Aurelia japonica: molecular and chromosomal evidence

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The genus *Aurelia* belongs to the family Ulmaridae, order Semaeostomeae, class Scyphozoa, type Cnidaria (Kramp, 1961). Mayer (1910) recorded 13 species of the genus Aurelia, after which Kramp (1961) mentioned only 7 and Russell (1970) reported only 2: *A. aurita* and *A. limbata*. At the end of the century again one of the species from «Synopsis of the medusae of the world" (Kramp, 1961), namely *A. labiata*, came back (Gershwin, 2001).

Traditionally, the jellyfish *Aurelia aurita* was deemed cosmopolitan species. It was reported in a variety of coastal and shelf marine environments between 70°N and 40°S (Kramp, 1961). However, the molecular genetic approach suggests that *A. aurita* contains 11 cryptic species *A.sp.1 – A.sp.11*. The name *Aurelia aurita* was saved to the initial population described by Linnaeus at the European North coast (Dawson, 2001; Dawson, 2003; Dawson et al., 2005). Kishinouye (1891) described a form of Aurelia from Tokyo Bay as *Aurelia japonica* (Gershwin, 2001). This form of Aurelia was designated *Aurelia* sp. *1* and considered to be endemic to the western North Pacific and, therefore, dispersed globally from Japan (Dawson et al., 2005).

In our previous study, the comparison of structural mesoglea protein mesoglein (Matveev et al., 2007, 2012) and its gene from three habitats White Sea (WsA), Black Sea (BsA), Japonic Sea (JsA) produced clear difference of two Aurelia populations. WsA and BsA belong to the boreal group, while JsA is a distinct group. It appears that the mesoglea protein of Japonic Aurelia has a molecular weight of approximately 53/55 kDa, while the mesoglein mass of *A. aurita* (WsA and BsA) is 47 kDa. 53/55 kDa protein do not react with antibodies against *A. aurita* mesoglein on immunoblots and paraffin sections. Differences in RNA structures of 53/55 kD protein and mesoglein were identified by PCR-analysis. So, the difference between mesoglein is obvious not only at protein level but at the level of RNA as well (Kotova et al., 2015).

Here, we addressed the latter issue by using Bayesian method to reconstruct the phylogenetic relationships among three populations from White, Black and Japonic seas, using partial sequence data from two nuclear genes: 18S and 28S rDNA. The sequences from 20 animals from all habitats were cloned and sequenced. The evolutionary distances were computed using the Kimura 2-parameter method (Kimura, 1980). The Bayesian Markov Chain Monte Carlo analyses was obtained using the MrBayes 3.2.2. For SSU and LSU the K2P substitution model was used. Starting trees were randomly generated. The Markov chain Monte Carlo (MCMC) was 10^6 steps

long and parameters were sampled every 10^3 steps after a burn-in of 10^6 steps. As result the sequence of 18S and 28S rRNA JsA allocated as a separate group. At the same time the sequences of WsA and BsA form the mixed group.

Also we performed 53/55 kDa (or JsA mesoglein) gene cloning. The resulting sequence was submitted to GenBank (accession № KM190145). JsA mesoglein is longer than WsA one (1582 bp versus 1421 bp) and its' calculated M_r is higher (50696.5 Da versus 47223 Da). The absence of 5′ untranslated region in the cloned mesoglein cDNA and presence of methionine at the start of the deduced protein sequence leads to the conclusion that the cDNA sequence is partial though only a small part of mesoglein cDNA remains uncloned. We analyse amino acid mesoglein sequences from different populations. The comparison confirms quite high degree of mesoglein diversity between WsA and JsA.

Karyotypes of Aurelia species from these three populations differ significantly: JsA karyotype has 17 pairs chromosomes (2n=34), while the karyotypes of BsA and WsA are the same and have 19 pairs (2n=38). The similarity of the WsA and BsA karyotypes and the difference of both from JsA karyotype is the serious argument among others for the species of *Aurelia aurita* and *Aurelia japonica* to be distinguished.

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