Biospheric coupling of terrestrial water and carbon fluxes: Implications for the climate system

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Terrestrial water and carbon fluxes represent one of the largest movements of mass and energy in the Earth's outer spheres, yet the relative contributions of abiotic water vapour fluxes and those that are regulated solely by the physiology of plants remain poorly constrained. By interpreting differences in the oxygen-18 and deuterium content of precipitation and river water, it is possible to partition plant transpiration from the evaporative flux that occurs directly from soils, water bodies and plant surfaces. The methodology was applied to fifteen large watersheds in North America, South America, Africa, Australia, and New Guinea, and results show that approximately two thirds of the annual water flux from the water-limited ecosystems that are typical of higher-latitude regions can be attributed to plant transpiration. In contrast to water-limited watersheds, transpiration in high-rainfall, densely vegetated regions of the tropics represents a smaller proportion of precipitation and is relatively constant, defining a plateau in response to incident solar radiation. Estimates of water transpiration behave similar to net primary productivity, confirming that, in agreement with small-scale measurements, the terrestrial water and carbon cycles are inherently coupled via the biosphere, offering a conceptual perspective on the dynamics of energy exchange between terrestrial systems and the atmosphere, where the carbon cycle is essentially driven by solar energy via the water cycle intermediary.

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Tracking the biogeochemistry of an Ediacaran basin in SW-Gondwana by isotopes and biomarkers

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In an ongoing project we trace the biogeochemical changes in Neoproterozoic to Cambrian sediments of the Corumba Group (CG, SW-Brazil), the Arroyo del Soldado Group (ASG, Uruguay), and Sierras Bayas Group (SBG, Argentina), all of them from the Rio de la Plata Craton, SW-Gondwana, by an isotopic and molecular approach.

The $\delta^{13}C_{carb}$ values range from -5.7 to 5.7% VPDB, and display coeval excursions in CG and ASG coinciding with global curves. The lowest values recorded for cap dolostones of the CG (Bocaina Formation) are typical in cap carbonates worldwide. The $\delta^{13}C_{ker}$ values varying from -26.4 to -22.8% in CG samples and from -27.4 to -12% in ASG are most likely due to variations in the primary composition of the organic matter (i.e., variable contribution of bacteria) and/or in the productivity rate during deposition. The highest $\delta^{13}C_{ker}$ values in ASG samples reflect isotopically heavy carbon primary sources or a ¹³C-enriched surface water during water column stratification. The $\delta^{15}N_{ker}$ range between -3.3 to 3.1% N2-Air, suggests primary contribution of molecular nitrogen fixers (cyanobacteria). Positive $\Delta^{13}C_{carb-ker}$ excursions, higher concentrations of redox sensitive elements (Mn, Fe and V), \sum REE and variations in the Ce anomaly can be explained by an enhanced primary productivity (increased pCO_2 or nutrients supply) and preservation of organic carbon favored by reducing conditions in bottom waters. The main resolvable compounds in the GC-MSD total ion chromatograms of the hydrocarbons saturated fraction are *n*-alkanes in the C_{12} - C_{30} range (maxima at C₂₁) for CG; C₁₄-C₃₅ range (maxima at C₂₆) for ASG and C14-C28 range (maxima at C25) for SBG samples with no odd/even C-number predominance. The high amount of $C_{>18}$ *n*-alkanes confirm a marine planktonic input. The identified biomarkers include extended C₂₉-C₃₄ hopanes, acyclic isoprenoids, branched alkanes (8-methyl heptadecane), alkybenzenes and traces of steranes. Gammacerane was identified in one sample. Biosynthesis of homohopanes is restricted to bacteria not strictly anaerobic, and steranes are derived from aerobic eukaryotes. The 8-methyl heptadecane is typically synthesized by cyanobacteria. The biomarker distribution reflects a mainly microbial ecosystem based on photosynthetic primary production, including chemotrophic bacteria.