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The Complete Genome Sequence of *Lythrypnus dalli*, the Bluebanded Goby

Kuk-Jeong Chin[1], Matthew S. Grober[1], Stacy Pirro

[1] Biology, Georgia State University

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The Bluebanded goby (*Lythrypnus dalli*) is a small, highly social marine goby. We present the whole genome sequence of this species. A total of 118,266,160 paired end reads consisting of 17.9G bases were obtained by sequencing tissue from a single individual. The reads were assembled by a *de novo* method followed by alignment to related species. The raw and assembled data is publicly available via Genbank: Sequence Read Archive (SRR5170315) and Assembly (GCA_011763505).

Introduction

The Bluebanded goby (*Lythrypnus dalli*) is a small [standard length 18–45mm], highly social marine goby that lives on rocky reefs in the Pacific Ocean, from Morro Bay, California to the Galapagos Islands, Ecuador. Mixed-sex social groups vary from small and isolated (3–10 fish) to aggregations of 120 fish/m2 and are usually comprised of harems with a dominant, territorial male and multiple subordinate females. Under natural conditions, *L. dalli* primarily undergoes socially regulated protogynous sex change (Black et al. 2005), and this could occur when a male is eliminated from his territory by predation or when multiple females converge on a territory that is not occupied by a male. In the laboratory, changes in social status can induce both protogynous and protandrous sex change in *L. dalli* (i.e., bidirectional sex change; Rodgers, Earley, and Grober 2007). Bluebanded gobies exhibit a remarkable lifelong plasticity in the social regulation of sexual phenotype and a complete genome sequence for this species will greatly assist with our understanding of the evolution and development of vertebrate sexual plasticity, as well as the genetic basis of the regulation of social behavior in vertebrates.

Methods

A single wild-caught individual Goby was used for this study. The specimen was collected off the coast of Catalina Island, CA, during the months of June–July of 2012 by SCUBA diving and using hand nets (permit numbers SC-10676 and SC-11879). After capture, the fish were kept in 2 l plastic Nalgene bottles, brought to the boat and then placed in a large bucket for transport to a laboratory at the Wrigley Institute for Environmental Studies. Fish were housed in 60 X 94 cm2 aquaria with continuous seawater and exposed to natural ambient light cycles. The specimen was euthanized in tricaine methanosulfate (MS-222; 1.0 mg/100 ml seawater).

All applicable international, national, and/or institutional guidelines for the care and use of animals were followed. All procedures performed were in accordance with the ethical standards of Georgia State University and the University of Southern California (IACUC protocol #A13023).

DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard process. A paired-end sequencing library was constructed using the Illumina TruSeq kit, according to the manufacturer's instructions. The library was sequenced on an Illumina Hi-Seq platform in paired-end, 2 × 150bp format. The resulting fastq files were trimmed of adapter/primer sequence and low-quality regions with Trimmomatic v0.33 (Bolger, Lohse, and Usadel 2014). The trimmed sequence was assembled by SPAdes v2.5 (Bankevich et al. 2012) followed by a finishing step using RagTag v1.0.0 (Alonge 2020) to make additional contig joins based on conserved regions in related fish species in the Gobiidae family: *Periophthalmus magnuspinnatus* (GCA_009829135), *Periophthalmus magnuspinnatus* (GCA_009829125), *Neogobius melanostomus* (GCA_007210695), *Lesueurigobius sanzi* (GCA_900303255), *Boleophthalmus pectinirostris* (GCA_000788275), *Periophthalmus magnuspinnatus* (GCA_000787105), *Periophthalmodon schlosseri* (GCA_000787095), and *Scartelaos histophorus* (GCA_000787155). Default parameters were used for all assembly steps.

Results

The genome assembly yielded a total sequence length of 830,691,505 bp over 570,462 scaffolds with an N50 of 2,577,483.

Data availability

Raw and assembled data is publicly available via GenBank:

Raw genome data:

https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR5170315

Assembled genome:

https://www.ncbi.nlm.nih.gov/assembly/GCA_011763505

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