Influence of Carbon Source on the Distribution of Carbon Isotopes in Bacteria

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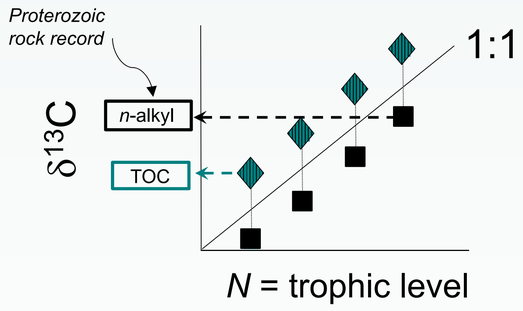
Abstract

"*You are what you eat, +1.5‰*" is a central principle of carbon isotope systematics. Although based on observations from multicellular organisms, this idea also has been applied to Precambrian ecosystems dominated by unicellular, microbial life, with the suggestion that such systems would develop ordered trophic levels [1]. Here we present a survey of several bacterial species grown on a variety of carbon sources to show that the concept of heterotrophic ^{13}C enrichment is not universal. Growth on complex food substrates produces the typical ^{13}C enrichment, yet growth on simple sugars produces ^{13}C depletion – in the same species. These results may be explained because microbes cannot ingest whole, complex foods; *i.e.*, they assimilate small-molecule metabolites. Bacterial carbon isotopic patterns must therefore reflect the type of substrate and the entry point of this substrate into central metabolism [2]. In agreement, the intracellular carbon isotope distributions in our experiments – as traced by the $\delta^{13}C$ values of amino acids reflecting different branch points of the intracellular reaction network [2, 3] – change as a function of the primary carbon metabolite. Isotopic patterns of amino acids and lipids in heterotrophs are indistinguishable from autotrophs when the primary food source is fresh photosynthate (sugar). When acetate is the food source, phytol becomes the most strongly ^{13}C-depleted cellular component and *n*-alkyl lipids have ^{13}C contents equal to biomass. These results can be explained by an isotope flux-balance model initiated with simple stoichiometric relationships and known kinetic isotope effects (ε). Together these observations suggest that organic ^{13}C isotopic patterns in Earth history may primarily reflect the changing nature of carbon inputs to the sedimentary environment.

"Logan Hypothesis" [1]

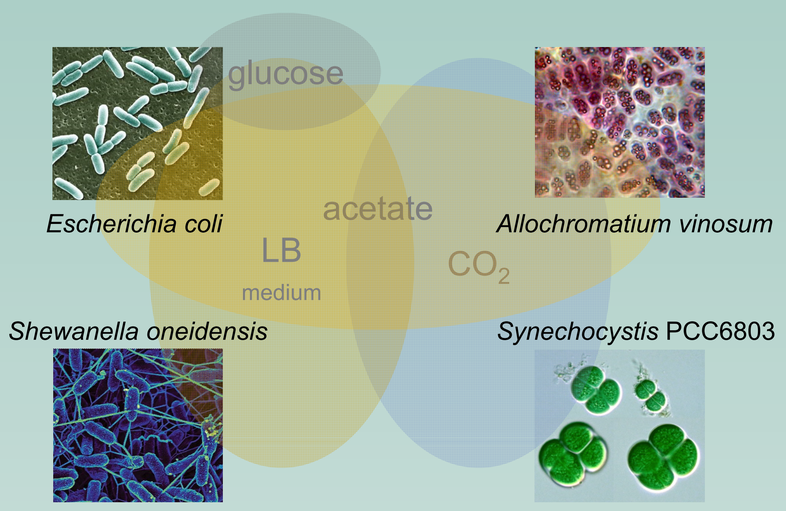


Microbial trophic levels?

- **Slow particle sinking, slow biological pump.**
- **Long residence time permits the development of an ecosystem containing many trophic levels**
- **Disappears in the latest Ediacaran due to intensification of grazing.**

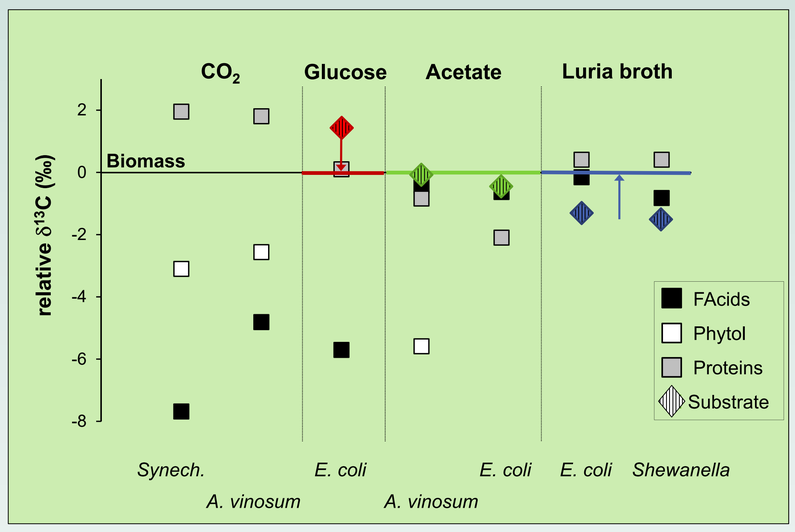
Microbes & C Sources

- **Carbon isotope distributions were studied for seven combinations of species and substrates [4, 5].**



4 species, 4 substrates, 7 combinations

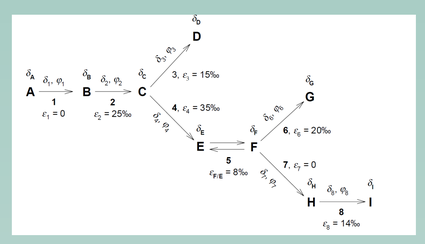
"…what you eat, +1‰?"



- **Sugar: …what you eat, -1.5‰.**
- **Acetate: …what you eat.**
- **Omnivory: …what you eat, +1.5‰.**
- **Fatty acids are -5‰ to -8‰ relative to biomass when living on CO_2 or sugar, but are equal to biomass when living on acetate or complex substrate.**
- **Phytol is the most ^{13}C-depleted component when cells are grown on acetate.**
- **Lipid vs. TOC (kerogen) relationships in the rock record will depend on the metabolic history of the buried biomass; microbes do not have simple trophic levels.**

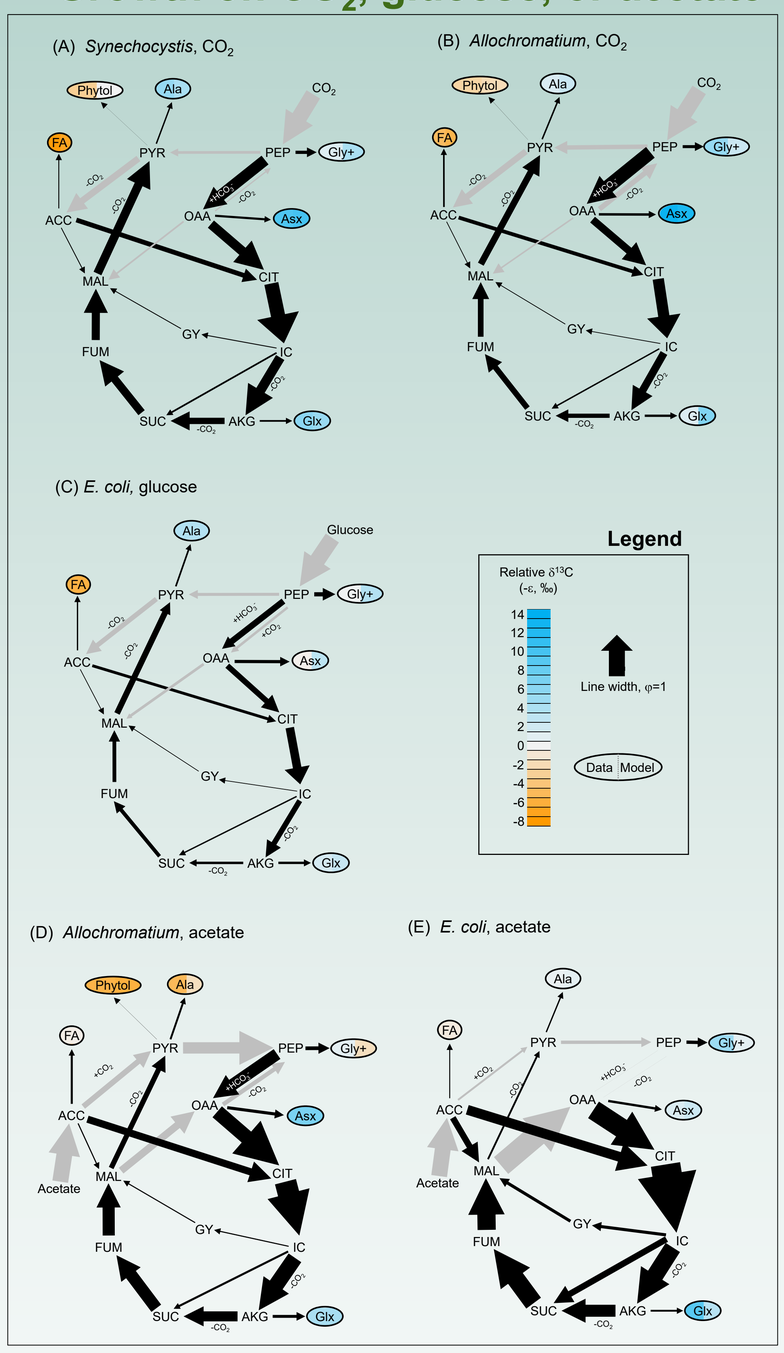
Isotope Flux-Balance

- **Flux-balance model to explain isotopic patterns and intracellular carbon flow.**



Letters indicate metabolites. Isotopic compositions of these metabolites are indicated by δ with alphabetical subscripts. Reactions are numbered, where δ_i, φ_i, and ε_i indicate respectively the isotopic composition of the carbon flux, the magnitude of the flux, and the isotope effect of the reaction. Adapted from [2].

Model solutions: Growth on CO_2, glucose, or acetate



Similar C fluxes for different species grown on the same carbon source

- **Incomplete TCA cycle in autotrophs.**
- **Role of malic enzyme (MAL→ PYR).**
- **Same topology, different efficiency, for glucose vs. CO_2.**
- **Modern application: Fingerprinting natural communities *via* carbon isotope patterns in amino acids and fatty acids.**

References & Acknowledgments

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