

Review Article

# Pigeonpea sterility mosaic virus a green plague-Current status of available drug and new potential targets

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## Abstract

Pigeonpea is one of the important legume crops with high protein content and nutritional traits. It has enormous potency for its widespread adoption by farming communities. It is affected by various kinds of biotic and abiotic stresses. In the context, of biotic stresses Sterility mosaic disease (SMD) is one of the severe diseases in pigeonpea which ultimately lead to the drastic yield loss. The virus belongs to the genus *Emaravirus*, family- Fimoviridae. SMD is associated with two diverse types of *emaravirus*, Pigeonpea sterility mosaic virus1 (PPSMV-1) and Pigeonpea sterility mosaic virus 2 (PPSMV-2). It is transmitted by the mite (*Aceria cajani*), mainly environmental contributing to the feasibility for the mites for the inoculation of the virus. The SMD is mainly governed by two genes SV1 that includes the dominant allele and serves as an inhibitory action on the resistance of the SV2. Methods for identification of the virus include RT-PCR, DIBA and ELISA using alkaline phosphatase or penicillinase. To control SMV disease farmers generally adopted intercropping methods. There are few potential drugs have been identified for the administration of the disease such as 0.1% Fenazaquin, Dicofol, Imidacloprid, Carbosulfan; Spiromesifin includes the inhibition of the mite inoculation on the pigeonpea plant. The present review describes compressive and systematic insights on SMV protein targets and potential drugs that could be utilized as the presumed drug targets for the finding of true drugs against the SMD in pigeonpea.

## Introduction

Pigeonpea (*Cajanus Cajan L. Millsp.*), also known as tur or red gram, a perennial shrub and tropical legume which enriches the soil through symbiotic nitrogen fixation [1]. In India, it is one of the important crops after chickpea and predominates the area of ~4.89 million tons (mt) and productivity is 762.4 kg ha<sup>-1</sup> respectively [2]. It is a cross pollinated and diploid legume with 22 chromosomes and 858 Mb, encodes a total of 47,180 protein-coding genes [3]. It is mainly known for its high protein content (vitamin B, carotene and ascorbic acid), with a substantial amount of amino acid content up to 43.61% [4]. Despite being the most populated crop, it faces several environmental challenges (abiotic and biotic stress). In abiotic stress (low and high moisture, salinity and water-logging hypoxia) and biotic stresses (fusarium wilt, sterility mosaic and several insect pests including pod borer insects, maruca, stresses) which affects the yield of the plant [5]. Many diseases

have led to low yield in the pigeonpea such as root-knot infestations (*Meloidogyne spp.*); Wilt (*Fusarium udum*) [6]. Sterility Mosaic Diseases are one of the biotic stresses which are highly disastrous and endemic in almost all agro-ecologies of pigeonpea growing in India. Apart from this, reniform nematodes (*Rotylenchulus.spp.*) also increases susceptibility to fusarium wilt and Sterility Mosaic Disease (SMD). The SMD is a major restriction on the production of pigeonpea and other legumes. SMD was first described in 1931 in Pusa, Bihar State and is mostly regional to India, Nepal, Bangladesh and Myanmar [7]. If infection of SMD occurs at an early stage i.e., less than 45-day-old plants, it leads to loss 95% - 100% yield [8]. SMD is one of repression on the pigeonpea that leads to the yield loss in consistency, thus leading to the epidemics. The symptomatic features of the seed are the stunting, bushy and pale green appearance of the plant with mosaic, mottling and reduced size of the leaves, but severely affected plants are seen with complete sterility of pods [9]. Pigeonpea and a few

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Keywords: Drug targets; Emaravirus; Pigeonpea; Protein structure SMD; SMV1 and SMV2

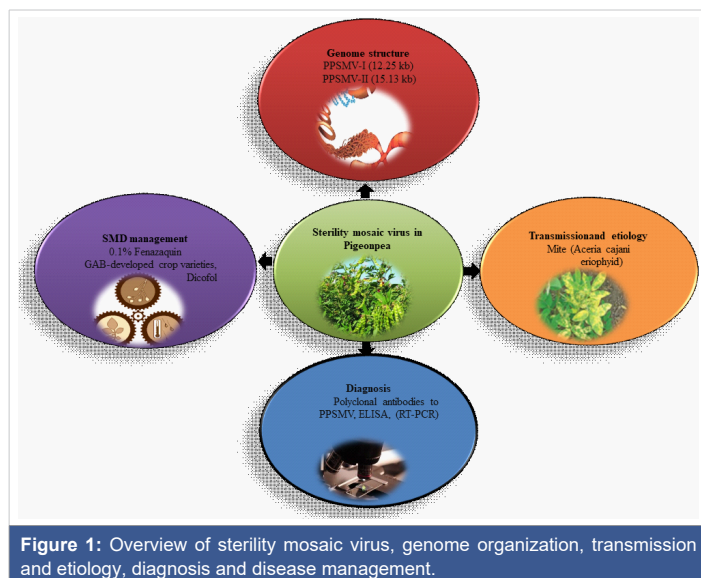
Abbreviations: AFLP: Amplified Fragment Length Polymorphism; DAS-ELISA: Double Antibody Sandwich ELISA; DIBA: Dot Immunobinding Assay; ELISA: The Enzyme-Linked Immunosorbent Assay; RT-PCR: Reverse Transcription Polymerase Chain Reaction; SMD: Sterility Mosaic Disease; SMV: Sterility Mosaic Virus



wild species of *Cajanus* were found to support the vector *Aceria cajani* (Acari: Arthropoda), the eriophyid mite. Many studies conducted in the last few decades showed that in nature, *A. cajani* populations were almost exclusively observed on SMD-infected pigeonpea, but not on healthy plants, indicating a strong communitistic relationship between the virus-infected plants and the vector. The epidemiology of SMD involves the virus, mite vector, cultivar and environmental conditions. Infected perennial and volunteer plants serve as a source for both the virus and its vector mites and play an important role in the disease cycle. Wild *Cajanus* serves useful genes which have the greater potential for crop improvement. Several tools have been developed using the genomics approach to boost the genetic performance such as different types of molecular markers were added to trace the disease resistance varieties [10]. Many genetic improvement techniques are evolved i.e., pure line selection from germplasm, hybridization followed by pedigree selection and mutation breeding. Management of the disease with very rare drugs has been found to be effective. The biological control can be done through use of entomopathogenic fungi [11]. In this review we provide an outline of SMV including its symptoms, transmission, etiology, genome organization, and proteomic structure with a list of few available and potent drugs for the management and control of SMV in pigeonpea crop improvement programs (Figure 1).

### The sterility mosaic disease in pigeonpea

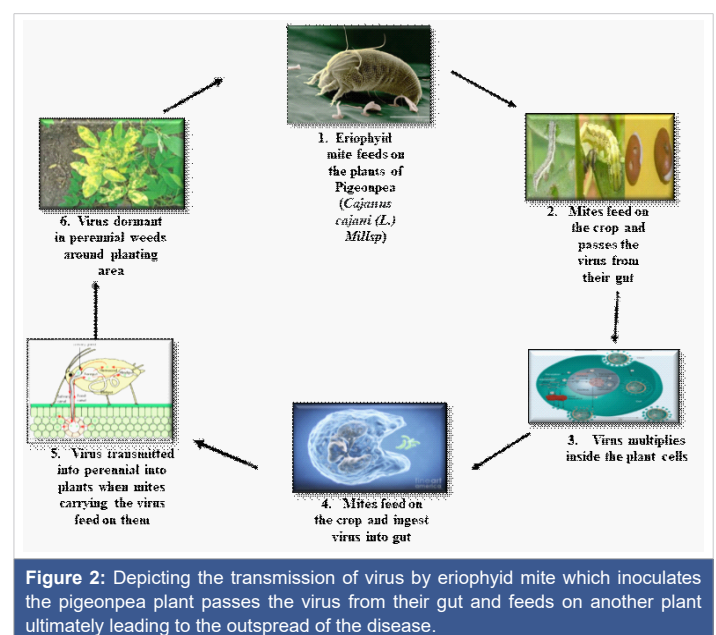
SMD is one of the major diseases in the Indian subcontinent associated with various factors that lead to different infections and it is transmitted by *A. cajani*. The main susceptible parts like branches show the mottling of the disease and diverse degree of mosaic affecting sterility of the infected plants [13]. Sterility Mosaic Disease is considered as one the major biotic stress causing disastrous damage to the yield leading to loss up to 95% [14]. A contingent agent of the disease is *emaravirus*. The disease is also designated as 'green plague' since infected



plants remain in the habitat [15]. SMD is characterized by one or more features such as partial cessation of production of flowers (sterility), mosaic or chlorotic ringspot. Symptoms of the leaves include excessive vegetative growth, stunting and decreased leaf size. Symptoms often depend on the infection time. Infection of susceptible species at the early stage of crop development, genotypes (< 30- to 45-day-old plants) result in characteristic disease expression symptoms within 10 to 15 days and nearly every other day complete cessation of the flowering process, but leaves plants grow, symptoms become masked [16]. The population of mites, their life cycle and the incidence of disease were observed to be affected by seasonal temperature fluctuations; relative humidity, direction of wind, speed and rainfall etc. [17]. SMV enters the plant cells through the mites which ejaculate the virus into the natural openings of the plant surface resulting in mechanical injury. Upon SMV entry, the viral genomic RNA is released and translated. Following translation, the viral proteins, and particles assemble new virus progeny and move to adjacent cells. Aphids spread the virus, relatively in a short time, after feeding on a virus-infected plant; mites instantly transfer to a healthy plant and transmit (spread) the virus as they feed on the other plant (Figure 2). Seeds are the source of primary inoculums, while secondary spreads are by aphids which happen at a rapid pace. Seed transmission efficiency varies by cultivar, with the incidence of seed transmission being higher in plants infected before flowering [18]. 5% of the transmission occurs in the majority of commercial cultivars produced, with older cultivars varying from no transmission to 75% transmission [19].

### Etiology and virus transmission

SMD has a distinctive attribute in stunted and bushy plants, reduced-size leaves with chlorotic rings or mosaic symptoms, and partial or complete cessation of flower production [20]. The causative agent of the disease is PPSMV, a single-stranded





RNA genome virus with a segmented, negative sense, transmitted semi-persistently by the eriophyid mite *Aceria cajani*. Several genotypes of cultivated and wild relatives of pigeonpea are affected by PPSMV. The experimental hosts are *N. Benthamian*, *N. Clevelandii*, *P. vulgaris*, *Chrozophorarottleri* was used for the identification and spread of disease [21].

The virus and the vector are both intensely pigeonpea-specific and its few wild relatives are *C. Scarabaeoides* and *C. Cajanifolius*. The presence of several PPSMV strains was suspected based on differential host reactions in different geographical areas. It spreads through the fields in an outbreak form under favorable conditions. Moreover, infection predisposes the plants to subsequent infection by fungal diseases and spider mite colonization [22]. The prevalence of asymptomatic field infections is normal and often much higher in areas of incidence of illness dependent on apparent foliar symptoms [23]. Differential host reactions are based on different regional reactions. The presence of different types of PPSMV strains can be detected in areas where pigeonpea is cultivated after a long gap. The epidemiology of SMD involves the virus, vector mite, cultivar and environmental conditions. Perennial infected and volunteer plants both serve as a source for the virus. Its vector mites have an important role to play in the disease cycle [24]. *A. cajani* was up to 53% but was 100% when > 5 mites were used per plant [25]. *A. cajani* has a short length of 2.03  $\mu\text{m}$  (approx.) which enables transmission to the epidermal and the underneath mesophyll cells [26]. The multiplication of mites on SMD-affected plants was very high compared to healthy pigeonpea plants. PPSMV has an incubation time of eight days for the expression of pigeonpea symptoms [27]. A number of central research foci, captivating research to determine critical pathogen targets for control, novel methodologies and methods of delivery, are evolving that will provide a strong basis for disease management into the future. As described below, assertive research and implementation for the development of natural resistance has led to development of resistance varieties of pigeonpea from various national and international crop breeding programs.

### Detection of SMD in pigeonpea plant

SMD symptoms are particular and show a diagnostic trait for its identification. Several attempts have been made since various strategies have been done for the detection of the disease agent to be characterized. The diagnosis of SMD and the selection of germplasm resistant to SMD are based on symptom expression. However, this diagnosis is complicated by the fact that many abiotic and biotic variables are governed in symptom expression and that pigeonpea is cross-pollinated so that genotypic heterogeneity, caused by cross-pollination, also plays an important role in symptomatology [28].

The host polyphenolic compounds on the pod surface which interfere with the stability and infectivity of the SMD agent, which obstructs virus infectivity and purification of

the virus particle. The purification procedure for minimizing the effects of components by extraction of infected leaves in buffers containing chelating and reducing agents, high concentrations of nonionic detergent, and the precipitation. Purification was achieved by quasi-equilibrium zoning centrifugation Sucrose and CsCl gradients [29]. In order to detect the presence of PPSMV from their virulent vector using whole mite extract as an antigen, serological diagnostic techniques such as DAS-ELISA (double antibody sandwich ELISA) and DIBA (dot immunobinding assay) were developed. For virus detection in vector mites, both DAS-ELISA and DIBA was susceptible [30]. Polyclonal antibodies to PPSMV are VLP (Virus like particles) preparations produced in rabbits have been very effective in the detection of PPSMV in plant tissues by double antibody sandwich (DAS) and direct antigen coating forms of ELISA using enzyme-labeled (alkaline phosphatase or penicillinase) immuno-gammaglobulin. At the genome level, using reverse transcription-polymerase chain reaction (RT-PCR) which uses primers based on sequence [31]. Recently, different approaches have been developed in the genomic regions responsible for genetic study and breeding traits using the Axiom 62K SNP array which allows the marker assisted breeding to transfer this trait into elite cultivars and germplasm [32]. The recent advances of omics technologies deliver large-scale multidimensional data sets, better to integrate and utilize them for the development of disease resistance pigeonpea cultivars [3].

### Management of SMD in pigeonpea plant

The numerous chemical methods such as organophosphorus (Sulphur with Propargite combination, Salicylic acid and acaricides viz; 0.1% Fenazaquin) were used for control of disease but these were not economically beneficial because the crop is grown in marginal conditions. Various conventional breeding programmes have been conducted in South India which among 115 wild *Cajanus* accessions belonging to six species, *C. albicans*, *C. platycarpus*, *C. cajanifolius*, *C. lineatus*, *C. scarabaeoides*, and *C. sericeus* which revealed about resistance of accessions, ICP 15614, 15615, 15626, 15684, 15688, 15700, 15701, 15725, 15734, 15736, 15737, 15740, 15924, 15925, and 15926 and can be cross compatible with pigeonpea [33]. The existence of separate PPSMV strains/ isolates in various locations, however, makes it difficult for the identification of the isolates. Genotypes that are SMD-resistant have an epidermal cell wall and thicker leaf cuticles than those of genotypes prone to mite's broad-spectrum resistance [34]. PPSMV exhibits that recessive gene are the key cause of resistance. Resistant trait was governed by two independent non-allelic genes, SV1 and SV2 in which one-gene SV1 which is a dominant allele has an inhibitory effect on the character (resistance) that regulates the other (SV2) gene. Based on this, the presence in one locus of the dominant SV1 gene allele suppresses the action of the dominant SV2 (resistance) gene allele found at another locus, resulting in susceptible phenotypes [35].



New sources of resistance to Fusarium wilt and SMD have been identified in a mini-core collection of pigeonpea germplasm. Molecular markers based on AFLP (Amplified fragment length polymorphism) is a PCR-based technique that uses selective amplification of a subset of digested DNA fragments to generate and compare unique fingerprints for genomes of interest. Various QTLs for resistance to isolates have been analyzed using composite interval mapping, which shows the involvement of different genes that grant resistance to these isolates [36].

### Genome organization of SMV

PPSMV is the seventh species in the genus of *Emaravirus*, family *Fimoviridae*, order *Bunyavirales*. It shows features which are associated with the *Tospovirus* members of the genera (Family: *Bunyaviridae*) and *Tenuivirus*, both consist of single-stranded RNA viruses encode proteins [37]. PPSMV shows resemblance in context to genomic organization and conserved 5' and 3'-end sequences with other *emaraviruses*. The phylogenetic analysis of the RNA-3 sequence of disease causing two viral agents such as PPSMV-I and PPSMV-II exhibited considerable variability among seven different geographical strains depicting four states in southern India [38]. PPSMV-1 was the first to be identified and, subsequently, another separate PPSMV-2 *emaravirus* was also reported to be involved in SMD. Both PPSMV-1 and PPSMV-2 consist of six genomic segments of RNA, namely RNA1 (7022 nucleotide in length) coding for RNA-dependent RNA polymerase (RdRp, 2295 amino acids); RNA2 (2223 nucleotide) coding for glycoprotein (GP, 649 amino acids); RNA3 (1442 nucleotide) coding for nucleocapsid protein (NP, 309 amino acids); RNA4 (1563 nucleotide) coding for p4 (MP, 362 amino acids); RNA5 (1689 nucleotide) coding for p4 movement protein (MP, 362 amino acids); (238 amino acids)[39]. The genome structure is spherical and segmented shape. It consists of four linear segments with negative-sense and single-stranded RNA. The genome size is around 12.2 kb. The genome structure consists of RNA1 (7.0kb) and RNA2 (2.3 kb). The viral RNA dependent RNA polymerase (L) binds to a promoter on each encapsulated segment and transcribes the mRNAs and is capped by L protein during synthesis using cap snatching [40]. The protein sequences of SMV were retrieved from UniProt database (<http://www.uniprot.org/>). In order to understand the structural properties of SMV, MODELLER is used for homology or comparative modeling of protein three-dimensional structures. The alignment of SMV sequences to be modeled with known related structures is provided and MODELLER automatically calculates a model containing all non-hydrogen atoms. MODELLER implements comparative protein structure modeling by satisfaction of spatial restraints [41]. The protein structure involves the two type *i.e. emaravirus1* and *emaravirus2* of base pair 2294 in length. By computer assisted analysis using MODELLER. The 3D structure was developed by the interaction of amino acid

residues in which SMV1 and SMV2 both showed an alpha helix of 16%. In SMV1 beta strand is one-fold higher than SMV2 beta strand (10%). Total 2% of TM helix present in SMV2 while absent in SMV1 (Figure 3).

### Proteomic structure of SMV

### Analysis of primary structure and secondary structure

The amino acid composition of SMV1 and SMV2 were analyzed. The amino acid composition reveals that SMV1 has 2294 amino acids and molecular weight of 266245.80 Daltons whereas SMV2 has 2294 amino acids and molecular weight of 267897.20 Daltons (Figure 4).

### Secondary structure

#### a) Hydrophobicity

Kyte and Doolittle method is used to evaluate mean hydrophobicity as it can recognize surface exposed regions and transmembrane regions with interaction of protein region towards lipid bilayer. Lipid bilayer acts as a barrier around the cell, thus enable the virus to bind the host cells. Hydrophobic moment was determined for each residue by keeping the same window size for all of the amino acids. In this X-axis show position of each amino acid in sequence and Y-axis shows mean hydrophobicity. Value above zero is observed to have more amino acid at a particular position and give its mean hydrophobicity value (Figure 5).

#### b) Hydrophilicity

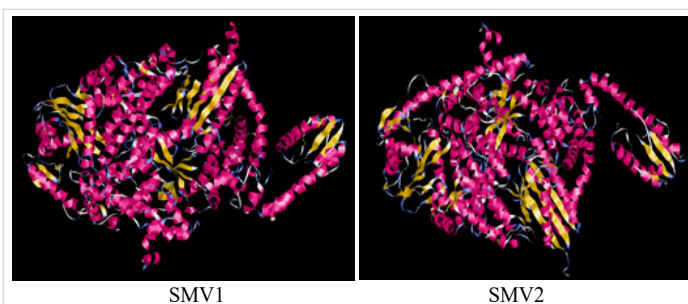


Figure 3: Depicts the 3D structure of SMV1 structure (left) and SMV2 structure (right).

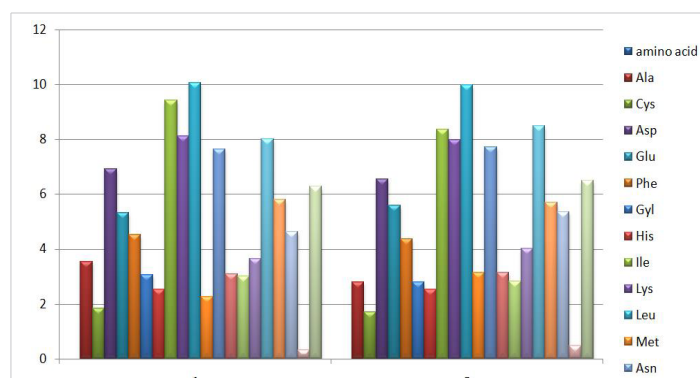


Figure 4: Depicts the molecular weight of number of amino acid included in sequence of SMV1 (1) and SMV2 (2) in pigeonpea.

Boyko plot is a quantitative analysis of hydrophilicity of amino acids in SMV1 and SMV2. It measures the degree of interaction of the polar solvent with amino acids. Hydrophilicity indicates the quantitative analysis of amino acids of protein and helps of characterize domains of SMV1 and SMV2. Higher hydrophilicity indicates that residues are in contact with solvent and likely to occupy the outer surface of protein (Figure 6).

### New potential drug targets

SMV is one of the tropical diseases which are being treated with the non-SMD drugs however; the exact antimicrobial activity of the drug is not clearly understood. Search of new potential drugs only targets biochemical and metabolic pathways necessary for the mite survival [42]. Narrow and Broad-spectrum drugs are:

Narrow spectrum drugs only inhibit the multiplication of the unwanted pathogen by infecting the other virus by various strategies such as prohibiting protein, nucleic acid synthesis and metabolic pathways (Table 1).

Broad spectrum drugs targets and inhibits replication and development of the viral proteins such as polymerase and proteases by interfering with their cellular machinery (Table 2).

### Conclusion

In this present review, we provide insights on the sterility mosaic disease in pigeonpea (*Cajanus Cajan*) which causes devastating damage to the yield of pigeonpea. There was a major dilemma in etiology and molecular biology regarding the causal organism of SMD. The sterility mosaic virus is transmitted through the *Aceria cajani* eriophyid as a mite vector. Mite inoculates the whole field with the virus from their gut. Many preventive measures are being taken to overcome yield loss. Recently the identification was dependent on the symptoms, but characterization of the causal agent has manifest SMD detection by various techniques such as DAS-ELISA (A double antibody sandwich ELISA) and DIBA (A dot immunobinding assay) and many purification methods quasi-equilibrium zoning centrifugation Sucrose and CsCl gradients. PPSMV antibodies react with the virus in viruliferous mites

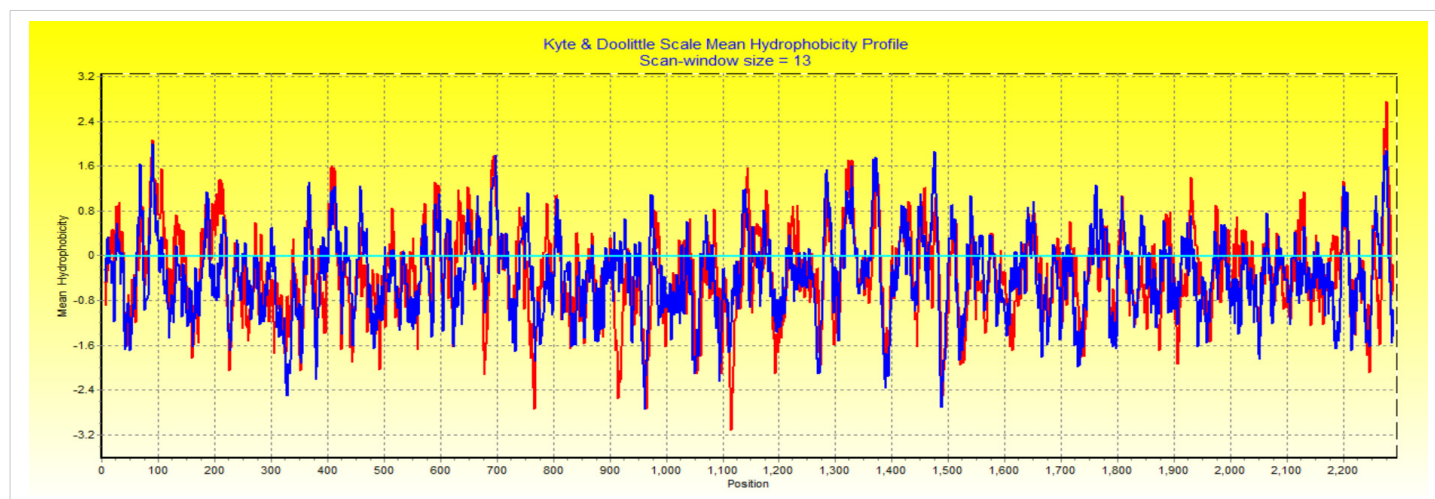


Figure 5: Kyte-Doolittle hydrophobicity of two distinct emaravirus SMV1 with the red region and SMV2 with the blue region.

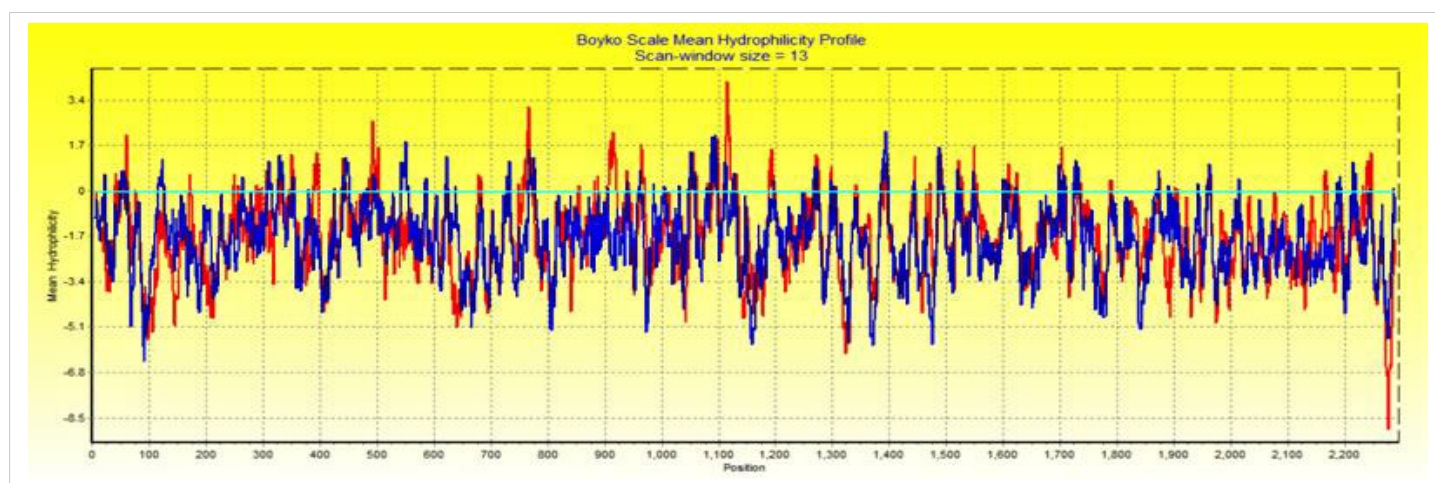
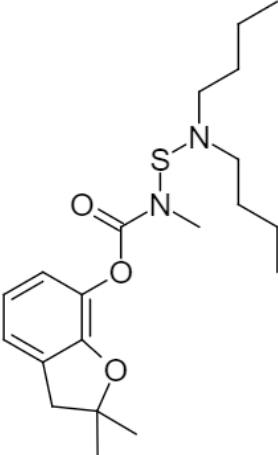
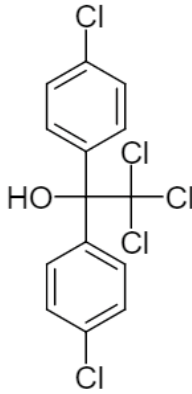
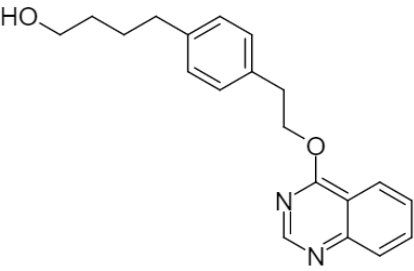
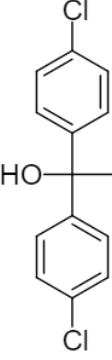


Figure 6: Boyko plot hydrophilicity of two distinct emaravirus SMV1 with red region and SMV2 with blue region.

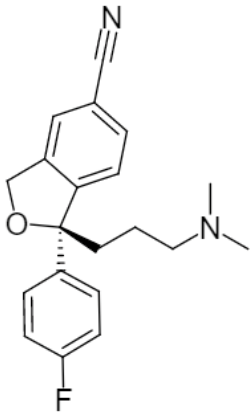
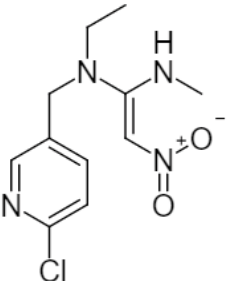
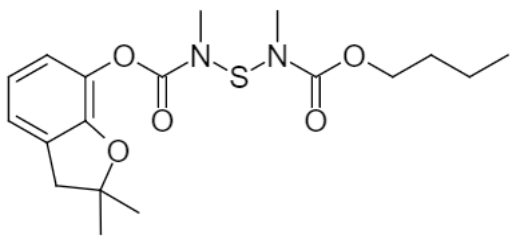
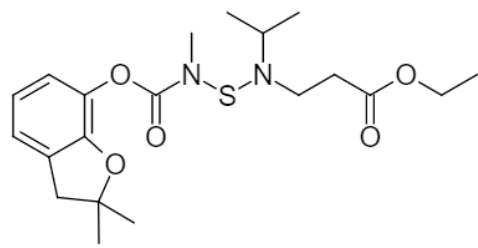
**Table 1:** Summary on the narrow spectrum drugs for treatment of SMV in pigeonpea.

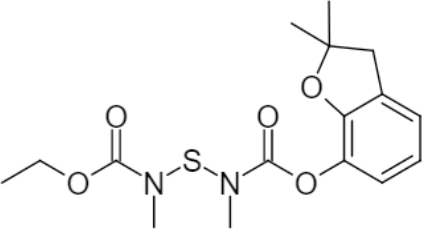
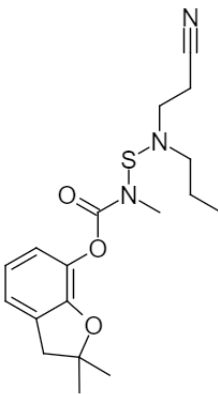
S.No.	Drug name	Chemical structure	IUPAC Name:	CID number
1.	Fenazaquin	 <chem>CC(C)(C)c1ccc(cc1)CCOC2=CN3C=CC=CC3=N2</chem> $C_{20}H_{22}N_2O$	4-[2-(4-tert-butylphenyl)ethoxy]quinazoline	86356
2.	Dicofol	 <chem>ClC1=CC=C(C=C1)C(O)(Cl)C2=CC=C(Cl)C=C2</chem> $C_{14}H_9Cl_5O$	2,2,2-trichloro-1,1-bis(4-chlorophenyl)ethanol	8268
3.	Spiromesifin	 <chem>CC(C)C(=O)OC12C=CC(=C1C2)C3=CC(=C(C)C)C=C3C4C5C=CC(=C4)OC5C</chem> $C_{23}H_{30}O_4$	[2-oxo-3-(2,4,6-trimethylphenyl)-1-oxaspiro[4.4]non-3-en-4-yl] 3,3-dimethylbutanoate	9907412
4.	Imidacloprid	 <chem>CC1=CN(C=C1)CN2C=CC(=CN2)Cl</chem> $C_9H_{11}ClN_4[N^+]O_2$	[[1-[(6-chloropyridin-3-yl)methyl]-4,5-dihydroimidazol-2-yl]amino]-hydroxy-oxoazanium	101618973

5.	Carbosulfan	 <p style="text-align: center;"><math>C_{20}H_{32}N_2O_3S</math></p>	(2,2-dimethyl-3H-1-benzofuran-7-yl) N-(dibutylamino)sulfanyl-N-methylcarbamate	41384
6.	Kelthane	 <p style="text-align: center;"><math>C_{14}H_9Cl_5O</math></p>	2,2,2-trichloro-1,1-bis(4-chlorophenyl) ethanol	8268
7.	CEMBL251502	 <p style="text-align: center;"><math>C_{20}H_{22}N_2O_2</math></p>	4-[4-(2-quinazolin-4-yloxy ethyl)phenyl] butan-1-ol	44441989
8.	Chlorfenethol	 <p style="text-align: center;"><math>C_{14}H_{12}Cl_2O</math></p>	1,1-bis(4-chlorophenyl)ethanol	6624

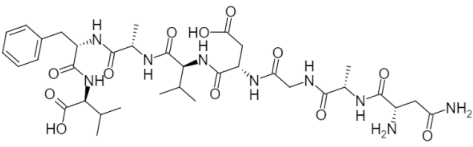
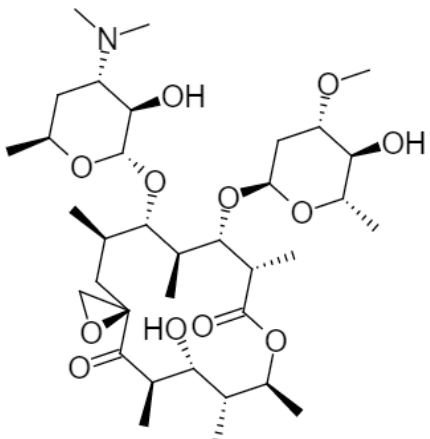
9.	Proclonol	 $C_{16}H_{14}Cl_2O$	bis(4-chlorophenyl)-cyclopropylmethanol	26450
10.	Brl 15268	 $C_{16}H_{12}Cl_2O$	1,1-bis(4-chlorophenyl)but-3-yn-1-ol	173320
11.	2,2-Dichloro-1,1-bis(4-Chlorophenyl) Ethanol	 $C_{14}H_{10}Cl_4O$	2,2-dichloro-1,1-bis(4-chlorophenyl)ethanol	160701
12.	CHEMBL3186301	 $C_{22}H_{28}O_4$	[2-oxo-3-(2,4,6-trimethylphenyl)-1-oxaspiro[4.4]non-3-en-4-yl] 2,2-dimethylpropanoate	11348842

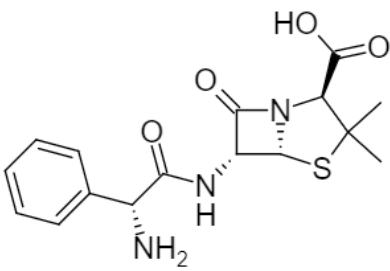
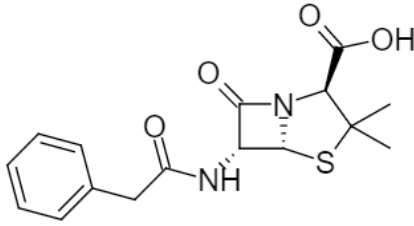
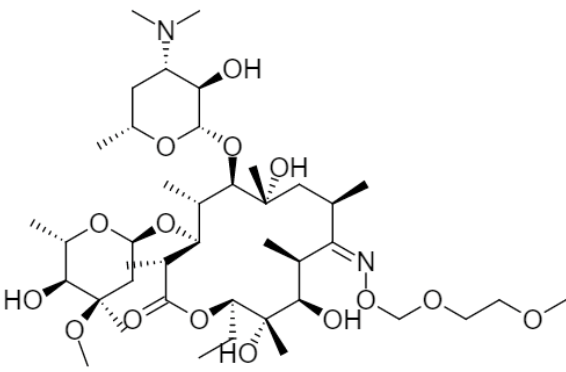
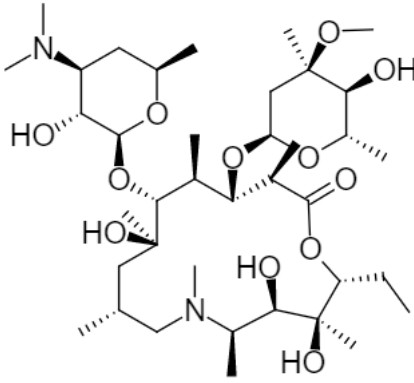


13.	Escitalopram	 <p style="text-align: center;"><math>C_{20}H_{21}FN_2O</math></p>	(1S)-1-[3-(dimethylamino)propyl]-1-(4-fluorophenyl)-3H-2-benzofuran-5-carbonitrile	2771
14.	Nitenpyram	 <p style="text-align: center;"><math>C_{11}H_{15}ClN_3[N^+][O^-]</math></p>	(NE)-N-[1-[(6-chloropyridin-3-yl)methyl]imidazolidin-2-ylidene]nitramide	86287518
15.	Furathiocarb	 <p style="text-align: center;"><math>C_{18}H_{26}N_2O_5S</math></p>	(2,2-dimethyl-3H-1-benzofuran-7-yl) N-[butoxycarbonyl(methyl)amino]sulfanyl-N-methylcarbamate	47759
16.	Benfuracarb	 <p style="text-align: center;"><math>C_{20}H_{30}N_2O_5S</math></p>	ethyl 3-[[[(2,2-dimethyl-3H-1-benzofuran-7-yl)oxycarbonyl-methylamino]sulfanyl-propan-2-ylamino]propanoate	54886

17.	Benzofuran	 <p style="text-align: center;"><math>C_{16}H_{22}N_2O_5S</math></p>	ethyl N-[(2,2-dimethyl-3H-1-benzofuran-7-yl)oxycarbonyl-methylamino]sulfanyl-N-methylcarbamate	47756
18.	Carbamic acid	 <p style="text-align: center;"><math>C_{19}H_{27}N_3O_3S</math></p>	(2,2-dimethyl-3H-1-benzofuran-7-yl) N-[butyl(2-cyanoethyl)amino]sulfanyl-N-methylcarbamate	3067994

**Table 2:** Summary on broad spectrum drugs for the treatment of SMV in pigeonpea.

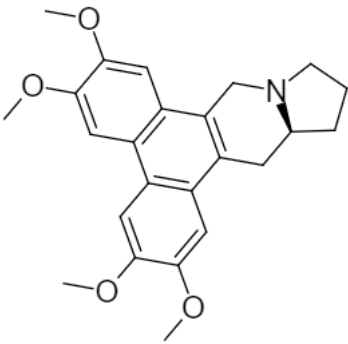
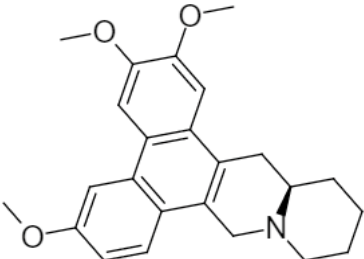
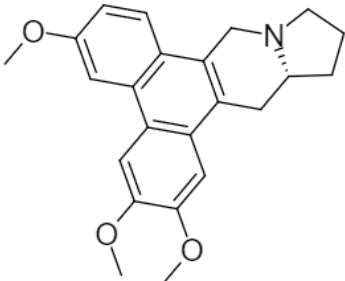
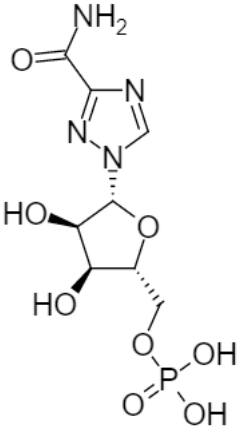
S.No	Drug name	Chemical structure	IUPAC Name:	Reference
1.	Lactoferrin	 <p style="text-align: center;"><math>C_{35}H_{53}N_9O_{12}</math></p>	(2S)-2-[[[(2S)-2-[[[(2S)-2-[[[(2S)-3-carboxy-2-[[[2-[[[(2S)-2-[[[(2S)-2,4-diamino-4-oxobutanoyl]amino]propanoyl]amino]acetyl]amino]propanoyl]amino]-3-methylbutanoyl]amino]propanoyl]amino]-3-phenylpropanoyl]amino]-3-methylbutanoic acid	131676698
2.	Oleandomycin	 <p style="text-align: center;"><math>C_{35}H_{61}NO_{12}</math></p>	(3R,5R,6S,7S,8S,9S,12S,13R,14R,15R)-6-[[[(2S,3R,4S,6S)-4-(dimethylamino)-3-hydroxy-6-methyloxan-2-yl]oxy-14-hydroxy-8-[[[(2R,4S,5S,6S)-5-hydroxy-4-methoxy-6-methyloxan-2-yl]oxy-5,7,9,12,13,15-hexamethyl-1,11-dioxaspiro[2.13]hexadecane-10,16-dione	72493

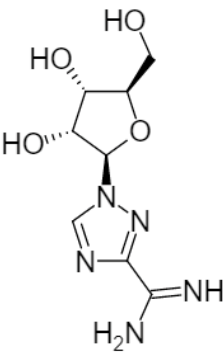
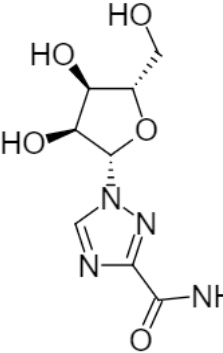
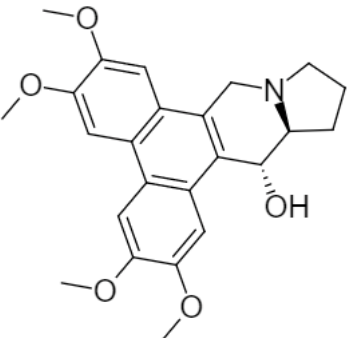
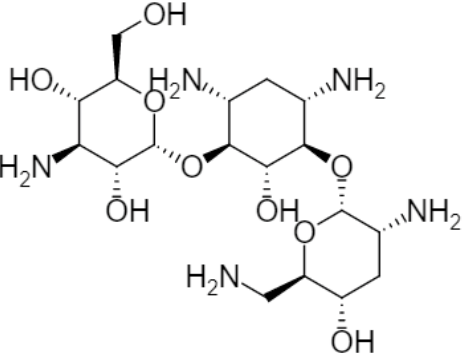
3.	Ampicillin	 <p style="text-align: center;"><math>C_{16}H_{19}N_3O_4S</math></p>	(2S,5R,6R)-6-[(2R)-2-amino-2-phenylacetyl]amino]-3,3-dimethyl-7-oxo-4-thia-1-azabicyclo[3.2.0]heptane-2-carboxylic acid	6249
4.	Penicillin G	 <p style="text-align: center;"><math>C_{16}H_{18}N_2O_4S</math></p>	(2S,5R,6R)-3,3-dimethyl-7-oxo-6-[(2-phenylacetyl)amino]-4-thia-1-azabicyclo[3.2.0]heptane-2-carboxylic acid	5904
5.	Roxithromycin	 <p style="text-align: center;"><math>C_{41}H_{76}N_2O_{15}</math></p>	(3R,4S,5S,6R,7R,9R,10Z,11S,12R,13S,14R)-6-[(2S,3R,4S,6R)-4-(dimethylamino)-3-hydroxy-6-methylhexan-2-yl]oxy-14-ethyl-7,12,13-trihydroxy-4-[(2R,4R,5S,6S)-5-hydroxy-4-methoxy-4,6-dimethyl oxan-2-yl]oxy-10-(2-methoxyethoxymethyl imino)-3,5,7,9,11,13-hexamethyl-oxacyclotetradecan-2-one	6915744
6.	Azithromycin	 <p style="text-align: center;"><math>C_{38}H_{72}N_2O_{12}</math></p>	(2R,3S,4R,5R,8R,10R,11R,12S,13S,14R)-11-[(2S,3R,4S,6R)-4-(dimethylamino)-3-hydroxy-6-methyloxan-2-yl]oxy-2-ethyl-3,4,10-trihydroxy-13-[(2R,4R,5S,6S)-5-hydroxy-4-methoxy-4,6-dimethyloxan-2-yl]oxy-3,5,6,8,10,12,14-heptamethyl-1-oxa-6-azacyclopentadecan-15-one	447043

7.	Isoprenaline	 $C_{11}H_{17}NO_3$	4-[1-hydroxy-2-(propan-2-ylamino)ethyl] benzene-1,2-diol	3779
8.	Riboflavin	 $C_{17}H_{20}N_4O_6$	7,8-dimethyl-10-[(2S,3S,4R)-2,3,4,5-tetrahydroxypentyl]benzo[g]pteridine-2,4-dione	493570
9.	Atropine	 $C_{17}H_{23}NO_3$	[(1S,5R)-8-methyl-8-azabicyclo[3.2.1]octan-3-yl]3-hydroxy-2-phenylpropanoate	174174
10.	Albendazole	 $C_{12}H_{15}N_3O_2S$	MethylN-(6-propylsulfanyl-1H-benzimidazol-2-yl)carbamate	2082
11.	Neomycin B	 $C_{23}H_{46}N_6O_{13}$	(2R,3S,4R,5R,6R)-5-amino-2-(aminomethyl)-6-[(1R,2R,3S,4R,6S)-4,6-diamino-2-[(2S,3R,4S,5R)-4-[(2R,3R,4R,5S,6S)-3-amino-6-(aminomethyl)-4,5-dihydroxyoxan-2-yl]oxy-3-hydroxy-5-(hydroxymethyl)oxolan-2-yl]oxy-3-hydroxycyclohexyl]oxyoxane-3,4-diol	8378



12.	L-Tyrosylglycyl L-isoleucyl L-phenylalaniamide	 $C_{26}H_{35}N_5O_5$	N-[(2S)-3-[4-[5-[2-(diethylamino)-6-methylpyridin-4-yl]-1,2,4-oxadiazol-3-yl]-2-ethyl-6-methylphenoxy]-2-hydroxypropyl]-2-hydroxyacetamide	25074253
13.	CHEMBL330666; BDBM50014232; 6-(4-Ethynyl-Phenyl)- 1,2,3,5,6,10b- Hexahydro- Pyrrolo[2,1-A] Isoquinoline	 $C_{20}H_{19}N$	(6S,10bR)-6-(4-ethynylphenyl)-1,2,3,5,6,10b-hexahydro-pyrrolo[2,1-a]isoquinoline	13903191
14.	Diazepine	 $C_5H_6N_2$	1H-diazepine	166734
15.	Ningnanmycin	 $C_{16}H_{25}N_7O_8$	(2S,3S,4S,5R,6R)-6-(4-amino-2-oxopyrimidin-1-yl)-4,5-dihydroxy-3-[[[(2S)-3-hydroxy-2-[[2-(methylamino)acetyl]amino]propanoyl]amino]oxane-2-carboxamide	44588235
16.	Ribavirin	 $C_8H_{12}N_4O_5$	1-[(2R,3R,4S,5R)-3,4-dihydroxy-5-(hydroxymethyl)oxolan-2-yl]-1,2,4-triazole-3-carboxamide	37542

17.	Tyloporine	 <p style="text-align: center;"><math>C_{24}H_{27}NO_4</math></p>	(13aS)-2,3,6,7-tetramethoxy-9,11,12,13,13a,14-hexahydrophenanthro[9,10-f]indolizine	5090648
18.	Cryptopleurine	 <p style="text-align: center;"><math>C_{24}H_{27}NO_3</math></p>	(14aR)-2,3,6-trimethoxy-11,12,13,14,14a,15-hexahydro-9H-phenanthro[9,10-b]quinolizine	92765
19.	Antofine	 <p style="text-align: center;"><math>C_{23}H_{25}NO_3</math></p>	(13aR)-2,3,6-trimethoxy-9,11,12,13,13a,14-hexahydrophenanthro[9,10-f]indolizine	639288
20.	Ribavirin monophosphate	 <p style="text-align: center;"><math>C_8H_{13}N_4O_8P</math></p>	[(2R,3S,4R,5R)-5-(3-carbamoyl-1,2,4-triazol-1-yl)-3,4-dihydroxyoxolan-2-yl] methyl dihydrogen phosphate	100252

21.	Taribavirin	 <p style="text-align: center;"><math>C_8H_{13}N_5O_4</math></p>	1-[(2R,3R,4S,5R)-3,4-dihydroxy-5-(hydroxymethyl)oxolan-2-yl]-1,2,4-triazole-3-carboximidamide	451448
22.	Leovirin	 <p style="text-align: center;"><math>C_8H_{12}N_4O_5</math></p>	1-[(2S,3S,4R,5S)-3,4-dihydroxy-5-(hydroxymethyl)oxolan-2-yl]-1,2,4-triazole-3-carboxamide	460516
23.	Tylophorincine	 <p style="text-align: center;"><math>C_{24}H_{27}NO_5</math></p>	(13aS,14R)-2,3,6,7-tetramethoxy-9,11,12,13,13a,14-hexahydrophenanthro[9,10-f]indolizin-14-ol	44443369
24.	Tobramycin	 <p style="text-align: center;"><math>C_{18}H_{37}N_5O_9</math></p>	(2S,3R,4S,5S,6R)-4-amino-2-[(1S,2S,3R,4S,6R)-4,6-diamino-3-[(2R,3R,5S,6R)-3-amino-6-(aminomethyl)-5-hydroxyoxan-2-yl]oxy-2-hydroxycyclohexyl]oxy-6-(hydroxymethyl)oxane-3,5-diol	36294

25.	TabavirinHcl	<p style="text-align: center;">HCl</p> <p style="text-align: center;"><math>C_8H_{14}ClN_5O_4</math></p>	1-[(2R,3R,4S,5R)-3,4-dihydroxy-5-(hydroxymethyl)oxolan-2-yl]-1,2,4-triazole-3-carboximidamide;hydrochloride	451447
26.	Dd-Rabvarin	<p style="text-align: center;"><math>C_8H_{12}N_4O_3</math></p>	1-[(2R,5S)-5-(hydroxymethyl)oxolan-2-yl]-1,2,4-triazole-3-carboxamide	451949
27.	Framycetin	<p style="text-align: center;"><math>C_{23}H_{46}N_6O_{13}</math></p>	(2R,3S,4R,5R,6R)-5-amino-2-(aminomethyl)-6-[(1R,2R,3S,4R,6S)-4,6-diamino-2-[(2S,3R,4S,5R)-4-[(2R,3R,4R,5S,6S)-3-amino-6-(aminomethyl)-4,5-dihydroxyoxan-2-yl]oxy-3-hydroxy-5-(hydroxymethyl)oxolan-2-yl]oxy-3-hydroxycyclohexyl]oxyoxane-3,4-diol	8378

seen in techniques such as DAS-ELISA and DIBA. Both of the techniques can detect the pathogen from the extracts of a minimum of 5 to 10 vector mites. The disease can be controlled by the various potential drugs such as Dicofol and 0.1% Fenazaquin as well as with molecular markers based on AFLP, SSR and SNPs markers. Beside genomics approach we can employ other approaches such as protein target interactions and chemoinformatics approach in this context few potential drugs against SMV which can provides stability

and effectiveness towards the resistance in pigeonpea and which will also help in systematic agronomic system in diseased localities and exercise as a component in the integrated disease management.

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