

Seed Composition and Amino Acid Profiles for Quinoa Accessions Grown in Washington State

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PURPOSE

Gap in Knowledge

Quinoa seed composition and amino acid profiles below the species level (e.g. genotype, commercial varieties, elite germplasm).

Research Questions

1. How do seed composition and essential amino acid profiles of WSU-grown quinoa compare to the literature?
2. How do genotypic differences influence essential amino acid profiles?
3. Which genotypes meet the daily essential amino acid requirements set by the World Health Organization (WHO)?
4. Which genotypes have the highest values for seed composition components and essential amino acids?

BACKGROUND

➤ Pseudocereal with potential to contribute to food security and nutritional security

- Broad genetic diversity and ability to adapt to harsh environments
- Balanced amino acid profile

➤ Food and Agriculture Organization of the United Nations classification as one of the most promising crops for food security in 21st century

➤ 2016 review on quinoa nutritional composition (Nowak *et al.*, 2016)

- Identified a lack of comparable data on quinoa nutrition (e.g. seed composition components and amino acids) below the species level
- High variation in nutrient content reported

METHODS

Sample Selection

Protein values were predicted for a representative selection of WSU field grown material (n=194), and samples were randomly selected across a protein content normal distribution for wet chemistry analysis (n=100). Protein values were predicted using a DA7250 NIR analyzer (Pertin Instruments, Springfield, IL) with a default quinoa calibration.

Wet Chemistry Analysis

Samples were sent to the University of Missouri-Columbia Agricultural Experiment Station Chemical Laboratories for determination of seed composition components via proximates analysis (crude protein, crude fat, crude fiber, moisture, ash, and carbohydrates) and determination of complete protein amino acid profiles (n=23).

Germplasm and Field Locations

Raw quinoa seed sent for analysis was comprised of F5:F6 advanced breeding lines (P102: CO407Dave X QQ74, n=21; P104: Kaslaea X QQ74, n=26; P105: QQ065 X QQ74, n=3; P106: QQ065 x Black, 5; P107: QQ74 X Black, n=10; P108: QQ74 X Cherry Vanilla, n=20) and check varieties (CO407Dave, Kaslaea, Cherry Vanilla; n=6) grown as hand sown single head rows in 2016 on three organic farms in Chimacum (n=24), Quilcene (n=37) and Sequim (n=30), WA. In 2017, germplasm (QQ74, Japanese Strain, Baer, 3UISE, 17GR; n=9) was grown either hand-planted or transplanted into 0.914 x 3.05 m plots at the WSU Extension and Research Center in (NWREC) Mount Vernon, WA under irrigated (n=4) and nonirrigated conditions (n=5).

Data Analysis

Data was analyzed and figures were generated using JMP 12 (Cary, NC) and Microsoft Excel 2010 (Seattle, WA).

RESULTS

1. How do seed composition and essential amino acid profiles of WSU-grown quinoa compare to the literature?

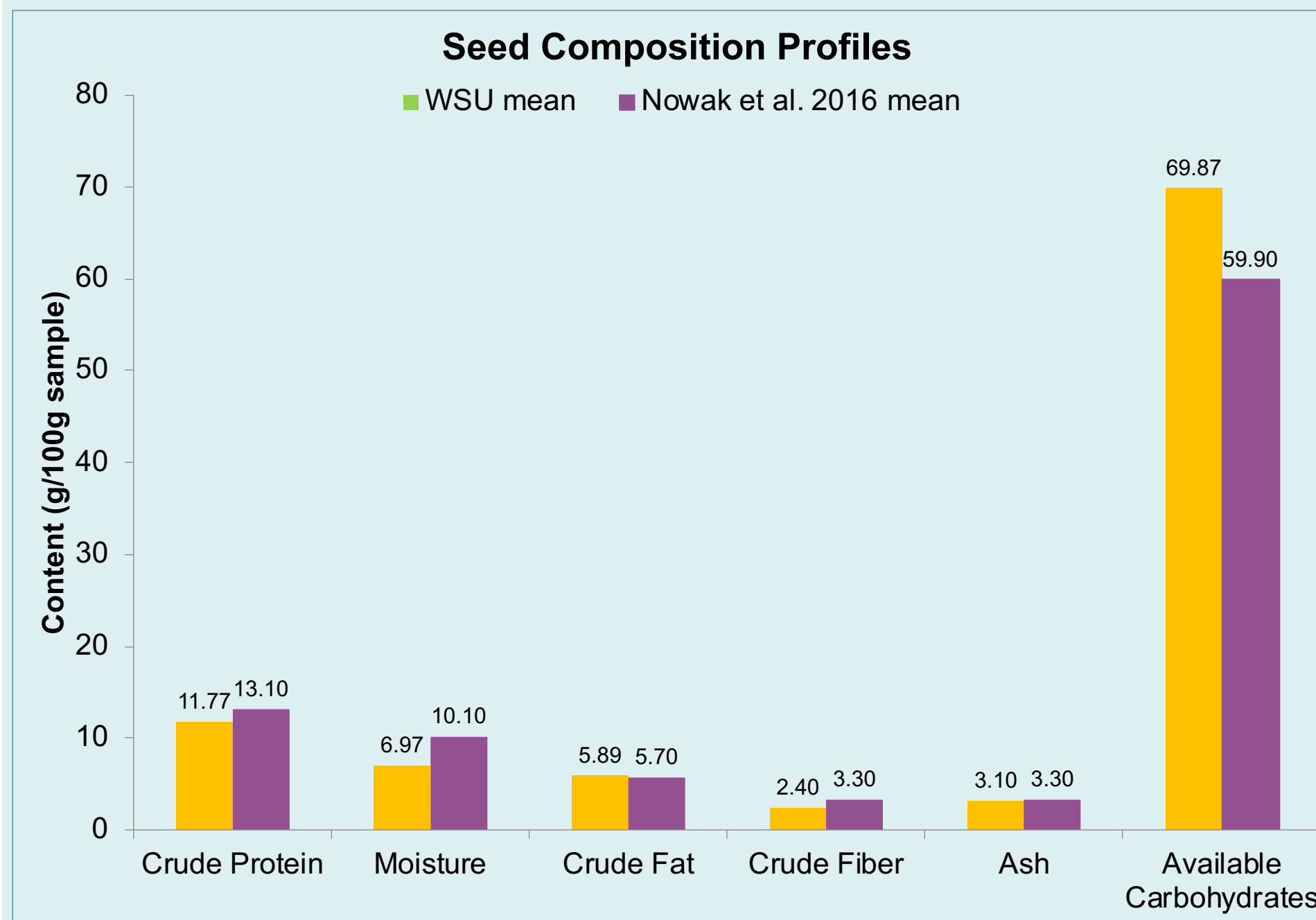


Figure 1. Seed composition profiles represented by the WSU mean and the mean value reported by Nowak *et al.*, 2016. Seed composition was determined by proximate analysis.

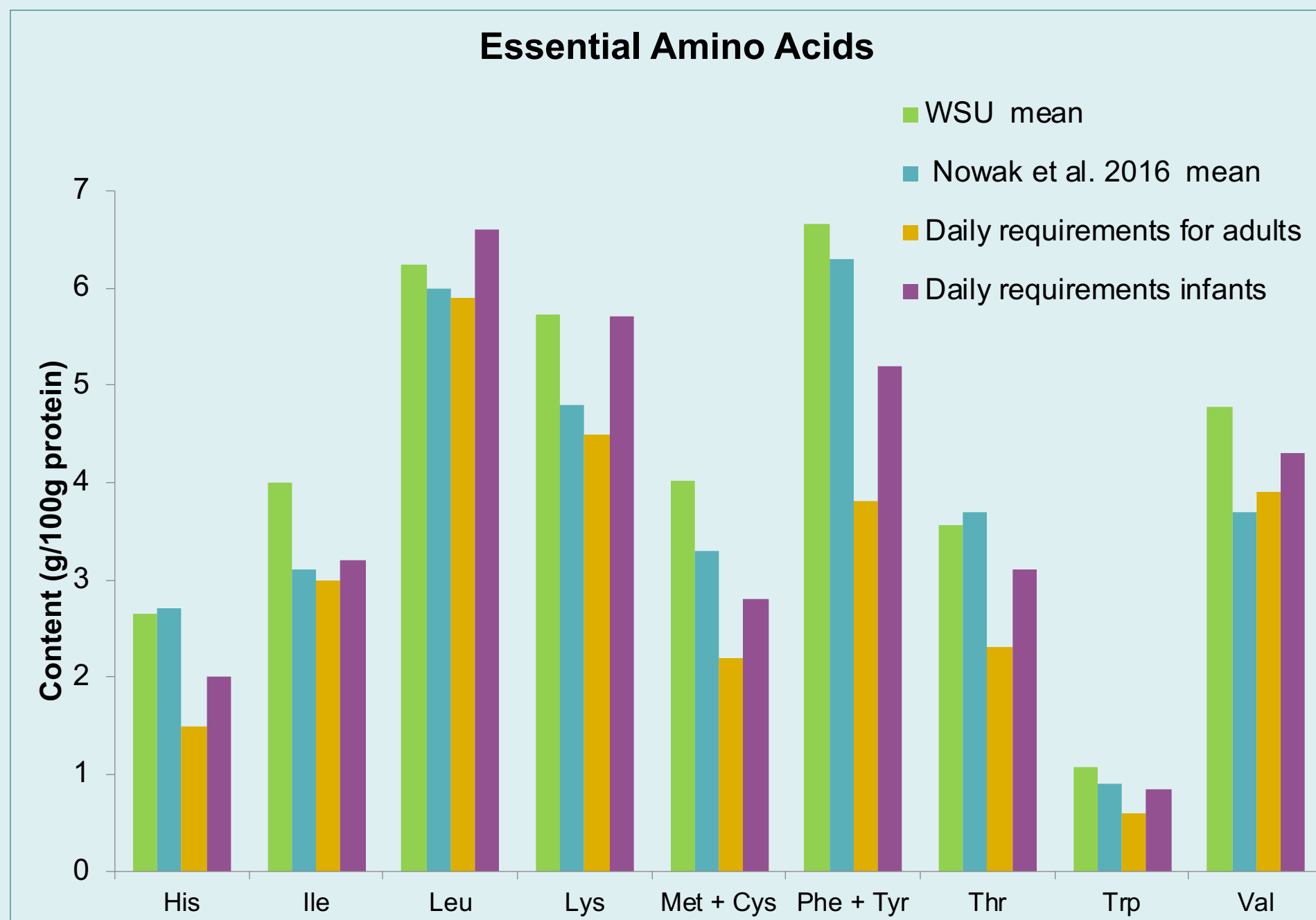


Figure 2. Essential amino acid content represented by the WSU mean value, the mean value reported by Nowak *et al.*, 2016, and the WHO daily requirements for adults and infants.

2. How do genotypic differences influence essential amino acid profiles? 3. Which genotypes meet the daily essential amino acid requirements set by the WHO?



Figures 3A-I. Essential amino acid profiles (g/100g crude protein) presented for samples (n=100) of raw WSU-grown quinoa. Each scatter plot features markers that are color and shape coded according to location (see legend above), a solid line for the mean value, and a dashed and dotted line for the WHO daily requirements for infants (i.e. 0.5) and adults (i.e. >18), respectively.



Our goal is to increase the genetic and biological diversity of cropping systems across the state of Washington through the development of new cultivars and ecologically sound production practices. The general traits and systems of importance across the crops we study include nutritional value, heat tolerance, drought tolerance, resistance to rusts and mildews, intercropping, deficit irrigation, and evolutionary participatory breeding.



DISCUSSION

Nutrients	Nowak <i>et al.</i> , 2016 mean (min-max)	WSU mean (min-max)	Sample with highest value (location; note)
Crude Protein	13.1 (9.1-15.7)	11.77 (10.04-13.68)	WWA15FS27 (Chimacum; pop 104)
Crude Fat	5.7 (4.0-7.6)	5.89 (4.56-7.19)	WWA15FS78 (Sequim; pop 107)
Crude Fiber	3.3 (1.0-9.2)	2.40 (1.79-4.76)	WWA15FS37 (Sequim; pop 106)
Moisture	10.1 (8.2-13.1)	6.97 (6.41-7.37)	WWA15FS37 (Sequim; pop 106)
Ash	3.3 (2.0-7.7)	3.11 (2.7-5)	3UISE (Mount Vernon; irrigated)
Carbohydrates	59.9 (48.5-69.8)	69.87 (66.87-71.95)	WWA15FS9 (Quilcene; 102)

Table 1. Mean, minimum, and maximum values (g/100g sample) for seed composition components (proximates) reported for WSU samples and Nowak *et al.*, 2016. The WSU sample with the corresponding highest value is reported.

Essential Amino Acids	Nowak <i>et al.</i> 2016 mean (min-max)	WSU mean (min-max)	Accession with highest value (location; note)
His	2.7 (1.4-5.4)	2.66 (2.29 - 2.91)	WWA15FS52 (Chimacum; 102)
Ile	3.1 (0.8-7.4)	4.00 (3.55-4.41)	WWA15FS52 (Chimacum; 102)
Leu	6.0 (2.3-9.4)	6.25 (5.63-6.85)	WWA15FS17 (Quilcene; 102)
Lys	4.8 (2.4-7.8)	5.72 (5.05-6.59)	WWA15FS17 (Quilcene; 102)
Met + Cys	3.3 (0.4-11.8)	4.02 (3.36-4.53)	Kaslaea & CO407 Dave (Chimacum)
Phe + Tyr	6.3 (2.7-10.3)	6.65 (5.95-7.33)	WWA15FS17 (Quilcene; 102)
Thr	3.7 (2.1-8.9)	3.57 (3.18-4.02)	WWA15FS17 (Quilcene; 102)
Trp	0.9 (0.6-1.9)	1.08 (0.68-1.48)	WWA15FS23 (Quilcene; 102)
Val	3.7 (0.8-6.1)	4.78 (4.31-5.20)	WWA15FS52 (Chimacum; 102)
Total Essential	38.7 (34-43.3)	38.72 (35.1-42.29)	WWA15FS17 (Quilcene; 102)
Total AA	NA	87.11 (77.87-95.54)	WWA15FS17 (Quilcene; 102)

Table 2. Mean, minimum, and maximum values (g/100g protein) reported for WSU and Nowak *et al.*, 2016 for each essential amino acid, total essential amino acids, and total amino acids. The WSU sample with the corresponding highest value is reported.



Figure 4. Advanced breeding line WWA15FS17

CONCLUSIONS

- Mean values for WSU-grown quinoa are **lower** for protein, moisture, and fiber, **comparable** for fat and ash, and **higher** for carbohydrates compared to mean values reported in the literature in the review by Nowak *et al.*, 2016 (Figure 1).
- The mean of residual values for WSU-grown quinoa were highest for lysine, indicating relatively high variation for this essential amino acid (Figure 3D).
- All essential amino acid daily requirements for infants and adults were met by the mean values for WSU-grown quinoa, except for the amount of leucine required by infants (Figure 3A-I)
- Advanced breeding line WWA15FS17 had the highest content for total amino acids, total essential amino acids, and 4/9 of the essential amino acids (e.g. lysine and leucine) (Figure 4). Breeding line WWA15FS52 had the highest content for 2/9 of the essential amino acids (Table 2).

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