Identification of a putative RNA dependent RNA polymerase encoded by a yeast double stranded RNA virus

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Consensus sequences have been established for a number of conserved regions in putative RNA dependent RNA polymerases (RDRPs) from 7 RNA viruses of eucaryotes by comparison to the known poliovirus RDRP (1). One of these conserved regions also appears in Qb synthetase and in several retrovirus reverse transcriptases. We report a partial (carboxy terminal) sequence for a putative RDRP from the yeast virus ScV (2), the first RDRP from a double stranded RNA virus of eucaryotes. The sequence was derived from the 3' 1135 bases of the L1 plus strand (EMBL accession number X07770). L1 (approximately 5 kb) is the only required viral dsRNA.

The predicted amino acid sequence is the 377 carboxy terminal amino acids of a protein sharing four highly conserved regions with all eucaryotic viral RDRPs examined. These occur in the same order in each. The second of these regions (the gly-asp-asp region) occurs twice in the ScV putative RDRP and is the only region also occurring in Qb synthetase and in viral reverse transcriptases. It is intriguing to speculate that both of these regions in ScV may be functional: one as part of a "replicase" RDRP and the other as part of a "transcriptase" RDRP.

The four conserved regions within the carboxy terminal sequences of all RDRPs are compared to those of ScV in Table 1, where the non-standard abbreviations are the following: - = any amino acid; X = K or R; B = S or T; J = hydrophobic; O = D, E, Q or N; U = D or E; and Z = K, R, D or E. The positions of the regions of the consensus sequence are reported as averages of the 8 sequences.

Table 1. Conserved sequences in RDRPs

Region	aa position (1 = COOH)	Sequence		Match (avg. or ScV)
1	~181 - 164	consensus	BG--JT-J-NBJJN-JJJ	12.2/13
1	328 - 311	ScV	SGWRLTTFMNTVLNWAYM	13.0/13
2	~148 - 139	consensus	JJ-JGDD-JJ	7.5/8
2a	297 - 288	ScV	SVHNGDDVMI	6.0/8
2b	177 - 168	ScV	IFGVGDDVVR	7.0/8
3	~127 - 119	consensus	JOJUJZJJZ	7.8/9
3	150 - 142	ScV	APVETKIIT	6.0/9
4	~91 - 85	consensus	LXR-JXJ	5.1/6
4	88 - 82	ScV	LKRKARI	6.0/6

In general, there is as much conservation of these sequences in ScV as in other eucaryotic RNA viruses.

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