Supplementary Information To the publication 'Gram-scale production of 4-vinyl guaiacol in the fast-growing cyanobacterium *Synechococcus* sp. PCC 11901'

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### 1. Supplementary figures and tables



Figure 1 Sequence alignment of PAD with the amplicon from the colony-PCR of S. PCC11901 fadA::pad.



Figure 2 SDS-PAGE for expression control. Samples were denatured with an SDS-buffer at  $95^{\circ}$ C for 10min and transferred into a polyacrylamide gel (12% bis-acrylamide) and run at 200V. The marker is shown in the middle (PageRuler, Fisher Scientific, Waltham, MA, USA). Synechococcus sp. PCC11901, with left fadA::pad strain, after induction with 1mM IPTG, the middle lane is the WT of S. PCC11901followed by the DNA marker, outer right is an E. coli strain expressing PAD as a positive control. The molecular weight of PAD is expected at ~19 kDa, indicated by a green arrow.



Figure 3 Synechococcus sp. PCC11901 fadA::pad was incubated with 10mM caffeic acid at 500 $\mu$ mol photons/s/m<sup>2</sup>. A shows cells after 24h, **B** the same tube, after centrifugation. **C** shows 10mM 3,4-dimethoxy styrene after 24h incubation in the same buffer and light conditions, without cells.



Figure 4 Synechococcus sp. PCC 11901WT (left) and fadA::pad (right) incubated with 10mM ferulic acid at 500µmol photons/s/m<sup>2</sup> after 24h.



Figure 5 NMR spectrum of 4-vinyl guaiacol, converted from ferulic acid by S. PCC 11901 fadA::pad. The product was extracted from the organic phase (DINP) by basic extraction. NMR code: <sup>1</sup>H NMR (400 MHz, DMSO)  $\delta$  9.07 (s, 1H), 7.04 (d, J = 2.0 Hz, 1H), 6.85 (dd, J = 8.2, 2.0 Hz, 1H), 6.73 (d, J = 8.1 Hz, 1H), 6.60 (dd, J = 17.6, 10.9 Hz, 1H), 5.62 (dd, J = 17.6, 1.1 Hz, 1H), 5.06 (dd, J = 10.9, 1.1 Hz, 1H), 3.79 (s, 3H).



Figure 6 Calculating the factor of OD<sub>750nm</sub> to dry cell weight.



*Figure 7 Optical density at 750nm (OD), Chlorophyll a and carotenoids content of S. PCC 11901, grown at 37°C, 1% CO<sub>2,</sub> and 500µmol photons/s/m<sup>2</sup>. The error bars indicate the standard error of the means from 3 replicates.* 



Figure 8 8 Growth comparison of S. PCC11901 and S. UTEX2973 in the CellDEG system. Cells were incubated at 500µmol photons/s/m<sup>2</sup> and 37°C. The arrows indicate an exchange of the carbonate buffer. S. UTEX2973 has been described as the fastest-growing cyanobacterium known<sup>1</sup>, but S. PCC11901 shows a higher total biomass accumulation.

Compound	LB	ТВ	AD7 <sup>2</sup>	MAD2 <sup>2</sup>	YBG11 <sup>3</sup>
Peptone	10 g/L				
Yeast extract	5 g/L	24 g/L			
NaCl	5 g/L		18 g/L	18 g/L	
Tryptone		20 g/L			
KH <sub>2</sub> PO <sub>4</sub>		17 mM	50 mg/L	50 mg/L	
K <sub>2</sub> HPO <sub>4</sub>		72 mM		0.27605 g/L	0.0305 g/L
MgSO <sub>4</sub> * 7H <sub>2</sub> O			5 g/L	5 g/L	0.074 g/L
KCI			0.6 g/L	0.6 g/L	
NaNO <sub>3</sub>			1 g/L	16 g/L	1.49 g/L
CaCl <sub>2</sub> *2H <sub>2</sub> O			0.37 g/L	0.37 g/L	36 mg/L
Na <sub>2</sub> EDTA*2H <sub>2</sub> O			30 mg/L	30 mg/L	5.95 mg/L
FeCl <sub>3</sub> *6H <sub>2</sub> O			15 µM	30 µM	0.97 mg/L
Vitamin B12			4 µg/L	12 µg/L	
H <sub>3</sub> BO <sub>3</sub>			2.86 µg/L	2.86 µg/L	2.78 mg/L
MnCl <sub>2</sub> * 4H <sub>2</sub> O			1.18 µg/L	1.18 µg/L	1.13 mg/L
ZnSO <sub>4</sub> * 7H <sub>2</sub> O			222 µg/L	222 µg/L	0.2 mg/L
Na <sub>2</sub> MoO <sub>4</sub> * 2H <sub>2</sub> O			1.26 mg/L	1.26 mg/L	0.39 mg/L
CuSO <sub>4</sub> *5H <sub>2</sub> O			79 µg/L	79 µg/L	0.07 mg/L
CoCl <sub>2</sub> * 6H <sub>2</sub> O			40.3 µg/L	40.3 µg/L	0.16 µM
Citric acid * H <sub>2</sub> O					6.3 mg/L
Na <sub>2</sub> CO <sub>3</sub>					160 µM
Tris (pH 8.4)			1.0375 g/L	1.0375 g/L	
HEPES (pH 7.8)					10/100 mM (depends on use)
Bacto-Agar	18 g/L (for plates)		12 g/L (for plates)		
$Na_2S_2O_3$			1 g/L (for plates)		
					Adjust to pH 7.2

Table 1 Media composition

2. Plasmids, primers, and sequences



Figure 9 Plasmid for genomic integration of PAD into S. PCC 11901. The integration site was the fadA locus, as described in Wlodraczyk et al., 2020.<sup>2</sup> The map was designed using SnapGene (Boston, USA).

# 2.1 Sequence of Phenolic Acid Decarboxylase (PAD) from *Bacillus coagulans* DSM11<sup>4</sup>

ATGAAAACCCTGGAAGAATTTTTGGGAACCCACATGATCTACACCTACGAAAATGGCTGGGAATACGAGTTCT ACGTCAAGAATCAAAACACTGTTGACTATCGAATTCACTCTGGCATGGTAGGTGGTCGCTGGGTTCGCGGTCA GAAAGCTGATATTGTCAAAATTACCGATGGCGTTTTCAAAGTCAGCTGGACGGAGCCGACAGGGACGGATGCC AGTCTAAACTTCATGCCTGACGACAAGCGGATGCATGGGGTGATTTTTTTCCCGAAGTGGGTGCATGAGCATCC CGAGATTACAGTCTGCTATCAGAATGATCACATCGATCTGATGGAAGAGTCGCGCGCAAAAATATGAAACCTAT CCCAAGTATGTGGTGCCAGAGTTTGCCGATATCACTTACATCAAAAATGAAGGCATCAACAACGAAAAGGTGA TCAGCGAGGCACCCTACGCCACGATGGCGGATGACATTCGTTCAGGCAAAACTCAAGTTTTCCTAA

#### 2.2 Primers used in this study

Table 2 List of primers used in this study.

#74 PAD into fadA_fwd	tcaagtaggagattaattccATGAAAACCCTGGAAGAATTTTTGGG
#75 PAD into fadA_rev	gtttgtacaagaaatctagaTTAGGAAAACTTGAGTTTGCCTGAACG
#76 fadA for PAD_fwd	GCAAACTCAAGTTTTCCTAAtctagatttcttgtacaaactcggccc
#77 fadA for PAD_rev	AATTCTTCCAGGGTTTTCATggaattaatctcctacttgactttatgagt

## 3. References

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