

Research Insight

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Computational Analysis of Growth Characteristics and Active Compound Accumulation in Zhejiang Medicinal Plants

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Abstract Zhejiang Province is recognized as one of the important regions for medicinal plant diversity in China, with abundant resources characterized by unique ecological adaptability and rich accumulation of bioactive compounds. However, the growth performance and medicinal quality of these plants are strongly influenced by complex interactions among genetic background, environmental conditions, cultivation practices, and metabolic regulation processes. Recent advances in computational biology, artificial intelligence, and multi-omics technologies provide new opportunities for systematically investigating plant growth dynamics and active compound accumulation. This review summarizes the biological characteristics and developmental patterns of Zhejiang medicinal plants and discusses computational frameworks integrating phenotypic data, environmental parameters, metabolomics, transcriptomics, and machine learning approaches. Particular emphasis is placed on computational modeling strategies for predicting growth traits, identifying key regulatory factors, and elucidating metabolic pathways associated with bioactive compound biosynthesis. Furthermore, advanced technologies, including remote sensing-based digital phenotyping, network biology, and deep learning models, are evaluated for their potential applications in precision cultivation and medicinal quality optimization. A case study framework is presented to demonstrate how machine learning models can integrate environmental variables, growth indicators, and metabolite profiles to predict plant productivity and medicinal compound accumulation. Despite significant progress, challenges remain in data standardization, model interpretability, and the integration of computational predictions with experimental validation. Future development of artificial intelligence-driven platforms, digital twins, and multi-scale biological models will facilitate sustainable cultivation, resource conservation, and quality improvement of Zhejiang medicinal plants. This computational perspective provides a theoretical and technological foundation for advancing intelligent medicinal plant research and precision herbal medicine production.

Keywords Zhejiang medicinal plants; Computational biology; Machine learning prediction; Active compound accumulation; Multi-omics integration

1 Introduction

Medicinal plants form the material foundation of traditional Chinese medicine and remain increasingly important for health care, industry, and regional bioeconomies. At the same time, sustainable development of this resource base is constrained by declining wild populations, uneven cultivation practices, and persistent variation in the quality of cultivated materials. These challenges are especially relevant in provinces such as Zhejiang, where medicinal-plant richness, industrial potential, and geographic heterogeneity coexist, yet development of planting systems, markets, and enterprise distribution remains imperfectly aligned with resource endowment (Shan et al., 2021). Environmental variation further complicates production because soil, climate, and terrain strongly influence plant growth and the accumulation of active ingredients, often causing substantial differences within the same species across habitats and medicinal parts. For Zhejiang medicinal plants, this means that evaluating growth vigor alone is insufficient; robust assessment must also address phytochemical quality, environmental responsiveness, and the interaction between agronomic performance and medicinal value.

Recent empirical work has reinforced the importance of linking growth traits with bioactive compound accumulation through quantitative analysis. In *Polygonatum cyrtoneura*, a medicinal and edible species of high economic relevance in southern China, multi-site provenance testing in Zhejiang showed highly significant