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The structure of *Pyrococcus horikoshii* 2′-5′RNA ligase at 1.94 Å resolution reveals a possible open form with a wider active-site cleft

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The structure of *Pyrococcus horikoshii* 2′-5′ RNA ligase at 1.94 Å resolution reveals a possible open form with a wider active-site cleft

Bacterial and archael 2′-5′ RNA ligases, members of the 2H phosphoesterase superfamily, catalyze the linkage of the 5′ and 3′ exons via a 2′-5′-phosphodiester bond during tRNA-precursor splicing. The crystal structure of the 2′-5′ RNA ligase PH0099 from *Pyrococcus horikoshii* OT3 was solved at 1.94 Å resolution (PDB code 1vgj). The molecule has a bilobal α+β arrangement with two antiparallel β-sheets constituting a V-shaped active-site cleft, as found in other members of the 2H phosphoesterase superfamily. The present structure was significantly different from that determined previously at 2.4 Å resolution (PDB code 1vdx) in the active-site cleft; the entrance to the cleft is wider and the active site is easily accessible to the substrate (RNA precursor) in our structure. Structural comparison with the 2′-5′ RNA ligase from *Thermus thermophilus* HB8 also revealed differences in the RNA precursor-binding region. The structural differences in the active-site residues (tetrapeptide motifs H-X-T/S-X) between the members of the 2H phosphoesterase superfamily are discussed.

1. Introduction

The tRNA precursors (pre-tRNA), the primary transcripts of tRNA genes, must undergo processing before becoming functional. This processing involves the removal of introns by splicing, the cleavage of extra 5′ nucleotides, the replacement of UU residues at the 3′ end with a CCA sequence and the modification of numerous bases (Abelson et al., 1998). To remove the introns, the pre-tRNA is cleaved by endonuclease to produce a 5′ exon with a 2′,3′-cyclic monophosphate end and a 3′ exon with a 5′-OH end (Peebles et al., 1983). In eukaryotes, the two half-molecules are joined by a 3′,5′-phosphodiester bond linkage, which is catalyzed by ATP-dependent tRNA ligase through three steps of nucleotidyl transfer. The yeast tRNA ligase consists of an N-terminal adenyltransferase domain, a central domain with kinase activity and a C-terminal domain that is similar to the 2H phosphotransferase superfamily. The present structure was significantly different from that determined previously at 2.4 Å resolution (PDB code 1vdx) in the active-site cleft; the entrance to the cleft is wider and the active site is easily accessible to the substrate (RNA precursor) in our structure. Structural comparison with the 2′-5′ RNA ligase from *Thermus thermophilus* HB8 also revealed differences in the RNA precursor-binding region. The structural differences in the active-site residues (tetrapeptide motifs H-X-T/S-X) between the members of the 2H phosphoesterase superfamily are discussed.
mammals and their sequence similarity is low. However, the three-dimensional structures of these proteins or corresponding domains are similar. It has been suggested that the four subclasses of this superfamily originated from a common ancestor (Kozlov et al., 2005). In this superfamily, CPDases (Holmann et al., 2000), fungal RNA ligases (Xu et al., 1990) and CNPases (Sakamoto et al., 2005; Kozlov et al., 2003) have one domain that possesses hydrolysis activity, while in yeast tRNA ligase the C- and N-terminal domains possess hydrolysis and ligation activities, respectively (Sawaya et al., 2003; Wang & Shuman, 2005). Only the subclass of bacteria and archaeal 2'-5' RNA ligases, which are single-domain proteins, possess both hydrolysis activity towards 2',3'-cyclic phosphodiester bonds and ligation activity towards two RNA exons with 2'-phosphate and 5'-OH ends. It is possible that the 2'-5' RNA ligase acts as a bridge between the structural homology of the 2H phosphoesterase superfamily and yeast tRNA ligase.

Table 1
Crystal parameters and data-collection statistics.

<table>
<thead>
<tr>
<th>Crystal</th>
<th>ScMet</th>
<th>Data quality</th>
</tr>
</thead>
<tbody>
<tr>
<td>Space group</td>
<td>P2_12_12</td>
<td>10839 (461)</td>
</tr>
<tr>
<td>No. of unique reflections</td>
<td>14330 (1394)</td>
<td>99.9 (99.6)</td>
</tr>
<tr>
<td>Completeness (%)</td>
<td>73.8 (6.6)</td>
<td>16.5 (3.8)</td>
</tr>
<tr>
<td>Redundancy</td>
<td>4.7 (38.4)</td>
<td></td>
</tr>
</tbody>
</table>

Values in parentheses are for the highest resolution shell.

Table 2
Summary of refinement statistics.

| Resolution range (Å) | 10.1-1.94 |
| Number of reflections (total/test) | 12780/1414 |
| No. of residues | 184 |
| No. of water molecules | 41 |
| Rmerge (%) | 21.6265 |
| R.m.s.d. bond lengths (Å) | 0.027 |
| R.m.s.d. angles (°) | 1.966 |
| Average B factor (Å²) | 33.7 |
| Protein molecules | 38.1 |
| Water molecules | |
| Ramachandran plot (%) | |
| Most favoured regions | 93.4 |
| Generously allowed regions | 6.6 |
| Disallowed regions | 0 |

2.2. Crystallization

Preliminary crystallization trials were performed using crystallization screening kits from Hampton Research. Each drop consisted of 1 μl sample solution and 1 μl reservoir solution and was equilibrated against 100 μl reservoir solution at 293 K. Initial crystals were obtained with Hampton Research PEG/Ion Screen (No. 3; 20% PEG 3350, 0.2 M ammonium fluoride pH 6.2). After optimization by changing the buffer and precipitant, crystals that diffracted well were obtained by the hanging-drop method with 2 μl protein solution mixed with an equal volume of mother-liquor solution containing 0.2 M ammonium fluoride, 24% PEG 4000 and 0.1 M sodium acetate pH 4.6.

2.3. Data collection and processing

X-ray diffraction data were collected at BL44B2 of SPring-8 (Hyogo, Japan). A single crystal was mounted in a loop and flash-cooled in a stream of nitrogen gas after soaking in mother liquor containing 15% glycerol. The X-ray diffraction data were processed using the HKL-2000 package (Otwinowski & Minor, 1997). The crystals belong to space group P2_12_12, with unit-cell parameters a = 41.5, b = 45.7, c = 97.6 Å. The asymmetric unit contains one molecule of PH0099, which corresponds to a solvent content of 43.5% (V_M = 2.1 Å³ Da⁻¹). A summary of data-collection and processing statistics is given in Table 1.

2.4. Structure solution and refinement

The structure of PH0099 was solved by molecular replacement with MOLREP (Vagin & Teplyakov, 1997) using the homologous (32.6% sequence identity) protein structure of T. thermophilus 2'-5' RNA ligase (PDB code 1iuh; Kato et al., 2003) as a search model. The difference in the resolution range 20–3.0 Å were used in both rotation and translation calculations, which gave an obvious solution with significant contrast. The initial model, which comprised 78.8% of 184 residues, was rebuilt automatically using ARP=WARP (Lamzin & Wilson, 1993). The fragmented initial model was extended and refined automatically using LAFILE (Yao et al., 2006) with CNS.

The recombinant protein PH0099 was expressed in Escherichia coli strain B834 (DE3) by adding 1 mM IPTG to LB broth (310 K) at an OD600 of approximately 0.6. After induction for 5 h, the cells were harvested and then resuspended in buffer A (50 mM Tris pH 9.0) and disrupted with a French press. The lysate was incubated at 343 K for 30 min and centrifuged (40 000 g for 30 min at 277 K). The supernatant was applied onto a 5 ml HiTrap QXL column (Amersham Bioscience) and ammonium sulfate, the samples were filtered (0.45 μm, Millipore) and applied onto a 1 ml Resource Phenyl column (Amersham Bioscience) and highly purified PH0099 was eluted. The buffer was exchanged and the sample was concentrated to 10 mg ml⁻¹ (in 20 mM Tris pH 9.0) using an Amicon column. The target protein was confirmed by MALDI-TOF mass spectrometry. For the production of SeMet-substituted PH0099, cells were cultured in minimum medium containing SeMet. The procedure for the purification of SeMet PH0099 was the same as that used for the native protein.

The structure of PH0099 was solved by molecular replacement with MOLREP (Vagin & Teplyakov, 1997) using the homologous (32.6% sequence identity) protein structure of T. thermophilus 2'-5' RNA ligase (PDB code 1iuh; Kato et al., 2003) as a search model. The difference in the resolution range 20–3.0 Å were used in both rotation and translation calculations, which gave an obvious solution with significant contrast. The initial model, which comprised 78.8% of 184 residues, was rebuilt automatically using ARP=WARP (Lamzin & Wilson, 1993). The fragmented initial model was extended and refined automatically using LAFILE (Yao et al., 2006) with CNS.
(Brünger et al., 1998) with slight manual intervention (R factor and Rfree = 23.8 and 27.2%, respectively). After a final check and correction, the R and free R factors for the model consisting of 184 amino-acid residues and 41 water molecules were 21.6 and 26.5%, respectively. The stereochemical quality of the final model was validated with PROCHECK (Laskowski et al., 1993). The Ramachandran plot indicated that 93.4% of the residues lie in the most favoured regions, with the remaining 6.6% in additionally allowed regions (Table 2).

3. Results and discussion
The final model of PH0099 is composed of one molecule in the asymmetric unit, containing all residues (184) and 41 water molecules. The overall structure of PH0099, which has dimensions 45 \times 40 \times 25 \text{ Å}, contains one 3_{10}-helix, four \( \alpha \)-helices and nine \( \beta \)-strands and resembles two lobes positioned symmetrically (Fig. 1a). The lobe harbouring the N- and C-terminal regions (the terminal lobe) consists of \( \beta_1, \beta_3, \alpha_2, \alpha_3, \beta_8 \) and \( \beta_9 \) and forms a four-stranded antiparallel \( \beta \)-sheet. The other lobe (the transit lobe) possesses a 3_{10}-helix, \( \alpha_1, \alpha_4 \) and a five-stranded antiparallel \( \beta \)-sheet (\( \beta_4, \beta_5, \beta_6, \beta_2, \beta_7 \)). The two antiparallel \( \beta \)-sheets (\( \beta_1-\beta_3-\beta_8-\beta_9 \) and \( \beta_4-\beta_5-\beta_6-\beta_2-\beta_7 \)) constitute a V-shaped active-site cleft (about 25 Å in width and 15 Å in depth), with two antiparallel \( \alpha \)-helices wrapping around the outer side of each \( \beta \)-sheet (Fig. 1a). Two structures of PH0099 were deposited in the PDB at around the same time: 1vgj (1.94 Å resolution) and 1vdx (Rehse & Tahirov, 2005; 2.4 Å resolution). The two crystals used for structural determination were obtained under different crystallization conditions and belonged to the same space group with slightly different unit-cell parameters [a difference of 2.6 Å (6%) in the \( a \) axis and 4.4 Å (4.5%) in the \( c \) axis]. With the exception of two regions, residues 165–175 forming a \( \beta \)-turn-\( \beta \) structure (\( \beta_8 \) and \( \beta_9 \)) and a loop containing residues 81–88 linking \( \beta_4 \) to \( \beta_5 \), the two structures superposed very well, with an r.m.s.d. (root-mean-square deviation) of 0.67 Å for the main chain. Compared with 1vdx, the maximum \( C^\alpha \) shifts of these two regions (residues 165–175 and 81–88) in the present structure are 5.8 and 1.6 Å, respectively. These shifts broaden the width of the entrance of the active-site cleft. In particular, the different orientation of the side chain of Lys170 in our structure almost doubled the opening width of the cleft in comparison with that of 1vdx (Fig. 1b).

There is no direct contact between residues situated on opposite sides of the V-shaped active-site cleft in both structures. In the above-mentioned regions (residues 165–175 and 81–88), only one water molecule (W230) was found in the cleft of the structure determined at the higher resolution (1vgj), which makes an interaction with residue Pro172. It is unlikely that this interaction is capable of causing such a conformational change of the residues 165–175 (particularly the side chain of Lys170). The plots of the \( B \) factors of the main chain for the two structures are shown in Fig. 2. For both structures, the average \( B \) factors of the main chain of the two regions (residues 81–88 and 165–175) are higher than that overall. Residues 168–171 (the turn between \( \beta_8 \) and \( \beta_9 \)) constitute the region with the highest average \( B \) factors in 1vgj and 1vdx (50.0 and 82.9 Å², respectively). The high \( B \) factors and the structural variations possibly suggest that conformational changes occur in these regions on binding RNA substrate. These changes occurring at the entrance of the active-site cleft can broaden its width (>8 Å) and form an open conformation that is beneficial for allowing RNA precursors to approach the active site. It is possible that the present structure (1vgj) and the previous one (1vdx) are open and closed forms of the \( P. \) horikoshii 2'-5' RNA ligase, respectively.

![Figure 1](image1.png)

**Figure 1**
Structure of PH0099 and the active site. The terminal lobe is shown in green and the transit lobe in blue. (a) Ribbon representation of PH0099. The active-site residues His40, Thr42, His125 and Thr127 in the tetrapeptide motif H-X-T/S-X are depicted explicitly in stick representation. (b) Comparison of this structure (green and blue) with that of PDB entry 1vdx (black).

![Figure 2](image2.png)

**Figure 2**
Plot of the \( B \) factors of the main chains of 1vgj (red) and 1vdx (black). The dashed lines indicate the average \( B \) factor (1vgj, 31.6 Å²; red; 1vdx, 41.8 Å²; black).
The *T. thermophilus* 2'-5' RNA ligase has a loop at residues 138–148; however, PH0099, CPDase (Hofmann et al., 2000) and CNPase (Sakamoto et al., 2005; Kozlov et al., 2003) have helices a4 corresponding to these positions. PH0099 possess two α-helices distributed on each of the outer sides of the bilobal arrangement, similar to the structures of the 2H phosphoesterase superfamily members CPDase (Hofmann et al., 2000) and CNPase (Sakamoto et al., 2005; Kozlov et al., 2003). Compared with *T. thermophilus* 2'-5' RNA ligase (Kato et al., 2003), the electrostatic surface potential shows that PH0099 has a smaller positively charged patch and that the centre of the active-site cleft is also positively charged, which is essential for recognizing the negatively charged RNA precursors (Fig. 3). The region containing β4, β5 and the C-terminus of α4 in PH0099 is mostly negatively charged (Fig. 3a), which implies that it is not involved in binding the RNA precursor. The corresponding region (β4, β5 and loop 138–148) in *T. thermophilus* 2'-5' RNA ligase is positively charged (Fig. 3b) and hence a larger positively charged region is formed compared with that of PH0099. In the case of *T. thermophilus* 2'-5' RNA ligase, the loop (138–148) may contribute to binding substrate by possibly changing its conformation. A loop is more suitable than a helix for such conformational changes. The different charged regions suggest that the substrates and their recognition may be different for the two ligases. The structure of PH0099 with two α-helices distributed in each lobe, similar to CPDase and CNPase, may act as a bridge between the structural homology of the 2H phosphoesterase superfamily.

The members of the 2H phosphoesterase superfamily share two prominent tetrapeptide motifs, H-X-T/S-X (X is generally a hydrophobic residue), in the antiparallel β-sheets. At the predicted active sites containing the two motifs, the structures of the *T. thermophilus* 2'-5' RNA ligase (Kato et al., 2003), plant CPDase in two forms (Hofmann et al., 2000, 2002) and the catalytic domain of human/rat CNPase (Sakamoto et al., 2005; Kozlov et al., 2003) were superimposed onto PH0099 and the result showed that the conserved residues in the tetrapeptide motifs (His, Thr or Ser) superimposed well in all proteins, with the exception of one conformation of His30 in *T. thermophilus* 2'-5' RNA ligase (data not shown). The structural similarity of the tetrapeptide motifs in those proteins is consistent with the common characteristic that the members of the 2H phosphoesterase superfamily catalyze the hydrolysis of 2',3'-cyclic phosphodiester bonds. In the tetrapeptide motifs H-X-T/S-X, the distances between the two NE atoms of the two histidines and the two OG1 atoms of the two threonines (Thr to Ser in CPDase) vary in the range 6.7–8.2 Å and 7.0–7.6 Å, respectively. It seems that the distance between the threonines is less varied. This is in agreement with the observation that all threonines are located within β-strands except for Thr132 in *T. thermophilus* 2'-5' RNA ligase, while all histidines lie in the loop except for the histidine corresponding to His40 (PH0099) in CNPase.

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References

Figure 3
Electrostatic surface potentials of (a) *P. horikoshii* and (b) *T. thermophilus* 2'-5' RNA ligase. The electrostatic potential was calculated using PyMOL (DeLano, 2002); positively charged regions are in blue and negatively charged regions in red.

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