The Bevilacqua Laboratory

Department of Chemistry, The Pennsylvania State University, University Park, PA, USA

The People

The Bevilacqua Laboratory currently consists of one undergraduate, eight graduate students, and two postdoctoral researchers. Left to right: Joshua Sokoloski (graduate student), Sarah Krahe (undergraduate), Rebecca Toroney (graduate student), Laurie Heinicke (graduate student), Joshua Blose (graduate student), Durga Chadalavada (postdoc), Trevor Brown (graduate student), Rieko Yajima (graduate student), Subbarao Nallagatla (postdoc), Andrea Cerrone-Szakal (graduate student), Nate Siegfried (graduate student), and Philip Bevilacqua (Associate Professor of Chemistry).

The Research

The Bevilacqua group is interested in the folding and catalysis of ribonucleic acid (RNA) and its interactions with proteins. Our group focuses on important biological systems that include replication of the hepatitis delta virus (HDV) and the human viral response. We apply a variety of techniques to these complex systems, including rapid-mixing kinetics, fluorescence spectroscopy, UV melting, site-directed mutagenesis, combinatorial selection of nucleic acids [systematic evolution of ligands by exponential enrichment (SELEX)], and nuclear magnetic resonance (NMR) spectroscopy. Research problems center on the role of nucleotides as general acids and bases in ribozyme cleavage, the influence of alternative base pairing in RNA folding, determination of thermodynamic parameters for various nucleic acid secondary and tertiary structural motifs, and the determination of the strategies viral RNAs use to regulate the activation of the double-stranded RNA (dsRNA)-activated protein kinase (PKR). Further details of the continuing research in the Bevilacqua laboratory, as well as a list of publications and contact information, can be found via The Pennsylvania State University's Department of Chemistry web site at www.chem.psu.edu/profs/Bevilacqua.html.

The Technique

The Benchmark article describes a technique to yield an appropriate ladder for marking RNase V1 digestion products. We utilized the 3′-phosphatase activity of T4 polynucleotide kinase (PNK) to remove the 3′-terminal phosphate from RNase T1 and RNase A cleavage products. This technique fits into the lab's goals of elucidating the importance of alternative base pairing in guiding RNA folding and in understanding the influence of dsRNA on enzyme function. When recently developing a model in which Na^+ facilitates native folding by destabilizing multiple alternative secondary structures with a higher order dependence, it became critical to accurately identify the RNase V1 digestion products without the ambiguity typically associated with structure mapping of short RNAs. In the future, this method will be applied in many of our research projects, including RNA catalysis and the activation of PKR by RNA.

Ongoing research in the lab will evaluate individual functional group involvement in RNA folding, investigate the interplay of folding and catalysis of the HDV ribozyme, and extend our mechanistic studies of dsRNA binding proteins. In the future, the lab plans to bring several new techniques to bear on these systems, including nucleotide analog interference modification (NAIM), single-molecule folding techniques, and isothermal titration calorimetry (ITC).

Method for assigning double-stranded RNA structures, p. 368.