Oil cracking in Chinese sedimentary basins

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Oil cracking in sedimentary basins depend on the thermal history of reservoirs not of the oil prone source rocks, there are no significant oil-cracking gas in many basins (such as Bahai Bay basin, Jugar Basin) with deep buried oil-prone source rocks (depths >5000m) because oil has expelled and escaped upwards from the cracking into gas. Oil cracking kinetics algorithms are similar for marine and non-marine oil, but sulphur content of oils have minor influence on cracking kinetic parameters, TSR enhanced oil cracking in lower temperature. Solid pyrobitumen is directly indicator of oil cracking in reservoirs, sometimes oil inclusions and solid pyrobitumen be likely to coexist in same assemblage of carbonate cements, which indicate that open system favor oil cracking, but oil inclusions are rare or absent because of thermal alteration when reflectance of solid bitumens are more than 2.0%.

Gas yields and isotope kinetics algorithms (GOR software) can be used in conjunction with basin modeling (Trinity) to quantify oil to gas cracking history and to explain GOR of petroleum, gas composition and carbon isotope in Sichuan, Tarim and Songliao basin. the possible scenario of oil cracking, gas generation and accumulation history were postulated through comparison measured data with calculated results. Oil have been entirely cracked into gas in the Sinian and Permian–Triassic reservoirs with remaining pyrobitumen in the southern and eastern Sichuan Basin, Condensate and gas in Tazhong and Tabei uplift in Tarim Basin were derived from the cracking of crude oil downward, where cracking products are manly high GOR petroleum. Qingshen gas field in Xujiaweizi rift depression, Songliao Basin, where mixing of oil cracking gas with humic gas result in the half of gas samples with the peculiar reversal in the distribution of the carbon isotopic values.

Metagenomics assisted investigations of the metabolic diversities of microbial communities in the chimneys at Juan de Fuca Ridge

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The metabolic diversity and dynamics of the deep-sea hydrothermal vent chimneys in the Endeavour Segment of Juan de Fuca Ridge were investigated using combined molecular approaches including microarray hybridization on the Geochip, quantitative real-time PCR, 16S rRNA gene- and functional gene libraries. The results suggest that the hydrothermal microbial communities are metabolically and physiologically highly diverse, and the communities are undergoing rapid dynamic succession and adaptation in response to the steep temperature and chemical gradients across chimney. Meanwhile, a fosmid library of the mature chimney sample which was proved having enrichment of the dominant gamma-, and epsilon- Proteobacteria, was constructed and pooled for pyrosequencing. A total of 308,034 reads with average sequence length of 250 bp were generated. The population genome suggests that the deep-sea vent chemoautotrophs have the ability to derive energy from a variety of redox couples, such as sulfur compounds and ammonium. The obtained metagenome has a large suite of chemotaxis genes detected, reflecting their adaptation to the fast evolving deep-sea vent environment.