The genome of the chiton Acanthopleura granulata: a model system for studying molluscan biomineralization

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BIOMINERALIZATION OF CHITONS (POLYPLACHOPHORA)

CHITONS

Marine molluscs that graze on algae, chitons are in clade Aculifera, the sister clade to all other molluscs



SHELL VALVES

Eight overlapping aragonite plates articulate, granting flexibility. Plates are made entirely of aragonite¹





Sensory organs contained within channels in the shell valves²

RADULA

Teeth transition from protein to ferric hydroxide and then magnetite

SCLERITES

Protective structures cover the chiton girdle, varying in form by species





SEQUENCING

- High molecular weight DNA extracted via CTAB-phenol-chloroform and cleaned with magnetic beads
- Short reads: one lane of Illumina HiSeq X (2 x 150 bp paired-end reads)
- Long reads: four flowcells on Oxford Nanopore GridION (two with LSK-108 and two RevD with LSK-109), trimmed with PoreChop³

	MaSURCa	MaSURCa + Redundans	+ BioNano SAPHYR
N50	1,043,656	1,184,807	23.921 Mbp
L50	156	129	9
# contigs (scaffolds)	3,242	1,235	(84)
Longest contig	5,641,081	5,641,081	5,641,081
BUSCO (complete)	96.2	96.0	96.2
CEGMA (complete/partial)	66.3 / 93.5	66.3 / 93.5	59.7 / 93.9
Estimated genome size	622,141,316	560,941,252	605.980 Mbp

CHITON GENOME



SEEKING GENES OF INTEREST

Molluscan biomineralization toolkit: Shell forming proteins including nacrein, mucins, metalloproteases



Iron metabolism and transport: Ferritin, carbonic anhydrases, iron permeases, pH regulatory proteins



ASSEMBLY

- Hybrid assembly with MaSuRCA^{4/5}, which assembles short reads into super-reads that are then scaffolded to long-reads
- Redundans used to filter and remove heterozygosity





Blob-plot of sequence + optical mapping



GC content

Transcriptomes generated from radula, foot, girdle, gonad, and ctenidia for annotation with the MAKER⁶ pipeline

FUTURE WORK

- Comparisons between chiton genes of interest and other molluscs/organisms can reveal innovations of chiton mineralization
- Differential gene expression among four regions of iron mineralization to identify genetic mechanisms of iron deposition



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Assembly combined with one run of BioNano

SAPHYR optical mapping

Training sets generated from CEGMA output and initial runs of *ab initio*

MAKER given to SNAP and AUGUSTUS for gene prediction

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