

Structural Basis of the Respiratory Syncytial Virus Polymerase Complexes

1. Preparation and characterization of the RSV polymerase.

Preparing high-quality and large-quantity of RSV L is the critical first step to understanding RSV catalytic core and has been proven challenging¹. We have successfully co-expressed and co-purified full-length wild-type (wt) RSV RdRP (L:P) and catalytically inactive L(D811A):P using sf21 insect cells (**Fig. 1**). We will generate a panel of L fragments with one or two functional domains.

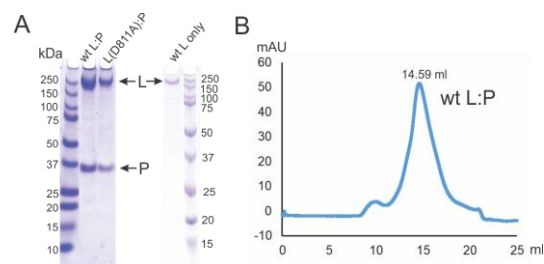


Figure 1: Preparation of the RSV L protein. (A) SDS-PAGE gel shows the expression of full-length wild-type (wt) and mutant RSV L:P, and L only in insect cells. (B) The size exclusion chromatography shows homogeneity. (Cao et al. Nat Comm 2020)

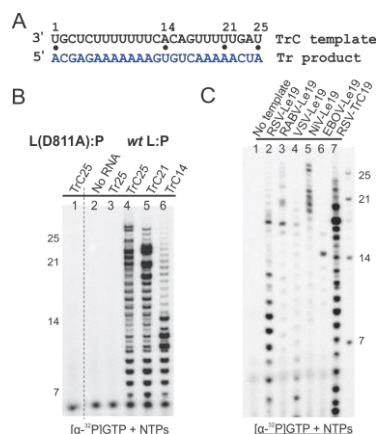


Figure 2: In vitro reconstitution of RSV RNA polymerization. (A) the template (TrC) and product (Tr). (B) Transcription assay using wt and mutant RdRP (L:P) on various RNAs. (C) Test RNA templates from different viruses for specificity. (Cao et al. JVI 2020, Viruses 2022)

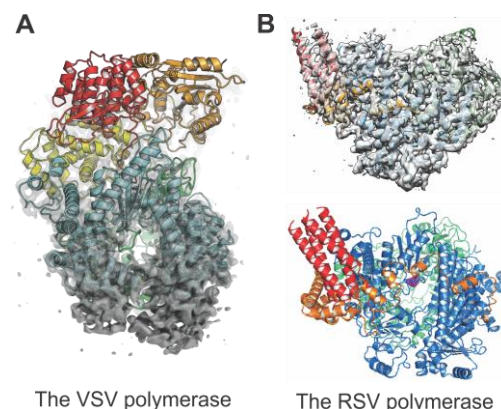
2. In vitro transcription assay.

We successfully adopted¹⁻³ and developed a novel RNA elongation assay to map key promoter features of RSV⁴ (**Fig. 2**). Our assay employs a short RNA template to incorporate [³²P]-NTP into the reaction. We will optimize the parameters (i.e., the length and sequence of the template and primers) to identify suitable constructs for in-depth structural analysis.

3. Capture the initiation and elongation of RSV polymerase.

We successfully determined multiple high-resolution structures of the polymerases from NNS RNA viruses using cryo-EM^{5,6} (**Fig. 3**). Using the template in the transcription assay and selected NTPs or NTP analogs; we will trap

the initiation and elongation stages of the RSV RdRP (**Fig. 4**).



The VSV polymerase The RSV polymerase
Figure 3: Cryo-EM structures of the polymerases of NNS RNA viruses determined by the PI. (A) 3.8 Å cryo-EM structure of the vesicular stomatitis virus (VSV) polymerase (Liang et al. Cell, 2015). (B) 3.67 Å cryo-EM structure of the respiratory syncytial virus (RSV) polymerase (Cao et al. Nat Comm 2020).

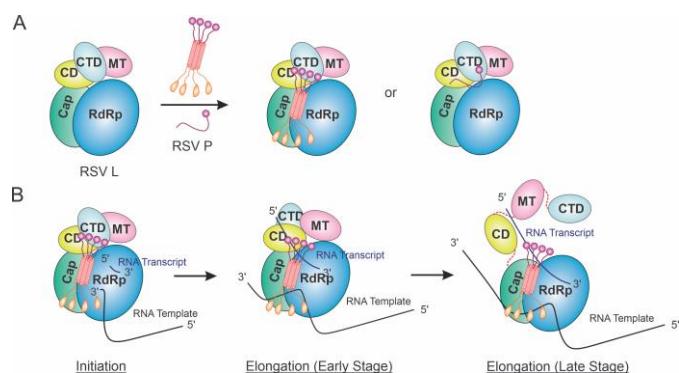


Figure 4: The overview of the proposed work. (A) The RSV RdRP (L:P). The domains of both monomeric L and tetrameric P are shown. Pfrag is the minimal P fragment used to stabilize the L protein domains in this proposal. (B) Initiation and elongation complexes. The RNA template and RNA transcript are shown as black or blue lines, respectively.

Preliminary data suggested that the RSV L:P:RNA complex showed reasonable homogeneity. The initial cryo-screen revealed good ice thickness and gradient in the cryo grids (**Fig. 5A, B**). The preliminary screen showed the particles are readily visible in the grid holes (**Fig. 5C**). A small cryo-EM dataset and the 2D class averages show both similar and different views compared to that of apo RSV L:P complex (**Fig. 5D**). In summary, we demonstrated the feasibility of preparing the high-quality RSV L:P:RNA complex. Besides the apo RSV RdRP, we determined multiple 2.5-3.5 Å cryo-EM structures of the RSV RdRP in complexes of RNA.

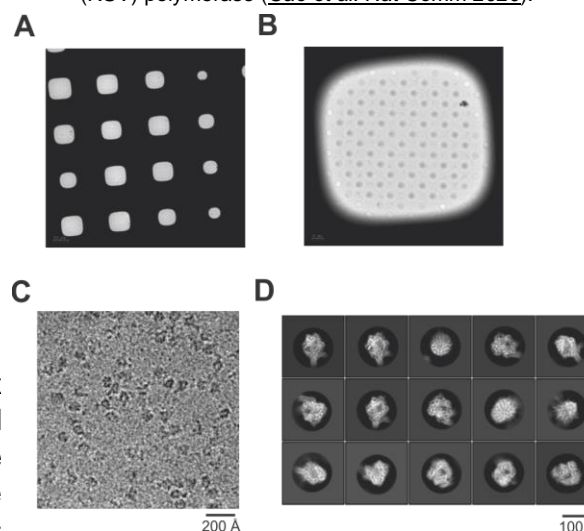


Figure 5: Preliminary cryo-EM analysis of RSV polymerase complex with its RNA (L:P:RNA). (A) The low magnification view of the grid. (B) The medium magnification view of a representative grid square. (C) The raw image of L:P:RNA complex. (D) The class averages show both similar and different views to that of apo RSV L:P complex.

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