

Transcriptome sequencing of 19 diverse species of choanoflagellates

Daniel Richter, Parinaz Fozouni, Michael Eisen, Nicole King

Abstract

The origin of animals, which occurred over 600 million years ago, left no evidence in the fossil record. To trace the earliest events in animal prehistory, we compare extant animals to their closest living relatives, the choanoflagellates, in order to reconstruct the gene content of their last common ancestor and how it evolved on the stem lineage leading to animals. In this project, we increase the accuracy of ancestral animal and choanoflagellate gene content reconstructions by sequencing the transcriptomes of 19 species of choanoflagellates selected for their phylogenetic diversity.

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Collection



1. [Modified Qiagen gel extraction with MinElute spin column.](#)

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2. [Modified Qiagen PCR purification \(no gel extraction\) with MinElute spin column.](#)

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3. [Phenol/chloroform genomic DNA extraction-1.5 ml Eppendorf tube.](#)

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4. [Lysis Buffer for Phenol/ chloroform genomic DNA extraction \(makes 20 mL of buffer\)](#)

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5. [RNA clean-up by phenol:chloroform](#)

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6. RNAqueous with TURBO DNA-free and SUPERase-In

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7. RNAqueous with No DNase, DNA Removal by Acid Phenol:Chloroform

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8. RNAqueous with DNase Clean-up by Phenol:Chloroform

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9. TruSeq RNA Preparation with Modification for Four Rounds of Poly-A Selection

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