Methylated hopanoid biosynthesis and function in modern bacteria

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The majority of life's history has been dominated by microbes whose metabolic inventions have significantly altered the Earth's surface environment and, in turn, impacted the evolution of life on Earth. Because unicellular microorganisms do not readily leave diagnostic morphological fossils, alternative strategies are necessary for studying microbial communities in the context of the Earth's distant past. One predominant strategy is to correlate organic compounds deposited by ancient microbes and preserved in sedimentary rock with lipid molecules produced by extant microorganisms. One such class of biomarkers are the hopanes, pentacyclic triterpenoid lipids that are clearly the diagenetic products of modern day hopanoids. Hopanoids are produced by a diverse set of bacteria and as a result most sedimentary hopanes do not provide any taxonomic specificity below the domain level. However, hopanoids methylated at the C-2 or C-3 position are produced by a limited number of bacterial taxa and thus have the potential to function as robust biomarkers. Traditionally, 2-methyl and 3-methylhopanoids have been utilized as proxies for cyanobacteria and aerobic methanotrophs, respectively. However, our discovery of the two proteins necessary to methylate at the C-2 (HpnP) and C-3 (HpnR) position revealed that the diversity of bacteria capable of producing methylhopanoids was underestimated. Subsequent ecological studies of the C-2 methylase have shown that alphaproteobacterial copies of the *hpnP* gene are found in diverse modern environments while cyanobacterial *hpnP* genes are rarer. Further, physiological studies of a C-3 methylase deletion mutant have demonstrated a potential role for 3-methylhopanoids in survival under nutrient limited conditions. Taken together, these studies illustrate that a proper interpretation of methylhopanes in the rock record requires us to look beyond simple taxonomic classification of methylhopanoid producers. In addition to understanding which organisms produce methylated hopanoids, a deeper knowledge of the physiological function and environmental factors that induce their expression in modern cells is needed.

Changes of the GWP due to shifts from flooded to upland rice cultivation

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Changes in climate and water distribution resulting in physical or economic water scarcity may have severe effects on rice production systems. Shifting to rotations with non-flooded crops entails pronounced implications in terms of C and N element cycling and associated greenhouse gas (GHG) emissions (CH_4, N_2O, CO_2). Higher soil aeration in upland systems might decrease CH_4 emissions, but increase N_2O emissions ("pollution swapping") and cause losses in soil organic carbon that translate into CO_2 emissions [1, 2].

An automated GHG measuring system was set up at the IRRI farm, Philippines to investigate changes in the total GHGs balance when shifting from flooded to upland rice cultivation in the dry season under consideration of different fertilizer regimes (zero, conventional, improved). The system consists of two analytical sampling units (valve steering and GCs) connected to a total of 18 chambers (2 treatments, 3 fertilizer regimes; 3 replicates).

The highest global-warming potential (GWP) (kg CO_2eq ha^{-1} $season^{-1}$) was found for flooded rice without N fertilization. Higher N application in irrigated plots resulted in lower CH_4 emissions. This finding supports theories that ammonium based fertilizers can decrease CH_4 emissions [3, 4]. Total GWPs (CH_4, N_2O) were about 70-80% lower in the upland systems due to lower CH_4 emissions but were offset by lower yields.

Upland rice cultivation using high yield varieties could help to mitigate GHG emissions and reduce water-use in rice production systems while further research of N fertilization-impacts on CH_4 emissions seems necessary.

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