

Future research should move beyond descriptive composition analysis toward developmentally resolved, mechanism-based design of soybean seed quality. Reviews of soybean functional genomics emphasize that hundreds of QTLs have already been identified, but relatively few genes have been functionally validated, and progress now depends on integrating genomics, transcriptomics, proteomics, and transformation technologies more effectively. A parallel design-oriented synthesis argues that resolving the protein-oil trade-off will require seed development-focused mutant analysis, multi-omics integration, and isotope-based metabolic flux studies that can capture rebalancing among protein, oil, and sucrose during filling.

Sustainable soybean production will also require linking seed quality improvement with climate resilience and resource efficiency. Soybean already contributes to sustainable agriculture through biological nitrogen fixation, but future breeding must address the fact that abiotic stress disrupts seed filling, shifts the balance among protein, oil, and fatty acids, and reduces protein yield per hectare even when concentration rises under drought or heat. The most promising roadmap combines climate-resilient breeding, optimized source-sink balance and nitrogen fixation, wider use of wild and diverse germplasm, and predictive approaches that incorporate nonlinear environmental effects on seed composition across regions and maturity groups.

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Conflict of Interest Disclosure

The author affirms that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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