



# Molecular identification of redfish (genus *Sebastes*) in the White Sea indicates patterns of introgressive hybridisation

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Received: 3 April 2020 / Revised: 3 July 2020 / Accepted: 11 July 2020 / Published online: 27 July 2020  
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## Abstract

The rare occurrence of redfish (genus *Sebastes*) in the White Sea encouraged Rolskii et al. (Polar Biol 43:385–389, 2020) to investigate the species identity of two animals captured near the Sredniy Island at 40 m depth. They reported that their morphological description proved unreliable and that genetic evidence “clearly demonstrated” these redfish belong to *S. norvegicus*. This was inferred using the S7 and the mitochondrial control region genes. However, while their S7 matched one *S. norvegicus* reference sequence, the *S. norvegicus* mitochondrial reference sequences used to infer species identity were previously shown to cluster with *S. mentella*. Therefore, both of their redfish samples belong to a *S. norvegicus* × *S. mentella* (deep-pelagic) hybrid which presents an interesting perspective into the complex species dynamics in this group.

**Keywords** *Sebastes* · redfish · hybridisation · White Sea

North Atlantic (NA) *Sebastes* are remarkably similar in external appearance and the absence of clear diagnostic morphological characters can obscure an accurate species assessment whereby phenotypic plasticity and hybridisation has blurred morphological limits of detection (Pampoulie and Daniélsdóttir 2008; Christensen et al. 2018). Therefore, it is reasonable to expect that misidentification occurs regularly and the resulting conclusions are hindered by taxonomic bias. Artamonova et al. (2013) documented some of the earliest mitochondrial DNA control region (or D-loop) sequence records for NA *Sebastes* from a small collection of samples. They characterised species, and subsequently sequence records, according to geographic distribution, morphology and allozyme analysis. However, they were

unable to unambiguously separate *S. mentella* from *S. norvegicus* based on their allozyme analysis and morphological assessments have been known to be ambiguous (Pampoulie and Daniélsdóttir 2008). Later, Shum et al. (2015) greatly expanded the mitochondrial D-loop sequence record by investigating the phylogeographic distribution of *S. mentella* in the NA, and screened over 250 samples generating 55 mitochondrial D-loop haplotypes as well as reference sequences (verified using microsatellite & mitochondrial DNA) for *S. viviparus*, *S. fasciatus* and *S. norvegicus*. In a following seafood authentication study, Shum et al. (2017) used all publicly available NA *Sebastes* mitochondrial D-loop sequences to identify redfish marketed in Europe and observed a common pattern: all previously published *S. norvegicus* sequences (Hyde and Vetter 2007; Artamonova et al. 2013) consistently clustered within *S. mentella*. They concluded that morphological misidentification may have led to inaccurate reference sequences deposited in public databases.

A prerequisite for the molecular identification of species using a DNA barcode is the generation of a reliable database containing all available reference sequences attributed to accurately identified taxonomic species (Hebert et al. 2003). Rolskii and colleagues noted the inadequacy of using a universal barcode, such as the cytochrome oxidase I, as it presents a challenge to discriminate between recently diverged species (Steinke et al. 2009), and this was

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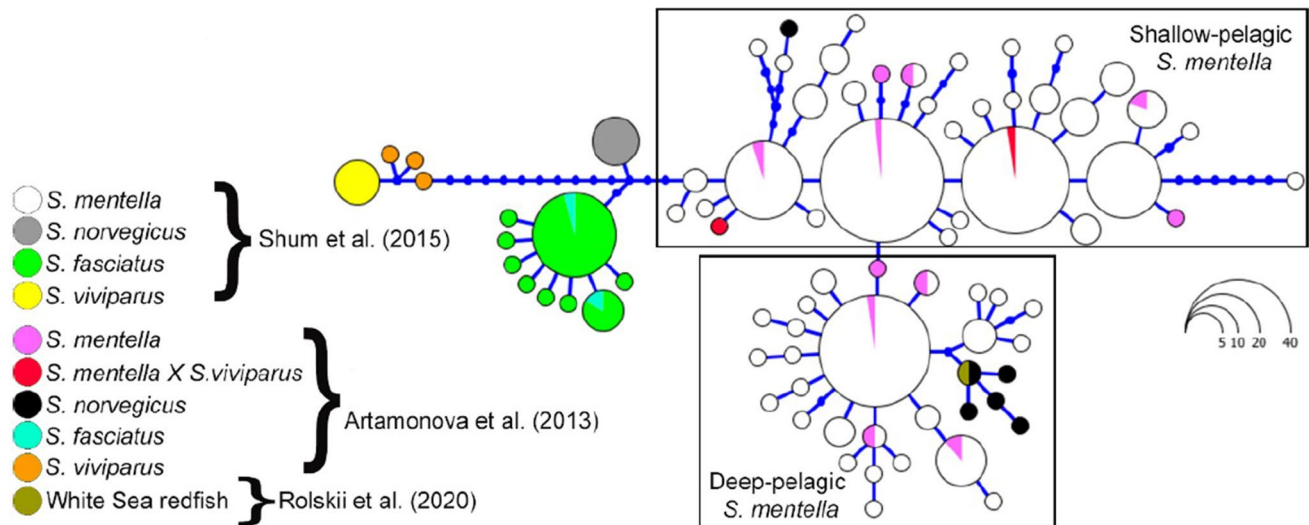
This is a comment to Rolskii, A.Y., Artamonova, V.S. and Makhrov, A.A., 2020. Molecular identification of golden redfish (*Sebastes norvegicus*) in the White Sea. Polar Biology, pp.1-5. DOI: <https://doi.org/10.1007/s00300-020-02629-y>

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**Fig. 1** Haplotype genealogy of North Atlantic *Sebastes* spp. from Shum et al. (2015) using mitochondrial DNA control region. Data from Artamonova et al. (2013) is visualised among reference haplo-

types where their *S. norvegicus* haplotypes cluster with shallow and deep-pelagic *S. mentella*. White Sea redfish collected by Rolskii et al. (2020) grouped with deep-pelagic *S. mentella*

recently corroborated for NA *Sebastes* species (Shum et al. 2017). To identify the two redfish individuals caught in the White Sea, Rolskii et al. (2020) shifted their attention to using a more informative mitochondrial marker and found that the two samples collected had identical haplotypes of the mitochondrial D-loop and were in complete agreement with the D-loop haplotype ‘MR1’ previously identified by Artamonova et al. (2013) as *S. norvegicus*. However, this haplotype unambiguously clustered with *S. mentella* (Shum et al. 2017), which suggested taxonomic misidentification prior to genetic analyses. To unravel the correct identity of the White Sea redfish samples collected by Rolskii et al. (2020), we present a network analysis with appropriate reference sequences and include Artamonova et al. (2013) D-loop data using a maximum likelihood phylogenetic framework (hapview, Salzburger et al. 2011). We confirmed that the White Sea redfish samples possessed a mitochondrial D-loop sequence identical to the MR1 haplotype which we previously identified as *S. mentella* (Fig. 1; Shum et al. 2015). Therefore, based on Rolskii et al. (2020) assessment of the S7 and evidence from the mitochondrial DNA control region based on Shum et al. (2015), the correct species identification is that of a *S. norvegicus* × deep-pelagic *S. mentella* hybrid.

Genetic data are frequently used to delimit species because traditional methods used to identify species are constrained by the exclusive reliance on morphological characters which can underestimate diversity by failing to detect cryptic taxa. Therefore, a critical review of all available data will have the greatest resolution, particularly when hybridisation is widespread, species are morphologically very similar and divergence occurred more recently (Pampoulie and

Daniélsdóttir 2008; Shum et al. 2015). Misidentification of *Sebastes* spp. remains a challenge for scientists, and there is, therefore, an urgent need to standardise the collection of new samples and deposition of reference sequences in public databases and ideally expand on current knowledge on this lineage using a more exhaustive genomic coverage.

The occurrence of hybrid redfish in the White Sea presents an interesting scenario for North Atlantic *Sebastes*. Rolskii et al. (2020) indicated that the ambiguous meristic characters could be attributed to local conditions or a result from biological isolation of the White Sea due to differences in diagnostic features and depth distribution that are typical of *S. norvegicus*. Interestingly, we revealed the identity of *S. norvegicus* × deep-pelagic *S. mentella* hybrids, which allows opportunities to consider novel explanations for ecomorphological traits observed in these redfish in such an unusual environment. Hybridisation is known to act as a generative force, facilitating adaptive evolution via introgression or promoting diversification through hybrid speciation (Mallet 2007). Given the substantial impact of hybridisation in this genus (Saha et al. 2017; Schwenke et al. 2018), it would seem prudent not to ignore such remarkable findings.

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