Confirmation of spring viremia of carp virus in wild common carp (*Cyprinus carpio* L.) in Mexico

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Background

Sanitary control measures associated with diseases in farmed carp in Mexico are scarce (1). Unpublished case reports have reported of infectious ascites by *Aeromonas* spp. and *Pseudomonas* spp (2). *Aeromonas bestiarum* was reported causing a septicaemia in common carp (3); whereas the occurrence of viral cases was largely ruled out, excepting one case in which coronavirus-like viral particles were microscopically identified (2). In October 2015, wild common carp (*C. carpio*) were collected as the result of a health-monitoring program for fish. The fishes were submitted to the lab with an anamnesis for routine diagnostic, with absence of any sign of disease. During necropsy, lesions suggestive of sepsis were observed and associated with the spring viremia of carp disease (SVC).

Objective

To confirm the presence of spring viremia of carp virus (SVCV) in wild common carp (*Cyprinus carpio* L) in central Mexico.

Methodology

- Ten common carp were collected from a natural freshwater lagoon where never disease outbreaks and/or disease-related mortalities had been reported. Internal organs samples were taken from each fish, fixed in 10% buffered formalin, dehydrated, and embedded in paraffin wax. Each tissue was sectioned at 5 µm and stained with hematoxylin and eosin (H-E) to describe histopathological alterations.
- The kidney were collected and processed for virus isolation in EPC cell monolayers according to OIE Manual (OIE,2018) (4).
- Electron microscopy images were obtained from monolayers of EPC cells infected with SVCV.
- For molecular diagnosis, total RNA was extracted from the cell culture supernatant and a semi-nested RT-PCR was performed according to Stone *et al* (2003). Samples were considered positive if the size of the first and second PCR products were 714 and 606 bp, respectively (5).
- The secondary amplification products were sequenced, and alignments were performed with the ClustalW algorithm and the two-nucleotide sequences were deposited in GenBank.

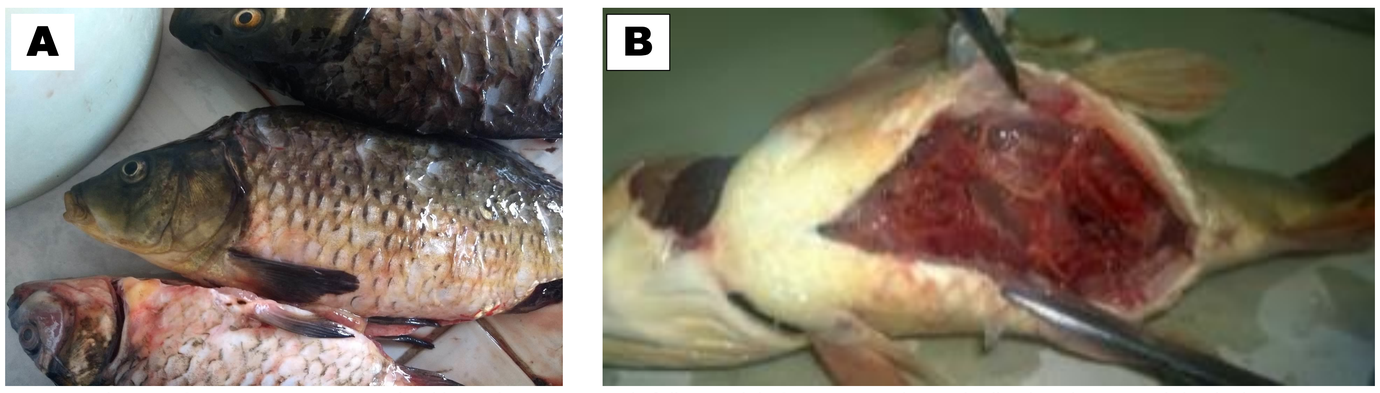

Figure 1. Common carp. Apparently without signs or external of disease (A). Carp; congestion and adhesions between abdominal organs (B).

Results.

- Fishes do not showed clinical signs, but exhibited lesions of septicemic disease, with sero-hemorrhagic ascites and adhesions between abdominal organs (Figure 1B).
- The kidney evidenced hemorrhagic and mononuclear interstitial nephritis, renal congestion, epithelial tubular degeneration, with tubular obstruction and dilation, melanomacrophages proliferation and perirenal steatitis (Figure 2).
- Liver presented perivascular hemorrhages with degeneration and infiltration in the vascular walls (Figure 3), multifocal mononuclear hepatitis, multi focal hyperemia, degeneration and necrotic pancreatitis (Figure 4).
- The spleen presented congestion and hemosiderosis (Figure 5), reticule endothelial hyperplasia and melano macrophage proliferation.
- The intestine showed perivascular inflammation and necrotic enteritis, with necrotic cryptitis of enterocytes and epithelial cells in the *lamina propria* (Figure 6), epithelial scaling, villous atrophy.
- The kidney homogenates showed a CPE between 24 and 48 h post-inoculation in EPC cells.
- The electron microscopy revealed the characteristic rhabdovirus structure and size of viral particles: (110-123 nm long, 75.5-78.1 nm wide) (Figure 7).
- The expected specific amplification product of semi-nested RT-PCR for SVCV was observed (716 bp and of 606 bp, respectively).
- The phylogenetic analyses of partial SVCV glycoprotein gene sequences of Mexican SVCV isolates were classified into the genogroup Ia (Figure 8).

Conclusion

- This study confirm the presence of SVCV in common carp in Mexico.
- The phylogenetic analyses classified the isolates into the Ia genogroup.
- It is difficult to estimate the risk of SVCV for other wild/feral cohabitating cyprinid species in the lagoon.
- The status of this virus in other water sources in the country is unknown.

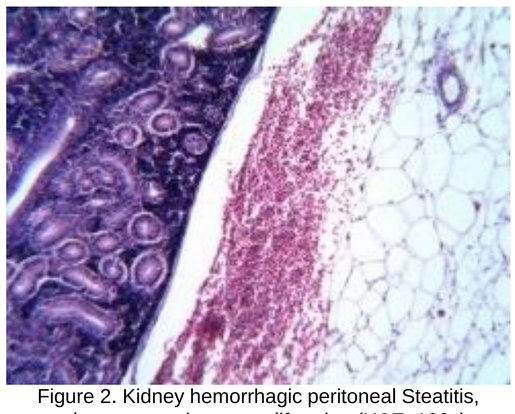

Figure 2. Kidney hemorrhagic peritoneal Steatitis, melanomacro-phages proliferation (H&E. 100x).

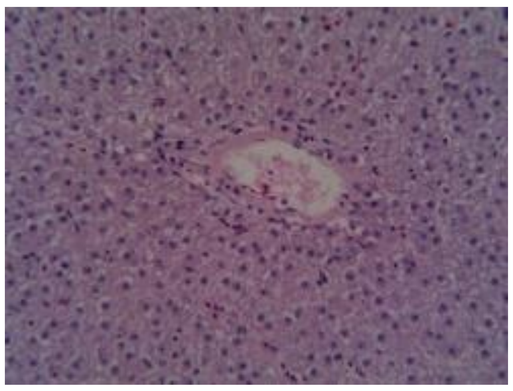

Figure 3. Liver, vascular wall degeneration (H&E. 250x).

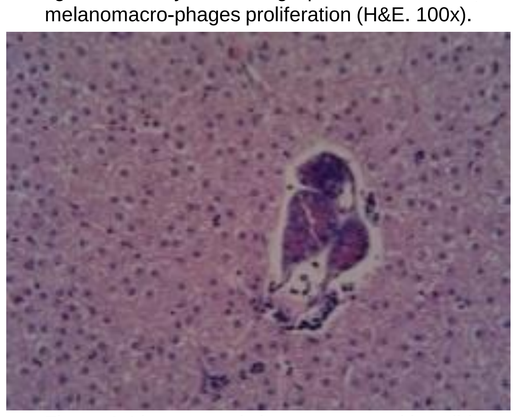

Figure 4. Liver, necrotic hepatopancreatitis, mild peripancreatic lymphocytic infiltrations (H&E. 250x).

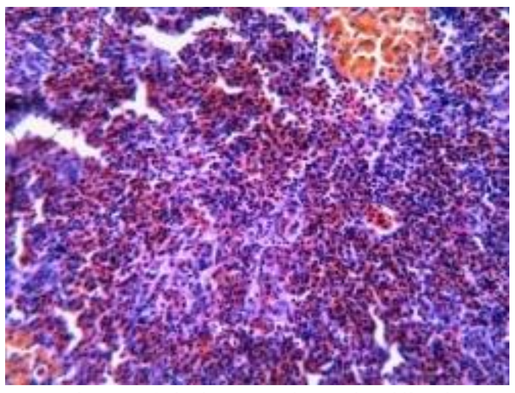

Figure 5. Splenic congestion and multifocal hemosiderosis (H&E. 250x).

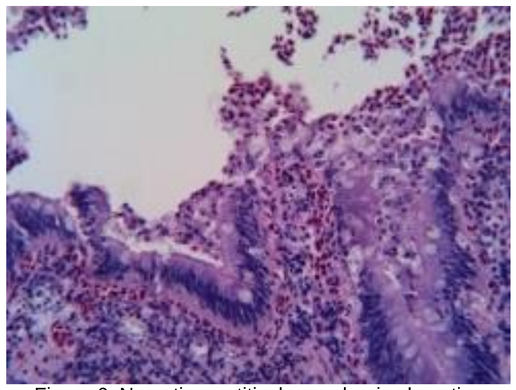

Figure 6. Necrotic cryptitis, hemorrhagic ulcerative enteritis (H&E. 250x).

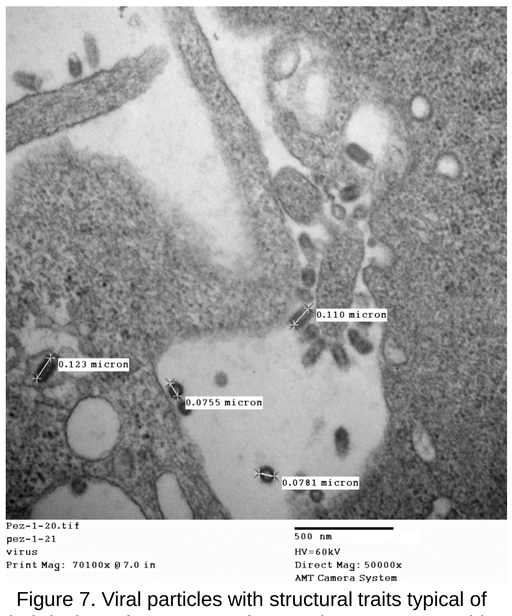

Figure 7. Viral particles with structural traits typical of rhabdovirus of 110-123 nm long and 75.5-78.1 nm wide.

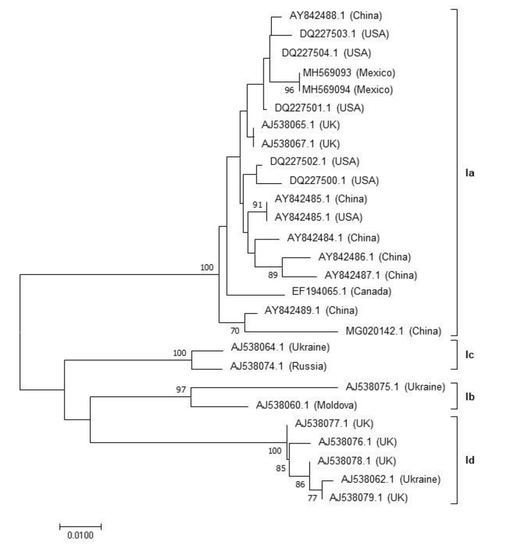

Figure 8. Phylogenetic tree for SVCV based on the obtained partial glycoprotein gene sequence, constructed using the neighbor-joining method. The values at the branches are bootstrap values with 1,000 replicates. The scale represents the evolutionary distance between two sequences. The accession number and origin of isolation are indicated.

References

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