<u>Supplementary File S1:</u> Details of the assumptions and simplifications in the metabolic model

Cell wall synthesis arises from activated carbohydrates (GDP-fucose, UDP-rhamnose, UDP-arabinose, UDP-xylose, UDP- and GDP-galactose, GDP-mannose and UDP-glucose), uronic acids (UDP-galacturonic and UDP-glucuronic) and lignin. Lignin is composed of syringyl lignin, p-hydroxy-phenyl lignin and guaiacyl lignin following Boerjan *et al.* (2003). The proportion of each precursor was taken from data on *Nicotiana tabacum* (Baucher *et al.*, 1998). Cell wall degradation is modelled as a simple hydrolysis forming glucose.

The synthesis and degradation of all individual amino acids was detailed. The degradation reactions of histidine and tryptophan were based on knowledge in animals, as they are still uncertain in plants (Hildebrandt *et al.*, 2015). The anaplerotic pathway of isoleucine formation from 2-methyl-malate (or citramalate, identified in the samples (Lacrampe *et al.*, 2023)) was added (Sugimoto *et al.*, 2021).

Protein synthesis was written as a fixed proportion of the twenty proteinogenic amino acids, according to that measured in grapevine petiole tissues by Buchs *et al.* (2018). Protein degradation was simplified as the restitution of all amino acids in the same proportions, with an expense in ATP.

Reactions towards the synthesis of purines and pyrimidines were included because of their relationship with C and N metabolism (cofactors, aminoimidazole carboxamide ribonucleotide [AICAR], 5-phosphoribosyl-1-diphosphate [PRPP], β-alanine, homocysteine, *etc.*). Nucleic acid synthesis was written according to the proportions of the different nucleotides described in tomato (The Tomato Genome Consortium, 2012; Kotwal *et al.*, 2016). This reaction was set as reversible, allowing for nucleic acid degradation.

The synthesis of phenolic compounds was simplified to account for the two major metabolites found in the biological samples, chlorogenic acid and rutin. They arise from the shikimate pathway, with dehydroquinic acid as a precursor. The mevalonate and 2-C-methyl-D-erythritol 4-phosphate/1-deoxy-D-xylulose 5-phosphate (MEP/DOXP) pathways were simplified and led to the terpenoid precursors geranyl-diphosphate and cholesterol. The latter is used for α-tomatine synthesis, with GABA as the nitrogen supplier (Sonawane *et al.*, 2016; Nakayasu *et al.*, 2021). Degradation of α-tomatine corresponds to hydrolysis, releasing the various carbohydrates and the aglycone moiety tomatidine.

Most reactions towards external compounds were bound from quantified metabolites. Five reactions associated with unmeasured compounds were added to balance the model: (i) chlorogenic acid accumulation, corresponding to a potential export to other

tissues for lignification processes (Mondolot *et al.*, 2006). The flux of chlorogenic acid (*Vcqa_ac*) was determined from the sum of the quantities of chlorogenic acid (3-O-caffeoylquinic acid) and its isomer neochlorogenic acid (trans-5-O-caffeoylquinic acid); (ii) cysteine accumulation, as cysteine may accumulate weakly in cells (Hildebrandt *et al.*, 2015); (iii) geranyl-diphosphate accumulation, accounting for precursors of terpenoid synthesis; (iv) tomatidine accumulation that balances the degradation of α-tomatine; and (v) nitrogen discharge reaction set as an accumulation of glutamine and glutamate with stoichiometric coefficients of 0.44 and 0.12, respectively, according to phloem sap concentration (Valle *et al.*, 1998).

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