Nucleotide sequence of *Physarum* U6 small RNA

Henry B. Skinner and David S. Adams

Department of Biology and Biotechnology, Worcester Polytechnic Institute, Worcester, MA 01609, USA

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**SEQUENCE ORIGIN:**
Small RNA molecule U6 was isolated from the total cellular RNA of vegetative *Physarum* microplasmodia (1) by preparative polyacrylamide electrophoresis (2,3). The molecule was radiolabeled *in vitro* to high-specific-activity using \(^{32}P\)-pCp and RNA-ligase, and sequenced by direct chemical methods as we previously described (3). In this sequencing process, pseudouridine scores as a uridine, methylcytosine scores as a cytosine, and methyladenosine scores as an adenosine.

![Sequence Diagram](image)

**COMMENTS:**
The primary sequence of *Physarum* U6 RNA is shown compared to the published (4) sequence of rat U6. *Physarum* U6 is 99 N long. One region, 93 N long, shows 65.5% homology (61/93) with nucleotides 10 to 108 of the rat U6 molecule. One 15 N subdomain, corresponding to nucleotides 18-32 of the rat molecule, is 100% conserved. Those rat U6 sequence domains proposed to base-pair with rat U4 RNA (5) are underlined in the Figure. Overall, these "functional" regions show 58.3% (21/36 N) homology with the rat sequence. Potential secondary structures of the *Physarum* U6 molecule were analyzed by computer programs (6). The programs predicted a secondary structure similar to the proposed structure for vertebrate U6 (4), basically, a simple hairpin structure with a single large single-stranded "bulge" in the center. Within the proposed stem regions, 86.7% (26/30) of the base changes preserved the hairpin structure. Interestingly, in those domains where primary structure shows poor homology, secondary structure is highly conserved.

**REFERENCES:**