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Measuring the 3D Size of Large RNA Molecules AJAYKUMAR GOPAL, DEFNE EGECIOGLU, LI TAI FANG, CHARLES M. KNOBLER, WILLIAM M. GELBART, University of California, Los Angeles, MARC NIEBUHR, Stanford Synchrotron Radiation Lab, Menlo Park, A. L. N. RAO, University of California, Riverside — Large single-stranded (ss) RNAs are ubiquitous in cells and constitute the genomic content of many viral species. Besides being the primary means of intra-cellular information transfer, some of their functions require them to form stable structural motifs. ssRNA molecules possess intrinsic self-complementarity leading to a partially double-stranded, branched, secondary structure. We measure, in solution, the physical dimensions of several sequences of ssRNA ranging from a few hundred to a few thousand nucleotides in length. Sizes are reported as radii of gyration (R_g) and hydrodynamic radii (R_h), respectively determined by small-angle x-ray scattering (SAXS) and fluorescence correlation spectroscopy (FCS). For RNAs of fixed nucleotide length ($\sim$2000) and composition, we find that R_gs and R_hs can vary by over 30%. By changing solvent conditions, we demonstrate that these size discrepancies are a generic property of the secondary structure arising from sequence-dependent base-pairing. Some viral RNAs that self-assemble into spherical protein capsids have highly evolved sequences that code for unusually compact size and shape.

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