Basic biology seas, share (Japan) latter genus Pacific includes Cohen (1983). In the Distribution of its Pacific range 2017. The latter species is almost cosmopolitan and is usually easy to identify by its large size. One Pacific flatfish represents a regular catch in deep-sea trawl, longline and trap fisheries and in some areas may occur in considerable amounts (Fitch, Lawen, 1968; Eschmeyer et al., 1983; Cohen, 1980). For example, on the continental slope of the Sea of Okhotsk their biomass is more than 3 tons per km1 of the fish biomass of the predatory flatfishes (Pholis, Espen, 1992). The biology of the species under consideration is poorly studied in comparison with blue hake (S vietrana, 1949; Cohen, 1990). In the literature there are only a few publications describing the structure of the otoliths of Pacific flatfish in connection with the taxonomy of morids (Kume, 1971; Fitch, Baker, 1972), as well as observations from the abalone (Cohen, 1977). A number of papers provide only general information on the spatial and vertical distributions, sizes and age of the species in question. (Shumits, 1957; Fitch, Lawen, 1968; Machak, 1971; Eschmeyer et al., 1983; Allen, Smith, 1988; Cohen et al., 1990; Orlo, Orlo, Almores, 2002, Frey et al., 2007). GOAL The goal of this poster is to present some results of studies performed during the years 1997-2017 in the framework of the initiative project ‘Basinology, micrometeorology, distribution, and biology of morid cods Arctos moridae; Moridae, Gadiformes, Teleostei of the World ocean’ supported by the Russian Foundation for Basic Research Grant 17-04-00131. RESULTS AND DISCUSSION Distribution The structure of Pacific flatfish was described by Cohen et al. (1990) in FAS Species Catalogue (Fig. 1) and recently revisited by Imasato (2010) in IASC Red List of Threatened Species. In the distribution map (Fig. 1) we present, both species come near name using data. The latter map does not display occurrence of the species in the Okhotsk and Bering seas and both maps indicate the occurrence of this species within the entire North Pacific. As our analysis of more than 10,000 records shows (Fig. 3), Pacific flatfish inhabits mostly continental slope from Mexico and Taiwan in the south to the northerly parts of the Bering Sea. The species is very common in the Okhotsk and Bering seas, and in the high seas occur only on seamounts (Emporer seamounts, Hawaiian ridge, seamounts of the Gulf of Alaska, Rogers and Shinkron underwater ridge). Fig. 1. Distribution of Pacific flatfish Arctos moridae (Cohen et al., 1990). Fig. 2. Distribution of Pacific flatfish Arctos moridae (after Imasato et al., 2010). The results obtained (Fig. 5) showed that the species from the Pacific waters of Japan is the most isolated from all others, which may be due to specific habitat conditions. A sample from the Emperor Seamounts also seems to be isolated with partial overlap with samples from southeastern Sakhalin, British Columbia, US West Coast (Fig. 6). Between these and the rest of the species there is a significant geographical distance, which may be due to similar habitat conditions on both coasts. At the same time the analysis of the relationships between the weight and length of otoliths (Fig. 6) shows that the colors of linear and power coefficients of the studied samples are markedly different from each other. Formas of these relationships have the following form (x = weight, y = length, cm, R = correlation coefficient): British Columbia: W = 1.505 (l2.006) * (R = 0.953), US West Coast: W = 1.923 + 0.151 * L (R = 0.849), Southeastern Sakhalin: W = 0.208 + 1.017 * L (R = 0.929), Emperor Seamounts: W = 1.080 + 0.107 * L (R = 0.787), Pacific waters of Japan: W = 3.749 + 0.270 * L (R = 0.954). Thus, the data obtained do not allow to make unambiguous conclusions about the intraspecific relations of A. moridae on the basis of the study of their otoliths. ACKNOWLEDGMENTS The amount of presentation research would not be possible without the assistance of numerous colleagues who provided us with the data on the occurrence, status, tissue, fish samples, and frozen specimens. We would like to thank Horst Frey, M. Feenstra (Japan), Gavin Henke, Maria Surzy, Katrina Temple (Canada), Linny Lundsten, Jeff Krause, Cara Riedelkin, Peter Frey (USA), Janne T. Drage (Norway), Igor Malinov (Russia). We are grateful to ARS, NARCC, BDF, IOS, ODF, SPC for open access to their databases. Special thanks to the Russian Foundation for Basic Research for financial support of the project Grant No. 16-04-00131. Otoliths To study the intraspecific relationships of individuals of A. moridae 704 samples from four different parts of their species’ range were studied (35 otoliths of fish from the waters of the Pacific coast of Honshu, Japan, 24 otoliths of fish from the waters of southeastern Sakhalin, 601 otoliths of fish from US West Coast, 28 otoliths of fish from British Columbia waters and 28 otoliths of fish from waters of the Emperor Seamounts). The total loses and blood loss of the fishes were measured. The length of otoliths was measured using an electronic caliper with 0.01 mm accuracy. The weight of otoliths was determined using electronic scales with 0.001 g accuracy. The data obtained were subjected to statistical analysis by the Principal Components method using Phyllo Stereometrics (PAST ver. 3.14 software; Hammer et al., 2001) using R. Ratios between fish length and of otolith, fish length and otolith weight, fish weight and otolith weight, fish length and otolith length and an otolith weight were used for comparative analysis of samples. Genetic analysis With the development of molecular genetic methods, interest in the study of macro- and microevolution processes in fish has increased significantly, including such deep-sea species, as Arctos moridae (Ozoguro et al., 1995, Rea-Verdier, 2001, 2009; Smith et al., 2011; White et al., 2011). Until now, however, genetic studies of members of the genus have been limited to the North Atlantic (Gardiner et al., 2011). In this study, tissue samples of 186 individuals from 7 samples from the eastern Pacific range were analysed using the COI gene (Table 1). The maximum haplotype diversity (14 haplotypes, not counting the unique one) was observed in the sample from British Columbia waters, which has not yet found any reasonable explanation. The haplotype diversity had a high frequency of occurrence (51.1% for all samples). In addition to this haplotype, considerable frequencies of occurrence were noted for haplotypes 5 (2.8%), 44 (1.4%), 42 (2.7%) and 77 (5.5%). The maximum numbers of unique (rare) haplotypes were found in the southeastern Sakhalin sample (20 individuals), the sample from the Emperor Seamounts (21 individuals). If we consider the distribution of haplotypes on the map of the North Pacific (Fig. 4), it is noteworthy to increase the share of the main haplotype 42 in the direction from north to south. So, its share steadily increased from 10.0% in the Gulf of Alaska to 62.5% in the waters of California, and finally reached 100% in the waters of Baja in 50% in the Pacific waters of Japan. It is also possible to note a high proportion of haplotype 3 of the Asian coast (low share in the Far East waters 2–3%) approx. 14.5%). The COI gene length is 649 bp (GenBank Accession Number: KJ51649). The (17.4%) and its low occurrence off the American coast (0.5%). Table 1. Composition of COI haplotypes in various Pacific flatfish Arctos moridae samples. Table 2. Species composition of parasites found in different Pacific flatfish Arctos moridae samples. Pacific flatfish (Arctos moridae, Moridae, Gadiformes) in the North Pacific: an overview of their distribution, genetic diversity, otoliths, and parasites Alexei M. Orlov 1,2,3, A. Svetlana Yu. Orlova 1, Alexei A. Baitaiulik 1, Ilya G. Gordeev 1,2, Pavel K. Afanasiev 1, Nikolai B. Korostylev 1 1 Russian Federal Research Institute of Fisheries and Oceanography (VNIRO), 17, V. Kosmosstoykaya St., Moscow, 107140, Russia 2 A. N. 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