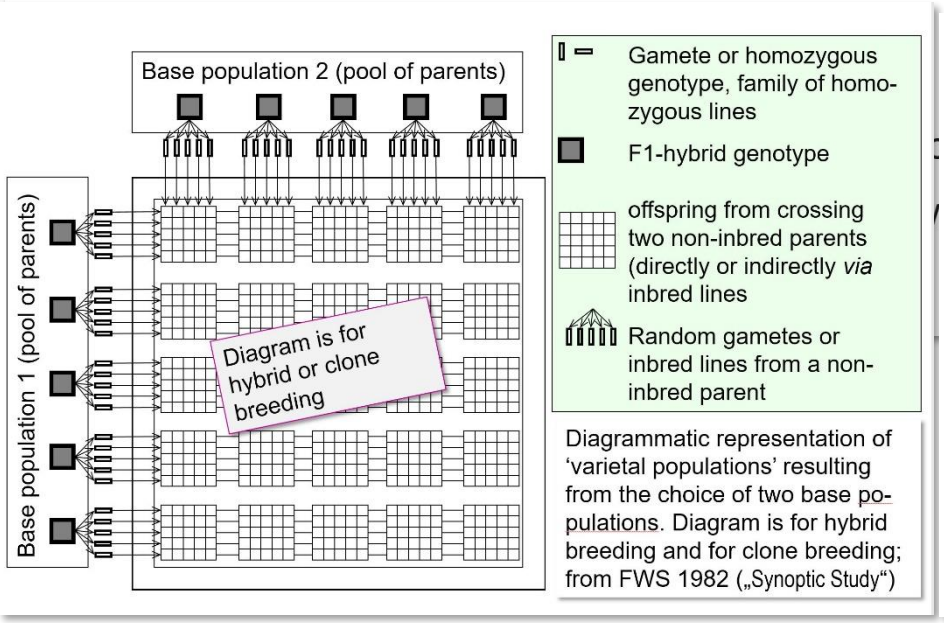
GEORG-AUGUST-UNIVERSITÄT GÖTTINGEN

CiBreed Retreat Oct. 2024
apl. Prof. Dr. Wolfgang Link
Status & Current Research in the ….
Division of Plant Breeding Methodology

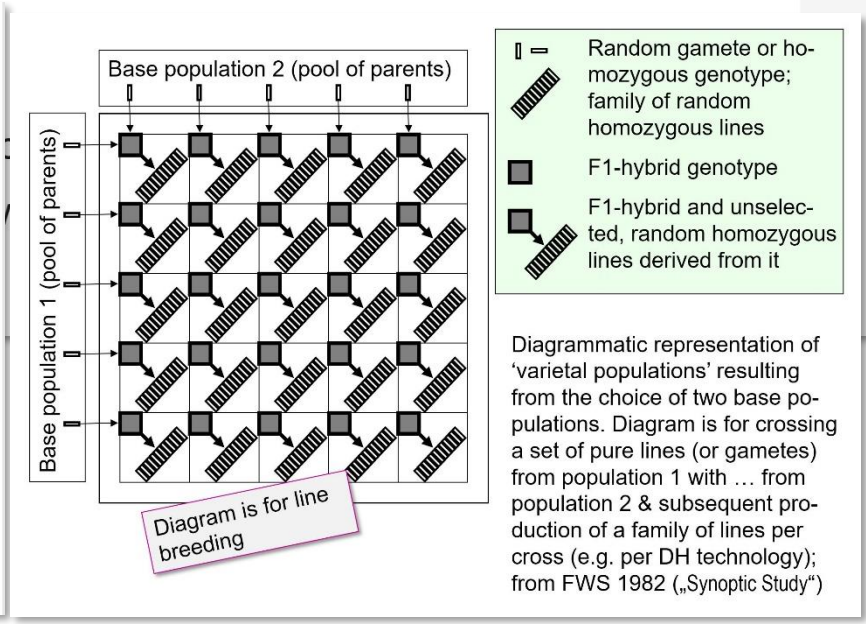
PEOPLE PUBLICATIONS RESEARCH TEACHING NEWS & ANNOUNCEMENTS HISTORY OF THIS CHAIR AND DIVISION

SEARCH DEUTSCH

Division of Plant Breeding Methodology



Diagrammatic representation of 'varietal populations' resulting from the choice of two base populations. Diagram is for hybrid breeding and for clone breeding; from FWS 1982 („Synoptic Study")



Diagrammatic representation of 'varietal populations' resulting from the choice of two base populations. Diagram is for crossing a set of pure lines (or gametes) from population 1 with … from population 2 & subsequent production of a family of lines per cross (e.g. per DH technology); from FWS 1982 („Synoptic Study")

Here are the hyperlinks to jump to the further Divisions (Working Groups) within the Department of Crop Sciences

Here is the hyperlink to CiBreed

We are, depending on how you count, 15 team members.
Office is administrated by E. Kistner.

Division of Plant Breeding Methodology, October 2024

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*D. Kaufmann, Senior Technician, is 50% ‘here’ and 50% in the Division of Crop Plant Genetics

This Division offers modules at BSc level, MSc level, PhD level.
For Agricultural Science, Crop Protection, integrated PAB, GFA.

Bachelor

- Pflanzenbau und Pflanzenzüchtung (Nr. 740372)
- Wissenschaftliches Arbeiten und professionelles Präsentieren in der Pflanzenproduktion (Nr. 740119)
- Experimentelle Pflanzenzüchtung (Nr. 740669)
- Spezielle Pflanzenzüchtung (Nr. 740161)
- Pflanzenbau, Pflanzenzüchtung und Graslandwirtschaft (Nr. 740969
- Planung und Auswertung experimenteller Bachelor-Arbeit in Nutzpflanzenwissenschaften (Nr. 740949)
- Datenmanagement, Versuchsplanung und graphische Darstellung mit Excel (Nr. 740919)

The Division offers modules at BSc level, MSc level, PhD level.
For Agricultural Science, Crop Protection, integrated PAB, GFA.

Master

- Genetische Grundlagen der Pflanzenzüchtung (Nr. 740053)
- Genome Analysis & Appl. of Markers in Plant Breeding (Nr. 740047
- Plant Breeding Methodology and Genetic Resources (Nr. 740411)
- Quantitative Genetics and Population Genetics (Nr. 740856)
- Breeding Schemes and Programs in Plant and Animal Breeding (Nr. 740885
- Journal Club: Evolutionary Genetics and Breeding (Nr. 740914)
- Selection Theory, Design and Optimisation of Breeding Programs (Nr. 740815)
- Planung und Auswertung experimenteller Master-Arbeit in Nutzpflanzenwissenschaften (Nr. 740948)
- Practical Statistics and Experimental Design in Agriculture (Nr. 740690)
- Methodisches Arbeiten: Versuchsplanung und –auswertung (Nr. 740023)

At BSc level, MSc level, PhD level.

PhD

- New Areas in Plant Breeding PhD (Nr. 740458)

We modernise the basic content of our plant breeding courses and prepare online-compatibility – still working on it.
Quentin Burandt: Plant Breeding Basics
Wolfgang Link: Population & Quantitative Genetics & Plant Breeding Methodology

Plant Breeding Basics

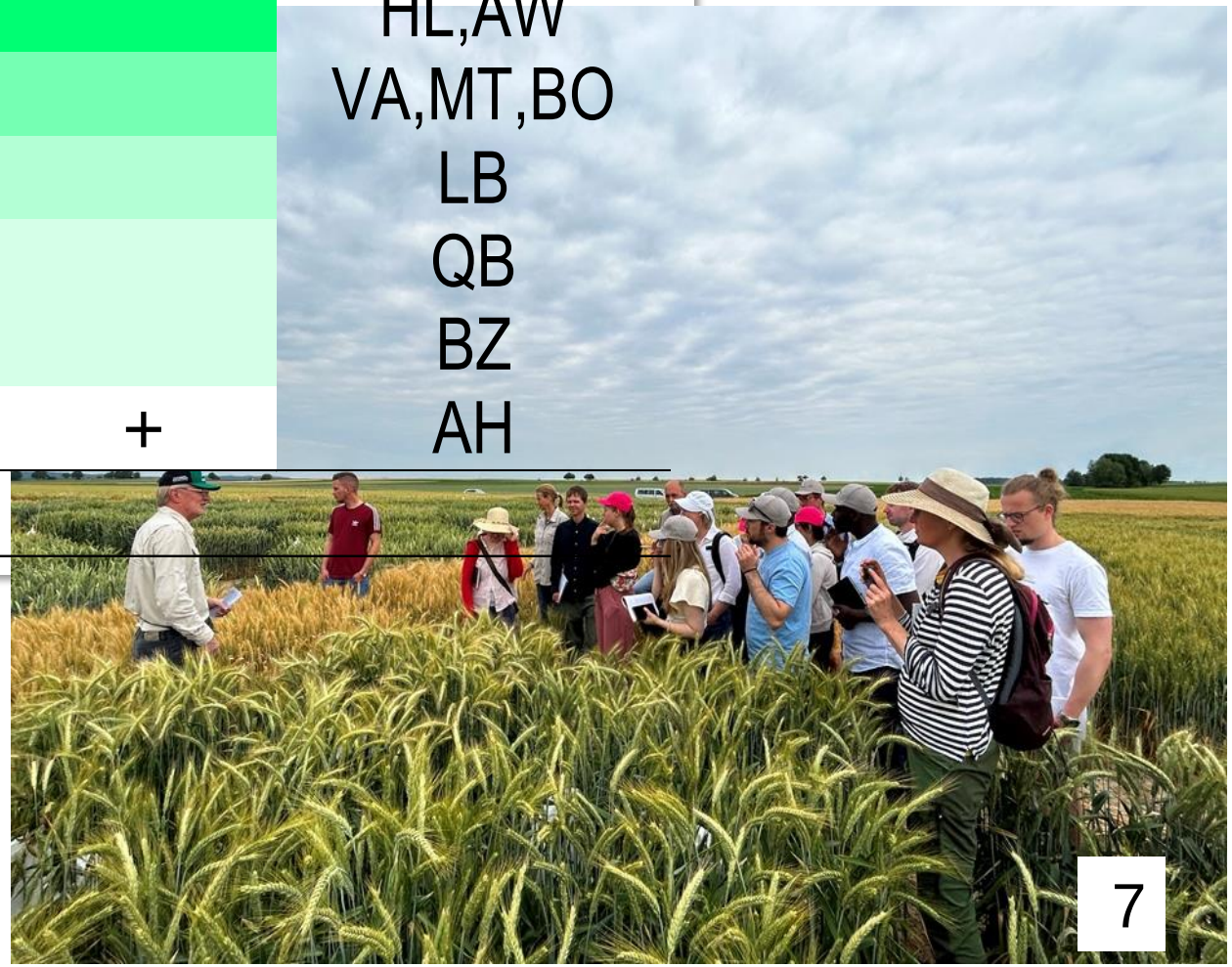
An ILIAS-based self-learning module;
especially for those starting the iPAB program.
If your BSc education in genetics and plant breeding has not well enough prepared you for the iPAB MSc program, then you invest 5 -10 hours here and make up for what is missing.
►►► Start in October 2024 ☺

Plant Breeding: Population and Quantitative Genetics and Breeding Methodology

A sequence of N>32 chapters (18-24 pages each), based on audio-enriched PowerPoint.
A streamlined, coherent, compilation of two MSc modules (Nr. 740053, Nr. 740411)
> Plant Breeding Methodology
> Genetic Principles of Plant Breeding

We are involved in several projects, acquired by us (TB, WL, LB, QB) or in cooperation

N	Fund acquired by			Project conduct by			Scientist
	us	coope-ration	others	us	coope-ration	others	
2	+			+			HL,AW
3	+				+		VA,MT,BO
1		+		+			LB
1		+			+		QB
2			+		+		BZ
1			+			+	AH
Σ=10							



Research of Birgit Zumbach. These two projects belong to the Divison of Crop Plant Genetics

Birgit Zumbach

- **Fungal disease resistance mapping exploring cross-kingdom: RNA interference in sugar beet (FUNBEET)**

→ Acquire fundamental understanding of pathogenic interactions between fungi and crops based on transcriptome analysis

Prepare joint DFG project application by the company Strube Research and the Division Crop Plant Genetics

EU-Project **CONSERWA** https://conserwa.eu

Evidence-based support for transition to agroecological weed management **in different** farming systems **and European regions**

→ Arrange group interviews/discussions with farmers and governmental advisors

Source: https://www.strube.net/global/products/sugar-beet/cultivation-lexicon/diseases-and-pests/cercospora

The DNPW budget for PostDocs is invested here to develop a Competetive & Innovative Research Project. Current target orientation:

- Breeding Pea for Vegetarian/Vegan Human diets
- Protein content, amino acid composition, mineral content

Lisa Brünjes

Pea-derived Protein Powder. ©Wikipedia

FABALOUS
Faba **b**ean **a**biotic stress to**l**erance for impr**o**ved yield **s**tability

Lisa Brünjes

- BMBF (February 2025 - January /2029), a project on faba bean, *Vicia faba*
- Multiple stresses at phenotypic, molecular, metabolic levels
  → Drought, Heat, *Uromyces, Botrytis*
- 15 project partners (Coordinator: Schießl-Weidenweber, **Universität Giessen**)

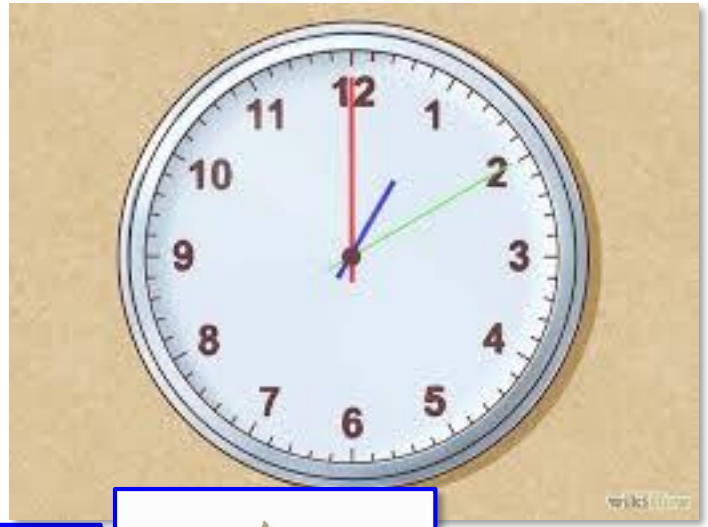
Göttingen Work Packages

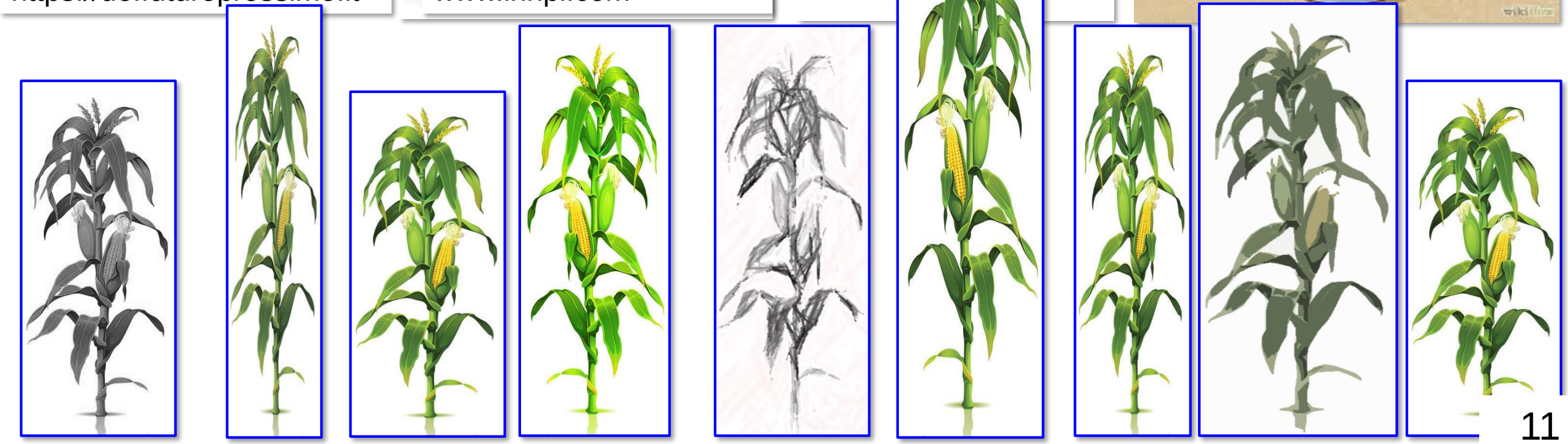
- Phenotyping stress response to heat & drought in rainout shelters; phenotypic data for systems biology and metabolomics
- Phenotyping pollen characteristics with Impedance Flow Cytometry
- Effects of abiotic stress on pollinator activity

TB: “Shorten maize breeding cycle by training GP model from phenotype data of individuals (instead of plot-based entries)”

https://de.futuroprossimo.it

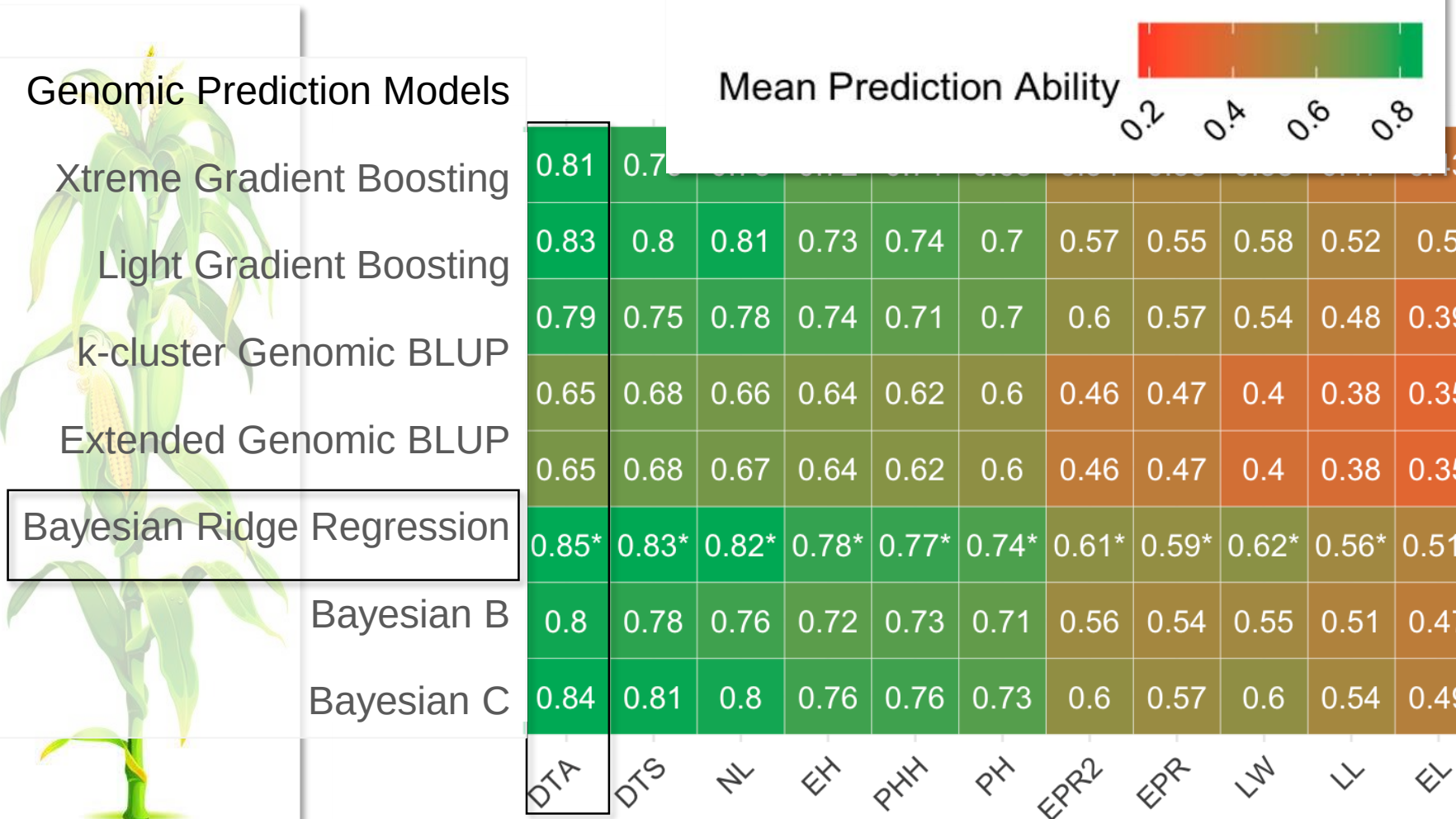
www.inhpl.com





Shorten maize breeding cycle by training GP model from phenotype data of individuals (instead of plot-based entries).
Prediction ability: Days to Anthesis (0.85), Grain Yield (0.50).
Bayesian Ridge Regression gave the highest prediction ability.

Leke Victor Aiyesa



DOI: https://doi.org/10.21203/rs.3.rs-4925882/v1
https://doi.org/10.21203/rs.3.rs-4337825/v1
PLBR-24-OAr-366 (manuscript ID – plant breeding journal)

Modelling non-addictive effects in genomic prediction using classical and machine learning methods. 1st supervisor: R. Sharifi

Improve the genomic prediction accuracy by combining modelling of
Additive effects; Dominance effects; Epistatic effects
... using locus-specific weighted **dominance effect** matrix transformation
... using Genomic Best Linear Unbiased Prediction, Gradient-Boosted Decision Trees, and Convolutional Neural Networks.

Bright E Osatohanmwen

Gen.

SNP MARKER MATRIX

	SNP 1	SNP 2	SNP 3	SNP 4	Trait value
1	AA	CC	AT	GG	2.85
2	AT	CG	AT	GG	1.72
3	TT	GG	TT	CC	2.92
4	AA	GG	AA	CC	2.81
5	AA	CC	TT	CG	2.86

Locus-specific weighted **dominance** effect matrix transformation

Transformed SNP MARKER MATRIX

SNP 1	SNP 2	SNP 3	SNP 4
0	2	2	2
0.92	0	2	2
2	0	0	0
0	0	0	0
0	2	2	1.4

Genomic Prediction & validation Using BLUP, GrBDTrees, Conv. Neur. Networks and more

PhD student at epartment of Forest Genetic and Tree Breeding

Experim. evolution in maize with replicated divergent selection

Preprint: https://doi.org/10.1101/2024.02.26.582128

Projects with the Dep. of Forest Genetic & Tree Breeding (Prof. Gailing)

- Environmental association analysis in European beech populations
- GWAS and identification of signals of polygenic selection in European beech pops.

Farbweizen. **Field & teaching based wheat breeding**

- Crosses of coloured tissue wheat x wheat elite varieties

Bachelor Thesis: Research into a non-destructive colour analysis in the breeding of coloured wheat“ (2021, 2023)

Mila Tost

And more

JO[illegible] LE

Ghat: an R package for identifying adaptive polygenic traits

Medhat Mahmoud, Mila Tost, Ngoc-Thuy Ha, Henner Simianer, Timothy Beissinger ✉ Author Notes

G3 Genes|Genomes|Genetics, Volume 13, Issue 2, February 2023, jkac319, https://doi.org/10.1093/g3journal/jkac319

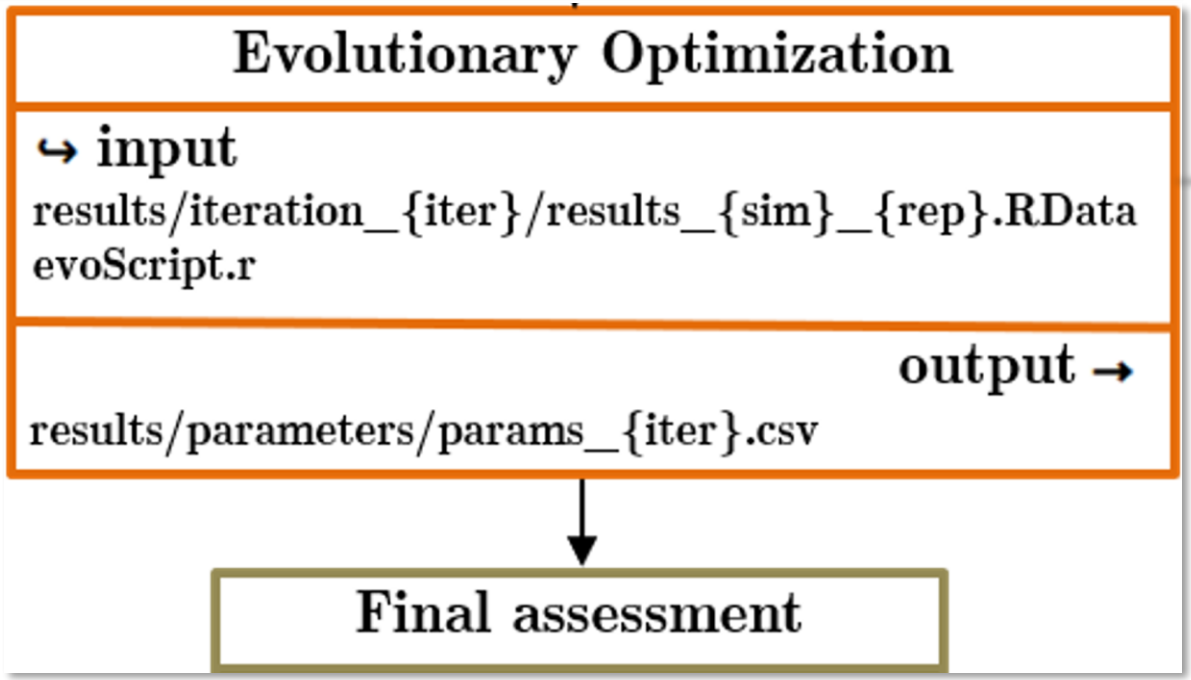
Published: 01 December 2022 **Article history** ▾

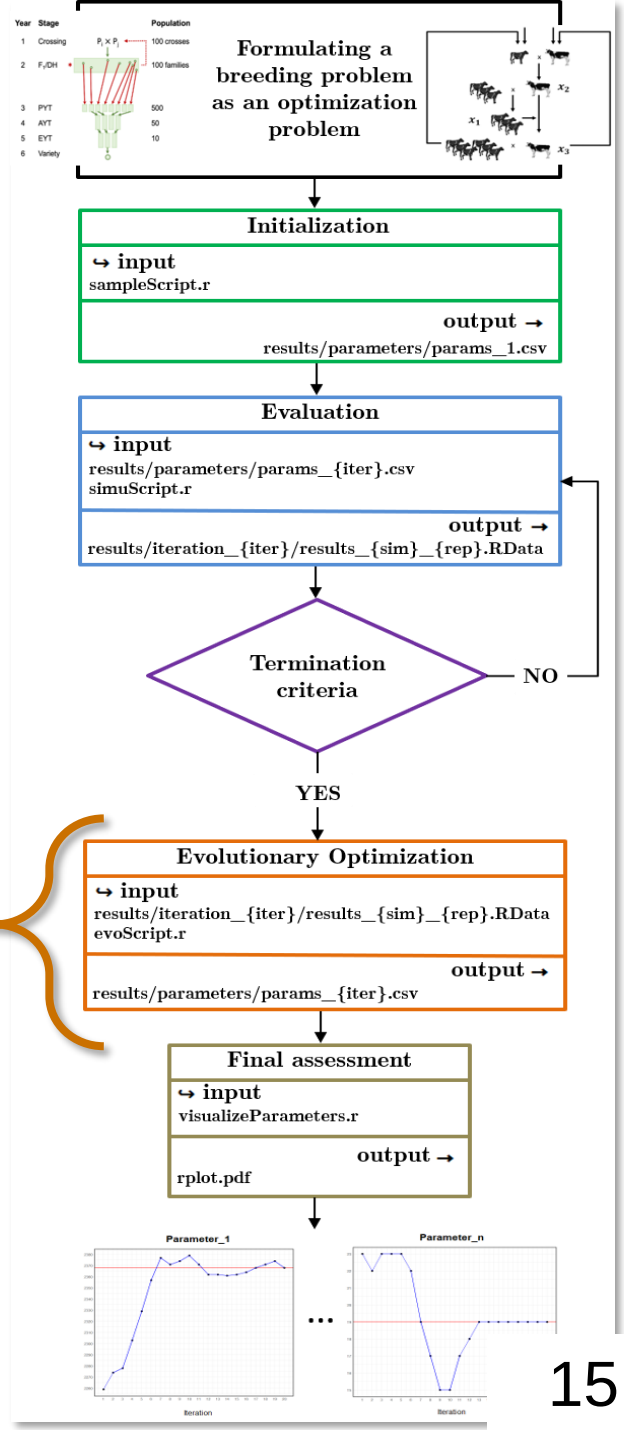
MoBPSopti Project. Development of an optimization framework for complex breeding programs. Supervs: Simianer, Schlater, Rohde, Pook.

- Transform the breeding problem into an optimization challenge
- Employ stochastic simulation to model and simulate various breeding scenarios
- Reduce the stochasticity of target functions via kernel regression
- Optimize breeding program design using an evolutionary algorithm
- Building optimization framework *via* the Snakemake workflow management system

The project is patent pending under application numbers EP24164947.4 and EP24188636.5 with collaboration with BASF Belgium Coordination Center

Azadeh Hassanpour

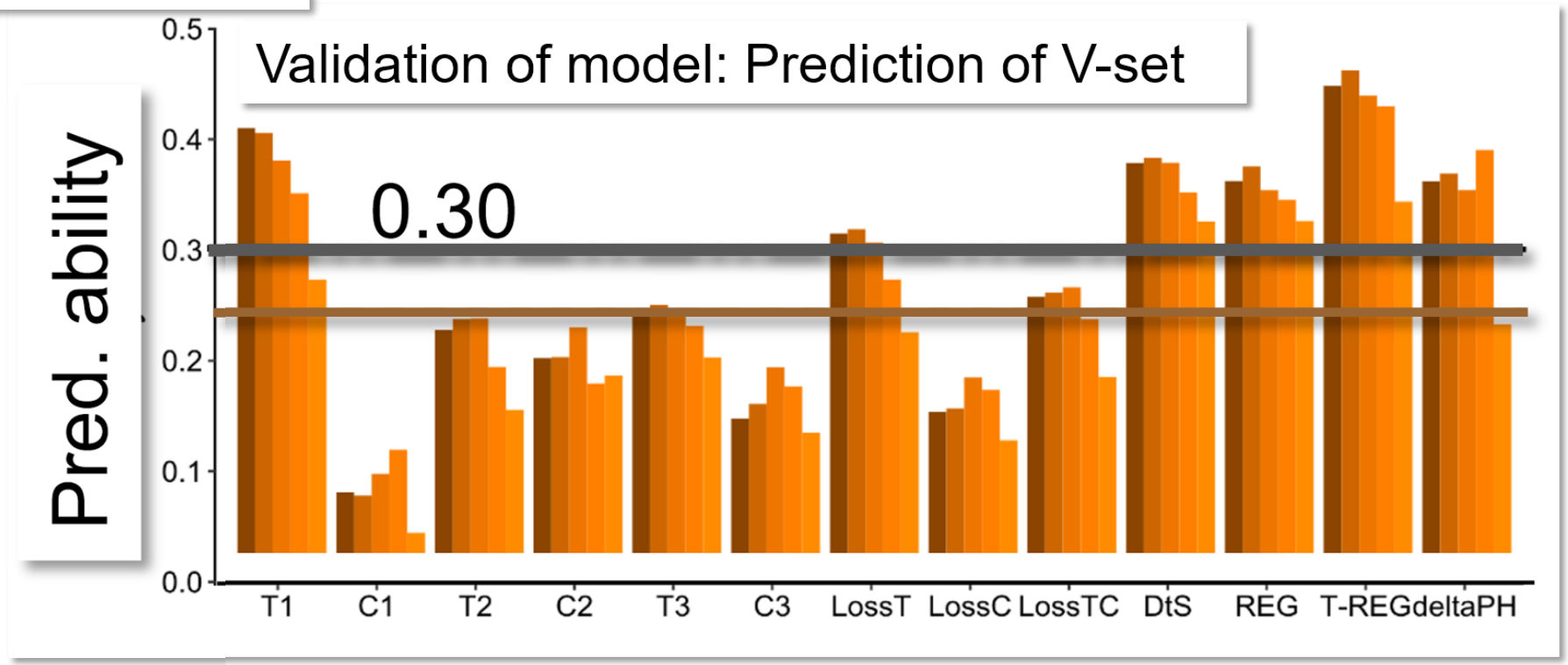




Faba bean. GWAS and GP of frost tolerance and winter hardiness, phenotyped in frost chamber (10-21 reps.) and field trials (E=22, 2005-2022)

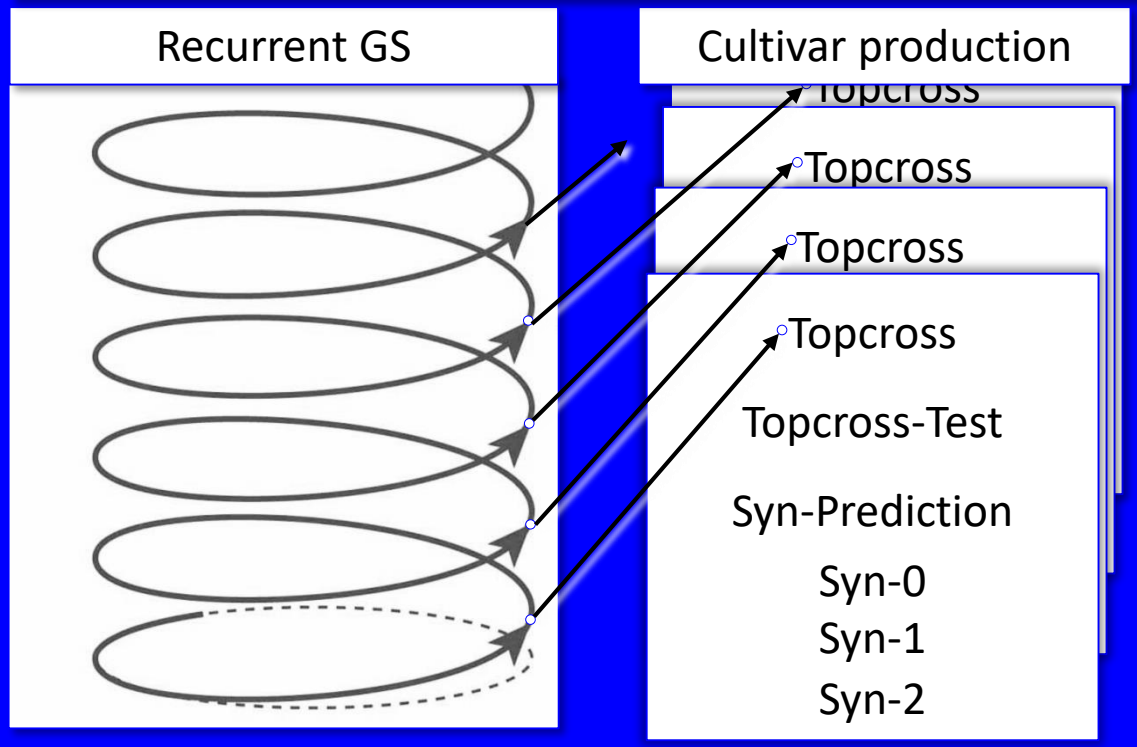
GBLUP in R; rrBLUP package, G matrix VanRaden 2008.
Training set 185 inbred lines, Validation set 64 inbred lines.
Hard validation with 'other' genotypes in 'other' experiments

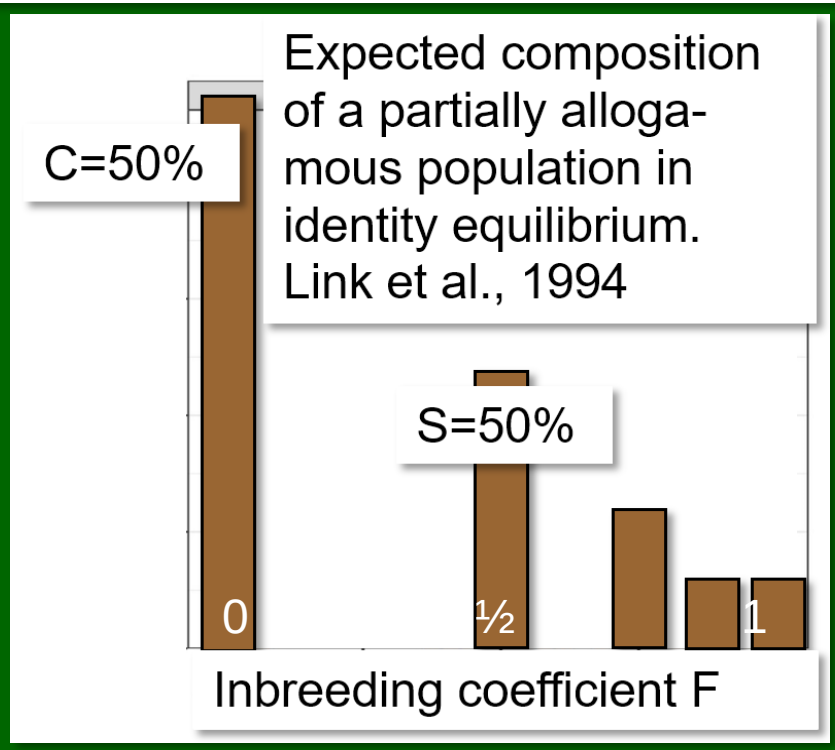
Vfaba_v2 Axiom SNP array 60k



Alex Windhorst

Faba bean. Abo-Direkt. Combine Gaynor et al., 2017 & Link et al., 1994; Link, 2013. New Breeding paradigm and GS to substitute missing DH technology.





Henri Laugel

Published online August 3, 2017

RESEARCH

A Two-Part Strategy for Using Genomic Selection to Develop Inbred Lines

R. Chris Gaynor, Gregor Gorjanc, Alison R. Bentley, Eric S. Ober, Phil Howell, Robert Jackson, Ian J. Mackay, John M. Hickey*

Vortr. Pflanzenzüchtg. 30, 201-230 (1994)

Zuchtmethodische Entwicklungen - Nutzung von Heterosis bei Fababohnen

W. Link[1], W. Ederer[2] und E. von Kittlitz[1]

[1]Universität Hohenheim (720), Landessaatzuchtanstalt

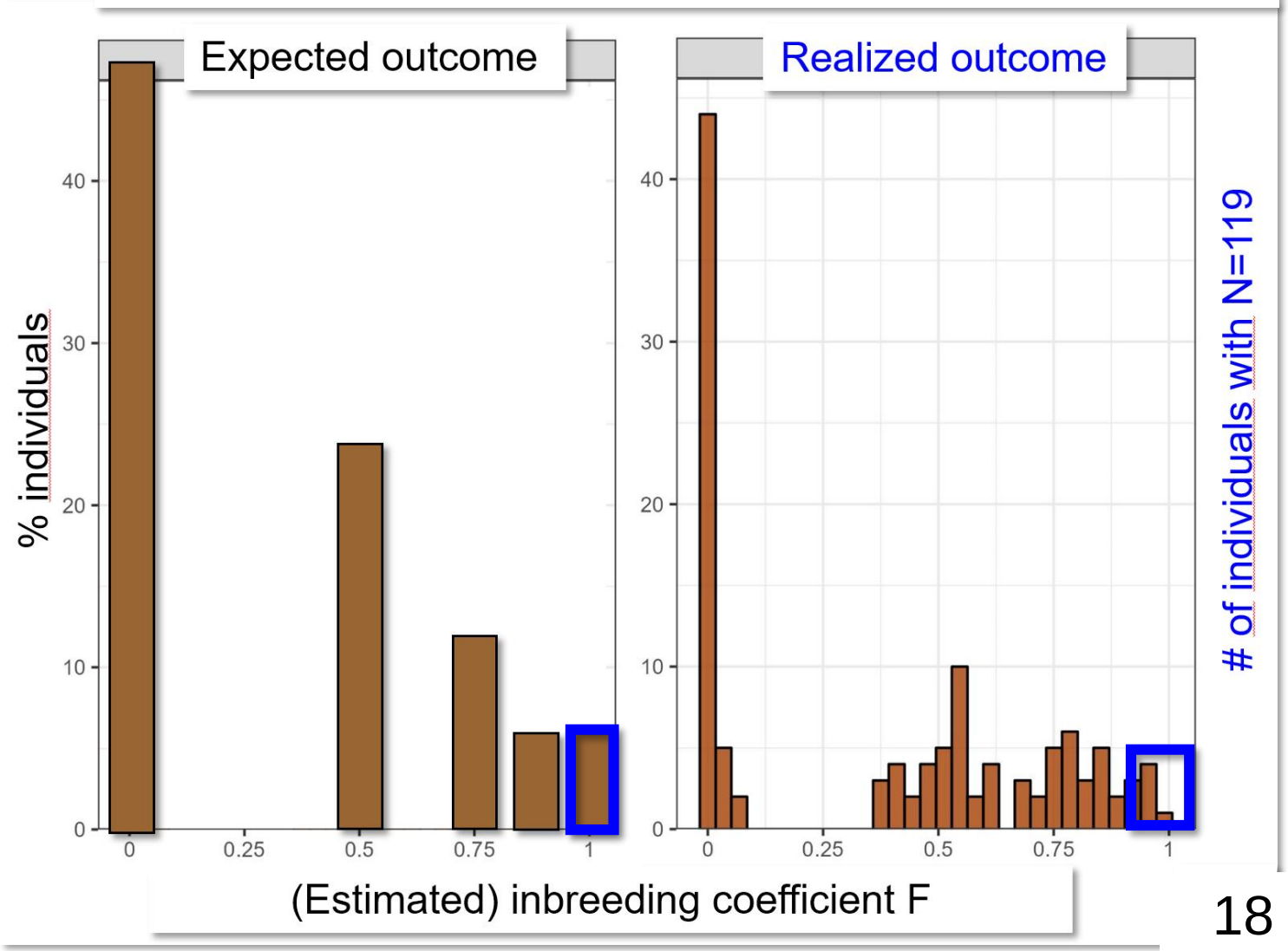
[2]Universität Hohenheim (350), Institut für Pflanzenzüchtung, Saatgutforschung und Populationsgenetik

D-70593 Stuttgart

Dissertation project of Henri Laugel ‚Abo-Direkt'. Make use of *à priori* available inbred individuals in faba bean population instead of DH technology

(●) Identify highly **homozygous** individuals in populations *via* DNA-markers
(●) Estimate their GEBV for agronomic traits (model trained from historical data); select
(●) Propagate (cage) most promising inbred individuals to have seed for plot-based field test
(●) Field-test inbred lines as Polycross or Topcross progenies (~GVA)
(●) Predict synthetic *cvs*., field test most promising ones from ex-trial seed …

So nice to see that the theoretical composition due to the partial allogamy is real!



Quentin Burandt speaks today himself: Prospects for future European Quinoa breeding

One of the two plants is Quinoa *Chenopodium quinoa* ;-)

Wikipedia

Göttingen team at the
GPZ conference 2024
Geisenheim near Frankfurt/M.,
March 2024

Thank you for listening