Identify all datasets that characterize DNA methylation in genus Mytilus and genus Crassostrea

Available DNA methylation datasets are limited to 10 studies of genus Crassostrea, with no characterization of genus Mytilus.

Abstract

DNA methylation datasets are available only for the oyster genus Crassostrea. Ten studies report data on Crassostrea species—nine on Crassostrea gigas and two on Crassostrea virginica (one study covers both species). The datasets rely primarily on whole genome bisulfite sequencing (seven studies) and reduced representation bisulfite sequencing (three studies, including two epiGBS variants); one study additionally combines a targeted bisulfite approach with WGBS. Tissue sources include gill, muscle, gonads, gametes, larvae, and spat. Several studies report genome-wide, single-base resolution data and note global methylation levels in the range of 14–18%, with patterns of gene-body methylation that correlate positively with gene expression. No studies were found that characterize DNA methylation in the genus Mytilus.

Paper search

Using your research question "Identify all datasets that characterize DNA methylation in genus Mytilus and genus Crassostrea", we searched across over 126 million academic papers from the Semantic Scholar corpus. We retrieved the 50 papers most relevant to the query.

Screening

We screened in sources that met these criteria:

- **Species Focus**: Does the study examine DNA methylation patterns in Mytilus or Crassostrea species?
- **Primary Research**: Does the study present original, primary DNA methylation data?
- **Methodology**: Does the study use validated DNA methylation detection methods (e.g., bisulfite sequencing, methylation-specific PCR, WGBS)?
- **Sample Type**: Does the study examine DNA methylation in organism samples (rather than cell lines)?
- **Epigenetic Focus**: Does the study include DNA methylation data (not exclusively other epigenetic modifications)?
- **Species Exclusivity**: Does the study include data from Mytilus or Crassostrea (not exclusively other bivalve species)?
- **Data Validity**: Does the study present actual methylation data using valid detection methods?

We considered all screening questions together and made a holistic judgement about whether to screen in each paper.

Data extraction

We asked a large language model to extract each data column below from each paper. We gave the model the extraction instructions shown below for each column.

- **Species and Genus Studied**:

  Identify the specific species and genus of Mytilus or Crassostrea examined in the study.

- Look in the title, abstract, and methods section
- Record the full scientific name (genus and species)
- If multiple species are studied, list all of them
- If no Mytilus or Crassostrea species are studied, mark as "Not applicable" Example format: Crassostrea virginica, Crassostrea gigas

- **DNA Methylation Methodology**:

  Identify and describe the specific DNA methylation analysis techniques used in the study.

- Look in the methods section for detailed methodology
- Record the full name of the technique (e.g., whole genome bisulfite sequencing, reduced representation bisulfite sequencing)
- Include any specific details about the technique's implementation
- If multiple techniques were used, list all of them Example format: Whole genome bisulfite sequencing (WGBS), with single-base resolution mapping

- **Methylation Patterns Characterized**:

  Extract key findings about DNA methylation patterns in the studied organism.

- Look in results and discussion sections
- Record specific observations about:
  - Global methylation levels
  - Methylation distribution across genome regions
  - Relationship between methylation and gene expression
- Be precise and use direct quotes or numerical data where possible Example format: "Majority of methylated sites mapped to intragenic regions, with methylated genes associated with high transcript abundance"

- **Biological Context of Methylation**:

  Identify the specific biological context or research focus of the methylation analysis.

- Look in introduction, methods, and discussion sections
- Record the primary biological process or research question being investigated
- Include specific contexts like sex determination, infection response, developmental processes Example format: "Sex reversal in Pacific oysters" or "Response to Perkinsus marinus infection"

- **Sample Size and Tissue Type**:

  Extract information about the study's sample size and tissue sources.

- Look in methods section for sample details
- Record total number of samples/individuals
- Specify tissue types analyzed (e.g., gonadal tissue, whole organism)
- Note any grouping or experimental conditions Example format: "n = 40 oysters, gonadal tissue from female and male individuals"

Results

Characteristics of Included Studies

Study	Species	Sequencing Method	Tissue Type	Coverage/Resolution	Full text retrieved
Tan et al., 2022	Crassostrea gigas	Whole genome bisulfite sequencing (WGBS), single-base resolution	No mention found	Genome-wide, single-base	No
Gavery and Roberts, 2013	Crassostrea gigas	Reduced representation bisulfite sequencing (RRBS), methylation enrichment	Gill tissue	More than 2.5 million cytosine-phosphate-guanine (CpG) loci, high resolution	Yes
Olson and Roberts, 2014	Crassostrea gigas	Whole genome bisulfite sequencing (WGBS)	Male gamete tissue	7.6 million CpG dinucleotides, single-base	Yes
Olson and Roberts, 2015	Crassostrea gigas	Whole genome bisulfite sequencing (WGBS)	Sperm and larvae	Single-base pair resolution	No
Rondon et al., 2017	Crassostrea gigas	Whole genome bisulfite sequencing (WGBS), targeted bisulfite sequencing (T-BS-Seq)	Whole spat tissue	Single nucleotide resolution	Yes
Li et al., 2022	Crassostrea gigas	Whole genome bisulfite sequencing (WGBS)	Muscle tissue	Single-base, genome-wide	Yes
Johnson and Kelly, 2020	Crassostrea virginica, Crassostrea gigas	Reduced representation bisulfite sequencing (RRBS, epiGBS variant)	Gill tissue	Locus-specific, genome-wide	Yes
Venkataraman et al., 2022	Crassostrea gigas	Whole genome bisulfite sequencing (WGBS)	Gonadal tissue (female)	Genome-wide, single-base	Yes

Study	Species	Sequencing Method	Tissue Type	Coverage/Resolution	Full text retrieved
Johnson et al., 2020	Crassostrea virginica	Reduced representation bisulfite sequencing (RRBS, epiGBS variant)	Gill tissue	Locus-specific, genome-wide	Yes
Sun et al., 2024	Crassostrea gigas	Whole genome bisulfite sequencing (WGBS)	Gonadal tissue	Single-base, genome-wide	No

Species:

- Crassostrea gigas:Nine studies included this species.
- Crassostrea virginica:Two studies included this species; one study included both Crassostrea gigas and Crassostrea virginica.
- Mytilus:We did not identify any datasets for genus Mytilus in the included studies.

Sequencing Method:

- Whole genome bisulfite sequencing (WGBS):Used in seven studies.
- Reduced representation bisulfite sequencing (RRBS):Used in three studies, with two using the epiGBS variant.
- Targeted bisulfite sequencing (T-BS-Seq):Used in one study, in combination with WGBS.
- Other methods:We did not find mention of other sequencing methods.

Tissue Type:

- Gill tissue:Studied in three studies.
- Gonadal tissue (female or unspecified):Studied in two studies.
- Muscle tissue, sperm, larvae, male gamete tissue, and spat:Each studied in one study.
- No mention found:One study did not mention tissue type.
- Multiple tissue types:Some studies included more than one tissue type.

Coverage/Resolution:

- Genome-wide, single-base resolution:Reported in four studies.
- Single-base resolution (not explicitly stated as genome-wide):Reported in three studies.
- Locus-specific, genome-wide coverage:Reported in two studies.
- High resolution (without further detail):Reported in one study.
- No mention of missing coverage/resolution information:All studies provided some detail, but the level of detail varied.

Thematic Analysis

Technical Approaches to Methylation Profiling

Study	Analysis Method	Data Type	Key Features	Technical Specifications
Tan et al., 2022	Whole genome bisulfite sequencing (WGBS)	Genome-wide methylation	Single-base resolution, comparative analysis	Illumina platform, WGBS
Gavery and Roberts, 2013	Reduced representation bisulfite sequencing (RRBS), methylation enrichment	CpG-rich regions	MethylMiner Kit, EpiTect Bisulfite Kit, Illumina HiSeq 2000	BSMAP mapping, more than 2.5 million CpG loci
Olson and Roberts, 2014	Whole genome bisulfite sequencing (WGBS)	Genome-wide methylation	High molecular weight DNA, single cell type	EpiTect Bisulfite Kit, Illumina HiSeq 2000, BSMAP
Olson and Roberts, 2015	Whole genome bisulfite sequencing (WGBS)	Genome-wide methylation	Single-base pair resolution, developmental stages	No mention found
Rondon et al., 2017	Whole genome bisulfite sequencing (WGBS), targeted bisulfite sequencing (T-BS-Seq)	Genome-wide and targeted	Single nucleotide resolution, validation of differentially methylated regions (DMRs)	WGBS, nested polymerase chain reaction (PCR) for T-BS-Seq
Li et al., 2022	Whole genome bisulfite sequencing (WGBS)	Genome-wide methylation	DNA shearing, bisulfite conversion, Illumina Hiseq	fastp, bsmap, BSeQC, MOABS (bioinformatics tools for methylation analysis)
Johnson and Kelly, 2020	Reduced representation bisulfite sequencing (RRBS, epiGBS variant)	Locus-specific methylation	Double enzyme digestion, Illumina sequencing	Trim Galore!, Bismark, MethylKit (bioinformatics tools)
Venkataraman et al., 2022	Whole genome bisulfite sequencing (WGBS)	Genome-wide methylation	Zymo-Seq WGBS Library Kit, NovaSeq	Bismark, methylKit
Johnson et al., 2020	Reduced representation bisulfite sequencing (RRBS, epiGBS variant)	Locus-specific methylation	epiGBS library, Trimmomatic, Bismark	MethylKit for DMR analysis
Sun et al., 2024	Whole genome bisulfite sequencing (WGBS)	Genome-wide methylation	Single-base resolution, sex reversal context	No mention found

Analysis Methods:

- Whole genome bisulfite sequencing (WGBS):Used in seven studies for genome-wide methylation profiling.
- Reduced representation bisulfite sequencing (RRBS):Used in three studies, with two using the epiGBS variant for locus-specific methylation.
- Methylation enrichment and targeted bisulfite sequencing (T-BS-Seq):Each used in one study.
- Multiple methods:Some studies used more than one method.

Data Type:

- Genome-wide methylation:Analyzed in seven studies.
- Locus-specific methylation:Analyzed in two studies.
- CpG-rich regions:Analyzed in one study.
- Targeted methylation analysis:Performed in one study.
- Multiple data types:Some studies included more than one data type.

Technical Specifications:

- Illumina sequencing platforms (HiSeq, Hiseq, or unspecified):Used in five studies.
- NovaSeq:Used in one study.
- No mention found:Two studies did not mention the sequencing platform.
- Bioinformatics tools:BSMAP, Bismark, and MethylKit were each used in three studies. Other tools (fastp, BSeQC, MOABS, Trim Galore!, Trimmomatic) were each used in one study.
- No mention found:Two studies did not mention technical specifications.

Summary of Technical Approaches:

- Predominant approach:Most studies used whole genome bisulfite sequencing (WGBS) for genome-wide methylation profiling.
- Sequencing platforms:Illumina platforms were most common.
- Bioinformatics tools:BSMAP, Bismark, and MethylKit were frequently used.
- Less common approaches:Reduced representation bisulfite sequencing (RRBS) and locus-specific methods were less common.
- Technical details:We did not find mention of technical details for two studies.

Biological Applications and Contexts

Study	Study Focus	Biological Process	Key Findings	Dataset Application
Tan et al., 2022	Growth regulation	Growth and shell color	Genic methylation hotspots, positive correlation with gene expression	Comparative methylome of fast/slow-growing strains
Gavery and Roberts, 2013	Gene regulation	Gene expression	Intragenic methylation, high transcript abundance, low expression variation	Genome-wide methylation and expression mapping

Study	Study Focus	Biological Process	Key Findings	Dataset Application
Olson and Roberts, 2014	Male gamete methylation	Spermatogenesis	15% CpG methylation, positive association with expression	Methylome of male gametes
Olson and Roberts, 2015	Developmental inheritance	Developmental processes	15-18% methylation, inheritance of patterns, transposable element (TE) concentration	Sperm and larval methylomes
Rondon et al., 2017	Environmental epigenetics	Parental diuron exposure	16.6% CpG methylation, differentially methylated regions (DMRs) in genes, weak expression correlation	Spat methylome post-exposure
Li et al., 2022	Inheritance, sex differences	Intergenerational transfer, sexual differentiation	Family-conserved patterns, sex-specific DMRs, gene-body methylation	Muscle methylome, diploid/triploid
Johnson and Kelly, 2020	Population divergence	Adaptation to environmental stress	14% methylation, gene body DMRs, population-specific profiles	Gill methylome across estuaries
Venkataraman et al., 2022	Ocean acidification	Gonad development under low pH	Differentially methylated loci (DML) in genic regions, expression variability, stress response	Gonad methylome under pH stress
Johnson et al., 2020	Infection response	Perkinsus marinus infection	Gene body methylation, immune genes, expression stability	Gill methylome by infection intensity
Sun et al., 2024	Sex reversal	Sex determination and reversal	Methylation remodeling, DNA methylase upregulation, heat shock protein (Hsp) genes	Gonadal methylome during sex reversal

Study Focus:

- Environmental response:Three studies focused on environmental response (Rondon et al., 2017; Venkataraman et al., 2022; Johnson et al., 2020).
- Inheritance or developmental processes:Two studies (Olson and Roberts, 2015; Li et al., 2022).
- Sex differences or sex reversal:Two studies (Li et al., 2022; Sun et al., 2024).
- Other focuses:One study each on growth regulation (Tan et al., 2022), gene regulation (Gavery and Roberts, 2013), reproduction/gamete methylation (Olson and Roberts, 2014), and population divergence/adaptation (Johnson and Kelly, 2020).

Biological Process:

- Environmental or stress-related processes:Three studies addressed these.
- Inheritance/developmental processes:Two studies.
- Sex differentiation/reversal and reproduction/gamete biology:Two studies each.
- Other processes:One study each on growth and shell color, gene expression regulation, and population adaptation.

Key Findings:

- Global methylation levels:Four studies reported global methylation levels (14-18%) (Olson and Roberts, 2014; Olson and Roberts, 2015; Rondon et al., 2017; Johnson and Kelly, 2020).
- Gene-body methylation or differentially methylated regions (DMRs):Four studies (Li et al., 2022; Johnson and Kelly, 2020; Johnson et al., 2020; Rondon et al., 2017).
- Positive correlation between methylation and gene expression:Two studies (Tan et al., 2022; Olson and Roberts, 2014).
- Inheritance of methylation patterns:Two studies (Olson and Roberts, 2015; Li et al., 2022).
- Sex-specific DMRs or sex-related methylation:Two studies (Li et al., 2022; Sun et al., 2024).
- Environmental or stress response:Three studies (Rondon et al., 2017; Venkataraman et al., 2022; Johnson et al., 2020).
- Expression variability or stability:Three studies (Gavery and Roberts, 2013; Venkataraman et al., 2022; Johnson et al., 2020).
- Other findings:Single studies reported transposable element (TE) concentration (Olson and Roberts, 2015), immune gene methylation (Johnson et al., 2020), methylation remodeling or DNA methylase upregulation (Sun et al., 2024), and heat shock protein (Hsp) gene involvement (Sun et al., 2024).

Cross-Species Methylation Patterns

- Mytilus datasets:No datasets characterizing DNA methylation in genus Mytilus were identified in the included studies.
- Crassostrea datasets:All included datasets are from Crassostrea (gigas and virginica).
- Methylation patterns within Crassostrea:
  - Global methylation:Four studies reported low global methylation (14–18% CpG methylation).
  - Intragenic methylation:Predominance of methylation within gene bodies was reported.
  - Gene body methylation and gene expression:A positive association was reported in multiple studies.
  - Consistency across tissues and contexts:These patterns were reported across gill, muscle, gonad, sperm, and larvae, and in contexts including development, environmental stress, infection, and sex reversal.
- Generality:The lack of Mytilus datasets limits the ability to generalize findings across bivalve genera. The consistency of methylation patterns within Crassostrea, as reported in the included studies, suggests conserved

epigenetic regulation in this genus.

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