Intratumor DNA methylation heterogeneity in glioblastoma: implications for DNA methylation-based classification

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Background. A feature of glioblastoma (GBM) is cellular and molecular heterogeneity, both within and between tumors. This variability causes a risk for sampling bias and potential tumor escape from future targeted therapy. Heterogeneous intratumor gene expression in GBM is well documented, but little is known regarding the epigenetic heterogeneity. Variability in DNA methylation within tumors would have implications for diagnostics, as methylation can be used for tumor classification, subtyping, and determination of the clinically used biomarker O6-methylguanine-DNA methyltransferase (MGMT) promoter methylation. We therefore aimed to profile the intratumor DNA methylation heterogeneity in GBM and its effect on diagnostic properties.

Methods. Three to 4 spatially separated biopsies per tumor were collected from 12 GBM patients. We performed genome-wide DNA methylation analysis and investigated intratumor variation.

Results. All samples were classified as GBM isocitrate dehydrogenase (IDH) wild type (wt)/mutated by methylation profiling, but the subclass differed within 5 tumors. Some GBM samples exhibited higher DNA methylation differences within tumors than between, and many cytosine-phosphate-guanine (CpG) sites (mean: 17 000) had different methylation levels within the tumors. MGMT methylation status differed in IDH mutated patients (1/1).

Conclusions. We demonstrated that intratumor DNA methylation heterogeneity is a feature of GBM. Although all biopsies were classified as GBM IDH wt/mutated by methylation analysis, the assigned subclass differed in samples from the same patient. The observed heterogeneity within tumors is important to consider for methylation-based biomarkers and future improvements in stratification of GBM patients.

Key Points
1. Methylation differences can be higher within tumors than between.
2. Multiple DNA methylation subclasses exist in GBM.
3. Intratumor DNA methylation heterogeneity is a feature of GBM.
**Importance of the Study**

GBM is a heterogeneous diagnostic category with poor survival despite multimodal treatment, highlighting the need for patient stratification and adapted treatment. DNA methylation is a valuable tool for classification and subgrouping of tumors with distinct differences in prognosis, and could potentially contribute to improving diagnostics. Considering the variety of tumor clones and transcriptomic expression profiles previously described within GBM tumors, it is of utmost importance to characterize the intratumor DNA methylation heterogeneity and how it affects methylation-based biomarkers and classification. We demonstrate a high intratumor methylation heterogeneity, but methylation-based classification assigns the correct tumor type (GBM *IDH* wild type/mutated). However, the subtype differs within 5 tumors, and the *MGMT* promoter methylation status, frequently used for treatment decision in elderly patients and inclusion in clinical trials, differs in one *IDH* mutated tumor. The methylation heterogeneity we demonstrate within tumors should be considered for methylation-based biomarkers and improvements in GBM subtyping.

Glioblastoma (GBM) is the most common primary malignant brain tumor in adults and is characterized by an extensive heterogeneity both between and within tumors on a regional as well as single-cell level regarding genomic aberrations and transcriptomic expression.2-4 Heterogeneity adds to the complexity of treating GBM, as the therapeutic response to radiation and chemotherapy varies between tumor clones.5-7 The current treatment for GBM is maximal safe surgical resection followed by concomitant and adjuvant temozolomide (TMZ) and radiotherapy, which still only results in a median survival of 15 months.8 O6-methylguanine-DNA methyltransferase (MGMT) is a DNA repair enzyme, which counteracts the damage induced by TMZ.9 This gene can be silenced by methylation in the promoter,10 and a survival benefit has been demonstrated for patients with methylated MGMT.11 MGMT is frequently used clinically for treatment allocation (e.g. TMZ or radiotherapy) in elderly patients12 and for stratification or selection to clinical trials.13

Molecular markers were implemented for the first time in the World Health Organization (WHO) 2016 classification,14 and we are moving toward more objective tools for classification—for instance, DNA methylation.15-17 DNA methylation can also be used to estimate the methylation age of tissues, which is accelerated in tumors,18,19 and to predict mortality in healthy subjects.20 Intertumor DNA methylation heterogeneity in GBM has been established by the existence of GBM subclasses with distinct prognosis,17 as well as for gliomas of different grades21 based on isocitrate dehydrogenase 1 (*IDH1*) mutation and glioma cytosine-phosphate-guanine (CpG) island methylator phenotype (G-CIMP).22 Considering the substantial heterogeneity within tumors described for gene expression, treatment response, etcetera, we asked whether intratumor heterogeneity in GBM exists also at the level of DNA methylation. This knowledge is essential for future improvements in tumor classification and methylation-based biomarkers, to avoid misdiagnosis due to tumor heterogeneity and sampling bias. We therefore sampled 3 to 4 biopsies, spatially separated, per tumor from GBM patients and processed the samples on Infinium EPIC methylation arrays and investigated variations within individual tumors. The 38 included biopsies (from 12 patients) were homogeneously classified as GBM *IDH* wild type (wt) or mutated by methylation profiling despite the heterogeneity we found within tumors regarding CpG sites with variable methylation values, methylation age, and GBM subclass (5/12). This demonstrates the potential for DNA methylation profiling for diagnosis of single samples in the clinic, but also highlights that the observed DNA methylation heterogeneity within tumors should be considered for biomarkers and future improvements in patient stratification.

**Materials and Methods**

**Patients and Samples**

The study was approved by the regional ethics committee (Dnr 604–12) and carried out in accordance with the relevant guidelines and regulations. Three to 4 spatially separated biopsies per tumor were collected from 12 adult GBM and 3 meningioma (MNG) patients undergoing primary tumor resection during 2016–2018 at Sahlgrenska University Hospital (Gothenburg, Sweden) after signed informed consent. Biopsies were taken as early as possible in the surgical procedure to reduce brain shift, which is known to reduce accuracy of neuronavigation. Clearly spatially separated biopsies (e.g. center vs periphery or diametric opposite peripheries) as determined by the neurosurgeon were collected after confirmation of fluorescence based on 5-aminolevulinic acid (5-ALA). The location of each biopsy was tagged in the neuronavigation system and based on MRI differentiated into the following categories: center, central in the tumor; periphery, clearly within tumor but with more peripheral location than center; border, in the border between contrast and normal (non–contrast enhanced) tissue; outside, outside contrast-enhancing tumor.

**Histology**

Samples were processed for histology (see Supplementary Materials) and tumor content was assessed (blinded) by a specialist in clinical neuropathology.

**Bisulfite Conversion and DNA Methylation Arrays**

DNA was extracted from the biopsies using DNeasy Blood and Tissue Kit and TissueLyser (Qiagen), and 500 ng DNA was bisulfite converted with the EZ DNA Methylation Kit.
DNA methylation levels were analyzed with Infinium MethylationEPIC BeadChip (Illumina) according to protocols supplied by the manufacturer.

**Data Analysis**

Methylation data were processed and normalized with Noob using the statistical software R with the package ChAMP. The generated methylation data are available at Gene Expression Omnibus, accession number GSE116298. The reliability and technical reproducibility of the EPIC array are well established in the literature, and we examined technical replicates from a recent publication to determine a robust threshold in our study to avoid calling the aforementioned technical replicates and was therefore determined as the threshold in our study to avoid calling DMP due to reproducibility issues. For tumor classification/subtyping of GBM samples we used the MethPed classifier and another published classifier. The methylation status of the MGMT promoter was predicted with the package MGMT-STP27. Methylation age was determined with Horvath age and epTOC. A stricter pre-processing method was applied with the R package SeSAMe to reduce artificial detection of methylation in deleted or hyperpolymorphic regions of the genome for certain analyses as indicated in the results section. Tumor deconvolution of the methylation data accounting for tumor purity was performed using the R package InfiniumPurify. Please see the Supplementary Methods for further details on the processing of methylation data.

**MGMT Pyrosequencing**

Pyrosequencing of 20 ng bisulfite converted DNA was performed using the PyroMark PCR kit, PyroMark Q24 CpG MGMT kit, and PyroMark Q24 Advanced CpG reagents on PyroMark Q24 Advanced (Qiagen) according to the manufacturer’s instructions. A total of 7 CpG sites were investigated; chromosome 10 129467243-129467275 (UCSC hg38). The reader is referred to the Supplementary Methods for further details.

**Sanger Sequencing**

Fifty ng of DNA from biopsies classified as IDH mutated by DNA methylation profiling was PCR amplified with IDH1 primers and purified with ExoSAP-IT PCR Product Cleanup Reagent (Affymetrix), and PCR products were Sanger sequenced (GATC Biotech).

**Results**

**Heterogeneous DNA Methylation Subclasses within GBM Tumors**

We sampled 3–4 spatially separated biopsies, fluorescent with 5-ALA, per tumor during tumor resection of GBM patients using neuronavigation and classified the biopsies as border, peripheral, and central (Figure 1A). Illumina methylation arrays were used to profile the genome-wide methylation pattern of the samples. Tumor content was evaluated by a neuropathologist by histology. Samples with ≥70% tumor content were included for further analysis, which left 38 biopsies from 12 GBM patients (Figure 1B).

We and others have previously developed DNA methylation-based diagnostic classifiers and we employed these to investigate the intratumor heterogeneity of the biopsies. All samples were classified as GBM with a high score by MethPed (>0.7; max 1.0) and as a match for GBM IDH wt or IDH mutant by the classifier by Capper et al (Supplementary Table 1). However, the subclass varied within 5 of 12 tumors; 3 had mesenchymal and receptor tyrosine kinase II (RTKII) subclasses, and 2 contained both RTKI and RTKII (Figure 1C). This demonstrates that several DNA methylation subclasses, according to the current classifier, exist intratumorally. There was no significant correlation in our cohort between the assigned GBM subclass and the regions that the biopsies were sampled from (data not shown). G-CIMP, which is associated with IDH mutations, can be used to predict length of survival and subtyping of glioma of different grades. One patient in the cohort (GU-HGG-216) was IDH mutated and G-CIMP positive according to methylation profiling, and both markers were consistent in all biopsies (Figure 1D).

**GBM Biopsies Can Be More Similar by DNA Methylation to Other Tumors than within Tumors**

To further evaluate heterogeneity in GBM, we included homogeneous intratumor MNG samples to use as comparison. Multiple samples, as described above, were analyzed from 3 MNG WHO grade I patients (tumor content ≥80%; Supplementary Table 2), which we, based on the benign nature of this tumor, expected to be homogeneous. The patient identity of all samples was first verified by single-nucleotide polymorphism clustering (Supplementary Figure 1A). The genome-wide heterogeneity in methylation was then investigated with a multidimensional scaling (MDS) plot based on all CpG sites (Figure 2A) and unsupervised hierarchical clustering based on the top 5000 deviating CpG sites (Figure 2B). As expected, the MNG samples formed a tight cluster in both analyses, while the GBM samples demonstrated a larger spread with biopsies from the same tumor interspersed with biopsies from other tumors, reflecting a higher similarity to samples from other tumors compared with their intratumor samples. We hypothesized that this could be dependent on the region the biopsy was sampled from or the GBM subclass, but neither showed any clear association in our cohort (Supplementary Figure 1B–C).

Copy-number alterations (CNAs) have been shown to differ within GBM tumors, which is in agreement with our study where hierarchical clustering based on the mean value of CNA segments showed that one patient (GU-HGG-204, who did not cluster by methylation either) did not cluster together and additional patients had biopsies at different branching levels (Figure 2C). The main intratumor CNA differences in GU-HGG-204 were loss of chromosomes 4, 6, and 8 (Supplementary Figure 2). We applied a stricter
Fig. 1. Diagnostics by DNA methylation profiling. (A) 5-ALA and neuronavigation were used to sample 3–4 biopsies per tumor from spatially separated regions categorized as border (B; left), peripheral (P; middle), and central (C; right) illustrated here with sagittal (top) and coronal (bottom) planes. (B) Data for the 12 included glioblastoma (GBM) patients including sampling region and histological tumor content of the biopsies. The listed diagnosis is the histological diagnosis of the patient based on tumor material separate from the biopsies. (C) DNA methylation profiling classified all biopsies as GBM IDH wt/mutated but the subclass, according to a previously published classifier, differed in 5 patients. (D) Unsupervised hierarchical clustering of the GBM biopsies (blue) and The Cancer Genome Atlas glioma samples, previously classified as positive for glioma CpG island methylator phenotype (G-CIMP; green) or G-CIMP negative (red), respectively. Three GBM biopsies (all GU-HGG-216) clustered as G-CIMP positive.
pre-processing method with the R package SeSAMe\textsuperscript{29} to reduce artifactual detection of methylation in regions with CNA and repeated the MDS and cluster analysis (Supplementary Figure 3A–B). The MDS plot based on all CpG sites was very similar to Figure 2A, suggesting that CNA differences within the tumors overall do not influence the heterogeneity in DNA methylation. GU-HGG-204, however, clustered together after the stricter pre-processing, thus indicating that the intratumor CNA differences were underlying the heterogeneity in the previous clustering (Figure 2B).

**Intratumor Heterogeneity in DNA Methylation Age and Median Methylation**

The global DNA methylation heterogeneity in GBM and MNG was assessed by examining the median methylation values within each tumor (Figure 3A) and the coefficient of variation (CV) of it. The CV between GBM tumors was 15\% and only 3\% for MNG. The CV within the individual tumors ranged 0.1–2\% for MNG, while it was 0.5–6.5\% for GBM, demonstrating that GBM can vary more intratumorally than MNG interpatient. Another proposed method to assess heterogeneity is to determine the proportion of intermediate methylation (PIM) score, since methylation has a bimodal distribution, and an intermediate value consequently evaluates heterogeneity within the sample (biopsy in this case). The PIM varied intertumor for GBM (range: 10–27\% PIM) as well as intratumor (range: 0.2–5\% Δ PIM) while the PIM was similar between MNG tumors (range: 13–16\%), but varied less intratumor than GBM (0.2–1.5\% Δ PIM; Figure 3B).

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**Fig. 2.** Genome-wide heterogeneity in glioblastoma. (A) Multidimensional scaling (MDS) plot based on all sites on the EPIC methylation array shows intratumor GBM heterogeneity as several samples are located closer, and are thus more similar, to samples from other tumors than their intratumor samples. (B) Unsupervised hierarchical clustering of the top deviating 5000 CpG sites on the methylation array clusters biopsies from each patient together for all patients except one. (C) Copy-number alterations (CNAs) were inferred from methylation data and hierarchically clustered.
Accelerated methylation age (higher DNA methylation age than chronological age) varies across GBM subclasses and has been suggested as a biomarker in glioma. A biomarker should ideally be homogeneous and we therefore investigated the methylation age within GBM tumors and compared it with MNG. The methylation age was assessed by Horvath age and epiTOC and the scores were in good agreement (Pearson correlation 0.61, $P$-value $6 \times 10^{-6}$; Supplementary Figure 4A). Differences within GBM tumors were detected both with Horvath age ($\Delta$Horvath age = 7 y) and epiTOC ($\Delta$epiTOC = 0.015), while the MNG tumors were more homogeneous ($\Delta$Horvath age = 3 y; mean $\Delta$epiTOC = 0.003; Figure 3C–D). Accelerated aging was seen in 45/47 GBM and MNG biopsies with the Horvath age ($\Delta$mean = 25 and 13 y, respectively; Supplementary Figure 4B).

**Individual CpG Sites Demonstrate Intratumor Heterogeneity**

Next, we characterized the number of DMP ($\Delta\beta > 0.3$) occurring between different patients in our cohort to use as a comparison for the intratumor DMP. The mean number of DMP between GBM patients was 86000 (Figure 4A) and 21000 between MNG patients. However, the mean number of DMP within GBM tumors was 17000 (range: 522–50684), but only 110 for MNG (range: 94–131) highlighting the intratumor heterogeneity in GBM (Figure 4B). GU-HGG-204, which did not cluster by CNA, was not significantly enriched for DMP on the chromosomes with differing copy number intratumorally compared with the other tumors. We also repeated the DMP analysis after applying the stricter pre-processing pipeline in SeSAMe to reduce erroneous detection of methylation in regions with CNA. This reduced the mean number of intertumor DMP slightly in GBM (72000 instead of 86000 previously) and MNG (17000 instead of 21000). The number of intratumor DMP was reduced in a similar manner; average of 13000 DMP in GBM (17000 without CNA correction) and in MNG (50 instead of 110; Supplementary Figure 5), showing that the majority of intratumor DMP were not influenced by differences in CNA.

The GBM intratumor DMP were mostly only present between 1 biopsy pair or 2 biopsy pairs, but not shared between all pairs of the biopsies (Figure 4C). The location of the intratumor DMP in GBM was significantly
enriched in open sea regions (P-value 0.001) and reduced in CpG islands, N-Shore and S- Shore (P-value 5*10^{-4}, 0.03 and 0.01) compared with the distribution of CpG sites on the array (Figure 4D). Given the pattern of enrichment in open sea regions, we investigated whether specific CpG sites were frequently altered in multiple tumors. However, this was not the case, as the same DMP was rarely detected in several tumors (only 36 CpG sites shared between 6/12 GBM tumors; Figure 4E).

Fig. 4. CpG site-specific intratumor heterogeneity in glioblastoma. (A) The frequency of the number of intertumor differentially methylated probes (DMP; Δβ > 0.3) in the GBM cohort. (B) The number of intratumor DMP in each tumor respectively and (C) between how many intratumor biopsy pairs the DMP occurred. (D) Distribution of where the intratumor DMP occurred and the black bar (EPIC) illustrate the distribution of all CpG sites on the methylation array as a point of reference; if the proportion of DMP in a certain region exceeds this bar there is an enrichment of DMP in this region. * denotes significant change of the GBM intratumor DMP compared with the distribution on the array, P-value < 0.05. ** denotes P-value < 0.01. (E) Depiction of the number of intratumor DMP occurring in multiple GBM tumors.
DNA Methylation Heterogeneity within the Same Tumor Occurs in the MGMT Promoter

The methylation status of the MGMT promoter is currently used clinically for treatment allocation in elderly patients. We predicted MGMT methylation based on methylation array values with the MGMT-STP27 package, and found that the only IDH mutated patient in our cohort (GU-HGG-216) was heterogeneous for MGMT, while 1/11 IDH wt were heterogeneous (Figure 5A–B). The MGMT-STP27 prediction, which is based on 2 CpG sites, is frequently used in clinical trials. In clinical diagnostics, however, other sites are more commonly analyzed, using pyrosequencing (Supplementary Figure 6A). We therefore also performed pyrosequencing on 4 and 7 commonly used CpG sites (chr 10 129467255-129467273 and 129467243-129467275, respectively) according to thresholds previously suggested. The results verified the heterogeneity in GU-HGG-216 and classified all IDH wt homogeneously (Figure 5C; Supplementary Figure 6B).

DNA Methylation Heterogeneity within Tumors Is Not Caused by Differing Tumor Content

The heterogeneity of GBM tumors also includes cell composition with a varying mix of tumor cells, normal cells, immune cells, etc. Differences in tumor content within individual tumors could as such affect methylation values. We therefore used the R package InfiniumPurify to estimate tumor purity differences within tumors and deconvolute the methylome accounting for tumor purity. The tumor purity difference within tumors correlated significantly with the number of intratumor DMP prior...
to deconvolution (Figure 6A). The number of intratumor DMP after tumor deconvolution increased for some samples and decreased for some (Figure 6B), but overall there was no significant difference (P-value 0.09, paired Wilcoxon test). Further, the MDS plot based on all CpG sites after tumor deconvolution still showed a high intratumor methylation heterogeneity as several biopsies were closer, and thus more similar, to samples from other tumors than samples from the same tumor (Figure 6C). Further, the cluster after tumor deconvolution (Figure 6D) also looked similar, which taken together with the results from the MDS plot and DMP analysis demonstrated that differences in tumor content within individual tumors is not the cause of the observed intratumor methylation heterogeneity.

**Discussion**

The WHO classification of brain tumors relies heavily on histopathological criteria, but high intra- and inter-observer variability has been demonstrated. Several DNA methylation-based classifiers have therefore been developed and successfully reclassified and stratified patients into subgroups with distinct survival times. The unbiased diagnosis offered by the DNA methylation-based classifiers is consequently considered for diagnostic use. One important factor to evaluate is whether the classification is homogeneous within tumors, particularly for heterogeneous tumors such as GBM. Heterogeneity in gene expression,
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In conclusion, we showed that intratumor DNA methylation heterogeneity is a feature of GBM, and our results suggest that the alterations mainly occur in less conserved regions (open sea), but not altering specific CpG sites within that region. DNA methylation-based classification was still able to provide homogeneous intratumor diagnoses (GBM IDH wt and GBM IDH mutated) using 2 methods: Horvath age and epiTOC. The methylation age has been suggested as a biomarker in glioma, and we therefore evaluated it in our cohort using 2 methods: Horvath age and epiTOC. The methods were in good agreement, and the Horvath age was accelerated in all except 2 samples, consistent with earlier studies. Methylation age, assessed by both methods, was homogeneous in MNG, but heterogeneous within GBM tumors, thus questioning its value as a prognostic biomarker. A robust biomarker should ideally be homogeneous within tumors, a criterion that is often overlooked but needs to be considered in future studies of candidate biomarkers.

Intratumor DNA methylation is less explored for this patient group, and further studies with larger cohorts are required to determine the relevance of MGMT methylation for IDH mutated patients. MGMT was homogeneous in our cohort for GBM IDH wt based on pyrosequencing, but one patient was heterogeneous according to the prediction from the methylation arrays. We noted, however, that the discordant biopsy (GU-HGG-271–3) had a lower probability score compared with the other biopsies.

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In conclusion, we showed that intratumor DNA methylation heterogeneity is a feature of GBM, and our results suggest that the alterations mainly occur in less conserved regions (open sea), but not altering specific CpG sites within that region. DNA methylation-based classification was still able to provide homogeneous intratumor diagnoses (GBM IDH wt and GBM IDH mutated, respectively). Caution should, however, be exercised regarding subgrouping of GBM, as we demonstrated that multiple methylation subclasses coexist within the same tumor. We further showed that a large number of CpG sites were differentially methylated within the GBM tumors and that...
the intratumor heterogeneity affected the suggested biomarker methylation age. The clinically implemented biomarker MGMT promoter methylation was heterogeneous for the IDH mutated tumor, warranting further studies on this patient group. All IDH wt tumors were homogeneous for MGMT based on pyrosequencing, but one was heterogeneous according to the prediction from the methylation arrays necessitating further studies. The observed intratumor heterogeneity in DNA methylation in this study needs to be considered for methylation-based biomarkers and future stratification of GBM subtypes to improve diagnostic accuracy for this heterogeneous disease.

Supplementary Material

Supplementary data are available at Neuro-Oncology online.

Keywords
classification | DNA methylation | glioblastoma | heterogeneity | MGMT

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