

BIOTECHNOLOGY OF LITTLE CHERRY VIRUS: FROM MOLECULAR STRUCTURE OF THE GENOME TO A DIAGNOSTIC KIT

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Little cherry virus (LCV) with long flexuous and filamentous particles is similar to closteroviruses. LCV is associated with major disease of cherry trees around the world. In British Columbia, Canada, LCV infection hampers the fruit development reducing yield and quality by producing small and tasteless fruits. Diagnosis of this virus through conventional woody indexing is very tedious and time consuming. Genomic organisation and molecular structure of LCV were determined in order to develop a rapid and less costly diagnostic kit. Double stranded RNA (12.6kb) of this virus was cloned and sequenced. Computer assisted analysis of LCV nucleotide sequence established strong similarities between proteins encoded by LCV and those of other closteroviruses while, the genomic organisation of this virus was significantly different. Thirteen open reading frames (ORF) have been identified containing sequences homologous to proteins from type members of closteroviruses. From 5' to 3', ORF1 contains an unknown protein, helicase and RNA dependent RNA polymerase (RdRp) as seen in members of Closteroviridae. ORF5 encodes the heat shock protein 70 (HSP70) homolog which is the hallmark of closteroviruses as reported in earlier studies. Unlike other closteroviruses LCV contains three ORFs homologous to coat protein gene of other closteroviruses, one being located upstream of HSP70 and the other two downstream of that gene. A small (49 amino acids) hydrophobic