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## A viroid structural compendium

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The subviral pathogens known as viroids are composed of a single stranded and circular RNA genome in the size range of 246-401 nt. The 30 species known are causing a wide array of symptoms to many plants. An important feature is their non-coding genome. This has for consequence that they depend on their sequence and structure to infect a host. The classification of viroids based only on their sequence was previously shown to be insufficient. To strengthen that classification, we believe that the use of the secondary structure of the viroids is useful. Generally, their structures were predicted with thermodynamics-based RNA folding programs, which were shown to lack precision for RNA longer than 200 nt. Thus the predicted structure of a viroid needs to have more information on its folding to produce accurate

models for interpreting any systematic studies. Following the adaptation of SHAPE probing and computer assisted structure prediction to the viroid, we have elucidated the structure of all the known species. In fact, the structures in solution for one variant of all *Avsunviroidae* members as well as 30 *Pospiviroidae* species have been elucidated. There were many significant differences compared to predicted structure in absence of probing data, confirming the importance of this study. In addition to providing a complete compendium of viroid structure, this analysis permitted to ascertain structural motifs that could be important for their biology and classification.

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