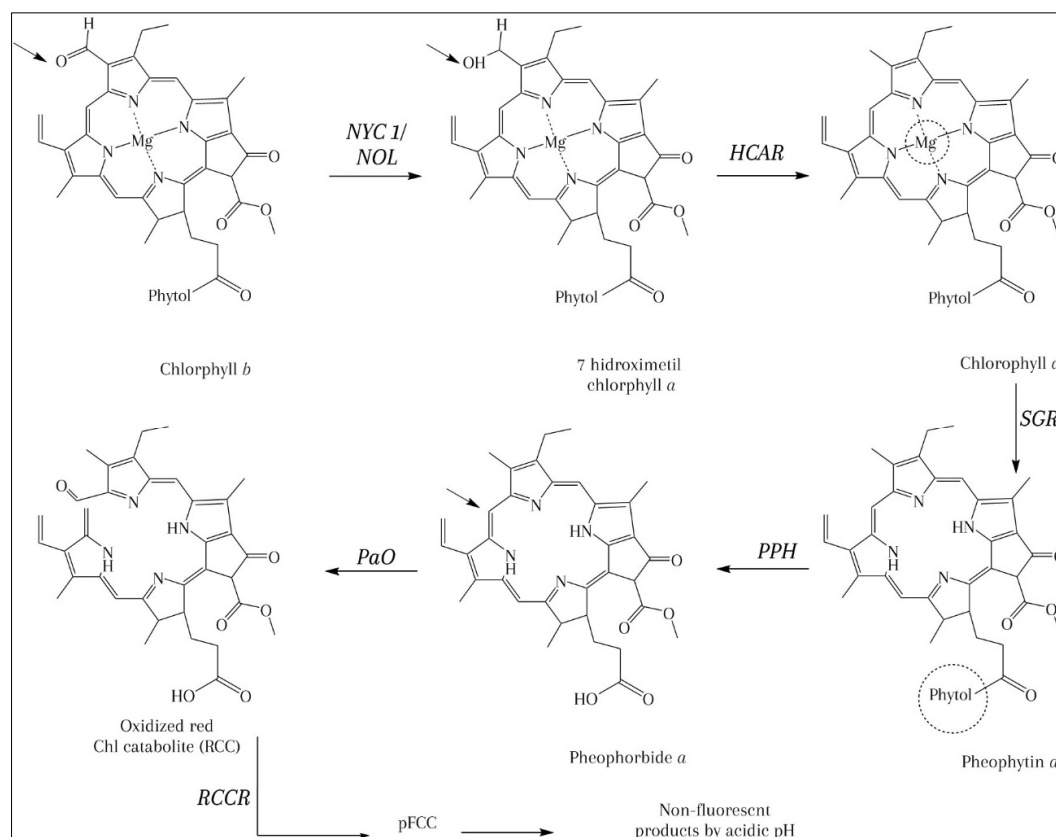
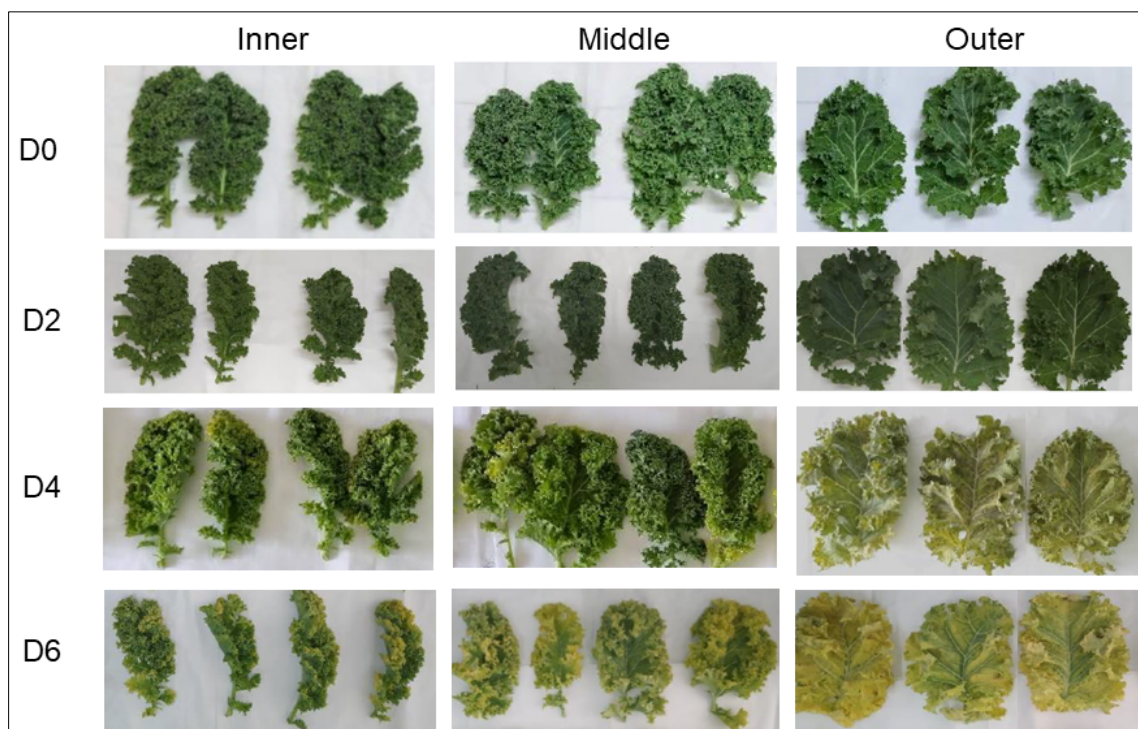
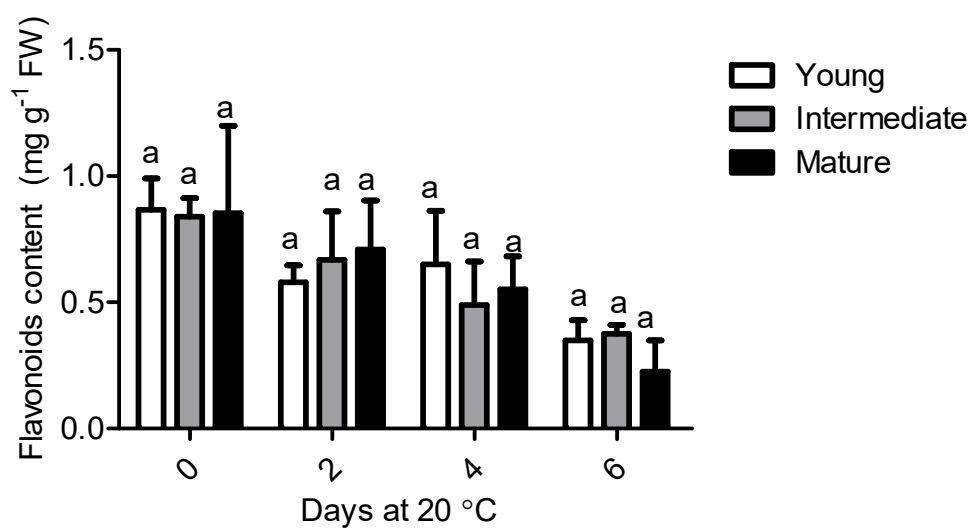




**Figure S1.** Chlorophyll catabolic pathway during leaf senescence. Schematic representation of chlorophyll degradation, showing the conversion of chlorophyll *b* to 7-hydroxymethyl chlorophyll *a* mediated by chlorophyll *b* reductases encoded by NYC1 and NOL, followed by conversion to chlorophyll *a* by HCAR. Chlorophyll *a* is subsequently converted to pheophytin *a* by SGR, followed by hydrolysis of the phytol chain by PPH to produce pheophorbide *a*. PaO catalyzes the formation of oxidized red chlorophyll catabolites (RCCs), which are further converted by red chlorophyll catabolite reductase (RCCR) into primary fluorescent chlorophyll catabolites (pFCCs) and subsequently into non-fluorescent chlorophyll catabolites under acidic conditions.



**Figure S2.** Representative photographs of kale leaves at different developmental stages during postharvest storage. Representative images of inner, middle, and outer leaves at harvest (D0) and after 2 (D2), 4 (D4), and 6 (D6) days of storage at 20 °C in darkness.



**Figure S3.** Total flavonoids content expressed as mg per g of fresh weight (FW) at day 0, 2, 4 and 6 of young (White), intermediate (gray) and mature (black) kale leaves. Data are presented as mean  $\pm$  standard deviation (SD). Different letters indicate significant differences at the same time of storage ( $p < 0.05$ ).

**Table S1.** Primers used for the relative gene expression analysis of chlorophyll catabolism-related genes in kale leaves. The table includes the forward and reverse primer sequences, amplicon size in basis pairs, and corresponding NCBI accession numbers [35] for *NYC*, *NOL*, *SGR*, *PPH*, and *PaO*, as well as *ACT*, which was used as the reference gene [42].

| Gene       | Forward primer          | Reverse primer            | Amplicon size (bp) | NCBI accession number |
|------------|-------------------------|---------------------------|--------------------|-----------------------|
| <i>NYC</i> | TTACATCTCGCAGTTCTGA     | GCAATACCAACTACCTTAGC      | 130                | XM_013780573          |
| <i>NOL</i> | ATGGCGGGGAAGGAGGACAGTGA | GGCGACGGTTGGGGAGGTGATTTA  | 159                | XM_013771448          |
| <i>SGR</i> | TTCCGACAACCGAAGTAA      | GTGAGCGTATAAGTTCTTGG      | 198                | XM_013748873          |
| <i>PPH</i> | AGAGGTTATCGGTGAGCCA     | GACGGATGAGGATGGG          | 91                 | XM_013760640          |
| <i>PaO</i> | CTCTTCTTCCTCTTCCTTC     | GACCCTTCTTCTTCCTTATC      | 315                | XM_013752085          |
| <i>ACT</i> | CCAGAGGTCTTGTTCCAGCCATC | GTTCCACCACTGAGCACAATGTTAG | 137                | XM_01373137           |

35 Kim J. Sugar metabolism as input signals and fuel for leaf senescence. *Genes Genomics*. 2019;41(7):737-746.

42 National Center for Biotechnology Information. National Center for Biotechnology Information [Internet]. Bethesda (MD): National Library of Medicine (US); [cited 2024 Oct 23]. Available from: <https://www.ncbi.nlm.nih.gov/>