Sporulation as a bacterial adaptation mechanism to high pressure

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Endospores represent bacterial dormant stages and can remain viable for thousands to millions of years. Recent findings challenge our traditional hypothesis (e.g. Kopke et al., 2005; Fang et al., 2017): Everything is everywhere, and the environment selects. Fang et al. (2017) isolated a number of gram-positive spore-forming meso- and thermopiezophilic bacteria and their endospores from the Shimokita coalbed sediment from a forearc basin in the western Pacific at depths of 1,999 and 2,406 mbsf (meters below the seafloor). Fang et al. (2017) hypothesized that the bacterial isolates were laboratory-germinated bacterial endospores that had been buried in the sediment which was transported from the terrestrial envrionment and deposited in the basin about 20 million years ago. To test this hypothesis, we conducted two experiments. First, *Bacillus subtillus* strain 168 was cultivated in a media prepared with artificial seawater amended with glucose, at 35^{o}C and under growth pressures of 0.1, 20, 40, 60 and 80 MPa (megapascal). Our results show that the abundance of endospores from this spore-forming bacterium increased by two-fold when pressure increased from 0.1 to 40 MPa, and then descreased with further increasing pressures. Then, bacterial isolate from the coalbed sediment, *Bacillus subtillus* strain 29R7-12 was cultivated under the same conditions. We found that the number of spores increased from 2.25 x 10^{7} ml^{-1} to 3.37 x 10^{7} ml^{-1}when growth pressure increased from 0.1 to 20 MPa, then decreased with pressure. Our results indicate that endospore formation (sporulation) appears to constitute a bacterial adaptation mechanism to the increased pressure, suggesting that the coalbed bacterial isolates might be from the germination of the buried endospores in the lab. This conclusion is further supported by the observation that the growth property of strain 29R7-12 spores was simiar to that of the bacterial isolate itself.

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Köpke et al., Appl. Environ. Microbiol., 2015, 71, 7819–7830.