Research article

Soybean seed yield, protein, and oil concentration for a modern and old genotype under varying row spacings

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A B S T R A C T

Progress in soybean (*Glycine* max L.) breeding has led to a reduction in optimal seeding rates due to enhanced branching capacity over time. However, less is known about the changes in canopy architecture between old and modern soybean genotypes at varying row spacing and their impact on yield and seed quality through the main stem and branches. Therefore, this study aimed to i) evaluate yield and seed quality responses of an old and modern soybean genotype at different row spacings and ii) examine the yield and seed quality of branches and the main stem. Trials were conducted in Kansas (United States, US) during 2020 and 2021, comparing two genotypes (old, released in 1980, and modern, released in 2013) at four row spacings (0.19, 0.38, 0.76, and 1.52 m) under rainfed conditions. Seed yield and quality (protein and oil concentrations, %) were assessed at the end of each growing season. In 2021, both genotypes had low and similar yields at all row spacings (averaging 2481 kg ha^{-1}) with 2.5 % less protein on branches compared to the main stem. However, 2022 resulted in a high-yielding environment, with the modern yielding 50 % more (3584 kg ha^{-1}) than the old (2315 kg ha^{-1}) genotype in narrow row spacings ($<$0.38 m). Additionally, the modern genotype showed a three-fold greater contribution to yield from branches (1113 kg ha^{-1}) relative to the old genotype (379 kg ha^{-1}). Despite the high yields observed in narrow rows, the modern genotype maintained protein levels. These results highlight the importance of row spacing as a key management practice for improving yield while maintaining protein levels in high yield conditions.

1. Introduction

Soybean accounts for 60 % (398 million Mg in 2023) of the global oilseed production [1], primarily intended for animal feed in the form of soybean meal (76 %) and for human consumption primarily as oil (20 %) [2]. The overall increase in global soybean production is driven by greater yields per unit area, with no signs of yield stagnation in 76 % of the harvested area [3,4]. The United States (US) accounts for 29 % of the global production, with farmer yields steadily increasing at 36 kg ha^{-1} year^{-1} during the last four decades [5]. Hence, future progress in genetic gain is promising not only for sustaining yield but also for improving seed composition

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On-farm yield improvements over time can be attributed to the continued adoption of modern genotypes and agronomic technologies [7]. The main agronomic technologies associated with these yield gains include earlier planting dates (approximately 12 days earlier to late April/early May) [8], narrower row spacings (reduced from 0.76 to 0.38 m), minimum or no-till system supported by herbicide-tolerant genotypes, and new planters that ensure uniform seed placement depth and spacing [9,10]. From a plant architecture standpoint, modern genotypes can set more seeds on the main stem and branches, enhancing the ability to adjust yield at varying plant densities [11]. Nonetheless, little is known about how row spacings affect the yield allocation to branches and main stem when comparing modern relative to older soybean genotypes.

Over the past decade, US growers in the north-central region have increasingly adopted narrow (below 0.76 m) over wide (>0.76 m) row spacing [7,12], with a current adoption rate of 66 % of producers using narrow and 34 % using wide spacing [13]. Although yield benefits associated with narrow rows are expected [14], studies have found inconsistent results [15–18]. Narrow rows can provide yield benefits when the crop growth cycle is shortened, such as with late sowing dates, short maturity groups (MG), or under high temperatures [19]. In optimum irrigated conditions with fast canopy closure, in the other hand, yield improvements might not be observed [20]. Different row spacings can also alter the contribution of yield from branches and main stems [21]. For instance, narrow rows show a potential to increase yield through branch growth [22]. However, further research is needed on the implications of varying row spacings for modern soybeans, particularly on the contribution of branches and main stem to yield formation and seed quality or composition, including protein and oil concentrations.

For both old and modern genotypes, seed quality on the main stem consistently shows greater protein and less oil concentrations on the upper relative to the bottom section (Bellaloui & Gillen, 2010; Moro Rosso et al., 2021). Conversely, branches can have similar protein but less oil concentrations compared to the main stem [23]. Evaluating these dynamics is particularly timely for formulating management practices intended to improve seed quality given the opportunity of future markets rewarding quality standards [6].

We hypothesize that modern soybean genotypes with high branching capacity have less yield penalties associated with changes in row spacing but present potential variations in seed quality due to changes in partitioning between main stem and branches. We have conducted a two-year trial with two genotypes (one released in 1980 and one in 2013) at four row spacings (0.19, 0.38, 0.76, and 1.52 m) to evaluate impacts on both yield and seed quality (oil and protein concentrations) on the entire plants and in plant fractions, mainly focusing on main stem, and branches.

2. Material and methods

2.1. Field conditions and management

Field experiments were conducted in 2020 and 2021 at Kansas State University in Manhattan, Kansas, US (39° 12′ 22″, −96° 35′ 37″). The experiment was arranged in a randomized complete block design in a split-plot layout with three replications. The whole plot consisted of row spacing with four levels (0.19, 0.38, 0.76, and 1.52 m), and the subplot consisted of a two-factor factorial of seeding rate with two levels (148 and 445 thousand seeds ha^{-1}) and genotype with two levels (P3981, "Williams 82" released in the 1980s, herein termed as "old," and P39T67R, released in 2013, herein termed as "modern") (Corteva Agriscience, Johnston, Iowa, US), both indeterminate growth with 3.9 MG. For each trial year, the soils were a smolam silt loam in 2020 (2.75 % OM, 41 % clay, 12 % sand, 47 % silt) and 2021 (2.70 % OM, 25 % clay, 29 % sand, 46 % silt). The plots were 10 ft long by 5 ft wide. The planting dates were June 12 in 2020 and May 25 in 2021, with harvesting dates on October 8 in 2020 and October 7 in 2021. Seasonal precipitation from planting to harvesting was 351 mm in 2020 and 443 mm in 2021. Seeds were not treated nor inoculated before planting, and weeds were manually controlled throughout the season.

2.2. Field determinations

At R2 (full flowering) and R5 (beginning of seed filling) growth and development stages [24], an area of 0.81 m^2 per plot was hand-cut, and the plants were counted and weighed. Three representative plants were selected, weighed and oven-dried (65 °C) until constant weight to obtain dry weight. Between R2 and R6 phenological stages, a Go-Pro Hero 5 camera placed at 2 m parallel to the soil was used to take weekly pictures of the canopy. Pictures were processed with Canopeo [25] to obtain the fractional of green canopy coverage (percentage basis).

At physiological maturity (R8), an area of 0.81 m^2 per plot was hand-cut, the plants were then counted, and oven-dried until constant weight to obtain the final seed weight. In addition, three plants were hand-cut, and the seeds from the main stem and branches were separated and oven-dried until constant weight to determine the seed weight. The seeds from the branches and main stem were ground to a particle size of 0.1 mm, and protein and oil concentration (percentage basis) were determined using near-infrared spectroscopy (NIR) with the Perten DA7200 Feed Analyzer (Perten Instruments, Stockholm, Sweden). Seed quality per plant was calculated as a weighted average between the seed quality components (%) and yield (%) from the branch and main stem plant fractions of the three plants harvested at the R8 stage.

2.3. Statistical analysis

The growing conditions in 2021 were more favorable and less variable compared to 2020, attributed to increased seasonal precipitation and an earlier planting. The result was lower biomass in R2 and R5 (Table 1), lower canopy coverage (Supplementary Fig. 2),

and lower average yields (Fig. 1) in 2020 compared to 2021. Hence, we analyzed the data separately for 2020 and 2021 due to the strong "by year" interaction effect. Additionally, density plots of the obtained plant densities were similar for both seeding rates in both years (Supplementary Fig. 1). Plant density was close to the target for the lower seeding rate, with 162 and 164 thousand plants ha^{-1} in 2020 and 2021, respectively. On the other hand, the high seeding rate resulted in a plant density 50 % below the target, with 207 and 221 thousand plants ha^{-1} in 2020 and 2021, respectively, mainly due to challenging early season and planting conditions. Therefore, the seeding rate treatment did not result in a factor impacting the main tested traits (yield and seed quality) and was not considered for the analysis.

Generalized linear models (GLM) were used to explain the variation in yield at the plot level, from main stem and branches, and plant biomass at R2 and R5 stages as a function of row spacing, genotype, and their interaction using a gamma distribution. GLMs were also utilized to model oil and protein concentration (%) in the whole plant and partitioned into main stems and branches as a function of row spacing, genotype, and their interaction, using a beta distribution. GLMs were fitted using the *glm* function from the *stats* package [26] in R programming [27]. The statistical model is as follows:

$$\left[y_{ij} \middle| \mu_{ij}, \psi \right]$$

$$g\left(\mu_{ij} \right) = x_{1i} \cdot \beta_1 + x_{2i} \cdot \beta_2 + \ldots + x_{8i} \cdot \beta_8$$

$$y_{ij} \sim Gamma\left(\mu_{ij}, \psi_{ij} \right)$$

$$y_{ij} \sim Beta\left(\mu_{ij}, \psi_{ij} \right)$$

$$g(u) = X_i \beta$$

where y_{ij} is the response variable (seed yield, biomass at R2 and R5 phenological stages, kg ha^{-1}; and protein and oil concentration, %) for the ith genotype and the jth row spacing, conditional on an expected value μ and dispersion ψ. The response variables in kg ha^{-1} follow a gamma distribution with an identity link function; and the response variables in % follow a beta distribution with a logit link function (i.e., $g(\cdot) = \text{logit}(\cdot)$).

To quantify uncertainty in our estimates, we obtained 999 bootstrapped samples using a second-order balanced design of bootstrap simulations [28]. This involved sampling at the row spacing by genotype level to respect the treatment structure. We calculated the median and the 95 % confidence interval (CI$_{2.5\text{-}97.5}$) as derived quantities for estimation of the expected value (effect size) and its uncertainty. Following guidance from the American Statistical Association regarding the use of p-values [29], our statistical modeling aimed not to test for 'statistical significance', but rather to quantify the effect size and our uncertainty around those estimates. Therefore, we report effect sizes and CI$_{2.5\text{-}97.5}$ rather than test for statistical significance. Additionally, density distributions of the difference between the modern and old genotypes at each row spacing are presented for each model to visualize the difference in effect sizes (Supplementary Figs. 3, 4, 5, and 6).
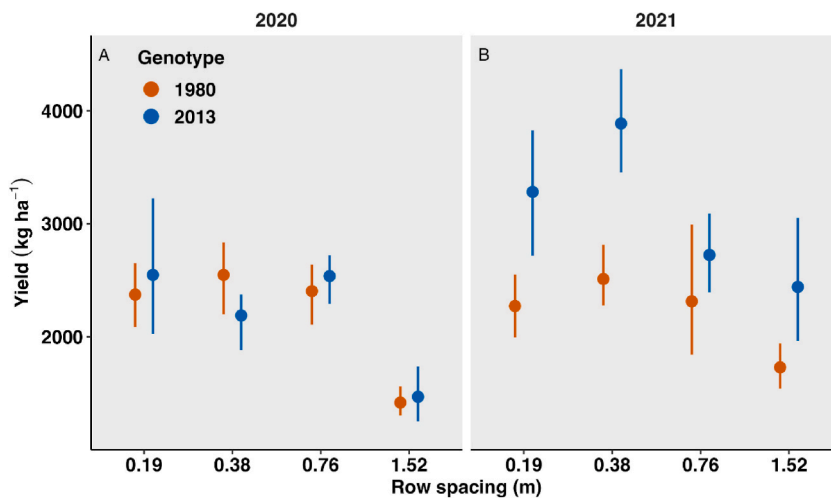

Fig. 1. Soybean seed yield (kg ha^{-1}) of old (1980) and modern (2013) soybean genotypes at row spacings of 0.19, 0.38, 0.76, and 1.52 m in 2020 (panel A) and 2021 (panel B) growing seasons. The error bars represent the 95 % confidence intervals around the estimated expected value.

3. Results

In the 2020 season, both genotypes had similar yields at row spacings of 0.19, 0.38, and 0.76 m with a median of 2481 kg ha^{-1}, while there was a clear reduction at 1.52 m with a median of 1451 kg ha^{-1} (Fig. 1A). In 2021, similar to 2020, the old genotype had similar yields for row spacing levels of 0.19–0.76 m with a median of 2315 kg ha^{-1}, while 1731 kg ha^{-1} was recorded at 1.52 m. In contrast, the modern genotype in 2021 presented greater yields, with the narrow rows (0.19 and 0.38 m) producing the highest yields with a median of 3584 kg ha^{-1} and wider rows (0.76, 1.52 m) yielding 2583 kg ha^{-1} (Fig. 1B, Supplementary Fig. 3).

Overall, plant biomass was higher in 2021 compared to 2020, with no differences observed between genotypes or row spacings (Table 1). Plant biomass at R2 was higher in 2021 (median of 6247 kg ha^{-1}) than in 2020 (median of 3716 kg ha^{-1}). Similarly, biomass at R5 was higher in 2021 (median of 8855 kg ha^{-1}) compared to 2020 (median of 5348 kg ha^{-1}).

Yield from branches was similar across row spacings and genotypes in 2020, with a median of 44 % (Fig. 2A). In 2021 however, the modern genotype had a higher contribution from branches (36 %) compared to the old genotype (18 %) (Fig. 2B). There were no differences in yield (kg ha^{-1}) from branches and main stem across genotypes and row spacings in 2020 (Fig. 2C). However, in 2021, the main stem showed a similar contribution for both genotypes with greater yields under narrow rows (0.19 and 0.38 m) at a median of 2226 kg ha^{-1}, compared to wide rows (0.76 and 1.52 m) at 1663 kg ha^{-1}. Remarkably, in 2021, the yield derived from branches was three-times greater for the modern compared to the old genotype (1113 vs. 379 kg ha^{-1}) (Fig. 2D, Supplementary Fig. 4). Pod number in branches across nodes of the main stem were consistently concentrated in the bottom section (nodes 1 to 6), with more pods observed for the modern genotype in 2021 (Fig. 2, insets A1 and B1).

Protein concentration was similar across genotypes and row spacings in 2020, with an overall median of 39.8 % (Fig. 3A). In 2021, the old genotype had a median protein concentration of 40.1 %, while the modern genotype had consistently lower values with a median of 37.1 %. Nevertheless, the modern genotype maintained protein levels despite the high yields observed under narrow rows (0.19 and 0.38 m) (Fig. 3B). The seed oil concentration in 2020 had an overall mean of 21.1 % across treatments (Fig. 3C). The old genotype in 2021, similar to 2020, had a median of 20.5 %, while the modern genotype tended to have greater oil concentration (median of 21.5 %) (Fig. 3D, Supplementary Fig. 5).

No apparent differences were observed in seed quality (or composition) between branches and main stems, except for protein in

Table 1
Soybean biomass (kg ha^{-1}) in R2 (full flowering) and R5 (beginning seed filling) phenological stages of old (1980) and modern (2013) genotypes at row spacings of 0.19, 0.37, 0.76, and 1.52 m, in 2020 and 2021. The numbers between parenthesis indicate the 95 % confidence interval around the estimated expected value.

Year	Genotype	Row Spacing (m)	Biomass (kg ha^{-1})	
			R2	R5
2020	1980	0.19	3926 (3372–4493)[a]	5547 (4280–7252)
		0.38	3615 (2347–5664)	4802 (3637–5498)
		0.76	3891 (2882–4802)	5925 (5118–6831)
		1.52	3817 (3137–4439)	4601 (4064–5114)
	2013	0.19	3284 (2866–3652)	6063 (5672–6457)
		0.38	2714 (1970–3424)	5222 (3438–7107)
		0.76	4437 (3847–5090)	5578 (4534–6634)
		1.52	2249 (1866–2635)	3460 (2726–4178)
2021	1980	0.19	6704 (5316–7965)	8718 (7732–9846)
		0.38	7639 (5775–9687)	8992 (8278–9722)
		0.76	5913 (4640–7515)	8153 (7039–9498)
		1.52	5366 (3910–6761)	7006 (5616–8635)
	2013	0.19	6581 (5643–7642)	9944 (8184–11958)
		0.38	8345 (7122–9476)	9454 (7369–11032)
		0.76	5519 (4048–6927)	9095 (8122–10359)
		1.52	4627 (3762–5783)	8039 (5749–11140)

[a] 95 % confidence interval of the parameter estimation.
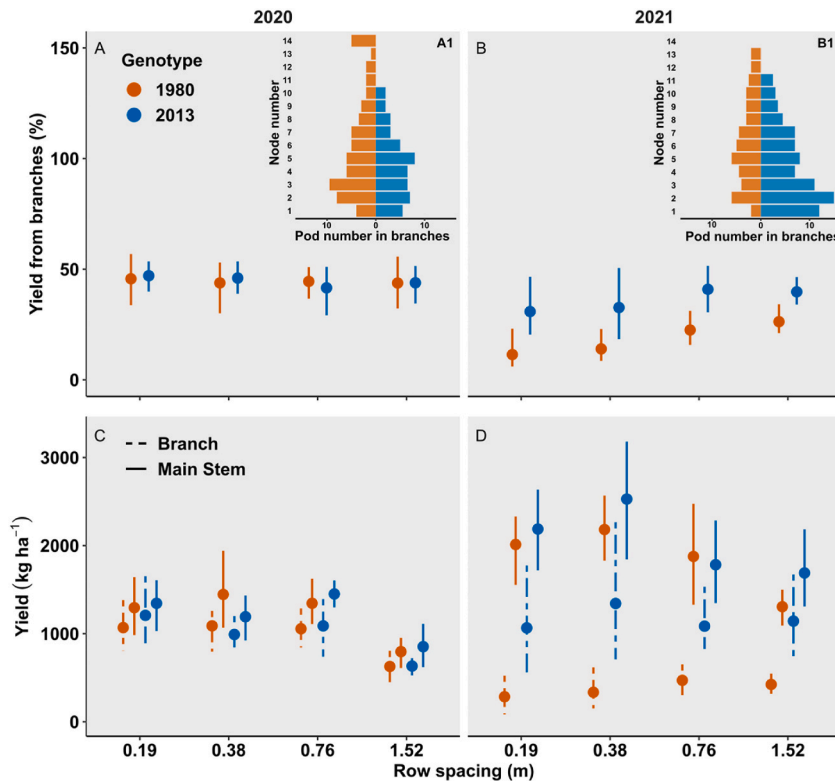
Fig. 2. Soybean seed yield from branches (%, A and B), and from branches and main stems (kg ha^{-1}, C and D; dashed and full line, respectively) of old (1980) and modern (2013) genotypes at row spacings of 0.19, 0.38, 0.76, and 1.52 m, in 2020 (panels A and C) and 2021 (panels B and D) growing seasons. The error bars represent the 95 % confidence intervals around the estimated expected value. Insets A1 and A2 present the median number of pods in branches across nodes of the main stem averaged over all tested row spacings in 2020 and 2021 growing seasons, respectively.

2020, where the main stem had a median of 40.8 % compared to 38.3 % in branches (Fig. 4A–D, Supplementary Fig. 6).

4. Discussion

This study provides evidence of the documented genetic yield gain for modern soybean genotypes [11,30,31], reflecting greater yield differences under narrow (<0.76 m) relative to wide row spacing (>0.76 m). Our results also expand on the ability of modern genotypes to tolerate plant-to-plant competition under high plant densities [11,32] to that observed in the intra-row under wide row spacings. Furthermore, the improved allocation of biomass to reproductive structures without major changes in vegetative biomass and time to canopy closure [33–35] are key factors sustaining yield gains for modern soybeans. Finally, the absence of a yield-protein trade-off in modern soybeans, likely due to high soil NO$_3^-$ and leaf N content late in the season, offers promising economic advantages for the seed quality-driven market [36,37].

Our findings align with previous research [11] indicating that branches contribute more to the yield of modern soybean genotypes. Branches can drive yield increases particularly when soybeans are planted early [38], and under narrow row spacings [39,40]. In this sense, our study confirms that branches tend to concentrate in the bottom and middle section of the canopy when growth is maximized [39,40], likely supported by enhanced light penetration [41]. Light interception has linearly increased with newer genotype releases [33], enhancing seed protein concentration at the base of the main stem [42]. Therefore, branches are crucial for stabilizing and increasing yields in modern soybean genotypes, significantly impacting seed quality composition [23].

From a seed quality perspective, maintaining protein levels at narrow rows despite higher yields could be linked to a better light distribution [42,43] and longer green canopy duration (Supplementary Fig. 2) relative to wide rows. Furthermore, although research has shown that seed protein concentration can be lower on branches than main stem [23], our results suggest that mainly low-yielding conditions favored less protein on branches. The latter could be linked to the delayed reproductive development of branches [44] and the fast senescence of the canopy (as for the 2020 season), suggesting a greater sensitivity to stress conditions on seed from branches. Studying seed quality dynamics of canopy portions (i.e., branch and main stem) could aim to identify farming practices to maximize seed quality and target protein and oil markets [6].

Despite the limitations of this study associated with the number of genotypes tested, these results report on the contribution of row spacing as a key management for achieving better yields for modern soybean genotypes, with implications on seed quality. Further research should explore a larger number of genotypes and investigate in detail changes linked to light interception and biomass
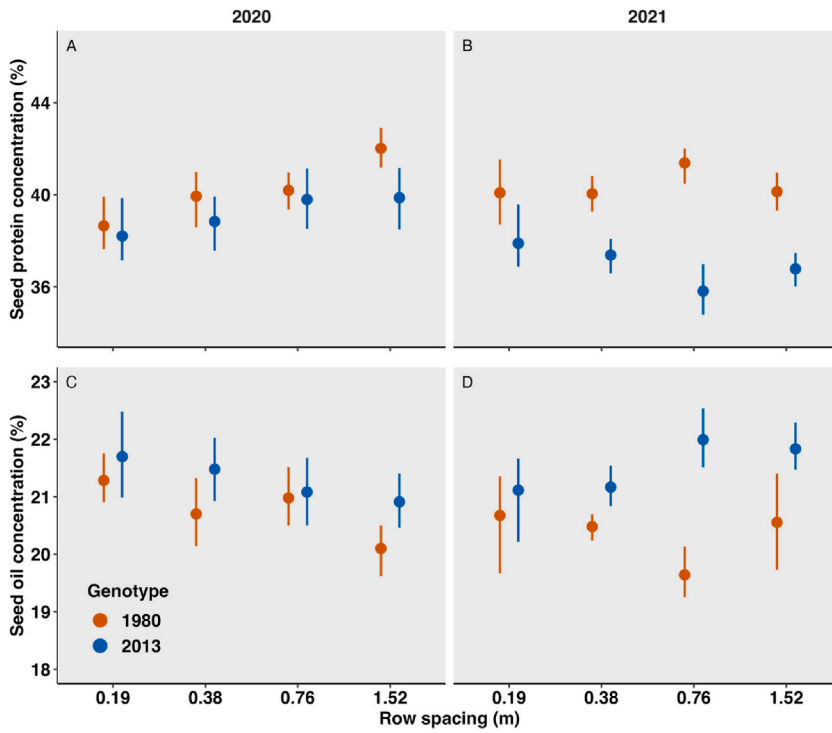
Fig. 3. Soybean seed oil (panels A and B) and protein (panels C and D) concentration (%) in the whole plant of the old (1980) and modern (2013) genotype at row spacings of 0.19, 0.38, 0.76, and 1.52 m, in 2020 (panels A and C) and 2021 growing seasons (panels B and D). The error bars represents the 95 % confidence intervals around the estimated expected value.
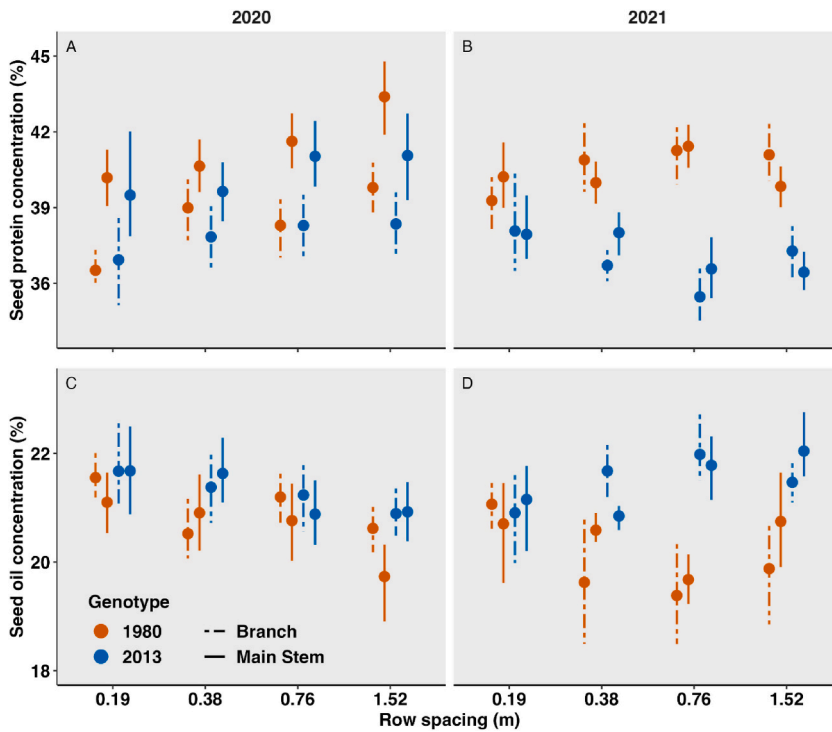

Fig. 4. Soybean seed oil (panels A and B) and protein (panels C and D) concentrations (%) in branches (dashed lines) and main stems (full line) (C and D) of the old (1980) and modern (2013) genotype at row spacings of 0.19, 0.38, 0.76, and 1.52 m, in 2020 (panels A and C) and 2021 growing seasons (panels B and D). The error bars represents the 95 % confidence intervals around the estimated expected value.

conversion efficiencies that could underpin underlying physiological processes. Branches and main stems should be considered as modulators of seed quality [23] with potential variations due to water and temperature stresses at different timings during reproductive development [19]. Canopy architecture traits, mainly branch angle and leaf shape, are key determinants of canopy closure [45]. Hence, branching architecture and light interception could be exploited by breeding to enhance not only yield but also protein concentration.

5. Conclusion

Our study revealed that soybean yield gain could be greater at narrow row spacings (<0.76 m) compared to the documented at 0.76 m and reinforces the important contribution from branches to yield. Protein concentrations for the modern genotype were maintained despite high yields under narrow rows. Future research should evaluate a larger number of genotypes and study different canopy architecture traits.

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Additional information

No additional information is available for this paper.

Data availability statement

Data associated with the study is not publicly available in a repository, and will be made available on request.

CRediT authorship contribution statement

Valentina M. Pereyra: Writing – review & editing, Writing – original draft, Visualization, Investigation, Formal analysis, Data curation, Conceptualization. **Trevor Hefley:** Writing – review & editing, Supervision, Formal analysis, Conceptualization. **P.V. Vara Prasad:** Writing – review & editing, Conceptualization. **Ignacio A. Ciampitti:** Writing – review & editing, Writing – original draft, Validation, Supervision, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Conceptualization.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.heliyon.2024.e35054.

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