The complete mitochondrial genome of the broad-nosed pipefish *Syngnathus typhle* (Linnaeus, 1758)

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The broad-nosed pipefish *Syngnathus typhle* (Linnaeus, 1758) occurs in Eastern Atlantic: Norway, Baltic Sea and the British Isles to Morocco. Usually, it is found along the coasts and estuaries at a temperature range from 8°C to 24°C (Dawson 1990). Spawns in summer (Muus & Nielsen 1999), the male carries the eggs in a brood pouch that is found under the tail (Breder & Rosen 1966). Its maximum length reached 35 cm in TL. The snout is compressed and taller than the eye diameter, and anterior trunk rings not fused ventrally.

Samples of the broad-nosed pipefish were live transported from Shanghai Changfeng Ocean World Aquarium (belonging to Merlin Entertainment Group, United Kingdom) and the muscle was preserved in pure alcohol. The specimens were stored in Fish Specimens Museum in Shanghai Ocean University, the accession number is SHOU20150044003. Then, their genomic DNA was extracted from muscle by using Genomic DNA Purification Kit (GeneMark, Taichung, Taiwan). The methods for genomic DNA extraction, library construction and next-generation sequencing were followed by previous publication (Shen et al. 2014). The raw next-generation sequencing reads were de novo assembled by commercial software (Geneious V8, Auckland, New Zealand) to produce a single, circular form of complete mitogenome with about an average 338.4 X coverage (13,496 out of 9,637,558, 0.0014%). The complete mitochondrial genome of the broad-nosed pipefish was 16,488 bp in size (GenBank: KU925872), includes 13 protein-coding genes, 22 transfer RNAs and two ribosomal RNAs genes. The overall base composition of the broad-nosed pipefish is 27.72% for A, 27.81% for C, 16.53% for G, 27.94% for T and show 87% identities to *Syngnathus schlegeli* (GenBank: AP012318). The complete mitogenome of the broad-nosed pipefish, provides essential and important DNA molecular data for further phylogeography and evolutionary analysis for seahorse family.
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Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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Figure 1. Neighbour-joining (NJ) tree of 12 species complete mitochondrial genome sequence. The phylogenetic relationships of broad-nosed pipefish show 87% identities to *Syngnathus schlegelii* using *Aulichthys japonicus* as an outgroup.