Optimización en el mejoramiento de quinua: Fenotipado de alto rendimiento y software para diseños, colecta y análisis de datos experimentales

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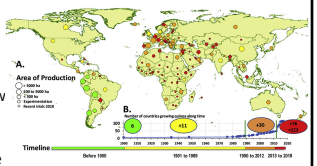
Why quinoa?

- 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)

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

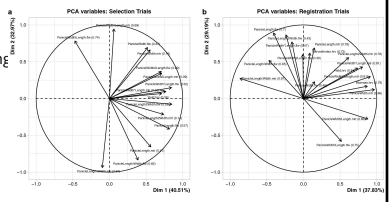
- Extract traits information from panicle images
- Use information for breeding purpose and genetic resource conservation
  - GenBank Phenomics
- Estimate panicle indices related to the yield

Panicle shapes

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

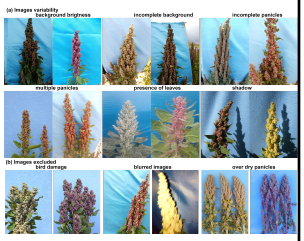
Materials and Methods

Field trials and image selection

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

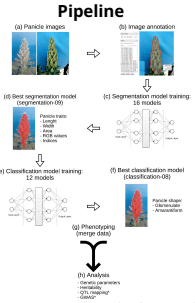
- Image variability
  - Different resolutions
  - Differents devices
- Unbalanced data for multi-location analysis
- Initial image annotation
  - Training set: 225
  - Validation set: 75

Field images

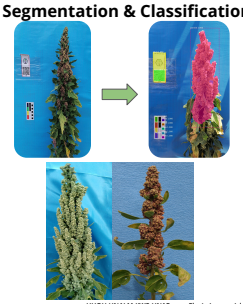


Results

Pipeline



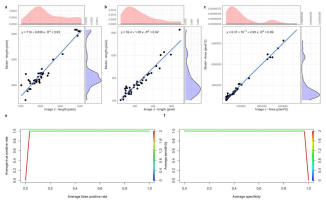
Segmentation & Classification



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

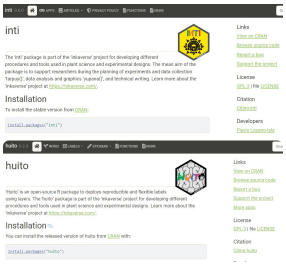


Inkaverse Project

Objectives

- Use open source software for data analysis and collection
  - CRAN packages
  - Interactive web applications
- Improve data quality and accelerate data analysis
- Tools to support design of experiments, data collection and analysis
  - Use in breeding programs

CRAN



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

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

Next steps

⇒ Publication
- Inti package
- Huito package
- H2cal() for genotype selection
  - H2cal() vs ASReml

⇒ Implementation
- Experimental designs
  - Split-plot
  - Latin square
- Genetic designs
  - Alpha lattice
  - p-reps
  - Sudoku
- Interactive labels design

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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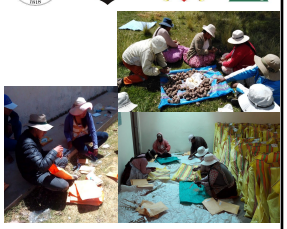
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