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Protein-Protein Interactions Leading to Recruitment of the Host DNA Sliding Clamp by the Hyperthermophilic *Sulfolobus islandicus* Rod-Shaped Virus 2

Andrew F. Gardner,[a] Stephen D. Bell,[b] Malcolm F. White,[c] David Prangishvili,[d] Mart Krupovic[d]

New England Biolabs, Ipswich, Massachusetts, USA[a]; Molecular and Cellular Biochemistry Department and Biology Department, Indiana University, Bloomington, Indiana, USA[b]; Biomedical Sciences Research Complex, University of St Andrews, Fife, United Kingdom[c]; Institut Pasteur, Unité Biologie Moléculaire du Gène chez les Extrêmophiles, Département de Microbiologie, Paris, France[d]

Viruses infecting hyperthermophilic archaea typically do not encode DNA polymerases, raising questions regarding their genome replication. Here, using a yeast two-hybrid approach, we have assessed interactions between proteins of *Sulfolobus islandicus* rod-shaped virus 2 (SIRV2) and the host-encoded proliferating cell nuclear antigen (PCNA), a key DNA replication protein in archaea. Five SIRV2 proteins were found to interact with PCNA, providing insights into the recruitment of host replisome for viral DNA replication.

Viruses infecting Archaea, the third domain of life, constitute one of the most enigmatic sections of the virosphere. Archaeal viruses, especially those infecting hyperthermophilic hosts thriving at temperatures above 70°C, are extremely diverse both morphologically and genetically (1, 2). The vast majority of them are unique to Archaea and do not resemble viruses infecting Bacteria or Eukarya. Furthermore, during the past few years, it became apparent that the ways hyperthermophilic archaeal viruses interact with their hosts are also often unprecedented in the viral world (3, 4). Indeed, proteins encoded by these viruses typically do not share similarity with proteins in the sequence databases (2), often display new structural folds (5), and play unexpected roles in the viral life cycles (6). An interesting feature of hyperthermophilic archaeal viruses is the general absence of recognizable DNA polymerase genes in their genomes; among the 41 virus isolates for which genome sequences are available, only one encodes a DNA polymerase (7), raising a question as to how genome replication in these viruses is achieved. To answer this puzzling question, in the present study we have investigated how *Sulfolobus islandicus* rod-shaped virus 2 (SIRV2) recruits the cellular machinery for the replication of its genome.

SIRV2 is one of the most extensively studied archaeal viruses (8) and is the type species of the family *Rudiviridae* within the order *Ligamenvirales* (9). The rod-shaped SIRV2 virions are nonenveloped and are formed from linear double-stranded DNA genomes coated with one major and three minor structural proteins. SIRV2 infects acidophilic hyperthermophiles of the archaeal order *Sulfolobales*, namely, *S. islandicus* (10) and *Sulfolobus solfataricus* (11). The infection cycle starts with rapid virus adsorption to the pilus-like structures on the host cell surface, which eventually leads to genome uncoating and internalization (12). Transcription of the viral genes commences within the first few minutes of infection (13) and is followed by the efficient replication of the viral DNA (3). SIRV2 virions, assembled in the cytoplasm, are released from the host ~8 to 10 h postinfection through large virus-encoded pyramidal structures (3). One of the least understood aspects of the SIRV2 infection cycle is genome replication in the absence of virus-encoded DNA polymerase. The only proteins which might be involved in the replication of the SIRV2 genome are the Holliday junction resolvase P121 (14) and the endonuclease P119c (15), which is related to enzymes involved in the initiation of the rolling-circle replication of various plasmids and single-stranded DNA viruses (16, 17). However, the exact steps of SIRV2 genome replication in which the two enzymes participate as well as the involvement of cellular players in this process remain unclear.

Viruses that do not encode their own DNA polymerases rely on the replication machinery of the host. However, viral proteins often play an important role in directing the replisome to the viral replication origins. Indeed, a considerable number of euryarchaeal viruses encode proteins involved in the initiation of DNA replication, including replicative MCM helicases, Cdc6/Orc1, or PCNA (proliferating cell nuclear antigen) homologues (18–24). Since rudiviruses encode neither a DNA polymerase nor any of the above-mentioned proteins involved in the initiation of DNA replication, we hypothesized that their genome replication should rely on the physical recruitment of the host replisome. To verify this possibility, we set out to investigate the interactions between SIRV2 proteins and the heterotrimeric *S. solfataricus* sliding clamp (SsoPCNA1 to -3) (25, 26). The latter was selected as a likely target because it is a key protein of DNA replication and repair in archaea and eukaryotes, allowing non-sequence-specific enzymes, such as replicative DNA polymerase PolB1, DNA ligase Lig1, and flap endonuclease FEN1, to associate with their DNA substrates (27–29). To explore which of the SIRV2 proteins might be involved in the recruitment of PCNA and, by extension, of the entire replisome, we employed yeast two-hybrid (Y2H) analysis. SsoPCNA subunits 1 (NP_341936), 2 (NP_342519), and 3 (NP_341944) were cloned into the "bait" vector (pGBKT7) encoding GAL4 DNA-binding domain, while the viral "prey" library was created by cloning a set

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Address correspondence to Mart Krupovic, krupovic@pasteur.fr, or David Prangishvili, david.prangishvili@pasteur.fr.

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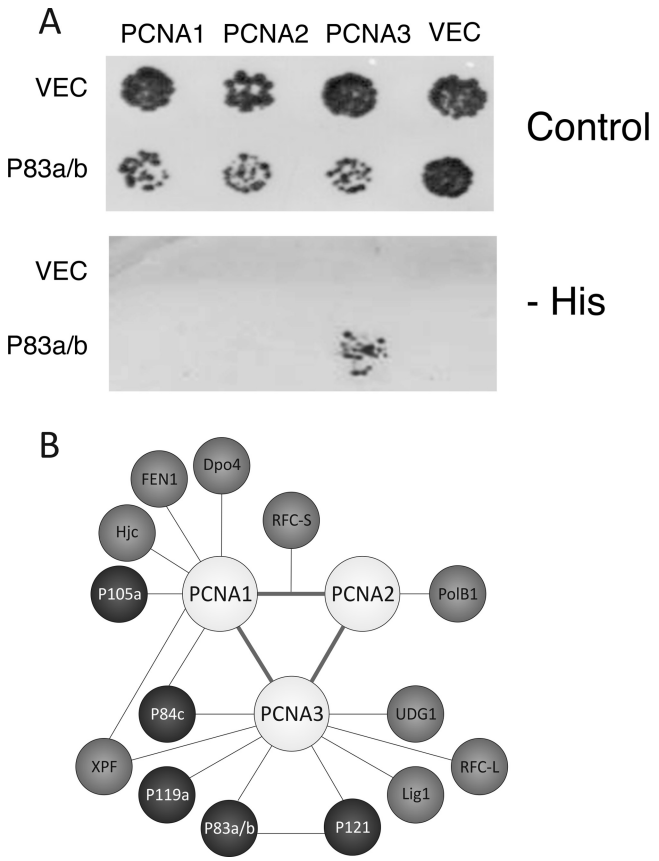

FIG 1 Results of yeast two-hybrid interactions between SIRV2 proteins and SsoPCNA. (A) An example of yeast two-hybrid analysis demonstrating the interaction between the SIRV2 protein P83a/b and SsoPCNA subunit 3. VEC, empty vector. Interaction between the bait (PCNA3) and prey (P83a/b) activates the *HIS3* expression, complementing histidine auxotrophy and allowing growth on yeast minimal medium lacking histidine (−HIS). (B) Schematic representation of the SsoPCNA interactome. SIRV2 proteins found to interact with SsoPCNA1 and -3 are represented by black spheres, while DNA replication and repair proteins of *S. solfataricus* previously reported to bind SsoPCNA are represented by gray spheres. Hjc, Holliday junction endonuclease (34); FEN1, flap structure-specific endonuclease 1 (25); Dpo4, DNA polymerase IV (36); RFC-S and -L, small and large subunits of the replication factor C, respectively (36); PolB1, replicative DNA polymerase (25); UDG1, uracil DNA glycosylase (37); Lig1, DNA ligase (25); XPF, nucleotide excision repair endonuclease (38).

of the PCR-amplified SIRV2 genes into the NdeI/XmaI site of the pGADT7 vector encoding the GAL4 activation domain. All clones were verified by DNA sequencing. *Saccharomyces cerevisiae* AH109 (Clontech) was sequentially transformed with prey and bait plasmids and selected on nutritional media lacking either leucine or tryptophan, respectively. Control assays with empty bait or prey vectors were performed to ensure that the fusion protein could not induce expression of the selection gene in the absence of a protein partner. In the case of interaction between the bait and prey, the fusion protein is expected to activate the *HIS3* expression and complement histidine auxotrophy, allowing growth on yeast minimal medium lacking histidine.

Our Y2H screen has revealed five SIRV2-encoded proteins that interacted with the SsoPCNA: proteins P105a (NP_666544) and P84c (NP_666565) were found to interact with SsoPCNA1, whereas proteins P83a/b (NP_666535/NP_666588), P84c, P119a (NP_666536), and P121 (NP_666569) were found to interact with SsoPCNA3 (Fig. 1). Notably, no interaction between viral proteins and SsoPCNA2 could be detected. Two of the PCNA-interacting SIRV2 proteins (P84c and P121) are conserved in all rudiviruses, two (P83a/b and P105a) are encoded in a smaller subset of more closely related viruses, while P119a is restricted to SIRV2 (Table 1).

PCNA is known as a "molecular toolbelt" (26) which interacts with multiple proteins involved in DNA replication and repair (27–29). These interactions are often mediated via the PCNA-interacting protein (PIP) box, with a consensus sequence of Qxxhxx@@, where h represents hydrophobic amino acid residues, @ corresponds to bulky aromatic residues, and x is any residue (30). Sequence analysis of the viral proteins, which were found to interact with SsoPCNA1 and SsoPCNA3, revealed the presence of potential PIP boxes in all proteins except for P84c (Fig. 2). Interestingly, P119a was found to contain three PIP boxes (Fig. 2D). Notably, whereas the presence of PIP boxes is suggestive of interaction with PCNA, the absence of the identifiable motif does not necessarily signify the reverse (i.e., lack of interaction), because (i) the exact sequence of PIP boxes is known to vary (30) and (ii) interactions might be mediated by motifs other than PIP (31). As has been previously observed for PCNA-interacting proteins from other viruses (32), the PIP boxes of SIRV2 displayed variable correspondence to the consensus sequence, which might be important for orchestrating the sequential binding of different protein partners to PCNA.

To more critically scrutinize the predicted PIP boxes, we have investigated their exact location within the four PCNA-interact-

TABLE 1 Conservation of SIRV2 PCNA-interacting proteins in other viruses[a]

SIRV2 protein (accession no.)	PCNA-interacting protein in:				Characteristic(s)
	SIRV1	SRV	ARV1	SMRV1	
P83a (NP_666535)	gp01	P57			Helix-turn-helix protein
P84c (NP_666565)	gp23	P75	gp22	gp22	C-terminal coiled-coil domain
P105a (NP_666544)	gp03				Novel fold; homologues in several lipothrixviruses and fusellovirus SSV6[b]
P119a (NP_666536)					No homologues
P121 (NP_666569)	gp27	P116c	gp25	gp19	Holliday junction resolvase; homologues in numerous bacterial and archaeal *Caudovirales*

[a] Genome accession numbers: SIRV2, NC_004086; SIRV1, NC_004087; SRV (*Stygiolobus* rod-shaped virus), FM164764; ARV1 (*Acidianus* rod-shaped virus 1), NC_009965; SMRV1 (*Sulfolobales* Mexican rudivirus 1), NC_019413.
[b] SSV6, *Sulfolobus* spindle-shaped virus 6.

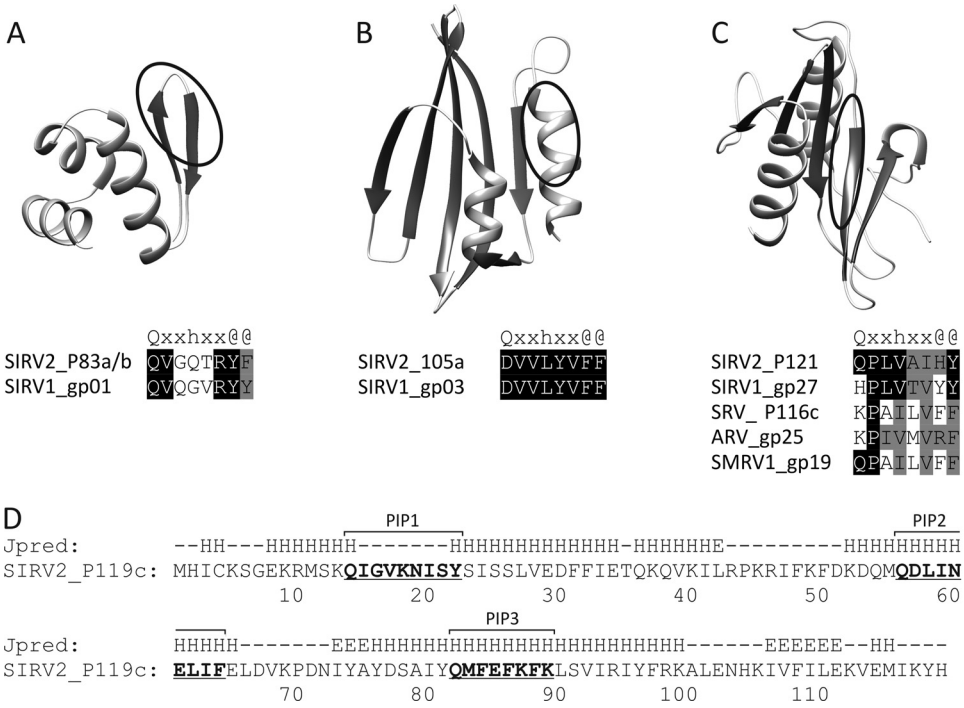

FIG 2 Potential PCNA-interacting protein (PIP) boxes in rudiviral proteins. (A to C) Structural homology models of three PCNA-interacting SIRV2 proteins for which structural homologues could be identified. The locations of the regions corresponding to predicted PIP boxes are circled. Qxxhxx@@ is the PIP consensus sequence, where h represents hydrophobic amino acid residues, @ corresponds to bulky aromatic residues, and x is any residue (30). (A) The P83a/b model was built using as a template the X-ray structure of SIRV1 protein P56a (PDB accession no. 2X48). (B) The P105a model was built using as a template the X-ray structure of protein ORF14 of the lipothrixvirus *S. islandicus* filamentous virus (SIFV) (PDB accession no. 2H36). (C) The P121 model was built using as a template the X-ray structure of *Sulfolobus solfataricus* Holliday junction resolvase (PDB accession no. 1HH1). SRV, *Stygiolobus* rod-shaped virus; ARV, *Acidianus* rod-shaped virus; SMRV1, *Sulfolobales* Mexican rudivirus 1. (D) Locations of the three PIP boxes in P119a. The secondary-structure elements predicted using JPred (39) are indicated above the sequence (H, α-helixes; E, β-strands).

ing viral proteins. For this purpose, we have constructed structural homology models using Modeler v9.11 (33) for three of the SIRV2 proteins for which structural counterparts could be identified (Fig. 2A to C). This analysis suggested that the PIP box of protein P121 is unlikely to be functional, since it is located within the core of the protein fold (Fig. 2C), and thus a different protein region must be responsible for the observed PCNA binding. Similarly, two of the three PIP boxes initially predicted in P119a are found within the secondary-structure elements, which are likely to be integral for the tertiary protein structure. The PIP box of P83a/b is located in the loop region between the two hairpin-forming β-strands (Fig. 2A). In contrast, the PIP box of P105a and the PIP1 box of P119a are located at the extremities of the proteins, lending credence to their functionality.

Out of five PCNA-interacting SIRV2 proteins, only one has been biochemically characterized: protein P121 is a Holliday junction resolvase (Hjr), which is implicated in the resolution of viral genome concatemers, a key step in SIRV2 genome replication (14). Interestingly, SsoPCNA has been previously shown to bind the Hjr of *S. solfataricus* and stimulate its enzymatic activity (34), suggesting that a similar effect might be exerted during the interaction with the viral Hjr. Another interesting protein that has been identified as an SsoPCNA partner in our Y2H analysis is P83a/b (genes *ORF83a* and *ORF83b* are located in inverted terminal repeats and encode identical proteins). Transcriptome sequencing (RNA-seq) analysis has shown that *ORF83a/b* transcripts are overwhelmingly dominant starting within the first minutes of infection and remain abundant throughout the infection (13), suggesting an important role for P83a/b during the replication cycle of SIRV2. In the course of a structural genomics initiative, the X-ray structure of a P83a/b homolog from a closely related virus, SIRV1, has been solved (35). The protein was found to form a hexameric ring and contain the helix-turn-helix DNA-binding domain, suggesting that it might be involved in DNA metabolism (5). Notably, a previous Y2H screen for interactions among SIRV2 proteins revealed that P83a/b interacts with the viral Hjr, P121 (13), suggesting that P83a/b, P121, and SsoPCNA form a tripartite complex (Fig. 1B). Whereas *ORF83a/b* transcripts are abundant from the beginning of infection, those of *ORF121* appear later in infection, suggesting that the intricate interplay between viral proteins and the cellular PCNA might be regulated by both hierarchical strengths of PIP box-mediated protein-protein interactions and transcriptional control of viral gene expression. Future studies will focus on revealing the molecular and structural details of the interactions between the host PCNA subunits and the five SIRV2 proteins identified here, which will clarify how SIRV2 hijacks the replisome of its host.

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