[1] The most basic function of the cell cycle is to duplicate accurately the vast amount of DNA in the chromosomes and then segregate the copies precisely into two genetically identical daughter cells. These processes define the two major phases of the cell cycle. DNA duplication occurs during S phase (S for synthesis), which requires 10–12 hours and occupies about half of the cell-cycle time in a typical mammalian cell. After S phase, chromosome segregation and cell division occur in M phase (M for mitosis), which requires much less time (less than an hour in a mammalian cell). M phase involves a series of dramatic events that begin with nuclear division, or mitosis. Mitosis begins with chromosome condensation: the duplicated DNA strands, packaged into elongated chromosomes, condense into the much more compact chromosomes required for their segregation. The nuclear envelope then breaks down, and the replicated chromosomes, each consisting of a pair of sister chromatids, become attached to the microtubules of the mitotic spindle. As mitosis proceeds, the cell pauses briefly in a state called metaphase, when the chromosomes are aligned at the equator of the mitotic spindle, poised for segregation. The sudden separation of sister chromatids marks the beginning of anaphase, during which the chromosomes move to opposite poles of the spindle, where they decondense and reform intact nuclei. The cell is then pinched in two by cytoplasmic division, or cytokinesis, and cell division is complete.

[2] Crop improvement by genome editing involves the targeted alteration of genes to improve plant traits, such as stress tolerance, disease resistance or nutritional content. Techniques for the targeted modification of genomes have evolved from generating random mutations to precise base substitutions, followed by insertions, substitutions and deletions of small DNA fragments, and are finally starting to achieve precision manipulation of large DNA segments. Recent developments in base editing, prime editing and other CRISPR-associated systems have laid a solid technological foundation to enable plant basic research and precise molecular breeding. In this Review, we systematically outline the technological principles underlying precise and targeted genome-modification methods. We also review methods for the delivery of genome-editing reagents in plants and outline emerging crop-breeding strategies based on targeted genome modification. Finally, we consider potential future developments in precise genome-editing technologies, delivery methods and crop-breeding approaches, as well as regulatory policies for genome-editing products.

[3] Biogeography is the study of species distribution and diversity within an ecosystem and is at the core of how we understand ecosystem dynamics and interactions at the macroscale. In gut microbial communities, a historical reliance on bulk sequencing to probe community composition and dynamics has overlooked critical processes whereby microscale interactions affect systems-level microbiota function and the relationship with the host. In recent years, higher-resolution sequencing and novel single-cell level data have uncovered an incredible heterogeneity in microbial composition and have enabled a more nuanced spatial understanding of the gut microbiota. In an era when spatial transcriptomics and

single-cell imaging and analysis have become key tools in mammalian cell and tissue biology, many of these techniques are now being applied to the microbiota. This fresh approach to intestinal biogeography has given important insights that span temporal and spatial scales, from the discovery of mucus encapsulation of the microbiota to the quantification of bacterial species throughout the gut. In this Review, we highlight emerging knowledge surrounding gut biogeography enabled by the observation and quantification of heterogeneity across multiple scales.

[4] The central role of MRI in neuro-oncology is undisputed. The technique is used, both in clinical practice and in clinical trials, to diagnose and monitor disease activity, support treatment decision-making, guide the use of focused treatments and determine response to treatment. Despite recent substantial advances in imaging technology and image analysis techniques, clinical MRI is still primarily used for the qualitative subjective interpretation of macrostructural features, as opposed to quantitative analyses that take into consideration multiple pathophysiological features. However, the field of quantitative imaging and imaging biomarker development is maturing. The European Imaging Biomarkers Alliance (EIBALL) and Quantitative Imaging Biomarkers Alliance (QIBA) are setting standards for biomarker development, validation and implementation, as well as promoting the use of quantitative imaging and imaging biomarkers by demonstrating their clinical value. In parallel, advanced imaging techniques are reaching the clinical arena, providing quantitative, commonly physiological imaging parameters that are driving the discovery, validation and implementation of quantitative imaging and imaging biomarkers in the clinical routine. Additionally, computational analysis techniques are increasingly being used in the research setting to convert medical images into objective high-dimensional data and define radiomic signatures of disease states. Here, I review the definition and current state of MRI biomarkers in neuro-oncology, and discuss the clinical potential of quantitative image analysis techniques.

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