Proposal Code MX-2215

Proposal Title Measles Virus Full-Length Nucleocapsid Structure

Experiment report

The proposal MX-2215, on the structure of full-length measles virus nucleocapsid was granted 9 shifts of data collection on CM01 in September 2019. Pre-screened grids were provided to CM01 staff, and the best one was used for data collection. 4300 movies were acquired with a pixel size of 1.3505Å, which allowed to extract 2 millions helical segments along the flexible helices formed by the nucleocapsids (figure 1).

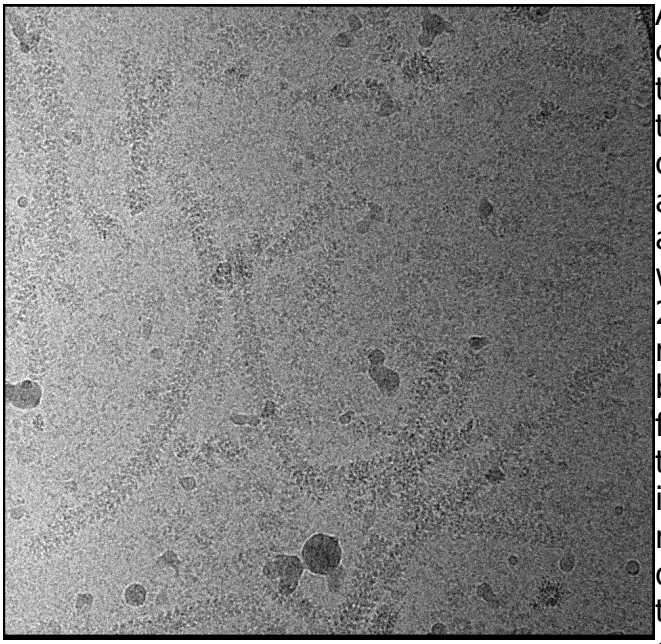

Figure 1 : an example micrograph of the MeV full-length nucleocapsids

As seen, the MeV-FL nucleocapsids are difficult objects for image processing : they are flexible and heterogeneous in term of helical symmetry. Despite these difficulties, extensive classification steps allowed us to solve 11 different structures at a resolution better than 5Å (figure 2A), with the best ones approaching 4Å (figure 2B). We could build 14 different atomic models, providing molecular insights behind the flexible nature of these filaments. The C-terminal 125 residues of the nucleoprotein (NTAIL), of particular interest for the biological function of the nucleocapsid, were known to be mostly disordered, but with a propensity for transient interaction and putative folding of a small stretch of residues onto the nucleoprotein.

By subtracting the ordered nucleoprotein region (residues 1-400) from the full-length nucleocapsid structure, we could locate the disordered region of interest, and validate one hypothesis for the location of stretch of residues with folding propensity (figure 2C).

The quality of the ESRF Titan Krios data and the number of micrographs obtained were critical for achieving the high goals of this project.

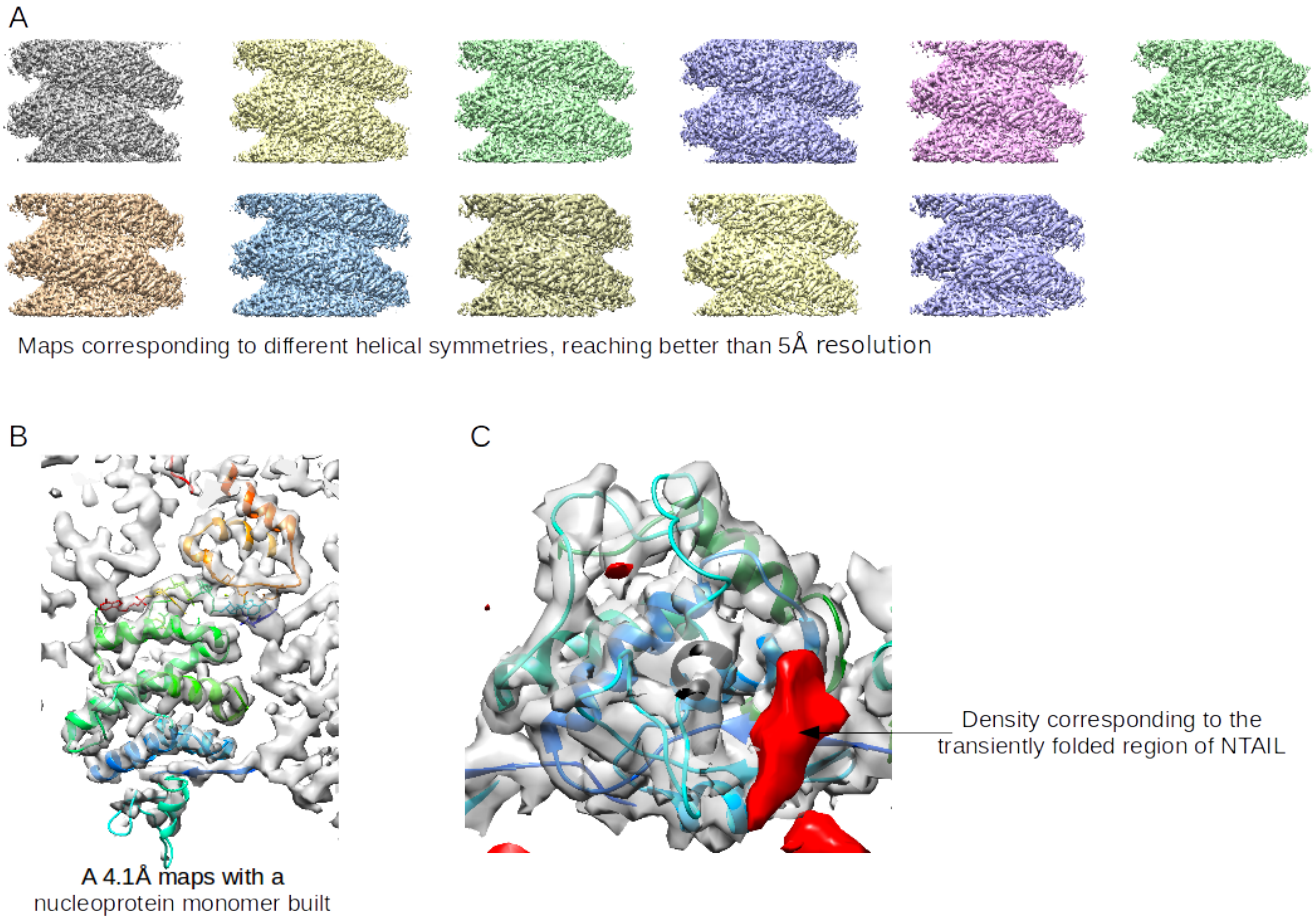

Figure 2 : Results