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Accumulation of anthocyanin and related genes expression during the development of cabbage seedlings

Xiaohua Li[a], Md Romij Uddin[a], Woo Tae Park[a], Yeon Bok Kim[a], Jeong Min Seo[b], Sun-Ju Kim[b], Ill-Sup Nou[c], Jeongyeo Lee[d], HyeRan Kim[d,*], Sang Un Park[a,**]

[a] Department of Crop Science, Chungnam National University, 99 Daehak-ro, Yuseong-gu, Daejeon 305-764, Republic of Korea
[b] Department of Bio Environmental Chemistry, Chungnam National University, 99 Daehak-ro, Yuseong-gu, Daejeon 305-754, Republic of Korea
[c] Department of Horticulture, Sunchon National University, Suncheon 540-742, Republic of Korea
[d] Plant Systems Engineering Research Center, Cabbage Genomics Assisted Breeding Supporting Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Daejeon 305-806, Republic of Korea

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ABSTRACT

In this study, we investigated anthocyanin accumulation and gene expression in response to light and dark conditions during the development of white and red cabbage seedlings. Two-day-old white cabbage seedlings expressed the highest transcript level for most of the genes under light conditions. Red cabbage also showed higher expression under light than under dark conditions, although gene expression (evaluated based on transcript levels normalized to that of a housekeeping gene) in 2-day-old red cabbage sprouts was much lower than that in the corresponding white cabbage sprouts. Trends in anthocyanin accumulation were similar for red and white cabbage but much greater accumulation was observed in red cabbage. Anthocyanin levels were higher in seedlings grown under light conditions compared to those grown under dark conditions for both cabbage cultivars. Especially, red cabbage accumulated 1.94–4.05 times greater total anthocyanin in 4-, 6-, 8-, and 10-day-old seedlings, when compared to white cabbage cultivar under light/dark and dark conditions. Our findings can improve understanding of the effects of light on accumulation of secondary metabolites in the seedling stages of various crops.

1. Introduction

Brassica oleracea L. var. *capitata* (cabbage) is one of the most important crop plants of the Brassicaceae, which has a long tradition of global cultivation and includes many important vegetable crops, such as cabbage, kale, Brussels sprouts, cauliflower, broccoli, and kohlrabi. Cabbage is a leafy white biennial that is grown as an annual vegetable for its dense-leaved (compact) heads. Many shapes, colors, and leaf textures are found among different cabbage varieties. Cabbages are generally categorized by leaf type as crinkled-leaf, loose-head or smooth-leaf, firm-head plants, while for the color spectrum, cabbage is differentiated into white head (*B. oleracea* L. var. *capitata* f. *alba*) and red head cabbage (*B. oleracea* L. var. *capitata* f. *rubra*).

Anthocyanin pigments are responsible for the red, purple, orange, and blue colors of many fruits, vegetables, cereal grains, and flowers [1–3], and have long been the subject of investigation by botanists and plant physiologists for their roles as pollination attractants [4] and phytoprotective (UV irradiation) agents [5]. Anthocyanins have also proven to be very useful in protecting human health against numerous diseases, including cancer, inflammation, coronary heart disease, and other age-related diseases [6–8]. The responses of anthocyanins to antioxidant and tumor-arresting activities have been widely studied [9–11].

Anthocyanin biosynthesis in plants is influenced by environmental factors, including light, and by various abiotic stresses, such as temperature [12,13], and is also regulated by internal factors (e.g., plant hormones, secondary metabolites, and nutrients) [14,15]. Light modulates the intensity of anthocyanin pigments by affecting the regulatory and structural genes involved in the biosynthesis, anthocyanin synthesis in the fruit of many agricultural crops is also enhanced by sunlight [16–20].

The main genes in the anthocyanin pathway had been well described in plant [2,21–23]. The first three steps of the pathway

Abbreviations: PAL, phenylalanine ammonium lyase; C4H, cinnamic acid 4-hydroxylase; CHI, chalcone isomerase; CHS, chalcone synthase; 4CL, 4-coumarate-CoA ligase; DFR, dihydroflavonol reductase; F3H, flavanone-3-hydroxylase; F3′H, flavonoid-3′-hydroxylase; ANS, anthocyanin synthase; UFGT, UDP Glc-flavonoid 3-*O*-glucosyl transferase.

* Corresponding author. Tel.: +82 42 860 4345; fax: +82 42 860 4149.
** Corresponding author. Tel.: +82 42 821 5730; fax: +82 42 822 2631.
E-mail addresses: kimhr@kribb.re.kr (H. Kim), supark@cnu.ac.kr (S.U. Park).

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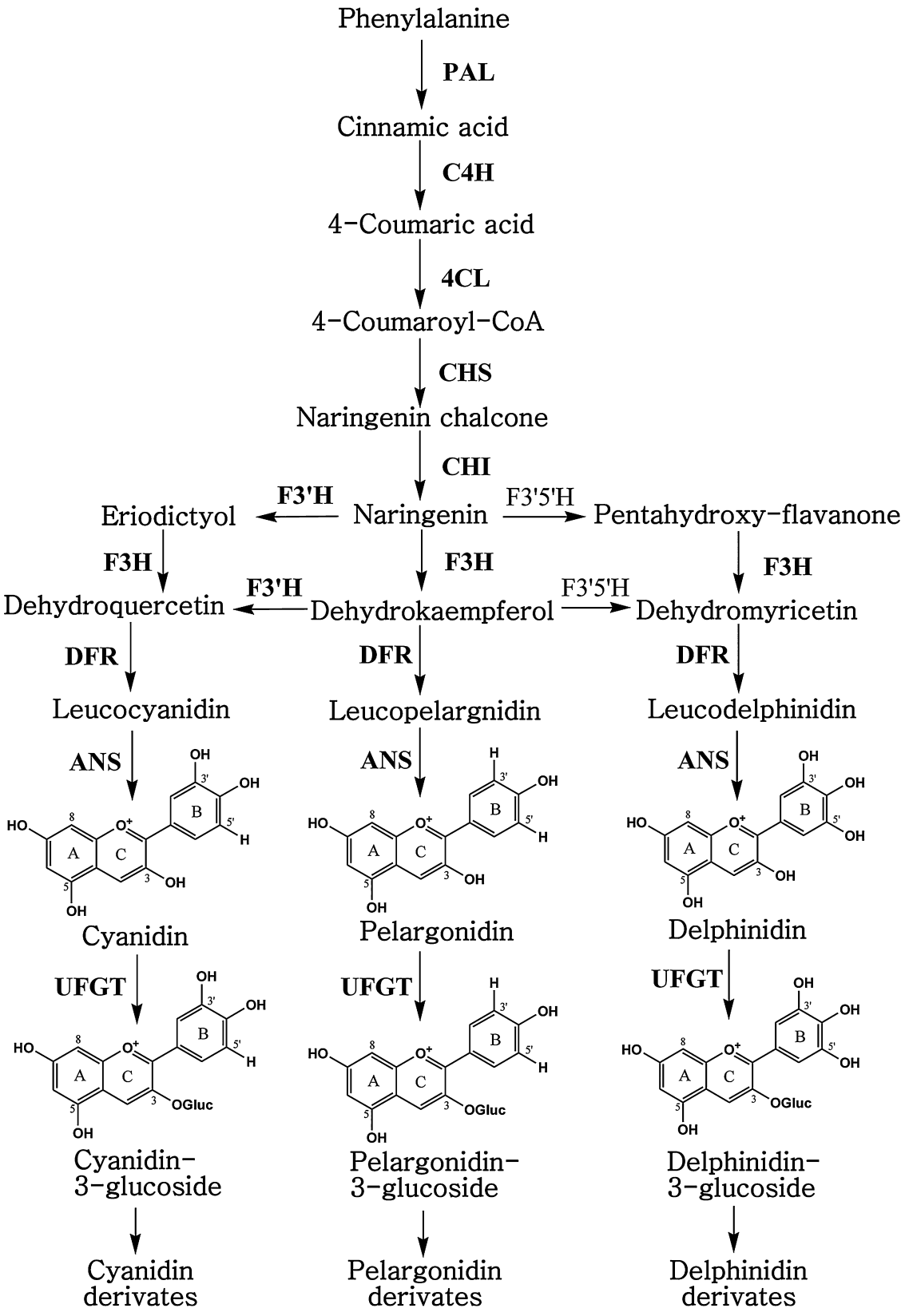

Fig. 1. A schematic representation of the anthocyanin biosynthetic pathway in cabbage. Expression of the genes presented in bold font was analyzed in this study. PAL, phenylalanine ammonium lyase; C4H, cinnamic acid 4-hydroxylase; CHI, chalcone isomerase; CHS, chalcone synthase; 4CL, 4-coumarate-CoA ligase; DFR, dihydroflavonol reductase; F3H, flavanone-3-hydroxylase; F3′H, flavonoid-3′-hydroxylase; F3′5′H, flavonoid 3′5′ hydroxylase; ANS, anthocyanin synthase; UFGT, UDP Glc-flavonoid 3-*O*-glucosyl transferase.

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