medicinal metabolite accumulation, which supports the broader principle that moderate-to-high but non-photoinhibitory light optimizes source strength and metabolic quality (Xu et al., 2024).

3.2 Effects of temperature and day-night temperature differences on carbon metabolism and polysaccharide accumulation

Temperature regulates polysaccharide accumulation by altering carbon turnover, respiration, and sugar-metabolic gene expression. Within a suitable range, rising temperature increases hydrolase activity, accelerates starch hydrolysis, and raises soluble sugar content, whereas lower temperature weakens respiration and sugar consumption, thereby favoring sugar accumulation (Chen et al., 2024). Seasonal monitoring in *D. officinale* confirms that sugar accumulation is strongly climate-dependent: stem sugars mainly accumulated from October to April, with rapid accumulation from October to February, and related genes were enriched in photosynthesis and starch-sucrose metabolism pathways. Weighted gene co-expression analysis further identified hub genes that appear to maintain sugar metabolism by coordinating photosynthesis-related pathways under low-temperature and drought stress. Developmental transcriptomics also supports this carbon-metabolic basis, because stages with changing stem water-soluble polysaccharide content were enriched in starch and sucrose metabolism, indicating that temperature effects act through a pathway already central to endogenous polysaccharide formation (Figure 1) (Yang et al., 2025).



Figure 1 Phenotypes of *D. officinale* at different developmental stages (Adopted from Yang et al., 2025)
Image caption: S1: 2 months after sprouting; S2: 5 months after sprouting; S3: 11 months after sprouting; S4: 13 months after sprouting; and S5: 15 months after sprouting (Adopted from Yang et al., 2025)

Day–night temperature difference is a particularly important regulatory lever in controlled environments. In protocorm-like bodies, the DIF treatment favored soluble polysaccharide accumulation and produced higher chlorophyll, polysaccharide, and flavonoid contents than constant-temperature treatments. Transcriptome analysis under DIF showed differential expression of genes involved in sugar metabolism, including *SUS, SUT, HKL1, HGL, AMY1,* and *SS3*, together with heat-stress-responsive HSPs and HSFs, indicating that temperature amplitude changes both carbon partitioning and stress adaptation networks (Chen et al., 2024). The response is not simply "larger DIF is better," because plant species differ in how diurnal temperature amplitude balances photosynthesis, respiration, and metabolite allocation: tea showed reduced photosynthesis at excessive DIFs and sorghum showed reduced soluble sugars and biomass when diurnal temperature amplitude narrowed through elevated night