

THE DEGRADATION OF DIFFERENT SCYPHOZOAN JELLYFISH SPECIES BY THE AMBIENT BACTERIAL COMMUNITY

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Abstract

The chemical composition and degradation of dead jellyfish tissue of *Aurelia* sp., *Pelagia noctiluca* and *Rhizostoma pulmo* by the ambient bacterial community was studied in laboratory experiments using samples from the Gulf of Trieste (northern Adriatic). Preliminary results showed rapid hydrolyses of proteins in the presence of the natural microbial community and significant release of dissolved and inorganic nutrients, which can significantly alter the carbon and nitrogen cycles and oxygen dynamics in the surrounding environment.

Keywords: *Adriatic Sea, Bacteria, Medusae, Nutrients, Organic Matter*

Introduction

The increasing frequency and intensity of jellyfish outbreaks in the northern Adriatic may have a significant impact on fisheries, tourism and the functioning of the food web. Although eight scyphomedusae species have been discovered over the last 150 years in the northern Adriatic, only a few, have been observed in large numbers [3]. The total organic content of jellyfish is 1-2 % of wet weight and generally consists of high protein (72±14 %) contents, low carbohydrate (7±5 %) and lipid (22±12 %) contents [4]. Proteins, as a quantitatively important component of the jellyfish body, are substantially organic-nitrogen containing compounds believed to be very labile. During the decomposition of blooms, jellyfish carcasses can serve as an important source of protein to the environment. Few studies have addressed the fate of dead jellyfish [6], [8] nor indicated rapid decomposition and nutrient release, either in the water column or on the sediment surface.

Materials and method

Jellyfish for our experiments were collected by dip net from the surface during bloom events in the Gulf of Trieste (northern Adriatic). Bell diameters and wet weight were measured for each jellyfish. Seawater samples were collected with a Niskin sampler at 3 m depth at station BF (45° 32.804 N; 13° 33.034 E) in the Gulf of Trieste. Immediately after sampling, seawater was filtered through a 200 µm mesh net and subsequently through GF/F filters (Whatman) to yield a filtrate containing microorganisms. The filtered seawater was collected in 8 L acid washed and autoclaved polycarbonate bottles (Nalgen) and was used for the jellyfish decomposition experiments. In each experiment equal amounts of jellyfish were selected and their whole tissues, including interstitial water, homogenized with an Ultra – Turrax TP 18/10 (Janke & Kundel) at 20 000 rpm for several minutes. The whole tissue of each jellyfish was used as substrate, diluted in 8 litres of pre-filtered sea water containing the ambient bacterial community. Bottles with filtered sea water without addition of jellyfish served as controls. The bottles were incubated *in situ* at 3m depth in front of the Marine Biology Station from 24 March to 15 April 2009. Part of the homogenate was frozen and stored for CHNS elemental analysis. All nutrient analyses were performed on a GF/F pre-filtered water sample, using the standard protocols ([2]) and protein concentrations were determined by the Bradford method [1] using the Bio Rad Protein Assay Kit. Dissolved oxygen (DO) concentration was measured in triplicate by the standard Winkler method. Bacterial abundance was determined according to standard protocol, by staining cells with 4',6-diamino-2-phenylindole (DAPI) and examining them under an epifluorescence microscope [5]. Bacterial carbon production was measured by the incorporation of ³H-leucine into newly synthesized proteins in the bacterial cells [7]. Bacterial community structure was analyzed using two approaches: (i) by isolation of colony - forming bacteria on ZoBell media and (ii) by culture-independent analysis using the denaturing gradient gel electrophoresis (DGGE) fingerprinting method.

Results and discussion

Elemental analysis of *Aurelia* sp., *Pelagia noctiluca* and *Rhizostoma pulmo* reveals low dry weight specific carbon and nitrogen content, and rather low C/N atomic ratios (3.9 – 4.9). Preliminary results showed variation in protein concentrations of added dead substrate between jellyfish species. Concentrations were twice as high in the experimental bottles with *Pelagia* and *Rhizostoma* compared with *Aurelia*. After 72 hours of incubation, the protein concentrations were reduced in all experimental bottles with the jelly-mixture, and significant bacterial growth with biomass increases was recorded. The initially high concentrations of protein, DOP and orthophosphate in the amended bottles, appear to support microbial mineralizations which consume oxygen and release dissolved inorganic nutrients, mainly ammonium. The rate

of degradation and bacterial growth depends on jellyfish chemical composition as indicated by the ratio of biomass, ammonium and phosphate accumulation of 1:3 between *Aurelia* and *Pelagia*.

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