

翻譯 共 5 題 (寫出正確的大意，不要逐字翻譯)

1. 20 %

Nitrification, the oxidation of ammonia via nitrite to nitrate, has always been considered to be a two-step process catalysed by chemolithoautotrophic microorganisms oxidizing either ammonia or nitrite. No known nitrifier carries out both steps, although complete nitrification should be energetically advantageous. This functional separation has puzzled microbiologists for a century. Here we report on the discovery and cultivation of a completely nitrifying bacterium from the genus *Nitrospira*, a globally distributed group of nitrite oxidizers. The genome of this chemolithoautotrophic organism encodes the pathways both for ammonia and nitrite oxidation, which are concomitantly activated during growth by ammonia oxidation to nitrate. Genes affiliated with the phylogenetically distinct ammonia monooxygenase and hydroxylamine dehydrogenase genes of *Nitrospira* are present in many environments and were retrieved on *Nitrospira*-contigs in new metagenomes from engineered systems. These findings fundamentally change our picture of nitrification and point to completely nitrifying *Nitrospira* as key components of nitrogen-cycling microbial communities.

2. 20%

The human gut microbiome provides us with functional features that we did not have to evolve ourselves and can be viewed as a structured microbial community that operates like a microbial organ within the human host. A minor but important part of this microbiome is the ability to colonise and thrive within the mucous layer that covers the colon epithelium. These mucosal microbes intimately interact with the intestinal tissue and seem to be important modulators of human health. Embedded in the host-secreted mucous matrix, they form a 'mucosal biofilm' with a distinct composition and functionality. In this review, we provide evidence that six specific (micro)environmental factors near the colon mucosa shape and determine mucosal biofilm formation and stability, that is, (1) mucous rigidity, (2) gradients of fluid shear, (3) radial oxygen gradients, (4) secretions of host defense molecules, (5) the presence of a rich but challenging nutrient platform and (6) the presence of niches at the colon epithelial surface. In addition, it appears that microbes actively participate in shaping their mucosal environment. Current insights into the interaction between mucosal microbes and their environment are rather limited, and many questions

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regarding the contribution of mucosal biofilm functionality and stability to human health remain to be answered. Yet, given the higher potency of mucosal microbes than their luminal counterparts to interact with the host, new insights can accelerate the development of novel disease-preventive or therapeutic strategies.

3. 20%

Numerous molecular mechanisms act in concert to enact changes in neuronal function in response to diverse inputs. Such synaptic plasticity is critical for learning, memory, and other cognitive processes and is often defective in neurological disease. Among the mechanisms required for synaptic plasticity, coordinated changes in gene expression are essential for the consolidation and maintenance of most lasting forms of memory. Indeed, multiple signaling cascades couple transcription factor activation to synaptic activity. An additional level of transcriptional regulation occurs in the form of chromatin modification, whereby the accessibility of specific regions of the genome to the transcription machinery can be modulated by local posttranslational modification of histone proteins. Acetylation is the best-studied histone modification, and in recent years, it has become clear that histone acetylation dynamics play important roles in various cognitive processes, as well as in multiple neurological disorders. Histone acetylation is tightly regulated by the opposing activities of lysine acetyltransferases (KATs) and histone lysine deacetylases (HDACs). The role of HDACs in brain function and dysfunction forms the focus of this review. Additional histone modifications also participate in cognitive processes and have been reviewed elsewhere.

4. 20%

Ever since its introduction to ecology, network theory has repeatedly reorganized our understanding of the laws and processes that drive ecological community dynamics. The architecture of ecological networks and its consequences for community stability have been intensively investigated in mutualistic interactions involving plants and their pollinating or seed-dispersing animal partners. These plant–animal interactions commonly exhibit a “nested” network architecture, in which specialists (that is, species with narrow partner ranges) mainly interact with subsets of the partners of generalists. Because nestedness is so prevalent in plant–animal mutualistic

networks, understanding its impact on plant community processes is the key to understanding how biotic environmental changes (for example, extinction of indigenous partners or introduction of alien partners) can alter plant community structure.

Theory predicts that a nested network architecture can promote plant species coexistence by offsetting among-plant competition, increasing persistence against random extinctions, and promoting facilitation. Moreover, a recent study argued that a nested architecture can enhance species coexistence in mutualistic networks by increasing structural stability, which is mathematically defined as the range of parameter values that realize both feasible and dynamically stable equilibria. Thus, knowledge of such a potential link between network nestedness and species coexistence is crucial to preventing further plant biodiversity loss and consequential degrading of terrestrial ecosystem services worldwide.

5. 20%

Mammoths arrived in Eurasia from Africa around 3 million years ago (Ma) and underwent remarkable adaptive evolution through species *Mammuthus meridionalis* and *M. trogontherii* to *M. primigenius* (the woolly mammoth), with changes in molar and skull structure adaptive to grazing in the increasingly open habitats of the Pleistocene. Although the pattern is well documented for Eurasia, our understanding of the origin and evolution of North American mammoths is much less clear. Our study focused on upper and lower last molars (M^3 and M_3), which show most clearly the lineage transformations. In Europe, the average number of enamel lamellae increases from 13 (*M. meridionalis*) to 19 (*M. trogontherii*) to 24 (*M. primigenius*), while hypsodonty (crown height) almost doubles between the first two species, which also show the most profound changes in skull morphology. The earliest mammoths in North America, and hence their likely time of arrival, date to ~ 1.5 to 1.3 Ma. The prevailing view is that early American mammoths were of "primitive" morphology, indicating a close relationship to *M. meridionalis*, the contemporary species in Europe. Early North American fossils have been referred either to that form or to the supposedly related *M. hayi* or *M. haroldcooki*. From here, an evolutionary sequence is posited, leading to the late Pleistocene Columbian mammoth *M. columbi*. The transformations would have paralleled those from *M. meridionalis* to *M. trogontherii* in Eurasia, and the species *M. imperator* is frequently cited as an "intermediate" stage. (結束)