Reverse Electron Transfer Completes the Catalytic Cycle in a 2,3,5-Trifluorotyrosine-Substituted Ribonucleotide Reductase

Kanchana R. Ravichandran, ‡ Ellen C. Minnihan, ‡ Yifeng Wei, ‡ Daniel G. Nocera, § and JoAnne Stubbe * ‡,ε

‡ Department of Chemistry and ‡ Department of Biology, Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, Massachusetts 02139, United States
§ Department of Chemistry and Chemical Biology, Harvard University, 12 Oxford Street, Cambridge, Massachusetts 02138, United States

Supporting Information

ABSTRACT: Escherichia coli class Ia ribonucleotide reductase is composed of two subunits (α and β), which form an α2β2 complex that catalyzes the conversion of nucleoside 5′-diphosphates to deoxynucleotides (dNDPs). β2 contains the essential tyrosyl radical (Y122•) that generates a thyl radical (C439•) in α2 where dNDPs are made. This oxidation occurs over 35 Å through a pathway of amino acid radical intermediates (Y122• → W48• → Y356• in β2 to Y711• → Y730• → C439• in α2). However, chemistry is preceded by a slow protein conformational change(s) that prevents observation of most of these intermediates. 2,3,5-Trifluorotyrosine site-specifically inserted at position 122 of the α2 subunit (F3Y) perturbs its conformation and the driving force for radical propagation, while maintaining catalytic activity (1.7 s⁻¹). Rapid freeze-quench electron paramagnetic resonance spectroscopy and rapid chemical-quench analysis of the F3Y enzyme shows generation of 0.5 equiv of Y356• and 0.5 equiv of dCDP, both at 30 s⁻¹. In the absence of an external reducing system, Y356• reduction occurs concomitant with F3Y reoxidation (0.4 s⁻¹) and subsequent to oxidation of all α2s. In the presence of a reducing system, a burst of dCDP (0.4 equiv at 22 s⁻¹) is observed prior to steady-state turnover (1.7 s⁻¹). The Y356• does not change, consistent with rate-limiting F3Y reoxidation. The data support a mechanism where Y122• is reduced and reoxidized on each turnover and demonstrate for the first time the ability of a pathway radical in an active α2β2 complex to complete the catalytic cycle.

INTRODUCTION

Ribonucleotide reductases (RNRs) catalyze the formation of deoxynucleotides from their corresponding ribonucleotides (Scheme 1) in almost all organisms; allosteric regulation of substrate specificity and activity contributes to fidelity of both DNA replication and repair.1,2 The class Ia RNRs contain two homodimeric subunits, α2 and β2, which form an active α2β2 complex in the case of the E. coli enzyme.3 The β2 subunit houses a diferric-tyrosyl radical (Y122•) cofactor that reversibly oxidizes C439 in the active site of α2 to a thyl radical.4,5 The C439• initiates nucleotide reduction by H atom abstraction from the 3’ position of the substrate (Scheme 1).6,7 On the basis of in silico docking of the individual X-ray structures of α2 and β2,8,9 the distance between Y122• and C439• is estimated to be >35 Å. This radical transport (RT) process occurs through a specific pathway that involves at least three transient aromatic amino acid radical intermediates (proton-coupled electron transfer or PCET) through Y122• → W48• → Y356• in β2 to Y731• → Y730• → C439• in α2, Figure 1.9,10 During turnover of wild-type (wt) RNR, only the resting state Y122• is observed. In this paper, we describe the perturbation of PCET kinetics by site-specific incorporation of 2,3,5-trifluorotyrosine (F3Y) at position 122 in β2 resulting in accumulation of a pathway tyrosyl radical intermediate (Y356•) that is kinetically and chemically competent to complete the catalytic cycle of RNR.

Received: August 30, 2015
Published: October 22, 2015

DOI: 10.1021/jacs.5b09189
J. Am. Chem. Soc. 2015, 137, 14387−14395

Scheme 1. Reaction Catalyzed by RNR

"Turnover requires reducing equivalents which are provided by a pair of cysteines in the active site of the enzyme."
multiple turnovers at 25% the steady-state wt activity. Hand-reaction of F3Y electron transfer (ET); the conjugate base NO2Y β ATP rapidly generates 0.5 equiv of Y356 responding Y122 phenol (Figure 1).18 In contrast, use of NO2Y a water molecule on the diferric cluster to generate the cor-
thus, this mutant could only perform a single turnover.12 This or using rapid kinetic methods.11 An approach adopted by our tion of radical intermediates either during steady-state turnover and reverse RT steps occur on a much more rapid time scale than the protein conformational change(s) preventing observa-
reduction potentials in an e effort to accumulate and characterize the proposed radical intermediates (Figure 1). Previously, we described the insertion of 3-nitrotyrosine (NO2Y) at residue 122 in β.12 The reaction of NO2Y*-β2, α2, CDP, and ATP rapidly generates 0.5 equiv of Y356 and dCDP (>100 s⁻¹). We have proposed that this stoichiometry is a consequence of half-sites reactivity in RNR where only 50% of Y122* in the α2β2 complex reacts at a time.13,17 We have recently shown that, upon radical initiation in wt RNR, a proton is transferred from a water molecule on the dimeric cluster to generate the corresponding Y122 phenol (Figure 1).18 In contrast, use of NO2Y*-β2 to initiate RT uncouples this proton transfer (PT) and electron transfer (ET); the conjugate base NO2Y- is generated instead of the anticipated phenol NOY. Furthermore, Y356* generated during reverse RT is unable to reoxidize NO2Y-, and thus, this mutant could only perform a single turnover.12 This prevented us from establishing the chemical competence of Y356 to complete the catalytic cycle and determining if it is a true intermediate on the PCET pathway.

In an attempt to engineer a smaller perturbation to the driving force, we inserted F3Y at position 122 in β2 and investigated the reaction of F3Y*-β2, α2, CDP, and ATP.15 Steady-state assays revealed that, unlike the NO2Y*-β2 mutant, F3Y*-β2 can catalyze multiple turnovers at 25% the steady-state wt activity. Hand-quench EPR experiments showed formation of a new tyrosyl radical, assigned to residue Y356 in β2 based on multiple lines of evidence. First, the new radical is observed when the redox inert F is inserted at position 731 but not at position 356.19 Second, the 9 GHz EPR spectrum of the new radical is remarkably similar to that of the radical observed in the NO2Y*-β2 studies.12,19 In NO2Y*-β2, pulsed electron–electron double resonance (PELDOR) spectroscopy experiments measured a distance of 30 Å between the new radical in one α/β pair and NO2Y* in the second α/β pair.20 Similar experiments with other un-natural amino acids inserted at position 356 (either 3,4-dihydroxyphenylalanine11 or 3-aminotyrosine22) provide an identical distance measurement (30 Å). In preliminary PELDOR experiments, a similar distance is also observed between F3Y* and the new radical (Nick, Bennati, unpublished results). These data together support that the radical observed in F3Y*-β2 is located at position 356. Studies with NO2Y*-β2, however, have shown that while the predominant location of the radical is at position 356 (85–90%), Y356* is in equilibrium with Y731* and Y730* in α2 (15–10%).20 These initial studies laid the foundation for the work described herein and gave us an opportunity to investigate the importance of Y356* and reverse RT in an active RNR complex.

In this work, we carry out thorough kinetic analyses of the reaction of F3Y*-β2, α2, CDP, and ATP in the absence and pre-

Figure 1. Proposed PCET pathway in E. coli class Ia RNR.20 The pink and blue arrows indicate the movement of electrons and protons through conserved aromatic amino acids (Y356 in β and Y731 and Y730 in α2). WAα and its putative proton acceptor D355 are shown in gray, as there is no evidence for their participation in RT. The positions of Y356 and E350 are unknown, as these residues are disordered in all crystal structures of β/2.

### MATERIALS AND METHODS

**Materials.** (Hiss)₃ wt-α2 (specific activity of 2500 nmol/min/mg) was expressed from pET28a-nrdA and purified using our standard protocol.25 Wt-α2 was pre-reduced by the addition of DTT and hydro-

Tyrosine phenol lyase (TPL) (1400 U/mg) that varies directly

with the radical content (0.6–1.0 F3Y*-β2) and E. coli TR (40 U/mg) and TRR (1400 U/mg) were purified using established protocols.22 CDP was purchased from Vitrix (Placentia, CA). Hepes, MgSO₄, EDTA, 2XYT microbial medium, ampicillin (Amp), chloramphenicol (Cam), ATP, CDP, and carrier deoxycytidine (dC) were obtained from Sigma-Aldrich. Promega provided isopropyl β-D-thiogalactopyranoside (IPTG) and DTT. Calf alkaline phosphatase was purchased from Roche. Assay buffer consists of 50 mM Hepes pH 7.6, 15 mM MgSO₄, and 1 mM EDTA.

14388

DOI: 10.1021/jacs.5b09189

J. Am. Chem. Soc. 2015, 137, 14387–14395
Reaction of F3Y•/β2, wt-α2, CDP, and ATP Monitored by RFQ-EPR Spectroscopy. RFQ experiments were performed on an Update Instruments 1019 syringe ram unit and a model 715 Syringe Ram controller (ram speed 1.25–1.6 cm/s) equipped with a Lauda RM6 circulating water bath set at 5 or 25 °C. F3Y•/β2 (0.6 vs 0.8 F3Y•/β2, 80 μM) and CDP (2 mM) CDP was added to 10 μM F3Y•/β2, 1 mM BSA, 1 mM NaN3 in assay buffer. The concentration of BSA was previously estimated using a Cu(II)SO4 standard.29 EPR spectra were recorded at 77 K on a Bruker EMX X-band spectrometer with a quartz field sides of the spectrum as previously reported (Figure S1).19

The reaction was quenched and worked up as described earlier. The time courses of the reactions were fit to eq 3:

\[ y = A_1(1 - e^{-kt}) + A_2(1 - e^{-k't}) \]

where \( A_1 \) and \( A_2 \) are the amplitudes of the two phases and \( k_1 \) and \( k_2 \) are the observed rate constants.

**Results**

"Two or None" Radical Distribution and Half-Sites Reactivity in F3Y•/β2. The dipheric-F3Y• cofactor is self-assembled from apo F3Y/β2 by the addition of Fe2+ and O2 to produce ~0.8 F3Y•/β2 (S1), slower than the 1.2 Y•/wt-β2.31 While the radical distribution in β2 has remained difficult to probe experimentally, evidence collected over the past few years supports that active β2 contains one Y• in each monomer ("two or none", Figure 2A), suggesting that only ~40% of β2 is active in our F3Y•/β2 samples.12,13,20–22,32,33 To provide support for this conclusion, we monitored the effect of F3Y• concentration on the amount of Y356• that accumulates. RFQ-EPR experiments were performed at 25 °C with F3Y•/β2 containing 0.4 F3Y•/β2 or 0.85 F3Y•/β2, wt-α2, CDP, and ATP. The kinetic analysis of these studies is discussed subsequently, but the amount of Y356• is 0.43 and 0.5 equiv/F3Y•, respectively (Table S1). This amount can be rationalized by the "two or none" radical distribution model (Figure 2A) as well as half-sites reactivity in RNR (Figure 2B); only one of the 2 F3Y• reacts at a time to generate Y356•.20–22

Kinetics in the Absence of a Reducing System. Kinetics of Formation and Disappearance of Y356• at 25 °C. To assess if Y356• is formed faster than the turnover number of the enzyme (1.7 s-1, Table 1), a RFQ-EPR experiment was performed in which wt-α2, F3Y•/β2, CDP, and ATP were mixed rapidly (16 ms to 15 s). EPR analysis of each sample revealed a mixture of F3Y• and Y356•, and spectral subtractions...
were performed to quantitate the relative fraction of each radical. The unique hyperfine interactions associated with the fluorine nuclei facilitated spectral deconvolution (Figure S1). The results of the experiment are shown in Figure 3A, and the data were fit to a biexponential equation. Rapid loss of 0.51 ± 0.02 equiv of F3Y• (not shown) concomitant with formation of identical amounts of Y356• occurs at 30 ± 5 s−1. Subsequently, reduction of the pathway radical with kapp 0.4 ± 0.1 s−1 is accompanied by reformation of F3Y• with the same kapp (not shown). These data show for the first time, accumulation of a pathway radical (Y356•) in an active RNR complex that can regenerate the stable radical at position 122 (F3Y•). We note that between 0.1 and 1 s, the concentration of Y356• varies minimally. As shown subsequently, F3Y•/β2 can make multiple dCDPs in the absence of a reducing system, and the reduction of Y356• and reoxidation of F3Y are only visualized after the last turnover when all α2s are oxidized. Finally, regeneration of F3Y• is incomplete with only 0.25 equiv of Y356• reoxidizing F3Y within 10 s.

Kinetics of Formation and Disappearance of Y356• at 5 °C.

The rapid formation of Y356• at 25 °C resulted in generation of 0.25 equiv (50% of total Y356•) prior to the first data point (16 ms, Figure 3A) prompting us to switch to lower temperatures to slow down the reaction. RFQ-EPR experiments were set up at 5 °C as described for 25 °C, and the results are shown in Figure 4A.

Table 1. DeoxyCDP Formation Kinetics in the Absence and Presence of TR/TRR/NADPH

| β2 | T (°C) | R | k1 (s⁻¹) | A/radical | k2 (s⁻¹) | A/radical | dC/α2 | dC/radical |
|----|--------|---|----------|-----------|----------|-----------|-------|-----------|
| F3Y | 25     | N | 30b      | 0.5b      | 0.5 (1)  | 2.9 (1)   | 2.8 (4)c | 3.5 (3)c  |
| F3Y | 25     | Y | 22 (9)   | 0.40 (5)  | 1.73 (4) |           |        |           |
| F3Y | 5      | N | 3 (1)    | 0.3 (1)   | 0.08 (1) | 2.9 (1)   | 2.7 (1) | 3.4 (1)   |
| F3Y | 5      | Y | 6 (3)    | 0.26 (5)  | 0.20 (1) |           |        |           |

*All experiments were performed with 10 μM wt-α2 and 10 μM F3Y•/β2. R notes the absence or presence of a reducing system. A represents the amplitude of each phase. bSee description in main text and SI for more details regarding fitting. cNumbers reported reflect the total amount of dC generated within the first two phases. Product generated in the third phase is cytosine.
A $k_{\text{app}}$ of 3.8 ± 0.5 s$^{-1}$ was measured for formation of Y$_{356}^{\alpha}$ concomitant with loss of F$_3Y^*$ (not shown). In contrast to our observation at 25 °C, only 0.32 ± 0.02 equiv of Y$_{356}^{\alpha}$ is formed at 5 °C reflecting temperature dependent changes in the rates of formation and decay of the pathway radical. Similar to our observation at 25 °C, the concentration of Y$_{356}^{\alpha}$ varies minimally between 0.8 and 5 s supporting the proposal that F$_3Y^*$-β2 catalyzes multiple turnovers prior to visualization of reverse RT. Unlike in the 25 °C reaction, Y$_{356}^{\alpha}$ reduction at 5 °C is accompanied by complete reformation of F$_3Y^*$ (0.3 equiv, 0.06 ± 0.01 s$^{-1}$) within ~40 s.

**Kinetics and dCDP Formation with F$_3Y^*$-β2 at 25 °C.** Each dCDP generated by RNR is accompanied by the formation of a disulfide bond in the active site of an α monomer (Scheme 1, Figure 5, step A). Re-reduction of the active site disulfide by a C-terminal cysteine pair on each monomer (step B) facilitates an additional turnover (step C),11 giving a theoretical maximum of 4 dCDP/α2 can be produced; however, only 3 dCDP/α2 are routinely measured. The reaction mixture contains only 40% active F$_3Y^*$-β2 (Figure 2A) supporting reorganization of active and inactive α2/F$_3Y^*$-β2 complexes to oxidize all α2s.

![Figure 5](image-url)

**Figure 5.** Amount of dCDP generated in the absence of a reducing system. A theoretical maximum of 4 dCDP/α2 can be produced; however, only 3 dCDP/α2 are routinely measured. The reaction mixture contains only 40% active F$_3Y^*$-β2 (Figure 2A) supporting reorganization of active and inactive α2/F$_3Y^*$-β2 complexes to oxidize all α2s.

To assess if Y$_{356}^{\alpha}$ is on-pathway, the kinetics of dCDP formation were determined. Wt-α2, F$_3Y^*$-β2, [3H] CDP, and ATP were mixed (5 ms to 300 s) and quenched rapidly with 2% HClO$_4$, CDP and dCDP were separated and analyzed by standard procedures14,30 and the results are shown in Figure 3B. The data are best described by eq 2 with a fixed first exponential phase, a variable second exponential phase, and a very slow third linear phase. We initially attempted to fit the data with an exponential phase and a linear phase with poor results (Figure 2A).

To obtain the fit shown in Figure 3B (black line), we fixed the amplitude and rate constant ($k_1$) of the first phase at 0.5 dCDP/F$_3Y^*$ and 30 s$^{-1}$, respectively. Fixing this phase was required due to the scatter in the data at early time points. This scatter is a result of “two or none” and half-sites reactivity associated with RNR (Figure 2A). The [3H] dCDP measured between 5 and 100 ms is close to the background measured with [3H] CDP in the absence of α2. The range of choices considered for the amplitude and $k_1$ of this phase were based on the amplitude and rate constant measured for Y$_{356}^{\alpha}$ formation by RFQ-EPR (Figure 3A) and the results obtained in the presence of the reducing system (presented in the next section). The detailed description of data fitting using different parameters for the first kinetic phase is shown in Figure S2A–D. An additional experiment to justify the fixed first phase is shown in Figure S3.

Once the first phase was fixed using eq 2, we obtained an amplitude and rate constant ($k_2$) of 2.9 ± 0.1 dCDP/F$_3Y^*$ and 0.5 ± 0.1 s$^{-1}$, respectively, for the second phase and a rate constant ($k_3$) of 0.012 ± 0.001 s$^{-1}$ for the linear phase. This slow linear phase is associated with cytosine release and not dCDP formation. It occurs during the reaction of F$_3Y^*$-β2 with oxidized α2 as shown in Scheme S1.34 In a second manuscript, we show that the inability to monitor complete reverse RT at 25 °C (Figure 3A) is associated with reoxidation of Y$_{356}^{\alpha}$ (0.25 equiv) by F$_3Y^*$-β2/oxidized α2.

The fit shown in Figure 3B suggests that the pathway radical is kinetically and chemically competent for nucleotide reduction at 25 °C. These data require that Y$_{356}^{\alpha}$ accumulates during reverse RT. k$_2$ for product formation correlates well with $k_{\text{app}}$ for Y$_{356}^{\alpha}$ disappearance at this temperature (0.5 s$^{-1}$ vs 0.4 s$^{-1}$, Figure 3A).

**Kinetics and dCDP Formation with F$_3Y^*$-β2 at 5 °C.** The kinetics of dCDP formation were also measured at 5 °C, and the results are shown in Figure 4B. The data were fit to a bi-exponential equation providing amplitudes of 0.3 ± 0.1 dCDP/F$_3Y^*$ and 2.9 ± 0.1 dCDP/F$_3Y^*$ with $k_1$ and $k_2$ of 3 ± 1 s$^{-1}$ and 0.08 ± 0.01 s$^{-1}$, respectively (Table 1). $A_1$ and $k_1$ for dCDP formation are very similar to the amplitude and rate constant measured for Y$_{356}^{\alpha}$ formation by RFQ-EPR spectroscopy at the same temperature (Figure 4A). These data suggest that Y$_{356}^{\alpha}$ is kinetically and chemically competent for dCDP formation and accumulates during reverse RT. Similar to our observations at 25 °C, k$_2$ of 0.08 s$^{-1}$ for dCDP formation is similar to $k_{\text{app}}$ of 0.06 s$^{-1}$ for reoxidation of F$_3Y$ by Y$_{356}^{\alpha}$ (Figure 4A).

The RCQ data were also analyzed relative to α2 to show that 2.7 ± 0.1 dCDPs/α2 are generated. DeoxyCDP formation was monitored for a total of 20 min, and in contrast to the 25 °C data, no third kinetic phase associated with cytosine was observed.

**Kinetics in the Presence of a Reducing System. EPR Analysis of Y$_{356}^{\alpha}$ Concentration During Steady-State Turnover.** The ability of F$_3Y^*$-β2 to perform multiple turnovers in the absence of a reducing system (3.5 dCDP/F$_3Y^*$, Table 1) and the observation of a plateau phase in the RFQ-EPR kinetic traces (Figures 3A and 4A) suggested that reverse RT is visualized subsequent to complete oxidation of α2. Thus, we predicted that the concentration of Y$_{356}^{\alpha}$ would vary minimally in the presence of the reducing system, TR/TRR/NADPH, as oxidized α2 is re-reduced. To test this prediction, F$_3Y^*$-β2, wt-α2, CDP, and ATP were combined in the presence of TR/ TRR/NADPH, and samples were quenched by hand in liquid isopropanol between 20 and 90 s. In accordance with our
prediction, the amount of Y\textsuperscript{356}• does not change: 0.26 to 0.28 equiv/F\textsubscript{3}Y\textsuperscript{•} at 5 °C and 0.40 to 0.46 equiv/F\textsubscript{3}Y\textsuperscript{•} at 25 °C (Table S2). No reverse RT was visualized during the time frame of the reaction.

Kinetics of dCDP Formation at 5 and 25 °C. The observation of Y\textsuperscript{356}• accumulation during reverse RT (Figures 3 and 4) in the absence of a reducing system and the lack of variation in [Y\textsuperscript{356}•] during steady-state turnover suggest that the rate-limiting step occurs subsequent to dCDP formation and Y\textsuperscript{356}• reformation during reverse RT. This model predicts that RCQ experiments in the presence of the reducing system would show a burst of dCDP representing the first turnover by an α/β pair. Reverse PCET regenerating F\textsubscript{3}Y\textsuperscript{*} is rate-limiting during steady-state turnover.

As predicted, a burst of dCDP formation is observed at both temperatures (0.26 ± 0.05 dCDP/F\textsubscript{3}Y\textsuperscript{*} at 6 ± 3 s\textsuperscript{-1} at 5 °C and 0.40 ± 0.05 dCDP/F\textsubscript{3}Y\textsuperscript{*} at 22 ± 9 s\textsuperscript{-1} at 25 °C) followed by a linear phase (0.20 ± 0.01 s\textsuperscript{-1} at 5 °C and 1.73 ± 0.04 s\textsuperscript{-1} at 25 °C). The large uncertainties observed in these parameters are associated with low amounts of dCDP arising from the “two or none” model (Figure 2A) and half-sites reactivity (Figure 2B). Unfortunately, we are unable to increase protein concentration in these experiments as studies with wt RNR have revealed kinetic complexities associated with the re-reduction process and potentially quaternary structure interconversions.

Scheme 2. Kinetic Model for wt RNR in the Absence and Presence of a Reducing System\textsuperscript{a}

\textsuperscript{a}The graphic shows only the key amino acids in the PCET pathway. Rate constants are shown for the reaction at 25 °C. Y\textsubscript{356}• cannot be visualized in wt RNR due to the rate-limiting conformational change(s). Figure adapted from ref 11.

**DISCUSSION**

The rate-limiting protein conformational change(s) that gate(s) E. coli class Ia RNR turnover has precluded insight into the 35 Å forward RT, nucleotide reduction, and reverse RT processes. Our current model for wt RNR based on studies similar to those described herein for F\textsubscript{3}Y\textsuperscript{*}/β2 is shown in Scheme 2.
Upon association of β2/α2/CDP/ATP, a conformational change(s) (5–10 s⁻¹, Scheme 2, step A) triggers rapid RT into α2 and nucleotide reduction (>100 s⁻¹, step B). DeoxyCDP formation is rate-limited by the conformational change(s) and occurs at 5–10 s⁻¹ as measured by RCQ methods reported previously and reproduced here under the same conditions utilized for the F3Yβ2 studies (Figure S4). Subsequent to dCDP formation, reverse RT to regenerate Y122 is required to be downhill and rapid (>10³ s⁻¹, step C) as modeled by Ge et al.¹¹ to account for our inability to observe Y122 disappear and reappear during turnover (±TR/TRR/NADPH). The physical steps in wt RNR preclude detection of intermediates in these processes. Thus, studying the chemistry has required engineering specific perturbations to the system initially through site-directed mutagenesis and the use of mechanism-based inhibitors and, more recently, with site-specific incorporation of unnatural amino acids. While with many of these approaches we were able to monitor the disappearance of Y122 concomitant with formation of new radicals, in none of these cases was the catalytic cycle of RNR completed, and no insight was obtained into reverse RT.

Our recent engineering of an orthogonal tRNA-synthetase tRNA pair that can incorporate di- and trifluorotyrosines (F3Y, n = 2, 3) with a range of reduction potentials and pKₐ values in RNR allowed us to introduce a tunable thermodynamic perturbation of PCET kinetics with minimal steric perturbations. F3Y is predicted as ~10 mV harder to oxidize than Y,¹⁷,⁴³ assuming that the first step in forward RT involves PT from the water on the diferric cluster to F3Y concomitant with ET from Y356 to F3Y (Figure 1). F3Y/β2 is capable of catalyzing multiple turnovers but allows detection of Y356 (±TR/TRR/NADPH) due to perturbed reverse RT kinetics. Our current model for F3Yβ2 turnover is shown in Scheme 3. The ability to accumulate Y356 in F3Yβ2 but not in wt RNR is directly related to the differences in the rate-limiting step in the two systems.

In our model, the F3Yβ2/wt-α2/CDP/ATP complex undergoes a conformational change prior to generation of Y356 in one α/β pair (Scheme 3, step A). The RFQ-EPR data reported in Figures 3A and 4A provide the rate constants for this step and suggest that F3Yβ2 perturbs the conformational gate relative to the wt enzyme (20–30 vs 5–10 s⁻¹). We expect that forward RT into α and dCDP production (step B in Schemes 2 and 3) occur with similar rate constants to wt RNR (>100 s⁻¹). DeoxyCDP formation is rate-limited by the slow, conformationally gated generation of F3Yβ2 during forward RT as measured by the first phase in the absence of a reducing system (Figures 3B and 4B) or the burst phase in the presence of TR/TRR/NADPH (Figure 6) in the RCQ studies. Subsequent to product formation, we propose that reverse RT to regenerate Y356 is fast as modeled in wt RNR where reverse RT to regenerate Y122 is ~10³ s⁻¹. However, unlike in wt RNR, slow reoxidation of F3Y (step C) rate-limits subsequent turnovers.

In the absence of a reducing system, the RFQ-EPR data (Figures 3A and 4A) provide the rate constants for step C. Upon regeneration of F3Yβ2, β2 rapidly dissociates from a partially oxidized α2, associates with a second reduced α2 and cycles through steps A–C until all α2s are completely oxidized. Y356 concentration does not vary significantly during this time as visualized by the plateaus in the RFQ-EPR kinetic traces (Figures 3A and 4A). The second phase of the RCQ studies described in Figures 3B and 4B provides the rate constants for turnover in the absence of TR/TRR/NADPH (Scheme 3, branch I). Altered reverse RT kinetics in F3Yβ2 allow us to observe for the first time the disappearance and reappearance of the radical at position 122 subsequent to complete oxidation of α2. The molecular bases for our ability to observe reverse RT are not well-understood but are likely related to the initiating step in the PCET process. In addition to perturbing the driving force for RT, the fluorotyrosine substitutions could alter the distance between the phenolic oxygen and the water on the diferric cluster, thus affecting PT between the two (Figure 1). F3Y also perturbs the pKₐ at position 122 compared to Y (solution pKₐ 6.4 vs 10). Depending on the pKₐ of the water on the diferric cluster, the phenolic F3Y could be generated instead of the anticipated phenol F3Y.

Additional insight into the differences between wt and F3Yβ2 catalysis is obtained from the amplitudes for dCDP formation in the absence of a reducing system (Table 1 and Figure S4). In the F3Yβ2 system, the first phase (0.5 dCDP/F3Y at 25 °C) reports on the very first turnover by an α/β pair (Figure 2B),
while the second phase (2.9 dCDP/F3Yβ) reports on consumption of all remaining reduced \( \alpha \)2s, rate-limited by reverse RT. This result is distinct from our previous\(^{1,11}\) and current observations for wt RNR (Figure S4) where two phases are also measured for dCDP formation. The first phase is presumed to report on the conformationally gated generation of 2 dCDPs by all \( \alpha \)2s (the experimental observation is 1.3 ± 0.2 dCDP/\( \alpha \)2, 6 ± 1 s\(^{-1}\)), and the second phase is interpreted to report on the generation of 2 additional dCDPs subsequent to re-reduction of the active site disulphide (the experimental observation is 1.6 ± 0.2 dCDP/\( \alpha \)2, 0.5 ± 0.1 s\(^{-1}\)). The variation in the amplitudes of the two phases between wt and F3Yβ/2 is consistent with different rate-limiting steps in the two systems. However, in both cases the total number of dCDPs generated is the same: 3 dCDP/\( \alpha \)2 (Schemes 2 and 3, branch I).

The EPR and RCQ data collected in the presence of a reducing system also lend support to Scheme 3. In F3Yα/Yβ, a burst of dCDP formation prior to steady-state turnover is observed. The amplitude of this phase (\( \sim 0.5 \) dCDP/F3Yα at 25 °C) again reflects that turnover occurs only on one \( \alpha \)/\( \beta \) pair prior to the rate-limiting step and is consistent with slow reverse RT. Upon regeneration of F3Yα after one turnover (Scheme 3, step C), re-reduction of oxidized \( \alpha \)2 by TR/TRR/NADPH resets the system for additional turnovers (branch II). Y156β under these conditions behaves in a similar fashion to Y122β in wt RNR; i.e., no changes in its concentration are detected during steady-state conditions (Table S2). Slow reoxidation of F3Y followed by rapid re-reduction, forward RT, nucleotide reduction, and regeneration of Y156β (Scheme 3, steps A–C) precludes observation of its disappearance and reappearance. We interpret the linear phases in Figure 6A,B as representative of the rate constants for reverse RT in the presence of a reducing system (Scheme 3, step C) and the rate constant limits for re-reduction of oxidized \( \alpha \)2. Although we set a lower limit for re-reduction from our experiments, we note that the rate constant for this step must be relatively fast, \( > 5 \times 10^{5} \) s\(^{-1}\), to account for our inability to monitor changes in Y156β concentration.

A comparison of the burst phase for F3Yα/Yβ and that for wt RNR in the presence of TR/TRR/NADPH reveals distinct behavior in the two systems (Figure 6 and Figure S5).\(^{11}\) Although the conformational change is rate-limiting for dCDP formation in wt RNR, we have previously noted that the rate-limiting step in the presence of a reducing system can switch to re-reduction of oxidized \( \alpha \)2 at the high protein concentrations required for RCQ studies (10 \( \mu \)M).\(^{11}\) In wt RNR, this results in a conformationally gated burst of 2 dCDPs by all \( \alpha \)2s (the experimental observation is 1.9 ± 0.1, 9 ± 2 s\(^{-1}\)) prior to steady-state turnover (Figure S5).\(^{11}\) The burst phase reflects oxidation of all \( \alpha \)2 active sites despite the presence of only 60% active wt-\( \beta \)2 (1.2 Yα/Yβ, Figure 2A) and does not represent a single turnover. In contrast to the wt system, we have isolated the very first turnover by an \( \alpha \)2/\( \beta \)2 complex with F3Yα/Yβ due to rate-limiting reverse RT.

As a final point, the rate constant measured for dCDP formation in the presence of a reducing system is 3-fold faster than that measured in its absence (Scheme 3, branch I vs I). A similar variation has been previously noted for dCDP formation in the wt system.\(^{11}\) It is possible that re-reduction of the active site disulphide by the C-terminal tail (Figure 5, step B) is reversible and only driven to completion when the TR/TRR/NADPH system is included in the assays. However, we currently cannot rule out other modes by which TR accelerates re-reduction of the \( \alpha \)2 active site.

### CONCLUSIONS

Radical initiation in the class I RNRs is proposed to involve long-range PCET through three pathway tyrosines.\(^{9,10,17}\) Using an engineered RNR system, we have observed one of the proposed intermediates and demonstrate for the very first time chemically competent reverse RT that completes the RNR catalytic cycle. We additionally obtained insight into radical stoichiometry within \( \beta \)2, half-sites reactivity, and the ability of \( \beta \)2 to act catalytically during turnover. This work highlights the utility of unnatural amino acids in engineering specific perturbations for the study of redox active tyrosine residues in proteins; F3Y could facilitate understanding of a number of additional tyrosyl radical mediated metabolic processes.\(^{45–48}\)

### ASSOCIATED CONTENT

#### Supporting Information

The Supporting Information is available free of charge on the ACS Publications website at DOI: 10.1021/jacs.5b09189.

Detailed experimental procedures, tables, figures, and scheme of cytosine release from CDP (PDF)

### AUTHOR INFORMATION

**Corresponding Author**

*stubbe@mit.edu*

**Present Address**

‡Merck Research Laboratories, 33 Avenue Louis Pasteur, Boston, MA 02115, United States.

**Notes**

The authors declare no competing financial interest.

### ACKNOWLEDGMENTS

This work was supported by NIH Grant GM29595 to J.S.

### REFERENCES

1. Stubbe, J.; van der Donk, W. A. Chem. Rev. 1998, 98, 705–62.
2. Jordan, A.; Reichard, P. Annu. Rev. Biochem. 1998, 67, 71–98.
3. Brown, N. C.; Canellakis, Z. N.; Lundin, B.; Reichard, P.; Thelander, L. Eur. J. Biochem. 1996, 9, 561–73.
4. Licht, S.; Gerfen, G. J.; Stubbe, J. Science 1996, 271, 477–81.
5. Stubbe, J. Proc. Natl. Acad. Sci. U. S. A. 1998, 95, 2723–4.
6. Licht, S.; Stubbe, J. Compr. Nat. Prod. Chem. 1999, 5, 163–203.
7. Stubbe, J.; Ackles, D. J. Biol. Chem. 1980, 255, 8027–30.
8. Nordlund, P.; Sjöberg, B. M.; Eklund, H. Nature 1990, 345, 593–8.
9. Uhlín, U.; Eklund, H. Nature 1994, 370, 533–9.
10. Stubbe, J.; Nocera, D. G.; Yee, C. S.; Chang, M. C. Y. Chem. Rev. 2003, 103, 2167–201.
11. Ge, J.; Yu, G.; Ator, M. A.; Stubbe, J. Biochemistry 2003, 42, 10071–83.
12. Yokoyama, K.; Uhlín, U.; Stubbe, J. J. Am. Chem. Soc. 2010, 132, 15368–79.
13. Seyedsayamdost, M. R.; Stubbe, J. J. Am. Chem. Soc. 2006, 128, 2522–3.
14. Sjöberg, B. M.; Gräsuldn, A.; Eckstein, F. J. Biol. Chem. 1983, 258, 8060–7.
15. Salowe, S.; Bollinger, J. M., Jr.; Ator, M.; Stubbe, J.; McCracken, J.; Peisach, J.; Samano, M. C.; Robins, M. J. Biochemistry 1993, 32, 12749–12760.
16. Artin, E.; Wang, J.; Loehman, G. J.; Yokoyama, K.; Yu, G.; Griffin, R. G.; Bar, G.; Stubbe, J. Biochemistry 2009, 48, 11622–9.
17. Minnihan, E. C.; Nocera, D. G.; Stubbe, J. Acc. Chem. Res. 2013, 46, 2524–35.
(18) Wörsdorfer, B.; Conner, D. A.; Yokoyama, K.; Livada, J.; Seyedsayamdost, M.; Jiang, W.; Silakov, A.; Stubbe, J.; Bollinger, J. M., Jr.; Krebs, C. J. Am. Chem. Soc. 2013, 135, 885–93.
(19) Minnihan, E. C.; Young, D. D.; Schultz, P. G.; Stubbe, J. J. Am. Chem. Soc. 2011, 133, 15942–5.
(20) Yokoyama, K.; Smith, A. A.; Corillius, B.; Griffin, R. G.; Stubbe, J. J. Am. Chem. Soc. 2014, 133, 18420–32.
(21) Seyedsayamdost, M. R.; Chan, C. T.; Mugnaini, V.; Stubbe, J.; Bennati, M. J. Am. Chem. Soc. 2007, 129, 15748–9.
(22) Minnihan, E. C. Ph.D. Dissertation, Massachusetts Institute of Technology, 2012.
(23) Minnihan, E. C.; Seyedsayamdost, M. R.; Uhlin, U.; Stubbe, J. J. Am. Chem. Soc. 2011, 133, 9430–40.
(24) Seyedsayamdost, M. R.; Xie, J.; Chan, C. T.; Schultz, P. G.; Stubbe, J. J. Am. Chem. Soc. 2007, 129, 15060–71.
(25) Chen, H.; Gollnick, P.; Phillips, R. S. Eur. J. Biochem. 1995, 229, 540–9.
(26) Seyedsayamdost, M. R.; Yee, C. S.; Stubbe, J. Nat. Protoc. 2007, 2, 1225–35.
(27) Chivers, P. T.; Prehoda, K. E.; Volkman, B. F.; Kim, B. M.; Markley, J. L.; Raines, R. T. Biochemistry 1997, 36, 14985–91.
(28) Russel, M.; Model, P. J. Bacteriol. 1985, 163, 238–242.
(29) Palmer, G. Methods Enzymol. 1967, 10, 594–610.
(30) Steeper, J. R.; Steuart, C. D. Anal. Biochem. 1970, 34, 123–30.
(31) Tong, W. H.; Chen, S.; Lloyd, S. G.; Edmondson, D. E.; Huynh, B. H.; Stubbe, J. J. Am. Chem. Soc. 1996, 118, 2107–8.
(32) Bennati, M.; Weber, A.; Antonic, J.; Perlstein, D. L.; Robblee, J. H. J. Am. Chem. Soc. 2003, 125, 14988–9.
(33) Bennati, M.; Robblee, J. H.; Mugnaini, V.; Stubbe, J.; Freed, J. H.; Borbat, P. J. Am. Chem. Soc. 2005, 127, 15014–5.
(34) Ator, M. A.; Stubbe, J. Biochemistry 1985, 24, 7214–21.
(35) Ando, N.; Brignole, E. J.; Zimanyi, C. M.; Funk, M. A.; Yokoyama, K.; Asturias, F. J.; Stubbe, J.; Drennan, C. L. Proc. Natl. Acad. Sci. U. S. A. 2011, 108, 21046–51.
(36) Olshansky, L.; Pizano, A. A.; Wei, Y.; Stubbe, J.; Nocera, D. G. J. Am. Chem. Soc. 2014, 136, 16210–6.
(37) Lawrence, C. C.; Bennati, M.; Obias, H. V.; Bar, G.; Griffin, R. G.; Stubbe, J. Proc. Natl. Acad. Sci. U. S. A. 1999, 96, 8979–84.
(38) Mao, S. S.; Holler, T. P.; Yu, G. X.; Bollinger, J. M., Jr.; Booker, S.; Johnston, M. I.; Stubbe, J. Biochemistry 1992, 31, 9733–43.
(39) Persson, A. L.; Eriksson, M.; Katterle, B.; Pötsch, S.; Sahlin, M.; Sjöberg, B. M. J. Biol. Chem. 1997, 272, 31533–41.
(40) Kasravy, A.; Persson, A. L.; Sahlin, M.; Sjöberg, B. M. J. Biol. Chem. 2002, 277, 5749–55.
(41) van der Donk, W. A.; Stubbe, J.; Gerfen, G. J.; Bellew, B. F.; Griffin, R. G. J. Am. Chem. Soc. 1995, 117, 8908–16.
(42) van der Donk, W. A.; Yu, G. X.; Pérez, L.; Sanchez, R. J.; Stubbe, J.; Samano, V.; Robins, M. J. Biochemistry 1998, 37, 6419–26.
(43) Seyedsayamdost, M. R.; Reece, S. Y.; Nocera, D. G.; Stubbe, J. J. Am. Chem. Soc. 2006, 128, 1569–79.
(44) Olshansky, L. Ph.D. Dissertation, Massachusetts Institute of Technology, 2015.
(45) Barry, B. A.; El-Deeb, M. K.; Sandusky, P. O.; Babcock, G. T. J. Biol. Chem. 1990, 265, 20139–43.
(46) Gupta, A.; Mukherjee, A.; Matsui, K.; Roth, J. P. J. Am. Chem. Soc. 2008, 130, 11274–5.
(47) Zhao, X.; Suarez, J.; Khajo, A.; Yu, S.; Metlitsky, L.; Magliziozzo, R. S. J. Am. Chem. Soc. 2010, 132, 8268–9.
(48) Tsai, A. L.; Kulmacz, R. J. Arch. Biochem. Biophys. 2010, 493, 103–24.