Large numbers of viruses are helical, but the structures of helical viruses are quite rare. The first virus to be isolated, tobacco mosaic virus (TMV), a helical virus, is also the first virus to be solved by x-ray fiber diffraction (Namba and Stubbs, 1986). TMV has been a model system in structural biology largely because it is anomalous: it is nearly crystalline in its order. For most other helical viruses, such as the flexible filamentous plant viruses, x-ray fiber diffraction is not possible, and EM of such samples has been problematic. The first three-dimensional reconstruction in electron microscopy was from a helical phage tail (DeRosier and Klug, 1968), and reconstructions from helical polymers have been very important given the centrality of such polymers to many aspects of biology. Two developments have changed our ability to determine the atomic structure of helical viruses: 1) single-particle algorithms for helical reconstruction (Egelman, 2000) that eliminate the stringent requirements for nearly crystalline symmetry in the Fourier-Bessel approach (DeRosier and Klug, 1968; Klug et al., 1958); 2) the development of direct electron detectors for cryo-EM (Li al., 2013) which yield a greatly improved signal-to-noise ratio, point spread function and detection efficiency. In spite of these advances, the determination of helical symmetry can still be ambiguous until one reaches a resolution where secondary structure becomes evident (Egelman, 2014). We show, using two helical viruses as examples, how the correct symmetry becomes obvious at better than 7 Å resolution, and how it can be very difficult or impossible to determine the correct symmetry in some cases at lower resolution. The two examples are the SIRV2 virus which lives in nearly boiling acid (DiMaio et al., 2015b) and bamboo mosaic virus (BaMV) which is a good representative of a large family of flexible filamentous plant viruses (DiMaio et al., 2015a).
References

(a) Micrograph showing frozen/hydrated SIRV2 virions in vitreous ice. The scale bar is 1,000 Å.
(b) A side view of the reconstructed virion with a ribbon model for the protein (magenta). The asymmetric unit in the virion contains a protein dimer, and one is shown with one chain in yellow and the other in green. (c) A cutaway view showing the hollow lumen with the all α-helical protein segments that line the lumen. These α-helices wrap around the dsDNA (blue) and encapsidate it. This region of the protein has been shown to be unstructured when the monomer is in solution. (d) A close-up view of the region shown within the rectangle in (c).