

quality and quantity and correspondingly regulating morphology and metabolism (Liu et al., 2018). These photoreceptors converge on core regulatory hubs such as the COP1-SPA E3 ubiquitin ligase complex and the bZIP transcription factor HY5, integrating multi-wavelength signals and reprogramming gene expression (Tissot and Ulm, 2020).

In shaded tea plants, UVR8-, HY5-, and *COP1-related* genes show co-expression relationships with flavonoid biosynthesis genes, and their expression levels decrease synchronously with catechin and flavonol contents, indicating that weakening of UV-B and its related signaling directly affects secondary metabolism (Liu et al., 2018). More broadly, different wavelengths of light can activate HY5 and related factors through UVR8, cryptochromes, and phytochromes, thereby inducing the synthesis of phenylpropanoid “sunscreen” metabolites and other protective metabolites (Leonardelli et al., 2024). Therefore, in *T. hemsleyanum*, shading-induced changes in the UVR8-HY5-COP1 signaling pathway are likely to be key upstream mechanisms regulating the accumulation of medicinal phenylpropanoid and flavonoid compounds.

6.2 Regulatory mechanisms of secondary metabolic pathways

Light regulates the biosynthesis of phenolic compounds, terpenoids, alkaloids, and other substances through conserved transcriptional regulatory networks. Specific photoreceptors can activate signaling cascades and regulate the expression of genes involved in phenylpropanoid and flavonoid metabolic pathways, such as PAL, C4H, 4CL, CHS, CHI, F3H, F3'H, FLS, DFR, ANS, ANR, and LAR, thereby leading to tissue- and condition-specific accumulation of catechins, flavonols, anthocyanins, and other metabolites (Liu et al., 2023). In tea plants, shading treatment, namely 20%-25% light transmittance, reduces catechin and flavonol contents by more than 40%-50%, accompanied by coordinated downregulation of multiple flavonoid structural genes and UVR8 pathway components, directly demonstrating a link between shading and reduced phenylpropanoid metabolic flux (Liu et al., 2018).

Comprehensive reviews indicate that the effect of shading on medicinal quality depends on species shade tolerance and light level: moderate shading can increase total phenols, flavonoids, and specific compounds, whereas deep shading usually downregulates genes related to phenylpropanoid and terpenoid biosynthesis and reduces metabolite accumulation. Reviews of phenylpropanoid metabolism emphasize that this pathway generates thousands of metabolites, including flavonoids and phenolic acids with strong antioxidant and defensive functions, and that it is strictly regulated at both transcriptional and post-transcriptional levels to adapt to changing environmental conditions (Deng and Lu, 2017; Ninkuu et al., 2025). For *T. hemsleyanum*, its key medicinal components mainly include flavonoids and related compounds derived from the phenylpropanoid pathway. Therefore, shading is expected to reshape metabolic pathway flux by altering photoreceptor signaling and the expression of core biosynthetic genes.

6.3 Regulation of key enzyme genes and transcription factors

Light signals regulate medicinal quality not only through structural genes, but also through complex transcription factor networks. Core light-responsive regulators such as HY5, PIFs, BBX proteins, and COP1 can integrate photoreceptor input signals and interact with transcription factors such as MYB, bHLH, WRKY, bZIP, and NAC, thereby directing the expression of genes related to secondary metabolism (Liu et al., 2023; Chen et al., 2025). In shaded tea plants, photoreceptor genes and UVR8-HY5 pathway genes show co-expression relationships with MYB12, MYB4, and MYB111, supporting a model in which light-regulated MYB transcription factors control catechin and flavonol biosynthesis (Liu et al., 2018). In medicinal and horticultural plants, MYB, bHLH, WRKY, and related transcription factors serve as “master switches” of phenylpropanoid and flavonoid metabolic pathways and respond strongly to changes in the light environment. In yam, light exposure can increase anthocyanin and flavonoid contents, and light-induced MYB and WRKY transcription factors are highly correlated with anthocyanin metabolites and structural gene expression.

In pear, the light-responsive WRKY transcription factor PpWRKY44 is activated by BBX18 and can directly bind to the PpMYB10 promoter, thereby driving anthocyanin accumulation (Alabd et al., 2022). Multi-omics studies further show that blue light can upregulate MYB transcription factors as well as key structural genes such as PAL,