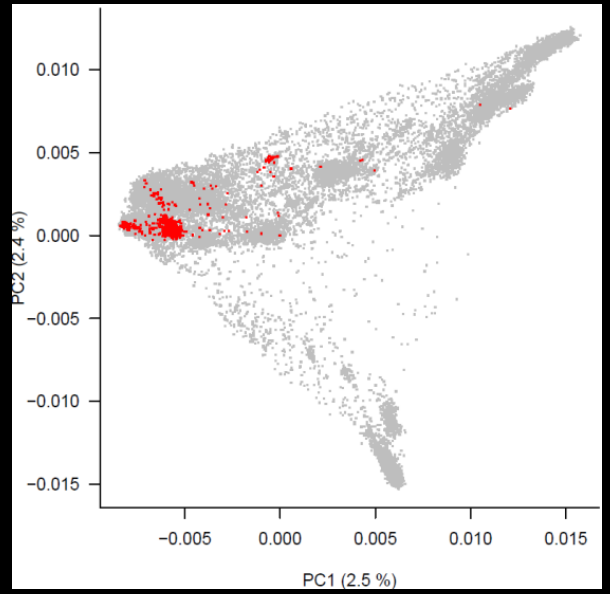
IPK/VIR: 500 (x2)



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

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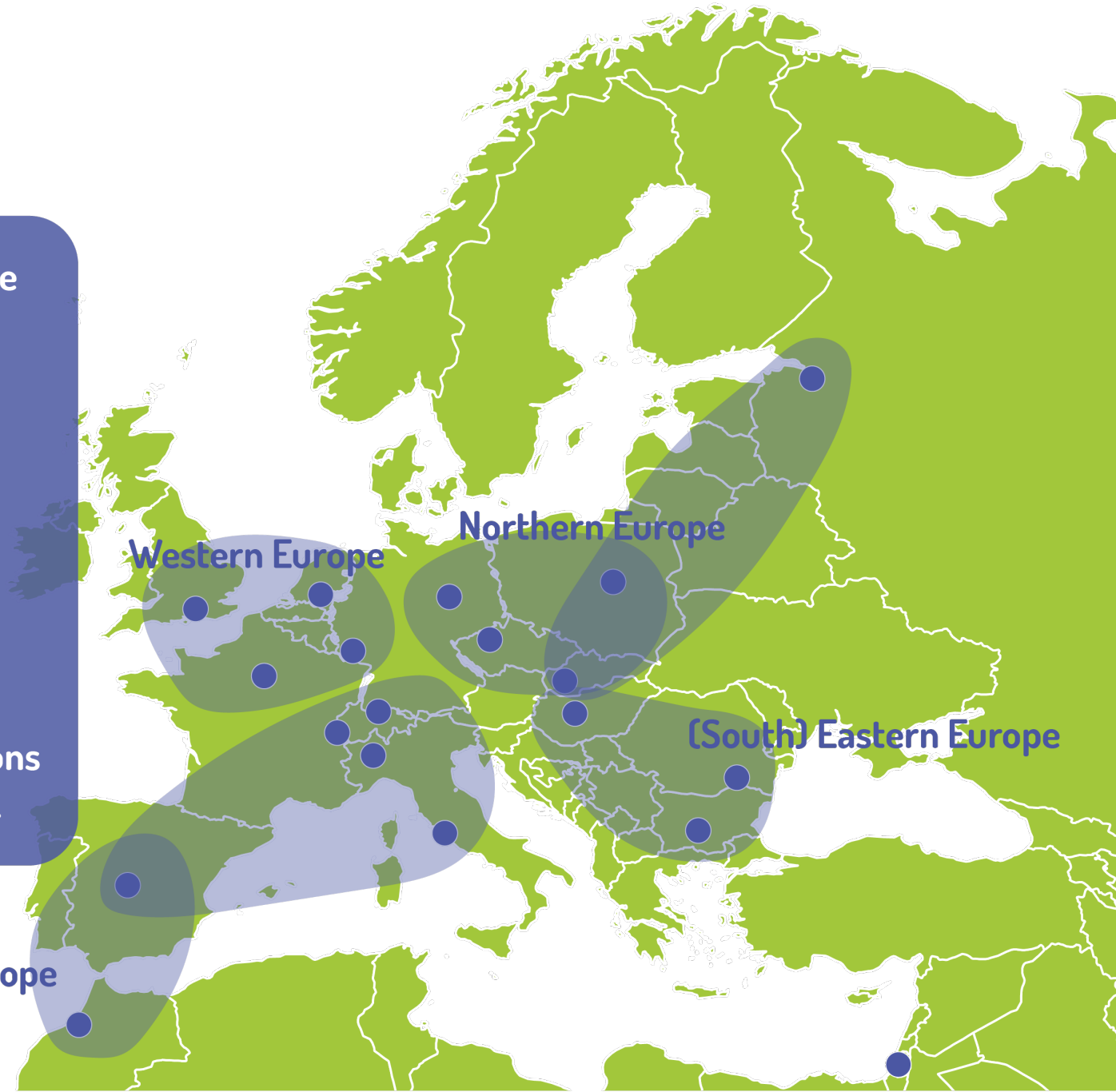
www.agent-project.eu

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').



AGENT

Training data and genomic prediction

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Summary - Discussion

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

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

Ploidy, zygosity, 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

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SAW Pakt f. Forschung und Innovation

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Activated GEnebank NeTwork

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