Comparison of two viruses in NCBI genome

P. Parameswari* and Sruthi M, R. Udayakumar Department of Bioinformatics, Bharath University, Chennai *Corresponding author:E-Mail: rsukumar2007@hotmail.com

ABSTRACT

Banana streak infection (BSV) could be a plant unhealthful infection of the family Caulimoviridae. Infective operator's leaf dash of banana, brought about by banana streak infection (BSV) contamination, could be an as of late depicted unwellness that happens in most banana-delivering nations. The unwellness, that is thought to affect singularly Musa and liliopsid variety, is develop by vegetative propagation, coarse bugs and through seed. BSV contamination in banana will antagonistically affect yield and organic product quality. We've analyzed the whole requesting grouping of banana streak infection and banana streak infection Mysore by recovering the arrangement in fasta organization from NCBI requesting. The sequencing information which can help the re-commenting of the banana streak infection requesting and known an arrangement insertion in banana streak infection specialist.

KEY WORDS: BSV, Caulimoviridae, Musa, Ensete, Genome Sequence.

1. INTRODUCTION

Banana streak infection (BSV) species are far reaching in Musa spp. They are actually transmitted by a few mealybug animal categories in a semipersistent mode and by actuation of endogenous arrangements incorporated in the genome of Musa balbisiana, one of the progenitorsof engineered and characteristic cross breeds. Regular indications incorporate yellow streaks on leaves, part of the pseudostem and anomalous rise of the group from the center of the pseudostem, bearing less products of littler size. Despite the fact that leaf streaks and pseudostem part side effects have been already seen in Cuba, BSV species were never recognized. Bacilliform particles were seen by immunosorbent electron microscopy in plantain FHIA21. The polyclonal antiserum utilized was raised against a few badnavirus animal categories and is along these lines not particular to BSV. Viral leaf dash of banana was initially depicted in Ivory Coast, Africa in 1968 and the causal operators, BSV, was distinguished in Morocco in 1985 [4, 5]. The impacts of BSV contamination on plant development, bundle yield and organic product quality may be extremely variable, for two reasons. Firstly, as specified beforehand, secludes of BSV vary significantly in the seriousness of indications delivered, going from periodic chlorotic streaking to deadly systemic rot. Also, the side effects brought about by BSV disease distinctively happen sporadically through the span of the year, and are connected with varieties in infection focus. Yield misfortunes because of BSV invection in banana have been archived for the AAA cultivar 'Poyo' in Ivory Coast. Diminishment in cluster size and mutation of fingers have likewise been accounted for BSV contamination in 'Dwarf Cavendish'. It has been recommended that BSV disease might significantly affect group measure and natural product quality when botanical start and early pack improvement agree with a time of expanded infection union. BSV is an individual from the plant infection class Badnavirus, speaking to infections which have bacilliform particles averaging 30 x 150 nm in size and which contain a roundabout twofold stranded DNA genome 7.2 kb in size. Badnaviruses are just the second gathering of ds DNA plant infections to be depicted. The limited host scope of BSV is that spread of BSV must of need happen from banana to banana. Weed has don't assume a part in the study of disease transmission of viral leaf streak as they do in contamination by CMV, which taints an extensive variety of plant species. Albeit grown-up mealybugs are inactive, the early instars or "crawlers" are very versatile. Mealybugs, which transmit badnaviruses in a semipersistent way. A few authoritative or provisional individuals from the badnavirus gathering have been appeared to be transmitted through seed, in a few occasions at rates of 60-90%. One badnavirus, Kalanchöe top-spotting infection (KTSV), is additionally dust transmitted.

2. MATERIALS AND METHODS

Databases used: NCBI, GENECARD

Tools used: APOLLO

Databases:

Gene bank: Databank of genetic sequences operated by a division of the National Institute of Health.

Gene card: Genecard is a database, which has collection of information about the genes.

Tools description:

Apollo: Apollo is a genomic annotation viewer and editorial manager. It was initially created as a coordinated effort between the Berkeley Drosophila Genome Venture (some portion of the FlyBase consortium) and The Sanger Establishment in Cambridge, UK. It was utilized by the FlyBase scholars to build the Discharge 3 and 4 annotations on the completed Drosophila melanogaster genome, and has additionally been an essential vehicle for offering these annotations to the group. Apollo permits specialists to investigate genomic annotations at numerous levels of subtle element, and to perform master annotation curation, all in a graphical domain. It is a Java application that is anything but difficult to introduce and keep running on Windows, Macintosh OS X, or any Unix-sort framework (counting

Journal of Chemical and Pharmaceutical Sciences

Linux). Apollo is presently bolstered by NIH gift 1R01GM080203-01 from the National Establishment of General Restorative Sciences (NIGMS).

Steps Included:

1. The genomic arrangement of Banana Streak GF infection and Banana Streak Mysore infection was looked in NCBI Genome database.2. The entire genomic informations graphical output was taken for analysis.

3. Genomic sequence in fasta as well as Genbank format was retrieved and stored in local hard disk for future use.

- 4. The entire genomic sequence in Genbank format was uploaded to the genome annotation tool Apollo.
- 5. The regions present in the genome was identified using Apollo software
- 6. The range of each region was predicted using sequence information function.
- 7. The exon regions present in all the regions was detected using exon finder.
- 8. Restriction site for EcoRI in the genome was predicted with the exact location.
- 9. The genome comparison for both the virus was analysed manually.

3. RESULTS & DISCUSSION

Eile S

Ge Ca

Carnation etched ring virus

Cassava vein mosaic virus Cauliflower mosaic virus

Cestrum yellow leaf curing viru Citrus yellow mosaic virus Commelina yellow mottle virus

Cycad leaf necrosis virus

Dioscorea bacilliform virus

Dracaena mottle virus

Elle Edit View History	Bookmarks Yahoo! Tools Help					0
	http://www.ncbi.nlm.nih.gov	/genomes/GenomesHome.cgi?taxid=10	39	ជ ។ 🚺	virus genome data	Nases D
S The Viral Genomes F	Resource		AD MODERNE-			•
S NCBI	Pital France 5000. 9 250	Gen 5Gen	ome			<u>^</u>
HOME SEARCH SITE MAP	All viruses		All viroids Help		Contact us	
Genome resources	Viral Genomes					
				hypothesis	read »	
Information	How to retrieve nucleo	otide and protein sequences of v	ral reference genomes?	Diduin		
About this site About viruses Statistics FAQs	Why is a particular full	 length genomic sequence missi 	ompiete viral genomes? g in Entrez Genomes? Is there a RefSeq genome fo	r this virus? invent [DNA?	
Advisors Help All Viral Genomes Alphabetical list RefSeq percentes Other genomes RefSeq PTP RefSeq FTP		Viruses have been found i serious diseases such as problems. Therefore, study understanding the principles	n all celular forms of life, from bacteria to chordates. NDS, encephaltides, hepatitides, influenza, SARS, in g various viruses and their interaction with hosts is of the organization of life.	Pathogenic human and an etc. Plant viruses are resp a prerequisite for finding	imal viruses are onsible for man remedies agains	causative agents of y major agricultural — t viral diseases and
All Viroid Genomes Alphabetical list RefSeq genomes Other genomes Taxonomy groups	Influenza A virus replication sche	A virus is a small, infectious newly synthesized compone	, obligate intracellular parasite, capable of replicating ints: the genome and a number of copies of at least or	tself in a host cell. Virions a ne viral protein. [more »]	re formed by de	novo assembly from
Tools	Click on it for explanations.	ane.				
PASC Protein clienter	A viral genome consists of either	single-stranded or double-stranded	d DNA or RNA in either linear or circular form, and car	comprise one or more seg	ments.	
Protein dusters	Entrez Genomes currently contains	s 3605 Reference Sequences for 2	443 viral genomes and 41 Reference Sequences for vir	oids.		
Related NCBI Resources	0.0.1.1.1.1.1		famile at the famil			
Genotyping		Retro-transcribing Vir	uses [102] @ Saterines [133]			
X Find:	🗍 Next 👚 Previous 🖗 Hi	ghlight all 🔣 Match case				
http://www.ncbi.nlm.nih.g	gov/genomes/GenomesGroup.cgi?taxid=35.	268				
Mozilla Firefox		S Cold	mhia: Top leftist rehel helieved killed			
w Higtory <u>B</u> ookmarks	s Yahoo! Iools Help		HIDRE TOP ILLIGATION FOR DURING MILLO			
CXAS	http://www.ncbi.nlm.nih.gov/genon	nes/GenomesGroup.cgi?taxid=3526	I.	<u></u>	- 👌 - virus g	enome databases
NCBI	Cost Column Column Column	-II-II SGen	ome			
CH SITE MAP	Viral Genomes Home	Taxon	omy groups All viruses	All viroids	Help	Contact us
(A)						
Retro-	transcribing viruses -	102 complete genomes				Sequence
noviridae [37] 🗶 He	epadnaviridae [8] 🔮 Retroviri	idae [57]				>Download th
		Accession	Source information	Segm	Length Prot	ein Nbrs Created U
iridae					10000	
streak GF virus		NC_007002	strain:Goldfinger		7263 nt	3 - 05/16/2005 03
streak Mysore virus		NC_006955			7650 nt	3 1 04/07/2005 10
streak OL virus		NC_003381			7389 nt	3 - 06/02/1998 10
streak virus		NC_008018	isolate:Acuminata Yunnan		7722 nt	3 3 05/10/2006 11
streak virus strain A	cuminata Vietnam	NC_007003	strain:Acuminata Vietnam	-	7801 nt	3 - 05/16/2005 07
y red ringspot virus		NC_003138			8303 nt	8 - 10/11/2001 03
villea spectabilis chlo	protic vein-banding virus	NC 011592			8759 nt	4 - 11/19/2008 11

Find:

D

VC 0034 NC_001648 NC_001497 NC_004324

NC_00338 NC_001343

NC 011097

NC 009010

🗍 Next 👚 Previous 🖉 Highlight all 📃 Match case

1 06/23/1988 12/08/2008

1 07/02/1996 12/08/2008 7 11/03/1982 12/08/2008 - 10/04/2002 11/04/2009 6 10/25/2001 09/15/2008

10/05/1990 07/10/2008

- 07/31/2008 07/31/2008

05/16/2006 07/30/2007

1 02/16/2007 05/24/2007

7932 nt

8159 nt 8024 nt 8253 nt 7559 nt 7489 nt

9205 nt

7261 nt

7531 nt

www.jchps.com Banana streak GF Infection:

1 200					
me > Viruses	> Banana streak (GF virus, co	omplete genome		t
e: <u>Viruses; Retro-tra</u>	unscribing viruses; Caulir	noviridae; Badn	avirus; Banana streak GF vi	<u>us</u>	
Genome Info:	Features:	BLAST homologs:	Links:	Review Info:	
Refseq: NC_007002	Genes: 3	COG	Genome Project	Publications: None	
GenBank: AY493509	Protein coding: 3	TaxMap	Refseq FTP	Refseq Status: PROVISIONAL	
Length: 7,263 nt	Structural RNAs: None	TaxPlot	GenBank FTP	Seq.Status: Completed	
GC Content: 42%	Pseudo genes: None	GenePlot.	BLAST	Sequencing center: University of Minnesota, Plant Pathology, USA, St.Paul	
% Coding: 87%	Others: None	gMap	TraceAssembly	Completed: 2005/05/16	
Topology: circular	Contigs: None		CDD	Organism Group	
Molecule: dsDNA			Other genomes for species		
Jene Classification bas	ed on COG functional categ	ones	Search gene, Genel	or locus_tag: Find Gene	
			Zoom	7263 nt	

Banana streak Mysore infection:

y Overview	• 5	show 20 -	Send to 🔹		
me > Viruse	s > Banana st	reak Mvso	re virus. complet	e genome	
e: <u>Viruses;</u> Retro	-transcribing viruse	s; Caulimovirio	lae; Badnavirus; Banana	streak Mys virus	
Genome Info:	Features:	BLAST homologs:	Links:	Review Info:	
Refseq: NC_006955	Genes: 3	COG	Genome Project	Publications: [1]	
GenBank: AY805074	Protein coding: 3	ТахМар	Refseq FTP	Refseq Status: Provisional	
Length: 7,650 nt	Structural RNAs: None	TaxPlot	GenBank FTP	Seq.Status: Completed	
GC Content: 42%	Pseudo genes: None	GenePlot	BLAST	Sequencing center: Queensland Department of Primary Industries and Fisheries, Horticulture and Forestry Science, Australia, Indooroopilly	
% Coding: 85%	Others: None	gMap	TraceAssembly	Completed: 2005/04/07	
Topology: circular	Contigs: None		CDD	Organism Group	
Molecule: dsDNA			Other genomes for species: 1		
Gene Classification	based on COG functio	nal categories	Search	gene. GenelD or locus tag	
	2001000			7650 nt	

From NCBI Genome Database, the objectives Banana Streak GF Infection and Banana Streak Mysore infection subtle elements were taken to investigate. Banana Streak Mysore Infection:

Complete genome:

Journal of Chemical and Pharmaceutical Sciences

www.jchps.com

NOBI RO	sources 🗇 How To 🛇	My NCBI Sign In
Alphabet of Li	Ide Search Nucleoside - Limits Advanced search Help	
Display Settings	k © Gentlank (kil) Send. ©	Change region shown •
Banana :	streak Mysore virus, complete genome e Sequence: NC_006955.1	Customize view ·
Go to. (*)		Analyze this sequence Run BLAST
LOCUS DEFINITION ACCESSION	NC_006955 7650 bp DNA oiroular VRL 08-DEC-2008 Banana atreak Nysore virus, complete genome. NC_006955 014292954	Pick Primera Find in this Sequence
DBLINK KEYWORDS SOURCE ORGANISM	Project: 15234 Banana streak Myy virus Banana streak Myy virus	All links from this record (*)
REFERENCE AUTHORS	Viruses/ Retrostranscribing viruses/ Caulimoviridae/ Badnavirus. 1 (bases i to 7650) Gesring,A.D., Pooggin,M.M., Olszewski,N.E., Lockhart,B.E. and Thomas,J.E.	Identical GenBank Sequence Protein
TITLE	Characterisation of Banana streak Mysore virus and evidence that its DNA is integrated in the B genome of cultivated Musa Arch, Virol, 150 (4), 787-796 (2005)	PubMed PubMed (Weighted)
PUBMED REFERENCE CONSETM	15785970 2 (bases 1 to 7650) MCRI Genome Project	Laxonomy
JOURNAL	Direct Submission Submitted (07-APR-2005) National Center for Biotechnology Information, NHM, Bethesda, MD 20894, USA	Recent activity
REFERENCE AUTHORS	3 (bases 1 to 7650) Geering,A.D.W.	NC_006955 Banana streak Mysore virus. complete genome Oenome
JOURNAL	Submitted (01-MOV-2004) Horticulture and Forestry Science, Queensland Department of Primary Industries and Fisheries, 80	complete genome Oenome
COMMENT	Meiers Road, Indocropilly, Queensland 4066, Australia PROVISIONAL <u>REFSEQ</u> : This record has not yet been subject to final NCBI review. The reference sequence was derived from AV005074.	See more
K Find:	🐥 Box 👚 Previous 🔊 Highlight all 🛅 Matgh case	

Figure.5. Complete genome

S NCBI Resources C How To C	My NCDI. Bign In 🦉
Nucleotide Search Nucleotide - Limits Advanced search Help Alphabet of Life Search Clear	
Display Bellings; (2) Graphics	Bend. 💿
Banana streak Mysore virus, complete genome NCBI Reference Bequence: NC_006955.1 Gendams: FAIXo	
	Link To This Page Help Eeedback Ennter Friendly Page
MC_000955.k (7,650 bases)	There Search
R	a * viaa ** /w * viaa * viaa ** viaa *** viaa **** viaa **** via
1:7,650 (7,650 bases shown, positive strand)	(a) (b)
- 20 Sequence dh Fip Strands (0, 0, 40 and "Tools"	🖓 🏴 Markers Details = 🛰 Options
- Sequence NC 000955.1: Danana streak Mysore virus, complete genome	- Sequence NC 006955 1: Banana streak Mysore \
	Genes
	otem
🛪 Find: 🗏 🕂 Det 🕆 Drevious 🖉 Highlight all 🖂 Matgh case	

Nucleotide	S NCBI Resources 🕑			My NG	CBI Sign I
Approache of Line Center Center Center Center Center Center Cente	Nucleotide	Search Nucleotide Limits Advanced search Help			
Construction State Change region shown Banana streak Mysore virus, complete genome Customize view Analyze filteria Customize view Distribution Customize view Distribution State Distribution </th <th>Alphabet of Life</th> <th>Search Clear</th> <th></th> <th></th> <th></th>	Alphabet of Life	Search Clear			
Banana streak Mysore virus, complete genome Customize view NCB: Reference Seguence: NC, 0009511 Analyze this sequence Val. (8237 k1) ref (NC, 0009513, 1) Bancas streak Nyore virus, complete genome Analyze this sequence Val. (8237 k1) ref (NC, 0009513, 1) Bancas streak Nyore virus, complete genome Analyze this sequence Val. (8237 k1) ref (NC, 0009513, 1) Bancas streak Nyore virus, complete genome Bancas Streak Nyore virus, complete genome Val. (8237 k1) ref (NC, 0009513, 1) Bancas streak Nyore virus, complete genome Bancas Streak Nyore virus, complete genome Val. (8237 k1) ref (NC, 000951, 1) Bancas streak Nyore virus, complete genome Bancas Streak Nyore virus, complete genome Val. (8237 k1) ref (NC, 000951, 1) Bancas streak Nyore virus, complete genome Bancas Streak Nyore virus, complete genome Val. (8237 k1) ref (NC, 000951, 1) Bancas streak Nyore virus, complete genome Bancas Streak Nyore virus, complete genome Val. (8238 k1) ref (NC, 000951, 1) Bancas streak Nyore virus, complete genome Bancas Streak Nyore virus, complete genome Val. (8238 k1) ref (NC, 000951, 1) Bancas streak Nyore virus, complete genome Bancas Streak Nyore virus, complete genome Val. (8238 k1) ref (NC, 000951, 1) Bancas streak Nyore virus, complete genome Bancas Streak Nyore Virus, complete genome Val. (8238 k1) ref (NC, 000951, 1) Bancas Streak Nyore Virus, complete genome Ba	Display Settings: 🕑 FASTA		Send 🕞	Change region shown	
Clutonize view Analyze this sequence Analyze this	Banana atroak	Nusara virus, complete geneme			
Analyze this sequence Built	Dallalla Sueak I	mysore virus, complete genome		Customize view	
and 162 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.002 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.0000 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.0000 Staller UK, 00553.11 Based a steek kysze virus, somjake genome start 0.00000 Staller UK, 00553.11 Based a steek kysze virus, somjake ge	CBI Reference Sequence:	: NC_006955.1			
STORAT CANADCASA DISTU CALCINATION CANCING AND AND CONTRACT CANCING AND AND CONTRACT CANCING AND CANCI	at 162327614 ref INC	006955.11 Ranana streak Musore virus, complete genome		Analyze this sequence	
AMAGESCITITITITICS/ALTICICUSATICICUSATICS/ALTICLARACICUSATICS/ALTICLARACICUSACIONALICICUSACIONALICICUSATICS/ALTICLARACICUSACIONALICICUSACIONALICICUSATICS/ALTICLARACIS/ALTICICUSATICS/ALTICLARACIS/ALTICICUSATICS/ALTICLARACIS/ALTICICUSATICS/ALTICLARACIS/A	IGGTATCAGAGCAGGGTTCF	ACTGTAAGTAAATTTATGGCTTTCATGGGGTAATTCCCTAGGATAGGAGCC		Run BLAST	
telected procession and an and a second a	TAAGGGCTCTTTTTATGCAT	TATTTCTGARTTTCTGTTARGACTATGCTTTATATACTCTGRAGCGAATTT		Pick Primers	
COMORDADORSANCTORIO DE CAMARTALACTION CONTRACTA CONCECTO DE CITATI TATALICI DE CONTRACTA CONTRACTA DE CONTRA	CIGGCAAGIAAGIIIIAAGA	AAGTAGATGGTAATACCTTATGAGGAGTAATACTACATATCTAGACTAAGG GBTGLGBGLTBBGGTGBCTLCTGGGLBTBGLCGTBLGCCCETTGTBBGTC		Find in this Sequence	
ANA TECHNIQUE CELLARA CONSULTION AND TRADE CONSULTION AND CALLSO CELLARA CONSULTION CONSULTION AND CALLSO CELLARA CONSULTION AND CALLSO CELLARA CONSULTION CONSULTION AND CALLSO CELLARA CONSULTION CONSULT	CCGAGGAAGGGCAGCTTGTC	ggcaaaaggtgactcagtataacctgaagatatcgcgtctctgtctaatt			
AI GARANALACODANOT TUTIAACTORTAACTIAACTIAACTIAACTIAACTIAACTIAACCAAA AI GARANALACODANOT TUTIAACTIAACTIAACTIAACTIAACTIAACTIAACTIA	AATATCCTGAGACTCCTAF	ARATCCGGATATGATAGTARARCTCTGATARAGCARARGCCTGARGCTTCG			
SCHALTOSORATCTACTOSORATACTACTOSORATACACTOSALACITICADASIALCTCTORATCASICATIONA SCHALTOSORATCTACTOSORATACACTOSALACITICADASIALCTCTORATCASICASICACTOS ANTICIDADASIANTI CARDONALTOSOCITATIONAL CONTROLOGICAL ANTICIDADASIA SCHALTOSOCITALIANTI CARDONALTOSOCITALIANDASIACTOSALASIACACTOSA CONTROL CARDONALTOSOCITATIONAL CONTROL CARDONAL ANTICIDADASIA SCHALTOSOCITALIANTI CARDONALTOSOCITALIANDASIACTORALASIANTI CONTROL SCHALTOSOCITALIANTI CARDONALTOSOCITALIANDASIANTI CONTROLACITICATIONAL SCHALTOSOCITALIANTI CARDONALTOSOCITALIANDASIANTI CONTROLACITICATIONAL SCHALTOSOCITALIANTI CARDONALTI CARDONALIANDASIA SCHALTOSOCITALIANTI CARDONALTI CARDONALIANDASIA SCHALTOSOCITALIANTI CARDONALIANDASIANTI CARDONALIANDASIA SCHALTOSOCITALIANTI CARDONALIANTI CARDONALIANDASIA SCHALTOSOCITALIANTI CARDONALIANTI CARDONALIANDASIA SCHALTOSOCITALIANTI CARDONALIANTI CARDONALIANDASIA SCHALTOSOCITALIANTI CARDONALIANTI CARDONALIANTI CONTROL CARDONALIANTI SCHALTOSOCITALIANTI CARDONALIANTI CARDONALIANTI CARDONALIANTI CONTROL SCHALTOSOCITALIANTI CARDONALIANTI CARDONALIANTI CONTROL CARDONALIANTI SCHALTOSOCITALIANTI CARDONALIANTI CONTROL CARDONALIANTI CONTROL SCHALTOSOCITALIANTI CARDONALIANTI CONTROL CARDONALIANTI CONTROL SCHALTOSOCITALIANTI CARDONALIANTI CONTROL CARDONALIANTI CONTROL SCHALTOSOCITALIANTI CARDONALIANTI CONTROL CARDONALIANTI CONTROL SCHALTOSOCITALIANTI CARDONALIANTI CONTROLACIALIANTI CONTROL SCHALTOSOCITALIANTI CARDONALIANTI CARDONALIANTI CONTROL SCHALTOSOCITALIANTI CARDONALIANTI CARDONALIANTI CONTROL SCHALTOSOCITALIANTI CARDONALIANTI CONTROLACIALIANTI CONTROL SCHALTOSOCITALIANTI CARDONALIANTI CONTROLACIALIANTI CONTROLACIALIA	ATGCATARATARCCCGARG	GGITCITIAICCIGCITCARAGCCITIAGITIACTIARACCITGARCCARA		All links from this record	
an CTITALINATI TELEVITE/OCUMANTI CALLADORT CONTAINADA: CTEADORTALINATI TELEVITE/CONTAINADA: CTEADORTALINATI CTE	GCTAATTCIGGATACTTACT	TGGGATAAARCCTTTGAAAATTACAAGAACTCTCATACTAAGTCAATTGCA		Gene	
TTO CALAXA SAN AND AND CTTO ANALACT TO ANALACIA TO TO ANALACT TO ANALACIANT Interfacil General Sequence Analacian Control Analacian Contro	ATCTTGAATATTTGAACTT	TAGCAGGAATTGARARGGTCTCARATARAGACCTAGCACATAACTTGCACG		Genome project	
arcalarColAAAAAACTIAAATCAAAAAAAAAAAAAAAAAAAAAAAAA	TTTGCAAAATAAAGAAGAGG	CTTGAAAAACTTCACAAGAAGCTTGAACTGTTTGGAGATCTAGACAAGATT		Identical GenBank Sequence	
Consider Transformer Construction Constructi	STCAGATCCCAAAGAACTGF	arctcararssctartcarsscttgrssrcttarcasssarctscars		Protein	
LAND TO SUBJUCT TANDA CONCURST CONTACT CONTACT AND CONTROL CONTACT CON	CCCTGCGTTCTGACTATCTC	CTCCAGGTGCCCTCTATCAAAGAAGGACGTAGAAGAACTTGTTCTACGTAT		PubMed	
CCCCCTTACLAGOBACCLATACTOCALCOLACIONALTALACIONA	AAGGTGGAGGCCCTTATCCJ	ACCGTCTGGAGAAAGTTATTATTGGATGAGTCTAGCCAACACCAAGGCTAG		PubMed (Weighted)	
ABGGBALTOLATOCTTOCITATTOCIALTONOODCOLACITAACACCTCATTIATCOGDDICAAATCA MAGGBALTONOODCOLACITAACAACCACCTCATTIATCOGDICAAATCAC TCTCTATATCAGDBALGAACTAGDICACCTCAAATCACCACCACGTCATTIACCACGTOGGAACCACGTOCTCAAGAA TCTCTATATCAGDBALGAACTAGDICACCTCAATCACGACGTOCTCAAGACCCGACGAGA MATATCAAATCACGTOCTCAATCACCACGACGTATTAGAACCACGACGACGACGACGACGACGACGACGACGACGA	CCCGCTTTACAAGGAAGCCF	atatctgctacatccaacggctgggaagaacaaggcgtaggatttactgaa		Taxonomy	
AND CONSTITUTION OF THE CO	AGGGGAACTGCATCCCTTGC	CTATTCTGACGCGCCRACTCAACACCCTCATTTACTCGGTGGTCAAAATCA			
TOTOTANTATA CAGO ANA CAMA CONTACTORADA TO CAMA ATTATA CAMA ATTATA CAMA ATTATA CAGO ANA ATTATA ATTATATA ATTATATA ATTATATA ATTATATA ATTATATA ATTATATA ATTATA ATTATATA ATTATA	ARGACGACATCGAAGGACTF ATCAGGGCAATCATCAGAAG	RAAGGARGARGTTACCCARATCCACCARAGGGTRARATCRATTGRGARGRA GGAGCCCCTGATTACAAGGCGGGACTTGGACGAARTCACCAARAGACTAAGT			
Image: Image: And State And St	TCTCTCACTATTCAGGGAGA	ACAAGATCCGAGAAGTAGGAGGCAATCTCAAAGTTTTCAAAAATCCCTACG		Recent activity	
UTRACTOROUGNOUS CONTRACTOR CONTRA	AAATTCTAAGATCCCTACAA	ATGACAACTCGAAGGTCCAGTCTACCCACGGTGACCGAAACAATGGGTCCC		Tur	a Off Ck
an voi a fundamental de construction de constr	AGTACATCIGGAAGAGAGATGG	GGACCCCACTTATTGAAGACCAAATTAGAGATTACCGGGGCATCCGCAAGGA		P NC_006955 Banana streak Myso	ore virus,
MARCATCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CGAGAGGATACCCTGGCCC	CTACTCATGGACCCGGAAGTAGAGTTACAAAGATCTATGCGGGGAACGAGCA		complete genome	Geno
an Change And An Annual Change	AGAACAGTCCCCGCCGAAGT	TATTATACATGTCAAGACGAGATGACGTTCACCATCGCGTCTACCACTTCA		NC_007002 Banana streak GF v	irus,
andale industries production of the industrial resonance in construction of the industrial sector of the industrial secto	ATCTGAGGAGCGAATGATG	GGTCAGTGACGCTGACCAAGATCGGACATTCATTTCTGAAGAATCTTT		complete genome	Gen
**************************************	CATAGGACCTTTGCTGGAA	CTATGGCGCTCCTGGTGTTCCGAGACACCAGATGGACGGCTGATGATCGGT			See mor
	CTATCATATCAGCCATGGA	AGTGGACCTAGCTGAAGGCAATCAGCTAATCTATGTCATCCCCCAACATAAT			

Banana Streak GF Virus:

S NCBI Resources (⊎ How To ⊎	My NCB	I Sign In
Nucleotide Alphabet of Life	Search; Nucleotde - Limits Advanced search Hep Search Clear		
Display Settings: 🕑 Geni	Bank Sens C	Change region shown	
Banana streal NCBI Reference Sequen EASTA Graphica	k GF virus, complete genome	Customize view	•
<u>Go to:</u> 🕑		Run BLAST	
LOCUS NC_00 DEFINITION Banan ACCESSION NC_00 VERSION NC_00	7002 7263 bp IDA circular VAL 04-MAX-2009 a streak G7 virs, complete genome. 7002 1 01:6372047	Pick Primers Find in this Sequence	
DBLINK Projec KEYWORDS . SOURCE Banani ORGANISM Banani	os: <u>1941</u> a streak GV virus a streak GV virus	All links from this record Gene Genome project	۲
REFERENCE 1 (b) AUTHORS Zhang, Olszer	es; Acto-Tañsorioug viuwes; (aulmoviridas; baanavius) ases 1 to 726 j.L. Jochard, S.E.L., Lheureux, F., Geering, A.D.W. and watz, M.E.	Identical GenBank Sequence Protein Taxonomy	
which genome	ng and sequencing of a second banana screak virus isotate : may also occur as a retroelement, integrated into the host :e		
JOURNAL Unpub) REFERENCE 2 (b) CONSRTM NCBI (TITLE Direct JOURNAL Submit	lished Become Project Topi (16-MBY-0003) National Center for Biotechnology	Recent activity <u>Turn O</u> Banana streak GF virus, complete g	enome Nucleotide
AUTHORS Zhang, Olazer	malion, NIM, Bethesda, MD 20094, USA ares 1 to 726, St.L., Lheureux,F., Gering,A.D.N. and wrig N.R.	 NC_006955 Banana streak Mysore complete genome NC_007002 Banana streak GF viru: 	virus, Genome s,
TITLE Direct JOURNAL Submit 1991 T COMMENT PROVIS	s Johnisson tsé (02-100-2-003) Plant Fathology, University of Minnesota, Upper Buford Circle, 5. Raul, 80 55100, USA SIGNAL <u>BIF185</u> , Inis record has not ynt heen authect to final	 complete genome Se 	Genome ee more
Find:	↓ Not ↑ Devices by Highlight 20 Match case		

Banana Streak GF Virus

Journal of Chemical and Pharmaceutical Sciences

Nucleotide								
Alphabet of Life	Search: Nucleotide	Limits Advance	dsearch Help Searc	Clear				
Display Settings: Graphics								Send 🕑
Banana streak GF NCBI Reference Sequence: NC GenBank FASTA	F virus, complete gen C_007002.1	iome						
						Link To This Page He	elp Eeedback Printer-Fri	endly Page
NC_007002.1 (7,263 bases)	n 🤨 Views & Tools •					P Markers Search		•
200 400 600 600	1K L200 L400 L600 L600 2K	2,200 2,400 2,600 2,000 3.K	3,200 3,400 3,600 3,00	0 *X 4,200 4,400 4	600 4,800 5.K 5,200	5,400 5,800 5,800 6 K	5200 5.400 5.600 5.600	78 22
1:7,263 (7,263 bases shown,	, positive strand)							* 2
 Sequence A Fip St 200 400 600 800 Sequence NC_007002.1: Ba 	trands Q Q III and Tools 1 K 1,200 1,400 1,600 1,600 2 K anana streak GF virus, complete genom	2,200 2,400 2,600 2,800 3 K	3,200 3,400 3,600 3,60	0 4K 4,200 4,400 4,	600 4,800 SK 5,200	5,400 5,600 5,600 6 K	Markers Details 6,200 6,400 6,600 6,600 IC_007002.1: Banana strea	Coptions 7 K 7,263 K GF virus
€&∋						- Genes		
BSGPVp1 YP_233105.1		• • • •	> > > > > > > > > > > > > > > > > > >	ESGFVo3 > 233107.1: polyprotein	· · ·	\rightarrow \rightarrow		
	VP_2331061							

APOLLO: Genome comparison was done between the target sequences Banana Streak GF Virus and Banana Streak Mysore Virus.

In Artigstop banana streak or virus		
Eile Edit View Tiers Analysis Bookmarks Agnotation Window Links He	lp	
have the same count of a start from the second start	en de Verten ander en de Stelen de Stelen Stelen de Stelen de St	ۇرى قىرىلارغان رەر مەربىيەتىر دىرىمىز بايەمەرىرىغە 1
ORFU		
ONP1 polyprotein II		
0 . 800 . 1600 . 2400	3200 4000 4800	3 5600 8400 7200
	entino, sere tradet and a series	
Position (1	
Zoom x10 x2 x.5 x.1 Reset Zoom factor = 1.0000 Banana streak GF vir	us:1-7263	
Position 3774 Feature Action		

Restriction site:



Restriction Site

Restriction site position for bsgfv 531 - 536, 3254 - 3259 and 3887 - 3892 fragment position 1 - 536, 531 - 3259 and 3254 - 3892 fragment length 536, 2729, 639 BSMV

Elle Edi	t ⊻iew	Tiers Analysi	s <u>B</u> ookmark	s Annotation	Window Lini	ks <u>H</u> elp			-						
1.1	1.1		1	S. 25.	de la contra	Street 5	10 Y 31		dia and	Aster States	a. 177 a 194	Sec. 1	1. Same	12.54	· · · · · · · · · · · · · · · · · · ·
20.00	n farfar	ta da se	11.00						1 1 1 10						•
			ORF II profein												
		ORF / profeir		ORF /II polyprote	ie										_
1				4800	240		2200	1000		1000		100	8400		7300
1		ayu		Topu	, 24pi	· ·	3200	, 4 000		4opu	, 9	spo ,	6400		7200
															<u></u>
	1.1			1000 111	di suit			1.5 1.1 1.	5. S.J			1.11.11			·····
				, 4 m. jun		(N. 19.200	a ta sun	0078 (J	برزيو مرد	900 A.V A	CONTRACTOR OF STREET	li notori		- 10 C C C
Position .	40 102		Team t	laster - 1 0000	Decesso street		7850								,
ZOOM	10 12	1.5 1.1 1	zoom	130000	ballana su'ea	Citys mus.r-	7050								
Positio	n 5647	Feature	Action	_				_	_	_	_	_		_	

Restriction Site:

🔬 Sequence Analysis Co	ntrols		101		
Restriction Enzymes	GC Window Size				
		Use the control key to select multiple	le restriction enzymes		
F-3 (F00000)					1.1
Ecal [ICCOCC]					A
Eco478 MGCGCT					
Eco57LICTGAAGI					
EcoRI [GAATTC]					
EcoRV [GATATC]					
Esp3I [CGTCTC]					
Faul [CCCGC]					-
	D	Clear			
Enz	sme	Restriction site positi-	n Fragment positi	ion Fragment length	Select
EcoRI (GAATTC)		3458-3463	1-3463	3463	
EcoRI [GAATTC]		3638-3643	3458-3643	185	
Downstream		7650-7650	3638-7650	4013	
		Show selected restriction frage	ent sequences		

Restriction Site

Restriction Site Position For BSMV 3458 – 3463 and 3638 - 3643 Fragment Position 1 – 3463 and 3458 – 3643 FRAGMENT LENGTH 3463 and 186

2. CONCLUSION

The genome investigation was finished Banana Streak GF Infection and Banana Streak Mysore Infection to discover the locales present in the genome .The consequences of apollo gave 3 areas for BSGFV and 3 districts for BSMV.

REFERENCES

Arumugam S, Ramareddy S, Simulation comparison of class D/ Class E inverter fed induction heating", Journal of Electrical Engineering, 12(12), 2012, 71-76.

Bouhida M and Lockhart BE, Increase in importance of cucumber mosaic virus infection in greenhouse-grown bananas in Morocco, Phytopathology, 80, 1990, 981.

Bouhida M, Lockhart BEL and Olszewski NE, An analysis of the complete nucleotide sequence of a sugarcane bacilliform virus genome infectious to banana and rice. Journal of General Virology, 74, 1993, 15-22.

Comstock JC and Lockhart BE, Widespread occurrence of sugarcane bacilliform virus in U.S. sugarcane germplasm collections. Plant Disease, 74, 1990, 530.

Daniells J, Thomas JE and Smith M, Seed transmission of banana streak virus confirmed. Infomusa 4, 1995, 1-7.

Francki RIB, Mossop DW and Hatta T, 1979. Cucumber mosaic virus. Descriptions of Plant Viruses No. 213. Commonwealth Mycological Institute/Association of Applied Biologists, Kew, Surrey, England. 6, 1979.

Hearon SS and Locke JC, Graft, pollen, and seed transmission of an agent associated with top spotting in Kalancöe blossfeldiana. Phytopathology, 74, 1984, 347-350.

Javer E, Identification of Banana streak virus species Goldfinger, Imové, Mysore and Obino l'Ewaï in Musa spp. in Cuba New Disease Reports, 18, 2009, 45.

Lassoudiere A, Mise en évidence des répercussion économiques de la mosaïque en tirets du bananier en Côte d'Ivoire. Possibilitiés de Lutte par eradication, Fruits, 34, 1974, 3-34.

Journal of Chemical and Pharmaceutical Sciences

Lockhart BE, Banana Streak Badnavirus Infection in Musa: Epidemiology, Diagnosis and Control Department of Plant Pathology, University of Minnesota, St. Paul, MN 55108, U.S.A, 1995-10-01

Lockhart BEL and Olszewski NE, Badnavirus Group. In: Encyclopedia of Virology, R.G. Webster, and A. Granoff (eds.), Academic Press, New York, 1, 1994, 139-143.

Lockhart BEL and Olszewski NE, Serological and genomic heterogeneity of banana streak badnavirus: Implications for virus detection in Musa germplasm. In: Breeding Banana and Plantain for Resistance to Diseases and Pests. J. Ganry, (ed.). CIRAD/INIBAP, Mont-pellier, France, 1993, 105-113.

Lydia Caroline M, Kandasamy A, Mohan R, Vasudevan S, Growth and characterization of dichlorobis l-proline Zn(II): A semiorganic nonlinear optical single crystal, Journal of Crystal Growth, 311 (4), 2009, 1161-1165.

Martin EM and Kim KS, A new type of virus causing striped chlorosis of mimosa, Phytopathology, 77, 1987, 935-940.

Medberry SL, Lockhart BEL and Olszewski NE, Properties of Commelina yellow mottle virus' complete DNA sequence: Genomic discontinuities and transcript suggests that it is a pararetrovirus, Nucleic Acids Research, 18, 1990, 5055-5513.

Ramkumar Prabhu M, Reji V, Sivabalan A, Improved radiation and bandwidth of triangular and star patch antenna, Research Journal of Applied Sciences, Engineering and Technology, 4 (12), 2012, 1740-1748.

Saravanan T, Srinivasan V, Udayakumar R, A approach for visualization of atherosclerosis in coronary artery, Middle - East Journal of Scientific Research, 18 (12), 2013, 1713-1717.

Srinivasan V, Saravanan T, Reformation and market design of power sector", Middle - East Journal of Scientific Research, 16 (12), 2013, 1763-1767.

Srivatsan P, Aravindha Babu N, Mesiodens with an unusual morphology and multiple impacted supernumerary teeth in a non-syndromic patient, Indian Journal of Dental Research, 18 (3), 2007, 138-140.

Sundarraj M, Study of compact ventilator, Middle - East Journal of Scientific Research, 16 (12), 2013, 1741-1743.

Thooyamani KP, Khanaa V, Udayakumar R, An integrated agent system for e-mail coordination using jade", Indian Journal of Science and Technology, 6 (6), 2013, 4758-4761.

Udayakumar R, Khanaa V, Kaliyamurthie K.P, Optical ring architecture performance evaluation using ordinary receiver, Indian Journal of Science and Technology, 6 (6), 2013, 4742-4747.

Udayakumar R, Khanaa V, Kaliyamurthie K.P, Performance analysis of resilient ftth architecture with protection mechanism, Indian Journal of Science and Technology, 6 (6), 2013, 4737-4741.

Udayakumar R, Kumarave A, Rangarajan K, Introducing an efficient programming paradigm for object-oriented distributed systems, Indian Journal of Science and Technology, 6 (5), 2013, 4596-4603.

Uma Mageswaran S, Guna Sekhar NO, Reactive power contribution of multiple STATCOM using particle swarm optimization, International Journal of Engineering and Technology, 5 (1), 2013, 122-126.

Vidyalakshmi K, Kamalakannan P, Viswanathan S, Ramaswamy S, Antinociceptive effect of certain dihydroxy flavones in mice, Pharmacology Biochemistry and Behavior, 96(1), 2010, 1-6.

Vijayaragavan S.P, Karthik B, Kiran Kumar T.V.U, Sundar Raj M, Analysis of chaotic DC-DC converter using wavelet transform, Middle - East Journal of Scientific Research, 16 (12), 2013, 1813-1819, 2013.

Vijayaragavan S.P, Karthik B, Kiran T.V.U, Sundar Raj M, Robotic surveillance for patient care in hospitals, Middle - East Journal of Scientific Research, 16 (12), 2013, 1820-1824.

Vuylsteke DR, Chizala CT and Lockhart BE, First report of banana streak virus in Malawi. Plant Disease, 80, 1996, 224.