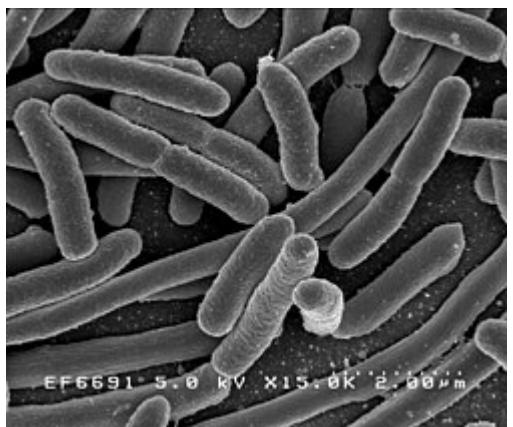


bacteria.231.1.genomic.fna.names

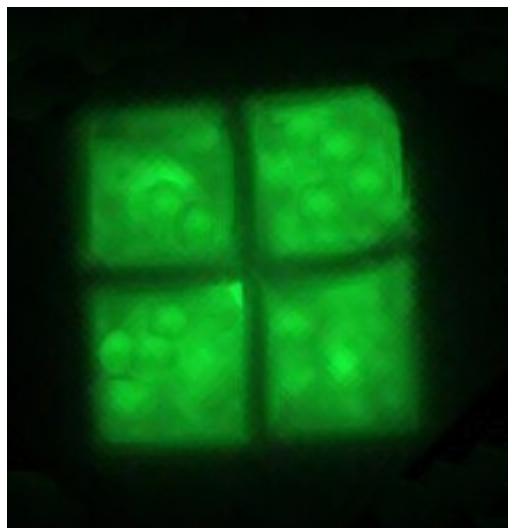
Escherichia coli (dar dažnai vadinama santrumpa ***E. coli***) – gramneigiamos, lazdelės formos bakterijos, fakultatyviniai anaerobai. Randamos šiltakraujų organizmų žarnyne. *E. coli* bei kiti fakultatyviniai anaerobai sudaro apie 0,1 % viso žarnyno floros. Dauguma *E. coli* padermių yra nepavojingos, bet kai kurie serotipai sukelia sunkų apsinuodijimą maistu. Nepavojingos padermės yra dalis natūralios žarnyno mikrofloros ir gali teikti šeimininkams naudą gamindamas vitaminą K2, taip pat užkirsdamas kelią patogeniškų bakterijų ištvirtinimui žarnyne. *E. coli* patenka į aplinką su išmatomis. Šios bakterijos sparčiai dauginasi šviežiose išmatose aerobinėse sąlygose 3 dienas, vėliau jų skaičius mažėja.



archaea.6.1.genomic.fna

Haloquadratum walsbyi is a species of Archaea in the genus *Haloquadratum*, known for its square shape and halophilic nature.

First discovered in a brine pool in the Sinai Peninsula of Egypt, *H. walsbyi* is noted for its flat, square-shaped cells, and its unusual ability to survive in aqueous environments with high concentrations of sodium chloride and magnesium chloride. The species' genus name *Haloquadratum* translates from Greek and Latin as "salt square". This archaean is also commonly referred to as "Walsby's Square Bacterium" because of its unique square shape. In accordance with its name, *H. walsbyi* are most abundantly observed in salty environments.



fungi.19.1.genomic.fna

Muscodor is a genus of fungi in the family Xylariaceae noted for its ability to produce a variety of volatile organic compounds, which inhibit the growth of other fungi. The first species to be identified was *M. albus*. Other known species include *M. roseus* and *M. vitigenus*.

Known habitats of *Muscodor* species include Honduras, Venezuela, Thailand, Brazil, and Australia's Northern Territory. Members of the genus are believed to prefer tropical or monsoonal rainforests as habitats; efforts made to find them in the temperate rainforests of southern Australia and southern Chile have been unsuccessful.



Bacteria & Archaea

Maximum Score:

Score = 4017 bits (2175), Expect = 0.0

Identities = 2175/2175 (100%), Gaps = 0/2175 (0%)

Strand=Plus/Plus

BLASTX:

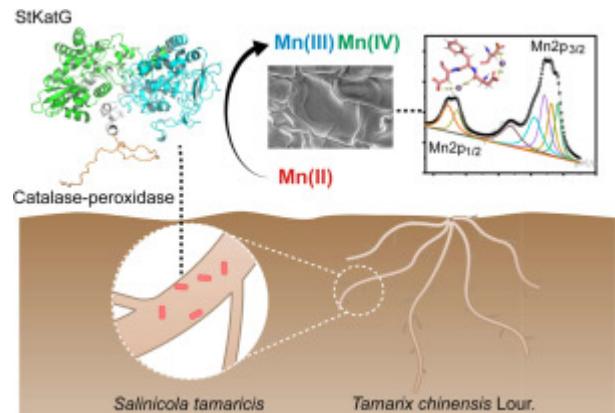
Cluster Acestor	Cluster Representative Sequence	Max Score	Total Score	Query Cover	E Value	Per. Ident	Acc. Len	Accession
high G+C Gram-positive bacteria	catalase/peroxidase HPI [Intrasporangium sp.]	189	274	100%	4e-53	93.16%	731	WP_317180654.1

catalase/peroxidase HPI [Intrasporangium sp.]

Sequence ID: [WP_317180654.1](#)

Length: 731

Number of Matches: 2



Conclusions:

The presence of catalase-peroxidase in both domains supports either ancient common ancestry or horizontal gene transfer between bacteria and archaea.

About:

- **Catalase/peroxidase HPI [Intrasporangium sp.]** - This enzyme is involved in **detoxification** of reactive oxygen species, particularly hydrogen peroxide. Catalase-peroxidases are widespread in bacteria and archaea and play a crucial role in oxidative stress resistance, especially in **aerobic** or facultatively **anaerobic** environments.
- Catalase-peroxidase StKatG is a bacterial manganese oxidase from endophytic *Salinicola tamaricis*. Manganese (Mn) oxides in iron/manganese plaques are widely distributed in the rhizosphere of wetland plants and **contribute significantly to elemental cycling and pollutant removal**. Mn oxides are primarily produced by **bacterial processes** using Mn oxidases.

(<https://www.sciencedirect.com/science/article/pii/S0141813022023650>)

Bacteria & Fungi

Maximum Score:

Score = 976 bits (528), Expect = 0.0

Identities = 1637/2166 (76%), Gaps = 101/2166 (5%)

Strand=Plus/Plus

BLASTX:

Cluster Ancestor	Cluster Representative Sequence	Max Score	Total Score	Query Cover	E Value	Per. Ident	Acc. Len	Accession
Klebsiella sp.	class A broad-spectrum beta-lactamase TEM-72, partial [Klebsiella sp.]	254	254	99%	1e-83	93.53%	215	BGI53802.1

class A broad-spectrum beta-lactamase TEM-72, partial [Klebsiella sp.]Sequence ID: [BGI53802.1](#)

Length: 215

Number of Matches: 1

About:

- **Class A broad-spectrum beta-lactamase TEM-72, partial [Klebsiella sp.]** - Beta-lactamases are enzymes that confer antibiotic resistance by hydrolyzing beta-lactam antibiotics. TEM-type beta-lactamases are among the most widespread resistance determinants in Gram-negative bacteria.
- Broad-spectrum β-lactamase genes (coding for extended-spectrum β-lactamases and AmpC β-lactamases) have been frequently demonstrated in the **microbiota of food-producing animals**. This may pose a human health hazard as these genes may be present in zoonotic bacteria, which would cause a direct problem. They can also be present in commensals, which may act as a reservoir of resistance genes for pathogens causing disease both in humans and in animals.

Fungi & Archaea

Maximum Score:

Score = 582 bits (315), Expect = 1e-161

Identities = 1472/2017 (73%), Gaps = 133/2017 (7%)

Strand=Plus/Plus

BLASTX:

Cluster Ancestor	Cluster Representative Sequence	Max Score	Total Score	Query Cover	E Value	Per. Ident	Acc. Len	Accession
Ascomycete fungi	hypothetical protein SLS58_001878 [Diplodia intermedia]	256	256	99%	1e-78	97.10%	747	KAL1648704.1

hypothetical protein SLS58_001878 [Diplodia intermedia]

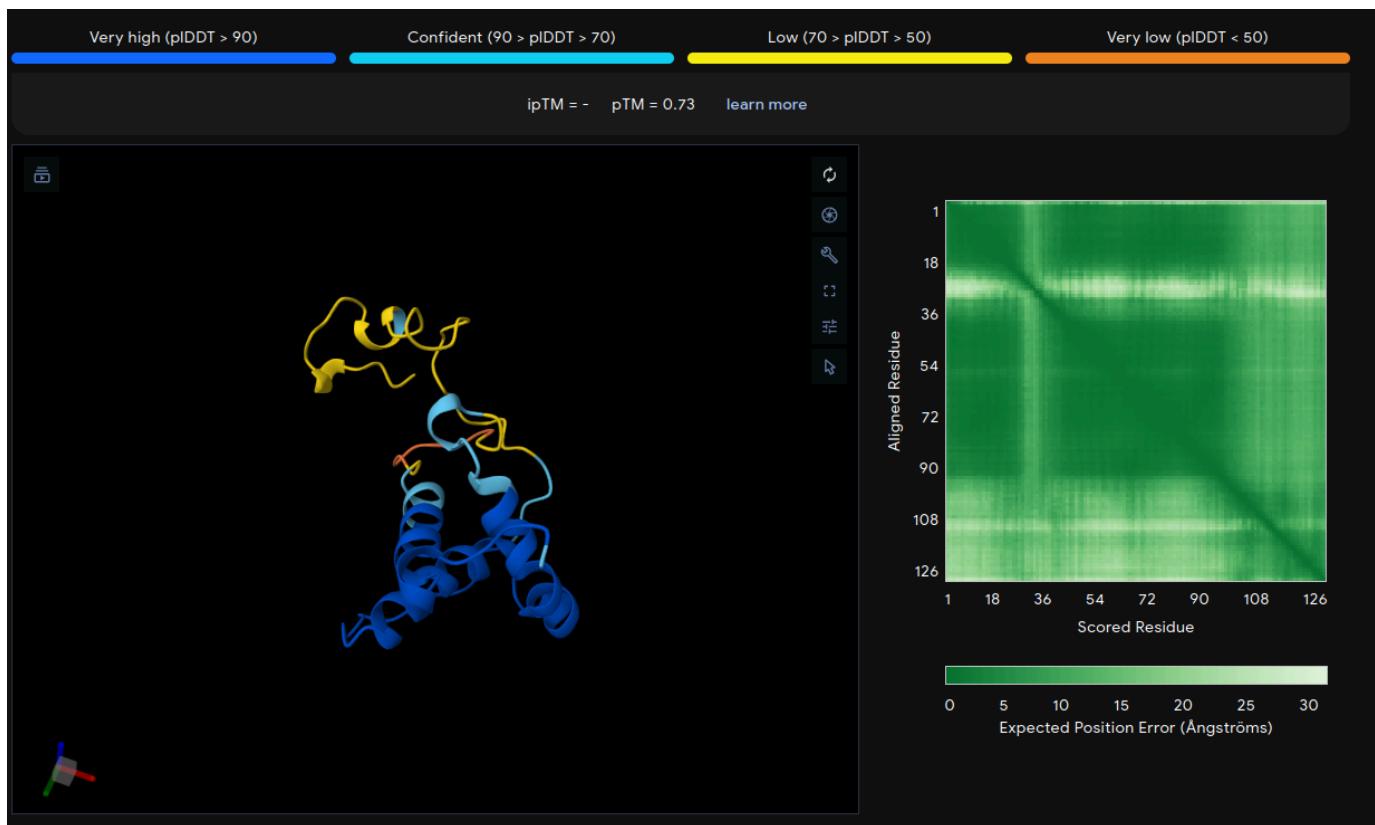
Sequence ID: [KAL1648704.1](#)

Length: 747

Number of Matches: 1

About:

- **hypothetical protein SLS58_001878 [Diplodia intermedia]** - This protein is currently uncharacterized.



Viral & Archaea

Maximum Score:

Score = 54.7 bits (130), Expect = 5e-05, Method: Compositional matrix adjust.

Identities = 76/318 (24%), Positives = 131/318 (41%), Gaps = 58/318 (18%)

Frame = -1

TBLASTN:

Description	Scientific Name	Max Score	Total Score	Query Cover	E Value	Per. Ident	Acc. Len	Accession
Sweet potato virus 2, complete genome	Sweet potato virus 2	431	580	92%	2e-132	88.11 %	10731	NC_017970.1

Sweet potato virus 2, complete genome

Sequence ID: [NC_017970.1](#)

Length: 10731

Number of Matches: 2

Conclusions:

This supports the idea that viruses occasionally share functional motifs with cellular life but are evolutionarily distinct.

About:

- **Sweet potato virus 2** - A plant virus belonging to the *Potyviridae* family, characterized by RNA genomes and polyprotein processing. Sweet potato is prone to virus infections, which are associated with substantial yield and quality loss.
(<https://www.arc.agric.za/arc-vop/Pages/Crop%20Protection/Viruses.aspx>)



Viral & Bacteria

Maximum Score:

Score = 70.5 bits (171), Expect = 7e-11, Method: Compositional matrix adjust.

Identities = 82/320 (26%), Positives = 141/320 (44%), Gaps = 31/320 (10%)

Frame = -2

TBLASTN:

Description	Scientific Name	Max Score	Total Score	Query Cover	E Value	Per. Ident	Acc. Len	Accession
Hippeastrum mosaic virus isolate Marijiniup 6, complete genome	Hippeastrum mosaic virus	610	610	100%	0.0	100.00%	9660	JQ723474.1
Nerine yellow stripe virus isolate 63, complete genome	Nerine yellow stripe virus	457	457	100%	7e-143	73.63%	10165	MT396083.1

Hippeastrum mosaic virus isolate Marijiniup 6, complete genome

Sequence ID: [JQ723474.1](#)

Length: 9660

Number of Matches: 1

Nerine yellow stripe virus isolate 63, complete genome

Sequence ID: MT396083.1

Length: 10165

Number of Matches: 1

About:

- **Hippeastrum mosaic virus** - A plant-infecting RNA virus known for encoding proteins involved in replication, movement, and host interaction.
 - **Nerine yellow stripe virus** - The genome consists of 10,165 nucleotides, excluding the 3'-terminal poly(A) tail. A single open reading frame encodes a large polyprotein of 3294 amino acids with typical potyvirus features. The nuclear inclusion b and coat protein region shares 95% identity with a previously reported partial NeYSV sequence (NC_043153.1). Phylogenetic analysis of the polyprotein amino acid sequence showed that NeYSV clustered with hippeastrum mosaic virus (HiMV YP_006382256.1).

First Report of Nerine Yellow Stripe Virus Infecting Crinum Lily (*Crinum* sp.) in Texas

(<https://apsjournals.apsnet.org/doi/10.1094/PDIS-06-23-1149-PDN>) 2023

Viral & Fungi

Maximum Score:

Score = 64.3 bits (155). Expect = 3e-08. Method: Compositional matrix adjust.

Identities = 103/427 (24%), Positives = 167/427 (39%), Gaps = 65/427 (15%)
Frame = +1

TBLASTN:

Description	Scientific Name	Max Score	Total Score	Query Cover	E Value	Per. Ident	Acc. Len	Accession
Hippeastrum mosaic virus isolate Marijiniup 6, complete genome	Hippeastrum mosaic virus	769	769	100%	0.0	100.00%	9660	JQ723474.1
Zucchini tigre mosaic virus isolate 15-283 cylindrical inclusion gene, partial cds	Zucchini tigre mosaic virus	472	472	99%	2e-15 8	62.19%	10165	KT992782.1
Malva vein clearing virus isolate DSMZ PV-0963 clone 1 polyprotein gene, complete cds; and PIPO gene, partial cds	Malva vein clearing virus	502	502	100%	3e-15 7	68.31%	10952	PV664460.1

Hippeastrum mosaic virus isolate Marijiniup 6, complete genome

Sequence ID: [JQ723474.1](#)

Length: 9660

Number of Matches: 1

Received: 22 December 2023 | Accepted: 2 June 2024

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New Disease Reports  WILEY

First report of *Zucchini tigré mosaic virus* naturally infecting two different cucurbit species in Argentina

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KEY WORDS
Cucurbita maxima, PRSV Cluster, ZTMV

In Argentina, *Cucurbita maxima* cv. Zapallo Plomo, an indigenous variety, and the hybrid *Cucurbita maxima* × *Cucurbita moschata* cv. Tetsukabuto contribute significantly to regional economies, being the fourth most popular vegetable in the domestic market. In March 2022, leaves



FIGURE 1 *Cucurbita maxima* cv. Zapallo Plomo leaf showing symptoms caused by Zucchini tigre mosaic virus.



FIGURE 2 *Cucurbita maxima* cv. Zapallo Plomo fruit showing symptoms caused by Zucchini tigre mosaic virus.

showing virus-like symptoms, including discolouration, blistering, distortion and mosaics were collected from both cultivars in Balcarce, Catamarca province (Figure 1). The fruits were severely affected, being covered in knobby warts, blisters and brown bumps (Figure 2).

Samples were tested by DAS-ELISA using commercial Papaya ringspot virus (PRSV) antiserum (BIOREBA AG, Switzerland), following

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wileyonlinelibrary.com/journal/ndr

| 1 of 3

Malva vein clearing virus isolate DSMZ PV-0963 clone 1 polyprotein gene, complete cds; and PIPO gene, partial cds

Sequence ID: [PV664460.1](#)

Length: 10952

Number of Matches: 1

Zucchini tigre mosaic virus isolate 15-283 cylindrical inclusion gene, partial cds

Sequence ID: [KT992782.1](#)

Length: 2058

Number of Matches: 1

Conclusions:

Matches are likely due to shared functional motifs rather than shared ancestry.

About:

- **Zucchini tigre mosaic virus** - A potyvirus encoding cylindrical inclusion proteins, which are important for viral movement and replication.
- **Malva vein clearing virus** also known as **MVCV**^[1] is a species of Potyvirus in the family Potyviridae that was isolated in 1957 from Malva sylvestris in Germany which is transmitted by the aphids Aphis umbrella and Myzus persicae. The insects mechanically inoculate the malvaceous hosts.^[1]

