Dynamics and efficiency of photoswitching in biliverdin-binding phytochromes

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Electronic supplementary information (ESI)
**Fig. S1.** Absorption and fluorescence spectra of PstBphP1 in the Pr (red) and Pfr (dark red) forms. Pfr is not fluorescent. Pr represents the dark adapted form.

**Fig. S2.** Absorption and fluorescence spectra of PaBphPin the Pr (red), darPfr (dark red) forms. The black line is the dark adapted state, = 100% Pfr. Pfr is not fluorescent.
**Fig. S3.** Absorption and fluorescence spectra of FphAN753 in the Pr (red) and Pfr (dark red) forms. Pfr is not fluorescent. Pr represents the dark adapted form.

**Fig. S4.** Comparison of matched ΔA values for detected wavelengths to the steady state absorption difference spectrum of PstBphP1, for the Pfr-to-Pr route (pump beam wl = 760 nm). Steady state spectrum and absorption values at the end of the flash photolysis experiment (at 20 °C) are presented with difference spectrum (Pr-Pfr). Steady state spectrum and absorption values at the end of the flash photolysis experiment (at 20 °C) are presented with different scales for the y-axes.
Fig. S6. Comparison of matched ΔA values for detected wavelengths to the steady state absorption difference spectrum of PaBphP, for the Pr-to-Pfr route (pump beam wl = 760 nm). Steady state spectrum and absorption values at the end of the flash photolysis experiment (at 20 °C) are presented with difference spectrum (Pfr-Pr). Steady state spectrum and absorption values at the end of the flash photolysis experiment (at 20 °C) are presented with different scales for the y-axes.
Fig. S7. Comparison of matched ΔA values for detected wavelengths to the steady state absorption difference spectrum of FphAN753 for the Pr-to-Pfr route (pump beam wl = 650 nm). Steady state spectrum and absorption values at the end of the flash photolysis experiment (at 20 °C) are presented with difference spectrum (Pfr-Pr). Steady state spectrum and absorption values at the end of the flash photolysis experiment (at 20 °C) are presented with different scales for the y-axes.

Fig. S8. Comparison of matched ΔA values for detected wavelengths to the steady state absorption difference spectrum of FphAN753 for the Pfr-to-Pr route (pump beam wl = 760 nm). Steady state spectrum and absorption values at the end of the flash photolysis experiment (at 20 °C) are presented with difference spectrum (Pr-Pfr). Steady state spectrum and absorption values at the end of the flash photolysis experiment (at 20 °C) are presented with different scales for the y-axes.
Fig. S9. Kinetics for the Pr-to-Pfr photoconversion in PstBphP1, detected at several wavelengths; note the logarithmic time axis.

Fig. S10. Kinetics for the Pfr-to-Pr photoconversion in PstBphP1, detected at several wavelengths; note the logarithmic time axis.
**Fig. S11.** Kinetics for the Pfr-to-Pr photoconversion in \textit{PaBphP}, detected at several wavelengths; note the logarithmic time axis.

**Fig. S12.** Kinetics for the Pr-to-Pfr photoconversion in \textit{PaBphP}, detected at several wavelengths; note the logarithmic time axis.
Fig. S13. Kinetics for the Pr-to-Pfr photoconversion in FphAN753, detected at several wavelengths; note the logarithmic time axis.

Fig. S14. Kinetics for the Pfr-to-Pr photoconversion in FphAN753, detected at several wavelengths; note the logarithmic time axis.
Figure S15. Sequence and secondary structure comparison of the photosensing PHY-GAF-PHY module for A. nidulans FhA with BphPs of known structure. The beginning of the core region (starting with a β-turn) is indicated with PAS, GAF and PHY. A structural homology model of FphA753 (not shown) was built with the FphA with BphPs of known structure. The global quality of the model was quite low (GMQE, 0.58), basically due to the long insertion of 50 aa (319-368) between the PAS and the GAF domain. Single domains could be modeled as good (PAS) and excellent (GAF and PHY). The PAS domain contain shorter, extra insertions. Important structural elements such as the "knot" and the "tongue" are preserved in FphA, but for the latter, in the conserved PRxSF motif, the chromophore-binding cysteine is in bold and underlined (N-terminal to the PAS core). The symbol ▼ indicates a residue in close vicinity of the chromophore (≤4.5 Å) in the template RpBphP2. For the other sequences: Dr = Rhodopseudomonas palustris, Pa = Pseudomonas aeruginosa, “r” and “fr” indicate the Pr and Pfr form respectively; PDB code are indicated in parenthesis. Note that in Pfr forms one of the α-helix with respect to Pr states. A model with a reduced ∼20 C-terminal residues was also built with RpBphP2_r(4r6l) and BphP2_r(4r6l). The quality of this model was slightly better (GMQE, 0.59), but the residues in close proximity of the chromophore were not preserved.

Reference text is added here.