

Discovery, prevalence and biogeographical distribution of a novel RNA virus in the seagrass *Thalassia testudinum*

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Introduction

Seagrass meadows fulfill numerous essential ecosystem functions. Unfortunately, seagrasses are currently under threat due to various stressors such as eutrophication, coastal development, dredging activities, global climate change and disease. Given global declines in coverage and increasing urbanization of coastal estuaries, it is critical to better understand the impact of pathogens on the ecology of seagrasses. Although studies have investigated bacteria, fungi and protists in seagrasses, virtually nothing is known about viral infection in these ecologically-important plants.



Fig. 1-2 *T. testudinum* of the Tampa Bay area (FL, USA)



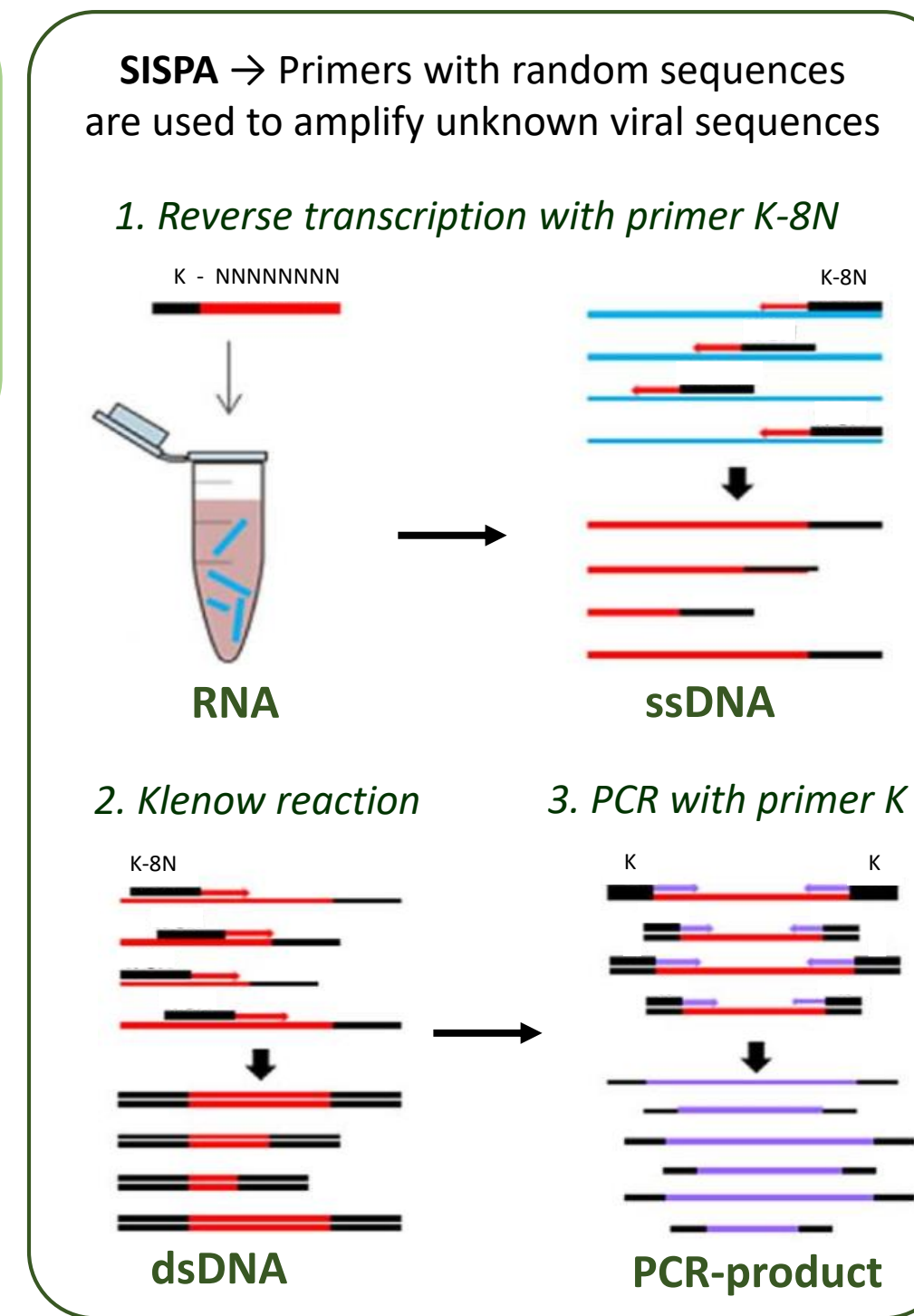
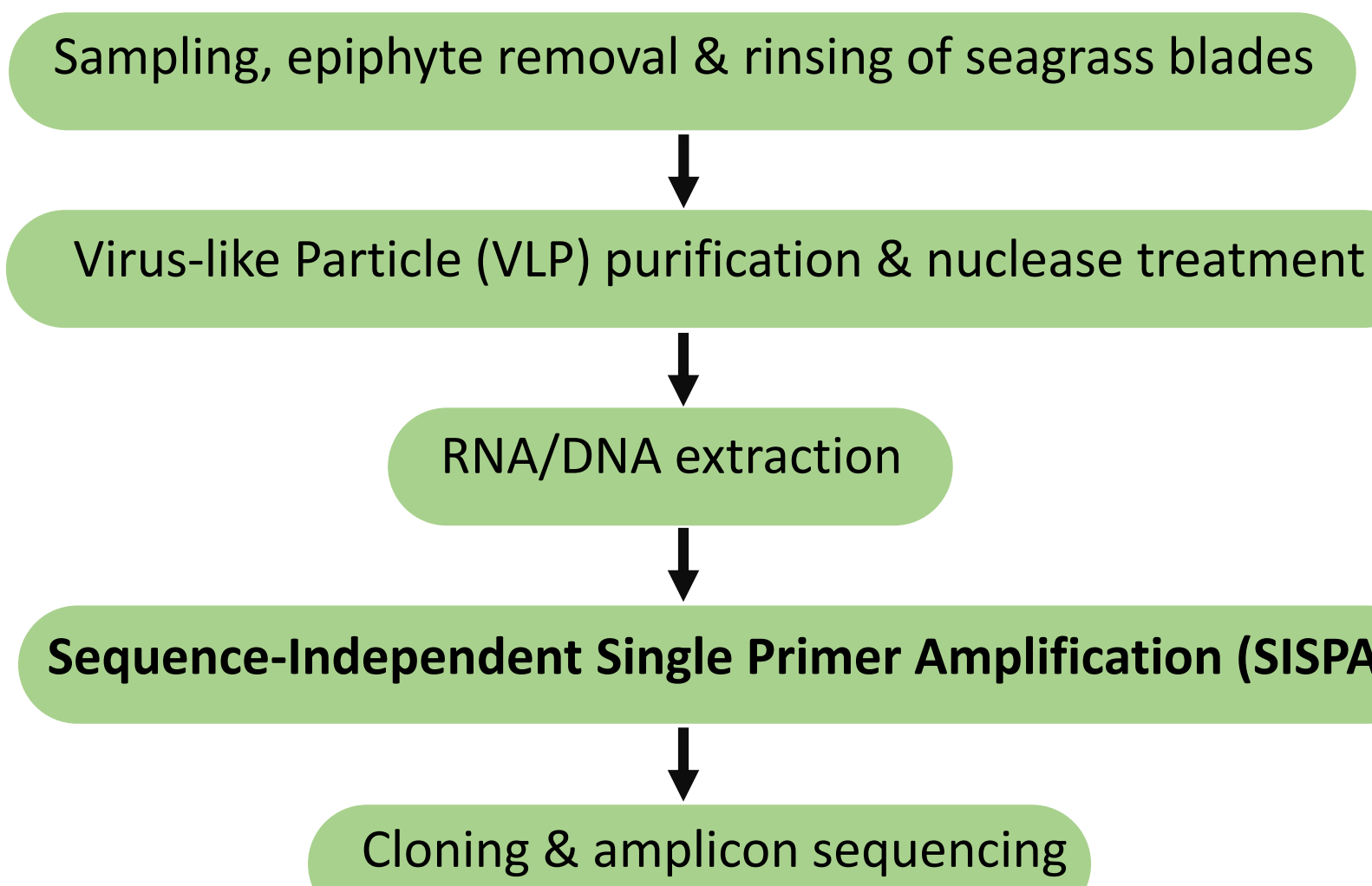
Objective

This study aimed to identify viruses in natural populations of the widespread subtropical seagrass species *Thalassia testudinum* (turtlegrass) in Tampa Bay, Florida (Fig 1-2). Here we describe a novel virus detected in these populations.

Methods

Virus detection

Ten individual seagrass leaves were sampled in December 2016 in the Terra Ceia Aquatic Preserve in Tampa Bay, FL, USA (at sampling location N01, Fig. 3) and pooled together for screening.



Modified from Chrzastek et al. 2017

Development of a qPCR-assay for individual testing

A qPCR assay targeting a segment of the RdRp coding region of TtPV was used to test a total of 40 individual seagrass blades collected at two time points (February & August) in 2017 from four locations (N01, N02, N03 and N04) in the Tampa Bay area (Fig. 3).

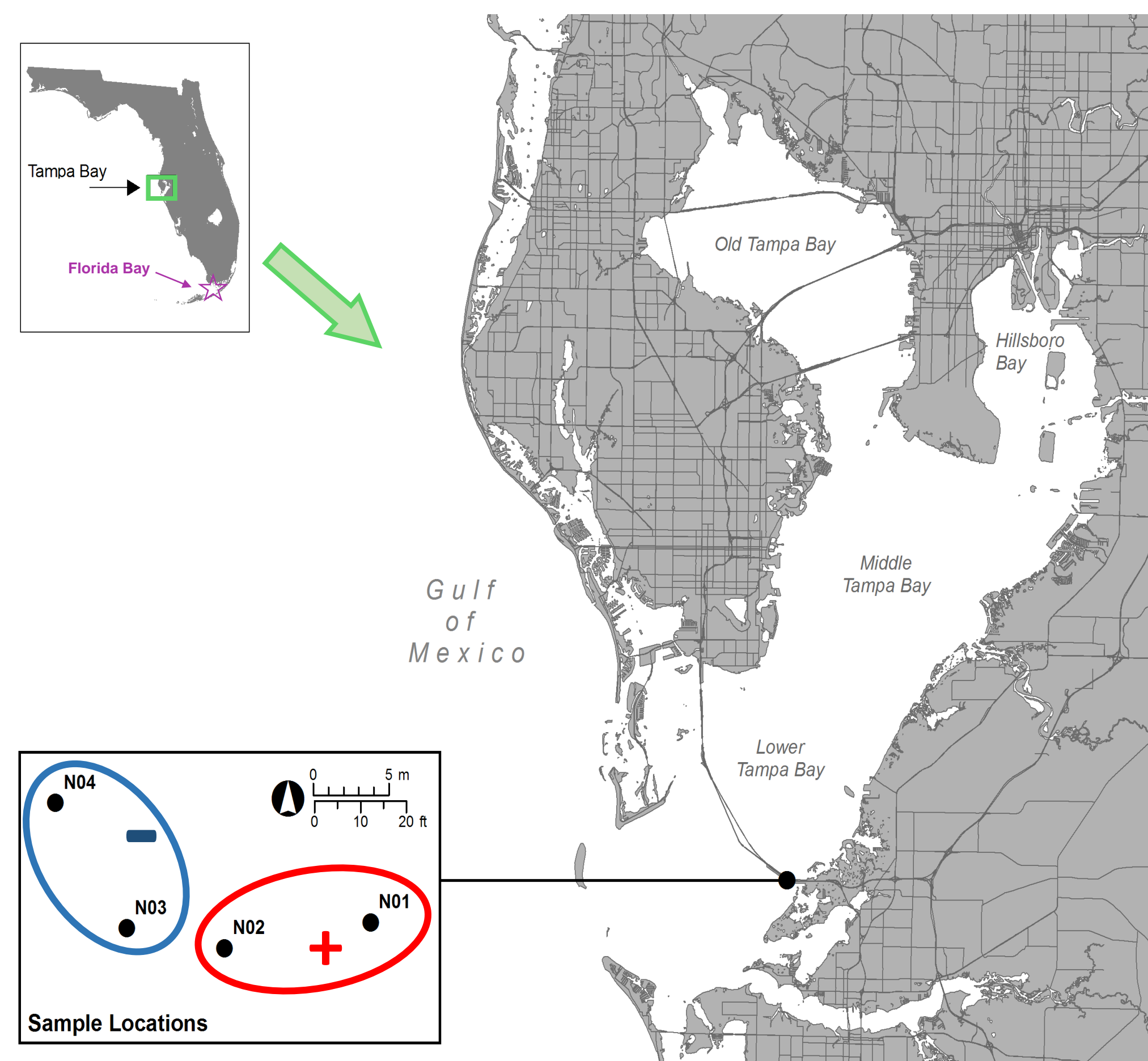


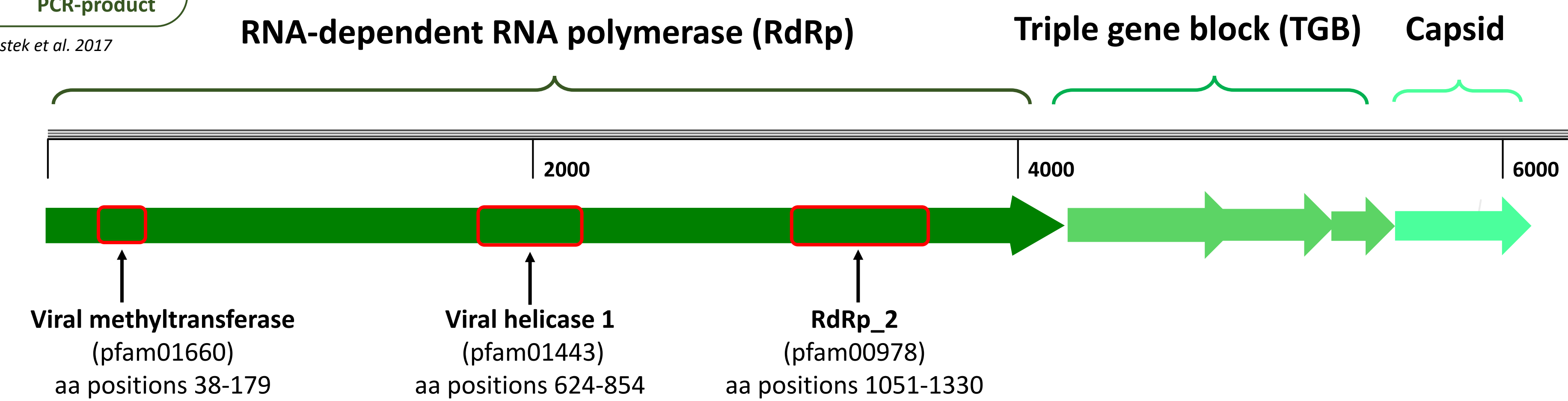
Fig. 3 Sampling location in the Terra Ceia Aquatic Preserve in Tampa Bay, FL

Results

Discovery of a new potexvirus infecting *T. testudinum*

- A new virus was discovered in the pooled sample of December 2016 (Fig. 3, location N01) with a filamentous morphology (Fig. 4)
- Proposed name: *Thalassia testudinum potexvirus* (TtPV)
- The TtPV genome, 6252 nt long, was completed through primer walking and RACE
- TtPV shares 66% genome-wide pairwise identity with the potexvirus *Foxtail mosaic virus* (FoMV) that infects terrestrial plants, mainly grasses (*Poaceae*)

TtPV genome organization



Prevalence, viral load and morphology of TtPV

Site	Viral load (VLPs/mg)		Prevalence (n = 10, %)	
	Feb	Aug	Feb	Aug
N01	2.27*10 ⁸	1.53*10 ⁹	80	60
N02	2.33*10 ⁶	1.00*10 ⁸	10	20
N03-N04	0	0	0	0

Viral load and prevalence for sites N01-N04 in Tampa Bay, FL

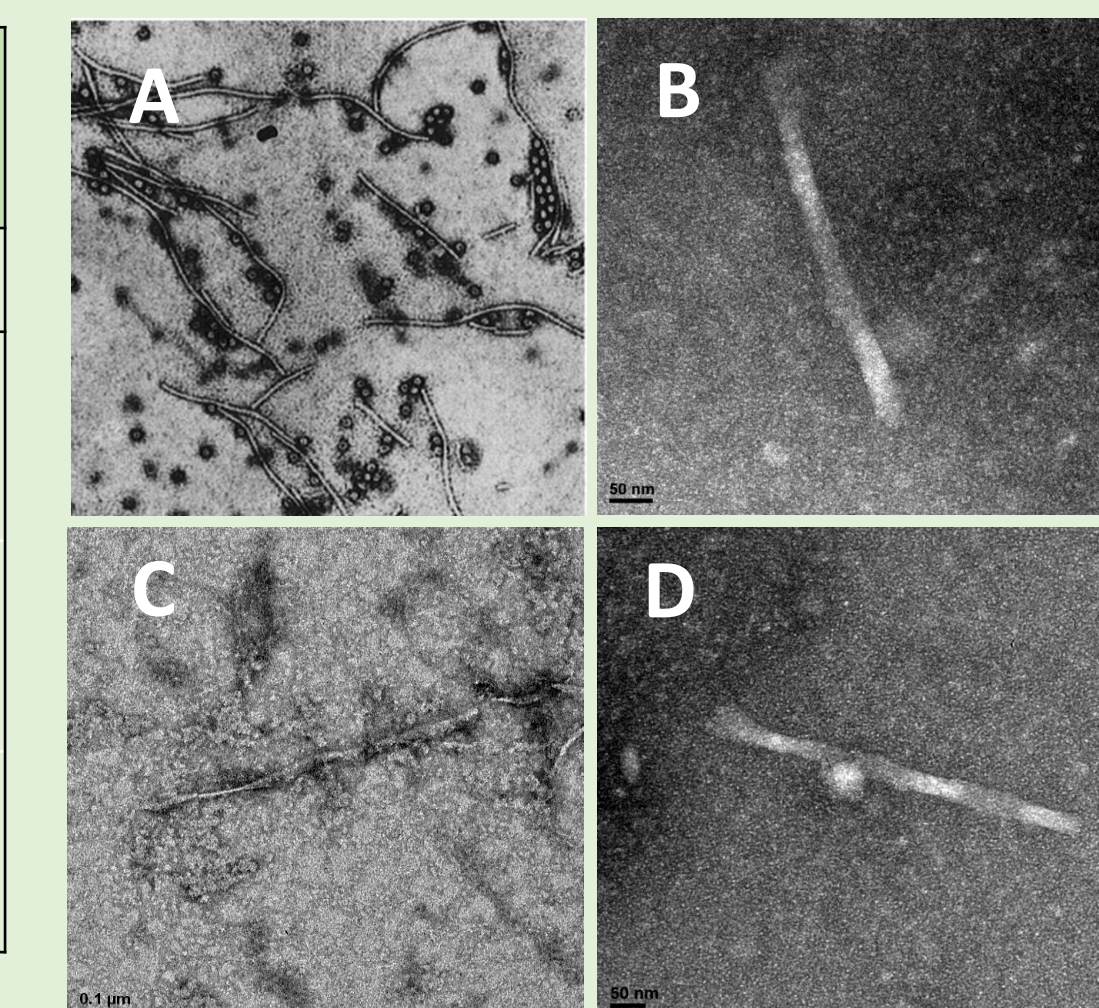


Fig. 4 TEM-images showing various filamentous VLPs from A) FoMV (Paulsen & Niblett 1977) and B-D) TtPV. Negatively stained TtPV virions ranged between 400 - 500 nm



TtPV was **not** found in *T. testudinum* samples obtained from 7 different sites in Florida Bay sampled in May 2017.

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