5.2 Regulation of genes associated with storage root development

Storage-root differentiation in sweet potato is governed by a relatively complex transcriptional regulatory network. He et al. (2021) applied dynamic network biomarker (DNB) analysis to continuous transcriptomic data from developing sweet potato roots and found that more than 9% of sweet potato genes displayed clear stage-specific expression patterns. The DNB signal reached a critical state when root diameter was approximately 3.5 mm, and this stage was therefore defined as a "critical transition point" from fibrous-root growth to storage-root swelling. Network analysis further identified the NAC transcription factor IbNAC083 as a central regulatory node. Suppression of IbNAC083 inhibited root swelling and simultaneously disrupted lignin, flavonoid/flavonol, and starch biosynthesis. These results indicate that storage-root formation is not triggered by the activation of a single "starch gene," but instead involves broad reprogramming of the metabolic network.

Genes associated with lignification deserve particular attention. Transcriptomic analyses of two cultivars differing in their rates of storage-root swelling generated 52,137 transcripts, from which 21,148 unigenes and 9,577 differentially expressed genes were identified. *swbp1*, *swpa7*, *IbERF061*, and *IbERF109* were selected as important candidate factors associated with lignin metabolism and storage-root expansion (Meng et al., 2023). Nitrogen supply can also alter the expression of genes such as *IbEXP1*, *Ibkn1*, and *Ibkn2*. Nitrogen management therefore ultimately intersects with the intrinsic developmental programs operating within the root.

5.3 Coordination between nitrogen and carbon metabolism

From a metabolic perspective, storage-root formation is essentially a process of carbon and nitrogen redistribution (Figure 3). During the early stage, a certain amount of nitrogen is required to support cell division and enzyme and protein synthesis. However, excessively high nitrogen concentrations in the roots often correspond to a low carbon-to-nitrogen ratio and continued dominance of vegetative growth.

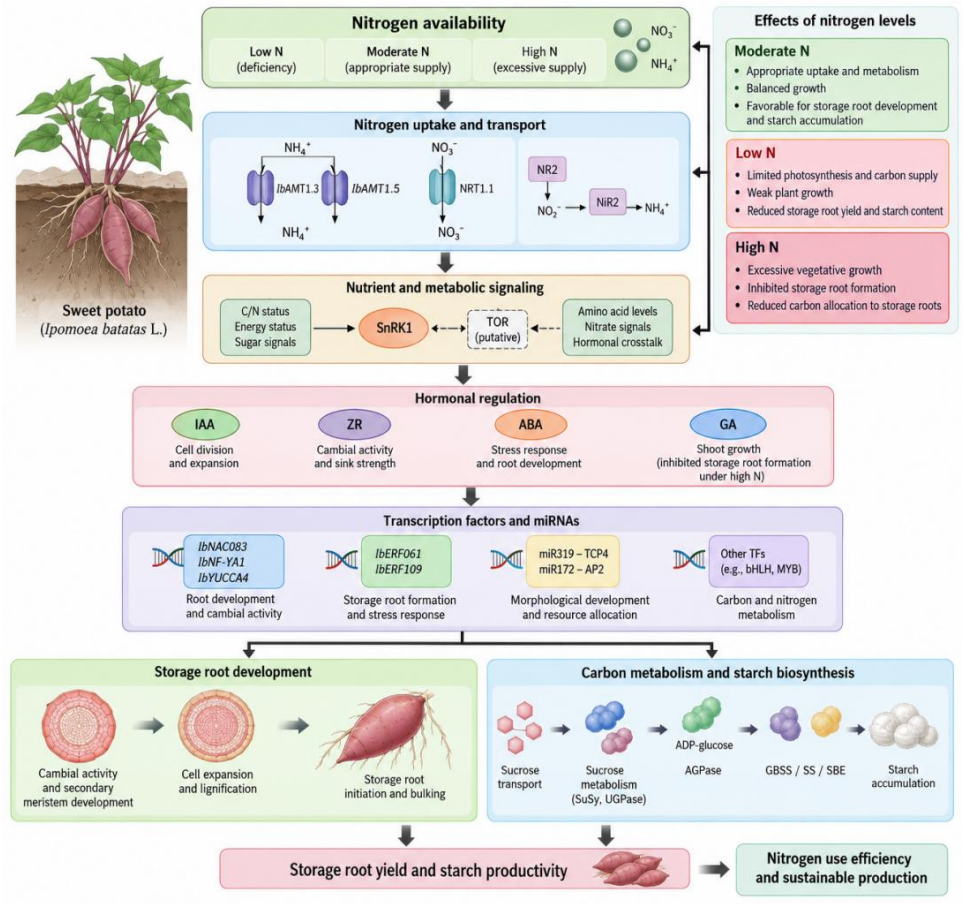


Figure 3 Proposed molecular and metabolic network underlying nitrogen regulation of storage root development and starch formation in sweet potato