

EVALUATING PEA PROTEIN CONCENTRATE YIELD AND FUNCTIONALITY: A COMPARATIVE STUDY OF GENOTYPE AND ENVIRONMENTAL IMPACT



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INTRODUCTION

The demand for plant-based proteins has increased, driven by the necessity for sustainable food solutions to support our growing population, a desire to minimize environmental impact, and the pursuit of enhanced public and individual health (Shanthakumar et al., 2022). Among the various options, field pea is gaining traction for its role in producing plant-based protein. A plant-based meat company that has facilitated growth in pea protein is Beyond Meat; their products feature pea protein as a primary ingredient (Daba et al., 2022). Furthermore, peas are linked to a reduction in diabetes and cardiovascular diseases Kumari et al. (2021). By gaining a deeper understanding of genotype-by-environment interactions, we can enhance both the yield and functionality of pea protein concentrate. This project aims to evaluate the performance of different pea genotypes in terms of protein yield and assess their functional characteristics. This work also explores the differences in wet chemistry versus NIR spectroscopy in calculating protein concentration.

METHODS

In 2024, two genotypes of yellow peas, PS1710002 and PS17100120, were cultivated at four locations in Montana: Havre, Huntley, Richland, and Sidney. We collected a total of 16 samples, with two field replications from each environment and genotype. The samples were dehulled and milled into a fine flour. Protein isolation was carried out using the method described in Daba et al. (2022), which involved isoelectric point precipitation. The oil and water holding capacities were evaluated using a modified method based on the research of Ma et al. (2022). To determine the protein concentration of the concentrate, we employed a fluorescence-based protein quantitation assay (Thermo Scientific, Waltham, USA). Additionally, an NIR Spectrophotometer (PerkinElmer, Waltham, USA) was used to measure the average protein, starch, and moisture concentration of the whole peas, the flour, and the protein concentrate.

Figure 1. Steps in the process of obtaining freeze dried protein concentrate from whole peas



RESULTS

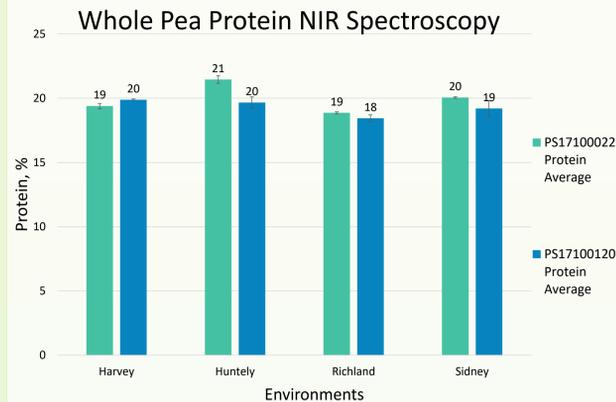


Figure 2. PS17100120 remained uniform through the four environments and outperformed PS17100022 in Havre. PS17100022 ranged in protein concentration from 18.86% to 21.45%. Both genotypes had the lowest protein in Richland.

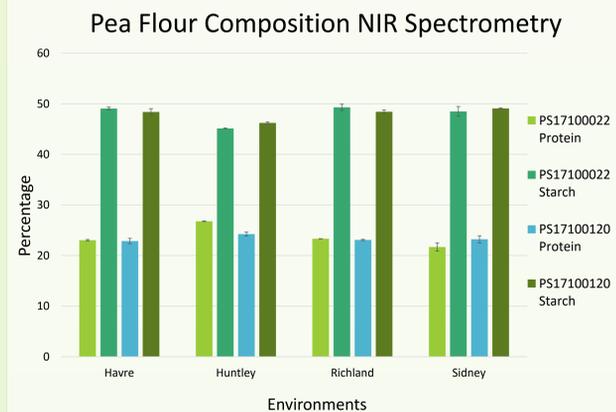


Figure 3. PS17100120 remains uniform in protein. PS17100022 outperforms PS17100120 in Richland and Sidney, with the highest protein in Richland. PS17100120 outperforms in Havre and Huntley. As expected, an inverse relationship is seen with starch and protein concentration; this is best shown in Richland.

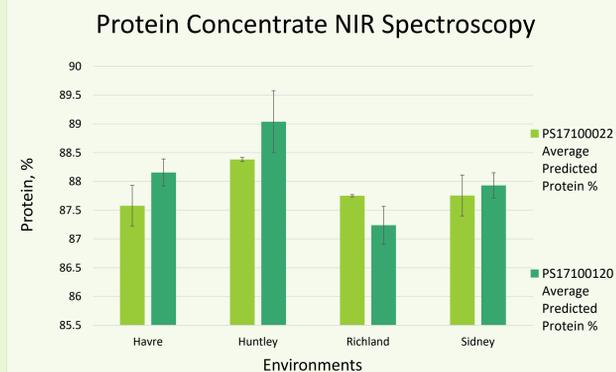


Figure 4. PS17100120 has a greater protein percentage than PS17100022 in three of the environments. Huntley produces the highest protein, while Richland produces the least amount in both genotypes.

DISCUSSION

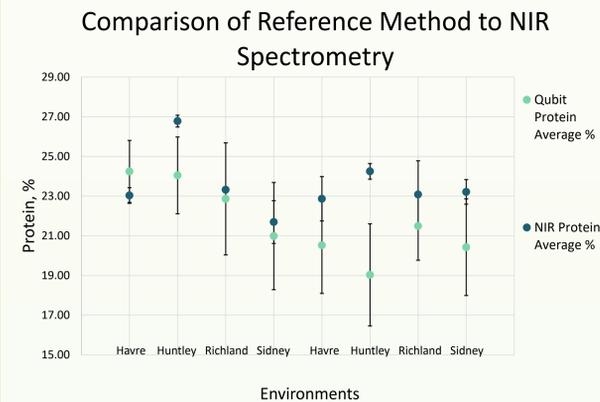


Figure 5. This illustrates the overestimation of protein using NIR spectrophotometry, as is evident at Huntley. Seeds produced at Huntley were outside the calibration of the NIR. Although we had a narrow range of samples and mostly nonsignificant differences, as more samples are collected, the NIR spectrophotometer will be calibrated.

Table 1. Total protein recovery

Environment	Genotype	Protein Recovery %
Havre	PS17100022	60.0
	PS17100120	61.8
Huntley	PS17100022	56.8
	PS17100120	54.3
Richland	PS17100022	60.0
	PS17100120	56.4
Sidney	PS17100022	59.5
	PS17100120	60.5

There were no significant differences across genotypes or locations for the protein recovery.

Table 2. Average water holding capacity (%)

Genotype	Environments			
	Havre	Huntley	Richland	Sidney
PS17100022	269	273	281	285
PS17100120	282	283	277	287

PS17100120 had significantly greater WHC at P = 0.010, however, there was variation across replications.

Table 3. Average oil holding capacity (%)

Genotype	Environments			
	Havre	Huntley	Richland	Sidney
PS17100022	262	241	245	245
PS17100120	248	245	246	248

OHC was uniform across the environments and genotypes. There were no significant differences across genotypes or locations, but replications were highly significantly different.

CONCLUSIONS

These results highlight the importance of both genotype characteristics and environmental factors in selecting pea varieties for protein yield, offering valuable insights for breeders aiming to optimize protein extraction. Due to time constraints, this project analyzed a limited number of samples. Future research will involve a larger sample size to understand protein yield and genotype-by-environment interactions better, while focusing on specific environmental conditions to enhance genotype advantages.

REFERENCES

- Daba, Sintayehu D., et al. "Trait associations and genetic variability in field pea (*pisum sativum* L.): Implications in variety development process." *Cereal Chemistry*, vol. 99, no. 2, 9 Nov. 2021
- Kumari, Tapasya, and Sankar Chandra Deka. "Potential health benefits of garden pea seeds and pods: A Review." *Legume Science*, vol. 3, no. 2, 9 Mar. 2022
- Ma, Kai Kai, et al. "Functional and physical properties of commercial pulse proteins compared to soy derived protein." *Future Foods*, vol. 6, Dec. 2022
- Shanthakumar, Parvathy, et al. "The current situation of pea protein and its application in the Food Industry." *Molecules*, vol. 27, no. 16, 22 Aug. 2022

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