

3502-470 Plant Genetic Resources

Prof. Karl Schmid SS 2025

Institute of Plant Breeding, Seed Science and Population Genetics University of Hohenheim

1/23

Background

Methods for allele mining

2 / 23



Background

- \cdot Very large *ex situ* and *in situ* genebank collections exist
- Allele mining: Identification and utilization of useful genetic variation
- Erwin Baur in 1913: Collect old landraces before they disappear to maintain future breeding progress

4/23

Use of PGR in plant breeding

In addition to the constant improvement PGR are useful for:

- Adaptation to global change by tolerating higher temperature and longer periods of low precipitation.
- Opening of new regions for cultivation for example in cooler regions such as Northern Europe by improving cold tolerance (of maize, for example)
- New uses such as biomass production for biogas production by selecting varieties with a later flowering time or a larger growth potential for an increased biomass production.

5/23





Approaches to mining PGR

Different types of information are available:

- Passport information (Geographic information)
- $\cdot\,$ Phenotypic data from field evalution
- Genotypic data
- \cdot Climatic data from the site of origin

7 / 23



8/23

Approaches to mining PGR

- Core collections that maximize genetic, ecological or geographic diversity
- Identification of association between environmental and phenotypic variation
- \cdot Allele mining of known genes based on geographic distribution
- $\cdot\,$ Discovery of new genes based on tests of selection
- Population genetic modeling to identify a large number of new alleles at candidate genes

Ongoing efforts

Large-scale characterization of PGR (phenotypic and genotypic): http://seedsofdiscovery.org

Outcome: Public databases

10 / 23

Simple queries of databases

e.g., GENESYS database

See: http://www.screencast.com/t/0pdvMs0pc81r for a video

11 / 23

Identification of new disease resistance alleles in wheat

- Trait: resistance against powdery mildew
- 733 worldwide wheat accessions
- Sequencing of *Pm3* gene and pathogenicity tests
- \cdot Out of 8 cloned sequences, two new functional alleles were identified

	cc	NBS	IS		LRR			
Pm3CS								
Pm3a		54	AND THE A		1.10			
Pm3m			ACCEPTION					
Pm3_4650			1 10 CONTRACT					
Pm3_8152					1	15	un dan 🖉	
Pm3_15011			1.		11		D	
Pm3_7524				в				
Pm3_11150				1		LLC.		
Pm3_2816				·		<u> </u>		
Pm3_2616				1			F	
Pm3_3220				1			9.0.0	
	50	0 1000	1500	2000 2500	300	0 350	10 400	00

Bhullar et al., BMC Plant Biology (2010)

Focused identification of germplasm strategy (FIGS)

- 1. Identify the geographic origin of a large collection of barley landraces from plant genetic resource databases
- Produce field trial data of a selected set of accessions representing a broad and climatically diverse range of regions-of-origin of accessions. Conduct field trials at multiple locations.
- 3. Measure a substantial number of traits (> 10) in the field trials.
- 4. Receive climatic data from climate databases such as the WorldClim database
- 5. Organise the data into a three-dimensional array with three dimensions: Genotype, trait, as well as year with location.
- 6. Create a second three-dimensional array with the dimensions: Genotype, 12 monthly means of climate data, and a set of climate variables.
- 7. Analyse with the PARAFAC (Generalized PCA for higher order arrays) and N-PLS method (N-way partial least squares for multiway regression).

13 / 23

Multidimensional data structure for FIGS





FIGS analysis in Faba beans

Rank	drought related parameter	model					
		rpart-caret	RF				
			mean decrease accuracy		mean decrease Gini		
1	Leaflet temperature	34.91	0.26	55.	41		
2	Canopy temperature	13.68	0.10	31.	64		
3	Relative water content	12.46	0.02	9.6	4		
4	Leaflet area	9.95	0.01	6.39	9		
5	Stomatal length	6.70	0.01	2.30)		
6	Fertile tillers	4.72	0.00	0.47	7		
7	stomatal area	4.13	0.00	1.01	1		
8	Transpiration rate	3.61	0.03	6.94	4		
9	Stomatal area per unit area of leaflet	2.75	0.01	3.52			
10	Photosynthetic rate	2.34	0.01	4.25			
11	Days to flowering	2.21	0.00	1.95	5		
12	Intercellular CO ₂	1.64	0.00	0.93	3		
13	Stomatal density	1.26	0.01	2.43	2		
14	Water use efficiency	1.21	0.01	1.89	9		
15	Stomatal conductance	0.86	0.01	1.83	3		
16	Stomatal width	0.14	0.00	0.82	2		

doi:10.1371/journal.pone.0063107.t005 Khazaei et al., PLOS ONE (2013)

FIGS to identify new resistance alleles

- Yellow rust in wheat (Bari et al., 2012)
- Russian wheat aphid (El Bouhssini et al., 2011)
- Stem rust in wheat (Endresen 2011)
- Net blotch in barley (Endresen 2011)
- Ug99 rust pathogen allele (Endresen et al., 2012)

17 / 23

Critique of FIGS

- $\cdot\,$ Depends strongly on quality of phenotypic evaluation
- Passport data often insufficient
- \cdot Based on pattern matching
- Predictive ability is often low
- Information about genetic history and biological mechanisms not used

Population genetic-based allele mining

Example: Resistance against barley yellow mosaic and barley mild mosaic virus

- All modern barley varieties have the *rym4/rym5* recessive resistance alleles
- Sequence eIF4E genes in 1090 barley landraces and old cultivars from 84 countries
- 47 new haplotypes
- In coding regions: all polymorphisms replace an amino acid

19 / 23

21/23

Geographic distribution of eIF4E haplotypes



Haplotype diversity at eIF4e haplotypes



Hofinger et al. (2011)

Summary of allele mining

- \cdot Many new, potentially functional alleles were discovered
- But no functional tests (yet): Functional tests are required

22 / 23

References i

Hofinger BJ, Russell JR, Bass CG, Baldwin T, Dos REIS M, Hedley PE, Li Y, Macaulay M, Waugh R, Hammond-Kosack KE, Kanyuka K (2011) An exceptionally high nucleotide and haplotype diversity and a signature of positive selection for the eIF4e resistance gene in barley are revealed by allele mining and phylogenetic analyses of natural populations. Molecular Ecology 20(17):3653–3668, DOI 10.1111/j.1365-294X.2011.05201.x, URL http://onlinelibrary.wiley.com/doi/10.1111/j. 1365-294X.2011.05201.x/abstract

23 / 23