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Muscle transcriptome profiling of *Kaupichthys hyoproroides*

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A high ecological diversity and a great number of species organized in 20 families define the Anguilliformes. Recent research in eels mainly focuses on the critically endangered freshwater eel *Anguilla anguilla* investigating survival risks and stress response due to anthropogenic introduced water pollution (mainly pesticides) or in systematics in general. Little is known about other non-migratory eel species inhabiting coral reefs, and nothing in regards to their genomics. *K. hyoproroides* is an Atlantic circum-tropical species and some authors proposed to place it in synonymy with Indo-Pacific species *Kaupichthys diodontus*. Here we present the first high throughout transcriptome data of this circum-tropical marine living False Moray, *Kaupichthys hyoproroides*. Two individual high quality muscle RNA seq data sets were obtained using Illumina Hi-seq, 80-bp paired endreads. De novo assembly with two main *de novo* assembly programs has highlighted the assembly statistics in these two datasets. Comparative transcriptomic analyses between these two individuals have led to identification of similarly expressed genes (essential as calibration for future studies). Furthermore, comparisons at the order level with existing transcriptome data and EST's of *A. anguilla* and *A. japonica* has shed light on order shared genes. Besides, these first annotated transcriptomes enable subsequent qualitative and quantitative studies in stress response and local adaptation using *K. hyoproroides* as ecologically important fish for anthropogenic reef destruction.

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