



VIII CONGRESO
MUNDIAL DE LA
QUINUA
Bolivia





Optimizing Quinoa breeding High-Throughput Phenotyping and Software for Experimental Designs and Data Collection

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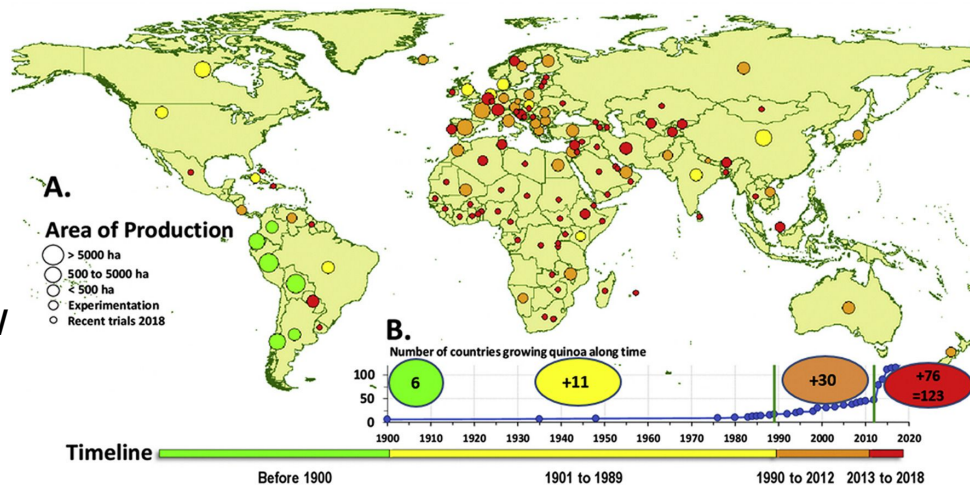
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Why quinoa?

- Ancient crop of the Andean region (Jacobsen et al., 2003)
- In 2013 its potential was recognized and was declared the “International Year of Quinoa”
- Nutritional grain, gluten-free and low glycaemic index (Vega-Gálvez et al. 2020)
- Quinoa is tolerant to a diverse range of abiotic stresses (Rao & Shahid, 2012) and adapted to marginal soils



Global expansion of quinoa (Alandia et. al 2020)

Capacity development

- Contribute to food security of Peruvian smallholder farmers by local capacity development
- Genetic resources conservation and crop improvement for maize and quinoa
- Utilizing genetic diversity of Peruvian quinoa landraces for breeding improved varieties
- Project partners:
 - UHOH (Germany)
 - UNAP (Peru)
 - UNALM (Peru)
 - KWS (Germany)



Die KWS Initiative
„Capacity Development“

KWS Saatgut-Projekte in Peru

Peru ist vielfältig.

Tropenklimate prägen die östlichen Regenwaldgebiete („Selva“). Im Westen und den Küstengebieten („Costa“) herrscht trockenes Wüstenklima. Gemäßigte bis kalte Zonen bestimmen die zentralen Anden („Sierra“) und das Hochplateau („Altiplano“).

Diese Vielfalt spiegelt sich auch in der Landwirtschaft wider. Peruanische Kleinbauern kultivieren in allen Landesteilen eine Vielzahl an Mais- und Quinoa-Sorten. Doch die Vielfalt ist bedroht: Extreme Klimaschwankungen nehmen zu, die Jugend wandert in die Städte ab und traditionelles Wissen zu Anbau, Nutzung und Erhalt der Kulturpflanzen geht verloren. Die Folgen: Chronischer Nahrungsmangel herrscht vor allem in entlegeneren Regionen. Insgesamt leben acht Millionen Menschen in Armut, das sind fast 30 Prozent der rund 30 Millionen Peruaner.

Ziel: Ernährungssicherheit erhöhen

Die Initiative besteht aus drei, vollständig von KWS finanzierten Projekten.

Overview

High-Throughput Phenotyping

- > New phenotyping methods for study the diversity and plant breeding application
 - Phenotyping and characterization of genetic resources in quinoa
 - Using deep learning
 - Use Mask R CNN for image segmentation and classification

Inkaverse Project

- > Software for Experimental Designs and Data Collection
 - Improve experimental data quality and analysis
 - Open source software in R programming environment
 - Interactive web applications
 - Easy to implement in small breeding programs

Quinoa panicles: High-Throughput Phenotyping

Rationale

Panicle shapes

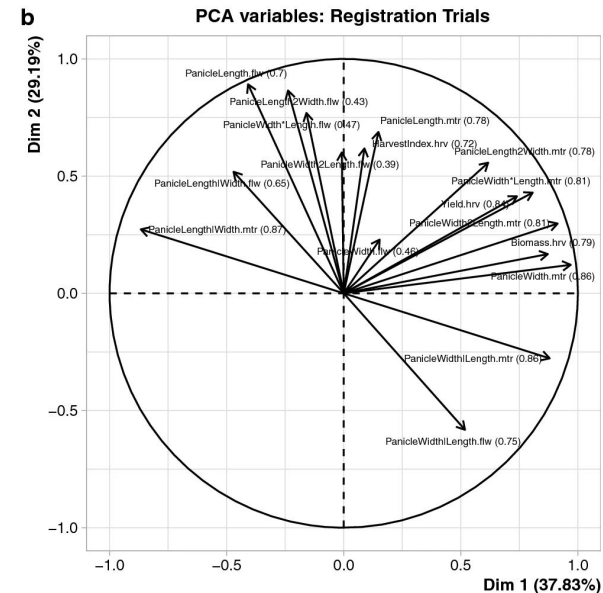
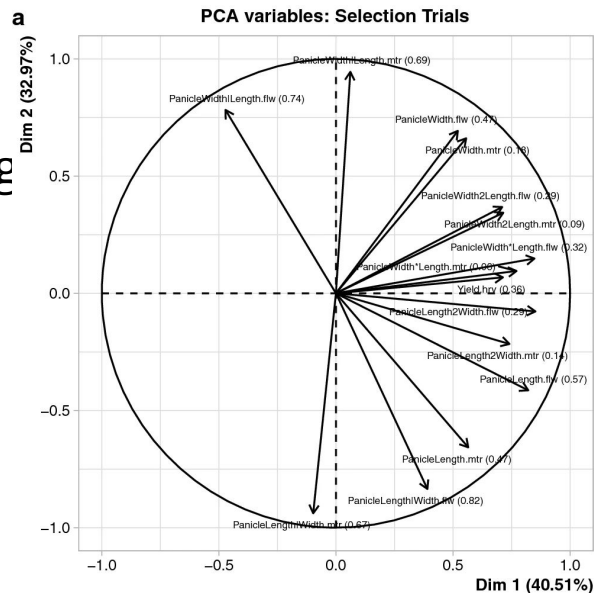
- Extract traits information from panicle images
- Use information for breeding purpose and genetic resource conservation
 - GenBank Phenomics
- Estimate panicle indices related to the yield



Association of grain yield with panicle indices

Previous results

- Phenotyping of quinoa panicles is time-consuming
- PCA and calculated the heritability of six panicle traits indices from the selection and registration trials
- The index panicle Width*Length



Lozano-Isla et al. (2023) Euphytica

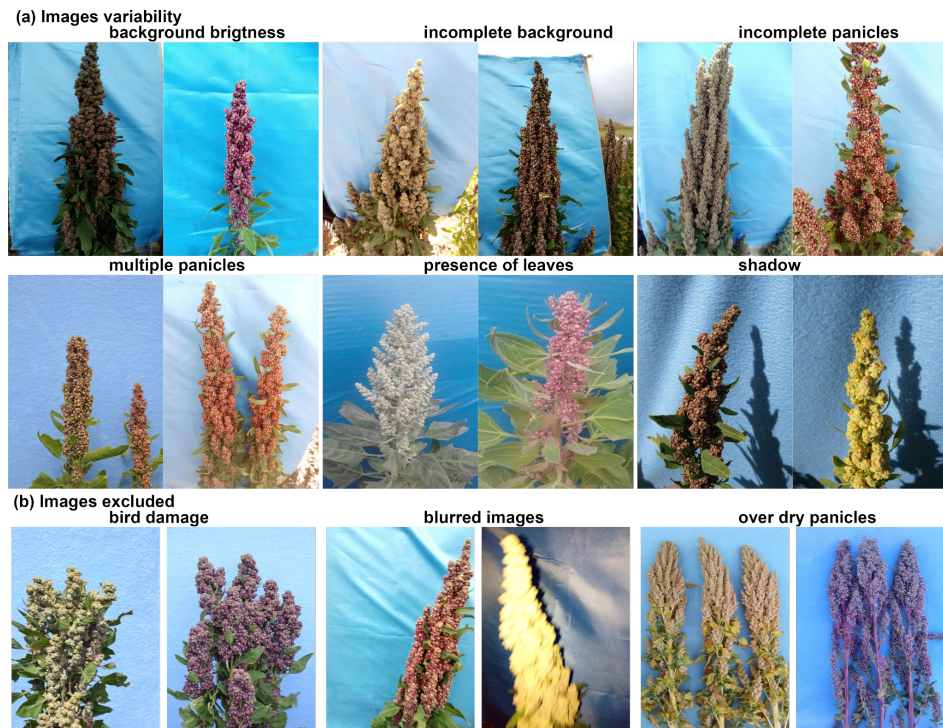
Materials and Methods

Field trials and image selection

Field images

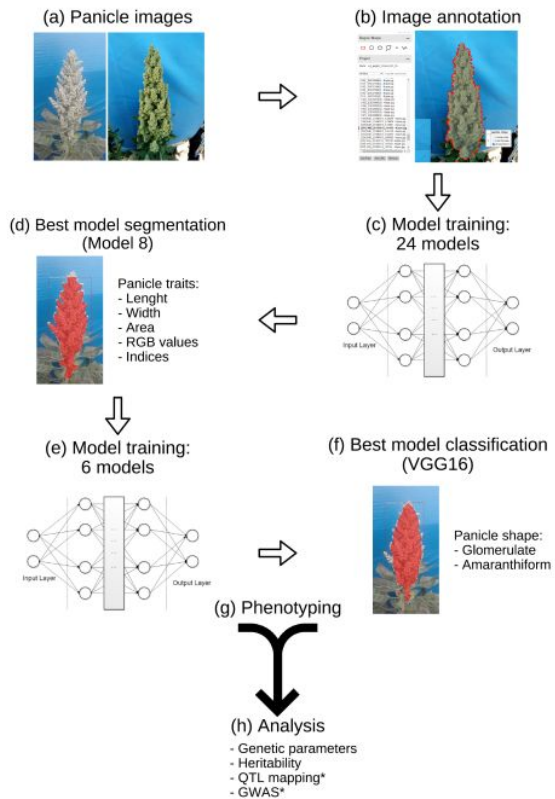
Season	Genotypes	Generation	Location	Exp. design	Photographic device	Resolution
2016-2017	1200	F6	Camacani, Puno	RCBD	Nikon D5101	9MP
2017-2018	600	F7	Illpa, Puno	Lattice 10x10	ZTE Blade A610	8MP
2018-2019	25	F8	Camacani, Puno	Lattice 5x5	Samsung SM-T285M	3.7MP
2018-2019	25	F8	Illpa, Puno	Lattice 5x5	Samsung SM-T285M	3.7MP

- Image variability
 - Different resolutions
 - Different devices
- Unbalanced data for multi-location analysis
- Initial image annotation
 - Training set: 225
 - Validation set: 75

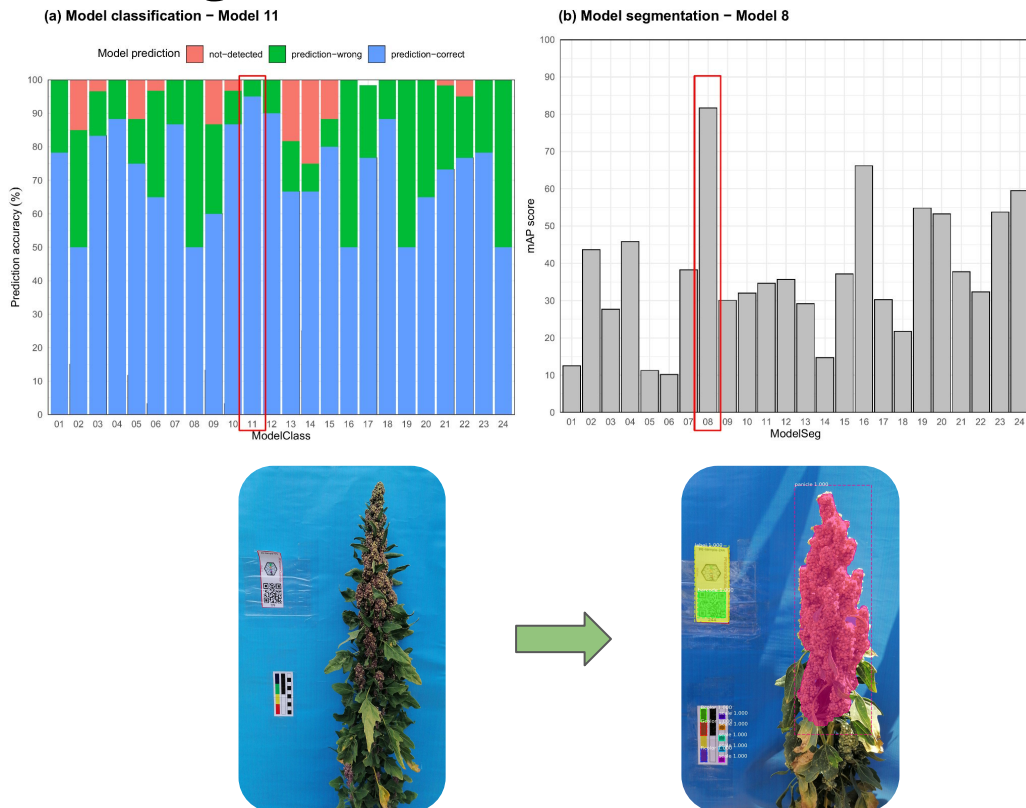


Results

Pipeline



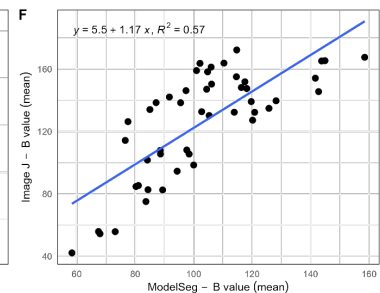
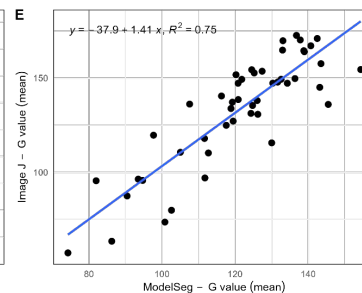
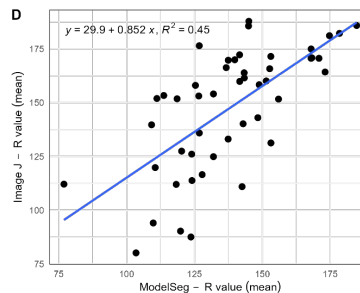
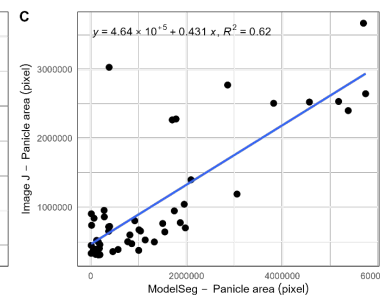
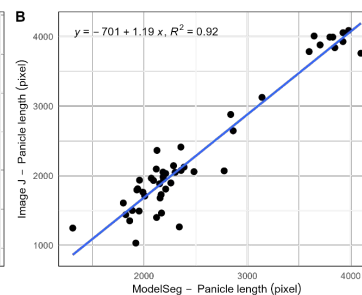
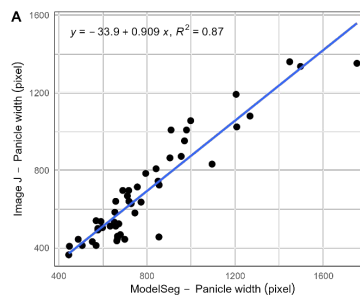
Segmentation and Classification



Results

Mask R-CNN vs Imagej

- High correlation between the phenotypic parameters
 - Panicle length, width and area
- Intermediate correlation between the RGB values
- Mask R-CNN allow to phenotype a several images after model training



Inkaverse Project

Rationale

- Use open source software for data analysis and collection
 - CRAN packages
- Improve data quality and accelerate data analysis
- Tools to support small breeding programs

CRAN

inti 0.6.0

APPS ARTICLES PRIVACY POLICY FUNCTIONS NEWS

inti

The 'inti' package is part of the 'inkaverse' project for developing different procedures and tools used in plant science and experimental designs. The main aim of the package is to support researchers during the planning of experiments and data collection 'tarpuy()', data analysis and graphics 'yupana()', and technical writing. Learn more about the 'inkaverse' project at <https://inkaverse.com/>.

Installation

To install the stable version from [CRAN](#):

```
install.packages("inti")
```

INKVERSE

YUPANA

INTI

TARPUY

Links

- [View on CRAN](#)
- [Browse source code](#)
- [Report a bug](#)
- [Support the project](#)

License

[GPL-3](#) | file [LICENSE](#)

Citation

[Citing inti](#)

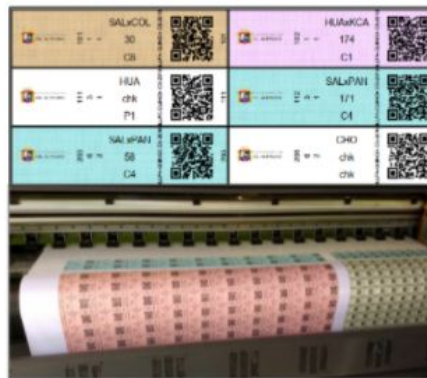
Developers

[Flavio Lozano-Isla](#)

R packages

Implementation

- Project for experimental designs, data collection and analysis
 - Inti R package
 - Yupana ⇒ Data analysis
 - Tarpuy ⇒ Fieldbook plan
 - MET ⇒ Genotype selection
 - BLUPs and BLUEs
 - Heritability
 - Huito R package
 - Reproducible and flexible labels design



Preparación de etiquetas



Etiquetado



Colecta de datos

Summary

- Importance of capacity development in latin america
- Use the high-throughput phenotyping for boost breeding and conservation of genetic resources in quinoa
 - GenBank phenomics
- Open source tools in R for support researchers for planning, collection and data analysis





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