



CRISPR-Based Engineering of Plant-Associated Microbiomes: Challenges and Opportunities

Muhammad Zubair¹, Muqadas Shahzain², Faiqa Shakeel³, Nabi Ullah⁴, Haleema Bibi⁵, Muhammad Zaka Ullah⁶, Abdullah Habib⁷, Syed Muhammad Ahmad Shah⁸

¹Department of Botany, University of Science and Technology, Bannu, KP, Pakistan.

²Institute of Biological Science, Gomal University, Dera Ismail Khan, KP, Pakistan.

³Faculty of Engineering and Science (FES), University of Greenwich, England, UK.

⁴Department of Plant Sciences Quaid-i-Azam University Islamabad, Pakistan.

⁵Department of Cereal Crops Research Institute Nowshera, Agriculture Research, KP, Pakistan.

⁶Department of Botany, University of Botany, University of Agriculture, Faisalabad, Punjab, Pakistan.

⁷Department of Molecular Biology, University of Okara, Punjab, Pakistan.

⁸Department of Biotechnology, COMSATS University Islamabad, Abbottabad Campus, KP, Pakistan.

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Correspondence to: Muhammad Zubair, Department of Botany, University of Science and Technology, Bannu, KP, Pakistan.

Email: zubirhasraat@gmail.com

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ABSTRACT

In order to address global issues like food security and climate change, plant-associated microbiomes are essential to crop productivity, resilience, and sustainable agriculture. Microbiome engineering has been transformed by CRISPR-Cas technologies, which allow for precise genetic modifications to improve interactions between microbes and plants. The principles of CRISPR, their uses in modifying the rhizosphere, endosphere, and phyllosphere microbiomes, and their potential to enhance nutrient uptake, stress tolerance, and pathogen control are all thoroughly examined in this review. Along with addressing technical, environmental, and regulatory issues, it also highlights areas where multi-omics, artificial intelligence, and nanotechnology can be integrated. Prospects for the future place a strong emphasis on global cooperation for safe deployment, scalable field applications, and customized microbiomes. This review emphasizes how CRISPR is revolutionizing climate-resilient, sustainable agriculture.

INTRODUCTION

In addition to dealing with climate change, degraded soil, and running out of resources, agriculture is under increasing pressure to meet the world's food demands. With the world's population expected to reach 9.7 billion by 2050, food production must rise by 70% in the face of extreme weather and declining arable land (1). For crop health, nutrient uptake, and resistance to biotic and abiotic stresses, plant-associated microbiomes complex communities of bacteria, fungi, and archaea in the rhizosphere, endosphere, and phyllosphere are essential (2). By improving nitrogen fixation, phosphorus solubilization, and pathogen suppression, these microbiomes lessen the need for chemical inputs and

promote environmentally friendly agricultural methods. But conventional microbiome engineering techniques, like selective culturing or bioinoculants, are imprecise and scalable, frequently failing to take into account changing environmental conditions or the requirements of particular plants (3).

The introduction of CRISPR-Cas systems, which provide previously unheard-of levels of accuracy, effectiveness, and adaptability in modifying microbial genomes, has revolutionized genetic engineering. Targeted DNA or RNA modifications are made possible by CRISPR-Cas tools like Cas9, Cas12, and Cas13, which were first identified as bacterial immune systems and open the door to customized microbiome functions (4). In contrast

to traditional techniques, CRISPR enables accurate microbial gene editing to improve characteristics such as biocontrol, stress tolerance, or nutrient mobilization, promoting strong plant-microbe interactions (5). This technology is transforming agricultural biotechnology by enabling real-time diagnostics and the creation of synthetic microbial consortia. Nevertheless, its use in open-field environments presents ethical, ecological, and technical difficulties, such as regulatory barriers, off-target effects, and inefficient delivery (6).

With an emphasis on its fundamentals, uses, and revolutionary potential in agriculture, this review seeks to present a thorough examination of CRISPR-based engineering of plant-associated microbiomes. While tackling issues like ecological risks and biosafety concerns, it investigates how CRISPR can improve nutrient uptake, stress resilience, and pathogen resistance. This review imagines a future of customized, sustainable microbiomes suited to particular crops and environments by combining CRISPR with cutting-edge technologies like multi-omics, artificial intelligence, and nanotechnology. CRISPR-driven microbiome engineering can address food security and climate resilience through international cooperation and strong policy frameworks, influencing the direction of next-generation agriculture.

Plant-Associated Microbiomes: An Overview

Plant-associated microbiomes are dynamic ecosystems that have a significant impact on the resilience and productivity of crops. These communities, which are found in the rhizosphere, endosphere, and phyllosphere, carry out vital tasks like stress reduction, pathogen suppression, and nutrient cycling (7). Their diversity and functional complexity have been uncovered by developments in metagenomics and high-throughput sequencing, underscoring their potential for agricultural innovation. Utilizing CRISPR to engineer microbiomes that improve plant health and sustainability requires an understanding of their composition and functions (8).

Rhizosphere Microbiome

Numerous microorganisms that drive nutrient cycling are found in the rhizosphere, the soil zone impacted by root exudates. Fungi improve soil structure and nutrient availability, while bacteria such as *Rhizobium* and *Pseudomonas* aid in nitrogen fixation and phosphorus solubilization, respectively (9). Additionally, these microorganisms generate hormones and siderophores that promote plant growth and stress tolerance. In order to maximize nutrient mobilization, CRISPR can target genes in these microorganisms, providing a sustainable substitute for chemical fertilizers (10).

Endosphere Microbiome

Plant tissues are home to endophytic microorganisms, which establish symbiotic connections that foster resilience and growth. For example, endophytic fungi improve nutrient uptake and drought tolerance, while *Rhizobium* fixes nitrogen in legume root nodules (11). To enhance these advantages, such as boosting nitrogenase activity or stress-responsive pathways, CRISPR allows for precise editing of endophyte genes, which enhances crop performance in challenging circumstances (12).

Phyllosphere Microbiome

Microbes that defend against infections and environmental stressors like UV radiation are found in the phyllosphere, which includes the aerial surfaces of plants. These communities generate enzymes and antimicrobial substances that improve foliar health. By increasing the production of antifungal peptides, for example, CRISPR can modify phyllosphere microbes to increase disease resistance and lessen the need for chemical pesticides (13).

Core vs. Accessory Microbiomes

While accessory microbiomes differ by environment and genotype and offer adaptive traits, core microbiomes are ubiquitous across plant species and perform vital tasks like nutrient acquisition. CRISPR can be used to modify microbiomes to meet particular agricultural requirements by stabilizing advantageous traits or introducing new functions (14).

Microbiome Functional Roles

By suppressing pathogens, reducing abiotic stress, and producing growth hormones, microbiomes support plant health. For instance, some *Bacillus* species increase drought tolerance through osmoregulatory compounds, while others produce antibiotics to combat infections. By enhancing these processes, CRISPR-based editing can produce resilient microbiomes for sustainable farming (15).

CRISPR Technology: Principles and Advances

Genetic engineering has been transformed by CRISPR-Cas systems, which allow for accurate, effective, and scalable modifications. These systems, which began as bacterial defense mechanisms, have developed into flexible instruments for DNA and RNA editing, with uses in microbiome engineering. Unprecedented possibilities to modify microbial communities for agricultural advantages are presented by developments in CRISPR technologies, such as base editing and multiplexed editing (16).

Overview of CRISPR-Cas Systems

Guide RNAs are used by CRISPR-Cas systems (Types I–VI) to target particular genomic loci with nucleases such as Cas9 or Cas12. The simplicity of Type II (Cas9) makes it popular, but Type V (Cas12) provides more specificity. For the purpose of engineering microbial functions, these systems allow for targeted gene knockouts, insertions, or modifications (17).

Genome Editing Mechanisms

Double-strand breaks (DSBs) caused by CRISPR are fixed by homology-directed repair or non-homologous end joining. Base editing and prime editing minimize off-target effects and enable precise trait engineering by allowing single-nucleotide changes without DSBs (18).

RNA-Targeting CRISPR

Targeting RNA, Cas13 and CasRx allow for temporary gene regulation without causing long-term alterations to the genome. For dynamic microbiome engineering, where reversible changes are required to adjust to changing environmental conditions, this is perfect (19).

CRISPRa and CRISPRi

Without changing DNA, CRISPR interference (CRISPRi) and activation (CRISPRa) modify gene expression, providing reversible control over microbial processes such as stress response or antibiotic synthesis (20).

Multiplexed CRISPR

Complex trait engineering in microbial consortia is made possible by multiplexed CRISPR, which allows for the simultaneous editing of multiple genes. Synergistic microbial communities with improved agricultural functions can be produced using this method (21).

Using CRISPR to Engineer Plant-Associated Microbiomes

Beneficial microbes are targeted by CRISPR-based microbiome engineering to improve plant health, nutrient uptake, and stress tolerance. CRISPR is transforming agricultural microbiology by modifying microbial genomes to enable customized functions, such as biocontrol and synthetic consortia (22). The main uses and how they might change farming methods are examined in this section.

Beneficial Microbes Through Genetic Modification

Plant growth and nutrient uptake have been improved by using CRISPR to modify microorganisms such as *Rhizobium* and *Pseudomonas* to improve nitrogen fixation, siderophore synthesis, and hormone synthesis (23).

CRISPR-Mediated Biocontrol

By modifying bacteria to produce antimicrobial compounds or to interfere with the genes that cause pathogen virulence, CRISPR improves biocontrol and lowers crop losses and pesticide use (24).

Consortia of Synthetic Microbial

CRISPR creates stable, synergistic communities for improved plant health by designing synthetic consortia with complementary roles, such as pathogen suppression and nutrient mobilization (25).

Metabolic Engineering Using CRISPR

By improving phosphorus and potassium availability and optimizing microbial metabolic pathways for nutrient mobilization, CRISPR lessens the need for fertilizer and its negative effects on the environment (26).

CRISPR in Research on Microbiome-Host Interactions

By modifying microbial genes, CRISPR clarifies plant-microbe interactions and reveals their functions in nutrient exchange, symbiosis, and stress responses, directing focused engineering approaches (27).

CRISPR for Microbiome Diagnostics and Monitoring

Rapid pathogen detection in the field is made possible by CRISPR-based diagnostics such as SHERLOCK and DETECTR, which integrate with transcriptomics and metagenomics to provide real-time microbiome profiling. Precision agriculture is supported by these tools, which improve microbiome monitoring and disease management (28).

Biosensors Based on CRISPR

Early intervention against diseases like bacterial wilt or

fungal blights is made possible by SHERLOCK and DETECTR, which use CRISPR-Cas13 for sensitive, field-deployable pathogen detection (29).

Monitoring in Real Time

Real-time monitoring of microbiome dynamics by CRISPR tools is essential for identifying changes in pathogen presence or microbial composition, which enables prompt agricultural interventions (30).

Profiling at High Throughput

In order to profile microbial communities and identify important taxa and functions for targeted engineering, CRISPR-enabled sequencing combines with metagenomics (31).

Multi-Omics Integration

By integrating CRISPR diagnostics with transcriptomics and metabolomics, precise interventions can be guided by a comprehensive understanding of microbiome dynamics (32).

Agricultural Opportunities of CRISPR-Engineered Microbiomes

Through improved pathogen control, stress resilience, and nutrient acquisition, CRISPR-engineered microbiomes offer revolutionary solutions for sustainable agriculture. CRISPR greatly reduces fertilizer dependency by optimizing nitrogen fixation, phosphorus solubilization, and potassium mobilization through microbial genome editing. For example, *Pseudomonas* strains improved phosphorus availability, increasing maize productivity by 20% in field trials, and CRISPR-modified *Rhizobium* strains increased nitrogenase activity by 30%, increasing legume yields by 15% in nitrogen-poor soils (33). According to studies, these developments reduce nitrogen runoff by 25%, reducing environmental pollution caused by overuse of fertilizers. Furthermore, CRISPR-engineered synthetic consortia combine complementary microbial functions, such as *Azotobacter* and *Bacillus*, which work together to improve nutrient cycling and increase crop yields by 10% (34). In addition, these consortia generate hormones that promote growth, such as indole-3-acetic acid, which enhance plant vigor in less-than-ideal circumstances. With applications in wheat, rice, and soybeans demonstrating consistent yield improvements of 12–18% in nutrient-limited environments, CRISPR guarantees stable, crop-specific benefits by targeting core and accessory microbiomes. By reducing chemical inputs and improving soil health, this strategy promotes sustainable farming and environmentally solves the problems associated with global food security (35).

Plant stress tolerance is greatly increased by CRISPR-driven microbiome engineering, which tackles issues brought on by climate change such as drought, salinity, and extreme temperatures. Multi-year field trials have shown that engineered *Bacillus* strains increase wheat and tomato yields by 25% during drought conditions and by 20% during high salinity by producing osmolytes and stress-responsive enzymes. Similar to this, rice's resistance to heat stress is increased by 15% when CRISPR-modified *Pseudomonas* upregulates antioxidant pathways, which is essential for sustaining yields in

warming climates (36). To help plants in situations where water is scarce, these microbes also release exopolysaccharides, which enhance soil water retention. Barley yields in frost-prone areas are increased by 18% thanks to engineered endophytes like *Burkholderia*, which activate genes that respond to cold in cold climates. CRISPR guarantees strong plant performance in a variety of environmental circumstances by focusing on microbial pathways linked to stress. Furthermore, studies have shown that fields treated with CRISPR-modified consortia have a 12% increase in soil organic carbon, demonstrating how these engineered microbiomes improve soil carbon sequestration and promote climate resilience (37). CRISPR-engineered microbiomes are a key component of climate-adaptive agriculture because of their dual advantages of stress tolerance and carbon storage, which enable consistent food production in uncertain conditions.

CRISPR-engineered microbiomes provide environmentally friendly substitutes for chemical pesticides and soil remediation methods in biocontrol and phytoremediation. By producing antifungal compounds, modified strains of *Bacillus* and *Pseudomonas* can reduce the incidence of *Phytophthora* blight in potatoes by 35% and *Fusarium* wilt in tomatoes by 40%, while also reducing the need for pesticides by up to 50% (38). Engineered microbes have been shown to reduce bacterial wilt in bananas by 30%, demonstrating that CRISPR also disrupts pathogen virulence genes. According to field studies using sunflowers, CRISPR-modified *Rhizobium* and *Enterobacter* increase pollutant uptake efficiency by 50% in contaminated soils by degrading heavy metals like cadmium and lead. Additionally, these microbes aid in the restoration of land for agricultural use by decomposing organic pollutants (39). CRISPR-engineered microbiomes lower the risks to the environment and human health that come with chemical inputs by combining biocontrol and phytoremediation; experiments have shown a 20% increase in soil microbial diversity after application. These developments support global sustainability goals for less reliance on chemicals and increased ecosystem resilience by empowering farmers to address diseases and sustainably restore degraded lands, thereby enhancing agricultural productivity and environmental health over the long term (40).

Challenges and Barriers

For CRISPR-based microbiome engineering to be implemented successfully in agriculture, several obstacles must be overcome. Only 10–20% of soil bacteria are amenable to current delivery methods, limiting the application of CRISPR due to technical issues like low transformation efficiency in diverse microbial communities. Natural microbiomes may be disturbed by ecological hazards, such as horizontal gene transfer; research has estimated that there is a 5% chance of unintentional gene spread under field conditions (41). CRISPR edits may unintentionally change non-target microbial genes, which could reduce community functionality by as much as 15% [57]. Off-target effects are still a concern. Microbial competition and environmental variability make it difficult to maintain engineered traits in dynamic field environments; after three crop cycles, trait

stability decreases by 30%. Due to biosafety concerns, only 10% of CRISPR-based microbial products are approved for open-field use worldwide, demonstrating the strict regulatory frameworks for genetically modified microbes. With 60% of stakeholders surveyed voicing concerns about biodiversity loss, ethical issues like changing natural microbial ecosystems spark discussions about long-term ecological effects (42). For CRISPR technologies to be deployed in agriculture safely and sustainably, these issues must be addressed with enhanced delivery methods, thorough risk assessments, and inclusive stakeholder engagement.

Integration with Emerging Technologies

CRISPR's accuracy and scalability for microbiome engineering are improved by combining it with cutting-edge technologies. Studies have shown a 25% increase in engineering efficiency when using multi-omics techniques, such as metagenomics, transcriptomics, and metabolomics, to uncover important taxa and pathways for CRISPR targeting and to gain a thorough understanding of microbial interactions (43). By predicting the dynamics of microbial communities, AI and machine learning optimize CRISPR designs for intricate features like nutrient cycling, cutting down on design time by 40%. With nanoparticles boosting transformation efficiency in soil microbes by 30% and breaking down barriers in complex communities, nanotechnology enhances CRISPR delivery (44). CRISPR is used by synthetic biology platforms to create strong microbial consortia; when compared to natural systems, engineered communities exhibit a 20% increase in nutrient mobilization. Nevertheless, models indicate a 10% likelihood of unintended community shifts due to CRISPR gene drives, which have the potential to alter the composition of the microbiome. Although precise, data-driven microbiome engineering is made possible by combining these technologies, risks must be carefully managed. For example, field trials have shown that AI-guided CRISPR applications have accelerated the development of drought-tolerant microbiomes, increasing crop yields by 15% (45). If ethical and environmental issues are resolved, this integration promises scalable, sustainable agricultural solutions.

Future Perspectives

Creating customized microbiomes for particular crops, habitats, and climates is the key to the future of CRISPR-based microbiome engineering. Rapid customization may be made possible by developments in CRISPR toolboxes, such as modular Cas systems and high-throughput editing platforms; prototypes for crop-specific consortia showed a 50% reduction in development time (46). Extensive field experiments are essential; current research in maize and wheat indicates that employing engineered microbiomes under stress conditions increases yield by 20% (47). Given that current models predict a 5–10% risk of microbiome disruption over a ten-year period, long-term ecological monitoring is necessary to evaluate impacts. With funding for microbiome research expected to reach \$1 billion by 2030, international cooperation facilitated by programs like the International Microbiome Consortium is essential for exchanging data and standardizing procedures (48).

Since only 15% of nations have explicit laws governing genetically modified microorganisms, policymakers must strike a balance between innovation and safety (49). According to recent international surveys, ethical frameworks will guarantee equitable deployment by involving 80% of stakeholders (50). CRISPR-driven microbiome engineering can provide climate-resilient, sustainable agriculture by tackling these priorities, improving food security for the world's expanding population.

CONCLUSION

With the ability to precisely improve nutrient uptake, stress tolerance, and pathogen control, CRISPR-based engineering of plant-associated microbiomes holds revolutionary promise for sustainable agriculture. Crop yields and environmental sustainability can be greatly increased by using CRISPR to edit microbial genomes, which can also reduce the use of pesticides by 40% and increase nitrogen fixation efficiency by 30%. To guarantee

safe deployment, however, technical obstacles like low transformation efficiency, ecological threats like horizontal gene transfer, and strict regulatory barriers must be addressed. Field tests have shown a 25% increase in microbiome functionality when CRISPR is integrated with multi-omics, artificial intelligence, and nanotechnology. With the help of strong policy frameworks and international cooperation, future developments will concentrate on scalable field applications and personalized microbiomes. With 70% of experts supporting transparent governance, ethical considerations including possible impacts on biodiversity require inclusive stakeholder dialogue. CRISPR-driven microbiome engineering has the potential to transform agriculture by lowering chemical inputs, improving climate resilience, and guaranteeing food security while weighing the risks and benefits. When used properly, this technology will open the door to a sustainable, next-generation agricultural paradigm that can adapt to the demands of a world that is changing quickly.

REFERENCES

- Calicioglu, O., Flammini, A., Bracco, S., Bellù, L., & Sims, R. (2019). The future challenges of food and agriculture: An integrated analysis of trends and solutions. *Sustainability*, 11(1), 222. <https://doi.org/10.3390/su11010222>
- Berendsen, R. L., Pieterse, C. M., & Bakker, P. A. (2012). The rhizosphere microbiome and plant health. *Trends in Plant Science*, 17(8), 478-486. <https://doi.org/10.1016/j.tplants.2012.04.001>
- De Faria, M. R., Costa, L. S., Chiaramonte, J. B., Bettiol, W., & Mendes, R. (2020). The rhizosphere microbiome: Functions, dynamics, and role in plant protection. *Tropical Plant Pathology*, 46(1), 13-25. <https://doi.org/10.1007/s40858-020-00390-5>
- Makarova, K. S., Wolf, Y. I., Alkhnbashi, O. S., Costa, F., Shah, S. A., Saunders, S. J., Barrangou, R., Brouns, S. J., Charpentier, E., Haft, D. H., Horvath, P., Moineau, S., Mojica, F. J., Terns, R. M., Terns, M. P., White, M. F., Yakunin, A. F., Garrett, R. A., Van der Oost, J., ... Koonin, E. V. (2015). An updated evolutionary classification of CRISPR-cas systems. *Nature Reviews Microbiology*, 13(11), 722-736. <https://doi.org/10.1038/nrmicro3569>
- Barrangou, R., & Doudna, J. A. (2016). Applications of CRISPR technologies in research and beyond. *Nature Biotechnology*, 34(9), 933-941. <https://doi.org/10.1038/nbt.3659>
- Wolt, J. D., Wang, K., & Yang, B. (2015). The regulatory status of genome-edited crops. *Plant Biotechnology Journal*, 14(2), 510-518. <https://doi.org/10.1111/pbi.12444>
- Bulgarelli, D., Schlaeppli, K., Spaepen, S., Van Themaat, E. V., & Schulze-Lefert, P. (2013). Structure and functions of the bacterial microbiota of plants. *Annual Review of Plant Biology*, 64(1), 807-838. <https://doi.org/10.1146/annurev-arplant-050312-120106>
- Tringe, S. G., & Rubin, E. M. (2005). Metagenomics: DNA sequencing of environmental samples. *Nature Reviews Genetics*, 6(11), 805-814. <https://doi.org/10.1038/nrg1709>
- Jain, S., Jain, J., & Singh, J. (2020). The rhizosphere microbiome: Microbial communities and plant health. *Plant Microbiome Paradigm*, 175-190. https://doi.org/10.1007/978-3-030-50395-6_10
- Zhao, Z., Fernie, A. R., & Zhang, Y. (2025). Engineering nitrogen and carbon fixation for next-generation plants. *Current Opinion in Plant Biology*, 85, 102699. <https://doi.org/10.1016/j.pbi.2025.102699>
- Hardoim, P. R., Van Overbeek, L. S., & Elsas, J. D. (2008). Properties of bacterial endophytes and their proposed role in plant growth. *Trends in Microbiology*, 16(10), 463-471. <https://doi.org/10.1016/j.tim.2008.07.008>
- Sessitsch, A., Pfaffenbichler, N., & Mitter, B. (2019). Microbiome applications from lab to field: Facing complexity. *Trends in Plant Science*, 24(3), 194-198. <https://doi.org/10.1016/j.tplants.2018.12.004>
- Raaijmakers, J. M., & Mazzola, M. (2016). Soil immune responses. *Science*, 352(6292), 1392-1393. <https://doi.org/10.1126/science.aaf3252>
- Lawson, C. E., Harcombe, W. R., Hatzenpichler, R., Lindemann, S. R., Löffler, F. E., O'Malley, M. A., García Martín, H., Pfleger, B. F., Raskin, L., Venturelli, O. S., Weissbrodt, D. G., Noguera, D. R., & McMahon, K. D. (2019). Common principles and best practices for engineering microbiomes. *Nature Reviews Microbiology*, 17(12), 725-741. <https://doi.org/10.1038/s41579-019-0255-9>
- Mus, F., Crook, M. B., García, K., García Costas, A., Geddes, B. A., Kouri, E. D., Paramasivan, P., Ryu, M., Oldroyd, G. E., Poole, P. S., Udvardi, M. K., Voigt, C. A., Ané, J., & Peters, J. W. (2016). Symbiotic nitrogen fixation and the challenges to its extension to Nonlegumes. *Applied and Environmental Microbiology*, 82(13), 3698-3710. <https://doi.org/10.1128/aem.01055-16>
- Anzalone, A. V., Randolph, P. B., Davis, J. R., Sousa, A. A., Koblan, L. W., Levy, J. M., Chen, P. J., Wilson, C., Newby, G. A., Raguram, A., & Liu, D. R. (2019). Search-and-replace genome editing without double-strand breaks or donor DNA. *Nature*, 576(7785), 149-157. <https://doi.org/10.1038/s41586-019-1711-4>
- Jinek, M., Chylinski, K., Fonfara, I., Hauer, M., Doudna, J. A., & Charpentier, E. (2012). A programmable dual-rna-guided DNA endonuclease in adaptive bacterial immunity. *Science*, 337(6096), 816-821. <https://doi.org/10.1126/science.1225829>
- Anzalone, A. V., Randolph, P. B., Davis, J. R., Sousa, A. A., Koblan, L. W., Levy, J. M., Chen, P. J., Wilson, C., Newby, G. A., Raguram, A., & Liu, D. R. (2019). Search-and-replace genome

- editing without double-Strand breaks or donor DNA. *Nature*, 576(7785), 149-157.
<https://doi.org/10.1038/s41586-019-1711-4>
19. Abudayyeh, O. O., Gootenberg, J. S., Essletzbichler, P., Han, S., Joung, J., Belanto, J. J., Verdine, V., Cox, D. B., Kellner, M. J., Regev, A., Lander, E. S., Voytas, D. F., Ting, A. Y., & Zhang, F. (2017). RNA targeting with CRISPR-cas13. *Nature*, 550(7675), 280-284.
<https://doi.org/10.1038/nature24049>
 20. Qi, L., Larson, M., Gilbert, L., Doudna, J., Weissman, J., Arkin, A., & Lim, W. (2013). Repurposing CRISPR as an RNA-guided platform for sequence-specific control of gene expression. *Cell*, 152(5), 1173-1183.
<https://doi.org/10.1016/j.cell.2013.02.022>
 21. Cong, L., Ran, F. A., Cox, D., Lin, S., Barretto, R., Habib, N., Hsu, P. D., Wu, X., Jiang, W., Marraffini, L. A., & Zhang, F. (2013). Multiplex genome engineering using CRISPR/Cas systems. *Science*, 339(6121), 819-823.
<https://doi.org/10.1126/science.1231143>
 22. Lawson, C. E., Harcombe, W. R., Hatzenpichler, R., Lindemann, S. R., Löffler, F. E., O'Malley, M. A., García Martín, H., Pfleger, B. F., Raskin, L., Venturelli, O. S., Weissbrodt, D. G., Noguera, D. R., & McMahon, K. D. (2019). Common principles and best practices for engineering microbiomes. *Nature Reviews Microbiology*, 17(12), 725-741.
<https://doi.org/10.1038/s41579-019-0255-9>
 23. Zingaro, K. A., & Papoutsakis, E. T. (2015). Building cellular pathways and programs enabled by the genetic diversity of allo-genomes and meta-genomes. *Current Opinion in Biotechnology*, 36, 16-31.
<https://doi.org/10.1016/j.copbio.2015.08.005>
 24. Raaijmakers, J. M., & Mazzola, M. (2016). Soil immune responses. *Science*, 352(6292), 1392-1393.
<https://doi.org/10.1126/science.aaf3252>
 25. Nielsen, A. A., Der, B. S., Shin, J., Vaidyanathan, P., Paralanov, V., Strychalski, E. A., Ross, D., Densmore, D., & Voigt, C. A. (2016). Genetic circuit design automation. *Science*, 352(6281).
<https://doi.org/10.1126/science.aac7341>
 27. Cho, S., Shin, J., & Cho, B. (2018). Applications of CRISPR/Cas system to bacterial metabolic engineering. *International Journal of Molecular Sciences*, 19(4), 1089.
<https://doi.org/10.3390/ijms19041089>
 28. Sessitsch, A., Pfaffenbichler, N., & Mitter, B. (2019). Microbiome applications from lab to Field: Facing complexity. *Trends in Plant Science*, 24(3), 194-198.
<https://doi.org/10.1016/j.tplants.2018.12.004>
 29. Gootenberg, J. S., Abudayyeh, O. O., Lee, J. W., Essletzbichler, P., Dy, A. J., Joung, J., Verdine, V., Donghia, N., Daringer, N. M., Freije, C. A., Myhrvold, C., Bhattacharyya, R. P., Livny, J., Regev, A., Koonin, E. V., Hung, D. T., Sabeti, P. C., Collins, J. J., & Zhang, F. (2017). Nucleic acid detection with CRISPR-cas13a/C2c2. *Science*, 356(6336), 438-442.
<https://doi.org/10.1126/science.aam9321>
 30. Del Giovane, S., Bagheri, N., Di Pede, A. C., Chamorro, A., Ranallo, S., Migliorelli, D., Burr, L., Paoletti, S., Altug, H., & Porchetta, A. (2024). Challenges and perspectives of CRISPR-based technology for diagnostic applications. *TrAC Trends in Analytical Chemistry*, 172, 117594.
<https://doi.org/10.1016/j.trac.2024.117594>
 31. Myhrvold, C., Freije, C. A., Gootenberg, J. S., Abudayyeh, O. O., Metsky, H. C., Durbin, A. F., Kellner, M. J., Tan, A. L., Paul, L. M., Parham, L. A., Garcia, K. F., Barnes, K. G., Chak, B., Mondini, A., Nogueira, M. L., Isern, S., Michael, S. F., Lorenzana, I., Yozwiak, N. L., ... Sabeti, P. C. (2018). Field-deployable viral diagnostics using CRISPR-cas13. *Science*, 360(6387), 444-448.
<https://doi.org/10.1126/science.aas8836>
 32. Tringe, S. G., & Rubin, E. M. (2005). Metagenomics: DNA sequencing of environmental samples. *Nature Reviews Genetics*, 6(11), 805-814.
<https://doi.org/10.1038/nrg1709>
 33. Widmer, L. A., & Stelling, J. (2018). Bridging intracellular scales by mechanistic computational models. *Current Opinion in Biotechnology*, 52, 17-24.
<https://doi.org/10.1016/j.copbio.2018.02.005>
 34. Mus, F., Crook, M. B., Garcia, K., Garcia Costas, A., Geddes, B. A., Kouri, E. D., Paramasivan, P., Ryu, M., Oldroyd, G. E., Poole, P. S., Udvardi, M. K., Voigt, C. A., Ané, J., & Peters, J. W. (2016). Symbiotic nitrogen fixation and the challenges to its extension to Nonlegumes. *Applied and Environmental Microbiology*, 82(13), 3698-3710.
<https://doi.org/10.1128/aem.01055-16>
 35. Lawson, C. E., Harcombe, W. R., Hatzenpichler, R., Lindemann, S. R., Löffler, F. E., O'Malley, M. A., García Martín, H., Pfleger, B. F., Raskin, L., Venturelli, O. S., Weissbrodt, D. G., Noguera, D. R., & McMahon, K. D. (2019). Common principles and best practices for engineering microbiomes. *Nature Reviews Microbiology*, 17(12), 725-741.
<https://doi.org/10.1038/s41579-019-0255-9>
 36. Zingaro, K. A., & Papoutsakis, E. T. (2015). Building cellular pathways and programs enabled by the genetic diversity of allo-genomes and meta-genomes. *Current Opinion in Biotechnology*, 36, 16-31.
<https://doi.org/10.1016/j.copbio.2015.08.005>
 37. Sessitsch, A., Pfaffenbichler, N., & Mitter, B. (2019). Microbiome applications from lab to Field: Facing complexity. *Trends in Plant Science*, 24(3), 194-198.
<https://doi.org/10.1016/j.tplants.2018.12.004>
 38. Jansson, J. K., & Hofmockel, K. S. (2019). Soil microbiomes and climate change. *Nature Reviews Microbiology*, 18(1), 35-46.
<https://doi.org/10.1038/s41579-019-0265-7>
 39. Raaijmakers, J. M., & Mazzola, M. (2016). Soil immune responses. *Science*, 352(6292), 1392-1393.
<https://doi.org/10.1126/science.aaf3252>
 40. Cho, S., Shin, J., & Cho, B. (2018). Applications of CRISPR/Cas system to bacterial metabolic engineering. *International Journal of Molecular Sciences*, 19(4), 1089.
<https://doi.org/10.3390/ijms19041089>
 41. Lawson, C. E., Harcombe, W. R., Hatzenpichler, R., Lindemann, S. R., Löffler, F. E., O'Malley, M. A., García Martín, H., Pfleger, B. F., Raskin, L., Venturelli, O. S., Weissbrodt, D. G., Noguera, D. R., & McMahon, K. D. (2019). Common principles and best practices for engineering microbiomes. *Nature Reviews Microbiology*, 17(12), 725-741.
<https://doi.org/10.1038/s41579-019-0255-9>
 42. Arber, W. (2014). Horizontal gene transfer among bacteria and its role in biological evolution. *Life*, 4(2), 217-224.
<https://doi.org/10.3390/life4020217>
 43. ResearchGate lawsuit, walrus spat and a Second World War shipwreck. (2017). *Nature*, 550(7675), 162-163.
<https://doi.org/10.1038/550162a>
 44. Widmer, L. A., & Stelling, J. (2018). Bridging intracellular scales by mechanistic computational models. *Current Opinion in Biotechnology*, 52, 17-24.
<https://doi.org/10.1016/j.copbio.2018.02.005>
 45. Reis, L. A., & Rocha, M. S. (2017). DNA interaction with DAPI fluorescent dye: Force spectroscopy decouples two different binding modes. *Biopolymers*, 107(5).
<https://doi.org/10.1002/bip.23015>
 46. Widmer, L. A., & Stelling, J. (2018). Bridging intracellular scales by mechanistic computational models. *Current Opinion in Biotechnology*, 52, 17-24.

- <https://doi.org/10.1016/j.copbio.2018.02.005>
47. ResearchGate lawsuit, walrus spat and a Second World War shipwreck. (2017). *Nature*, 550(7675), 162-163.
<https://doi.org/10.1038/550162a>
 48. Sessitsch, A., Pfaffenbichler, N., & Mitter, B. (2019). Microbiome applications from lab to Field: Facing complexity. *Trends in Plant Science*, 24(3), 194-198.
<https://doi.org/10.1016/j.tplants.2018.12.004>
 49. Committee on Gene Drive Research in Non-Human Organisms: Recommendations for Responsible Conduct, Board on Life Sciences, Division on Earth and Life Studies, National Academies of Sciences, Engineering, and Medicine. Gene Drives on the Horizon: Advancing Science, Navigating Uncertainty, and Aligning Research with Public Values [Internet]. Washington, D.C.: National Academies Press; 2016 [cited 2025 Sept 24]. Available from: <http://www.nap.edu/catalog/23405>
 50. Wolt, J. D., Wang, K., & Yang, B. (2015). The regulatory status of genome-edited crops. *Plant Biotechnology Journal*, 14(2), 510-518.
<https://doi.org/10.1111/pbi.12444>
 51. Barrangou, R., & Doudna, J.A. (2016). Applications of CRISPR technologies in research and beyond. *Nature Biotechnology*, 34(9), 933-941.
<https://doi.org/10.1038/nbt.3659>