chlorophyll content, net photosynthetic rate, and stomatal conductance in the sweet potato cultivar Sushu 16. RNA-Seq analysis further identified 34 differentially expressed genes in storage roots under the optimal ammonium treatment. These genes were mainly involved in photosynthesis, starch biosynthesis, and hormone signaling pathways. Under low-nitrogen conditions, the contents of soluble sugars, sucrose, and starch increased in vegetative organs, while biomass allocation shifted toward roots rather than shoots, reflecting enhanced carbon utilization by sink organs (Amoah et al., 2025). In contrast, excessive nitrogen application tends to promote excessive vine growth at the expense of storage-root development, thereby reducing carbon allocation to sink tissues (Duan et al., 2019; Pan et al., 2026).

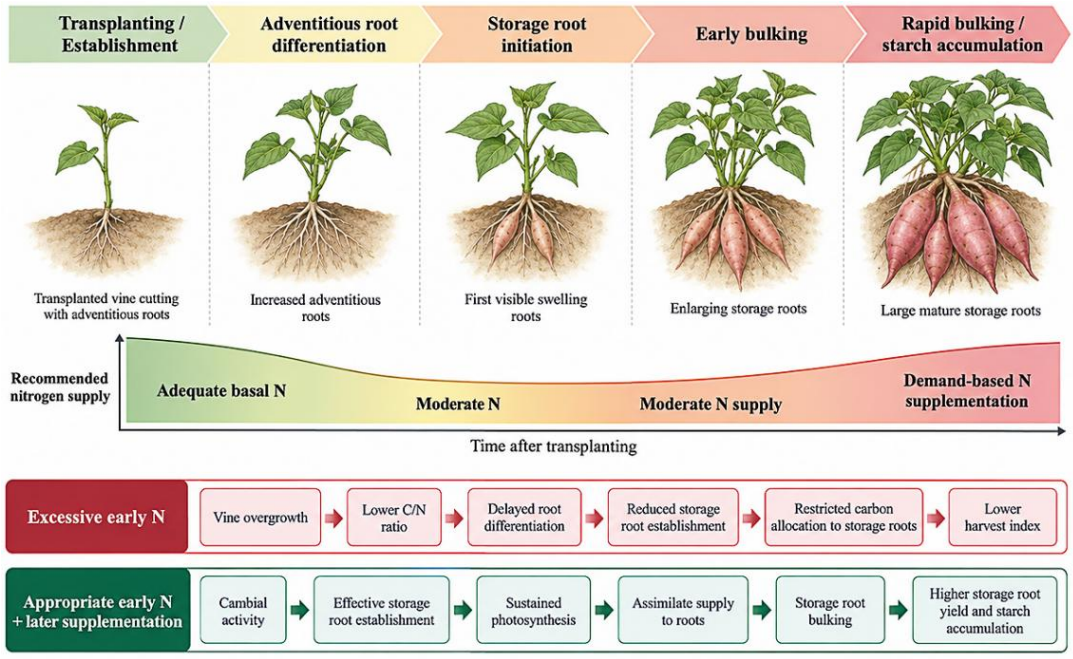


Figure 1 Stage-dependent regulation of sweet potato storage root development by nitrogen supply

Image caption: Moderate nitrogen availability during the early developmental stage favors cambial activity and effective storage root establishment, whereas excessive early nitrogen can promote shoot growth and delay storage root differentiation. After storage roots are established, nitrogen demand increases again, and appropriate supplemental nitrogen helps maintain leaf photosynthesis, assimilate supply, and storage root bulking

Efficient transport of sucrose from source leaves to storage roots through the phloem is an important prerequisite for starch accumulation in sink organs. Fan et al. (2021) found that sucrose transporters (SUTs) participate in sucrose loading into phloem sieve elements, and their overexpression can improve carbohydrate allocation to sink organs. Overexpression of the H^+-pyrophosphatase gene *IbVP1* increased *SUT1* expression, enhanced phloem loading and long-distance sucrose transport, and increased sucrose content in storage roots by 28%-67%. Similar results were reported by Jiang et al. (2024), who showed that the plasma membrane H^+-ATPase gene *IbPMA1*, regulated by the transcription factor *IbbHLH49*, plays an important role in sugar transport and starch biosynthesis in both source and sink tissues. Under relatively high nitrogen supply, nitrogen-tolerant cultivars such as Xushu 32 can reduce carbon flux into secondary metabolic pathways by downregulating genes involved in lignin and flavonoid biosynthesis, thereby redirecting more carbon toward starch metabolism and maintaining a relatively high sugar supply to sink organs (Duan et al., 2021). Source-sink coordination is therefore critical in this process. Even in high-starch genotypes, starch accumulation in storage roots can still be strongly constrained when the production or transport of photosynthates from leaves is limited (Jiang et al., 2024).

4.2 Starch biosynthesis in storage roots

Starch biosynthesis in sweet potato storage roots is coordinated by a series of enzymes (Figure 2). ADP-glucose pyrophosphorylase (AGPase) catalyzes a rate-limiting step in starch synthesis by producing ADP-glucose, which serves as the precursor substrate for the formation of amylose and amylopectin. Granule-bound starch synthase