Deep-Sea Research II 111 (2015) 34–43

Contents lists available at ScienceDirect

Deep-Sea Research II

journal homepage: www.elsevier.com/locate/dsr2

New insights into the abyssal sponge fauna of the Kurile–Kamchatka plain and Trench region (Northwest Pacific)

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ARTICLE INFO

Available online 21 August 2014

Keywords:
Porifera
Benthic environment
Abyssal zone
Species diversity
Distribution
Kurile Islands
Kamchatka
NW Pacific Ocean

ABSTRACT

The under-explored abyssal depths of the Kurile–Kamchatka region have been re-examined during the KuramBio (Kurile–Kamchatka Biodiversity Study) expedition. Combining new KuramBio data with previous expedition data in this region has enhanced our understanding abyssal sponge fauna, in particular, the patchiness, rarity, and exceptional richness of the Cladorhizidae family. In total, 14 sponge species, from 7 genera, in 5 families, within two classes (Demospongiae and Hexactinellida) were collected. Of the 14 species, 29% (4 spp.) have been found previously in this region, 36% (5 spp.) were new to the regional abyssal fauna, and 21% (3 spp.) were new to science. The number of abyssal species in this region has now been increased by 26% (8 spp.) and genera by nearly 15% (2 genera). Rarity is a prominent feature of this abyssal fauna, with more than half of species only found at one station, and 83% (19 spp.) of species found previously in this region were not re-found during KuramBio. Cladorhizid sponges dominate demosponge species and genera richness in the abyssal Kurile–Kamchatka region; accounting for 87% (20 spp.) of all demosponge species, and accounting for over 60% (5 genera) of all demosponge genera. Sponge richness in this region is potentially aided by the productivity of the ocean waters, the geological age of the Pacific Ocean, low population densities, and the varied topographic features (ridges, trenches, and seamounts) found in this region. Unusually, the dominance of demosponges in the Kurile–Kamchatka sponge faunal composition is not replicated in other well-sampled abyssal regions, which tend to be richer in deep-sea hexactinellid fauna. Broad depth, latitudinal and longitudinal ranges in Kurile–Kamchatka abyssal fauna are a key characteristic of this faunal assemblage. Strong abyssal faunal connectivity is found between the Kurile–Kamchatka region and North Pacific abyssal fauna, with weaker faunal connections found with the adjacent semi-enclosed seas of Japan and Okhotsk. The importance of the dominant sub-Polar Gyre currents, the vast area of abyssal plain and similar levels of productivity, are likely to be driving the strong faunal connectivity in the North Pacific. The importance of utilising several forms of sampling equipment has been illustrated in this study, with half of all specimens caught with non-AGT (Agassiz trawl) equipment.

1. Introduction

Chronic under-sampling is evident in all marine taxa that inhabit remote and open ocean regions, and particularly deep-sea habitats at bathyal to hadal depths (e.g. Smith et al., 2006; Webb et al., 2010). The abyssal realm (3000–6000 m depth) is one key region in which considerable research effort is essential in order to fully understand global biodiversity, assess current and future climatological and ecological trends, and implement effective conservation management (Boero and Bonsdorff, 2007; Williams et al., 2010). The North Pacific Ocean is currently under-sampled, with only ~9% of global sponge records known from this region at all depths (OBIS, 2014). In particular, the NW Pacific is considerably under-sampled for sponges at all depths, with less than 1% of global sponge records found in this sector (OBIS, 2014).

Previous benthic sampling in the Kurile–Kamchatka Trench and abyssal plain sector of the NW Pacific focused on the shallow coastal zones of the Kurile Islands and Kamchatka Peninsula under the US Fisheries Steamer Albatross in 1906. This expedition sampled across the North Pacific, with only three stations sampled in the Kurile–Kamchatka region, two on the shelf (~420 m depth) and one on the Kamchatka Peninsula continental slope (~1250 m), with all stations yielding a large number of sponge species; 5 calcareous (4 new to science) and 8 hexactinellid (7 new to science) (Hôzawa, 1918; Okada, 1932). The next, and until recently, last expedition in this sector of the NW Pacific, focused

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http://dx.doi.org/10.1016/j.dsr2.2014.08.010
0967-0645/

on sampling all marine habitats, from shelf to hadal, and was conducted by the R/V *Vityaz* in 1949, 1953 and 1966. Major results from these expeditions included: 154 additional descriptions of sponge species, with 44% (68 spp.) of these species new to science (Koltun, 1955, 1959, 1962, 1966, 1967, 1970); sponges were found to a depth of 8800 m in the Kurile–Kamchatka Trench; a discernible decline in sponge abundance and diversity from the continental slope to the abyssal zone; and it was proposed that hadal sponges were potentially a 'sink population' of abyssal species from this region (Koltun, 1970). Abyssal sampling from these expeditions was sparse due to the immense size of this region, with 22 stations trawled at these depth ranges, and 23 sponge species collected (Koltun, 1970). Of these species, eight are currently considered endemic, and one of the 12 genera represented is considered endemic. Despite under-sampling and the limited types of sampling equipment used in this region, moderate regional richness and endemism of abyssal sponges was found.

The main aim of this study is to investigate and re-assess the abyssal sponge diversity of the Kurile–Kamchatka abyssal plain and trench region. The 2012 KuramBio expedition was the first systematic sampling scheme undertaken in the Kurile–Kamchatka Trench and abyssal plain sector of the NW Pacific region since the *Vityaz* expeditions. Applying modern deep-sea sampling techniques and methods developed under CeDAMar (Census of the Diversity of Abyssal Marine Life), all new data has been analysed, alongside previous data, in order to gain a more comprehensive understanding of Kurile–Kamchatka abyssal sponge faunal richness, abundance, endemism, and distribution patterns.

2. Material and Methods

The sponge material from this study was collected between July and September 2012 in the NW Pacific during the KuramBio expedition utilising the R/V *Sonne*. Sponge specimens were found at nine of the eleven stations sampled (absent from stations 11 and 12). Sponges were collected at depths between 4862 and 5422 m by Agassiz trawl (AGT), Camera-Epibenthic Sledge (C-EBS), box-corer (GKG) and multi-corer (MUC). During this expedition the AGT was deployed twice at each of the 11 stations, except stations 2, 3 and 12, where it was deployed once. The C-EBS was deployed twice at each station, except stations 3 and 12 where it was deployed once. The GKG was deployed twice at each station except station 12, which had one deployment; and the MUC was deployed 3 times at each station, but only once at station 12. The AGT material was separated into major taxonomic groups on the vessel, whereas macrofauna from the other sampling equipment was sorted utilising stereo microscopes at the Zoological Museum of the University of Hamburg. All sponges were fixed either initially in 96% ethanol or re-fixed in 96% ethanol after a 4% formaldehyde preparation for preservation. For the purposes of analysis, epi- and supra-macrofauna fractions of the C-EBS from the same sample were combined.

Sponge taxonomy of the skeletal architecture and spicules was undertaken by dissolving either small parts of the sponge tissue or the entire sponge if it was $< 1\ cm^3$, in nitric acid (following the standard protocol, Boury-Esnault and Rützler, 1997) and mounted on microscopic slides using Euparal for light-microscopic analysis (LM). Measurements of spicules were made using high-resolution light microscope with an ocular micrometre. Spicules were placed on stubs and sputter-coated for scanning electron microscope (SEM) identification. The specimens, SEM stubs, and slides for this study are currently deposited in the Porifera collection of the Forschungsinstitut und Naturmuseum Senckenberg, Frankfurt am Main (SMF).

Analysis of community diversity, similarity and evenness were carried out by the use of PRIMER E v. 6.1.6 (Clarke and Gorley, 2006). To analyse α-diversity, the Shannon–Wiener Index (log e) (Shannon and Weaver, 1949) and Pielou's Evenness (Pielou, 1966) were used. To test for under-sampling during the entire KuramBio expedition, a species accumulation plot was drawn (index: UGE, sample order: 999 permutations, Ugland et al. 2003). Five estimators of species richness were used: Chao 1 and Chao 2 (Chao, 1987), Jacknife 1 and Jacknife 2 (Burnham and Overton, 1979), and Bootstrap (Smith and Belle, 1984).

All KuramBio data and previous abyssal sponge data from the Kurile–Kamchatka plain and trench were analysed to assess regional sponge diversity, endemism, depth distributions, and faunal connectivity. In this publication, the abyssal environment is defined by oceanic floor found at depths between 3000 and 6000 m (e.g. Gage and Tyler, 1991; Smith et al. 2006). The geographical extent of the region under study is defined by the major oceanic floor features (trenches and ridges). The Kurile–Kamchatka Trench defines the north and north-western boundary, the Japan Trench defines the west and south-western boundary, and the eastern and south-eastern boundary is defined by the Emperor Seamounts. All previous data from this study region was collated from both OBIS (2014) and additional publications (Hôzawa, 1918; Okada, 1932; Koltun 1955, 1959, 1962, 1966, 1967, 1970). All sponge taxonomy was checked and updated using WORMS: World Register of Marine Species (2014) for this study.

3. Results

3.1. Sponge abundance and taxonomic composition

In total, 69 sponge specimens were collected from the KuramBio expedition, of which 39 (57%) were of the Demospongiae class and 30 (43%) were of Hexactinellida class (Tables 1 and 2). No calcareous or homoscleromorph sponges were found in the abyssal study region. Taxonomy of the Hexactinellida was difficult as most specimens were small and juvenile. Fourteen species of sponges have been preliminarily identified from the KuramBio material. Eleven species are from the demosponge class and three are hexactinellid species. Demosponges are represented by four genera in two families, whereas Hexactinellids are represented in three genera and in three families. The Cladorhizidae family (37 specimens) dominated the demosponge taxonomic composition, specifically in the genera of *Cladorhiza* (5 spp.) and *Chondrocladia* (4 spp.).

Three species believed to be new to science were found in the *Cladorhiza* and *Chondrocladia* genera, with the former acquiring two new species, and the latter one new species (Table 2). In the non-Cladorhizid demosponges, one species from the Polymastiidae family was found at abyssal depths. Three species have been added to the known species list from this abyssal region: *Chondrocladia* (*Chondrocladia*) *koltuni* Vacelet, 2006, (*Asbestopluma* (*Asbestopluma*) *globularis* Lévi, 1964, and *Cladorhiza mirabilis* (Ridley and Dendy, 1886) (Table 2). Two genera, *Farrea* and *Sphaerotylus*, were also newly added to the known genera of the abyssal NW, previously found at shelf to continental slope depths in the NW Pacific (Okada, 1932; Koltun, 1970).

The greatest number of specimens were found at station 1 (14), with the lowest number of specimens collected at both stations 5 and 6 (2) (Table 1). Demosponges dominated in number of specimens at most stations; however, stations 1 and 10 were found to be dominated by hexactinellid sponge specimens (Fig. 1). The greatest number of species found at any one station during the KuramBio expedition was five, found only at station 2 (Fig. 1). Two stations had 4 spp. (1 and 3), three stations had 3 spp. (7, 9 and 10), and two stations recorded 2 spp. (5 and 6). Demosponge species dominated each station except station 1 in which half the species found were hexactinellid and at station 2, where 40% the species