

Cryo-EM offers novel insights into the RNA-nucleoprotein interactions in the measles virus nucleocapsids

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Measles is one of the most contagious human diseases. Recently we determined the cryo-EM structure of the helical nucleocapsid formed by the folded domain of the measles virus nucleoprotein encapsidating an RNA at 4.3 Å resolution (Gutsche et al, Science 2015). This structure revealed the molecular determinants of the nucleoprotein packing into a helix and provided first insights into the mode of nucleoprotein-RNA interaction in the nucleocapsid. In that work, we used recombinant nucleocapsids produced by overexpression of the nucleoprotein in insect cells where it non specifically wraps around cellular RNA. Consequently, although the RNA density was well defined in the 3D map, it reflected the random composition of the bound RNA and was further averaged by image processing procedures. Now however we are able to produce helical nucleocapsids with a defined RNA composition. We are using such nucleocapsids to gain precise structural information about the rationale of the nucleoprotein-RNA interaction by high resolution cryo-EM.