Engineering Carboxylic Acid Reductase for Bio-based Chemical Synthesis

Background

Enzymes are biological catalysts that accelerate chemical transformations for life. Enzymes are also becoming essential in a wide range of industrial applications.

Problem: Kinetic performance of an enzyme may limit its industrial use.

How to overcome the limitation? We can improve the catalytic properties and substrate scope of the enzyme via protein engineering.³

Carboxylic Acid Reductase (CAR)s (EC 1.2.1.30) are large multi-domain enzymes that can catalyze the ATP- and NADPH-dependent reduction of carboxylic acids into aldehydes. These enzymes consist of three domains: the adenylation domain (A-domain), the phosphopantetheine carrier protein domain (PCP-domain), and the reduction domain (R-domain).^{1, 2}



Methods

We have developed a novel growth-coupled selection method for the engineering of NADPH-dependent enzymes, i.e., CARs.³

Host strain engineering: Genes pgi (G6P isomerase) and sthA (soluble transhydrogenase) were deleted from *E. coli* genome to construct R- $\Delta 2$.

CAR mutant library construction: Single-site saturation mutagenesis (SSM) libraries of CAR enzyme from *Mycobacterium avium* (MavCAR) were constructed. Ten sites were randomized with the NNK codon (N =A, C, T, or G, K = T or G, 32 variants at nucleotide level).

Growth-coupled selection of CAR mutants: A single SSM library was transformed into *E. coli* R- $\Delta 2$ containing the phosphopantetheinyl transferase-expressing plasmid. Cells were washed and plated on M9 glucose agar plates with carboxylic acid substrate. Colony formation and growth were monitored.

Activity assay: Kinetic assay was performed by monitoring the oxidation of NADPH at 340 nm at 25 °C.

not selected are in purple.

To demonstrate the feasibility of the selection strategy, the mutant libraries were selected on a less favorable substrate adipate. Six out of the ten libraries (N276, S299, N335, M389, T390, and G391) showed improved growth. All mutants had lower K_m values than wild-type, while N335R showed a 17-fold improvement in catalytic efficiency.³

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Growth-Coupled NADPH Recycling Strategy



adipate	Variant	K _m (mM)	K _{cat} (min⁻¹)	K _{cat} /K _m (mM ⁻¹ min ⁻¹)
	wild-type	62.0 ± 3.9	59.5 ± 1.6	1.0 ± 0.1
	N335R (8)	2.6 ± 0.1	44.9 ± 0.6	17.0 ± 1.0
	S299K (2)	4.4 ± 0.2	30.1 ± 0.3	6.9 ± 0.3
	M389K (8)	5.4 ± 0.3	32.3 ± 0.4	5.9 ± 0.4
	N276P (2)	11.1 ± 0.5	47.3 ± 0.5	4.2 ± 0.2
	N276R (1)	13.2 ± 0.5	49.3 ± 0.6	3.7 ± 0.2
adipate semialdehyde	S299R (4)	13.3 ± 0.8	45.2 ± 0.9	3.4 ± 0.2
	N335K	9.4 ± 1.3	18.0 ± 0.6	1.9 ± 0.3
	M389R	9.7 ± 0.7	33.2 ± 0.8	3.4 ± 0.2

In Vivo Bioconversion of Adipate to 1,6-Hexanediol

A whole-cell bioconversion of adipate to 1,6-hexanediol (1,6-HDO) was done using MavCAR variants and E. coli aldehyde reductase (EcYahK). After 24 h, different ratios between 6-hydroxyhexanoic acid (6-HHA) and 1,6-HDO were observed. These varying ratios were due to the different activities of the MavCAR variants toward adipate and 6-HHA. Notably, the N335R variant was able to convert nearly all of the adipate to the final product 1,6-HDO.³



Figure 4. Whole-cell bioconversion of adipate to 6-hydroxyhexanoate and 1,6hexanediol using MavCAR and EcYahK. (A) In vivo biocatalytic cascade for the synthesis of 1,6-HDO. (B) Bioconversion of 1,6-HDO from 10 mM adipate after 24 h. Reaction was performed in M9 minimal media (pH 7.0) containing 10 g/L glucose, 0.25 mM IPTG, 10 mM adipic acid, and appropriated antibiotics. Conversion of 6-HHA and 1,6-HDO was analyzed and quantified by HPLC.





Growth characterization on dia (1 % glucose) with concentrations of 6hexanoate in R- $\Delta 2$ host. ector, 1; MavCAR, 2; -YahK, 3; Wild-type E. coli, 4.

Lactamization using MavCAR

Figure 5. Biosynthesis of caprolactam by MavCAR. (A) Overview of the synthesis of caprolactam by CAR adenylation domain. (B) Biosynthesis of caprolactam by MavCAR-WT (WT), MavCAR-WT A-domain (WT-Adom), MavCAR-M389E (M389E), and MavCAR-M389E A-domain (M389E-Adom). (C) ¹H-NMR of the biosynthesis of caprolactam. Reaction was performed with 12 µM CAR, 5 mM 6aminocaproic acid, 15 mM ATP, 10 mM MgCl₂, 1 µL *E. coli* Pyrophosphatase, in 50 mM Tris buffer pH 9.0 at 45 °C for 24 h.

Conclusion and Future Work

- The growth-coupled NADPH recycling strategy allows the identification of MavCAR variants with enhanced activity toward less favorable substrates
- Selection results showed that five positions N276, M296, S299, N335, and M389 have important roles in substrate recognition.
- This method allows a high-throughput and accessible selection with a low rate of false positive variants.
- Truncated A domain of MavCAR-M389E catalyzed the formation of caprolactam from 6-aminocaproic acid.
- Future work will focus on improving the selection scheme and further engineering CARs to produce C6 industrial chemicals.

Acknowledgements



NEBRASKA CENTER R ENERGY SCIENCES RESEARCH

This research is supported by the Nebraska Center for Energy Sciences Research and the National Science Foundation CBET-1805528.

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PDB ID: 5MSW







PDB ID: 5MSS





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