Available online at www.ijrbp.net

DOI: http://dx.doi.org/10.18782/2322-0392.1306

ISSN: 2322 – 0392

Int. J. Rec. Biotech. (2022) *10*(1), 1-7

Review Article

International Journal of Recent Biotechnology

Peer-Reviewed, Refereed, Open Access Journal

The Gene Expression Strategies in Plant Viral Genome

Ashok Kr Singh*

SRTC PG College Utraula, Balrampur -271604 UP India

*Corresponding Author E-mail: ashokarsingh@gmail.com

Received: 15.01.2022 | Revised: 24.02.2022 | Accepted: 7.03.2022

ABSTRACT

The small size of virus genome the genetic information is extremely compact, and non-coding regions are very limited as compared to those of prokaryotic and eukaryotic cell systems. The virus utilize cell components at all levels of the replication cycle for their own benefit. They have evolved a number of highly sophisticated strategies to produce and regulate the production of the proteins required for their propagation. These proteins are often multifunctional, encoding several essential virus-specific proteins. The virus adapted different strategies include splicing, the production of sub genomic RNAs from virus templates and cap-snatching. The viruses frequently resort to post-translational cleavage of a polyprotein precursor to yield the mature proteins.

Keywords*: Virus, Genome, Expression, Strategies.*

INTRODUCTION

The majority of known plant viruses have RNA genomes which show a wide variation in their genome structure, organization and have different terminal structures such as cap structures or genome-linked proteins at the 5' end, and poly(A)-tail or t-RNA-like structure at the 3' end of their RNA (Bouloy et al., 1990). The some viruses genome needed for infection is divided between two or more segments which may be encapsidated in the same particle or in separate particles and even have associated satellite RNAs (Hull & Davies, 1992). All plants virus genomes encode protein for functions that operate at various stages in the infection cycle.

The major problem facing RNA viruses with limited genome size is their obvious dependence on the host eukaryotic protein-synthesizing system. These small genomes are expected to encode a range of virus proteins. The strategies of expression that have emerged from recent studies suggest that the viral genomes appear to have evolved to overcome the obvious constraints of the plant host system.

Modes of Gene Expression

The eukaryotic 80S ribosome is usually able only to translate the first ORF in the 5' region of an m-RNA. The 40S ribosomal subunit carrying met- t RNA and various initiation factors binds initially at the 5’ end of m-RNA.

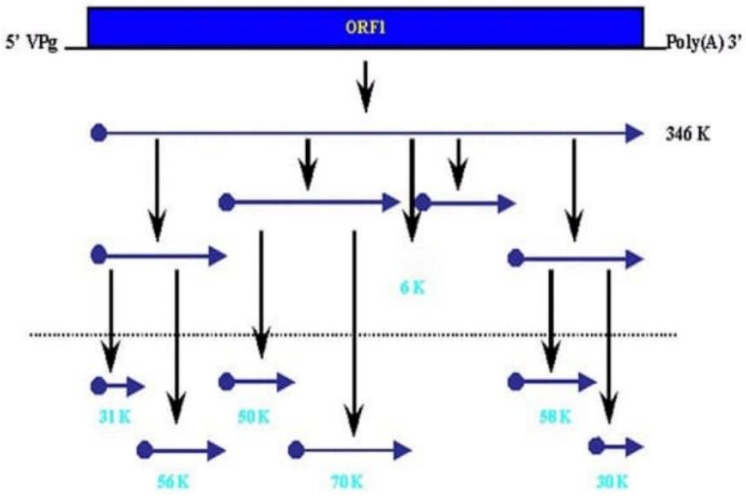
Cite this article: Singh, A. K. (2022). The Gene Expression Strategies in Plant Viral Genome, *Int. J. Rec. Biotech. 10*(1), 1-7. doi: http://dx.doi.org/10.18782/2322-0392.1306

The ubiquitous m7G cap and the associated cap-binding protein explain the predilection of eukaryotic ribosomes to engage m-RNA at the 5'-end. Then the migrating 40S ribosomal subunit stalls at the first AUG codon, which is recognized in large part by base pairing with the anticodon in met-tRNA. However, the stop-scanning step and selection of the initiator codon, is susceptible to modulation, by context and selection of more distal AUG is permitted under certain defined circumstances (Kozak, 1991).

The main strategies used by plant viruses to allow protein synthesis in eukaryotic system from RNA genome are discussed below:

2.1. Polyprotein

The viral genome contains a long ORF which is translated and then cleaved into smaller functional proteins by viral proteinases (Goldbach, 1990). These proteinases form part of the polyprotein, initial cleavages should be autocatalytic. The potyvirus group is one of the most important groups of plant viruses and members characteristically express their genome through a polyprotein process. The potyviral genome is approximately 10 kb in length and encodes a single polyprotein that is processed by three viral proteinases to yield nine or more mature proteins (Reichmann et al., 1992). Two of the proteinases, P1 and helper component-proteinase each catalyze cleavage only at their respective C termini. The remaining cleavage sites are processed by the NIa proteinase, a homologue of the picornaviral 3C proteinase. This enzyme posses a serine-type proteinase fold but contains a nucleophilic cys residue rather than ser at the active site (Gorbalenya et al., 1989).



Protein functions: 31K, cell to cell movement; 58K, proteinase and insect transmission; 50K, proteinase; 70K, rep lication; 6K, ?; 49K,

Polyprotein strategie, Potyvirus

2.2. Sub Genomic RNAs

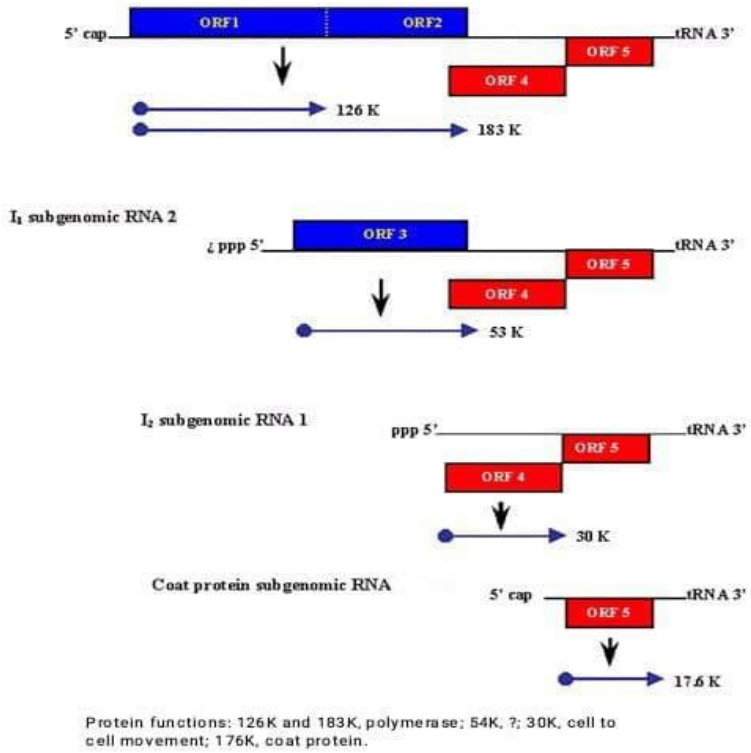
The expression of internal genes such coat protein of the positive RNA viruses is frequently mediated via sub genomic RNAs considered as m-RNAs. The plant RNA viruses mechanism of synthesis of the sub genomic RNA encoding the coat protein has been examined in TMV (Palukaitis et al., 1983). The two mechanisms have been proposed to explain the synthesis of sub genomic RNAs:(1) The minus RNA strand synthesis by the RdRp premature termination could lead to the formation of minus RNA strands of sub genomic length that could serve

as template to generate the sub genomic plus strand RNA. (2) The sub genomic plus strand RNA could be synthesized via internal initiation on minus RNA strands of genomic length.

Miller et al. (1985) studying the mechanism of BMV sub genomic RNA4 formation from genomic RNA3 by using the *in vitro* RdRp system provided, the evidence that the sub genomic RNA of a positive strand RNA virus is synthesized by internal initiation of positive strand RNA synthesis on a negative strand template.

2.3. Non AUG Start Codon

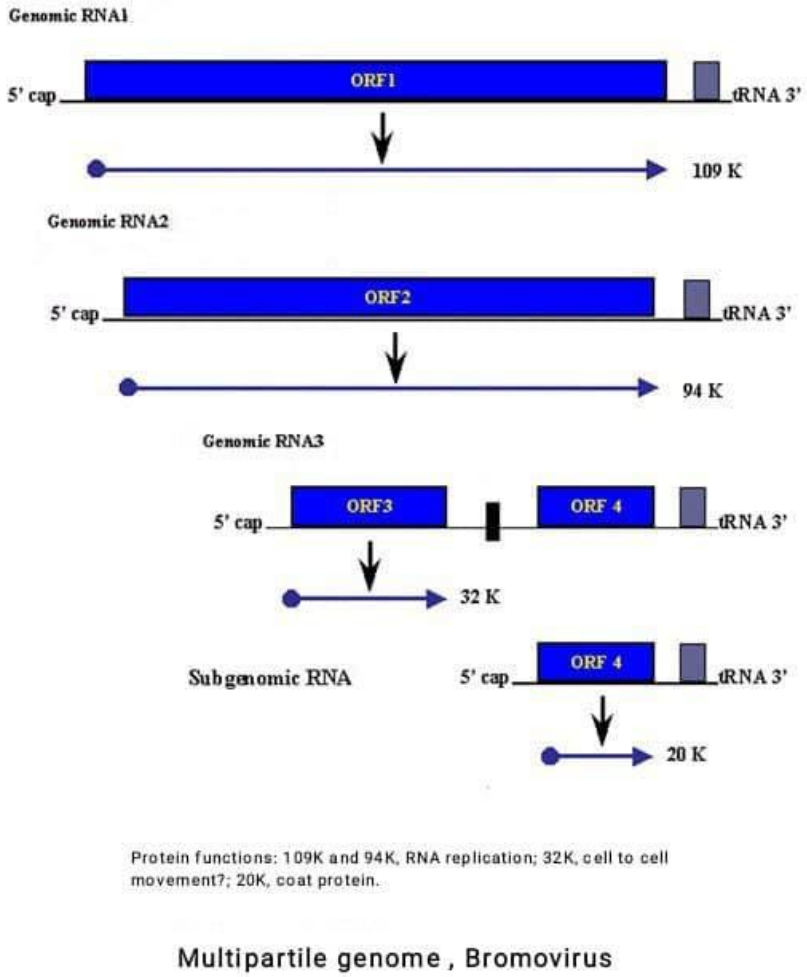
The some virus ORFs appear to start with codon that is not the conventional AUG start codon. The initiation of these ORFs is insufficient. RTBV the initiation codon is AUU.



Subgenomic RNAs, Tobanovirus genome

2.4. Multipartite Genome

The multipartite is a class of virus that have segmented genomes and each segment enclosed in a separate viral particle. The advantage of multipartite genome is its ability to synthesize multiple m-RNA strands to avoid the cellular constraint of mono cistronic. It was not known how multipartite viruses could efficiently infect a single cell with all the segments that comprise their genome simultaneously, which was necessary for replication. It has been shown that the segments accumulate in different cells and the viral system functions through exchange of material between cells. Thus, multipartite viruses are not localized in space but rather more like a distributed network of chemical reactions. The genome of BMV consists of three RNA segments as RNA1, RNA2 and RNA3 containing single cistron the sub genomic RNA4 encoding coat protein is also encapsidated (Allison et al., 1988).



Multipartile genome , Bromovirus

2.5. Leaky Scanning

The leaky scanning is a mechanism used during the initiation phase of eukaryotic translation that enables regulation of gene expression. During initiation, the small 40S ribosomal subunit moves in 5'-->3' direction along the 5'UTR to locate a start codon to commence elongation. Sometimes, the scanning ribosome by passes the initial AUG start codon and begins translation at further downstream AUG start codons (Kozak, 1999) Translation in eukaryotic cells according to most scanning mechanisms occurs at the AUG start codon proximal to the 5' end of m-RNA.

There are certain instances where initiation has been found to occur upstream at a non-AUG codon. Eukaryotic genes containing consistent G-C rich leader sequences are frequently observed performing this mechanism.

The viruses use a leaky scanning mechanism to produce vital proteins which implies that leaky scanning is not a consequence of inadequacy, but instead allows viruses to overcome the high selective pressures of competing with their hosts (Ryaboba, 2006).

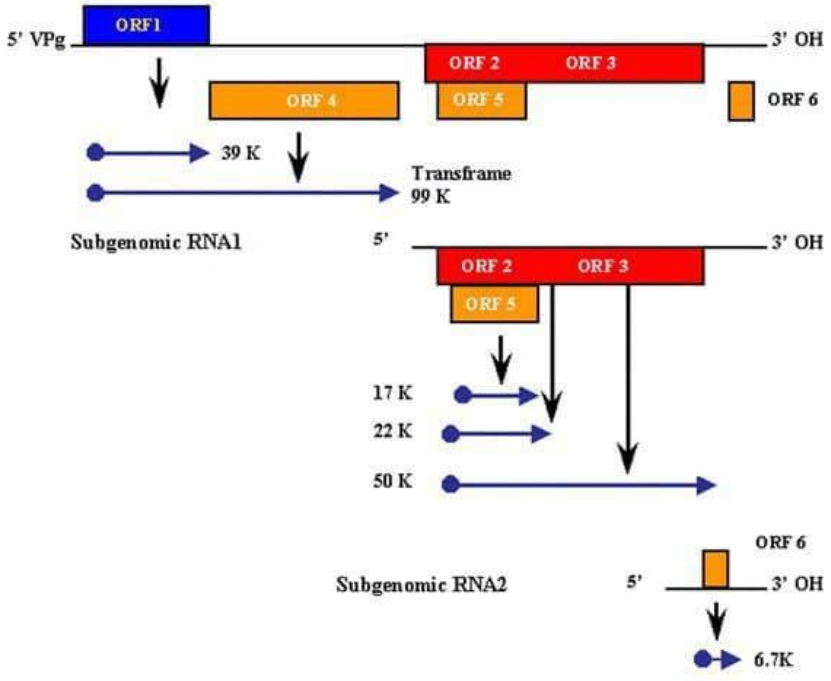
2.6. Read Through Protein

The first cistron in the genomic RNA have a leaky termination codon UAG or UGA that can be suppressed by a host transfer RNA there by permitting some of the ribosomes read through into a downstream cistron as a result, giving rise a second longer functional polypeptide. The protein are either replicase as in TMV or extension to coat protein as in luteovirus to be involved in transmission vector interaction. The stop codon is read by a suppressor t-RNA instead of the ribosome being released by the eukaryotic release factor. (Zaccomer et al., 1995).

The read through process requires at least two elements. First, a suppressor t-RNA the nature of a possible candidate has been proposed for TMV and for tobacco rattle tobravirus (Zerfass & Beier, 1992). Second, the nucleotide context surrounding the termination codon and in particular the two downstream codons appear important for read through of TMV RNA *in vivo* (Skuzeski et al., 1991).

2.7.Translational Frame Shift

The ribosomal frame shifting is a strategy frequently employed by virus to produce more than one protein from overlapping reading frames. It may occur in either 3' direction know as +1 frameshift whereas a shift in the 5' direction know as -1 frameshift (Vickers & Ecker, 1992). The frame shift allow a ribosome to by pass the stop codon at 3' end in one reading frame and swift to another reading frame so translation can continue to the next stop codon. The frame shift give two protein the frame and frame shift. They are identical from N- terminus. The luteovirus genome consist of 5.8 kb single strand plus RNA with six major ORFs. They expressed by -1 ribosomal frame shift in the region where the ORFs of the protein 2a and 2b overlap (Keese et al., 1990).



Protein functions 22 K, coat protein; 60 K, polymerase; 17 Vpg

Frame shift Luteovirus genome

2.8. Ribosomal Shunt

The studies carried out to analyze the translation of the CaMV genome suggested a mechanism by which ribosomes enter at the 5'cap site begin scanning but at some point near the 5' end of the leader they transferred to a region at the 3' end of the leader without scanning linearly through the central portion of the leader. This process has been termed ribosome shunt and the sites between which it occurs have been defined (Futterer et al., 1993).

The genome of RTBV contains four ORFs. The ds DNA genome is transcribed to

give a 35S RNA which spliced to form the m-RNA for ORF4.The ORF1 has AUU start codon and next two have AUG codon in any reading frame for ORF 2 and ORF3.The shunt process ribosome enters at 5' cap which translocate and across the stable hairpin from donor site to landing site of ORFs (Hull, 1992).

2.9.Translational Transactivation

Translation of down stream ORFs on the polycistronic RNAs of caulimo viruses depends on the presence of a virally encoded translational trans activator which is the product of ORF VI. TAV is a complex protein that appears to be involved in many aspects of the virus life cycle (De Tapia et al., 1993). Its role is to control translation from the polycistronic CaMV 35S RNA. Translational transactivation has been demonstrated for CaMV and appears to enhance expression of all the majors ORFs on the pre genomic 35S RNA (Scholthof et al., 1992). The TAV itself translated from the 19S RNA can probably also transactivated its own expression from ORF VI on the 35 S RNA (Driesen et al., 1993). The process of transactivation seems to allow ribosomes that have translated one ORF to remain competent to translate further down stream ORFs (Rothnie et al., 1994).

2.10. Splicing

It was previously though that there was no obligate role for splicing in either plant viruses. Kiss-Laszlo et al. (1995) have described the detection of spliced CaMV RNAs in infected plants and transfected protoplasts. Transient expression experiments revealed a splice donor site in the leader sequence of CaMV 35S RNA and three additional splice donor sites within ORF I. The splicing between the leader and ORF II produces an mRNA from which ORF III and, in the presence of TAV ORF IV can be translated efficiently. The other three splicing events produce RNAs encoding ORF I and II in frame fusions. All four spliced CaMV RNAs were detected in CaMV infected plants. Virus mutants in which the splice acceptor site in ORF II is inactivated are not infectious, indicating that splicing plays as essential role in the CaMV life cycle.

These are different strategies which virus used exclusively or a combination for a expression of genome.

REFERENCES

Allison, R. F., Janda, M., & Ahlquist, P. (1988). Infectious in vitro transcripts from cowpea chlorotic mottle virus c-DNA clones and exchange of individual RNA components with bromo mosaic virus. *J of Virology 62*, 3581-3588.

Bouloy, M., Pardigon, N., Vialat, P., Gerbaud, S., & Girard, M. (1990). Characterization of the 5' and 3' ends of viral m-RNAs isolated from BHK21 cells infected with germiston virus. *Virology 175*, 50-58.

De Tapia, M., Himmelbach, A., & Hohn, T. (1993). Molecular dissection of the cauliflower mosaic virus translation trans activator. *EMBO Journal 12*, 3305-3314.

Driesen, M., Benito Moreno, R. M., Hohn, T., & Fuetterer, J. (1993). Transcription from the CaMV 19S promoter and autocatalysis of translation from CaMV RNA. *Virology 195*, 203-210.

Gorbalenya, A. E., Koonin, E. V., Donchenko, A. P., & Blinov, V. M. (1989). Two related super families of putative helicases involved in replication, recombination, repair and expression of DNA and RNA genomes. *Nucleic Acids Research 17*, 4713-4730.

Hull, R., & Davies, J. W. (1992). The approaches to non conventional control of plant virus diseases. *Critical Rev in Plant Sciences 11*, 17-33.

Keese, P., Martin, R. R., Kawchuk, L. M., Waterhouse, P. M., & Gerlach, W. L. (1990). Nucleotide sequences of an Australian and a Canadian isolate of potato leafroll lute virus and their relationships with two European isolates. *J of General Virology 71*, 719-724.

Kiss-Laszlo, Z., Blanc, S., & Hohn, T. (1995). Splicing of cauliflower mosaic virus 35S RNA is essential for viral infectivity. *EMBO Journal 14*, 3552-3556.

Kozak, M. (1991). Structural features in eukaryotic m-RNAs that modulate the initiation of translation. *J of Biological Chemistry 266*, 867-870.

Kozak, M. (1999). Initiation of translation in prokaryotes and eukaryotes. *Gene 234*,187-208.

Marsh, L. E., Pogue, G. P., an& d Hall, T. C. (1989). Similarities among plant virus plus and minus RNA termini imply a common ancestry with promoters of eukaryotic t-RNAs. *Virology 172*, 415-427.

Miller, W. A., Dreher, T. W., & Hall, T. C. (1985). Synthesis of brome mosaic virus sub genomic RNA in vitro by internal initiation on minus sense genomic RNA. *Nature 313*, 68-70.

Palukaitis, P., Garcia Arenal, F., Sulzinski, M. A., & Zaitlin, M. (1983). Replication of tobacco mosaic virus and characterization of single stranded and double stranded virus related RNAs from TMV infected plants. *Virology 131*, 533-545.

Rothnie, H. M., Reid, J., & Hohn, T. (1994). Para retrovirus and retroviruses: a comparative review of viral structure and gene expression strategies. *Adv. in Virus Research 44*, 1-67.

Ryaboba, L. (2006). Translation reinitiation and leaky scanning plant science. *Virus Research, 119*, 52-62.

Scholthof, H. B., Gowda, S., Wu, F. C., & Shepherd, R. J. (1992). The full-length transcript of a caulimo virus is a polycistronic mRNA whose genes are trans activated by the product of gene VI. *J of Virology 66*, 3131-3139.

Skuzeski, J. M., Nichols, L. M., Gesteland, R. F., & Atkins, J. F. (1991). The signal for a leaky UAG stop codon in several plant viruses includes the two downstream codons. *J of Molecular Biology 218*, 365-373.

Vickers, T. A., & Ecker, D. J. (1992). Enhancement of ribosomal frameshifting by oligonucleotides targeted to the HIV gag pol region. *Nucleic Acids Research 20*, 3945-3953.

Zaccomer, B., Haenni, A. L., & Macaya, G. (1995). The remarkable variety of plant RNA virus genomes. *J of General Virology 76*, 231-247.

Zerfass, K., & Beier, H. (1992). Pseudo uridine in the anticodon GYA of plant cytoplasmic t-RNA Tyr is required for UAG and UAA suppression in the TMV sspecific context. *Nucleic Acids Research 20*, 5911-5918.