

same salt-tolerant and salt-sensitive millet materials. Research on wild soybean under salt stress has already provided a useful example. Researchers found that salt stress induced roots to secrete xanthine, which then recruited beneficial *Pseudomonas* species and improved host salt tolerance. Such studies indicate that only by placing “root exudates-microorganisms-host tolerance” within the same experimental system can the active recruitment mechanism of plants truly be explained. For millet, future work should further identify which organic acids, phenolic acids, amino acids, or sugars are associated with the enrichment of salt-tolerant rhizosphere microbial communities, and verify whether these metabolites can consistently induce beneficial microbial colonization.

### **7.3 Microbiome-assisted breeding strategies**

Microbiome-assisted breeding should not be considered an additional technique outside traditional salt-tolerance breeding. Instead, it should become an important part of improving millet adaptation to saline-alkali soils. The basic concept is that host genotype not only determines root structure, ion transport, and antioxidant capacity, but also affects root exudate composition and rhizosphere microbial assembly. Therefore, two millet materials with similar phenotypes may show completely different field stability under continuous saline-alkali cultivation because of differences in their ability to recruit beneficial microorganisms.

In recent years, plant microbiome breeding studies have proposed that plant genetic backgrounds should be matched with compatible microbial inoculants, rather than treating microbial products as universal inputs independent of crop genotype. Future breeding should simultaneously consider plant genetics, microbial functions, and environmental adaptability, and enhance stress resistance through matching host genotypes with microbial inoculants (Shi et al., 2026). This idea is especially suitable for millet because it is often cultivated on marginal lands affected by drought, nutrient deficiency, and salinity, where environmental heterogeneity is high and simple selection for high-yield materials cannot guarantee stable field performance.

Breeding indicators with greater practical value for millet should expand from yield alone to comprehensive adaptability traits, including stable  $K^+/Na^+$  selectivity, root recovery ability, biomass regeneration after salt stress, root exudate plasticity, enrichment capacity of beneficial rhizosphere microbes, and stability of microbial community networks. The rhizosphere microbiome is regulated by both environment and host genotype. Using the plant's natural ability to recruit beneficial microorganisms is becoming an important direction for precision microbial engineering and stress-resistant agriculture in the future (Shen et al., 2024). Therefore, salt-alkali breeding in millet should not only select materials that are “salt tolerant themselves,” but also materials that can “stably establish beneficial rhizosphere systems.”

### **7.4 Synthetic microbial communities and biofertilizers**

In future millet production on saline-alkali land, microbial intervention technologies will likely shift from single-strain inoculation to synthetic microbial communities (SynComs). Although single strains are easier to screen and produce, they often face weak colonization ability, competition from native microorganisms, and unstable performance in the field. In contrast, synthetic communities can be designed according to functional complementarity, allowing different members to perform functions such as phosphate solubilization, nitrogen fixation, IAA production, extracellular polysaccharide secretion, antioxidant induction, and ion homeostasis regulation. In this way, they can provide more stable growth-promoting and stress-resistant effects.

SynComs are not only modular tools for studying plant-microbe interactions, but can also be used to promote plant growth and improve stress adaptation. Their construction strategies include bottom-up screening of functional strains and top-down simplification and reconstruction of native microbial communities (Xu et al., 2025). This provides a clear path for millet cultivation on saline-alkali land: first isolate locally adapted strains from the rhizosphere of millet grown long-term in saline soils, then construct functional microbial consortia based on complementary traits, and finally test their compatibility with different millet genotypes.

However, commercialization of synthetic microbial communities still faces major challenges. Plant microbiome research requires more unified standards for community construction, causal verification, data reporting, and field