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Interactions between the prion protein and nucleic acids



In their recent report [1] concerning interactions between the prion protein (PrP) and nucleic acids, Bera and Biring present a number of RNA secondary structures which are erroneously described as pseudoknots. In the caption of Figure 2 it is stated "Normally, the pseudoknot contains two stems and three loops". An RNA pseudoknot is formed when the bases within a loop undergo Watson-Crick pairing with another otherwise single-stranded region of the same molecule [2]. The structures "MNV" in Figure 1 and "Hm45" and "Cm48" in Figure 2 of the Bera and Biring report [1] do not satisfy that criterion; they are simply multiple stem-loop structures. This in no way invalidates the experimental findings, but it does complicate the interpretation of them.

Many pseudoknots are capable of adopting a variety of alternative conformations, sometimes involving triple-base interactions that are determinative in relation to protein binding, so a proper understanding of protein binding can only be achieved once the three dimensional structure of the RNA in the RNA-protein complex has been identified. The "classic pseudoknot" first postulated by this author [3] has never been verified experimentally, in spite of its *possibility* having been demonstrated across the wide phylogenetic spectrum of PrP mRNA species [4]. However, the binding of the HIV tat protein, among others, to the tandem repeat region of the PrP mRNA [5,6] has been interpreted as indicative of a structure which is very different from the hypothetical pseudoknot, resembling instead the stemloop required for the tat-dependent transactivation of HIV [7].

The finding of Bira and Biring [1] that PrP can bind to the tandem repeat region of its own mRNA is very interesting in relation to hypothetical role of this interaction in the replication of the ætiological agent of transmissible spongiform encephalopathy through ribosomal frameshifting [8,9]. On the other hand extensive experimental investigations (unpublished results) have so far failed to verify the

existence of any special structural motifs—particular stemloops [8], pseudoknots [3] or G-quadraplexes [10]—that could facilitate such a process, highlighting the difficulty in progressing from calculated to actual RNA structures.

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