

Complete nucleotide sequence of filamentous phage Cf1c from *Xanthomonas campestris* pv. *citri*

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In 1987 the filamentous phage Cf1t was isolated from *Xanthomonas campestris* pv. *citri*, which is a phytopathogenic bacterium of citrus canker on orange trees. Cf1t is a small virus and contains a positive single stranded DNA molecule, which, upon infection, is converted into a double stranded replicative form of 7,308 base pairs in length. The DNA is encapsulated in a long protein coat (1, 2). This phage forms a turbid plaque, does not greatly affect the growth of the host cell, and integrates its viral DNA into the host chromosome and undergoes a lysogenic cycle. Recently we have observed clear plaque mutants, named Cf1c derived from Cf1t at an appreciable frequency of approximately 1×10^{-3} . The phage yield of Cf1c infected cells is higher than that of Cf1t infected cells, and the growth of Cf1c infected cells is drastically reduced. It is suggested that Cf1c might be a virulent form of Cf1t.

The complete sequence of Cf1c DNA was obtained from both strands with overlapping fragments by Sanger's method (3). The table shows the sequence homologs between typical filamentous phage f1 and Cf1c. Only a putative TATA Box, which is located at position 5590–5620 in Cf1c was found, and the f1 genes display no significant similarity, lower than 60% to Cf1c. Because the gene structure and sequence are highly conserved between f1, fd, M13 and Ike (4, 5, 6). It is suggested that the filamentous phage Cf1c is a novel one, and the functions of Cf1c genes are under investigation now.

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TABLE Sequence homologs between f1 and Cf1c

	Position	% Identity (nt)
TATA Box	5590–5620	99
f1 gene I	288–500	52.5
f1 gene III	4534–5569	50.62
f1 gene VI	1519–1287(??)	50.5
f1 gene II	1731–2288	49.8
f1 gene IV	5788–6909	48.2
others		<48.0