Supplementary

Fluorescence Properties of a Novel Cyanobacteriochrome GAF Domain from *Spirulina* that Exhibits Moderate Dark Reversion

Xian-Jun Wu [1,2,*], Hong Yang [1], Yi Sheng [1], Yong-Li Zhu [1,2], and Ping-Ping Li [1,2]

[1] College of Biology and the Environment, Nanjing Forestry University, Nanjing 210037, China; yanghong0406108@163.com (H.Y.); shengyi_1993@163.com (Y.S.); lyly1262011@126.com (Y.-L.Z.); ppli@njfu.edu.cn (P.-P.L.)

[2] Collaborative Innovation Center of Sustainable Forestry in Southern China of Jiangsu Province, Nanjing Forestry University, Nanjing 210037, China

* Correspondence: xjwu@njfu.edu.cn; tel.: +86-25-8542-7210

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1173  ATCCGACGTTCTTTAAACCTGCAAACCATTTTTAACACGGCGACTCAAGAAGTGCGGCAG
392   I  R  R  S  L  N  L  Q  T  I  F  N  T  A  T  Q  E  V  R  Q

1233  GTTTTACAAGCGGAACGGGTGGTGATTTACCGCTTTCTGCCGGATTGGAGCGGGGAATTT
412   V  L  Q  A  E  R  V  V  I  Y  R  F  L  P  D  W  S  G  E  F

1293  ATGGCGGAGTCCAAAGGGGAAGAATGGCGGACTGTGGTGGGGAAAAACTGCCCAATTATT
432   M  A  E  S  K  G  E  E  W  R  T  V  V  G  K  N  C  P  I  I

1353  TCGGACAAACATTTGCGAGAAACTCAGGGGGGTCGCTATGCTGCCCATGAAACCTCAACA
452   S  D  K  H  L  R  E  T  Q  G  G  R  Y  A  A  H  E  T  S  T

1413  GTTACGGATATTTATGAGGTGGGTTTTTCCCCTTGTCATCTCCAAATGTTAGAACAATTA
472   V  T  D  I  Y  E  V  G  F  S  P  C  H  L  Q  M  L  E  Q  L

1473  CAAGCCCGGGCTTATATGATTGTTCCCATTTTCTTGGGGGAGAATCTCTGGGGCTTGTTA
492   Q  A  R  A  Y  M  I  V  P  I  F  L  G  E  N  L  W  G  L  L

1533  GCGGCCTATCAAAATTCGGCCCCTCGTTACTGGCAAGCTGATGAGGTGGAACTGTTGACC
512   A  A  Y  Q  N  S  A  P  R  Y  W  Q  A  D  E  V  E  L  L  T

1593  CAAATTGGTTCTCAGTTGGGGATGGCCATTCAACAGGGGCAATATTTGCAACAAATGCAG
532   Q  I  G  S  Q  L  G  M  A  I  Q  Q  G  Q  Y  L  Q  Q  M  Q

1653  GCACAATCA
552   A  Q  S
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Figure S1. Nucleotide and amino acid sequence of SPI1085(GAF3, 397-552aa) from *Spirulina subsalsa* FACHB351. The conserved cysteine-483-binding site is underlined with a solid line; the unconserved cysteine-448 residue is underlined with a wavy line, and boxes show the conserved motifs in CBCR GAF domains.

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1      ATGGGTGTTAGTTTAGCAGAAGTGAATTTAGCCACAATGCTACGGGAAGGGACGAAAAAA
1      M  G  V  S  L  A  E  V  N  L  A  T  M  L  R  E  G  T  K  K

61     TCCCATACTATGGCGGAAAATATGGGGTTTATTAAATGTTTCCTCAAAGGCGTAGTCGAA
21     S  H  T  M  A  E  N  M  G  F  I  K  C  F  L  K  G  V  V  E

121    AAAAATTCCTACCGTAGATTAGCGGCTAATCTCTACTATGTTTATGGGGCGATGGAAGAA
41     K  N  S  Y  R  R  L  A  A  N  L  Y  Y  V  Y  G  A  M  E  E

181    GAAATGGAACGCCTCAAAGATCATCCCATTTTGTCTAAGGTCTATTTCCCTGAATTAAAT
61     E  M  E  R  L  K  D  H  P  I  L  S  K  V  Y  F  P  E  L  N

241    CGGAAAGCTAATTTAGAGCGGGATTTGTTCTATTACTACGGAGCAAACTGGCGGGAGGAA
81     R  K  A  N  L  E  R  D  L  F  Y  Y  Y  G  A  N  W  R  E  E

301    ATTGAACTTTCTCCTACAGGTCAAGCCTATGTTAATCGCATTCATCATGTGGCGAATGAA
101    I  E  L  S  P  T  G  Q  A  Y  V  N  R  I  H  H  V  A  N  E

361    AAGCCAGAACTCTTGGTGGCACATCTTTACACCCGCTATCTGGGGGATCTCTCTGGGGGA
121    K  P  E  L  L  V  A  H  L  Y  T  R  Y  L  G  D  L  S  G  G

421    CAAATCCTCAAGAAAATTGCTCAGACGGCGATGAATCTTTCTGAGGGTGAAGGGACGGCT
141    Q  I  L  K  K  I  A  Q  T  A  M  N  L  S  E  G  E  G  T  A

481    TTTTATCAGTTTGAGCAGATTCCCGATGAGAAGGCGTTCAAAACCCAATATCGGGCTGCA
161    F  Y  Q  F  E  Q  I  P  D  E  K  A  F  K  T  Q  Y  R  A  A

541    ATGGACAGTTTACCTGTGGATCAACAAACGGCCGAGGCTATTGTTGATGAAGCCAATGAT
181    M  D  S  L  P  V  D  Q  Q  T  A  E  A  I  V  D  E  A  N  D

601    GCGTTCGGCATGAATATGAAAATGTTCGGAGAATTAGAAGGGGAATTTGATCAAAGCTAT
201    A  F  G  M  N  M  K  M  F  G  E  L  E  G  E  F  D  Q  S  Y

661    TGGTCAATGCTGTTTAATTCTTTAACTCGTCGTCGCAGTCGTGGGAGTACCGATGGCGAA
221    W  S  M  L  F  N  S  L  T  R  R  R  S  R  G  S  T  D  G  E

721    TTAGCCACCGCCGAATAG
241    L  A  T  A  E  *
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Figure S2. Nucleotide and amino acid sequence of heme oxygenase 1 (HO1) from *Spirulina subsalsa* FACHB351. Underline indicates the ATG start codon and the TAG stop codon, and boxes show the conserved active sites.

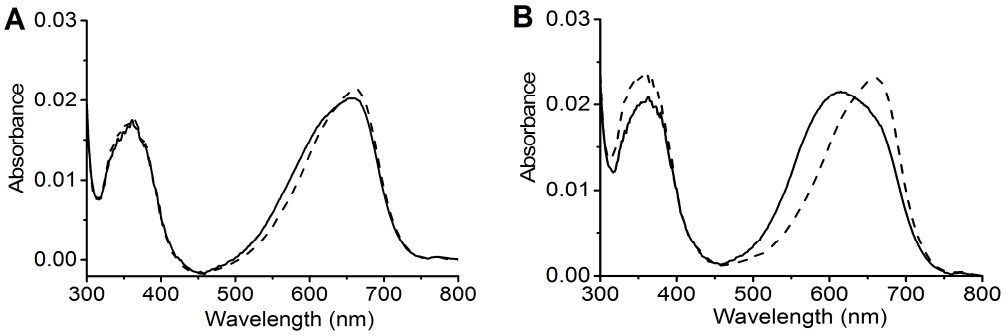

Figure S3. Acid denaturation of SPI1085g3. (A) Absorbance spectra of acid-denatured SPI1085g3 Pr state: absorbance spectra just after denaturation (solid line) and after while light illumination (dashed line). (B) Absorbance spectra of acid-denatured SPI1085g3 Pg state: absorbance spectra just after denaturation (solid line) and after while light illumination (dashed line).