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### CHAPTER

# 6

## Viroid Structure

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### INTRODUCTION

The elucidation of the structures adopted by viroids is paramount for understanding the different mechanisms involved in their replication, pathogenesis, and transport. In general, the secondary structures of viroids have been predicted using computer software. However, the characterization of biological structures in solution (in vitro) and in the cell (in vivo) is obviously more important for the elucidation of the structure–function relationships of a viroid. Recent advances have now revealed the structure in solution of several viroid species (Steger and Perreault, 2016).

### STRUCTURE OF THE POSPIVIROIDAE

The native structure of circular forms of members of the family *Pospiviroidae* is generally described as rod-like without any bifurcation (Fig. 6.1A). This structure consists of five domains that are described below:

The terminal left (TL) domain of most pospi- and apscaviroids (type members are potato spindle tuber viroid, PSTVd, and apple scar skin viroid, respectively) contains an imperfect repeat that could form either a rod-like or a Y-shaped (Fig. 6.1B) structure. However, the rod-like

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