

development, nutrient acquisition, and metabolic activities. In orchids such as *D. officinale*, rhizosphere and endophytic microorganisms not only enhance the uptake of water and mineral nutrients but may also contribute to the biosynthesis of quality-related metabolites, including polysaccharides, alkaloids, and flavonoids.

Studies of the *D. officinale* microbiome have provided important evidence for understanding substrate-microbe-plant interactions. Wang et al. (2022) conducted metagenomic analyses of *D. officinale* growing in nutrient-poor Danxia habitats and identified highly diverse microbial communities in both rhizosphere and endophytic compartments. These communities included plant growth-promoting rhizobacteria such as *Massilia*, *Pseudomonas*, *Bradyrhizobium*, *Paenibacillus*, and *Streptomyces*, as well as beneficial fungi including *Tulasnella* and *Serendipita*. Functional annotation revealed significant enrichment of pathways related to carbohydrate, amino acid, and energy metabolism, indicating that these microorganisms facilitate nutrient mobilization and transformation, thereby supporting plant survival and growth under low-fertility conditions (Wang et al., 2022). A review of rhizosphere microbiomes in *Dendrobium* species further suggested that plant growth-promoting bacteria and fungi can enhance nitrogen and phosphorus uptake, produce phytohormones such as indole-3-acetic acid and gibberellins, and suppress pathogens, collectively improving plant growth, stress tolerance, and quality (Sarsaiya et al., 2025).

Different cultivation systems and root-zone conditions may also alter microbial community composition and their influence on metabolite production. Studies on *Dendrobium denneanum* cultivated under tree-mounted, rock-mounted, and pot cultivation systems showed that soil properties, particularly total phosphorus and pH, simultaneously affected root microbial communities and metabolite profiles. Correlation analyses revealed associations between specific microorganisms, including *Occallatibacter* and *Clonostachys*, and the pharmacologically active compound gigantol, suggesting that root-associated microorganisms participate in regulating secondary metabolite biosynthesis (Chen et al., 2023). Broader rhizosphere microbiome studies have likewise demonstrated that the rhizosphere represents a hotspot for nutrient cycling and root nutrition, with enrichment of genes involved in organic compound transformation, nitrogen fixation, and denitrification relative to bulk soil (Ling et al., 2022). In crops such as maize and pea, arbuscular mycorrhizal fungi and rhizobia have been shown to enhance phosphorus and nitrogen uptake, reshape rhizosphere bacterial communities, and improve yield and nutrient-use efficiency (Lu et al., 2023; Calderon and Dangi, 2024). Collectively, these findings suggest that substrate-associated microbiomes may be regarded as extensions of root function in *D. officinale*, influencing growth and medicinal quality through enhanced nutrient acquisition, improved stress resistance, and regulation of metabolic pathways.

5.3 Relationship between substrate-induced stress and secondary metabolite accumulation

The formation of plant secondary metabolites is regulated not only by genetic factors but also by environmental conditions. Bioactive constituents of *D. officinale*, including polysaccharides, dendrobine, flavonoids, and phenolic compounds, are closely associated with plant responses to environmental stimuli. By altering water availability, aeration, salinity, nutrient balance, and rhizosphere microecological conditions, different cultivation substrates may impose varying degrees of physiological stress on plants, thereby influencing defense responses and the activation of secondary metabolic pathways. Moderate substrate-induced stress may stimulate defense mechanisms, redirecting carbon, nitrogen, and energy resources toward the biosynthesis of flavonoids, alkaloids, and other protective metabolites. However, excessive stress can inhibit photosynthesis and biomass accumulation, resulting in reduced growth and quality.

Previous studies investigating salt, temperature, and osmotic stresses have provided valuable insights into the relationship between environmental stimuli and the accumulation of quality-related metabolites in *D. officinale*. Under treatment with 250 mmol/L NaCl, significant transcriptomic and metabolomic reprogramming occurred in leaves, including marked changes in phenylalanine metabolism, flavonoid biosynthesis, and α -linolenic acid metabolism. Genes involved in jasmonic acid biosynthesis were upregulated, accompanied by increased levels of flavonoids, carbohydrates, and alkaloids. These findings suggest that jasmonic acid may act as a signaling molecule promoting flavonoid biosynthesis, enabling plants to adapt to salt stress through enhanced secondary