Diversity for seed protein content in the PCGIN diversity pea panel

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Introduction

The genetic improvement of seed protein content (SPC) has been a primary objective in breeding programs for food crops such as soybean and wheat. However, in peas (*Pisum sativum*), breeding efforts have historically prioritized agronomic traits like disease resistance and yield, as there are currently no premium market incentives for higher protein quality. However, the growing demand for plant-based protein in food industries and advancements in food processing technologies provide a new interest and potential market for high-protein pea varieties.

This short report highlights the variability of SPC in the PCGIN pea diversity panel, its relationship with seed morphology (round vs. wrinkled accessions), and the potential trade-offs between yield and protein content. The same panel was also screened for variation in protein composition, which is reported in (Warsame *et al.*, 2024).

Materials and Methods

The PCGIN pea diversity panel of 230 lines were grown in micro plots in 2021 and 2022 at the JIC de Winton experimental field station in Bawburgh, Norfolk. In 2021, 186 lines yielded sufficient seeds for analysis and in 2022 we successfully harvested seeds of 2011 lines. Initially different methods were tested for SPC, including Direct Detect and the Bradford assay, both for aqueous protein extract. However, the full data set reported here was obtained using a DA 7250 Near-Infrared (NIR) spectrometer (Perkin Elmer). This method is non-destructive and utilizes pre-developed calibration models based on reference wet chemistry data.

Results and Discussion

The SPC ranged from ~20% to ~32% of dry weight in both years (Figure 1A), which is similar to other studies including a recent report on 487 accessions of the USDA diversity panel (Uhdre *et al.*, 2024). Consistency between two harvests for each pea accession was relatively poor, and no GWAS loci for protein variation could be identified.

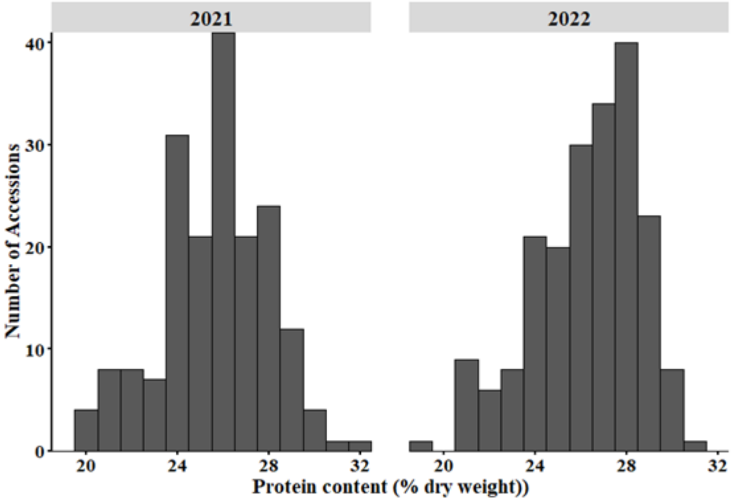

Figure 1. Seed protein content in accessions of the PCGIN pea diversity panel grown in micro plots in 2021 (n=186) and 2022 (n=211).

However, a statistically significant difference ($p < 0.005$) in SPC was noted between round-seeded and wrinkle-seeded accessions (Figure 2A). Wrinkled accessions consistently displayed higher SPC in both years. This trend is attributed to a mutation in the starch-branching enzyme (*SBEI*) gene, which results in reduced starch content and compensatory increased protein content.

Based on data from the 2022 trial, which included additional entries and per-plot yield assessments, a weak negative correlation was detected between yield and SPC in wrinkled accessions (Figure 2B). This suggests a potential trade-off between protein and yield, a common challenge in breeding for high-protein crops. However, further investigations with multi-environment trials are necessary to confirm this trend and identify accessions suitable for breeding high-protein pea cultivars.

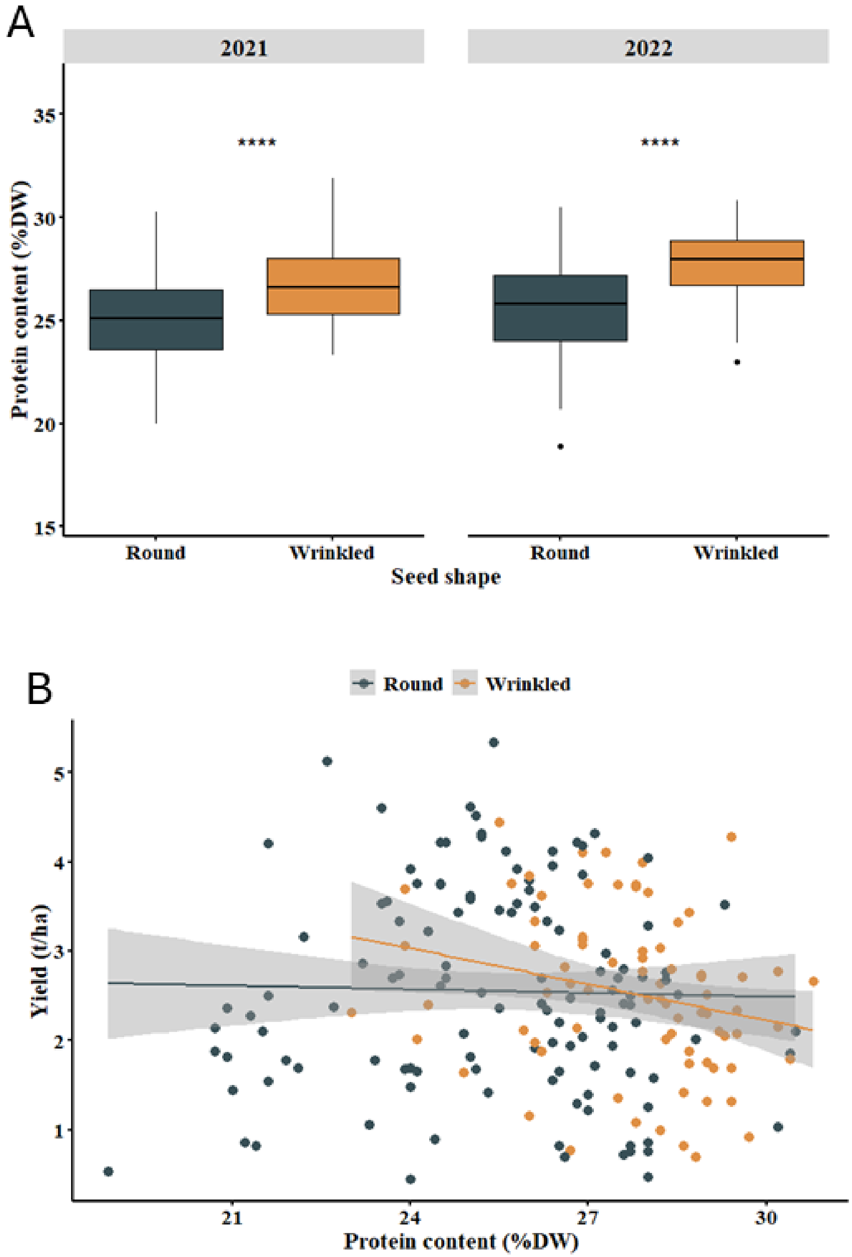

Figure 2. (A) Comparison of seed protein content in round (*RR*) and wrinkled (*rr*) accessions.

(B) The relationship between yield and seed protein content in 2022.

Future Directions

To fully capitalize on the genetic diversity observed in this panel and develop high-protein pea varieties suitable for commercial production, several steps are recommended:

1. Conduct rigorous multi-environment trials to assess the stability of protein content across different growing conditions.
2. Investigate the genetic basis of the observed variation in protein content, particularly in high-protein accessions.
3. Explore the potential for developing round-seeded varieties with elevated protein content.
4. Evaluate the nutritional quality and functional properties of high-protein accessions to ensure their suitability for various food applications.

By pursuing these research directions, breeders can work towards developing pea varieties that meet the growing demand for plant-based proteins while maintaining other essential agronomic characteristics.

References

Warsame, A. O., Balk, J., & Domoney, C. (2024). Identification of significant genome-wide associations and QTL underlying variation in seed protein composition in pea (*Pisum sativum*, L.). *bioRxiv*, 2024.2007.2004.602075. https://doi.org/10.1101/2024.07.04.602075

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