Single molecule-level detection and long read-based phasing of epigenetic variations in bacterial methylomes

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Beyond its role in host defense, bacterial DNA methylation also plays important roles in the regulation of gene expression, virulence and antibiotic resistance. Bacterial cells in a clonal population can generate epigenetic heterogeneity to increase population-level phenotypic plasticity. Single molecule, real-time (SMRT) sequencing enables the detection of N6-methyladenine and N4-methylcytosine, two major types of DNA modifications comprising the bacterial methylome. However, existing SMRT sequencing-based methods for studying bacterial methylomes rely on a population-level consensus that lacks the single-cell resolution required to observe epigenetic heterogeneity. Here, we present SMALR (single-molecule modification analysis of long reads), a novel framework for single molecule-level detection and phasing of DNA methylation. Using seven bacterial strains, we show that SMALR yields significantly improved resolution and reveals distinct types of epigenetic heterogeneity. SMALR is a powerful new tool that enables de novo detection of epigenetic heterogeneity and empowers investigation of its functions in bacterial populations.
n the bacterial kingdom, DNA methylation is catalysed by three families of DNA methyltransferases (MTases) that typically add methyl groups to DNA bases in a sequence-specific manner. One family of MTases attaches methyl groups to adenine residues, creating N6-methyladenine (6mA), whereas the other two families introduce methyl groups to cytosine residues to create either N4-methylcytosine (4mC) or 5-methylcytosine (5mC). Many bacterial DNA MTases act in concert with and are encoded in close proximity to cognate restriction endonucleases (REs); the MTase protects DNA from digestion by the RE with which it forms a restriction-modification (R-M) system. R-M systems are generally believed to have an ‘immune’ function, protecting cells from invading foreign DNA. They are also studied as selfish elements that protect themselves against removal through the post-segregational killing of new progeny by pre-existing and stable RE molecules. In addition, so-called ‘orphan’ MTases, which occur in the genome without an associated RE, have been found to play important regulatory roles in global gene expression and other biological processes. Furthermore, the ability of MTases to target their recognition motifs for methylation often depends on competitive binding at the target site between several DNA-binding proteins. These epigenetic regulators of gene expression, including both MTases and competing DNA-binding proteins, are a source of phase variation. The robustness of the population and provides opportunities to modulate transcription in response to changing environmental conditions.

In some bacteria, the behaviour of certain MTases can vary markedly due to slipped-strand mispairing during DNA replication. Often occurring in homopolymer-rich regions, this slippage can cause frameshift mutations that result in truncated and usually inactive MTases. Alternatively, recombination events can result in the movement of type I and III target recognition domains, which can alter the target sequence specificity of the MTase. These mechanisms can yield heterogeneity in the methylomes of descendants from a single cell and can cause differential regulation of multiple genes, termed a phase-variable regulon. It has been postulated that epigenetic control of gene expression mediated by phase variation (epigenetic control of a single gene) or phasevarions (multiple genes regulated simultaneously) allows an essentially clonal population to adopt multiple distinct phenotypes. Such heterogeneity can facilitate adaptation to diverse environmental niches, including complex host environments and the presence of antibiotics, as has been reported in several studies.

Genomic analyses suggest that some form of DNA methylation is present in nearly all bacteria, as putative DNA MTases have been found in 94% of >3,300 sequenced bacterial genomes. Given the large number of MTase target sites in bacterial genomes and the growing evidence suggesting complex regulatory roles of methylation by both R-M and orphan MTases, the potential scope for exploring the diversity of bacterial methylation and methylation-mediated gene regulation is vast. However, the precise sequence targets and biological roles of most MTases remain largely unknown. While recent progress in bisulfite sequencing facilitates the accurate detection of 5mC methylation, there has not been a high-throughput genome-wide sequencing technology that can detect the naturally occurring 4mC and 5mC, although the reduced signal-to-noise ratio with 5mC makes detection of such events challenging. SMRT sequencing molecules consist of a double-stranded native DNA fragment that has been circularized by ligating hairpin adapters to each end. During sequencing, a DNA polymerase proceeds around the circularized DNA template multiple times, the exact number depending on fragment size and polymerase performance. The sequencing instrument monitors not only the pulse fluorescence associated with each incorporated nucleotide, but also the time between the incorporation events, termed the inter-pulse duration (IPD). Variation in IPDs (referred to as kinetic variation) is highly correlated with the presence of modifications within the DNA template, including 6mA, 4mC, 8-oxoguanine and so on.

Many studies have used SMRT sequencing to conduct de novo identification of MTase target motifs, revealing surprising diversity in motifs among bacterial species and even among closely related strains. However, the heterogeneities within bacterial populations cultured under different conditions have not been thoroughly explored. This is primarily limited by the current SMRT sequencing-based bacterial methylation analysis protocol, which relies on assessments of aggregate IPD values at each genomic position across populations of cells, the individual reads (each from a single DNA molecule) are aligned to the same genomic region and then statistically modelled as an ensemble. This approach enhances the statistical power for methylation detection at single-nucleotide resolution, but fundamentally limits the ability to resolve epigenetic heterogeneity within the sample. Although progress beyond traditional population-level analysis has recently been reported, new methods are needed to provide improved resolution on complex methylomes.

Here, we present SMALR, a novel framework for single molecule-level detection and phasing of bacterial DNA methylation using SMRT sequencing data. This approach relies on two complementary methods that use molecule-specific IPD information to infer methylation states at single-molecule resolution. We demonstrate the effectiveness of SMALR through comprehensive and quantitative characterization of seven bacterial methylomes and by identifying distinct types of heterogeneity in these methylomes. The enhanced resolution provided by SMALR allows de novo detection of bacterial epigenetic heterogeneity, and should broaden our understanding of the diverse roles of methylation in modulating bacterial physiology. SMALR is freely available through GitHub.

Results

Single molecule-level methylation detection and phasing. We first present the rationale and description of the two complementary methods within SMALR for (i) single molecule, single nucleotide, strand-specific detection of methylation events and (ii) single molecule-level epigenetic phasing analysis. Our strategy revolves around the interrogation of circular consensus sequence data generated from short-insert SMRT sequencing libraries and continuous long-read data generated from long-insert SMRT sequencing libraries. Using short insert templates, we achieved average read lengths between 4,735 and 9,023 bp (Supplementary Table 1; Methods), although recent releases of the sequencing chemistry kits promise significantly longer-read lengths (12,000 bp on average). The multiple passes of the polymerase over the same template sequence (Fig. 1a,c) allow the calculation of a single molecule, single-nucleotide (SM$_{SN}$) score, which is defined as the difference between the mean site/strand-specific log (natural) IPD value from a native DNA molecule and the corresponding mean site/strand-specific log IPD value from whole-genome amplified (WGA) DNA molecules (Methods). This score provides the statistical power to detect shifts in kinetic variation at a specific nucleotide position on a given DNA molecule.
Complementing the short-insert libraries are the long-insert libraries (our data generated in early 2014 achieved mean insert sizes of 3,357–7,304 bp and mean read lengths of 4,957–7,965 bp, although a mean read length of 12,000 bp can now be achieved; Supplementary Table 1; Methods). Most of the reads generated from this protocol represent long stretches of contiguous DNA (as opposed to the circular consensus of shorter libraries). The long library sequencing protocol has been applied to de novo bacterial genome assembly because of its ability to resolve genomic regions with complex repeated elements 43–45. Here, we instead leverage the continuous long reads for methylation phasing at single-molecule resolution. The methylated motifs profiled in this study are represented in their genomes between 210 and 42,186 times (Supplementary Table 2), a number largely dependent on both the motif complexity and evolutionary selection. As such, a motif may be represented many times in a single long read, providing multiple data points revealing the kinetic variation for the motif. By pooling these kinetic variation statistics for a single read, it becomes possible to not only infer whether the cell that provided that DNA fragment contained MTase activity targeting that motif, but also to quantitatively estimate the processivity of the MTase (Fig. 1d). We therefore created the single molecule, pooled (SM P) score, which is defined as the difference between the mean log IPD value from all motif sites in a single native subread and the mean log IPD value from those same motif sites in WGA DNA molecules (Methods).

Figure 1 | SMALR methods for methylation detection in SMRT reads. Schematic illustrating the general approaches of both the existing and two proposed SMALR methods for detecting DNA methylation in SMRT sequencing reads. (a) A single SMRT sequencing molecule (short DNA insert + adapters) and the subreads that are produced during sequencing. (b) The existing methylation detection method is based on a molecule-aggregated, single-nucleotide (AggSN) score. For a given strand and genomic position, the IPD values from all the subreads aligning to that strand and position are aggregated together across all molecules to infer the presence of a consensus methylated base. (c) The proposed single molecule, single nucleotide (SM_{SN}) method for detecting DNA methylation relies instead on separate consideration of subreads from different molecules. The SM_{SN} scores are calculated for each molecule, strand and genomic position. (d) A single SMRT sequencing molecule (long DNA insert + adapters) with a single long subread and the proposed single molecule, pooled (SM_{P}) approach for assessing MTase activity. This approach pools together IPD values from multiple motif sites along the length of a single long subread.
Although this estimation procedure is more powerful for shorter methylation motifs than for the longer motifs that occur less frequently, the relatively longer-read lengths (reads up to 60,000 bp are now possible with recent updates to the SMRT chemistry kit) provide an opportunity to estimate the SM$_M$ scores accurately for longer motifs.

Sensitivity and specificity of SM$_{SN}$ detections. An accurate mean log IPD for each nucleotide in a single molecule permits confident estimation of the IPD ratio. The accuracy of the mean log IPD increases as the number of subreads for each molecule increases$^{33,34}$, as each subread provides an independent estimate of the IPD. For a given read length, the number of subreads (that is, single-molecule coverage, cov$_{SM}$) is negatively correlated with the insert size of the sequencing library. To quantify the sensitivity and specificity for SM$_{SN}$ detection, we analysed methylated 5$'$-CTGCAG sites in a native E. coli O104:H4 C227-11 strain$^{35}$ (referred to as C227), and a matching WGA sample that is free of methylation (Fig. 2a; Methods). As expected, the sensitivity of the method increased with increasing cov$_{SM}$. For the SM$_{SN}$ approach, cov$_{SM} \geq 15$ enables detection of 6 mA with a sensitivity of 98.5% and a specificity of 99.5%. Although smaller library sizes can provide higher values of cov$_{SM}$, a minimum library size of 150–200 bp is recommended to avoid loss of genomic DNA during library construction and to facilitate removal of adapter-dimer constructs during purification.

Estimating the sensitivity and specificity of detecting 6mA at single-molecule resolution for other 6 mA motifs, we found the results to be comparable to 5$'$-CTGCAG in strain C227 (Supplementary Fig. 1a,b). We found that 4mC also can be accurately detected at single-molecule resolution, albeit with slightly lower sensitivity and specificity (Supplementary Fig. 1c). We did not attempt similar analysis of 5mC motifs due to the removal of adapter-dimer constructs during purification.

SM$_{SN}$ scores for estimating global methylation heterogeneity. The methylome of Chromohalobacter salexigens characterized in a recent study was found to contain a substantial number of non-methylated 5$'$-RGATCY sites$^{37}$. In particular, 23.5% of the motif sites were predicted to be non-methylated based on the standard population-level analysis, which we replicated using molecule-aggregated, single-nucleotide (Agg$_{SN}$) scores (Fig. 2b; Methods). As shown, the distribution of Agg$_{SN}$ scores does not show clear separation between methylated and non-methylated 5$'$-RGATCY sites, indicating that quantifying the methylated fraction of 5$'$-RGATCY sites in the genome with Agg$_{SN}$ scores relies on a subjective and ad hoc threshold. In contrast, there is clear bimodality in the distribution of SM$_{SN}$ scores, where the components centred near SM$_{SN} \approx 0$ and SM$_{SN} \approx 2$ represent the non-methylated and methylated fractions, respectively (Fig. 2b). A distribution of SM$_{SN}$ centred at zero correspond to motif sites that are not methylated because the IPDs do not differ between native and WGA DNAs; in contrast, a distribution of SM$_{SN}$ centred near two corresponds to motif sites that are methylated (specific to 6 mA; consistently observed across multiple bacterial species and motifs as shown in Supplementary Figs 3–8). This bimodality allows the percentage of methylated motif sites to be estimated at 60.4% using a standard expectation maximization (EM) algorithm$^{47}$ (Methods) without need for a subjective input threshold.

SM$_{SN}$-based quantification at low sequencing coverage. As the SM$_{SN}$ scores depend on cov$_{SM}$ rather than the genomic-sequencing coverage, we conducted an in silico experiment to test the accuracy of SM$_{SN}$-based estimates of global methylated fraction at varying levels of genomic coverage. By mixing native and WGA-sequencing molecules at varying proportions and by gradually reducing the total number of molecules, we found that the SM$_{SN}$-based estimates of the global methylated fraction are stable even when the genomic sequencing coverage is as low as 1 (Fig. 2c; Methods). This finding could have implications for the characterization of in vivo isolates, for which low sequencing coverage due to limited DNA input is often a challenge.

Global methylation heterogeneity in six bacteria. We applied the SM$_{SN}$ analysis to six bacterial methylomes that were recently sequenced$^{35,37,38}$ or were specifically sequenced for this study (Supplementary Table 1). We first detected methylation motifs based on existing methods$^{24,35,37}$ and divided them into two groups based on the global distribution of SM$_{SN}$ scores. In the first group (Fig. 3a), most (>95%) motif sites were methylated, with only a small proportion non-methylated, likely due to competitive binding between the MTases and other DNA-binding proteins such as transcription factors$^{2,3,11,13,14}$. In the second group (Fig. 3b), a substantial (>5%) percentage of motif sites

![Figure 2](image-url) Performance of SM$_{SN}$ level detection of DNA methylation. Multiple metrics showing the performance of the proposed single molecule, single nucleotide (SM$_{SN}$) detection method. (a) Performance of the approach for detecting 6mA modifications in the 5$'$-CTGCAG motif of E. coli C227 using three thresholds for minimum single-molecule coverage (cov$_{SM}$). (b) Distribution of the aggregate, single nucleotide (Agg$_{SN}$) and SM$_{SN}$ methylation scores for the partially non-methylated 5$'$-RGATCY motif in C. salexigens. The bimodal distribution of the SM$_{SN}$ scores enables the accurate and objective estimation of this fraction. (c) Accuracy of SM$_{SN}$-enabled estimations of the methylated fraction (using cov$_{SM} \geq 10$) for the 5$'$-CTGCAG motif of E. coli C227 at various levels of genomic-sequencing coverage.
were non-methylated, suggesting the existence of alternative mechanisms that drive methylene heterogeneity. After analysing the SM\textsubscript{SN} scores for all bacterium-motif pairs (Supplementary Figs 3-8), we observed that while most motifs belong to the first group and do not show extensive non-methylation, the second group includes the 5'-RGATCY motif of C. salexigens and three motifs from Helicobacter pylori J99. Most intriguingly, the H. pylori motif 5'-GWCAY shows a very high (75.3%) percentage of non-methylated sites, which we subsequently investigated using the SM\textsubscript{MT} analysis (see below).

**SM\textsubscript{SN} score distributions show regional methylation dynamics.** The Caulobacter crescentus genome encodes a methyltransferase (CcrM) targeting 5'-G\textsubscript{ANTC} sites\textsuperscript{38}. The corresponding gene, ccrM, is only expressed at late stages of the cell cycle. Consequently, fully methylated 5'-G\textsubscript{ANTC} sites transition to hemi-methylated as the replication fork proceeds from the origin of replication (Cori) to the terminus (Ter)\textsuperscript{38}. Recently, Kozdon et al.\textsuperscript{38} used SMRT sequencing to study such transitions at five time points spanning a single, synchronized round of the cell cycle. This allowed us to conduct an approximate SM\textsubscript{SN} analysis (approximate due to lack of WGA sequencing in the original data; Methods) to test the use of SM\textsubscript{SN} for detecting regional methylation heterogeneity, focusing specifically on five distinct 200-kilobase regions in each of five time points (Fig. 3c).

As the replication fork proceeds from the Cori to the Ter in the five time points, the SM\textsubscript{SN} score distributions reveal an increasing fraction of the genome that has been converted from fully methylated to hemi-methylated 5'-G\textsubscript{ANTC} sites. At the first time point (5 min post-synchronization), the fully methylated state of the cells is shown by the single mode in approximate SM\textsubscript{SN} scores (Methods) in all five genomic regions. As the cells begin to differentiate (40 min), there are bimodal SM\textsubscript{SN} scores in regions (i) and (ii) that are closest to the Cori, reflecting the passage of the replication fork through those regions. The next two time points reveal the transition of the single-mode approximate SM\textsubscript{SN} distributions in regions (iii) and (iv) to clear bimodal distributions, reflecting the passage of the replication fork through those regions. The unequal bimodal distribution after 80 min in regions (iii) and (iv) indicates that the molecules from that region have not all been converted from fully to hemi-methylated, likely due to stochastic variance in the position of the replication fork 80 min post-synchronization. The final time point reveals a genome that has almost completely converted to a hemimethylated state, with the exception of the region immediately

Figure 3 | SM\textsubscript{SN} score distributions reveal epigenetic heterogeneity. (a) Single molecule, single nucleotide (SM\textsubscript{SN}) score distributions for multiple bacterium-motif pairs (and the genome-wide motif count, N, of each motif) that exhibit near complete methylation, along with a non-methylated motif for comparison. (b) SM\textsubscript{SN} score distributions for multiple bacterium-motif pairs that display significant non-methylated fractions. The H. pylori J99 motifs show minor variation in the SM\textsubscript{SN} associated with each peak due to subtle differences in the chemistry version used for SMRT sequencing of the native and WGA samples. (c) SM\textsubscript{SN} interrogation of 5'-G\textsubscript{ANTC} methylation at five genomic positions (columns) in a synchronized C. crescentus culture during a single round of DNA replication. Five time points (minutes post-synchronization; rows) provide snapshots of the bidirectional progression of the replication forks from the origin of replication (Cori) to the terminus (Ter). Grey wedges in the chromosome schematics show the 200-kb genomic regions where the SM\textsubscript{SN} scores are queried for each time point. Two regions are on either side of the Cori: (i) Cori - 0.1 Mbp and (ii) Cori + 0.1 Mbp. Another two are halfway between Cori and Ter: (iii) Cori - 1 Mbp and (iv) Cori + 1 Mbp. The final region covers the terminus: (v) Ter. Light (hemi-methylated) to dark (fully methylated) colour shading in the schematic illustrates the approximate position of the replication fork at each time point. The bimodal distributions of approximate SM\textsubscript{SN} scores (Methods) reveal the progressive hemi-methylation of 5'-G\textsubscript{ANTC} sites following the passage of the replication forks. Hemimethylated sites cannot transition back to full methylation until the MTase gene, ccrM, is transcribed, which does not occur until late in the replication process.

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surrounding the Ter (v), which shows only a small amount of hemi-methylation. Analysis at this time of regions (i)-(iv) indicates that these sites have already begun to transition from equal bimodality (universal hemi-methylation) towards their starting single-mode distributions (universal full methylation). This likely is also due to imperfect synchronization, allowing some replication forks to progress past the ipaM gene at the FDR time point, thus activating transcription and beginning the process of re-methylating all the 5'-GANTC sites that had been rendered hemi-methylated by passage of the replication fork.

**SMₚ identifies distinct types of epigenetic heterogeneity.** We considered three potential explanations for the heterogeneous methylation observed in select bacterium-motif pairs (Fig. 3b). First, we hypothesized that methylation motifs, especially degenerate motifs, may be inaccurately annotated; the observed heterogeneity would simply be due to a mixture of truly methylated motifs and motifs falsely identified by the motif enrichment algorithm. For example, the heterogeneous methylation of the 5'-RGATC motif in *C. salexigens* (Fig. 2b) may result from only three of the four explicit specifications (A/G/GATC/C/T) being truly methylated. However, we can reject this hypothesis as the SMₚ scores of the four explicit specifications showed similar heterogeneity (Supplementary Fig. 9).

A second possibility is that the MTase is stochastically methylating only a fraction of its recognition motif sites in each cell, in which case the SMₚ-based estimates of methylated fraction reflect a universally active MTase, albeit one without the ability to methylate all of its target motifs. In that case, we would expect the methylated motif sites to be interspersed with non-methylated sites throughout a single copy of the genome.

A third potential cause of heterogeneity in SMₚ scores is phase variation of the MTase responsible for targeting the motif. Phase-variable MTases have been well-documented in a variety of bacteria, in which stochastic mutations in homopolymers or other simple sequence repeats in the MTase can induce changes in the transcribed product that either activate/deactivate the MTase or modify its target specificity. Either of these two switching modes can induce cell-wide methylation patterns that might differ between neighbouring cells in a single population. In this scenario, the methylated fraction estimated by SMₚ scores reflects the fraction of cells with an active MTase targeting the motif.

We can differentiate between these latter two hypotheses (intra-cellular stochastic methylation versus stochastic phase-variable MTase with different phases in different cells) by using the SMₚ method to phase epigenetic information across the full length of each read (that is, methylation co-occurrence on a single molecule). If some molecules within a sample are methylated at all sites while others are completely non-methylated, this supports the existence of a stochastic phase-variable MTase. In contrast, a mixture of methylated and non-methylated motif sites on a single read suggests intracellular stochastic methylation as the source of heterogeneity in the SMₚ scores.

**Direct detection of phasevarion in single *H. pylori* colonies.** Phase-variable genes regulated by length variation of homopolymeric tracts have been well-documented in *H. pylori*. Several putative MTases contain inactivating frameshift mutations that prevent the transcription of an active protein. By experimentally correcting frameshifts in several MTases and SMRT sequencing the mutated populations, Krebes *et al.* were able to detect methylation (using aggregation-based methods) by the re-activated MTases and identify their target motifs. However, because most *H. pylori* isolates are likely not clonal and significant homopolymer length variation has been observed in MTases between closely related strains of *H. pylori*, it is possible that active copies of the phase-variable MTases are already present in the wild-type isolates, but at levels too low to detect using the aggregation-based method. This problem provided an opportunity to use the SMₚ method for direct detection in wild-type isolates of minor subpopulations with active and inactive MTases.

We first tested the SMₚ method on an *H. pylori* J99 isolate that was sequenced using libraries with long (~20 kb) DNA inserts. We targeted the 4-mer 5'-GATC motif, where >95% of sites are expected to be methylated based on its SMₚ distribution (Fig. 3a), and calculated a SMₚ score for each long read containing at least 10 GATC sites. The distribution of SMₚ scores for 5'-GATC was compared with a control distribution of SMₚ scores calculated after randomly shuffling IPD values between molecules (Fig. 4a). No bimodality is present in the 5'-GATC SMₚ distribution and it is nearly identical to the IPD-shuffled SMₚ distribution, suggesting that the MTase responsible for targeting the 5'-GATC motif in *H. pylori* (Hpy99V1) is constitutively active. Through false-discovery rate (FDR) estimation (Methods), we found that only 0.07% of the molecules with at least 10 5'-GATC sites had evidence of non-methylation (maximum FDR = 1%). This level of non-methylation is consistent with several other motifs for which we expect to observe near-universal methylation activity (5'-CATG, 5'-GANTC and 5'-GAGG), suggesting that the small number of non-methylated molecules may have originated from transiently hemi-methylated regions directly behind the DNA replication fork. Furthermore, phase variation of M.Hpy99V1 was considered unlikely as no significant sequence variation was observed in its coding sequence (Supplementary Fig. 10).

Next, we applied the same analysis to a motif, 5'-GWCA/GA, targeted by a known phase-variable MTase in *H. pylori* J99. The modification (M) subunit of the type III R-M system Hpy99XXI contains a 10-12G homopolymer locus, the exact length of which determines whether transcription downstream of the locus is in-frame (active MTase) or out-of-frame (inactive MTase). Methylation of the 5'-GWCA/GA motif is constitutively active. Through false-discovery rate (FDR) estimation (Methods), we found that only 0.07% of the molecules with at least 10 5'-GWCA/GA sites had evidence of non-methylation (maximum FDR = 1%). This level of non-methylation is consistent with several other motifs for which we expect to observe near-universal methylation activity (5'-CATG, 5'-GANTC and 5'-GAGG), suggesting that the small number of non-methylated molecules may have originated from transiently hemi-methylated regions directly behind the DNA replication fork. Furthermore, phase variation of M.Hpy99XXII was considered unlikely as no significant sequence variation was observed in its coding sequence (Supplementary Fig. 11; Methods).

Hpy99XXII is another R-M system in *H. pylori* J99 known to contain phase-variable components. In contrast to the Hpy99XXI system, the phase variation in this system is due to homopolymer length variation within the specificity (S) subunit that targets the 5'-TCANₐTRG/5'-CYANₐTGA motif. The SMₚ scores for this motif show that, although the majority of molecules have scores suggesting active methylation, there is a subpopulation of molecules with SM$_P$ ≈ 0 (Fig. 4c), indicative of cells within the culture lacking a functional Hpy99XXII system. MisSeq sequencing of the same DNA supported this mechanism, revealing a substantial length variation in the M.Hpy99XXII homopolymer (Supplementary Fig. 11; Methods).

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that true length variation, rather than sequencing error, is driving the considerable read-level variation seen in these two homopolymers.

The *H. pylori* J99 strain used in this study has been passaged many times over the 15 years since its original isolation. While phase variation refers to rapid state switching in response to the environment, it is also possible that, over the course of many passages, stable subpopulations have diverged within the isolate, each containing distinct and fixed homopolymer lengths. To investigate this possibility, we isolated five single colonies (HPXZ1383-1387; Methods) from the original isolate for Illumina sequencing and subjected the reads to analysis of read-level variation (Methods). Even in these clonal isolates, significant length variation was observed in the homopolymers within the *M. Hpy99XXI* and *S. Hpy99XXII* genes (Supplementary Fig. 13). This indicates that homopolymer length variation at these loci develops rapidly, generating heterogeneity in MTase activity in the descendants from a single cell. It is also worth noting that one of the five colonies revealed a large percentage of deletions in *M. Hpy99XXII* (that is, mostly 10G homopolymer rather than 11G), suggesting that this single colony is likely derived from a parent cell with a 10G homopolymer.

Interestingly, although a similar distribution of SMP scores was observed for both the 5'¯TCAN₅TRG/5'¯CYAN₅TGA (Fig. 4c)
and 5′-TCNNGA (Fig. 4e) motifs, no sequence variation was observed in or near the coding region of the genes involved in the Hpy99XVIII R-M system that methylates 5′-TCNNGA (Supplementary Fig. 14). This finding suggests that regulatory elements outside the coding region (genetic or epigenetic) may be responsible for the observed fraction of 5′-TCNNGA non-methylated molecules. Analysis of SM_{P} scores for other methylated motifs in \(H.\ pylon\ i\) \(J99\) did not reveal significant bimodality, suggesting full MTase activity (Supplementary Fig. 15).

### Gene expression in M.Hpy99XXI and S.Hpy99XXII mutants.

To assess the effect of a genome-wide absence of methylated 5′-GWCA\(Y\) and 5′-TCAN\(_{6}\)TRG5′-CYAN\(_{6}\)TGA motifs, we compared the transcriptomes of the five clonal wild-type \(J99\) isolates and the two mutant strains lacking \(M.\ Hpy99XXI\) and \(M.\ Hpy99XXII\) (HPXZ1401 and HPXZ1398, respectively; Methods). In the strain lacking 5′-GWCA\(Y\) methylation (HPXZ1401; Supplementary Table 5), 38 genes were significantly differentially expressed, while the strain lacking 5′-TCAN\(_{6}\)TRG5′-CYAN\(_{6}\)TGA methylation (HPXZ1398; Supplementary Table 6) contained 41 significantly differentially expressed genes \((P<0.001;\ \text{an\ adapted\ Fisher’s\ exact\ test\ (ref\ 70);\ FDR<0.05})\). The most striking changes in HPXZ1401 were the upregulation of \(flgE\), which encodes the flagellar hook protein FlgE, and two other flagellum-related genes, \(flgB\) and \(flaG\) (Supplementary Table 5).

Flagella are essential for \(Helicobacter\) motility and are subject to phase variation via reversible length variation in a short homopolymeric sequence repeat in the \(flgP\) gene\(^{54}\). The upregulation of three flagella-related genes in HPXZ1401 may suggest that other novel mechanisms are involved in \(H.\ pylon\) motility switching. Two other significantly upregulated genes, \(groEL\) and \(groES\), which reside in the same operon based on \textit{in silico} prediction\(^{25}\) and transcription start site mapping in another strain\(^{26}\), showed 2.0- and 5.4-fold enrichment, respectively, of 5′-GWCA\(Y\) motif sites (Supplementary Fig. 16) compared with the average genome-wide frequency. Such chaperone-related genes play important roles in bacterial stress responses to the host environment\(^{27}\). The expression changes in HPXZ1398 also include the flagellar hook-encoding gene, \(flgE\), and several genes related to DNA processing and metabolism (Supplementary Table 6). These results demonstrate that genome-wide alterations of methylation patterns can significantly impact gene expression, although the specific mechanisms by which methylation regulates the expression of these genes are unknown.

### Intracellular stochastic methylation in \(C.\ salexigens\).

In contrast to 5′-GWCA\(Y\), 5′-TCAN\(_{6}\)TRG5′-CYAN\(_{6}\)TGA and 5′-TCNNGA in \(H.\ pylon\ i\) \(J99\), the SM_{P} scores of the 5′-RGATCY motif in \(C.\ salexigens\) do not support the existence of phase-variable MTase activity (Fig. 4f). Instead of a peak near SM_{P} \(\approx 2\), there is a peak near SM_{P} \(\approx 0.9\), indicating that the IPD values used to calculate SM_{P} scores for each molecule reflect a mixture of both non-methylated and methylated motif sites. This observation combined with a lack of detected sequence variation in the coding sequence of the 5′-RGATCY-targeting \(M.\ Csa\) gene (Supplementary Fig. 17) and that \(M.\ Csa\) is an orphan MTase without a corresponding RE\(^{37}\) indicates that intracellular stochastic methylation by \(M.\ Csa\) is the likely mechanism driving the observed heterogeneity in SM_{SN} scores (Fig. 3b). Therefore, \(M.\ Csa\) in \(C.\ salexigens\) may have stochastic methylation activity \((~ \sim 60\%)\) in each cell, constituting an alternate form of epigenetic heterogeneity in a bacterial population.

### Discussion

Here, we present SMALR, the first systematic framework for single molecule-level characterization of epigenetic heterogeneity in bacterial methylomes using SMRT sequencing. We demonstrate the enhanced resolving power of our approach in analyses of seven methylomes that show distinct types of epigenetic heterogeneity in bacterial populations. The short library-based SM_{SN} method enables accurate estimation of the fractions of methylated and non-methylated motif sites without the use of subjective thresholds, even at low levels of genomic sequence coverage. Furthermore, the robust separation between methylated and non-methylated sites based on SM_{SN} scores at low levels of genomic sequence coverage suggests the possibility of reference-free, \textit{de novo} discovery of methylation motifs from SMRT sequencing data at a much lower coverage than is currently required. The long library-based SM_{P} method uses long reads to assess the co-occurrence patterns of methylated motif sites at single-molecule resolution. By surveying MTase activity at the single molecule-level, the SM_{P} scores can reveal small fractions of cells in a bacterial population that contain active or inactive MTases, and quantitatively estimate the processivity of an MTase of interest.

The existing, consensus-based methods for methylation detection cannot provide the resolution necessary to survey complex MTase activity. The application of SMALR and its integration with other single molecule- or single cell-level data, such as RNA and protein expression will enable a more detailed understanding of the functions of DNA methylations in bacterial physiology.

DNA methylation in promoter regions of bacteria has been extensively linked to the regulation of nearby genes\(^{2,3,12,58}\), but there is growing appreciation for the potential roles of methylation in the gene body\(^{31,39,60}\). More generally, the importance of epigenetic regulation in bacteria is emphasized in a recent study that proposed an epigenetics-driven adaptive evolution model\(^{24}\). In this model, heterogeneous methylomes may drive unique patterns of gene expression and cellular phenotypes, thereby serving as units of natural selection. The methods presented here make it possible to characterize the epigenetic modes that induce transcriptional diversity, analogous to the many known genetic modes\(^{17,26,49,54,61}\).

While SMRT sequencing enables \textit{de novo} detection of a wide variety of DNA modifications, it also poses challenges unique to third-generation sequencing technology. Specifically, detection of DNA modifications from SMRT reads fundamentally depends on the number of repeated observations for each single molecule. For a given read length, there is a resulting tradeoff between library size and accuracy in single molecule, single nucleotide-level methylation detection. The methods proposed here provide examples of effectively leveraging the unique features of SMRT sequencing using a combination of short- and long-library designs. This general methodology can be modified to accommodate forthcoming third-generation real-time sequencing techniques\(^{62}\).

While the current study uses SM_{SN} scores from a single site to detect DNA methylation, previous work has demonstrated that some DNA modifications (DNA methylation or damage) can create kinetic signatures that extend into surrounding bases\(^{34}\). Although beyond the scope of the current work, the single molecule-level approaches presented here can be expanded to include more sophisticated algorithms required for detection of these modification types.

Finally, while the current study focused on cultures of single bacterial strains, the single-molecule resolution methods proposed here can also be applied to mixed populations of bacteria. Such samples could include diverse clinical isolates, including...
samples that contain a high abundance pathogen or even diverse microbiome samples. The methods are also applicable outside the bacterial kingdom, such as in the analysis of human mitochondrional DNA or DNA viruses, both of which present significant genetic and epigenetic heterogeneity.

Methods

Code availability. SMALR is implemented in a stand-alone software package (written in Python) and available at https://github.com/fanglab.

Bacterial strains and culture conditions. The E. coli C227 sample was isolated from a 64-year-old woman from Hamburg, Germany, who was hospitalized in Copenhagen, Denmark after presenting with bloody diarrhoea. Rasko et al.44 isolated DNA using a Qiagen DNeasy Blood and Tissue Kit as per manufacturer’s instructions. The isolate was grown overnight in standard LB broth and the extraction was performed according to the kit instructions using 1 ml overnight culture per reaction and treating with proteinase K for 2 h. The DNA was eluted in 100 µl AE buffer per column.

H. pylori 199 was originally isolated in Nashville Tennessee from an American patient with a duodenal ulcer45 and sequenced in 1999 (ref. 53). Cells (50 µl of frozen H. pylori 199 stock from the original isolating lab were first spotted on trypticase soy agar (TSA) plates with 5% sheep blood (TSA, BBL Microbiology Systems, Cockeysville, MD) at 37 °C with 5% CO₂ for 48 h incubation, then were spread on new TSA plates in the same conditions64. After 24-h incubation, H. pylori cells were collected in 1.0 ml phosphate-buffered saline (PBS, pH 7.4) and centrifuged at 800 x g. Bacterial genomic DNA was prepared using the Wizard Genomic DNA purification kit according to manufacturer’s instructions (Promega, Madison WI). DNA concentration was measured by Nanodrop 1,000 spectrophotometer (Thermo Scientific, Rockford, IL). DNA for Chromohalobacter salexigens strain H111 was ordered from DSM (http://www.dsmz.de/catalogues/details/culture/DSM-3043.html).

Koodson et al.38 grew C. crescentus cells at 28 °C in M2-glucose minimal media (M2G) and performed small-scale synchrony. To have sufficient volume to remove large aliquots at each time point, swimmer cells were pooled from 16 small-scale synchronies. Cells were allowed to proceed synchronously through the cell cycle at 28 °C in M2G. Genomic DNA was isolated using the Wizard Genomic DNA purification kit according to manufacturer’s instructions (Promega, Madison WI). DNA concentration was measured by Nanodrop 1,000 spectrophotometer (Thermo Scientific, Rockford, IL). DNA for Chromohalobacter salexigens strain H111 was ordered from DSM (http://www.dsmz.de/catalogues/details/culture/DSM-3043.html).

Methods

SMA detection of methylation states. Considering each native molecule separately, the IPD values for a given motif that survive filtering are grouped by their strand only, irrespective of their mapped genomic positions. The natural log is taken for all values in this group and the mean calculated. Second, the strand/position-matched WGA IPD values are averaged across all molecules, as they were with the SMA method. However, here the WGA IPD values are additionally aggregated across each motif site covered by the native molecule in question. Then, these WGA strand- and motif-site-matched IPD values are natural log-converted and their mean value is subtracted from the native molecule/strand-specific mean, resulting in the SM value.

Whole-genome amplification. The Qiagen REPLI-g amplification kit was used to perform whole-genome amplification to exclude epigenetically modified bases. The method produced micrograms of DNA from 50 ng of input genomic DNA, following the manufacturer’s guidelines and 10 h of amplification time at 30 °C followed by deactivation at 65 °C for 3 min.

SM detection of MTase activity. First, considering each molecularly sequenced, the native IPD values for a given motif that survive filtering are grouped by their strand only, irrespective of their mapped genomic positions. The natural log is taken for all values in this group and the mean calculated. Second, the strand/position-matched WGA IPD values are averaged across all molecules, as they were with the SMA method. However, here the WGA IPD values are additionally aggregated across each motif site covered by the native molecule in question. Then, these WGA strand- and motif-site-matched IPD values are natural log-converted and their mean value is subtracted from the native molecule/strand-specific mean, resulting in the SM score.

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Modified fraction estimates with Gaussian mixture modelling. The mixture module of the Python package PyMix was used to run the EM algorithm for Gaussian mixture estimation.

To evaluate the ability of EM with a Gaussian mixture model to estimate the modified fraction, we applied the algorithm to distributions of SMAIPD values that were generated from in silico mixing of WGA and native SMRT sequencing molecules at known proportions. 100,000 total molecules sequenced from E. coli C227 were used for each specific mixture fraction, with the native fraction of molecules reduced in 5,000 (5%) to 100,000 (100%). The SMIPD-based methylation fraction for the motif 5'-CTGCAG was analysed with the EM algorithm for each in silico mixture. To assess the stability of EM-mediated estimation of
methylated fraction at lower levels of genomic coverage (that is, the number of total sequenced bases in relation to the genome size), we downsampled the scores in the SM$_{SN}$ distribution for the in silico mixtures of WGA and native molecules. The EM algorithm was then applied to these downsampled SM$_{SN}$ score distributions.

The EM algorithm slightly, yet consistently, underestimated the native fraction in this mixture. To determine whether any non-normality in the methylated and non-methylated SM$_{SN}$ score distributions might be causing the EM algorithm to underestimate the size of the modified fraction, we created Gaussian mixtures consisting of two entirely simulated normal distributions. To represent the non-methylated and methylated SM$_{SN}$ score distributions, the scores were simulated with $\pm 2$ and $\pm 0$, respectively ($\sigma = 0.5$ for each). As an alternative, we also created SM$_{SN}$ score distributions exclusively from WGA molecules where $\pm 2$ was added to a subset of the SM$_{SN}$ scores in order to get between 5 and 100% methylated SM$_{SN}$ values, the distributions of which will retain any non-normality found in the WGA SM$_{SN}$ distribution. The EM estimations of methylated fraction for these two types of simulated mixtures were both very similar and very accurate (Supplementary Appendix Fig. 2). This indicates that non-normality of SM$_{SN}$ score distribution is not the reason for the observed slight underestimation of native fraction. Instead, this evidence suggests that stably non-methylated 5'-CTGCAG sites in E. coli C227 are the reason for this phenomenon.

Approximate SM$_{SN}$ scores for C. crescentus. WGA sequencing was unavailable for analysis in this study, so the approximate SM$_{SN}$ score shown in Fig. 3c is simply the mean of native molecule-, strand-, and position-specific log IPD values (rather than its deviation from the mean of strand- and position-matched WGA log IPD values). This approximate SM$_{SN}$ score is susceptible to IPD biases introduced by local sequence contexts, but provides a sufficient ability to resolve the methylated and non-methylated components in the bimodal distributions.

FDR estimation for identifying methylated molecules. To assess the significance of observed methylated and non-methylated fractions based on SM$_{F}$ scores, we established negative control SM$_{F}$ distributions. When assessing the FDR for calling actively methylated molecules (for example, for the 5'-GWCAV motif in H. pylori J99), the negative control SM$_{SN}$ distribution is generated by running the SM$_{SN}$ method on WGA sequencing data. Alternatively, when assessing the FDR for calling non-methylated molecules (for example, for the 5'-TCAGN$_{2}$TRG5'-CY$_{2}$N$_{2}$TAGA and 5'-TCNCGA motifs in H. pylori J99), the negative control SM$_{SN}$ distribution is created by randomly shuffling IPD values among molecules to disrupt any signal of observed methylated and non-methylated fractions based on SM$_{SN}$ scores, reflecting molecules that are mostly methylated at the sequenced bases in relation to the genome size), we downsampled the scores in the SM$_{SN}$ distribution of SM P scores reflecting molecules that are mostly methylated in silico.

Fragments jhp1365up and jhp1365down were digested with SacI and PstI, respectively, and then ligated together into SacI/PstI-digested pGem-T Easy, creating pXZ757 (Supplementary Table 4). Similarly, a 0.9 Kb fragment upstream of jhp111 (jhp111up) was obtained by PCR using primers JHP111L-SacII and JHP111R-LSpeI (Supplementary Table 3). For FDR estimation for identifying methylated molecules, we ligated fragments jhp111up and jhp111down into SacI/SpeI digested pGEM-T Easy, creating pXZ759 (Supplementary Table 4). The sacB-cat cassette, conferring chloramphenicol resistance (Cm$^R$), was obtained by PCR using primers pZ0032 (ref. 64) as template and primers SC-F-XbA and SC-R-XbA (Supplementary Table 3). The sacB-cat cassette was digested with XbaI, and then ligated with SpeI-digested pXZ759, creating pXZ758 and pXZ850, respectively (Supplementary Table 4). All plasmid constructions were confirmed by sequencing using primers pGMET-seqF and pGMET-seqR (Supplementary Table 3).

The wild type H. pylori strain J99 was transformed to Cm$^R$ with these plasmids, pXZ758 and pXZ850, to create mutant HPXZ1398 (jhp111-sacB-cat) and HPXZ1401 (jhp111-sacB-cat), respectively (Supplementary Table 4), as previously described$^{44}$. Genomic DNA of these mutants was isolated and PCR was performed to confirm that HPXZ1398 and HPXZ1401 carry the correct mutation of jhp111-sacB-cat and jhp111-sacB-cat, respectively, with sacB-cat cassette-specific primer Catup and genome locus-specific primer JHP1365RR-PstI or JHP111RR-PstI (Supplementary Table 3).

Sensitivity and specificity of SM$_{SN}$ methylation detection. To measure the sensitivity and specificity of the SM$_{SN}$ scores for assessing methylated molecules (and by extension MTase activity), we applied the method to the 5'-GATC motif in H. pylori J99. The responsible MTase, M.Hpy99VI, is not suspected to be phase-variable and SM$_{SN}$ scores revealed a very small non-methylated fraction (Fig. 3a). We therefore expect that nearly 100% of molecules in the sample will be targeted for modification at the 5'-GATC motif. As the sensitivity and specificity curves show (Supplementary Fig. 1B), the power of the SM$_{SN}$ scores to detect methylated molecules increases with an increasing threshold on the number of motif sites present on the molecule. Although lower values of this threshold have limited ability to correctly identify methylated molecules, some methylated motifs are directed too sparsely in the genomes to be interrogated using higher thresholds. Shorter motifs are usually present at higher densities in a genome, but there are some exceptions to this rule (Supplementary Table 2). Therefore, we suggest using the number of motif sites on each molecule (rather than motif length) as the threshold for SM$_{SN}$ analysis.

**References**


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Author contributions
J.B. and G.F. designed the SM$_{10}$ and SM$_{19}$ methods; J.B. developed the SMALR package; J.B., X.-S.Z., E.E.S. and G.F. designed the experiments; X.-S.Z., R.S., C.R., G.D., N.S., D.M., M.K.W., A.C. and M.J.B. carried out sample-preparation experiments; R.S. and G.D. conducted all the sequencing; J.B., X.-S.Z., S.Z., R.S., M.K.W., A.C., M.J.B., E.E.S. and G.F. jointly analysed the data sets; J.B., E.E.S. and G.F. wrote the manuscript with input from all coauthors; G.F. conceived and supervised the project.

Additional information
Accession codes: Sequence data have been deposited at the NCBI Sequence Read Archive (SRA) with BioProject under project ID PRJNA281410 and the DNA Database of Japan under accession code SRP057274. The assembled reference genomes used in this study have been deposited in GenBank under the accession codes CP011331 (E. coli C227) and CP011330 (H. pylori J99).

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Competing financial interests: E.E.S. is on the scientific advisory board of Pacific Biosciences.

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