CHINA

The EU H2020 INVITE project “Innovations in plant Variety Testing in Europe”
欧盟“地平线2020计划” INVITE项目（“欧洲植物品种测试创新”）

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Francois Laurens，法国国家农业食品与环境研究院（INRAE） / INVITE项目协调员
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Joseph Peller，荷兰瓦赫宁根 / WP2联合负责人
Karl Schmid, University of Hohenheim, Germany / WP3 leader
Karl Schmid，德国霍恩海姆大学 / WP3 负责人
Aurélia Gouleau, GEVES, France / WP5 leader
Aurélia Gouleau，法国植物品种保护办公室（GEVES） / WP5 负责人

Plant Variety Rights online technical training for Chinese experts; 28 Nov 2023
中国专家植物品种权在线技术培训；2023年11月28日
www.ipkey.eu

Funded by the European Union
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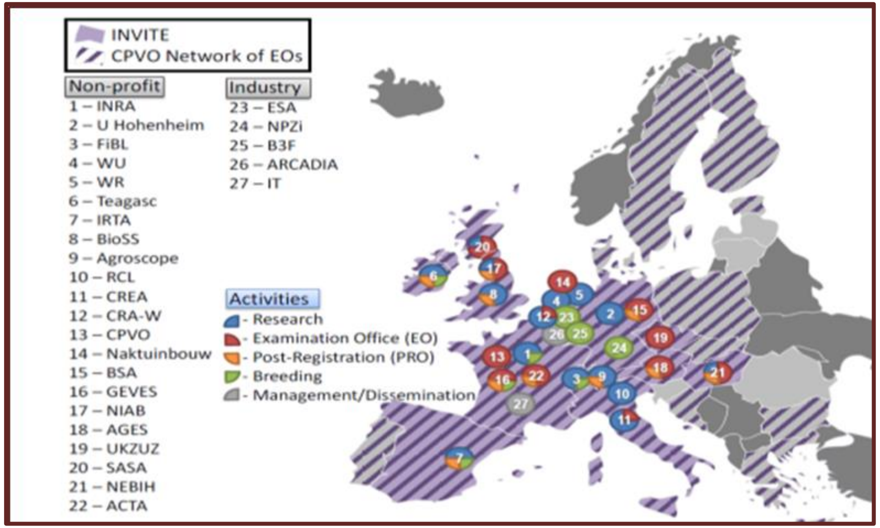
Agenda /// 日程

- General introduction on the INVITE project (F. Laurens)
  INVITE项目概述 (F. Laurens)
- Designing new tools for phenotyping using Human Centered Design (J. Peller)
  用人性化理念设计表型分析新工具 (J. Peller)
- Designing genotyping tools to better characterize varieties and their performance (K. Schmid)
  设计基因分型工具，更好表征品种及其性能 (K. Schmid)
- Integration of new tools in advanced variety testing (A. Gouleau)
  高级品种测试中对新型工具的综合运用 (A. Gouleau)
- Concluding remarks (F. Laurens)
  结束语（F. Laurens）

The INVITE project as a glance /// INVITE项目概览

Funded by the European Union /// 欧盟资助

Duration: 5 years : 1/01/2020 – 31/12/2024 /// 项目周期5年：2020年1月1日至2024年12月31日



29 partners /// 29个合作伙伴
Consortium ≈ 180 members /// 联合体 ≈ 180名成员
From 13 countries /// 来自13个国家
- Academic research /// 学术研究
- Breeders /// 育种者
- Technical institutes /// 技术机构
- Examination Offices (EOs) /// 测试中心（EOs）
- Post-registration Offices (Pros) /// 登记后事务办公室
- Management /// 管理
- Dissemination /// 推广

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General Objective and frame of the INVITE project /// INVITE项目总体目标框架

- The general objective of the INVITE project is to improve both efficiency of variety testing and the information available to stakeholders on variety performance under a range of production conditions and biotic and abiotic stresses. /// INVITE项目的总体目标是提高品种测试效率，向利益相关方提供品种在一系列生产条件及生物 / 非生物胁迫下的表现信息。

- The INVITE project is working on a small but representative set of selected crops:
  INVITE 项目正在研究一小部分具有代表性的作物：

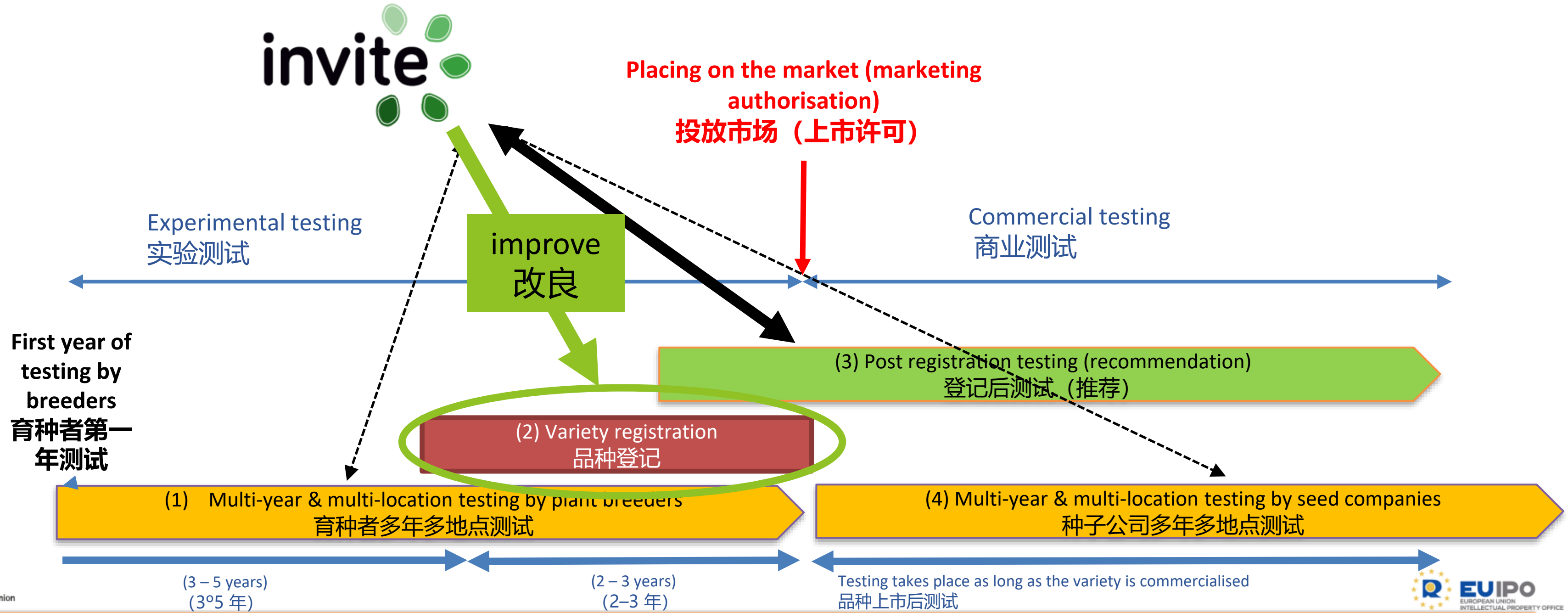
Maize	**Wheat**	**Sunflower**	**Perennial Ray Grass**	**Apple**	**Tomato**	**Potato**
玉米 + Soybean 大豆	小麦 Lucerne 紫苜蓿	向日葵 oilseed rape 油菜	多年生黑麦草	苹果	番茄	土豆

Specific objectives /// 具体目标

- Identify bioindicators associated with plant resource use efficiency, sustainability and resilience /// 确定植物资源利用效率、可持续性和恢复力相关生物指标
- Develop new phenotyping and genotyping tools /// 开发表型和基因分析新工具
- Implement models and statistical tools allowing to predict variety performance under a range of environments and crop management practices, while considering the economic return for farmers /// 使用模型和统计工具，预测品种在各种环境和作物管理措施下的表现，同时考虑农民的经济回报
- **Improve existing variety testing protocols for variety characterisation (DUS) and performance testing to enhance speed, precision and efficiency /// 改进现有品种表征（DUS）和性能测试规程，提升速度、精度和效率**
- Define new procedures for the management of reference collections /// 定义参考品种集管理新程序
- Propose organisational innovations to improve the management of variety testing networks /// 提出组织创新方案，完善品种测试网络的管理方法
- Propose guidelines to policy makers for including new traits and improving harmonisation of DUS and VCU at EU-level, and for the testing of heterogeneous plant reproductive material /// 向决策者提议政策方针，纳入新型性状，在欧盟层面进一步协调DUS测试和VCU测试，并对异质植物繁殖材料开展测试
- Facilitate data interoperability and exchanges within the consortium and set up a prototype of common DB to store phenotypic and genotypic data /// 促进联合体内数据交换互通，建立通用数据库原型，用于存储表型和基因型数据
- **Disseminate results and new technologies to stakeholders /// 向利益相关方推广工作成果和新型技术**

Context of variety testing Europe and positioning of INVITE /// 欧洲品种测试背景和INVITE项目定位

The complementary components of plant variety testing (principles) /// 植物品种测试的补充环节（及原则）



invite

Placing on the market (marketing authorisation)
投放市场（上市许可）

Experimental testing
实验测试

improve
改良

Commercial testing
商业测试

First year of testing by breeders
育种者第一年测试

(3) Post registration testing (recommendation)
登记后测试（推荐）

(2) Variety registration
品种登记

(1) Multi-year & multi-location testing by plant breeders
育种者多年多地点测试

(4) Multi-year & multi-location testing by seed companies
种子公司多年多地点测试

(3 – 5 years)
(3°5 年)

(2 – 3 years)
(2–3 年)

Testing takes place as long as the variety is commercialised
品种上市后测试

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Structure of the INVITE project /// INVITE项目结构

创新工具 / 方法，评价可持续性、恢复力标准，提升DUS和性能测试的速度 / 效率

示范新工具 / 方法，完善DUS和性能测试规程及基础设施

WP1：与可持续性、DUS测试标准相关的作物性状和生物学指标

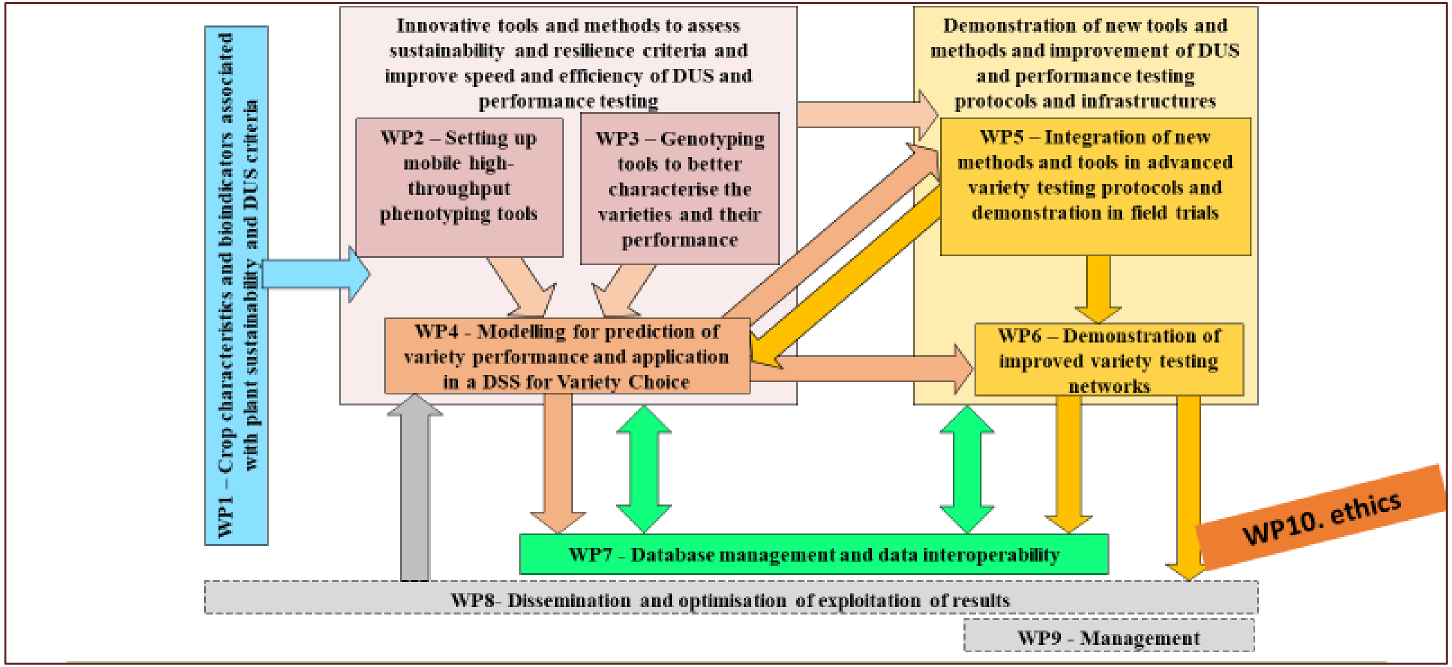
WP2：部署移动式高通量表型分析工具

WP3：使用表型分析工具更好表征品种及其性能

WP4：通过建模预测品种性能及应用（用于品种选择决策支持系统）

WP7：数据库管理和数据互通性

WP8：推广、优化、利用相关成果



Innovative tools and methods to assess sustainability and resilience criteria and improve speed and efficiency of DUS and performance testing

Demonstration of new tools and methods and improvement of DUS and performance testing protocols and infrastructures

WP1 – Crop characteristics and bioindicators associated with plant sustainability and DUS criteria

WP2 – Setting up mobile high-throughput phenotyping tools

WP3 – Genotyping tools to better characterise the varieties and their performance

WP4 - Modelling for prediction of variety performance and application in a DSS for Variety Choice

WP5 – Integration of new methods and tools in advanced variety testing protocols and demonstration in field trials

WP6 – Demonstration of improved variety testing networks

WP7 - Database management and data interoperability

WP8- Dissemination and optimisation of exploitation of results

WP9 - Management

WP10. ethics

WP5：在高级品种测试规程和试种示范中对新型工具进行综合运用

WP6：示范更完善的品种测试网络

WP9：管理

WP10：伦理道德

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Crops in the project /// 项目中的作物

WP1：与可持续性、DUS测试标准相关的作物性状和生物学指标

WP2：部署移动式高通量表型分析工具

WP3：使用表型分析工具更好表征品种及其性能

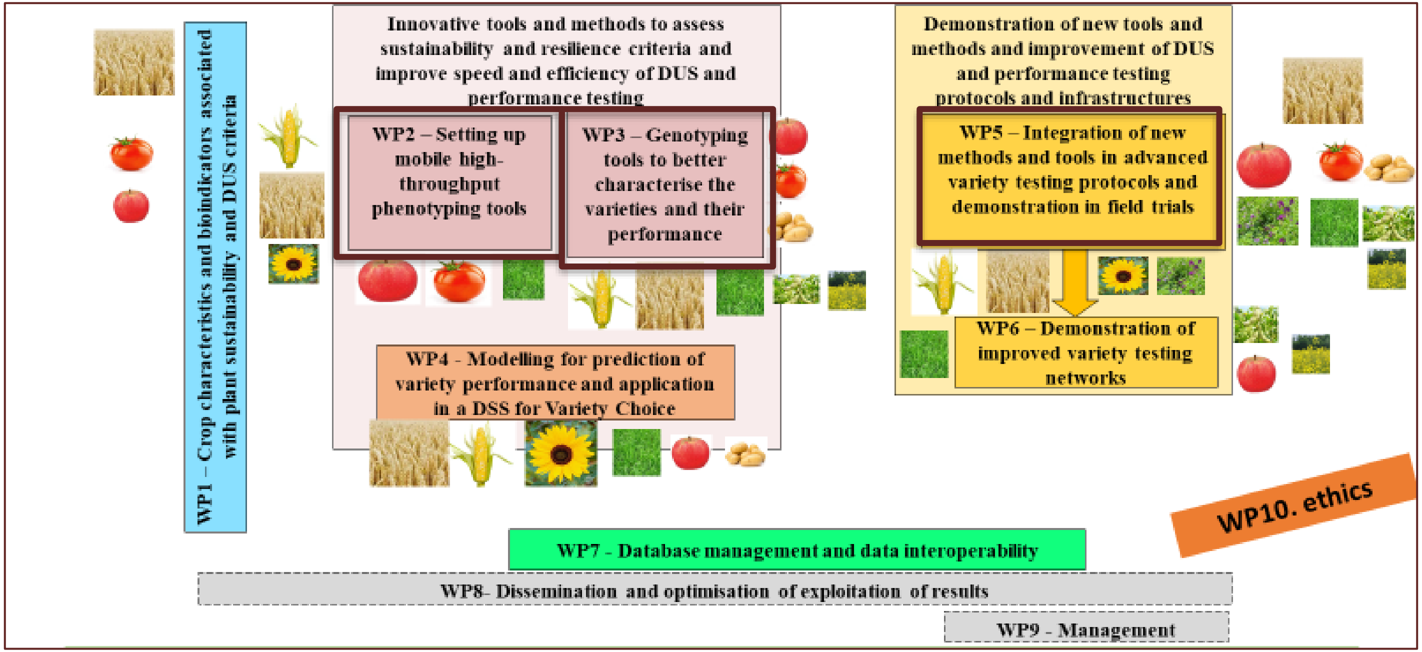
WP4：通过建模预测品种性能及申请（用于品种选择决策支持系统）

WP7：数据库管理和数据互通性

WP8：推广、优化、利用相关成果

创新工具 / 方法，评价可持续性、恢复力标准，提升DUS和性能测试的速度 / 效率

示范新工具 / 方法，完善DUS和性能测试规程及基础设施



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WP9：管理

WP10：伦理道德

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CHINA

Designing new tools for phenotyping using Human Centered Design
用人性化理念设计表型分析新工具

Joseph Peller | Wageningen, Netherlands | 28-11-2023
Joseph Peller | 荷兰瓦赫宁根 | 2023年11月28日

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Directed by the European Commission, IP Key is implemented by the European Union Intellectual Property Office (EUIPO). IP Key由欧盟委员会指导，欧盟知识产权局（EUIPO）实施。

Objectives of WP2 /// WP2目标

To create New Low Cost Phenotyping tools
开发低成本新表型工具

To make available these tools to Eos and Pros in WP5 (cf A. Gouleau part)
将工具提供WP5的测试中心和登记后事务办公室（参见A. Gouleau介绍内容)

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The Problem with Tool Development /// 工具开发问题

CultivarJ ImageJ Plugin for Plant Variety testing

WAGENINGEN UR
For quality of life

nak tuinbouw

Flax Analysis	Flax Boll Analysis	Pea/Pod Analysis	Bean Analysis	Cotyledon Analysis	Carrot Analysis
Onion Analysis	General Analysis				

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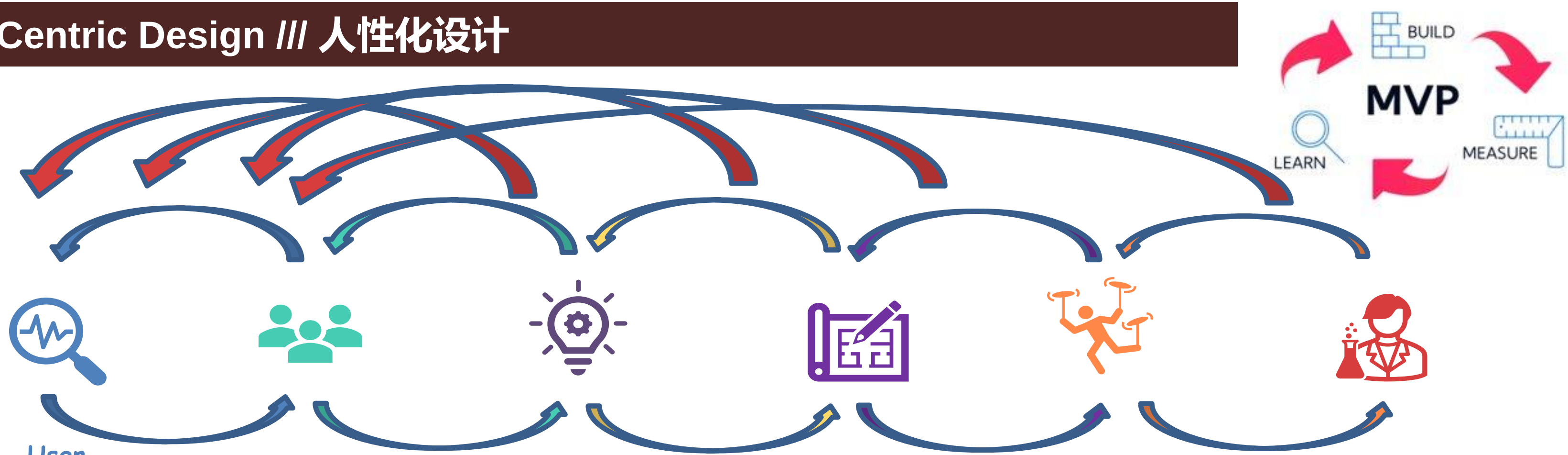
Human Centric Design /// 人性化设计



User Research 用户研究

- ✓ Identify users 确定用户
- ✓ Needs 需求
- ✓ Behaviour 行为
- ✓ Challenges 挑战
- ✓ Pain points 痛点
- ✓ Desires 诉求
- ✓ Values and norms 价值观和规范

Create Personas 创建用户画像

- ✓ Fictional representers of users 模拟用户代表

Concept development 概念开发

- ✓ Generate ideas 概念生成
- ✓ Brainstorm ideas 集思广益
- ✓ Consider needs and technical restrictions 需求和技术限制考量
- ✓ Consider business and ELSA aspects 业务和ELSA考量
- ✓ Match the values 价值匹配
- ✓ **interdisciplinary 跨学科**

Design and demonstrate 设计和演示

- ✓ Prototypes 原型
- ✓ Sketches 设计草图
- ✓ Visuals 视觉设计

Implement and evaluate 实施和评估

- ✓ Identify evaluation method 确定评估方法
- ✓ Newer version 版本更新
- ✓ Involve multiple stakeholders 多方参与

Test 测试

- ✓ With end-users (farm workers) 终端用户（田间工作人员）测试
- ✓ Feedback 接收反馈
- ✓ With other stakeholders 其他利益相关方测试
- ✓ Observe 观察使用情况

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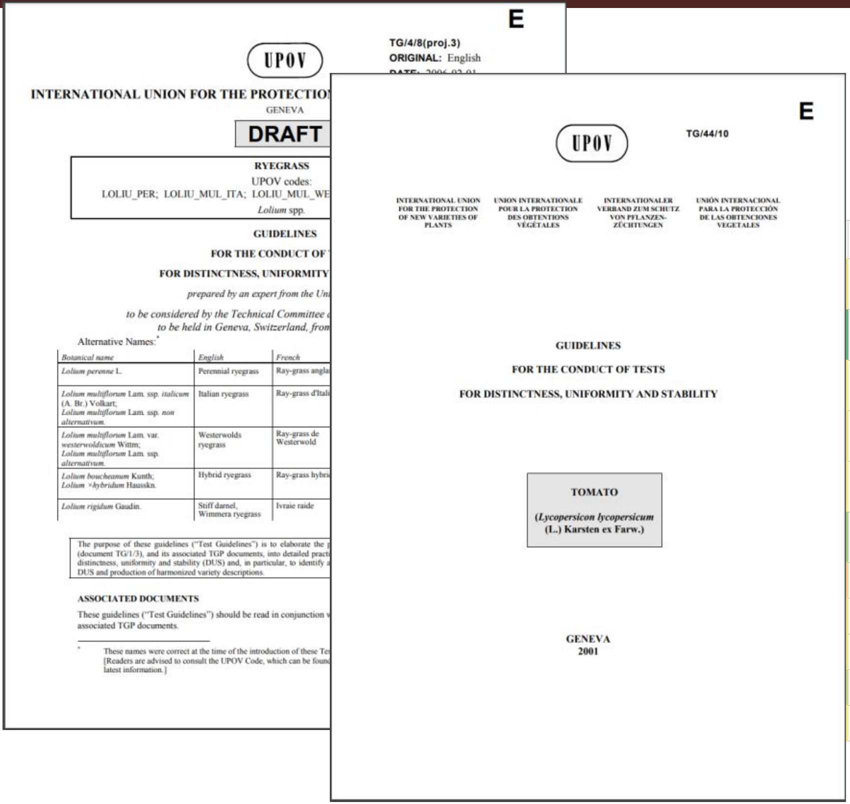
Surveying and Feedback /// 调查和反馈



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UPOV

TG/4/8(proj.3)
ORIGINAL: English
DATE: 2006-02-01

INTERNATIONAL UNION FOR THE PROTECTIO
GENEVA

DRAFT

RYEGRASS
UPOV codes:
LOLIU_PER; LOLIU_MUL_ITA; LOLIU_MUL_WE
Lolium spp.

GUIDELINES

FOR THE CONDUCT OF

FOR DISTINCTNESS, UNIFORMITY

prepared by an expert from the Un

to be considered by the Technical Committee
to be held in Geneva, Switzerland, from

Alternative Names:*

Botanical name	*English*	*French*
Lolium perenne L.	Perennial ryegrass	Ray-grass angla
Lolium multiflorum Lam. ssp. *italicum* (A. Br.) Volkart; *Lolium multiflorum* Lam. ssp. *non alternativum*.	Italian ryegrass	Ray-grass d'Itali
Lolium multiflorum Lam. var. *westerwoldicum* Wittm; *Lolium multiflorum* Lam. ssp. *alternativum*.	Westerwolds ryegrass	Ray-grass de Westerwold
Lolium boucheanum Kunth; *Lolium ×hybridum* Hausskn.	Hybrid ryegrass	Ray-grass hybri
Lolium rigidum Gaudin.	Stiff darnel, Wimmera ryegrass	Ivraie raide

The purpose of these guidelines ("Test Guidelines") is to elaborate the
(document TG/1/3), and its associated TGP documents, into detailed practi
distinctness, uniformity and stability (DUS) and, in particular, to identify
DUS and production of harmonized variety descriptions.

ASSOCIATED DOCUMENTS

These guidelines ("Test Guidelines") should be read in conjunction
associated TGP documents.

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* These names were correct at the time of the introduction of these Te
[Readers are advised to consult the UPOV Code, which can be foun
latest information.]

E

UPOV

TG/44/10

INTERNATIONAL UNION FOR THE PROTECTION OF NEW VARIETIES OF PLANTS

UNION INTERNATIONALE POUR LA PROTECTION DES OBTENTIONS VÉGÉTALES

INTERNATIONALER VERBAND ZUM SCHUTZ VON PFLANZEN-ZÜCHTUNGEN

UNIÓN INTERNACIONAL PARA LA PROTECCIÓN DE LAS OBTENCIONES VEGETALES

GUIDELINES

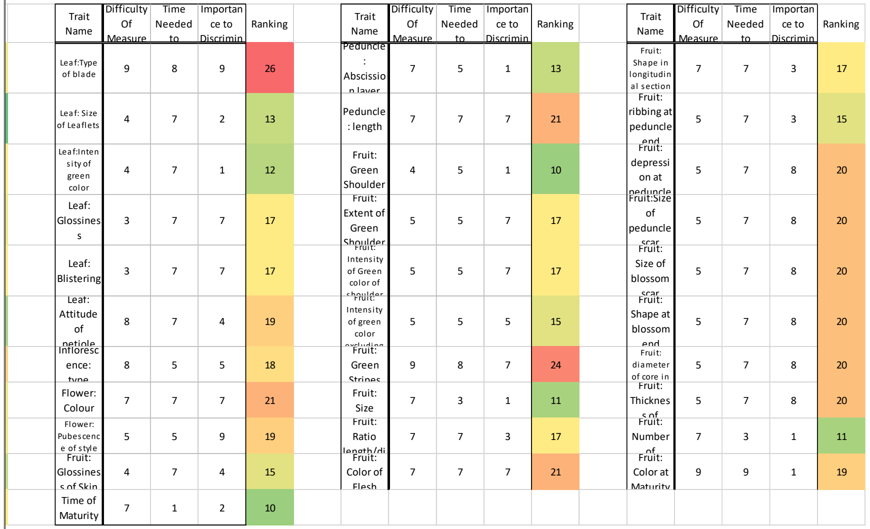
FOR THE CONDUCT OF TESTS

FOR DISTINCTNESS, UNIFORMITY AND STABILITY

TOMATO

(*Lycopersicon lycopersicum* (L.) Karsten ex Farw.)

GENEVA
2001



Trait Name	Difficulty Of Measure	Time Needed to	Importance to Discrimin	Ranking
Leaf:Type of blade	9	8	9	26
Leaf: Size of Leaflets	4	7	2	13
Leaf:Intensity of green color	4	7	1	12
Leaf: Glossiness	3	7	7	17
Leaf: Blistering	3	7	7	17
Leaf: Attitude of petiole	8	7	4	19
Inflorescence: type	8	5	5	18
Flower: Colour	7	7	7	21
Flower: Pubescence of style	5	5	9	19
Fruit: Glossiness of Skin	4	7	4	15
Time of Maturity	7	1	2	10

Trait Name	Difficulty Of Measure	Time Needed to	Importance to Discrimin	Ranking
Peduncle: Abscission layer	7	5	1	13
Peduncle: length	7	7	7	21
Fruit: Green Shoulder	4	5	1	10
Fruit: Extent of Green Shoulder	5	5	7	17
Fruit: Intensity of Green color of shoulder	5	5	7	17
Fruit: Intensity of green color excluding	5	5	5	15
Fruit: Green Stripes	9	8	7	24
Fruit: Size	7	3	1	11
Fruit: Ratio length/di	7	7	3	17
Fruit: Color of Flesh	7	7	7	21

Trait Name	Difficulty Of Measure	Time Needed to	Importance to Discrimin	Ranking
Fruit: Shape in longitudinal section	7	7	3	17
Fruit: ribbing at peduncle end	5	7	3	15
Fruit: depression at peduncle	5	7	8	20
Fruit:Size of peduncle scar	5	7	8	20
Fruit: Size of blossom scar	5	7	8	20
Fruit: Shape at blossom end	5	7	8	20
Fruit: diameter of core in	5	7	8	20
Fruit: Thickness of	5	7	8	20
Fruit: Number of	7	3	1	11
Fruit: Color at Maturity	9	9	1	19

Computer Vision as a Process /// 计算机视觉应用流程

第一步：图像获取

Step 1
image acquisition

from past and future funded experiments

过往及管线内获得资金支持的实验项目

第一步：图像打标

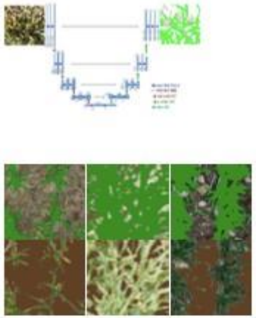
Step 2
annotation

from collaborative platform

协作式平台

第三步：深度学习

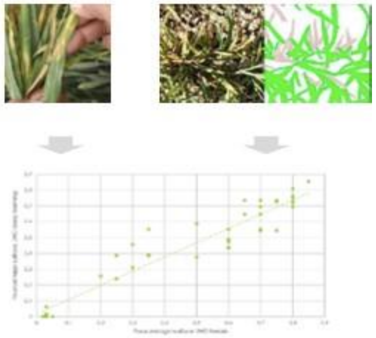
Step 3
Deep learning



from didactic version of U-Net
U-Net教学版

第四步：数据分析

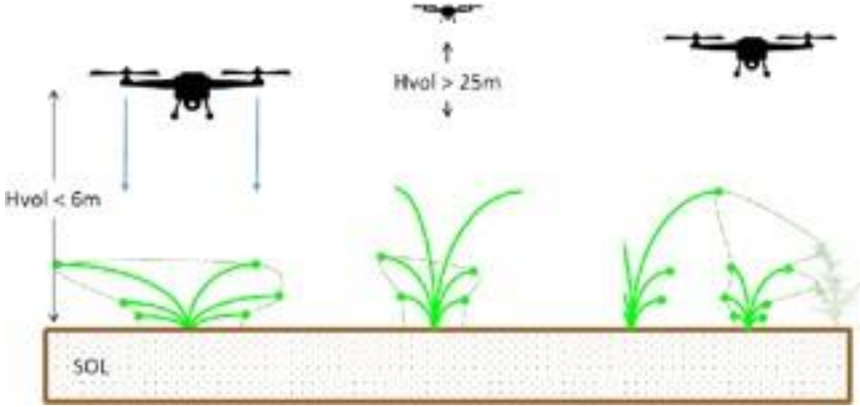
Step 4
Data analysis

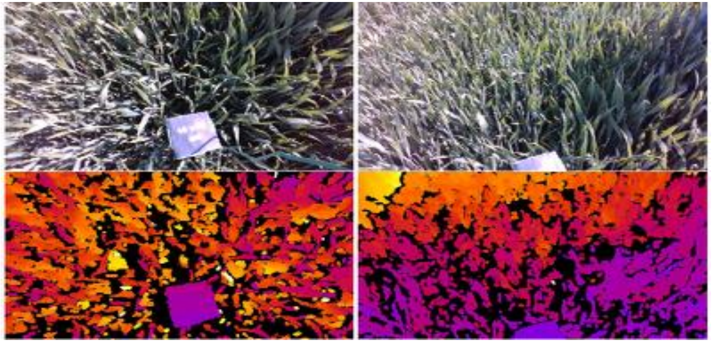


Comparison with ground truth
Automatic cluster of types of errors

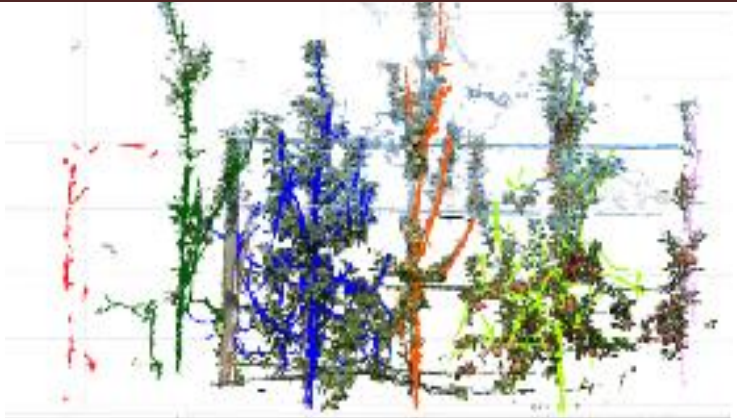
与现场真实数据对比；自动错误分类

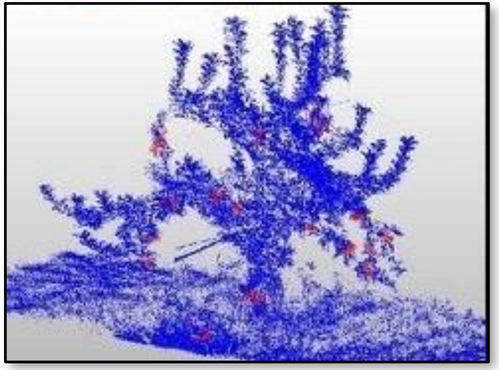
UAV Open Field Applications /// 无人机野外应用





Orchard 3D Reconstructions - Scouting /// 果园3D重建–勘探





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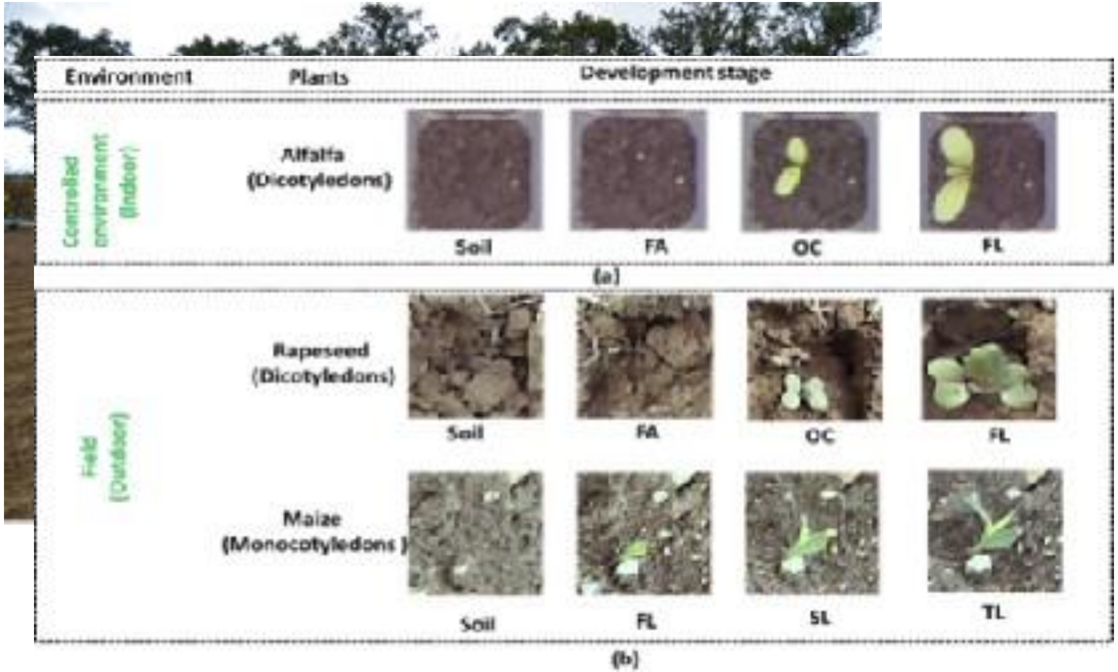
Open field Scouting /// 野外勘探



Tomato Phenotyping and Naktuinbouw /// 番茄表型分析：荷兰园艺检验局

Important Traits /// 重要性状

Traits of interest:

关注性状:

1. **Peduncle scar size /// 果梗痕大小**
2. **Color /// 颜色**
3. **Shape ratios /// 形状比**
4. **Volume /// 体积**
5. **Blossom-end scar size /// 果脐大小**
6. **Ribbing /// 果梗端的棱**

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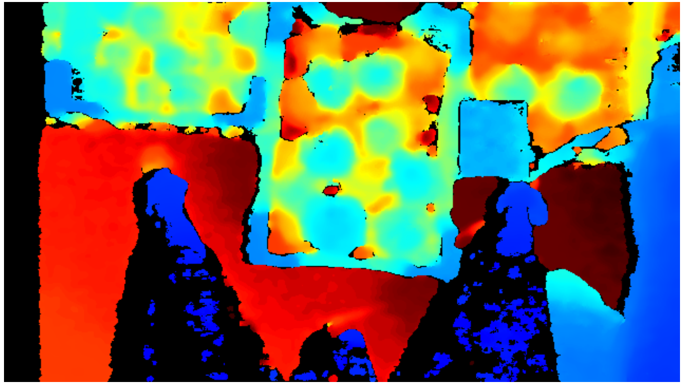
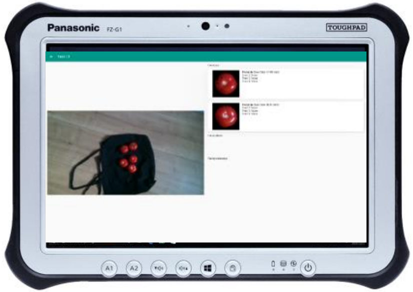
Initial Cycles – 3D Cameras /// 初始周期–3D相机



Current Cycles – Phone Applications /// 当前周期–手机app



Expected applications from INVITE WP2 /// INVITE WP2：开发项目

A general pipeline for any crop to implement low cost Phenotyping
可以对任意作物进行低成本表型分析的通用流程

An example App (moRPH) for tomato phenotyping as a baseline for other apps
番茄表型分析的示范app（moRPH），作为未来其他app的原型

Feedback and creation of a community of phenotypers in Europe
收集用户反馈，建立欧洲表型专家社区

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IPKey

CHINA

Genotyping tools to better characterize varieties and their performance
改善品种表征及性能表征的基因分型工具

Karl Schmid | University of Hohenheim, Stuttgart, Germany | 28 November 2023
Karl Schmid | 德国霍恩海姆大学，德国斯图加特 | 2023年11月28日

Plant Variety Rights online technical training for Chinese experts; 28 Nov 2023
中国专家植物品种权在线技术培训；2023年11月28日

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Overview
概述

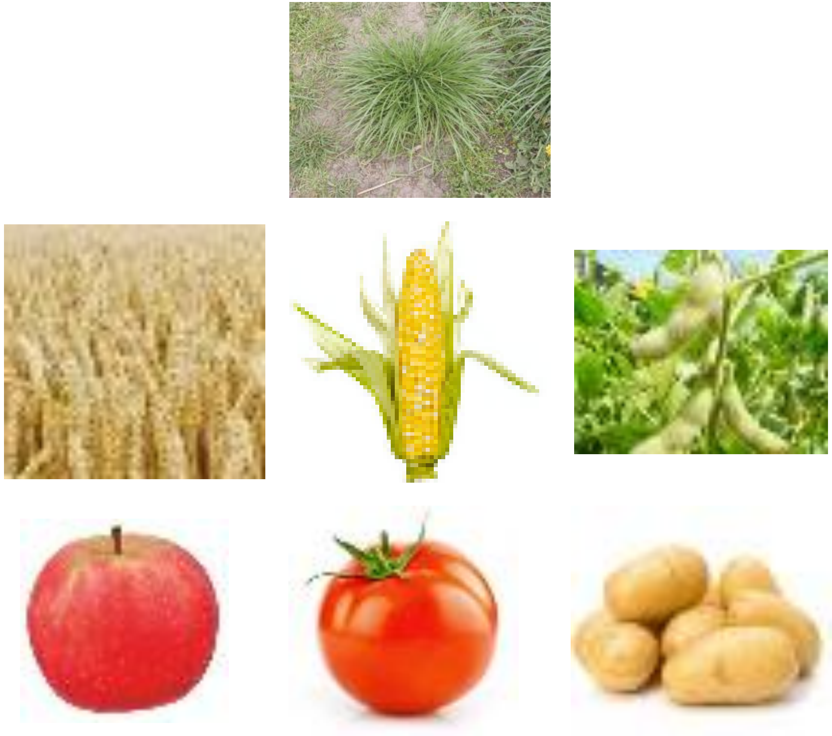
Objectives
目标

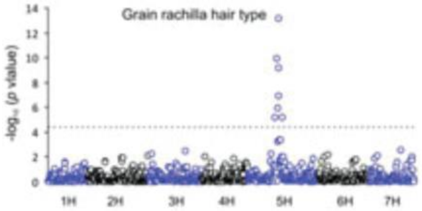
Achievements with some examples
成绩及实例

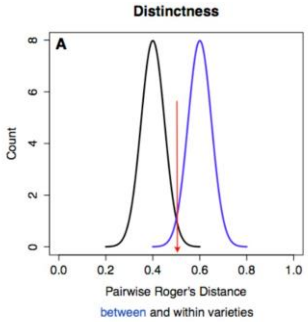
Challenges
挑战

Expected innovations
未来创新

Genotyping tools to better characterize varieties and their performance
改善品种表征及性能表征的基因分型工具







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Objectives /// 目标

- Identify genome-wide marker sets in different types of varieties and different crops

  鉴定各类品种、作物的全基因组标记集

- Develop low-cost genotyping arrays from genome-wide markers to support evaluation of DUS and VCU criteria

  以全基因组标记为基础，开发低成本基因分型阵列，支持对DUS、VCU测试标准的评估

- Identify novel markers associated with accepted and novel DUS traits

  鉴定与已知及全新DUS性状相关的新标记

- Develop models for marker-based evaluation of DUS and VCU criteria and reference collection management

  开发模型，用于基于标记的DUS和VCU测试标准评估和参考品种集管理

- **Improved models for marker-based evaluation of distinctness and uniformity in wheat, maize, PRG, and soybean**

  改进基于标记的特异性和一致性评价模型（用于小麦、玉米、多年生黑麦草和大豆）

Key achievements /// 主要成绩

DUS Marker trait associations (GWAS) -> Marker development

DUS标记性状协会（GWAS，全基因组关联分析研究）-> 标记开发

Genome-wide markers -> Genomic prediction of DUS traits

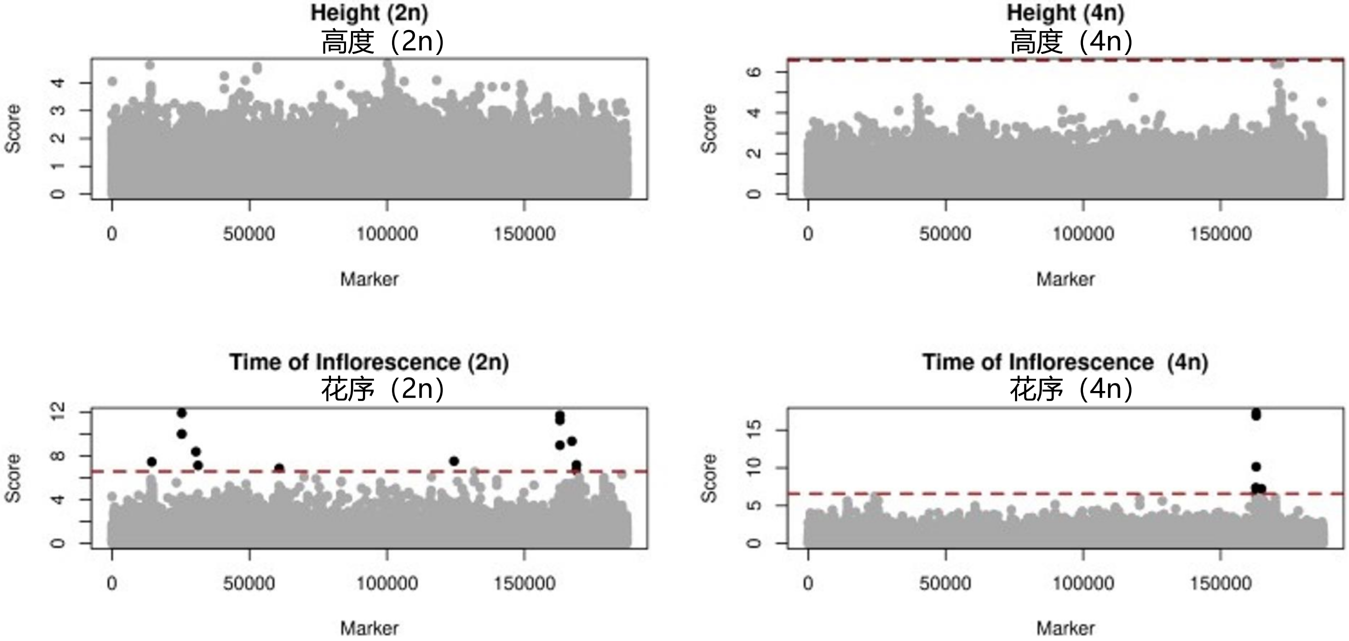
全基因组标记 -> DUS性状的基因组预测

New computational/statistical methods for DUS criteria and management of reference collections

DUS标准和参考品种集管理的新型计算 / 统计方法

Some selected examples: Genome-wide association studies for DUS traits
部分实例：DUS性状的全基因组关联研究

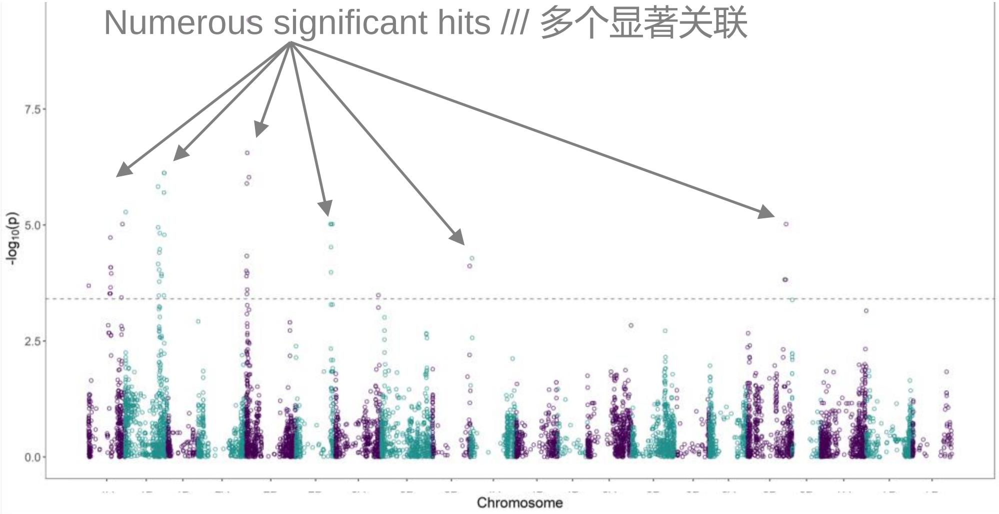
Perennial ryegrass (PRG) /// 多年生黑麦草



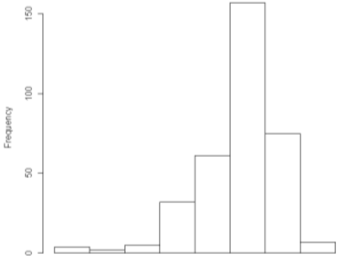
Dan Milbourne TEAGASC, Adrian Roberts BioSS

Some selected examples: Genome-wide association studies for DUS traits
部分精选实例：DUS性状的全基因组关联研究

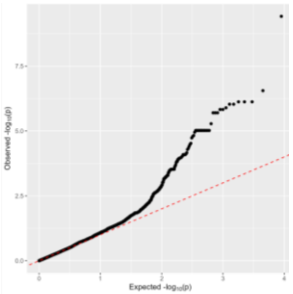
Flag leaf in wheat /// 小麦旗叶


Numerous significant hits /// 多个显著关联

Histogram of trait scores
性状分直方图



Q-Q plot /// 分位数–分位数点图



Trait scored on a 1-9 (quantitative) scale. Multiple GWAS hits identified.
性状按1–9（定量）评分。已识别多个GWAS关联。

James Cockram, Bethan Love, Tally Wright, NIAB, UK

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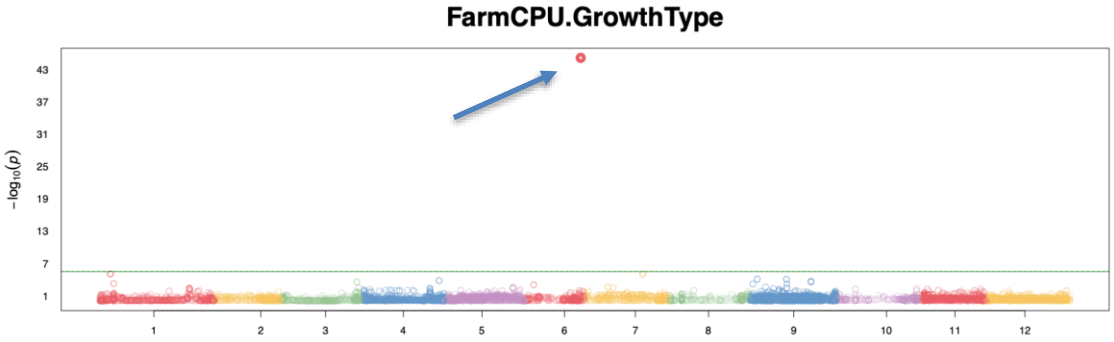
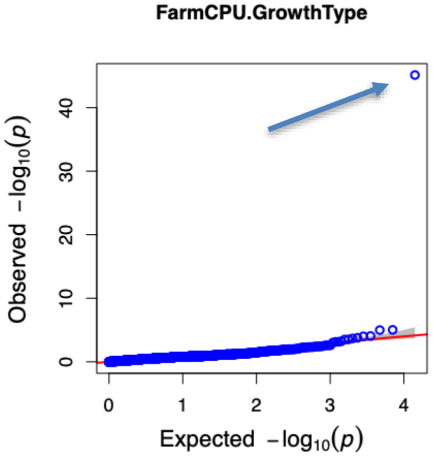
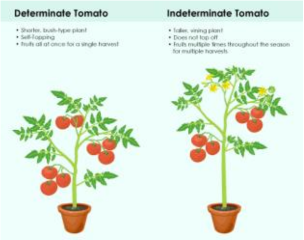
Some selected examples: Genome-wide association studies for DUS traits
部分实例：DUS性状的全基因组关联研究

Tomato - Trait: Determinate vs. indeterminate growth type
番茄–性状：有限生长型 vs. 无限生长型





Mathilde Causse INRAE



Determinate Tomato

- Shorter, bush-type plant
- Self-Topping
- Fruits all at once for a single harvest

Indeterminate Tomato

- Taller, vining plant
- Does not top off
- Fruits multiple times throughout the season for multiple harvests

Genome-wide markers to differentiate varieties /// 区分品种的全基因组标记

Select adequate SNPs for verifying uniqueness and identity of any unique apple genotypes
选择适当的单核苷酸多态性（SNPs），以便验证任意独特苹果基因型的特异性和身份

Use SNPs instead of SSRs to facilitate international comparisons
使用SNPs而非微卫星，以便促进国际比较

Identify a reference set of 96 SNP with high discrimination power
发现具有高鉴别力的参考组，包含96个SNP

INRAE

Charles-Eric Durel

Final selection of 96 SNP allowing at least 6 differences within all pairs of genotypes

最终选择96个SNP，允许所有基因型对中存在至少6个差异

currently tested for large set of ~800 individuals

目前对约800个体进行了大规模测试

Implementation in cheap and high throughput genotyping array (e.g., KASP, Fluidigm

在廉价和高通量基因分型阵列（如流达公司KASP法）中实施

Example: Trait-specific SNP assays for apple /// 实例：苹果的性状特异性SNP分析

Goal: Gather SNPs known to tag other disease-pest resistances, fruit quality, phenology
目标：收集已知的SNPs来标记其他病虫害抗性、果实品质和物候学
-> transfer to KASP as chemistry
-> 迁移至KASP（竞争性等位基因特异性PCR）

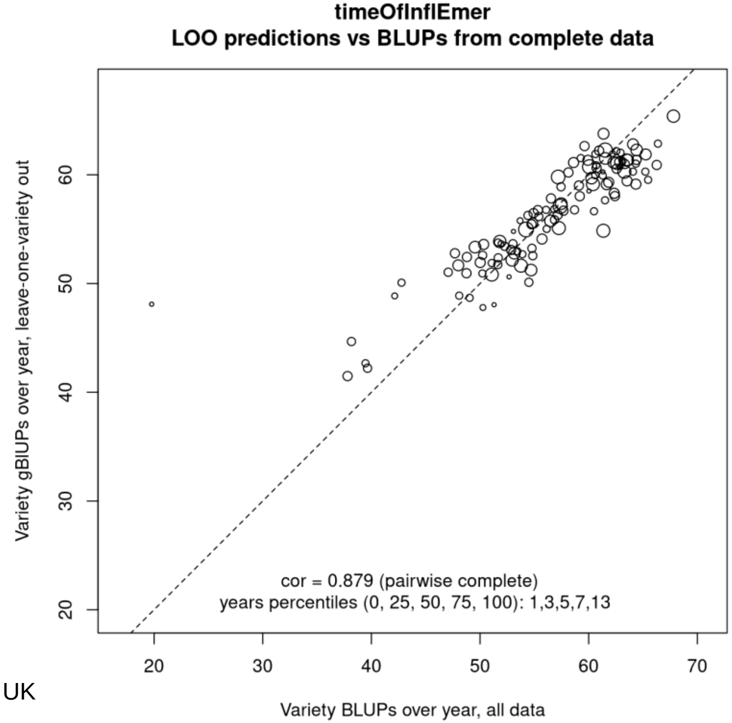
Approach: Webtool (GenoVarView) to search for variability in a target genomic region to design primers without mismatches
方法：WebTool（GenoVarView）搜索目标基因组区域的变异性，以设计无错配引物

IRTA

Maria José Aranzana

Example: Genomic prediction of DUS traits using genome-wide markers
实例：用全基因组标记对DUS性状进行基因组预测

Genomic BLUP in ryegrass
黑麦草基因组最佳线性无偏预测（BLUP）



Dan Milbourne TEAGASC Ireland, Adrian Roberts BioSS Scotland UK

Example: Improved management of reference collections /// 示例：参考品种集管理改进

Reference collection management using markers /// 用标记管理参考品种集

- Use markers to reduce number of reference varieties in DUS trials /// 用标记减少DUS试验中参考品种数量
- **Are markers more efficient than current UPOV models, whilst staying true to UPOV principles? 在忠实于UPOV原则的前提下，标记是否比当前的UPOV模型更有效?**

Approach to be tested in INVITE: /// INVITE项目中待测方法:

- Predict distinctness for each character in turn using genomic prediction /// 使用基因组依次预测每个性状的特异性
- Collate information over characters to get overall decision /// 整合性状信息，获得整体结论

Potential Advantages: /// 潜在优势：

  - **Phenotype driven /// 表型驱动**
  - Easier to correlate markers with individual characters than overall distances /// 与总距离相比，更容易将标记与单个性状相关联
  - Uses concept that distinctness only needed in one character /// 使用在单一性状中才需要的特异性概念

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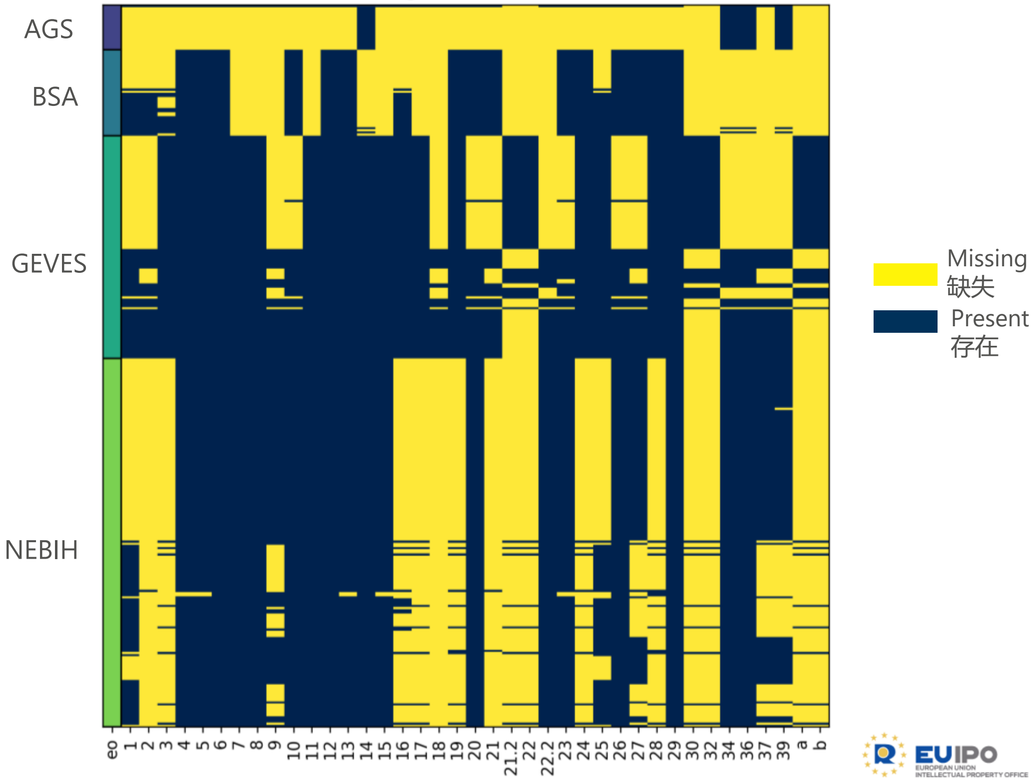
Challenge: Data type, quantity and quality /// 挑战：数据类型、数量和质量

- Missing data of genotypes (technical causes) /// 基因型数据缺失（技术原因）
- Missing data of DUS traits /// DUS性状数据缺失
- Numbers of varieties obtained not sufficient for some tasks /// 获得的品种数量不足以完成某些任务
- New phenotypes (e.g. arising from WP2) /// 新表型（来源包括WP2等）



Anurag Daware, Karl Schmid UHOH

Challenge diversity of genotyping technologies /// 挑战：基因分型技术多样性

Genotyping by sequencing

测序基因分型

Low coverage whole genome sequencing
低覆盖率全基因组测序

SPETs genotyping

SPETs基因分型

Sequence capture

序列捕获

SNP array genotyping

SNP阵列基因分型

KASP markers

KASP标记

Take home messages /// 结论：

- Identification of trait-specific and genome-wide markers easily possible /// 易于鉴别性状特异性标记和全基因组标记
- Which concepts for using markers given technical possibilities? /// 考虑到技术可能性，使用哪些标记？

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Genotyping tools to better characterize varieties and their performance
能更好表征品种及其性能的基因分型工具

Trait-specific markers implemented in marker assays (esp. tomato, potato, apple)
在标记分析中运用性状特异性标记（尤其是番茄、土豆、苹果）

Genome wide diversity of European material characterized for wheat, maize, soybean, PRG -> Management of reference collections
表征了小麦、玉米、大豆和多年生黑麦草欧洲材料的全基因组多样性->管理参考品种集

Updated methods and software implementations using genome-wide markers for distinctness and uniformity testing
使用全基因组标记进行特异性和一致性测试，更新了测试方法和软件实施

IPKey

CHINA

Integration of new tools in advanced variety testing
高级品种测试中对新型工具的综合运用

Aurélia Gouleau, GEVES, France | 28th November 2023
Aurélia Gouleau，法国植物品种保护办公室 | 2023年11月8日

Plant Variety Rights online technical training for Chinese experts; 28 Nov 2023
中国专家植物品种权在线技术培训；2023年11月28日
www.ipkey.eu

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Objectives of the integration of new tools in variety testing in INVITE project
INVITE项目品种测试中新工具集成目标

Testing of phenotyping tools for variety evaluation in INVITE project
INVITE项目品种评估表型分析工具测试

Testing of molecular markers for variety evaluation in INVITE project
INVITE项目品种评估分子标记测试

Expected applications from INVITE project
INVITE项目的预期应用

Objectives of the work /// 工作目标

Test and validate phenotyping and genotyping tools and methods for improved speed, precision and efficiency of variety testing
测试并验证表型和基因分型工具方法，提高品种测试的速度、精度和效率

Improve the management of DUS reference collections by the use of molecular tools
使用分子工具，提升DUS参考品种集管理

Develop new variety testing protocols to integrate sustainability criteria into variety testing
制定新的品种测试规程，纳入可持续性标准

Propose recommendations to policy makers for the evaluation of heterogeneous plant material
向政策制定者提出评估异质植物材料的建议

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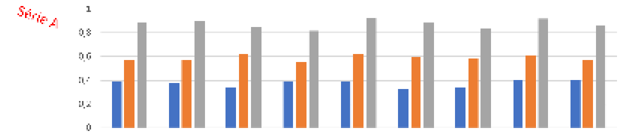
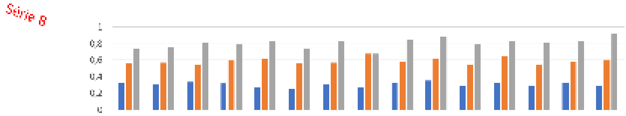
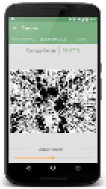
Testing of phenotyping tools - Sunflower /// 表型分析工具测试–向日葵

- coverage fraction at early stage
  早期覆盖率

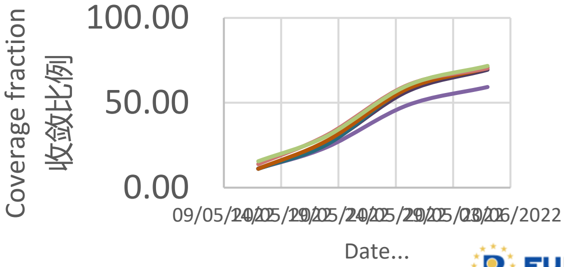


Drones
无人机





Canopeo software
Canopeo 软件



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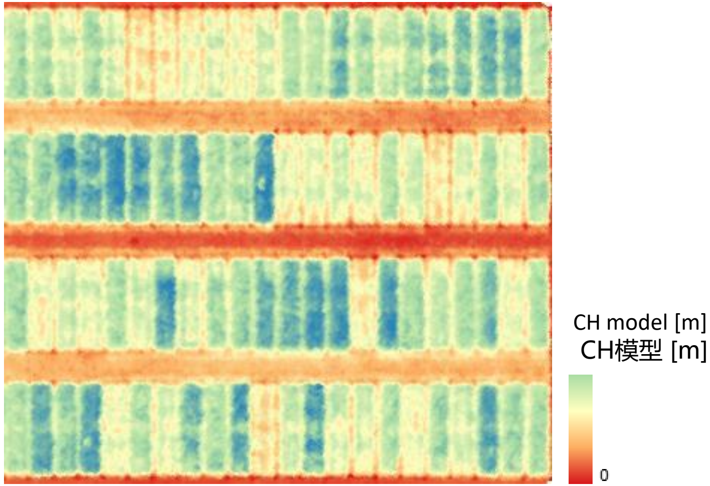
Testing of phenotyping tools - Ryegrass /// 表型分析工具测试–黑麦草

Forage grasses/Lolium perenne: canopy height/persistency
牧草/黑麦草：冠层高度/持久性

ILVO
Flanders Research Institute for Agriculture, Fisheries and Food



Canopy Height model (CH), variety trial, 20/05/2021
冠层高度模型 (CH)，品种测试，2021年5月20日

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Persistency, RGB orthomosaic, Schelderode, autumn 2021, much variability
持久性，RGB 正射影像，比利时Schelderode，2021 年秋季，变异性较大

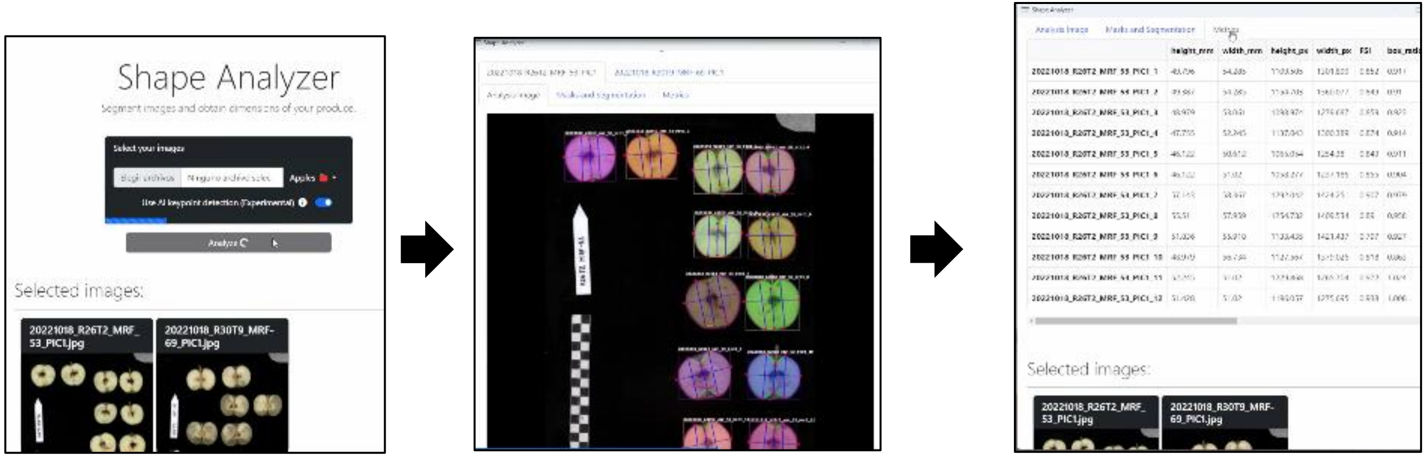
Testing of phenotyping tools - Apple /// 表型分析工具测试–苹果

- Development of a downloadable software for shape analysis previously in INVITE project

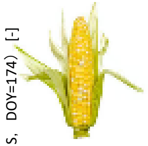
在INVITE项目中开发可下载的形状分析软件

- Demonstrated in apple collection of 120 local apple varieties; extended to almond (100 accessions) and pear (130 local varieties). Publication in preparation

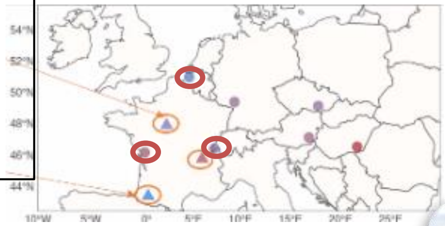
已在120个本地苹果品种的品种集中得到验证；拓展到100个扁桃品种和130个本地梨品种。准备发表。



Testing of phenotyping tools - Maize /// 表型分析工具测试–玉米



- Early vigor /// 发芽势
- Leaf area index /// 叶面积指数
- Plant height /// 植株高度
- Senescence /// 衰老



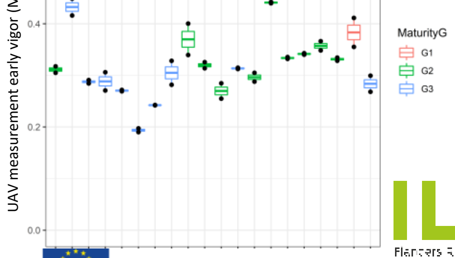
Drones /// 无人机

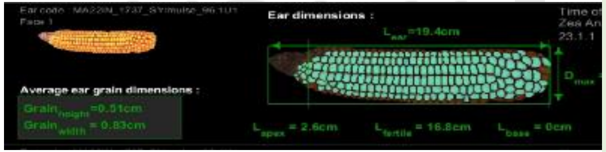
Literal stick /// 测量杆

Phenofield

Km scan /// KM扫描

Earbox /// 穗盒





Ear code : MA22N_1737_S?muise_96.1U1
Face 1

Ear dimensions :

L_{ear}=19.4cm

D_{max}

Time of
Zea An
23.1.1

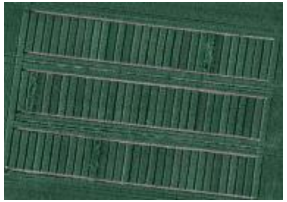
Average ear grain dimensions :

$Grain_{height}$=0.51cm
$Grain_{width}$ = 0.83cm

L_{apex} = 2.6cm $L_{fertile}$ = 16.8cm L_{base} = 0cm

- Ear characteristics
  穗性状

Testing of phenotyping tools - Wheat /// 表型分析工具测试–小麦



Wallonie recherche CRA-W
GEVES Expertise & Performance
Agroscope
AGES

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- 抽穗和开花始期
- 穗数
- 成熟期高度
- 衰老
- 出苗
- 越冬返青

- Heading and flowering time
- Number of spikes
- Height at maturity
- Senescence
- Emergence
- Growth after winter

Drones

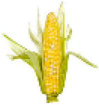
Literal stick

Spectrometer

Multispectral and RGB Cameras

- 无人机
- 标尺
- 光谱仪
- 多光谱和RGB照相机

Testing of phenotyping tools – Possible applicability for DUS testing
表型分析工具测试——可能适用于DUS测试


Species 物种	Traits 性状	Tools 工具
Rye-grass 黑麦草	Persistency, plant height and biomass estimation 持久性、植株高度和生物量估值	drones 无人机
Maize 玉米	Plant counting, early vigor, canopy height, ear characteristics 植株计数、发芽势、冠层高度、穗性状	drones, connected sticks 无人机，连接杆 phenotyping platform, Earbox (Phymea) 表型分析平台、穗盒（Phymea）
Wheat 小麦	Heading and flowering time, number of spikes, height at maturity, senescence, emergence, growth after winter 抽穗和开花始期、穗数、成熟期高度、衰老、出苗、越冬返青	drones, connected sticks, spectrometer, multispectral and RGB cameras 无人机、连接杆、光谱仪、多光谱相机和RGB相机 phenotyping platform 表型平台
Sunflower 向日葵	Coverage fraction at early stage 早期覆盖率	Drones, Canopeo 无人机，Canopeo
Apple 苹果	Fruit shape analysis 果形分析	Shape analysis software 形状分析软件

Benefits /// 优点

- more precise /// 更精确
- adaptation to environmental conditions /// 适应环境条件

Limits /// 限制

- weather dependent /// 依赖天气
- training of users /// 需要用户培训

Testing of molecular markers - Tomato /// 分子标记检测–番茄

Test of molecular markers linked to 3 disease resistances
与3种疾病抗性相关的分子标记测试
Tomato Mosaic Virus (ToMV) /// 番茄花叶病毒
Tomato Spotted Wilt Virus (TSWV) /// 番茄斑萎病毒

- *Fusarium oxysporum f. sp. lycopersici Fol: 1EU/2US /// 番茄枯萎病菌*

Testing of molecular markers – Apple (1/2) /// 分子标记检测–苹果（1/2）

- Test the SNP marker linked to Pl1 resistance gene in progenies. /// 在子代中检测与PL1抗性基因相关的SNP标记。
- The marker predicts well the trait in different genetic backgrounds and is suitable for MAS and could be helpful for DUS /// 该标记能很好地预测不同遗传背景下的性状，适用于MAS，可能也有助于DUS测试

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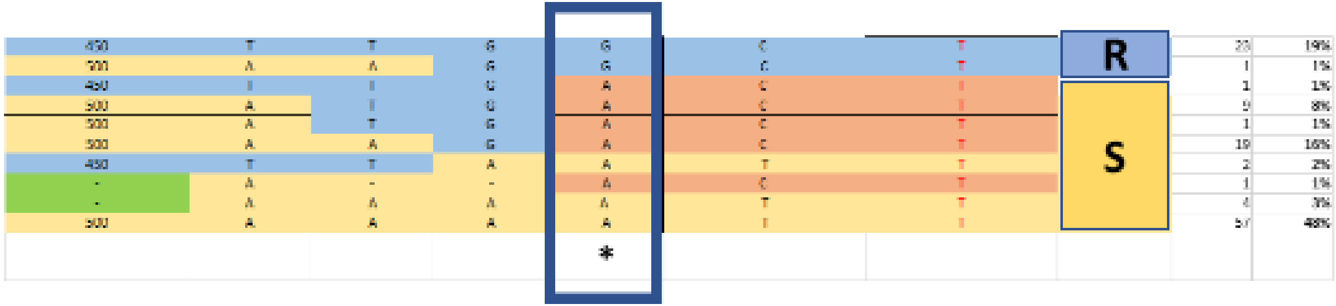

490	T	T	G	G	C	T	R	23	19%
500	A	A	G	G	C	T		1	1%
490	T	T	G	A	C	T	S	1	1%
500	A	T	G	A	C	T		9	8%
500	A	T	G	A	C	T		1	1%
500	A	A	G	A	C	T		19	16%
490	T	T	A	A	T	T		2	2%
-	A	-	-	A	C	T		1	1%
-	A	A	A	A	T	T		4	3%
500	A	A	A	A	T	T		57	48%
				*					

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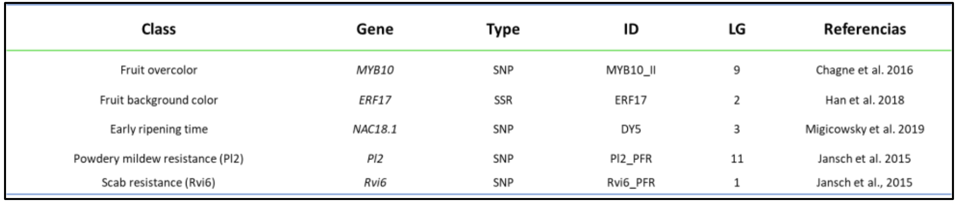
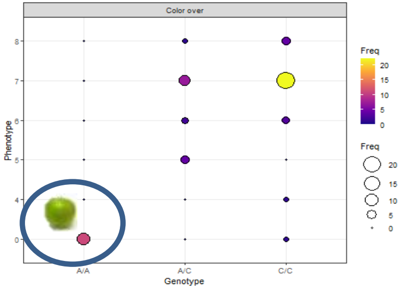
Testing of molecular markers – Apple (2/2) /// 分子标记检测–苹果（2/2）

Available at https://bioinformatics.cragenomica.es/projects/genovarview/
参见网址

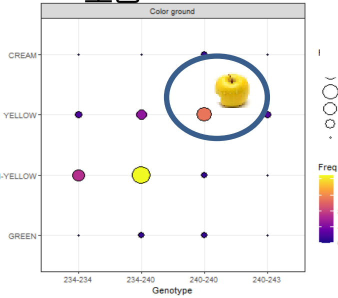


Class	Gene	Type	ID	LG	Referencias
Fruit overcolor	*MYB10*	SNP	MYB10_II	9	Chagne et al. 2016
Fruit background color	*ERF17*	SSR	ERF17	2	Han et al. 2018
Early ripening time	*NAC18.1*	SNP	DY5	3	Migicowsky et al. 2019
Powdery mildew resistance (Pl2)	*Pl2*	SNP	Pl2_PFR	11	Jansch et al. 2015
Scab resistance (Rvi6)	*Rvi6*	SNP	Rvi6_PFR	1	Jansch et al., 2015

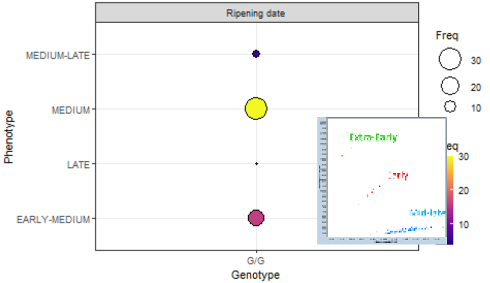
Markers developed from published information and tested in germplasm
根据公开信息开发的标记，已经完成种质测试



Overcolor
次色

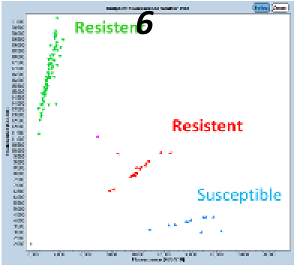


Background color
主色

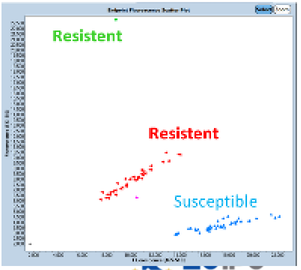


Early maturity
早熟

Rvi6



Pl2



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Testing of molecular markers - Lucerne /// 分子标记检测–紫花苜蓿

- Test a new technical approach (NGS-like) in order to manage the DUS reference collection /// 测试新的技术方法（类似于NGS），以管理DUS参考品种集
- Choice of markers done: 37 500 genome portions identified; development of a capture tool including 35,500 SNP markers /// 已完成标记选择：鉴定了37500个基因组部分；开发了含35500个SNP标记的捕获工具
- Sequencing in progress using the RAD capture tool developed by INRAE instead of genotyping-by-sequencing (GBS) /// 使用INRAE开发的RAD捕获工具代替测序基因分型（GBS）进行测序

INRAE
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GEVES Expertise & Performance
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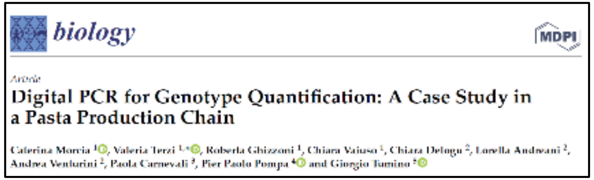
Testing of molecular markers - Wheat /// 分子标记检测–小麦

Evaluation of the digital PCR potentialities for a rapid description of genotype content in wheat autogamous, composite crosses and mixture /// 评估数字PCR在小麦自交、复合杂交和混交中快速描述基因型含量的潜力

- Method for the identification and quantification of wheat varieties in grains, flour and derived products /// 谷物、面粉和衍生产品中小麦品种的鉴定和定量方法
- Chip digital PCR method for the identification and quantification of hulless and hulled Triticum species /// 芯片数字PCR法对无壳和有壳小麦品种的鉴定和定量
- Rapid method for mycotoxin detection for wheat chain /// 小麦链真菌毒素快速检测方法
- Study of the adaptive traits and genetic diversity in traditional wheat landraces /// 研究传统小麦地方品种适应性性状及遗传多样性


biology MDPI

Article

Digital PCR for Genotype Quantification: A Case Study in a Pasta Production Chain

Caterina Morcia 1, Valeria Terzi 1,*, Roberta Ghizzoni 1, Chiara Vaiuso 1, Chiara Delogu 2, Lorella Andreani 2, Andrea Venturini 2, Paola Carnevali 3, Pier Paolo Pompa 4 and Giorgio Tumino 5

Morcia et al., Biology 2021a


biology MDPI

Article

A Digital PCR Assay to Quantify the Percentages of Hulled vs. Hulless Wheat in Flours and Flour-Based Products

Caterina Morcia 1, Raffaella Bergami 2, Sonia Scaramagli 2, Chiara Delogu 3, Lorella Andreani 3, Paola Carnevali 4, Giorgio Tumino 5, Roberta Ghizzoni 1 and Valeria Terzi 1,*

Morcia et al., Biology 2021b

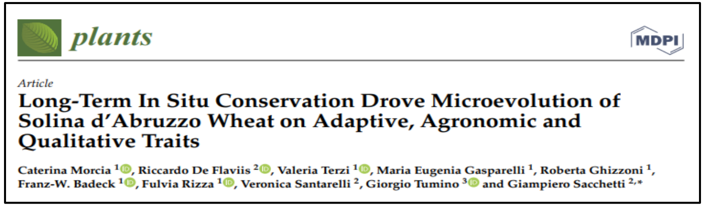

agronomy MDPI

Communication

A Point-of-Care Assay Based on Reflective Phantom Interface (RPI) Technology for Fast, Multi-Toxin Screening in Wheat

Matteo Salina 1, Giovanni Tagliabue 1, Roberta Ghizzoni 2, Valeria Terzi 2 and Caterina Morcia 2,*

Salina et al., Agronomy, 2022


plants MDPI

Article

Long-Term In Situ Conservation Drove Microevolution of Solina d’Abruzzo Wheat on Adaptive, Agronomic and Qualitative Traits

Caterina Morcia 1, Riccardo De Flaviis 2, Valeria Terzi 1, Maria Eugenia Gasparelli 1, Roberta Ghizzoni 1, Franz-W. Badeck 1, Fulvia Rizza 1, Veronica Santarelli 2, Giorgio Tumino 3 and Giampiero Sacchetti 2,*

Morcia et al., Plants, 2023

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EUIPO EUROPEAN UNION INTELLECTUAL PROPERTY OFFICE

Expected applications from INVITE /// INVITE项目的预期应用

Information about the applicability of phenotyping tools for variety testing
关于品种测试表型分析工具适用性的信息

Information about the applicability of molecular markers for distinctness and management of reference collection
关于分子标记在特异性和参考品种集管理上适用性的信息

Recommendations for the testing of heterogeneous plant material
异质植物材料测试建议

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CHINA

Concluding remarks: general outputs of INVITE
结束语：INVITE项目的整体成果

Francois Laurens, INRAE France / coordinator of the INVITE project
Francois Laurens 法国国家农业食品与环境研究院(INRAE) / INVITE项目协调员

Plant Variety Rights online technical training for Chinese experts; 28 Nov 2023
中国专家植物品种权在线技术培训；2023年11月28日
www.ipkey.eu

Funded by the European Union
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Main general outputs of INVITE (1) /// INVITE项目的整体成果（1）

- Setting-up a research community dedicated to support the variety testing scheme

建立致力于支持品种测试计划的共同体

- Improve links between research and users of research findings:

加强研究与研究结果使用者间的联系：

  - **DUS: links with the CPVO and several EOs /// DUS测试：与CPVO和若干测试中心的联系**
  - **VCU and post-registration: Links with VCU Expert network established with agreements that research should be regularly invited to present their activities. /// VCU测试和注册后：与VCU专家网络建立联系，达成定期邀请研究人员介绍活动的共识。**
  - **Breeding testing: EUROSEEDS liaison established /// 育种测试：建立欧洲种子联络处**

- ↗ strong links outside the consortium with other projects (National, European and international)

加强联合体外与其他国家级、欧洲和国际项目的联系

Main General outputs of INVITE (2) /// INVITE项目的整体成果（2）

- Setting-up a research community dedicated to support the variety testing scheme /// 建立致力于支持品种测试计划的共同体
- Improve links between research and users of research findings: /// 加强研究与研究结果使用者间的联系：
- ↗ strong links outside the consortium with other projects (National, European and international) /// 加强联合体外与其他国家级、欧洲和国际项目的联系

☐ Collect huge volumes of historical data that could (should) serve other purposes than just INVITE research. /// **收集大量历史数据，或可（应可）用于INVITE项目外的其他用途**

☐ Improve knowledge /// **提升认知**

☐ Develop tools and methods to be implemented in the EU variety testing /// **开发将在欧盟品种测试中使用的工具和方法**

THANK YOU
感谢聆听

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