

## Conceptualising carbon turnover in the rhizosphere

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Plants use belowground carbon inputs as a regulatory means to create, exploit and even condition the soil ecosystem towards optimum resource strength. They access resources of the mineral matrix through variations in root mass, root morphology, fine root turnover dynamics and the amount, composition and timing of root exudate production.

In order to assess the fate of these combined carbon inputs and their potential impact on preexisting carbon stocks, it is useful to remember that, when algae began to evolve into plants some 400-500 million years ago, they did so in an environment that was already inhabited by microorganisms. It thus appears reasonable to assume that, from the beginning, the evolution of root systems involved the development of sophisticated plant-microbial relationships covering the full scope of the mutualism-symbiosis-parasitism continuum, effectively forming a plant-microbial metaorganism or holobiont in the sense of Zilber-Rosenberg and Rosenberg [1].

These considerations help to understand why plants direct between 40-60% of photosynthetically fixed carbon to roots and associated microorganisms via sloughed-off root cells, tissues, mucilage and a variety of exuded organic compounds. We deduce that to gain mechanistic insight into soil carbon turnover processes, we must shift focus from isolated views of the individual plant or some specific decomposer community towards the more complex metaorganism in its respective soil environment.

When the plant is conceptualised as one organ of the metaorganism and the micro/mesobiota as its other organs, we become immediately aware that the rhizosphere is the place where mechanisms of sustenance, recycling, transport, communication and adaptation operate to allow the metaorganism to function and to evolve. The implications of this insight for soil carbon sequestration will be discussed.

[1] Zilber-Rosenberg, I., and E. Rosenberg (2008), Role of microorganisms in the evolution of animals and plants: the hologenome theory of evolution, *Fems Microbiology Reviews*, **32(5)**, 723-735.