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Research article

Effect of low-intensity white light mediated de-etiolation on the biosynthesis of polyphenols in tea seedlings

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A B S T R A C T

Light is an important source of energy as well as environmental signal for the regulation of biosynthesis and accumulation of multiple secondary metabolites in plants. Polyphenols are the major class of secondary metabolites in tea, which possess potential antioxidant properties. In order to investigate the effect of light signal on the regulation of biosynthesis and accumulation of polyphenols in tea seedlings, a low-intensity white light was used and the change in trends of polyphenol contents, patterns of gene expression, and corresponding enzymatic activities were studied. LC-TOF/MS analysis revealed that light signal promoted the accumulation of hydroxycinnamic acid derivatives and nongalloylated catechin (EGC), while it restrained the accumulation of β-glucogallin and galloylated catechins. The quantitative reverse transcription-PCR analysis showed that the expression levels of the regulator genes and some structural genes involved in photomorphogenesis and biosynthetic pathway of nongalloylated catechins, respectively, were up-regulated. In contrast, the expression of *DHD/SDH* and *UGT* genes, which may be involved in biosynthetic pathway of βG, was down-regulated. The corresponding *in vitro* enzyme assays revealed decrease in the activity of ECGT (galloylates nongalloylated catechins) and an increase in activity of GCH (hydrolyzes galloylated catechins) during de-etiolation. The present study yielded inconsistent accumulation patterns of phenolic acids, flavan-3-ols, and flavonols in tea seedlings during de-etiolation. In addition, the accumulation of catechins was possibly jointly influenced by the biosynthesis, hydrolysis, glycosylation, and galloylation of polyphenols in tea plants.

1. Introduction

Polyphenols, the potential antioxidative compounds, are the major category of secondary metabolites in tea plants, which comprise approximately 18%–36% of the dry leaf weight (Wan et al., 2008). There are more than 96 types of phenolic compounds found in tea plants and manufactured tea samples, some of which have been detected by the LC-DAD-ESI/MS analysis of 41 green tea and 25 fermented tea samples; these include 15 phenolic acid derivatives, 12 catechins, 6 proanthocyanidins (PAs), 19 *O*-glycosylated flavonol, 7 C-glycosylated flavones, and 28 acylated glycosylated flavonols (identified for the first time) (Lin et al., 2008). A total of 50 phenolic compounds in tea plants were analyzed qualitatively in a single chromatographic run using LC-TOF/MS and UPLC-QqQ-MS/MS, while 29 of these compounds could be simultaneously quantified, based on their fragmentation behavior (Jiang et al., 2013). Catechins (both, galloylated and non-galloylated) and proanthocyanidins are the predominant phenolic compounds found in fresh leaves and roots of tea plants, respectively (Jiang et al., 2013), which indicates that the biosynthesis and accumulation of polyphenols are tissue specific.

The phenolic compounds are primarily derived from the shikimic acid pathway, phenylpropanoid pathway, and flavonoid pathway (Fig. 1), and a full-scale investigation has been carried out on the functional verification and transcriptional regulation of some key enzymes and genes involved in these pathways (Winkel-Shirley, 2001; Dixon et al., 2005; Akagi et al., 2009; Baudry et al., 2004; Gigolashvili et al., 2007; Lepiniec et al., 2006).

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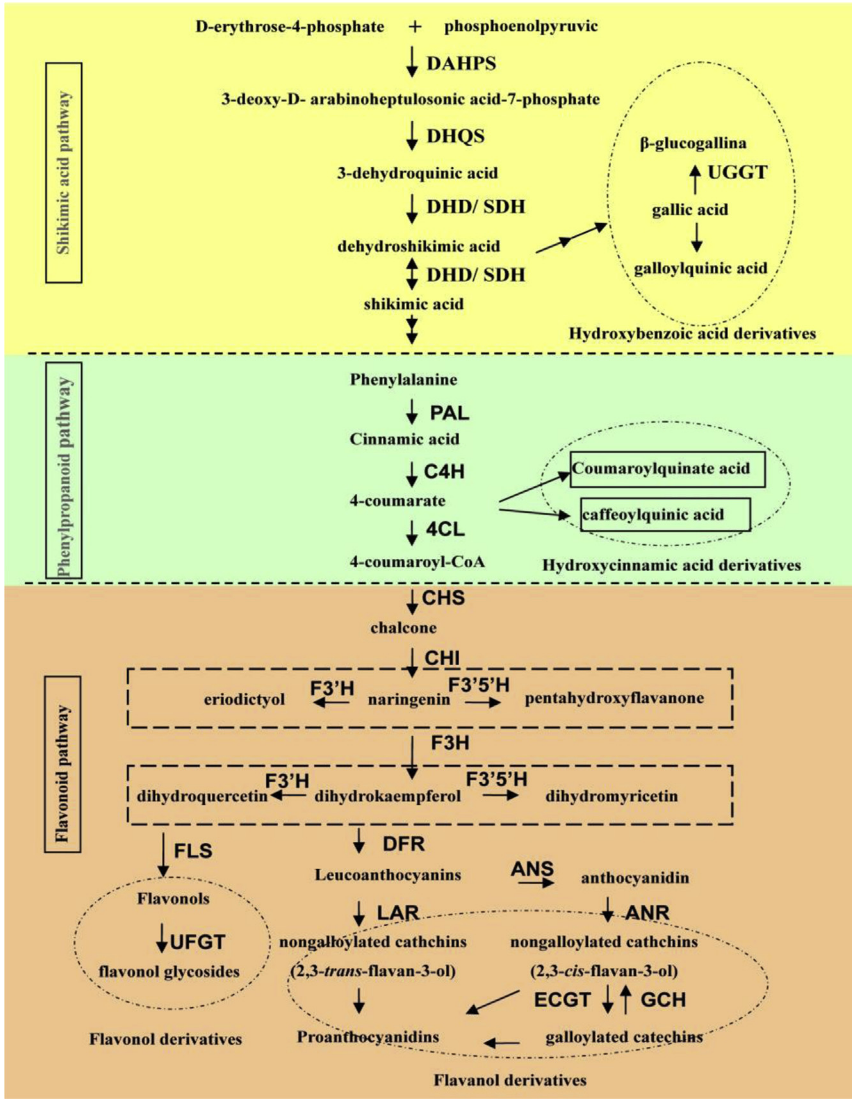

Fig. 1. Biosynthesis pathway of phenolic compounds in tea plants.

Nongalloylated catechins act as a precursor for the biosynthesis of galloylated catechins and proanthocyanidins. The biosynthesis and genetic regulation of these compounds have drawn wide interests across the scientific community and significant progress has already been made at the biochemical and genetic levels (Dixon et al., 2005; Lepiniec et al., 2006). At present, the focus of many studies has shifted to the transcriptional regulation (Hichri et al., 2011; Dubos et al., 2010), transportation, and polymerization, involved in the synthesis of proanthocyanidins and other phenols (Zhao et al., 2010).

Light is known to have a complicated effect on the cultivation of tea plants and the quality of tea beverage. During the process of tea production, shading treatment is the most common agronomic practice followed, which can contribute to enhancing the flavor and reducing astringency in manufactured tea (Ku et al., 2010). Some studies have suggested that shading treatment decreases the content of phenols, while increasing the production of amino acids in tea plants (Lee et al., 2013). We have previously studied the effect of light and shade on the metabolism of phenolic compounds in the callus of tea plants grown in fields, and reported that light promoted the synthesis of nongalloylated catechins, restrained the accumulation of gallic acid (a type of phenolic acid), but scarcely influenced the accumulation of galloylated catechins (Wang et al., 2012a,b). However, it still remains unclear if these effects are a result of a decrease in solar energy or an insufficiency of light signal during shading treatment.

Many studies have reported the accumulation of polyphenols induced by light acting as an environmental signal, such as ultraviolet light (UV)/blue-induced biosynthesis of anthocyanin in grapes (Kataoka et al., 2003), the swollen hypocotyls of turnip (Zhou et al., 2007), tomato (Guo and Wang, 2010), and turnip and Arabidopsis seedlings (Noh and Spalding, 1998; Wang et al., 2012c); induction of proanthocyanidins biosynthesis in poplar (Mellway et al., 2009), and of flavonols in Arabidopsis (Serrano et al., 2012). The existing reports believed flavonoids and anthocyanins act as photoprotective pigments, and are biosynthesized to protect the seedlings from more damaging effects of light in de-etiolation (Bowler et al., 2013). In addition, functional CONSTITUTIVE PHOTOMORPHOGENIC1 (COP1) and ELONGATED HYPOCOTYL5 (HY5) are required for UV-B-responsive flavonoid accumulation.