

dryland farming, functional foods, feed resources, and farmer income growth. In the future, if coordinated development can be achieved among breeding salt-tolerant varieties, saline-land cultivation systems, forage utilization, functional food development, and regional brand building, proso millet may become not only an alternative crop for marginal lands, but also a strategic minor cereal for improving agricultural system resilience under climate change.

## 7 Current Challenges, Future Perspectives, and Conclusions

### 7.1 Limitations in understanding rhizosphere microbial networks

In recent years, research on salt-alkali stress in proso millet (*Panicum miliaceum* L.) has gradually expanded from simple physiological measurements to studies of the rhizosphere microbiome. However, this field is still transitioning from descriptive studies to mechanism-based research. Salt-tolerant millet materials can alter rhizosphere bacterial and fungal communities under salt stress and enrich microbial groups related to nutrient cycling, salt buffering, and organic matter transformation. Nevertheless, there is still limited understanding of how these microorganisms form stable networks, how they influence the host through metabolic interactions, and whether different microbial functions can replace one another.

One major difficulty in rhizosphere microbial network research is that community behavior is not equal to the behavior of a single strain. Salt stress can induce plants to recruit specific rhizosphere bacteria, but long-term salt tolerance is usually supported by bacterial communities with complementary functions rather than by one “universal strain” (Li et al., 2021). Even if some bacterial genera are enriched in the rhizosphere of salt-tolerant millet, it cannot be directly concluded that inoculation with a single strain will stably improve salt tolerance. The actual effect may come from a functional rhizosphere network jointly formed by bacteria, fungi, and their metabolites.

In addition, field saline-alkali environments are highly complex. Salinity level,  $\text{Na}^+/\text{Cl}^-$  ratio, carbonate and bicarbonate content, soil pH, texture, organic matter level, irrigation system, and previous crops can all influence rhizosphere microbial assembly. Therefore, microbial communities that perform well in one saline soil may fail to colonize effectively in another soil type, or may not show growth-promoting effects at all. For millet, future research should not only answer “which microorganisms are enriched,” but also clarify “under which soil conditions,” “recruited by which millet genotype,” “through which metabolic pathways,” and “whether the effect can remain stable across continuous growing seasons in the field.” These are the key issues that must be solved before rhizosphere microbiome research can move from basic science to agricultural application.

### 7.2 Multi-omics approaches in rhizosphere research

An important future direction for millet salt-alkali adaptation research is the establishment of an integrated multi-omics framework linking “host genotype–root exudates–rhizosphere microorganisms–ion homeostasis–yield and quality.” Previous studies usually measured physiological traits, transcriptomes, metabolites, or microbial communities separately. Although such studies can reveal changes at a specific level, they often fail to explain the causal relationships among different biological layers. For example, a salt-tolerant material showing a high  $\text{K}^+/\text{Na}^+$  ratio may be related to transporter gene expression, regulation of microbial communities by root exudates, or interactions among root architecture and soil nutrient status. Without integrated analysis, it is difficult to identify the real limiting factor.

The improvement of millet genomic resources has provided the basis for this type of research. Zou et al. (2019) completed a high-quality chromosome-level genome assembly of millet, identifying 55,930 protein-coding genes and 339 miRNAs. They suggested that this genomic resource could support studies on stress resistance, C4 photosynthesis, and breeding improvement. This means that traits such as salt tolerance, alkali tolerance, root development, and rhizosphere recruitment ability can now be connected with genomic variation, promoting millet breeding from traditional experience-based selection to genome-assisted and microbiome-assisted breeding.

Methodologically, an ideal experimental design should simultaneously conduct phenotypic analysis, ionomics, root exudate metabolomics, rhizosphere metagenomics, metatranscriptomics, and host transcriptomics using the