

## Hops Latent Viroid – Technical Details

Hops Latent Viroid (HLVd) is a member of the Pospiviroidae family, which is characterized by their small, circular, single-stranded RNA (ssRNA) molecules. The RNA structure of HLVd, like other viroids, is highly structured and contains several distinct features that are crucial for its infectivity, replication, and interaction with the host plant's cellular machinery. The following provides an overview of the fundamental characteristics of HLVd:

### Size and Composition

- *Length:* HLVd RNA molecules typically consist of about 250 to 370 nucleotides, making them among the smallest known pathogens capable of causing disease in plants.
- *Circularity:* The RNA is circular and does not possess a 5' cap or a 3' poly-A tail, distinguishing it from typical messenger RNAs (mRNAs) found in cells.

### Secondary Structure

- *Rod-like Conformation:* The secondary structure of HLVd RNA adopts a rod-like conformation, which is a common feature among viroids. This structure is stabilized by intramolecular base pairing, forming a compact and highly paired molecule.
- *Central Conserved Region (CCR):* The CCR is a characteristic feature of members of the Pospiviroidae family, including HLVd. This region is critical for replication and is highly conserved among different viroid species. It plays a key role in the interaction with the host's RNA polymerase II, which is essential for viroid replication.
- *Terminal Loops:* The RNA structure features terminal loops that protrude from the rod-like structure. These loops are involved in the viroid's mobility within the plant and possibly in the recognition and binding to host factors necessary for replication and pathogenesis.

### Tertiary Interactions

- *Pseudoknots and Kissing Loops:* Tertiary structures, such as pseudoknots and kissing loops, contribute to the stability and function of the viroid RNA. These structures can facilitate the circularization of the RNA molecule and are thought to be involved in the replication process by providing specific binding sites for host enzymes.

## Functional Implications

- *Replication*: The replication of HLVD occurs in the nucleus of the host cell and involves a rolling-circle mechanism<sup>1</sup>. The structured RNA interacts with the host's RNA polymerase II to initiate synthesis of complementary RNA strands.
- *Pathogenicity*: Certain structural features of HLVD RNA, including specific sequences and structural motifs, are associated with the viroid's pathogenicity. These elements may interfere with normal plant cell processes, leading to disease symptoms.

The RNA structure of HLVD is a key determinant of its ability to infect, replicate within, and cause disease in host plants. The precise folding and specific structural features enable the viroid to interact effectively with host cellular components, despite its small size and the absence of encoded proteins.

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<sup>1</sup> **Rolling circle replication** (RCR) is a process of nucleic acid replication that proceeds in one direction and is capable of quickly producing numerous copies of circular DNA or RNA molecules. This process is applicable to plasmids, bacteriophage genomes, and the circular RNA genomes of viroids. Additionally, certain eukaryotic viruses employ this mechanism to replicate their DNA or RNA.