Comment on “The [4Fe4S] cluster of human DNA primase functions as a redox switch using DNA charge transport”

Andrey G. Baranovskiy,1 Nigar D. Babayeva,1 Yinbo Zhang,2 Luis Blanco,3 Youri I. Pavlov,1,4,5 Tahir H. Tahirov1

O’Brien et al. (Research Article, 24 February 2017, eaag1789) proposed a novel mechanism of primase function based on redox activity of the iron-sulfur cluster buried inside the C-terminal domain of the large primase subunit (p58C). Serious problems in the experimental design and data interpretation raise concerns about the validity of the conclusions.

The human p58C protein used by O’Brien et al. (1) contains the I271S mutation and exhibits an anomalous structure at the DNA:RNA-binding interface that is drastically different from the conserved structure of human p58C and its yeast ortholog determined by two independent groups in four different protein assemblies (2–5) (Fig. 1A). Without any explanation or qualification, O’Brien et al. assumed that the β-hairpin structure in their mutated p58C binds the RNA:DNA substrate in the same way as the α-helical structure in wild-type (WT) p58C [see figure 3, A and B, and figure S6 in (1)]. Moreover, the authors concluded that Y345 and Y347, which are adjacent in the mutated p58C (Fig. 1A), participate in the charge transfer (CT) between the iron-sulfur cluster and the DNA substrate. However, these two residues are 16.1 Å apart and oriented differently in the conserved p58C structure (Fig. 1, A and B). Consequently, results of CT and DNA-binding experiments are not applicable to WT primase.

DNA substrates used by O’Brien et al. in the binding and CT experiments are biologically irrelevant. Both the 5′-triphosphate of a primer and the 3′ overhang of a template are critical for DNA-RNA binding by p58C and primase (4, 6) (Fig. 1C, highlighted in blue). However, the substrate used by O’Brien et al. lacks these key binding elements (Fig. 1D), which results in affinity for mutated p58C less than 1/150 that of the natural substrate for WT p58C (Kd = 5.5 μM versus 33 nM) (see figure S1 in (1) and table 2 in (6), respectively). Previously, Chazin’s group obtained a Kd of 0.3 μM (table S2 in (7)) instead of 5.5 μM as reported in (4) using the same protein, substrate, and experimental procedure (1). This almost 20-fold difference was not explained.

The only supporting evidence by O’Brien et al. for the redox switch involvement in primer synthesis is the rate reduction of de novo RNA synthesis by the Y345F mutant (figure 4A in (1)). However, the rate reduction can be explained by a completely different mechanism. In the conserved p58C/substrate complex structure, Y345 interacts with the γ-phosphate of the initiating nucleotide triphosphate (NTP) (Fig. 1B) (4), which is rather sensitive to the binding environment (8, 9). For example, mutation of Arg306 analog in yeast primase, which makes two contacts with

Fig. 1. Comparison of functionally relevant primase substrate and correctly folded p58C (4) with the substrate and misfolded p58C used by O’Brien et al. (1). (A) Side-by-side comparison of p58C structures with correctly folded [Protein Data Bank (PDB) code 5F0Q] and misfolded (PDB code 3L9Q) substrate-binding regions highlighted in different colors. These regions are overlapped in the left bottom quarter. The positions of Y309, Y345, and Y347 relative to [4Fe-4S]2+ in two structures are shown in the right bottom quarter. The reason for p58C misfolding might be explained by substitution of structurally important I271 by serine in erroneously named “wild-type” p58C (PDB code 3L9Q) or by asparagine in its mutants Y345F and Y347F (PDB codes 5I7M and 5DQO, respectively). (B) Crystal structure of p58C in complex with a duplex containing 5′-triphosphate RNA and 3′-overhang DNA (4). (C) Primase substrate (6) with the 5′-triphosphate of a primer and the 3′ overhang of a template that are required for p58C binding and are shown in blue. (D) Substrate used by O’Brien et al. (1) for electrochemistry experiments. In (C) and (D), the red-colored 5′ overhanging do not participate in binding of correctly folded p58C. The figure was prepared using the PyMOL Molecular Graphics System (version 1.8, Schrödinger, LLC).
A 5′-(Pu)αGGAGAGAACAAGCCGGCCAAACACG-3′
5′-triphosphate/3′-overhang
Enzyme concentration (nM)

B 5′-(Pu)αGGAGAGAAG(A)3-3′
3′-(U)15(T)15-5′

<table>
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<tr>
<th>Reaction time (min)</th>
<th>Reaction</th>
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<th>Primer synthesis from T29</th>
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<td>2</td>
<td>1</td>
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<td>12-mer</td>
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Fig. 2. Side-by-side comparison of experimental setups for examination of RNA synthesis termination by human primase. (A) Example of primer elongation reactions showing the effect of template:primer structure on the efficiency of RNA synthesis termination by human primase, as described by Baranovskiy et al. (6). When using the correct substrate containing 5′-triphosphate and 3′-overhang, there is pronounced termination of reaction mainly at 9-nucleotide oligomer primers (lanes 3 and 4), which are optimal for extension by Polα (4). However, in the case of template:primer without 5′-triphosphate and 3′-overhang, primase loses the ability to terminate synthesis at 9-nucleotide oligomer primers (lanes 6 and 7) and has dramatically reduced activity, which requires a higher load of the enzyme and longer reaction time. Primase activity reactions were reproduced as in (6). The products were labeled by incorporation of [α-32P]GTP (guanosine triphosphate) at the seventh position of primer. The negatively charged triphosphate moiety increases the mobility of RNA primers. Lanes 1 and 5 control incubations in absence of enzyme or primer, respectively. Lane 2 reaction was not supplied with CTP and UTP. (B) Example of incorrectly designed primer elongation reactions, which are not capable of capturing physiologically relevant primer termination. The image was adopted from figure 5A in (1); note the high enzyme concentrations and long reaction time. The products with a length of 29 nucleotides or less are the result of RNA synthesis initiated from T29 in the template. Appearance of primers longer than 10 nucleotides is due to the absence of Polα or its catalytic core, which allows primase to rebind the 9-nucleotide oligomer primer without involvement of p58C and extend further (6, 14). Unfortunately, the gel provided does not allow visualization of the products of de novo synthesis from 2-nucleotide oligomer to 9- to 12-nucleotide oligomer. Counting of bands below 29-nucleotide oligomer product indicates that the lowest visible band corresponds to 18-nucleotide oligomer primer, not to 10-nucleotide oligomer as shown in figure S14 in (1).

5A and S14 (1) is a result of de novo RNA synthesis termination due to reaching the end of the primer [similar to termination in figure 4A in (1)] rather than abrogation of extension of a 31-nucleotide oligomer primer. Indeed, figure S14 in (1) confirms that Y345F substitution reduces the number of de novo synthesized primers, without any relation to CT. In the same manner, the absence of products with a length of ~30 nucleotides or less [as observed in figure 5A (right panel) in (1)] relates to abrogation of de novo primer synthesis and not to disruption of CT, because the introduced mismatch definitely disturbs the short (6 base pair) and AT-rich DNA:RNA duplex.

No direct evidence was provided that the oxidized [4Fe-4S]$^{2+}$ cluster was obtained during electrochemical experiments with p58C. Moreover, the affinity of DNA to p58C with the oxidized cluster was not measured to confirm the statement that this form binds more strongly to the template:primer. Actually, p58C without any electrochemical manipulations binds tightly to the correct substrate under aerobic conditions (6), in which the [4Fe-4S]$^{2+}$ cluster of primase is stable (9, 12). The authors avoided comparison of primer synthesis in aerobic versus anaerobic conditions but claimed the advantage of the latter. In fact, primase efficiently initiates and terminates RNA synthesis under aerobic conditions (6, 8), and the presence of an iron-sulfur cluster in Polα is still under debate (13). Moreover, Polα is absent in the primer elongation assay in (1), which renders the conclusion of its proposed role in termination of RNA primer synthesis a mere speculation.

Given the questionable results and the conclusions contradicting the biochemical, structural, and genetic data cumulated over three decades (13), we ask O’Brien et al. to re-examine their experiments and reconsider the conclusions.

REFERENCES AND NOTES


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