

Plant to Protein: Phenotypic Relationships Within a Quinoa World Core Collection

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C1/C9 Breeding for Improved Nutrition to Feed the World Oral

Translating Visionary Science to Practice



Overview

Introduction to Quinoa

Study Design

Results and Significance



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PERSPECTIVE ARTICLE

Front. Plant Sci., 09 May 2016 | <https://doi.org/10.3389/fpls.2016.00608>

Murphy *et al.*, 2016



Development of a Worldwide Consortium on Evolutionary Participatory Breeding in Quinoa



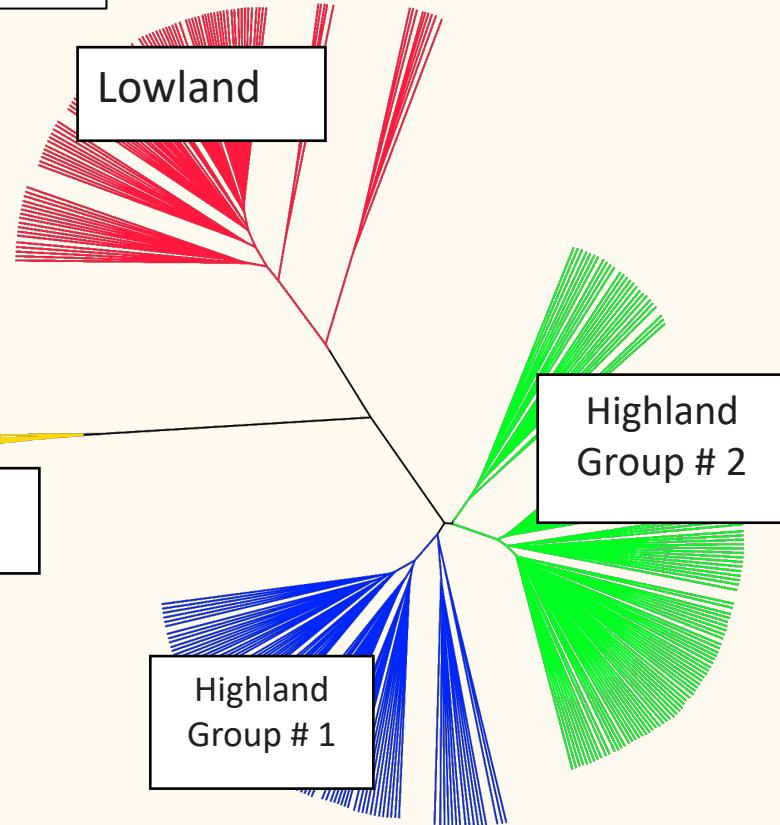
Kevin M. Murphy^{1*}, Didier Bazile², Julianne Kellogg¹ and Maryam Rahamanian³

- Excellent nutritional quality & potential to improve global food security, especially in marginal environments
- Tremendous variation to support strategic germplasm development



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World Core Collection



Unrooted NJ-Tree population structure based on filtered SNPs performed with GAPIT V.3 Van-Raden method

1. Aimed at capturing geographic diversity
2. Limited by germplasm access
3. Represents germplasm available to support global expansion
4. Genotyping: ~1.2M SNPs based on quinoa genome V2

Research Objectives

1. Characterize collection
2. Identify sources of variation
3. Understand relationships
4. GWAS



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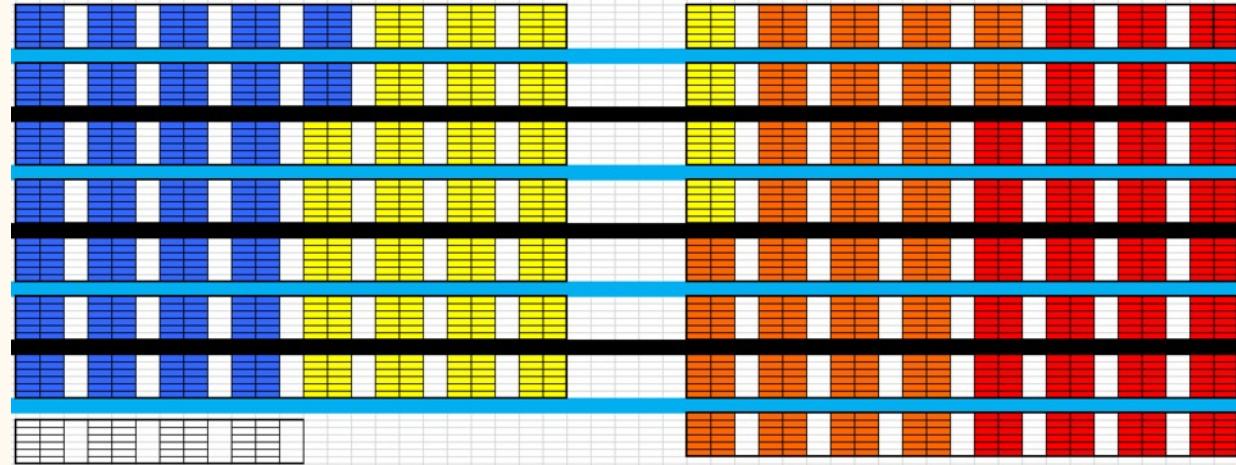
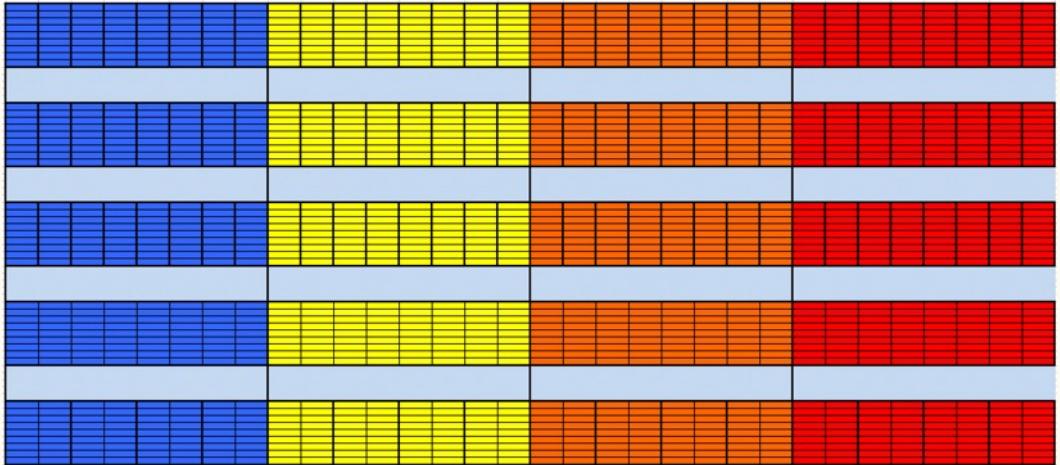
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Study Design

KAUST World Core Collection (n=334) + WSU Variety Trials (n=26)



Randomized Complete Block Design (4 blocks)

16:8 hours; light:dark
20-25°C

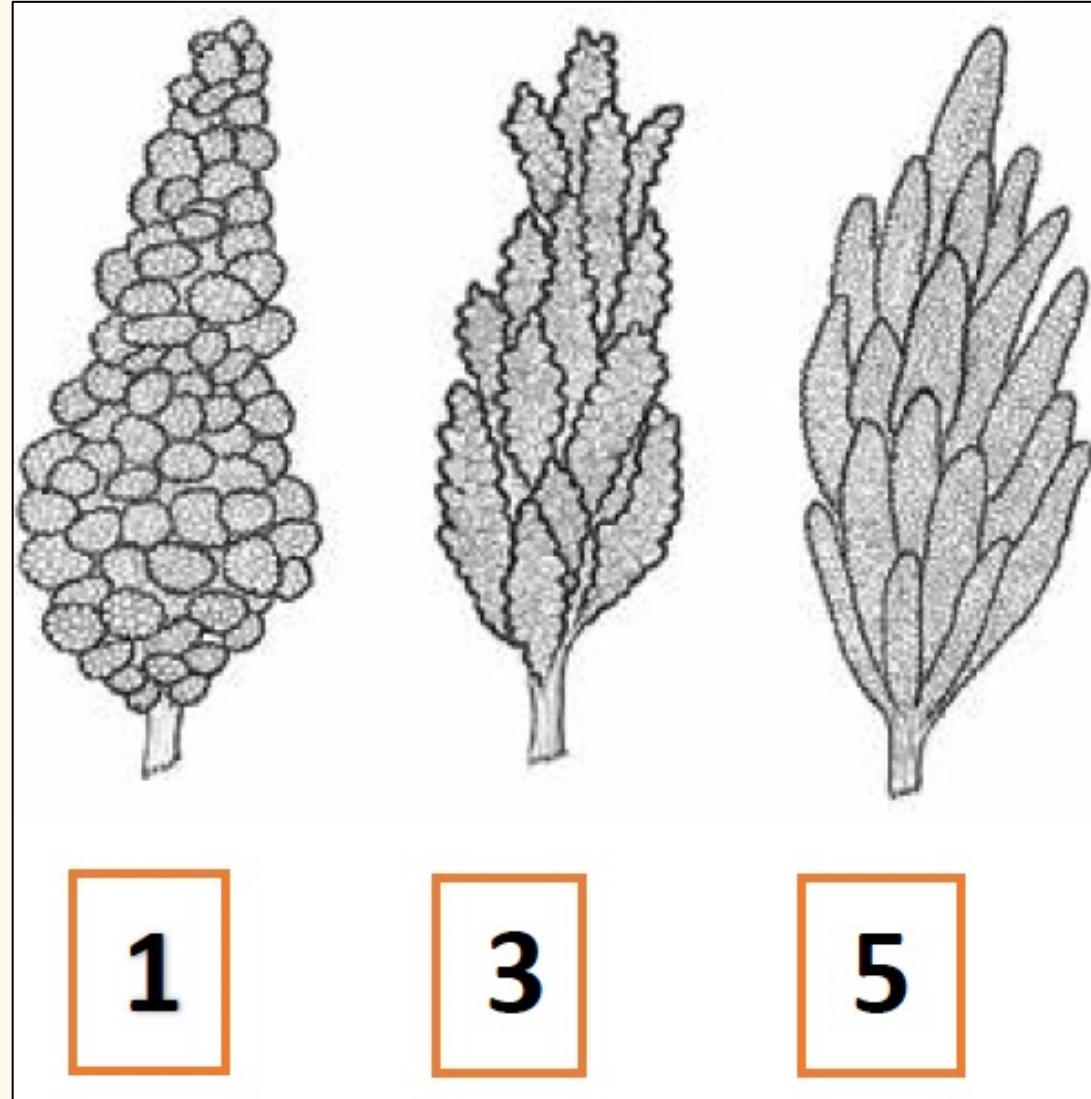


- Days to harvest
- Height at harvest
- Inflorescence length and width
- Photo



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Inflorescence Shape



Inflorescence Density



1



3



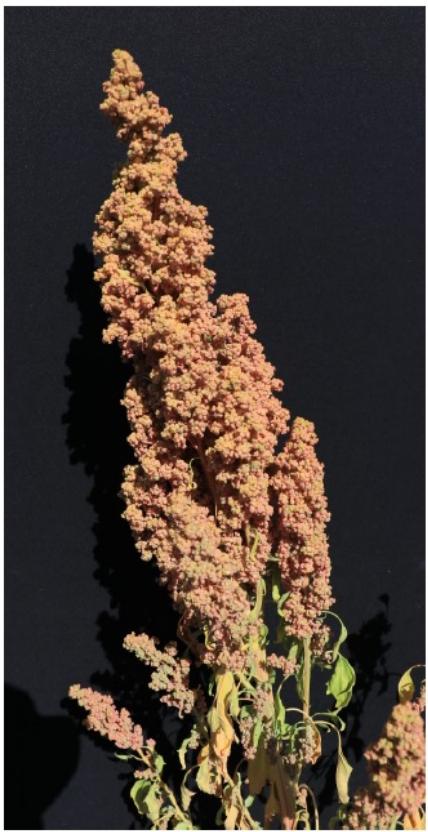
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7



Inflorescence Leafiness



1



3



5



7



Inflorescence Color





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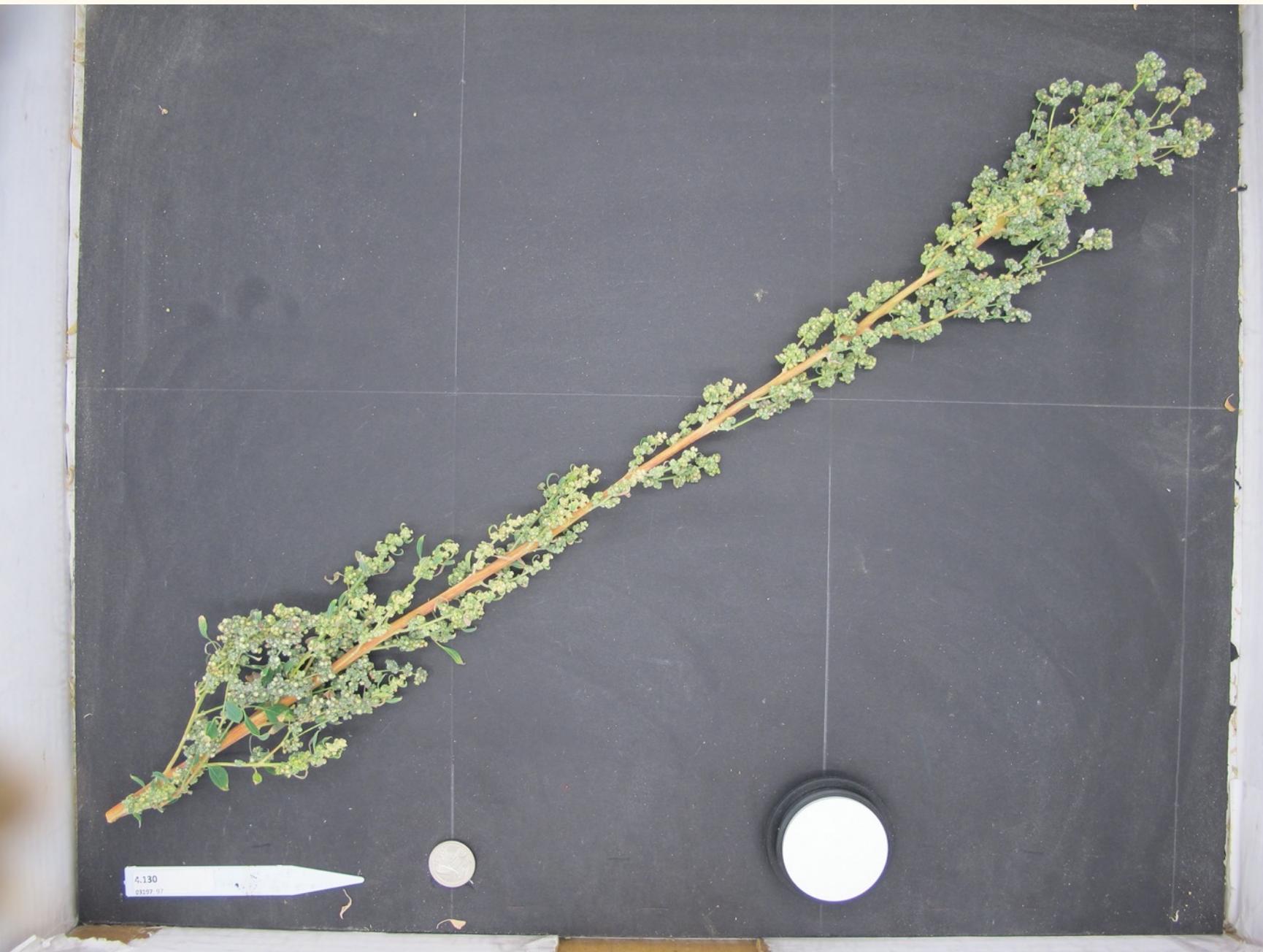
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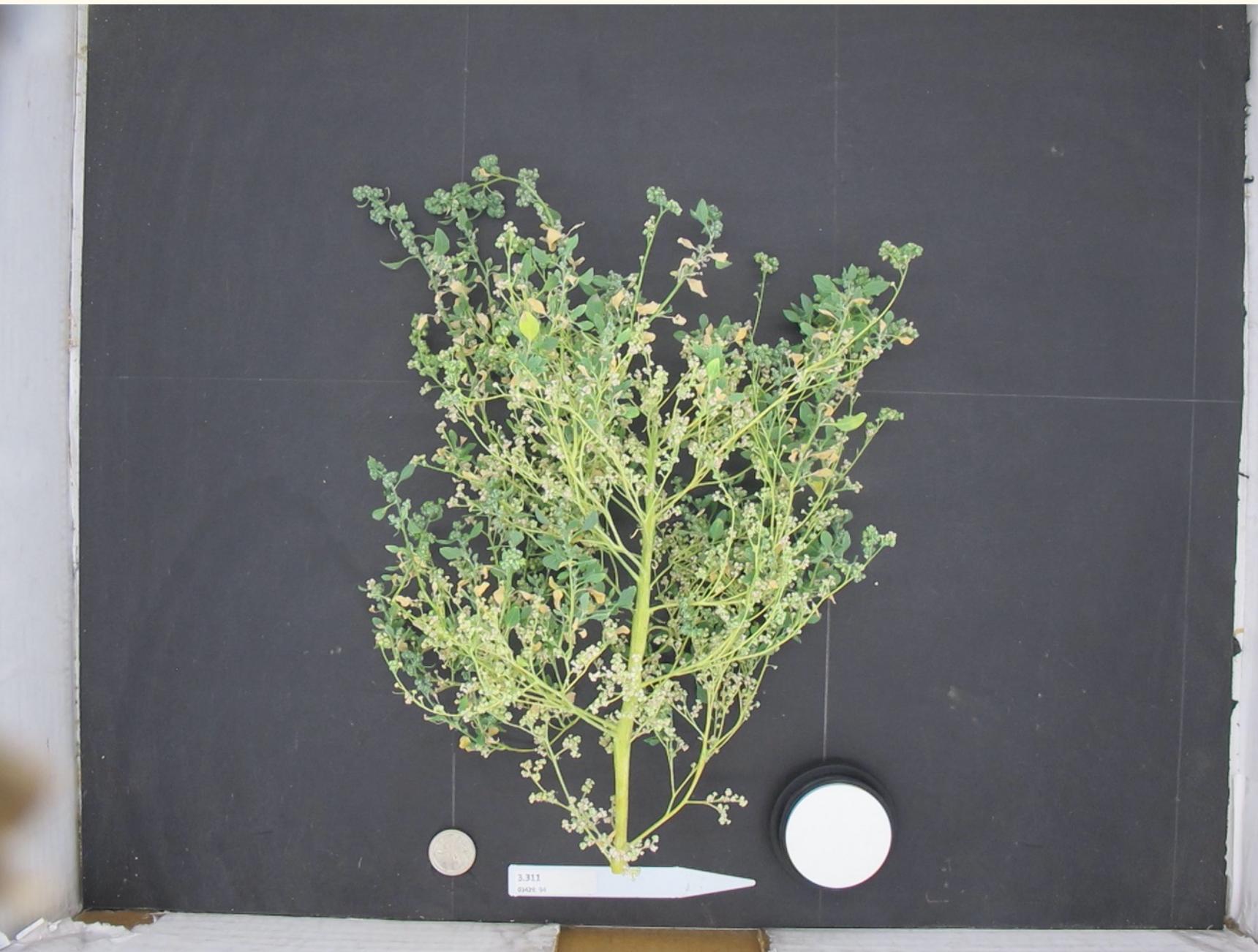
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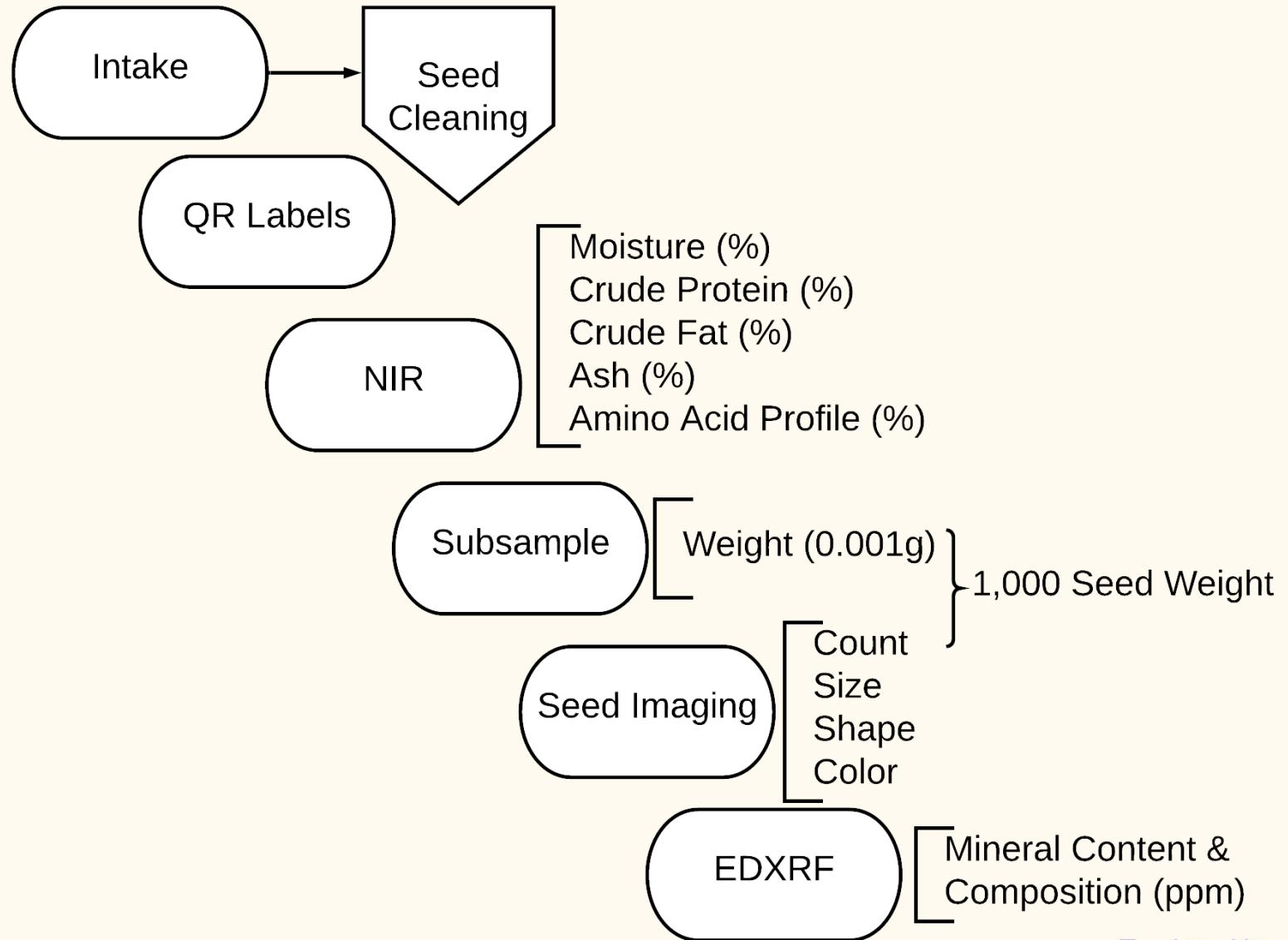




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WSU Nutritional Phenotyping Pipeline



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Postharvest Traits

Seed
Composition

Protein Content

Protein
Composition



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Yield

Thousand Seed
Weight

Size

Shape

Color

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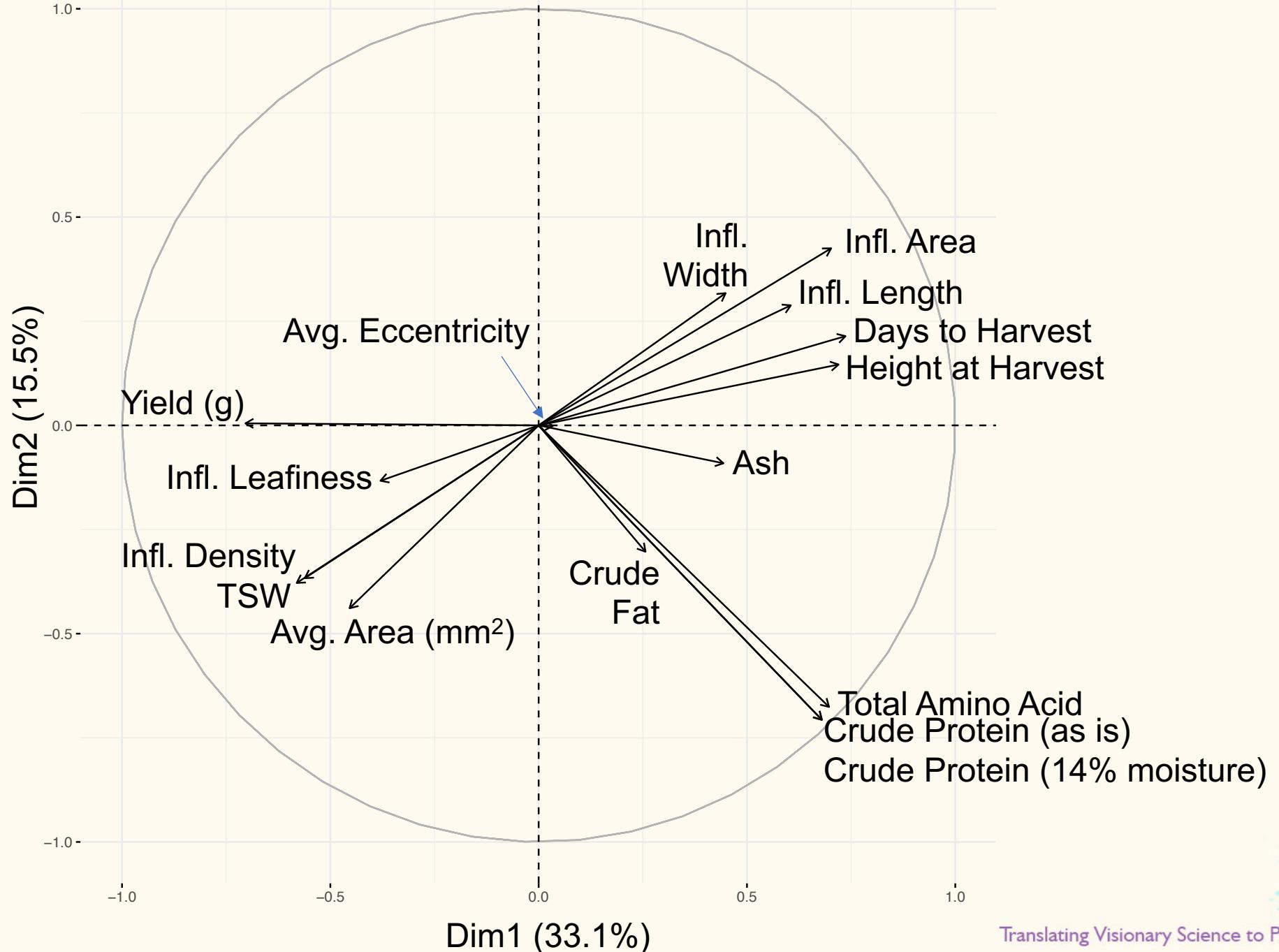
Results and Significance



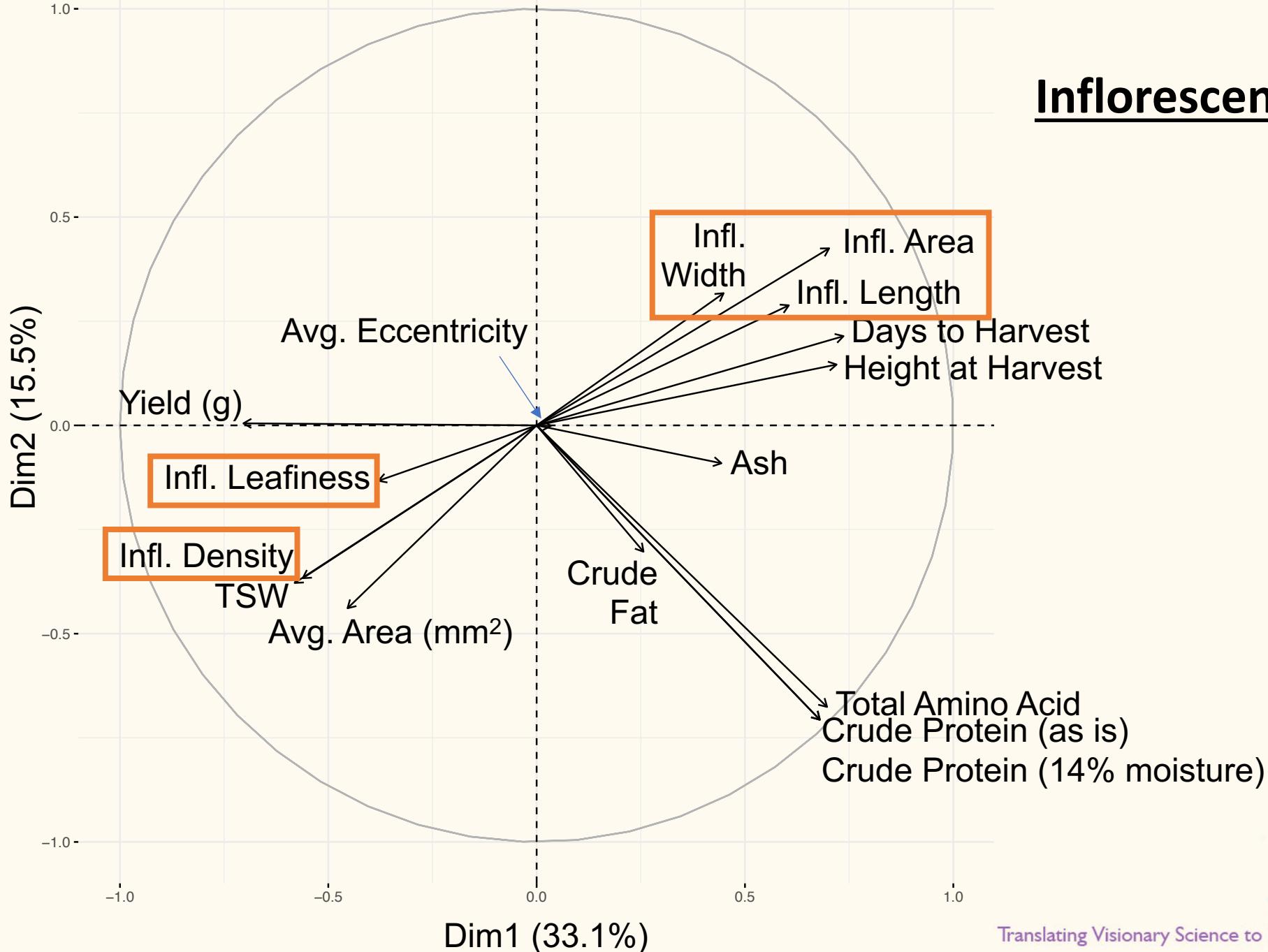
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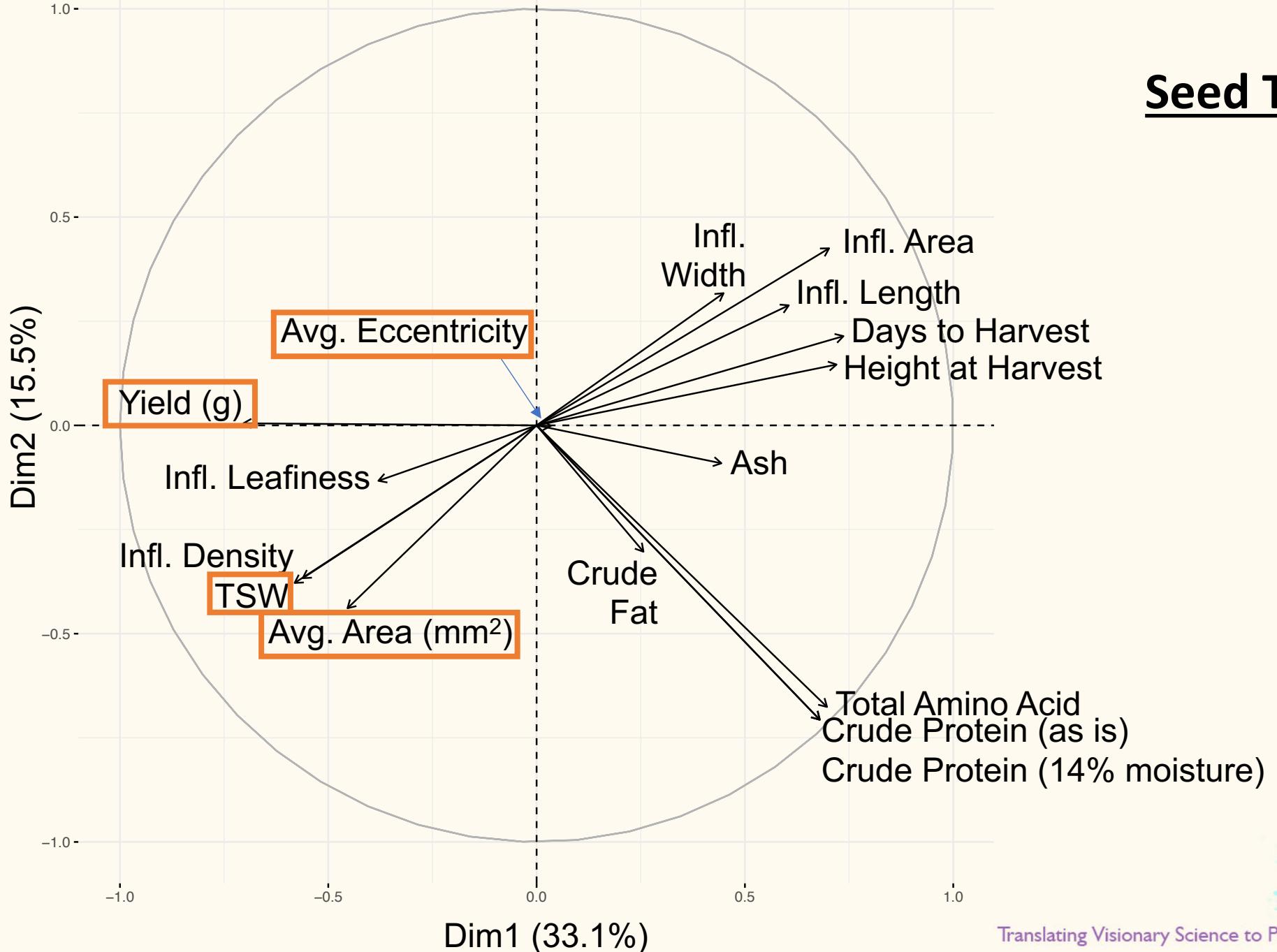




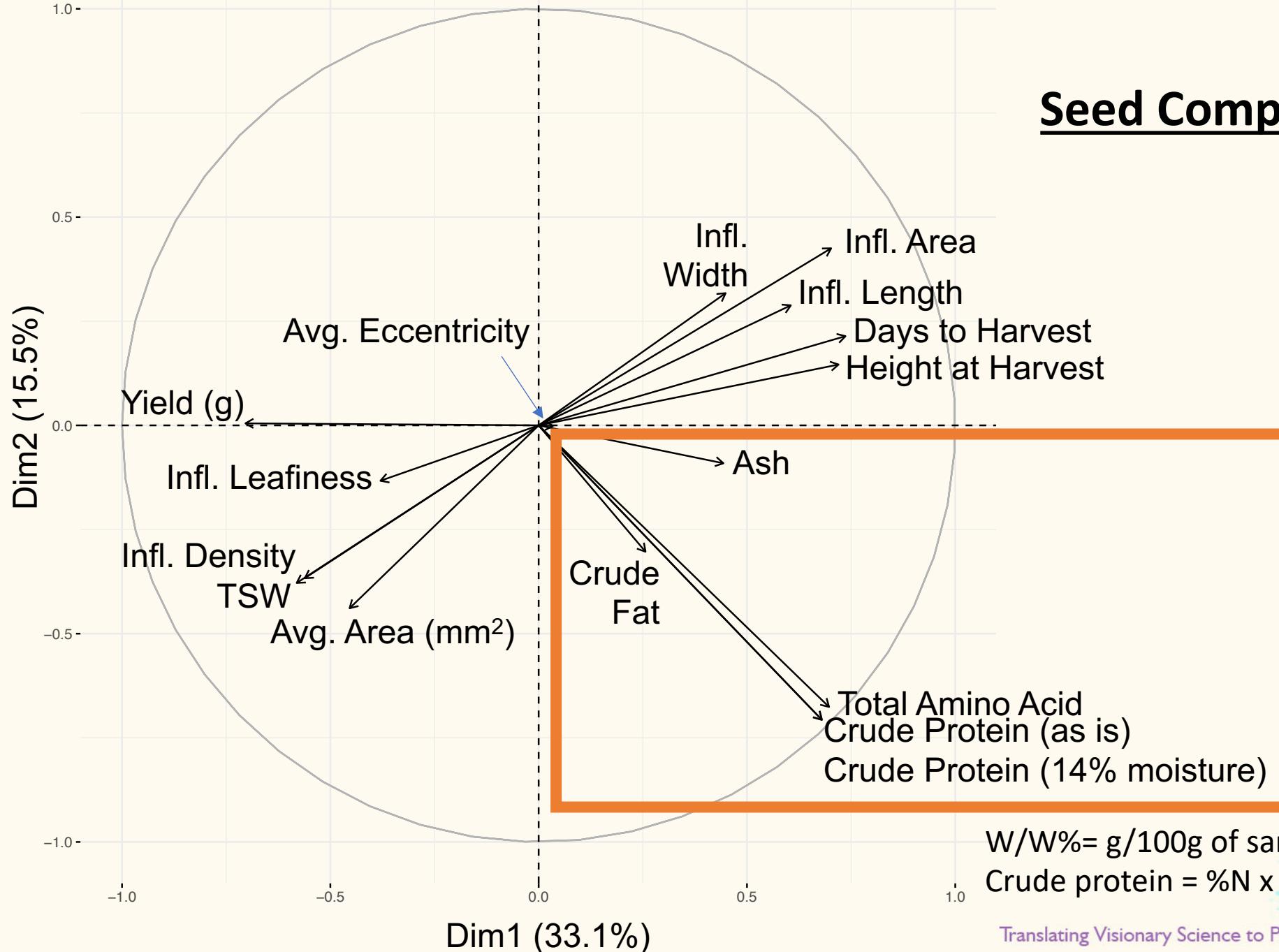
Inflorescence Traits

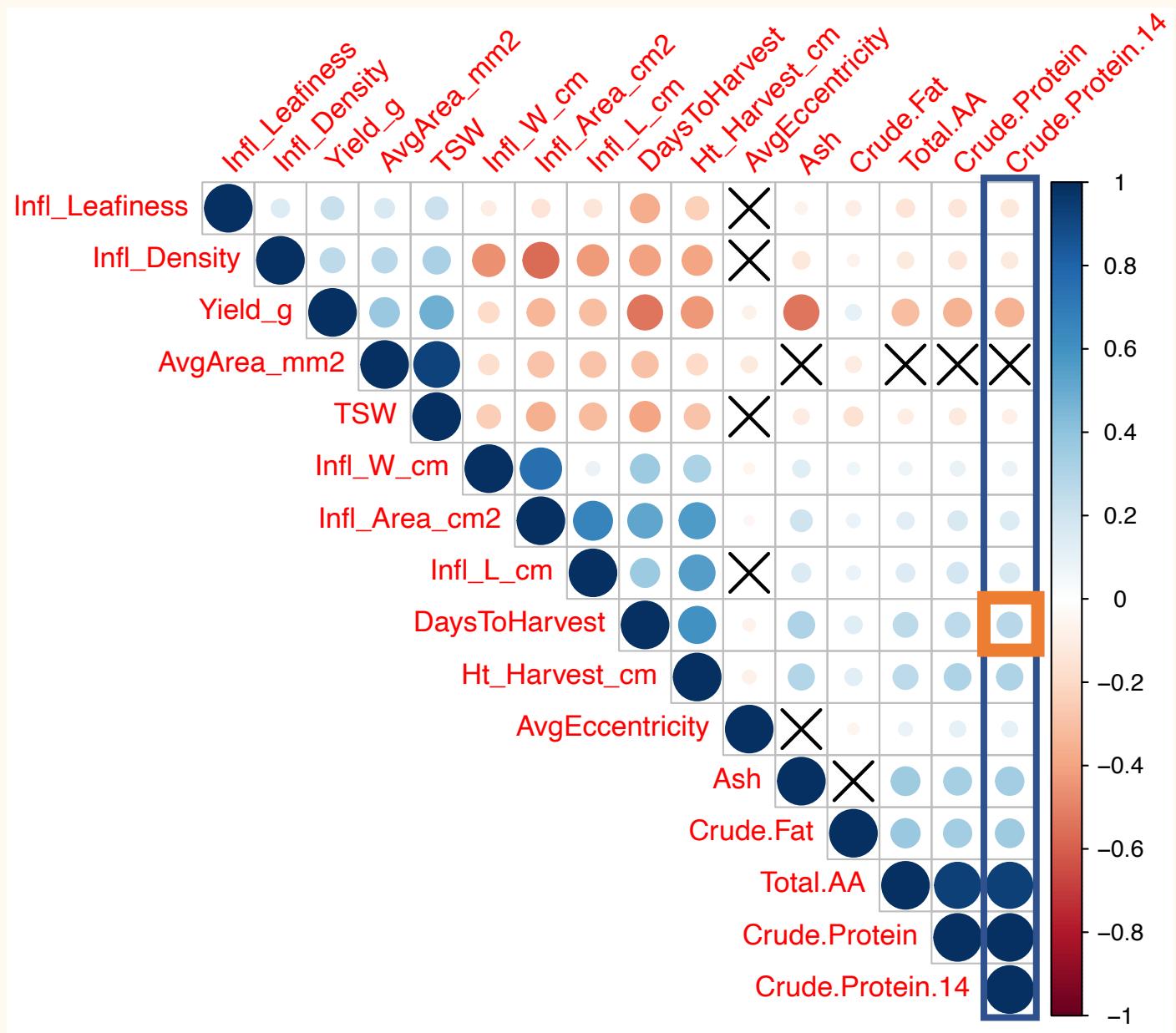


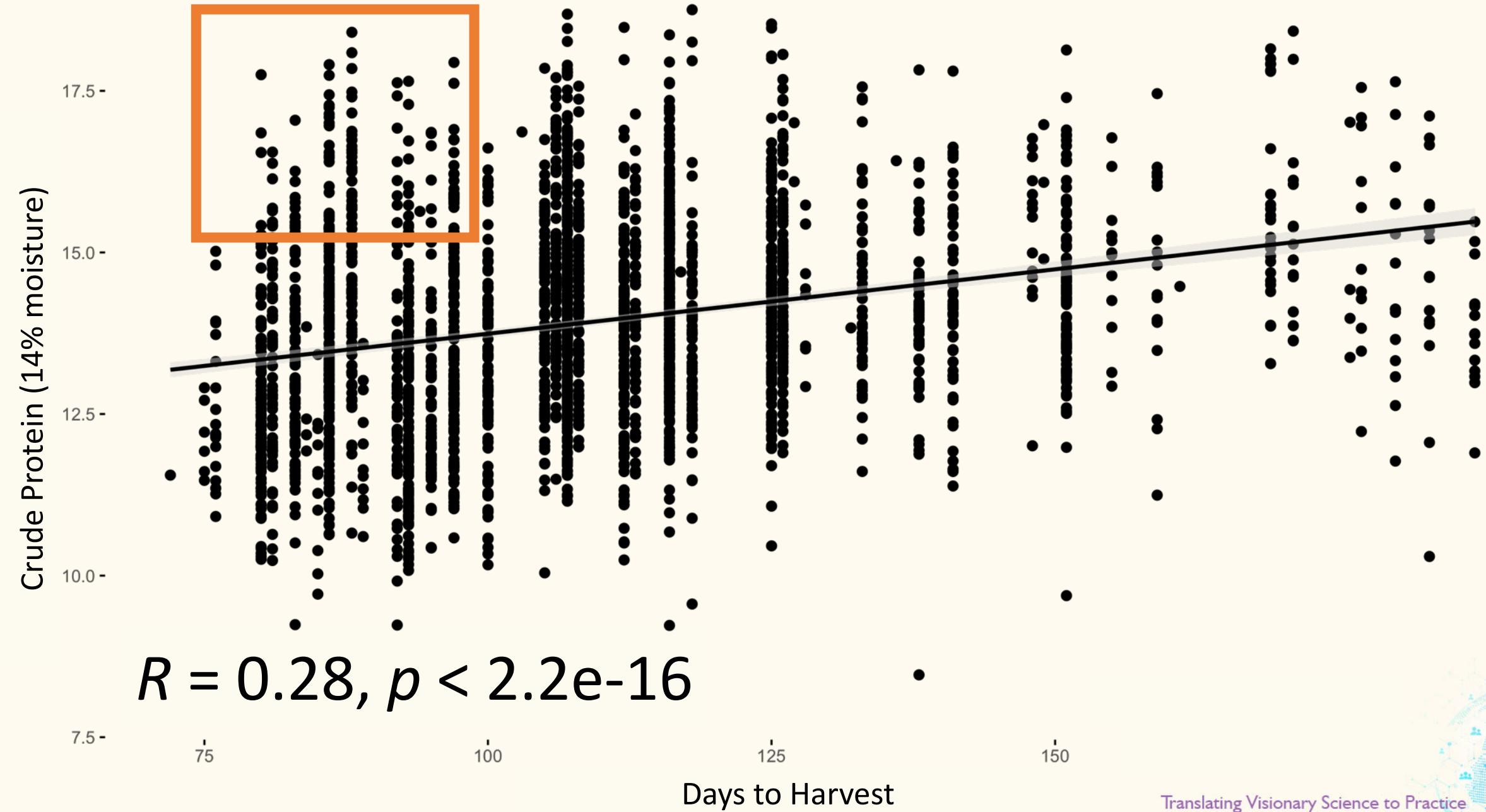
Seed Traits

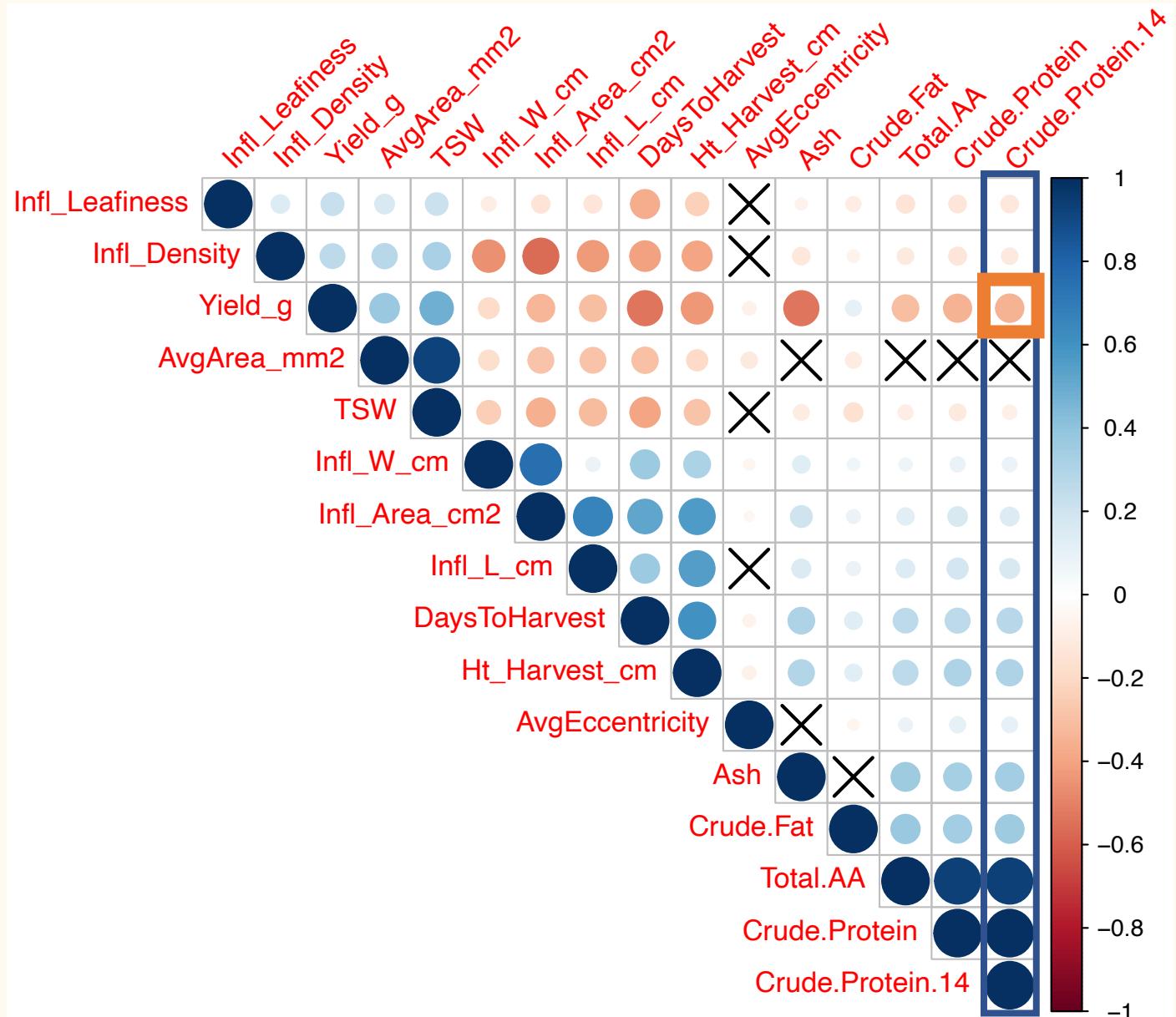


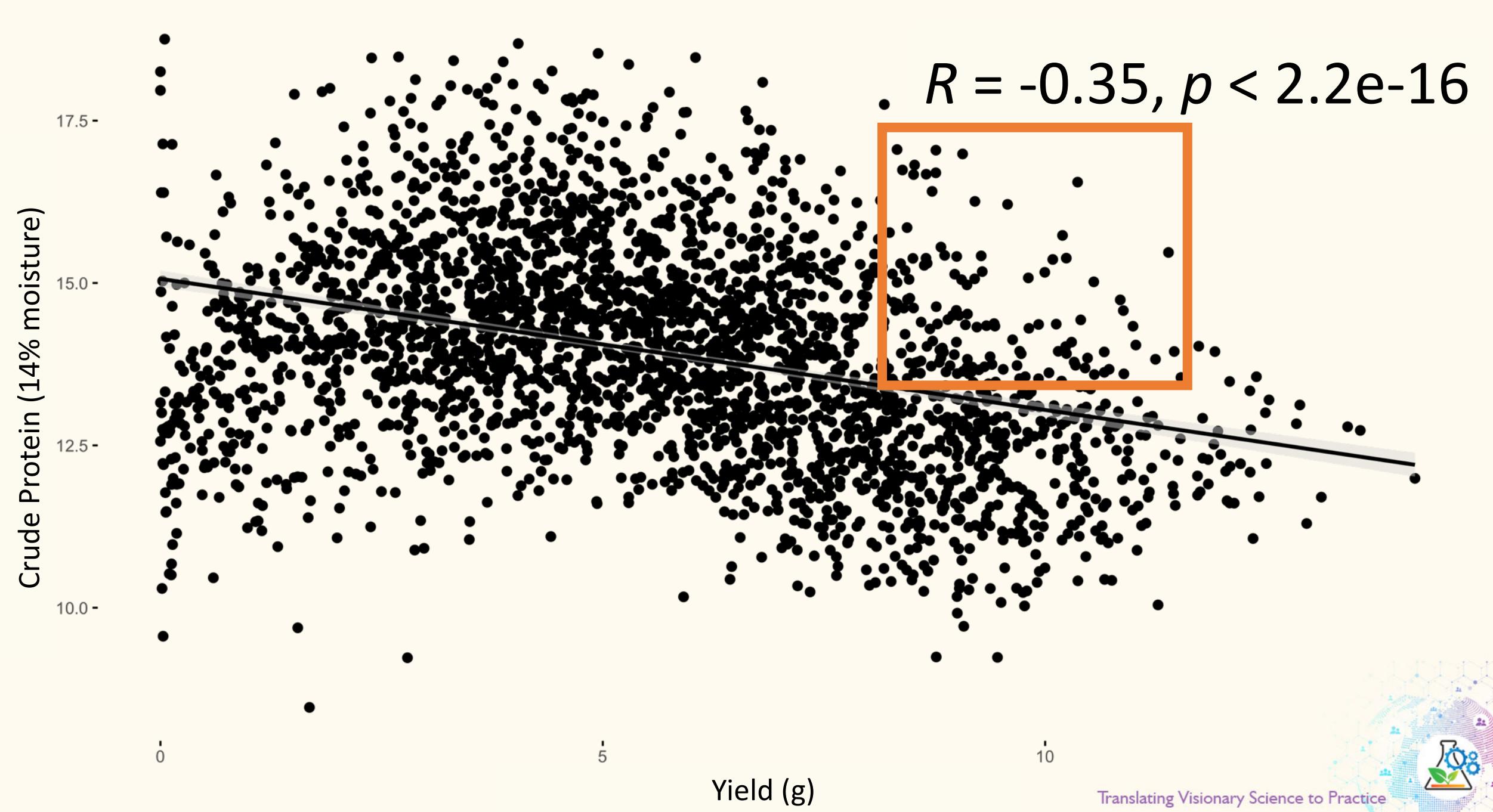
Seed Composition

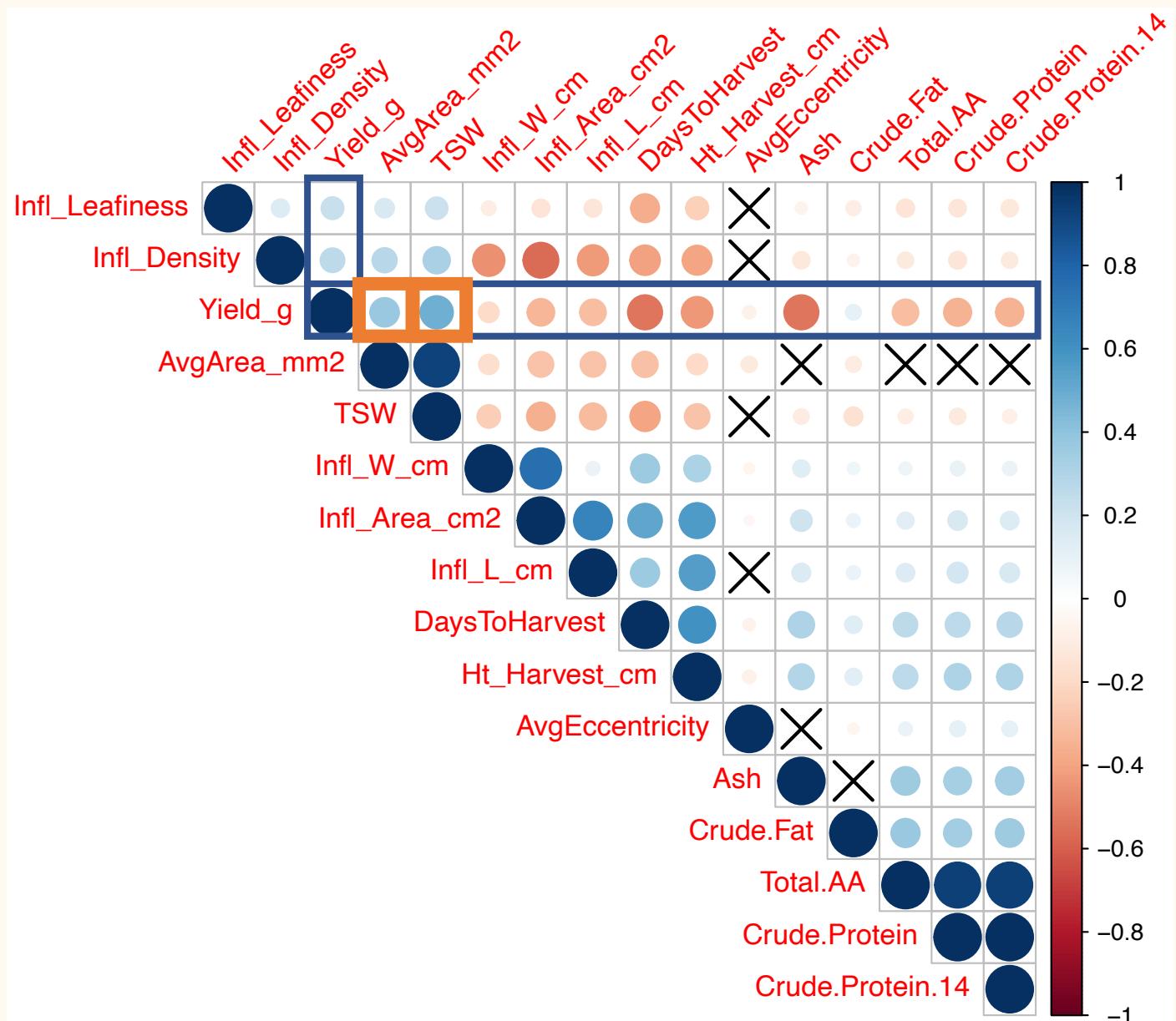




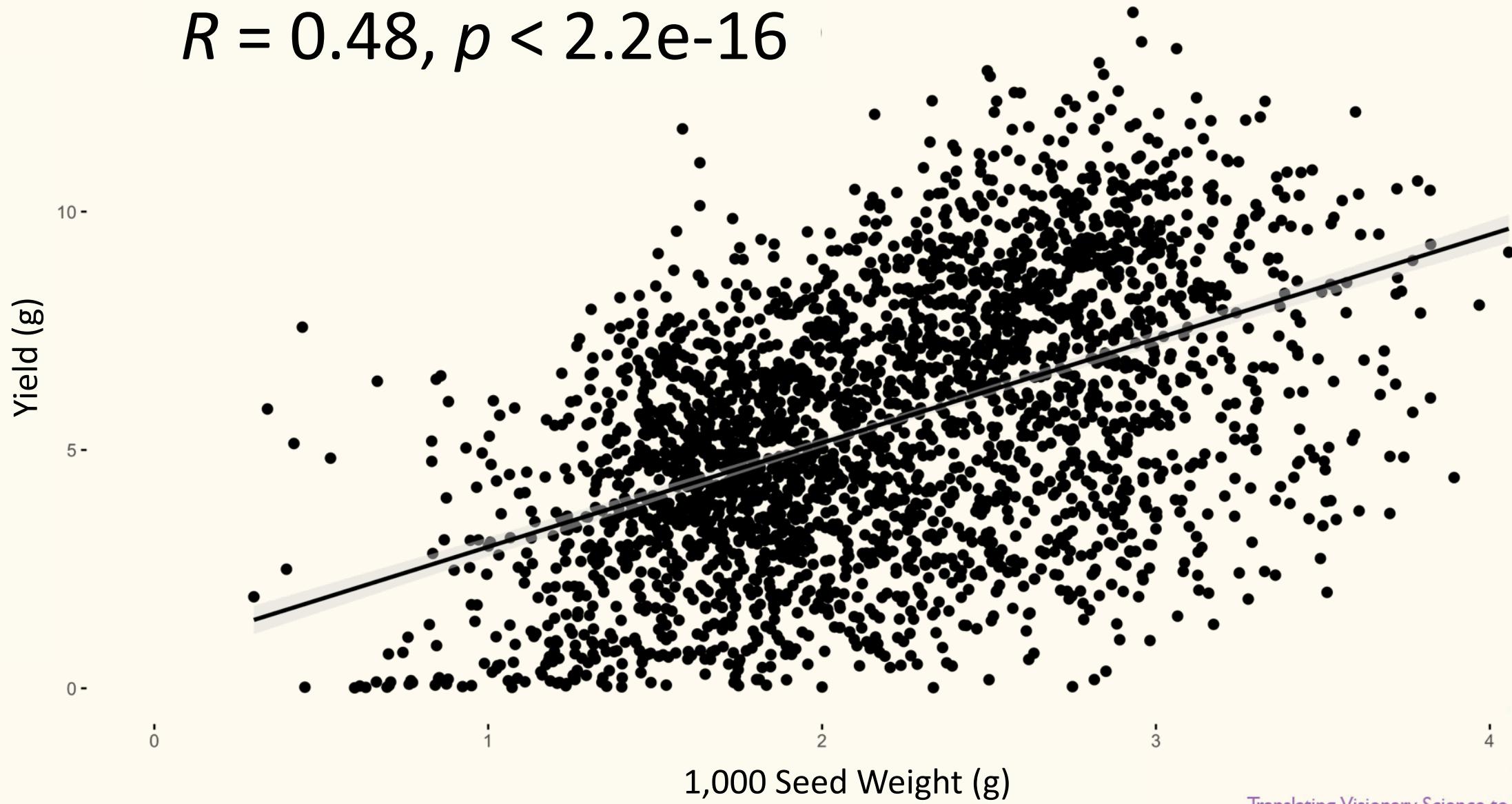




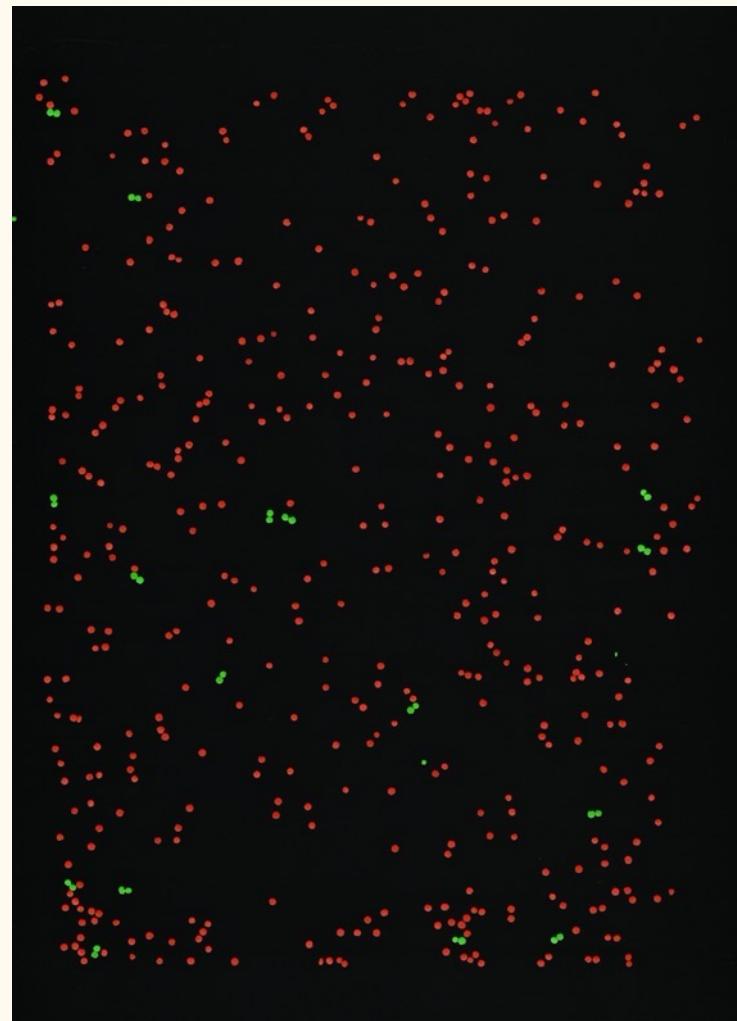
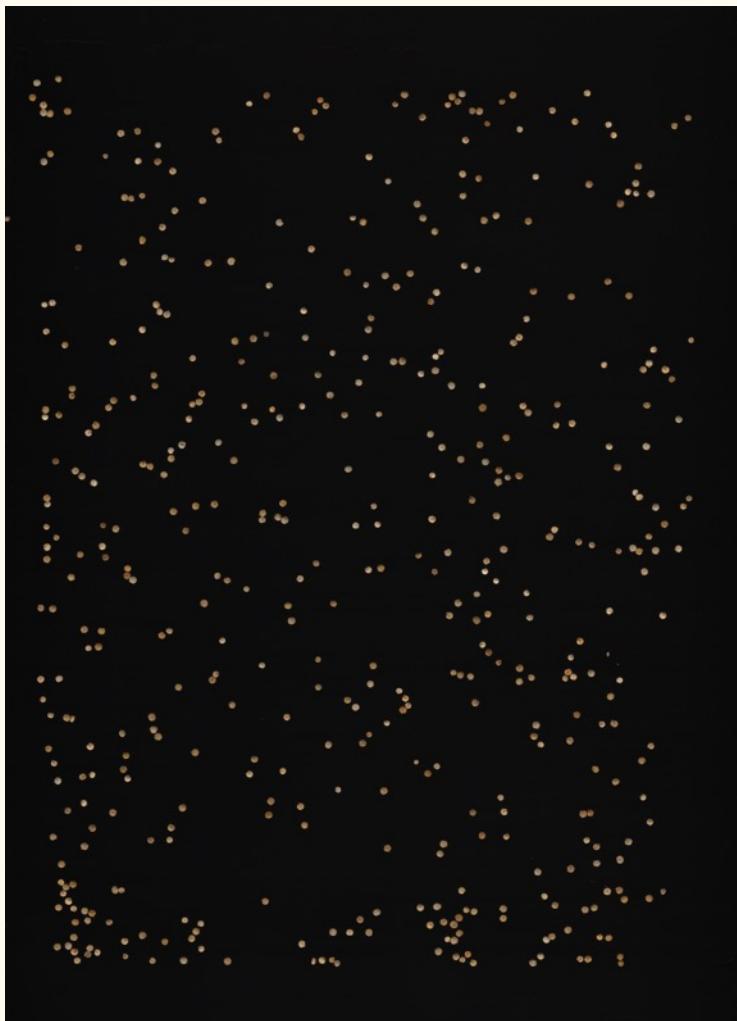




$$R = 0.48, p < 2.2e-16$$



1,000 Seed Weight (g)



Subsample weight = ~1.5g

Subsample count = 600-1200 seeds

$$TSW = \left(\frac{1.5 \text{ (g)}}{688 \text{ (seeds)}} \right) \times 1,000$$

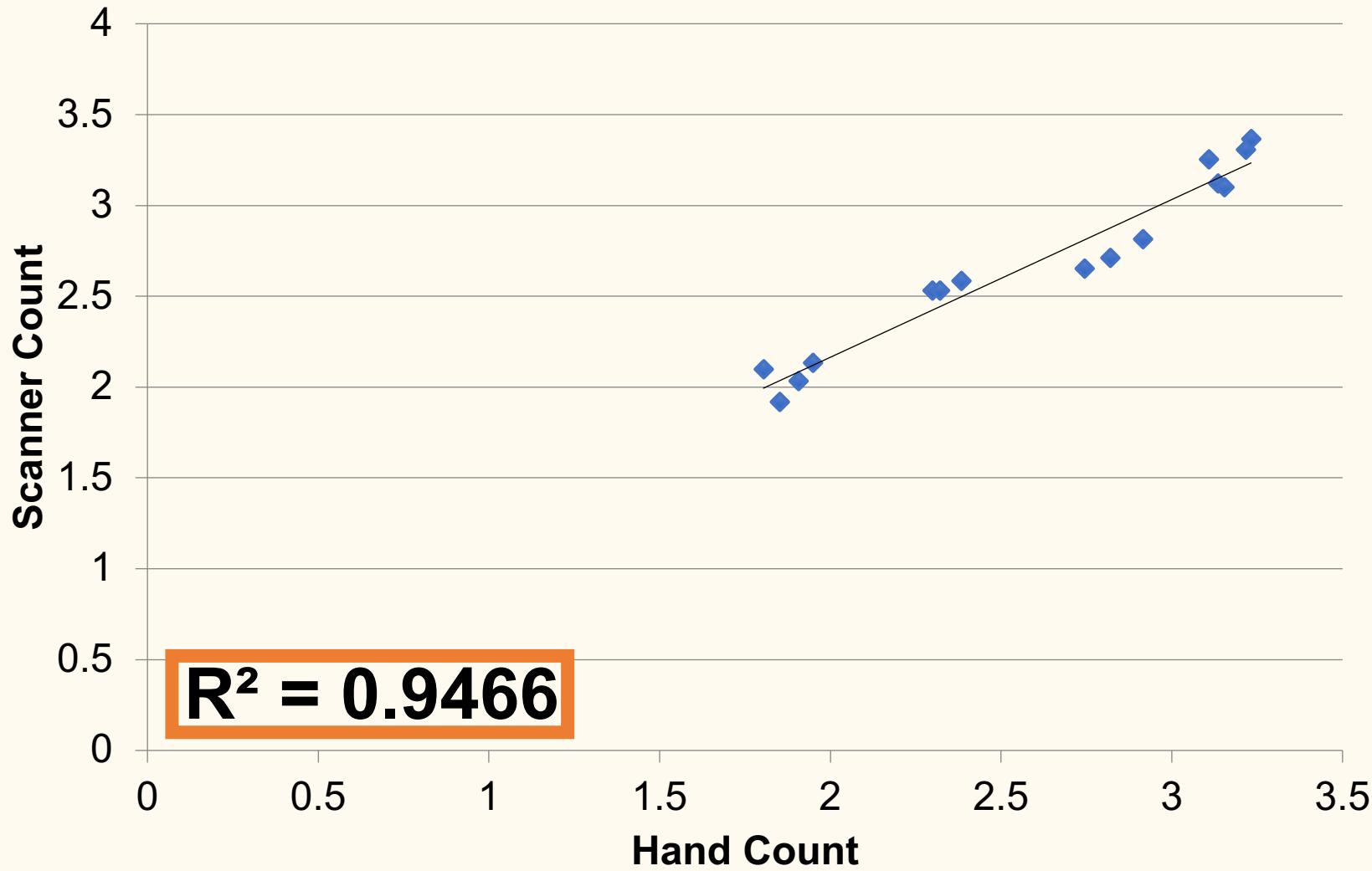
Cyverse App
phytoMorph Image Phenomics Tool Kit

Nathan Miller



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Thousand Seed Weight (g)



15-

$R = 0.48, p < 2.2\text{e-}16$ ← 1,000 Seed Weight (g)

$R = 0.38, p < 2.2\text{e-}16$

10 -

Yield (g)

5 -

0 -

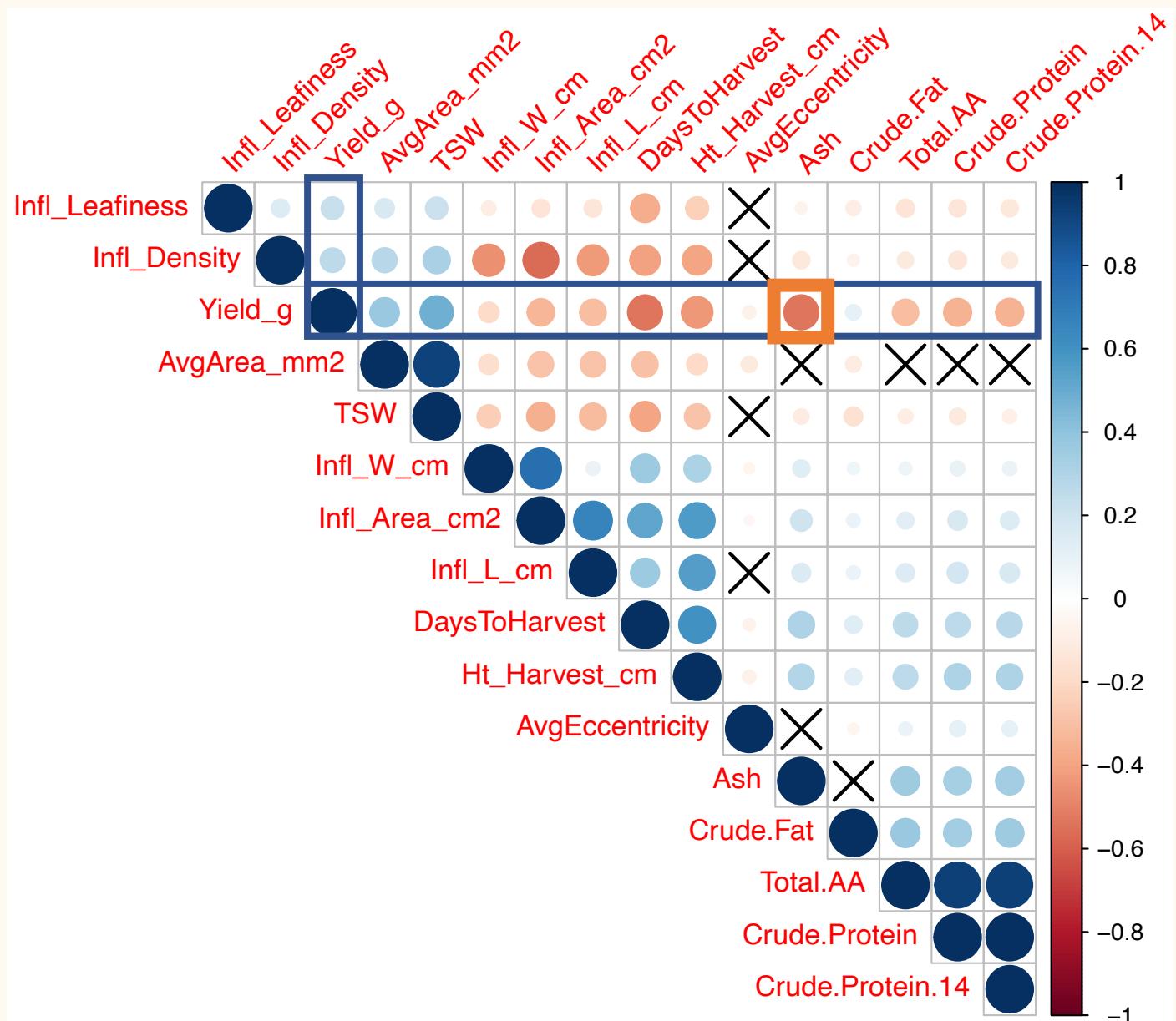
1

2

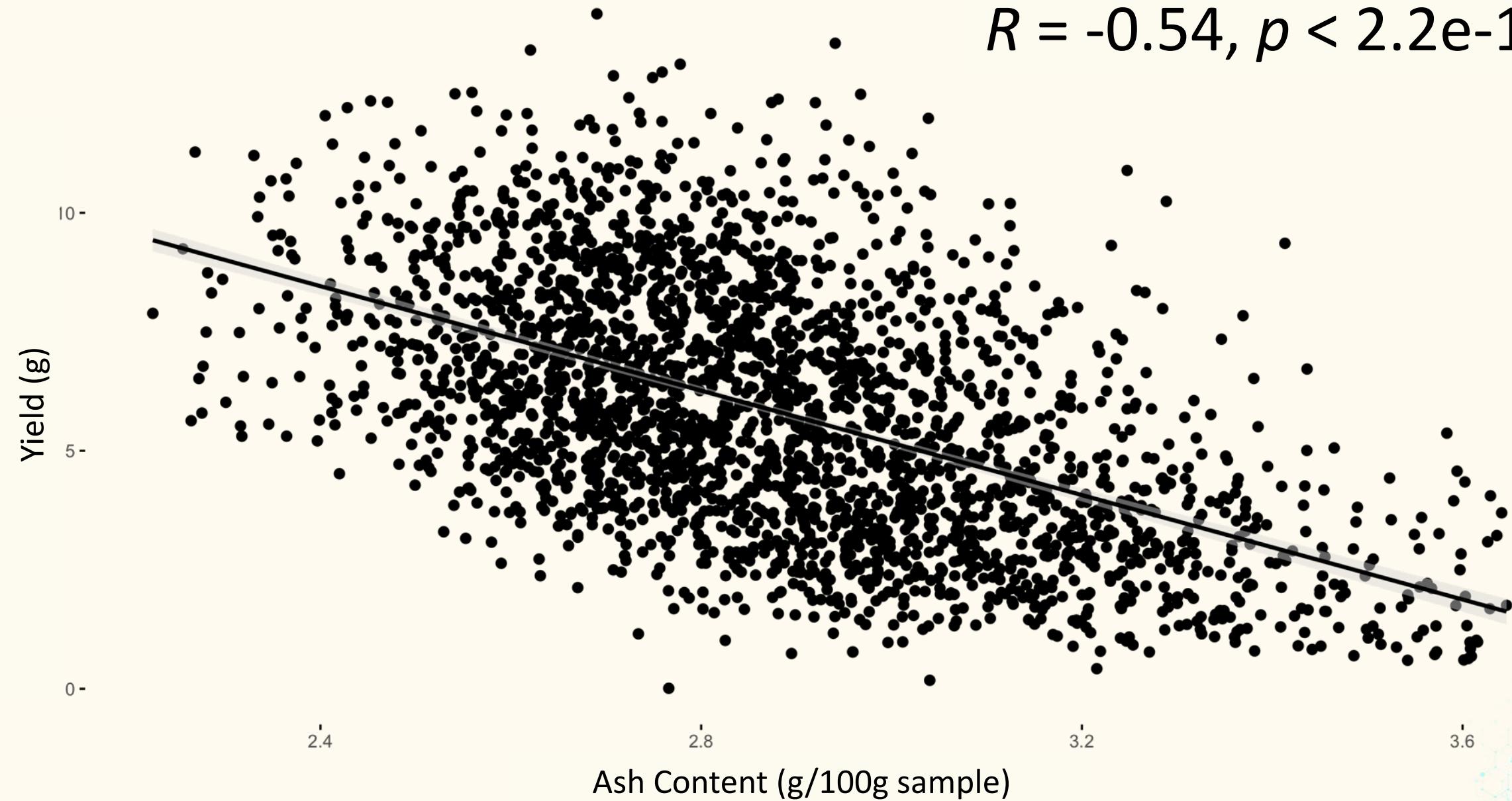
3

Average Seed Area (mm^2)



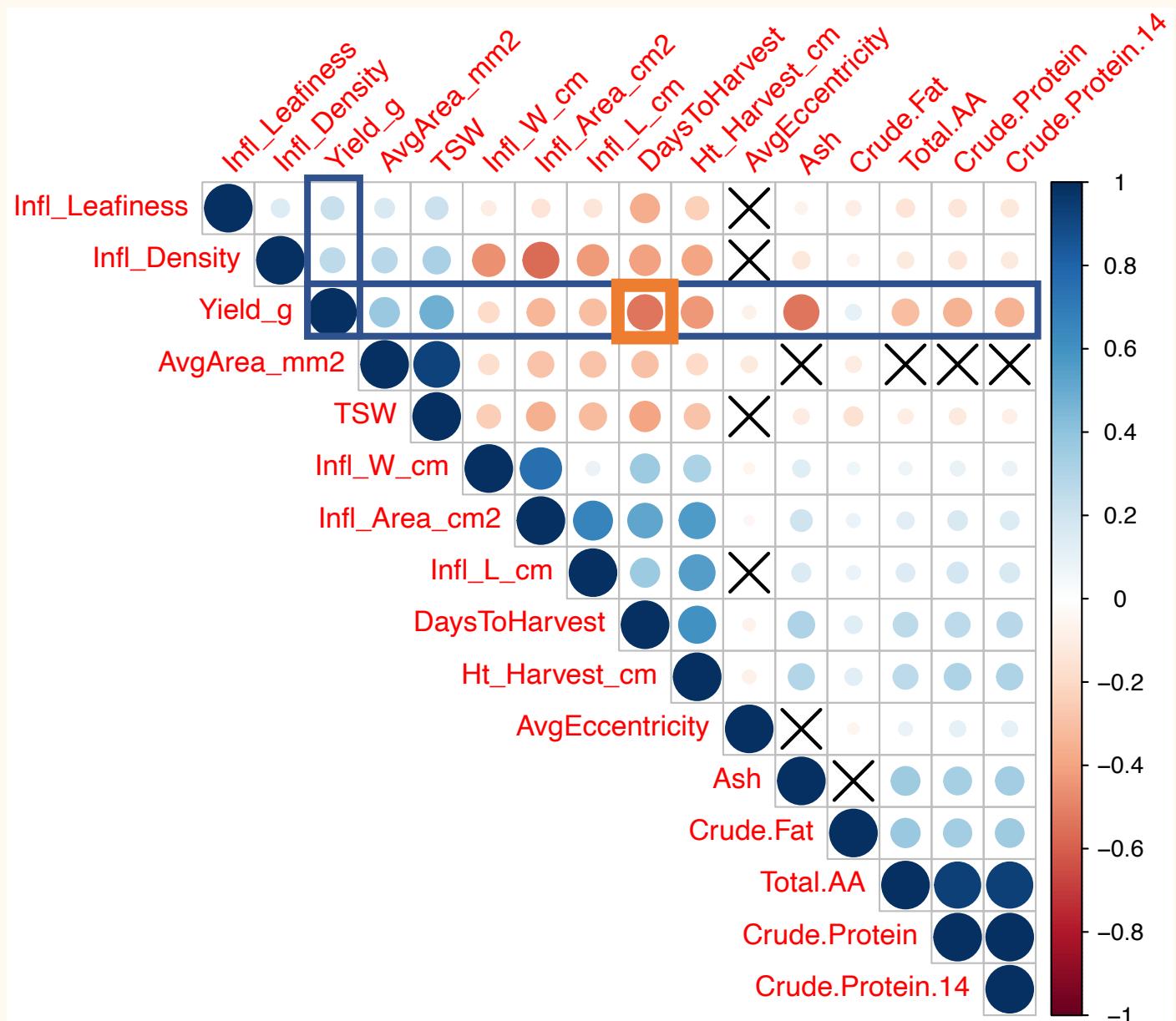


$$R = -0.54, p < 2.2\text{e-}16$$



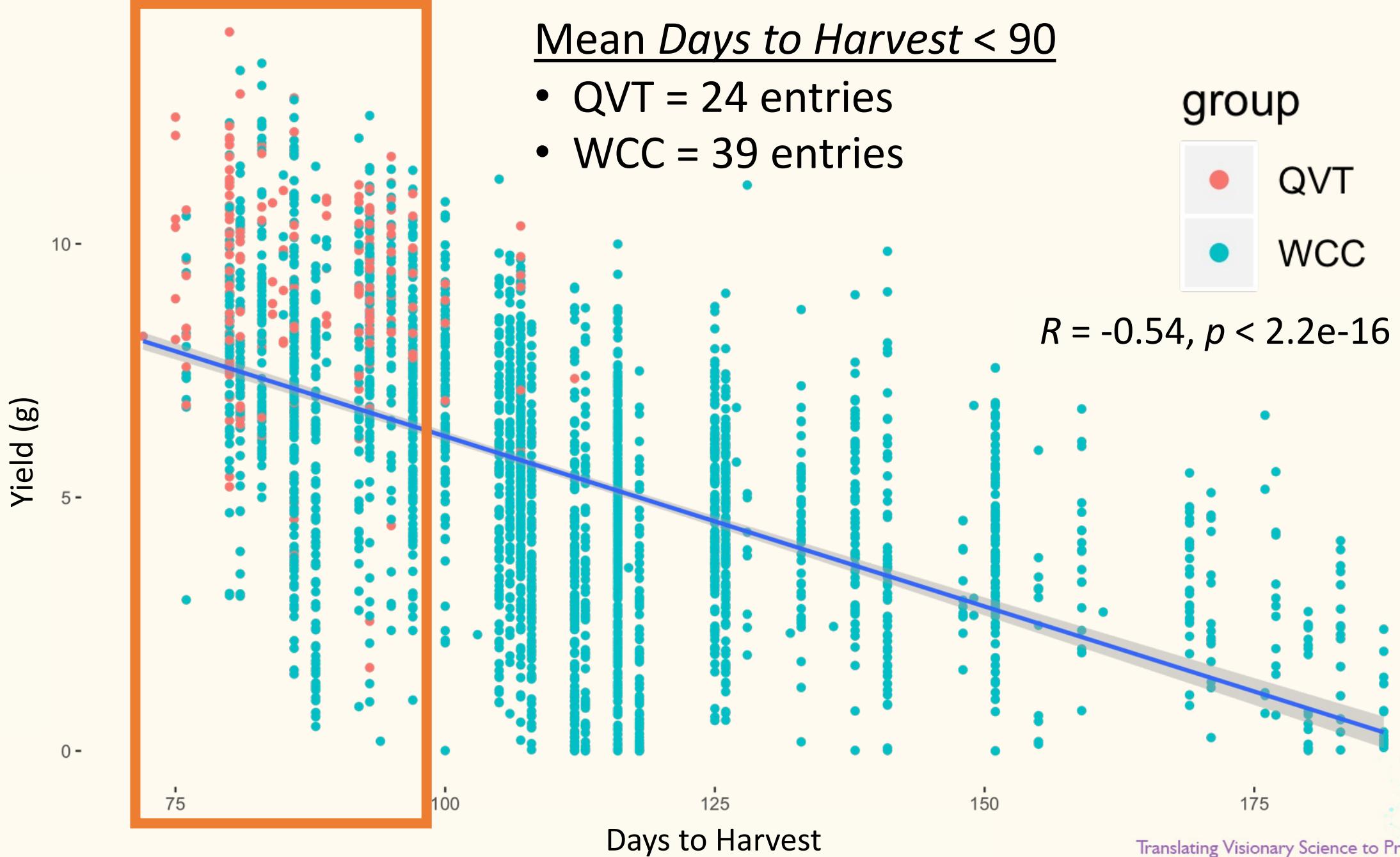
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Mean Days to Harvest < 90

- QVT = 24 entries
- WCC = 39 entries



Summary

- Crude protein (+) correlation with total amino acids & days to harvest; (-) with yield
- Yield (+) correlation with 1,000 seed weight & area; (-) with ash and days to harvest

- World Core Collection available to support quinoa global expansion
- Genotypic and phenotypic data available from greenhouse and ongoing field trials



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Future Directions

- Online database to support breeding efforts worldwide
- 2 years, 3 international locations with international collaborators
 - field & postharvest phenotyping
 - GWAS study to determine genetic architecture of traits
- WSU variety trials and projects in Rwanda, Malawi and Kenya



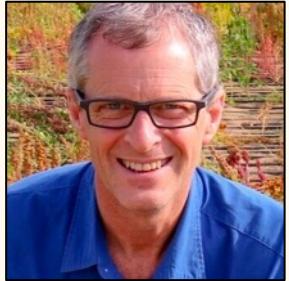
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Grand Challenges

STRATEGIC REALLOCATION



Search “Postharvest Phenotyping” on YouTube

Search “Nutritional Phenotyping Pipeline” on YouTube

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