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High-Throughput Non-Destructive Prediction of Duckweed Protein Content Using Hyperspectral Imaging and Deep Learning

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Duckweed is a promising plant-based protein and biomass resource, but efficient breeding and large-scale cultivation require rapid, high-throughput, and non-destructive evaluation of key traits. Conventional methods for determining crude protein and chlorophyll contents are labor-intensive, chemically demanding, and destructive, limiting their application in large-scale germplasm screening and real-time cultivation management. In this study, we developed an integrated high-throughput phenotyping platform combining hyperspectral imaging (HSI) and deep learning for simultaneous non-destructive prediction of crude protein content, leaf area-based relative growth rate (RGR), and chlorophyll content in duckweed. More than 200 duckweed samples cultivated in standardized 12-well microplates were scanned using an HSI system covering 400–2000 nm with a spectral resolution of 3 nm. A DeepLab v3+ semantic segmentation model was used to delineate duckweed fronds and quantify leaf area, enabling automated extraction of growth-related phenotypes. A Transformer-based spectral-spatial feature fusion model was further developed to integrate RGB-derived spatial features with hyperspectral signatures for biochemical and growth trait prediction. The platform achieved strong predictive performance for crude protein content (R^2 = 0.938, RMSE = 1.030, prediction accuracy = 95.8%), chlorophyll content (R^2 = 0.893, RMSE = 1.514, prediction accuracy = 94.7%), and leaf area-based RGR (prediction accuracy = 98.5%). With a throughput of up to 120 samples per hour, this HSI- and deep learning-based platform provides an efficient tool for duckweed germplasm evaluation, high-protein strain selection, and precision cultivation management.

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