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The figwort mosaic virus gene VI promoter region contains a sequence highly homologous to the octopine synthase (ocs) enhancer element

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Plant viruses from the caulimovirus group have attracted considerable interest as their double-stranded DNA genome makes them attractive candidates for use in plant genetic engineering. The most extensively studied member of this group is cauliflower mosaic virus (CaMV), although the genomes of two other members have been sequenced [4, 7, 8]. Two promoters of transcription have been found in the genomes of these three viruses, located upstream from the gene VI open reading frame and in the long intergenic region, and have been named respectively 19S and 35S promoters on the CaMV genome, based on the sedimentation coefficients of their transcription products. The 35S promoter of CaMV has been particularly used as a component of vectors for plant transformation as it is a strong promoter which is active in most cell types [1]. More recently, the equivalent promoter (34S) from figwort mosaic virus (FMV), which shows sequence homology with the 35S promoter, has also been tested and shown to be of comparable efficiency to the 35S promoter [9].

We have been working on *in vitro* transcription from the CaMV 19S promoter [3], which is less efficient than the 35S promoter in transient expression assays in plants, but which is used with approximately equal efficiency in a Hela cell-free extract (our unpublished results) and, in contrast to the 35S promoter, is active in our tobacco extracts. In the course of our work, we have carried out sequence comparisons between the 19S promoter regions and equivalent regions on the FMV and carnation etched ring virus (CERV) genomes in an attempt to detect conserved elements which could be important in the control of transcription from these promoters. While we detected no significant homology apart from the TATA box region, we were surprised to find a 20 bp sequence, located about 20 bp upstream from the FMV gene VI TATA sequence at 5293 bp, showing considerable homology with the CaMV 35S enhancer sequence ([1], Fig. 1). The homology is particularly striking as it covers the 'TGACG' sequence which has been shown to interact with a protein factor whose binding is correlated with the transcriptional activity of the

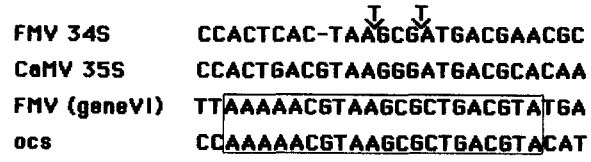

Fig. 1. Comparison of upstream sequences from the two FMV promoters, the CaMV 35S promoter and the ocs element. Sequences are from the FMV 34S (DxS isolate, 6843–6869 bp [8]), CaMV 35S (CM1841 isolate, 7347–7372 bp [5]), FMV gene VI (DxS isolate, 5245–5270 bp, [8]) and octopine synthase (20 bp element [2]) promoters. The region of homology between the FMV gene VI and ocs sequences is boxed.

The nucleotide sequence data reported will appear in the EMBL, GenBank and DDBJ Nucleotide Sequence Databases under the accession number X52754 FMV gene VI.

promoter. Within this region the homology with the 35S sequence is greater than that observed between the 34S and 35S promoters.

The fact that the FMV sequence is an imperfect palindrome led us to compare it with similar sequences upstream from other plant genes and which have been shown to play a role in the control of transcription. Bouchez *et al.* [2] have demonstrated the existence of a conserved 20 bp sequence upstream from the TATA box of ten T-DNA and plant viral genes and which binds a transcriptional regulatory factor which is present in healthy plant extracts. They have named this sequence the octopine synthase gene element (ocs element). The FMV sequence shows striking homology with this element ([8], Fig. 1), the two sequences being identical over a 21 bp stretch. The presence of such a sequence located immediately upstream from the TATA box strongly suggests that this element may be important in the expression of FMV gene VI. This possibility is supported by the recent demonstration that the FMV gene VI upstream region is more efficient than that of the CaMV 35S in promoting transactivation of gene expression in coelectroporation experiments [6], indicating that this FMV promoter is a particularly strong promoter of transcription.

The presence of highly similar sequence elements in the two promoters of FMV, in contrast to the other sequenced caulimovirus genomes, raises the intriguing possibility that gene VI expression may not be regulated by the same mechanisms in these three viruses. While further tests will be necessary to elucidate the role played by this ocs-type element in the expression of the FMV genome, these observations suggest that the FMV gene VI promoter could be a serious candidate for use in chimaeric constructs in which maximal gene expression is desired.

Acknowledgements

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