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贺兰山地区中元古代微生物席成因构造 [点此下载全文](#)

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摘要:

贺兰山中段中元古界黄旗口组石英砂岩中发现丰富的微生物席成因构造(MISS), 包括由微生物席生长、破坏和腐烂过程形成的3种类型、9种不同形态的构造; 与华北大红峪组发现的同类构造在成因类型与多样性方面具有很强的可对比性。砂岩中发育双向交错层理、冲洗层理、高角度单斜层理系和波痕, 泥质粉砂岩夹层中发育波痕与泥裂, 表明微生物席主要发育于潮间带上部至潮上带下部环境。MISS构造在华北地台长城系下部砂岩中的广泛存在表明在1.6 Ga前以蓝细菌为主的微生物群在环湖坪碎屑环境也很活跃, 可能代表了微生物由海洋向陆地环境发展的过渡阶段。具光合作用功能的制氧蓝细菌的蓬勃发展可能是引发中元古代海洋化学条件发生转变、含氧量增高的重要原因, 并为真核生物及宏观藻类的兴起创造了条件。研究表明, 黄旗口组与华北大红峪组大致同时, 反映了Columbia超大陆裂解期华北地台开始拉伸—张裂、缓慢沉降的构造古地理背景。

关键词: [贺兰山中段](#) [中元古界黄旗口组](#) [微生物席成因构造\(MISS\)](#) [环湖坪碎屑沉积](#) [华北地台西缘](#)

Pervasive Microbial Mat Colonization on Mesoproterozoic Peritidal Siliciclastic Substrates: an Example from the Huangqikou Formation(ca. 1.6 Ga) in Helan Mountains, NW China [Download Fulltext](#)

Fund Project:

Abstract:

The Mesoproterozoic Huangqikou Formation (ca. 1.6 Ga) in the Helan Mountains, NW China, consists mainly of quartz sandstone. In the lower part of this unit, abundant microbially induced sedimentary structures (MISS) are present, with nine distinctive types that can be grouped in to three genetic categories including mat growth, mat destruction and mat decay structures. These structures are closely associated with herringbone, swaley, and high angle planar cross stratification, ripple cross lamination, ripple marks, and mud cracks, suggesting microbial mat colonization and growth in shallow subtidal to supratidal environments with moderate to high hydraulic energy. The presence of mat growth structures and reworked mat chips in cross bedded sandstone indicates microbial mat colonization in high energy sandy substrates where biostabilization of mobile sediments prevented a complete removal of microbial mats and translucent quartz sand allowed microbial mats to grow out of the sediment burial. The association of MISS with mud cracks and ripple marks indicates that microbial mat growth in intermittently exposed silty and muddy substrates. These MISS are similar to those found in modern peritidal siliciclastic environments where periodic low or non deposition allowed microbes (most likely cyanobacteria) to grow into thick microbial mats and mat generated organic matter decay resulted in gas release and escape features. However, the MISS structures in the early Mesoproterozoic North China platform are widespread. The plethora of MISS from the Huangqikou Formation is present in coeval stratigraphic units including the Dahongyu Formation (Pt2) near Beijing, hundreds of kilometers away from the Helan Mountains. The widespread distribution and diversity of MISS in the lower Mesoproterozoic North China Platform thus indicate that microbes (particularly cyanobacteria) thrived in Mesoproterozoic peritidal siliciclastic environments. The abundance of MISS in sediments with mud cracks implies that, by the time of early Mesoproterozoic, microbes may have started to colonize the terrestrial substrates. Comparing the abundance and diversity of eukaryotes with the abundance of MISS in the Mesoproterozoic North China platform suggested that the widespread and diversity of MISS may have recorded the great thriving of cyanobacteria, an event that may have had significant influences on the oceanic redox changes, atmospheric oxygen increases and the evolution of eukaryotic microorganisms and macro algae. The study also suggests that the Huangqikou Formation in NW China is approximately equivalent to the Dahongyu Formation in North China, both of them were formed in a slowly subsiding tectono paleogeographical background resulted from the extension and rifting of the North China Platform in response to the break up of the Paleoproterozoic Columbia supercontinent.

Keywords: [Mesoproterozoic Huangqikou Formation](#) [microbial mat](#) [MISS\(microbially induced sedimentary structures\)](#) [peritidal sandstone](#) [Helan Mountains](#) [Ningxia](#)

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