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| Sommario/riassunto      | <p>Microbial mat communities consist of dense populations of microorganisms embedded in exopolymers and/or biomineralized solid phases, and are often found in mm-cm thick assemblages, which can be stratified due to environmental gradients such as light, oxygen or sulfide. Microbial mat communities are commonly observed under extreme environmental conditions, deriving energy primarily from light and/or reduced chemicals to drive autotrophic fixation of carbon dioxide. Microbial mat ecosystems are regarded as living analogues of primordial systems on Earth, and they often form perennial structures with conspicuous stratifications of microbial populations that can be studied in situ under stable conditions for many years. Consequently, microbial mat communities are ideal natural laboratories and represent excellent model systems for studying microbial community structure and function, microbial dynamics and interactions, and discovery of new microorganisms with novel metabolic pathways potentially useful in future industrial and/or medical applications. Due to their relative simplicity and organization, microbial mat communities are often excellent testing grounds for new technologies in microbiology including micro-sensor analysis, stable isotope methodology and modern genomics. Integrative studies of microbial mat communities that combine modern biogeochemical and molecular biological methods with traditional microbiology, macro-ecological approaches, and community network modeling will provide new and detailed</p> |

insights regarding the systems biology of microbial mats and the complex interplay among individual populations and their physicochemical environment. These processes ultimately control the biogeochemical cycling of energy and/or nutrients in microbial systems. Similarities in microbial community function across different types of communities from highly disparate environments may provide a deeper basis for understanding microbial community dynamics and the ecological role of specific microbial populations. Approaches and concepts developed in highly-constrained, relatively stable natural communities may also provide insights useful for studying and understanding more complex microbial communities.

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