Genome-wide identification and analysis of the SGR gene family in *Cucumis melo* L.

R.G. Bade¹², M.L. Bao¹, W.Y. Jin¹, Y. Ma³, Y.D. Niu¹ and A. Hasi¹

¹Inner Mongolia Key Laboratory of Herbage & Endemic Crop Biotechnology, School of Life Sciences, Inner Mongolia University, Hohhot, China
²Biomedical Research Center of Center Laboratory, Baotou Medical College, Baotou, China
³Department of Biological Science and Technology, Baotou Teacher’s College, Baotou, China

Corresponding author: A. Hasi
E-mail: hasind@sina.com

Received January 25, 2016
Accepted August 22, 2016
Published October 17, 2016
DOI http://dx.doi.org/10.4238/gmr15048485

Copyright © 2016 The Authors. This is an open-access article distributed under the terms of the Creative Commons Attribution ShareAlike (CC BY-SA) 4.0 License.

**ABSTRACT.** Chlorophyll (CHL) is present in many plant organs, and its metabolism is strongly regulated throughout plant development. Understanding the fate of CHL in senescent leaves or during fruit ripening is a complex process. The stay-green (SGR) protein has been shown to affect CHL degradation. In this study, we used the conserved sequences of STAY-GREEN domain protein (NP_567673) in *Arabidopsis thaliana* as a probe to search SGR family genes in the genome-wide melon protein database. Four candidate SGR family genes were identified in melon (*Cucumis melo* L. Hetao). The phylogenetic evolution, gene structure, and conserved motifs were subsequently analyzed. In order to verify the function of *CmSGR* genes in CHL degradation, *CmSGR1* and *CmSGR2* were transiently overexpressed and silenced using different plasmids in melon. Overexpression of *CmSGR1*
or *CmSGR2* induced leaf yellowing or fruit ripening, while silencing of *CmSGR1* or *CmSGR2* via RNA interference delayed CHL breakdown during fruit ripening or leaf senescence compared with the wild type. Next, the expression profile was analyzed, and we found that *CmSGR* genes were expressed ubiquitously. Moreover, *CmSGR1* and *CmSGR2* were upregulated, and promoted fruit ripening. *CmSGR3* and *CmSGR4* were more highly expressed in leaves, cotyledon, and stem compared with *CmSGR1* or *CmSGR2*. Thus, we conclude that *CmSGR* genes are crucial for fruit ripening and leaf senescence. CmSGR protein structure and function were further clarified to provide a theoretical foundation and valuable information for improved performance of melon.

**Key words:** Melon; Stay-green; Bioinformatic analysis; Chlorophyll degradation; Leaf senescence