A spatiotemporal analysis of sargassum impacting the eastern Caribbean: morphotypes and sub-origins

Un análisis espaciotemporal del impacto del sargazo en el Caribe oriental: morfotipos y suborígenes

Une analyse spatio-temporelle des sargasses impactant la Caraïbe orientale : morphotypes et sous-origines

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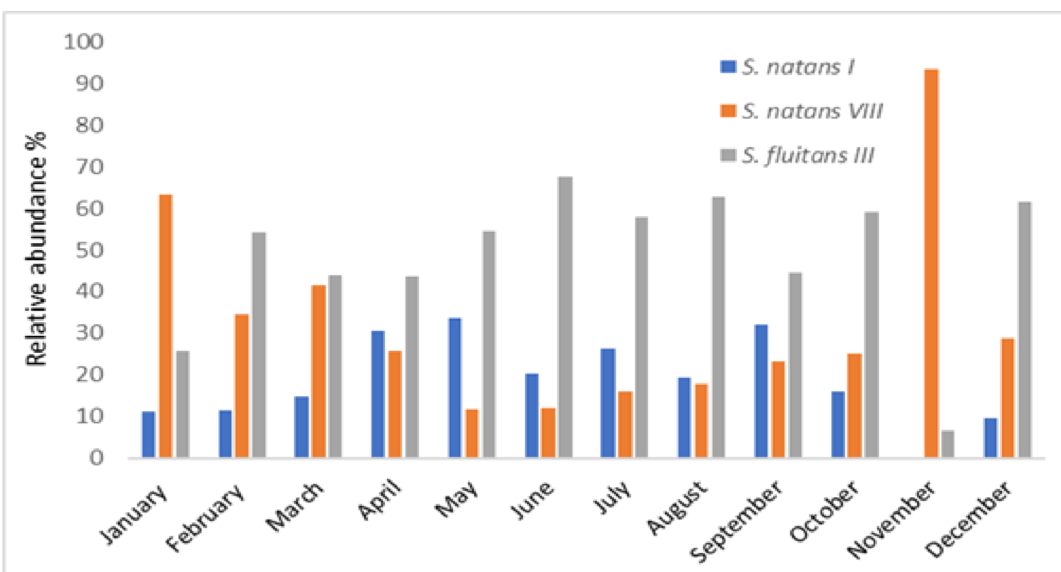
EXTENDED ABSTRACT

The unprecedented proliferation of pelagic sargassum in the Tropical Atlantic since 2011 stems from a new source region just north of the equator known as the North Equatorial Recirculation Region (NERR) (Johnson et al. 2020). Ocean eutrophication and climate change have been identified as key driving factors (Skliris et al. 2022) and sargassum influx events are now considered a new norm to which countries must adapt. In an attempt to turn a hazard into opportunities, stakeholders are trying to develop commercially viable uses for stranded sargassum. Valorisation of sargassum would certainly contribute to its sustainable management. Interestingly, pelagic sargassum morphotypes have been found to vary in their biology and chemical composition (Davis et al. 2020), and thus in their potential use in different applications. As such, knowledge on the morphotype composition of stranding sargassum, and how it changes over space and time is necessary to help define and guide possible uses (Oxenford et al. 2021).

In this study, we assessed the morphotype composition of sargassum stranding in Barbados during 2021-2022, and examined the possible influence of origin and route travelled using a backtracking algorithm based on ocean drifter data. Three morphotypes (*Sargassum natans* I, *S. natans* VIII and *S. fluitans* III) were identified using gross morphological features and a volume displacement method was used to estimate the relative abundance of each morphotype. The relative composition of morphotypes were assessed for 24 collection days over the one-year period and backtracks were simulated to determine potential origins of the sampled sargassum.



Monthly

Figure 1. Monthly relative composition of *S. natans* I, *S. natans* VIII *and S. fluitans* III arriving at Morgan Lewis beach in Barbados, during 2021-2022.

analyses of the relative composition of the three prevalent morphotypes revealed *S. fluitans* III as the predominant morphotype in 80% of the samples. However, noticeable changes were observed in November, January, and February with a change from the predominant *S. fluitans* III to the previously rare *S. natans* VIII (Figure 1). Backtracks indicate that temporal variations in the relative composition of the three morphotypes is potentially linked to two distinct sub-origins and/or transport pathways within the NERR. Sargassum stranding in Barbados between March and early August originated close to the equator (between 0 to 7°N) and travelled along northeast Brazil before arriving in Barbados; these tracks are hereafter referred to as sub-origin A (Figure 2). In contrast, sargassum arriving between late August and February originated further north (between 9 to 18°N) and travelled a relatively direct route to Barbados, these are referred to as sub-origin B (Figure 2). Moreover, we found that the relative abundance of *S. natans* I, *S. natans* VIII and *S. fluitans* III differed significantly between the two sub-origins. Sub-origin A showed a predominance of *S. fluitans* III while sub-origin B showed higher levels of *S. natans* VIII, with reduced quantities of *S. fluitans* III.

The findings of this study help to address valorisation constraints surrounding variation in the supply of the three prevalent sargassum morphotypes. Moreover, the identification of the two sub-origins/transport pathways can play a critical role in advancing the region's understanding of the factors responsible for the continued proliferation and extensive interannual variability of sargassum in the NERR since the initial bloom in 2011.

KEYWORDS: sargassum morphotypes, morphotype composition, backtracking, sub-origins

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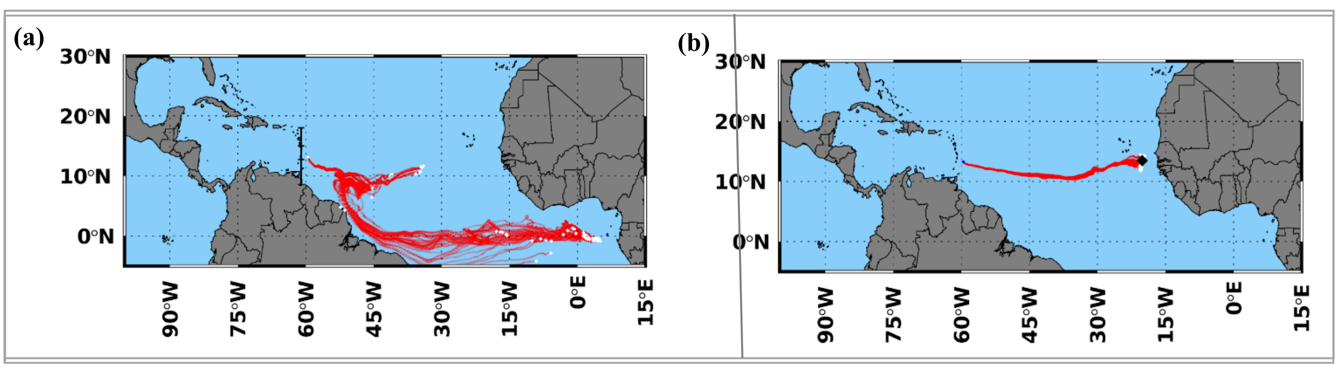

Figure 2. Example of sargassum backtracks originating from sub-origin/ transport pathway A (a) and sub-origin/ transport pathway B (b).