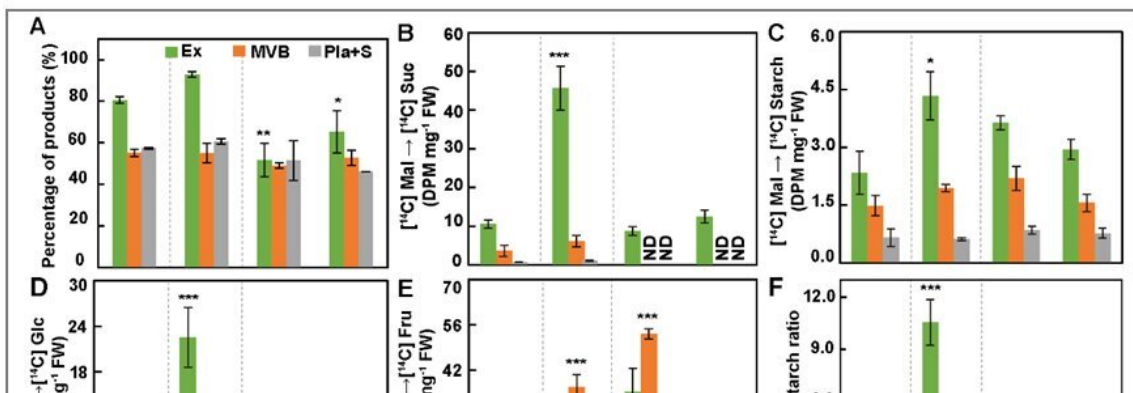
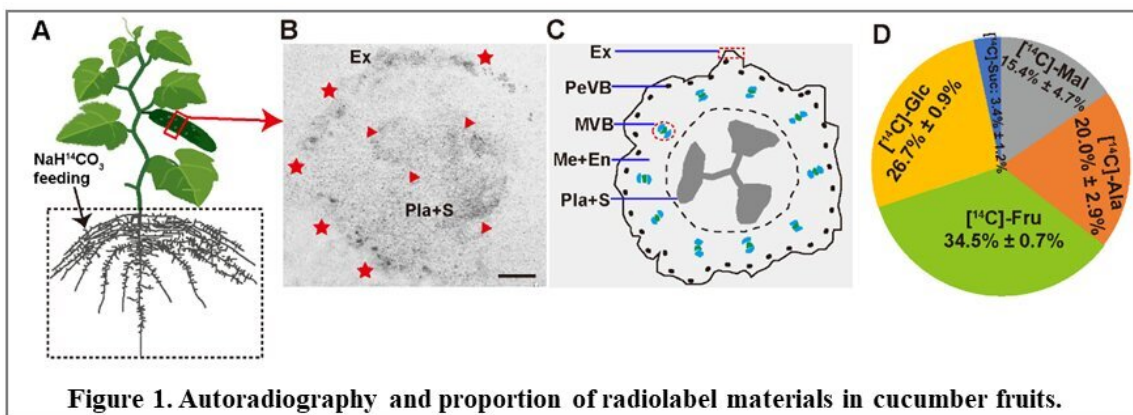


The role of malate decarboxylate CsNADP-ME2 in mediating the balance of carbon and amino acid metabolism in fruit

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Credit: *Horticulture Research*

Central metabolism produces carbohydrates and amino acids that are tightly correlated to plant growth and thereby crop productivity. Malate

is reported to link mitochondrial respiratory metabolism with cytosolic biosynthetic pathways. Although the function of malate metabolism-related enzymes in providing carbon has been characterized in some plants, evidence conferring this role in the fleshy fruit of cucumber (*Cucumis sativus*) is lacking.

A [research paper](#), titled "[Cucumber malate decarboxylase, CsNADP-ME2, functions in the balance of carbon and amino acid metabolism in fruit](#)," was published online in the journal of *Horticulture Research*.

Conducted by the joint team of Prof. Xiaolei Sui (from Beijing Key Laboratory of Growth and Developmental Regulation for Protected Vegetable Crops, College of Horticulture, China Agricultural University) and Prof. Alisdair R. Fernie (from Max-Planck-Institute of Molecular Plant Physiology), the research revealed the important role of CsNADP-ME2 in the balance of carbon and amino acid metabolism in cucumber [fruit](#).

The rapid development and growth of fleshy cucumber fruit require significant sources of carbon and nitrogen. Researchers have reported that monosaccharides like glucose and fructose are the primary carbohydrates that accumulate in mature cucumber fruit. Organic acids coincidentally accumulated during cucumber fruit development. Cucumber fruits displayed complicated vascular anatomy.

Peripheral (PeVB), main (MVB), carpel (CVB), and placental vascular bundles (PIVB) are among the four sets of functionally differentiated vascular bundles from the outside to the inside of the fruits of cucumber plants. However, so far, the *in vivo* functions of CsNADP-ME in the metabolism of nitrogen and carbon in cucumber fruits are not clear.

Here, ¹⁴C-labeled bicarbonate fed into the xylem stream from the cucumber roots was detected to be incorporated into [amino acids](#),

soluble sugars, and organic acids in the exocarp and vasculature of fruits.

Histochemical localization showed that the NADP-dependent malic enzyme coding gene CsNADP-ME2 was mainly located in the exocarp and vascular bundle system of fruit. Radioisotope tracer and gas exchange analysis showed that overexpression of CsNADP-ME2 gene significantly increased the contents of starch, sucrose and glucose in cucumber fruit exocarp, as well as the ratio of sucrose to starch, indicating that CsNADP-ME2 could promote the carbon flux into soluble sugars and starch in fruits.

Further studies combined with metabolic profiling showed that down-regulation of CsNADP-ME2 by RNA interference resulted in the accumulation of malate in exocarp.

In addition to the inhibition of the glycolysis-related genes' expression and the reduction of the activities of the corresponding enzymes, increased amino acid synthesis and decreased sugar abundance were also observed. In the fruit of CsNADP-ME2- overexpression line, the opposite trend was detected.

Overall, this study indicates that CsNADP-ME2 may play potential roles both in central carbon reactions and amino acid metabolism in cucumber fruits. This study also offers a promising approach for collaborative regulation of yield and quality of fleshy fruit in [cucumber](#).

More information: Nan Shan et al, Cucumber malate decarboxylase, CsNADP-ME2, functions in the balance of carbon and amino acid metabolism in fruit, *Horticulture Research* (2023). [DOI: 10.1093/hr/uhad216](https://doi.org/10.1093/hr/uhad216)

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