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The long non-coding RNA HOTAIR is transcriptionally activated by HOXA9 and is an independent prognostic marker in patients with malignant glioma

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ABSTRACT

The IncRNA HOTAIR has been implicated in several human cancers. Here, we evaluated the molecular alterations and upstream regulatory mechanisms of HOTAIR in glioma, the most common primary brain tumors, and its clinical relevance. HOTAIR gene expression, methylation, copy-number and prognostic value were investigated in human gliomas integrating data from online datasets and our cohorts. High levels of HOTAIR were associated with higher grades of glioma, particularly IDH wild-type cases. Mechanistically, HOTAIR was overexpressed in a gene dosage-independent manner, while DNA methylation levels of particular CpGs in HOTAIR locus were associated with HOTAIR expression levels in GBM clinical specimens and cell lines. Concordantly, the demethylating agent 5-Aza-2’-deoxycytidine affected HOTAIR transcriptional levels in a cell line-dependent manner. Importantly, HOTAIR was frequently co-expressed with HOXA9 in high-grade gliomas from TCGA, Oncomine, and our Portuguese and French datasets. Integrated in silico analyses, chromatin immunoprecipitation, and qPCR data showed that HOXA9 binds directly to the promoter of HOTAIR. Clinically, GBM patients with high HOTAIR expression had a
significantly reduced overall survival, independently of other prognostic variables. In summary, this work reveals HOXA9 as a novel direct regulator of HOTAIR, and establishes HOTAIR as an independent prognostic marker, providing new therapeutic opportunities to treat this highly aggressive cancer.

INTRODUCTION

Gliomas encompass the majority of primary central nervous system tumors, and have been historically classified based on their histopathological features, according to four grades of malignancy (World Health Organization – WHO – grade I-IV). Glioblastoma (GBM; WHO grade IV) represents the most common and malignant primary adult brain tumor [1], with a median patient overall survival (OS) of approximately 15 months [2]. The remarkable tumor heterogeneity, invasive phenotype, and resistance to radio- and chemotherapy are main determinants of this poor prognosis [3–5]. Additionally, several molecular alterations (epigenetic, genetic, transcriptional and proteomic) contribute to GBM tumorigenesis and may represent putative biomarkers of GBM prognosis and aggressiveness [6].

Recent studies have explored the complexity of the transcriptome and reported the existence of a large number of transcripts that do not code for a protein, which nonetheless have the critical ability to regulate gene expression [7]. Among others, these transcripts include long non-coding RNAs (lncRNA) [8, 9] that are defined as spliced, polyadenylated and >200 nucleotides long RNAs that modify the genome in a highly tissue-specific manner [9, 10]. LncRNA have also emerged as new players in cancer development and progression, with recent studies highlighting the importance of both tumor suppressor and oncogenic lncRNAs in the deregulation of cellular pathways and gene expression programs [11]. The HOX Transcript Antisense Intergenic RNA (HOTAIR) is a trans-acting lncRNA, involved in the genome-wide reprogramming of the chromatin [10]. HOTAIR is transcribed at the HOXC locus in chromosome 12 (between HOXC11 and HOXC12), and its 5′-domain interacts with the Polycomb Repressor Complex 2 (PRC2), and the 3′-domain interacts with the lysine specific demethylase 1/REST corepressor 1/RE1-silencing transcription factor (LSD1/CoREST/REST) complex. Thus, HOTAIR can act as modular scaffold, with different binding sites for harboring demethylase (LSD1), that mediates the enzymatic demethylation of histone H3 dimethyl lysine 4, H3K4me2) and methylase (PRC2) and the histone H3 lysine 27 – H3K27 – methylase EZH2) complexes, resulting in the transcriptional inhibition of the HOXD locus on chromosome 2 by epigenetic control of the chromatin structure [10, 12].

HOTAIR has also been shown to have functional roles in a variety of human cancers (reviewed in [13–15]), being associated with patients’ decreased OS, increased metastatic potential, tumor recurrence and chemotherapy resistance. In glioma, HOTAIR was reported to be involved in proliferation, invasion, cell cycle and colony formation ability, in vivo tumor growth, and GBM patients’ OS [16–20]. However, the molecular mechanisms underlying its aberrant activation in glioma remain elusive. In this context, we aimed to investigate the integrated molecular status (gene copy number, expression, and DNA methylation levels) of HOTAIR in glioma samples, unravel the underlying mechanisms regulating HOTAIR expression in these tumors, and assess its clinical significance in independent large cohorts of GBM.

RESULTS

HOTAIR expression is associated with high-grade gliomas

In a first approach, we analyzed the expression levels of HOTAIR in grades II and III gliomas, and in grade IV GBM patients using gene expression microarray data and RNA-sequencing (RNA-seq) data from The Cancer Genome Atlas (TCGA). Globally, HOTAIR was highly expressed in GBM, particularly in IDH-wt GBM, as compared to lower-grade gliomas and normal brain (Figure 1A and Supplementary Figure 1A). Of note, in the RNA-seq data, IDH-wt grade III gliomas presented higher HOTAIR expression than the remaining grade II and III gliomas entities (Supplementary Figure 1A). Concordantly, four additional datasets from the Oncomine database (Murat [21], Freije [22], Sun [23], and Phillips [24]) and two independent Portuguese and French glioma series, confirmed that HOTAIR expression is far more frequent in grades III and IV than in grade II gliomas and normal brain (Supplementary Table 1 and Supplementary Figure 1B). In all tested glioma datasets, HOTAIR expression was not significantly associated with any other clinicopathological feature (patient age, sex, Karnofsky performance status [KPS], and exposure to radiotherapy or chemotherapy, except for associations with patient age in Phillips [24], Repository of Molecular Brain Neoplasia Data (REMBRANDT) and the French datasets, and associations with IDH mutation status in the French dataset; data not shown). Moreover, HOTAIR expression was not associated with any particular GBM molecular subtype as defined by Wang et al. [25] (Supplementary Figure 1C and 1D; p > 0.9999 for microarray and RNA-seq data). Together, these data suggest that HOTAIR is highly expressed in high-grade gliomas, being particularly frequent in IDH-wt cases.
DNA methylation regulates HOTAIR levels in glioma

In order to understand the molecular mechanisms underlying HOTAIR expression increase in GBMs, we analyzed gene copy number aberrations (Figure 1B) and DNA methylation levels in the HOTAIR locus (Figure 1C). In 250 IDH-wt GBMs analyzed for gene copy number, HOTAIR amplification and deletion (either focal or chromosomal) were found in 0.8% (2/250) and in 3.2% of the samples (8/250; Figure 1B), respectively, while no amplifications or deletions were found in 20 IDH-mut GBMs (Figure 1B). While HOTAIR levels were high in 3 of the 5 HOTAIR-amplified tumors, it was also present in 1 tumor with gene deletion and in 116 without copy number aberrations (Figure 1B). These data show HOTAIR copy number aberrations are rare in GBM, and unlikely associated with its increased expression levels ($p = 0.182$). Analysis of 56 methylation probes spanning from HOTAIR’s most proximal genes (HOXC11 and HOXC12) revealed a wide spectrum of methylation levels across different GBM samples (Figure 1C). Of note, some probes consistently presented similar methylation levels across all samples (e.g., several probes within the HOTAIR intragenic region consistently showed low methylation levels), suggesting those regions are not prone to de novo methylation in GBM. In a subset of 70 GBMs (66 IDH-wt and 4 IDH-mut) for which both gene expression and methylation data were available, we found the methylation levels of 3 probes located in the intragenic region of HOTAIR (cg00079219, cg18824990 and cg24895871) to be significantly inversely correlated with HOTAIR expression levels ($r = -0.36$, $p = 0.002$; $r = -0.43$, $p = 0.0002$; and $r = -0.35$, $p = 0.003$, respectively; Figure 1D). Of note, performing the same analysis exclusively for the IDH-wt GBMs showed that the methylation levels of the probes cg00079219 and cg18824990 were inversely correlated with HOTAIR expression ($r = -0.39$, $p = 0.0002$; $r = -0.39$, $p = 0.0014$), while methylation levels at the probe cg24895871 lost their association with expression ($r = -0.26$, $p = 0.167$). We further corroborated the relevance of these associations in IDH-wt GBM patients in the French dataset as the 3 intragenic methylation probes were also found to inversely correlate with HOTAIR expression (cg00079219 $r = -0.53$, $p = 0.016$; cg18824990 $r = -0.523$, $p = 0.017$; cg24895871 $r = -0.521$, $p = 0.018$), and in the combination of IDH-wt glioma grade III and IDH-wt GBM patients (cg00079219 $r = -0.43$, $p = 0.004$; cg18824990 $r = -0.453$, $p = 0.002$; cg24895871 $r = -0.431$, $p = 0.004$).

To further explore the relevance of DNA methylation in HOTAIR regulation, we treated glioma cell lines with the global DNA demethylating agent 5-Aza-2′-deoxycytidine (5-Aza) followed by methylation-specific PCR (MSP) and quantitative PCR (qPCR) analyses (Figure 1E and 1F). Interestingly, HOTAIR intragenic CpGs were found to be mostly methylated in untreated glioma cells. In addition, 5-Aza treatment resulted in DNA demethylation (Figure 1E) and associated increase in HOTAIR transcriptional levels in most but not all of the cell lines (Figure 1F), suggesting a cell line-dependent regulation. Together, our data suggest an association between methylation and HOTAIR’s expression in GBM patients and glioma cell lines, but other mechanisms may be crucial in reactivating HOTAIR in these tumors.

HOXA9 directly binds the HOTAIR promoter in GBM cells

Previously published transcriptomic data from our group (GEO accession number GSE56517) [26, 27] suggested a possible regulation of HOTAIR by the homeoprotein HOXA9, an important protein in the aggressiveness, chemotherapy resistance, and prognosis of GBM [21, 26, 28, 29]. Specifically, GBM cell lines with overexpression or silencing of HOXA9 presented increased or reduced expression of HOTAIR, respectively; raising the hypothesis that HOXA9 may directly regulate HOTAIR expression. Indeed, an in silico analysis using MatInspector (Genomatix) revealed 3 putative binding sites for HOXA9 with high matrix similarities to HOXA9.02 (0.899), PBX-HOXA9.01 (0.849), and MEIS1B-HOXA9.01 (0.837) matrixes (Figure 2A), suggesting that HOXA9 may bind to the promoter region of HOTAIR and regulate its transcription. To test this, we studied the expression pattern of HOTAIR and HOXA9 in adult and pediatric glioma-derived cell lines by semi-quantitative reverse transcription-PCR (RT-PCR) and qPCR, and found these genes to be frequently co-expressed in glioma (Figure 2B and 2C). Moreover, U87MG-HOXA9 cells (with exogenous overexpression of HOXA9) presented significantly increased expression of HOTAIR as compared to their HOXA9-negative counterpart (U87MG-MSCV; Figure 2B and 2C). We then performed anti-HOXA9 chromatin-immunoprecipitation (ChIP) on U251 GBM cell line (endogenously expressing HOTAIR and HOXA9), U87MG-HOXA9 (HOXA9 overexpression models) and their HOXA9-negative counterparts. In both U251 and U87MG-HOXA9, ChIP-qPCR revealed significantly increased HOXA9 occupancy of the promoter region of HOTAIR in comparison to their respective controls (Figure 2D and 2E; $p < 0.0002$ for U251; $p = 0.0148$ for U87MG-HOXA9), confirming that HOXA9 directly interacts with the promoter region of HOTAIR. Together, these results indicate that HOXA9 is a direct activator of HOTAIR expression in GBM cells, thus supporting the strong co-expression of these genes observed in glioma cell lines.
Co-expression of *HOTAIR* and *HOXA9* is a frequent event in clinical specimens of glioma

To verify if the frequent co-expression of *HOTAIR* and *HOXA9* in glioma cell lines is present in glioma clinical specimens, we evaluated their expression levels and potential correlations in the Portuguese, French, and TCGA datasets. We found that *HOTAIR* and *HOXA9* frequently have a coherent transcriptional activation status in grade IV glioma (Portuguese dataset Pearson’s *r* = 0.642, *p* < 0.0001; IDH-wt GBM in French dataset Pearson’s *r* = 0.649, *p* = 0.002; IDH-wt GBM in TCGA microarray dataset Pearson’s *r* = 0.494, *p* < 0.0001; IDH-wt GBM in TCGA RNA-seq dataset Pearson’s *r* = 0.525, *p* < 0.0001; Figure 3A–3C, Supplementary Figure 2H and Table 1). Similarly, significant correlations between *HOTAIR* and *HOXA9* expression were also observed in specific combinations of glioma grades (Portuguese dataset WHO grades II+III, III, II+III+IV and II+III+IV; French dataset IDH-wt WHO grade III and grade IV; Table 1 and Supplementary Figure 2A–2G). While *HOTAIR* and *HOXA9* co-expression did not reach statistical significance for grade II gliomas (*n* = 6; Supplementary Figure 2A), this is likely due to the small sample size, and the same trend for co-expression was observed; indeed, all of these tumors were either double-positive or double-negative (Table 1).

Further analysis in 4 independent datasets showed a statistically significant correlation between the expression of *HOTAIR* and *HOXA9* in all glioma sets (Table 2). Furthermore, in IDH-wt (*n* = 55) and IDH-mut (*n* = 137) grades II and III glioma with available RNA-seq data from TCGA, a statistically significant correlation between the expression of *HOTAIR* and *HOXA9* was also found (IDH-wt Spearman’s *r* = 0.65, *p* < 0.0001, and IDH-mut *r* = 0.21, *p* = 0.01; data not shown), while in 1p19q codeleted and IDH-mut grades II and III glioma no correlation was found (*n* = 85, *r* < 0.01, *p* = 0.999; data not shown).

Interestingly, no significant correlations between *HOTAIR* and *HOXA9* were found for other cancer types, including lung, leukemia, colorectal, and breast cancers (Table 2). Taken together, our results strongly suggest that *HOTAIR* and *HOXA9* are concomitantly co-expressed in human gliomas, but not in other cancer types.

High levels of *HOTAIR* expression associate with shorter survival in patients with malignant glioma

To validate the prognostic value of *HOTAIR* expression reported in GBM patients from the Chinese population [16], we firstly analyzed two independent datasets of GBM patients from TCGA and REMBRANDT. In 554 GBM patients from TCGA with available survival data, a statistically significant decrease in OS was observed in patients with high *HOTAIR* expression (*n* = 177, median OS = 383 days) as compared to patients whose GBMs presented low *HOTAIR* levels (*n* = 377, median OS = 447 days; *p* = 0.026 Log-rank test; Figure 4A). Similarly, associations were found in the subset of 387 IDH-wt GBMs (*HOTAIR*-high *n* = 126, median OS = 370 days and *HOTAIR*-low *n* = 241, median OS = 447 days; *p* = 0.032 Log-rank test; Figure 4B and Supplementary Table 2). As expected, classic prognostic factors including patient age at diagnosis, KPS, and use of radio-chemotherapy, were significantly associated with OS (*p* < 0.05, Log-rank test, Supplementary Table 2). Importantly, *HOTAIR* expression was significantly associated with shorter OS of IDH-wt GBM patients in a multivariable Cox model (*p* = 0.036), independently of other prognostic factors (age, gender, KPS, use of chemoradiotherapy, and treatment with additional chemoradiotherapy; Supplementary Table 2). Consistently, in an independent dataset of 67 GBM patients from the REMBRANDT dataset, high *HOTAIR* expression was present in 72% of patients (*n* = 48) who...
Figure 2: HOXA9 transcriptionally activates HOTAIR via direct interaction with its promoter region. (A) MatInspector representation of specific binding sites for HOXA9 matrix in HOTAIR promoter region. Each matrix match is represented by a half round symbol and each color symbolizes a matrix family. Pink, blue and violet colors represent the matrixes HOXA9.02 (matrix sim = 0.899, sequence: ctgtgacTAA attgg and family ABDB), PBX-HOXA9.01 (matrix sim = 0.849, sequence: gaggTGTTtgag and family HOXC) and MEIS1B-HOXA9.01 (matrix sim = 0.837, sequence: TGCCattttatgc and family HOXH), respectively. Basepairs in italic appear in a position with a high conservation profile in the matrix (ci-value > 60). Basepairs in capital letters represent the core sequence used by the program. Matches represented on the top of the sequence line were found on the positive strand, while below the sequence line reside matches found on the negative strand. The red arrows represent HOTAIR putative transcription start sites (TSS). (B–C) HOTAIR and HOXA9 expression were evaluated by reverse-transcriptase PCR (B) and quantitative PCR (C) in a panel of adult and pediatric glioma-derived cell lines, and in the GBM-L18 primary GBM-derived cell culture. GBM cell line U87MG-MSCV does not present detectable levels of endogenous HOTAIR expression, which were significantly increased upon retrovirally-mediated HOXA9 overexpression (U87MG-HOXA9). White and grey bars represent HOTAIR and HOXA9 expressions, respectively. qPCR levels were normalized to the expression of HPRT1. The results are representative of triplicates (mean ± SD). *p = 0.029; **p = 0.0088. (D–E) The putative binding of HOXA9 protein to the promoter region of HOTAIR was assessed by chromatin immunoprecipitation (ChIP) analysis followed by quantitative PCR in U251 cells (D), and U87MG-HOXA9 and their HOXA9-negative counterparts (E). IgG was used as negative control for the ChIP. Chromatin immunoprecipitated with an anti-HOXA9 antibody shows direct binding of HOXA9 to the HOTAIR promoter. Relative enrichment is normalized to input DNA (not subjected to immunoprecipitation) and to the IgG background signal (D), whereas fold change occupancy is normalized to input, IgG and HOXA9-negative cells (E), from three independent experiments (mean ± SD). (D) ***p = 0.0002; (E) p = 0.0148.
had a significantly shorter OS (median OS = 15.8 months) than those with low expression (median OS = 37.4 months), both in univariable and multivariable analyses (p = 0.005 Log-rank test; p = 0.034 Cox regression, Figure 4C and Supplementary Table 3). Since HOXA9 expression is a known prognostic factor in GBM patients [26, 28, 29], we investigated in the large TCGA dataset whether HOTAIR was still prognostically valuable in the subset of HOXA9-negative IDH-wt GBM patients. Indeed, high expression of HOTAIR was able to identify a subgroup of HOXA9-negative IDH-wt GBM patients that presented a significantly shorter OS (median OS = 375 days) than those with low HOTAIR levels (median OS = 463 days; Supplementary Figure 3; Log-rank p = 0.037).

Additionally, we tested the prognostic value of HOTAIR expression among 28 glioma grade III patients from the French dataset with available survival data. Similarly to GBM, we found for the first time an association between high HOTAIR expression levels and shorter OS in grade III glioma patients with high HOTAIR expression (p = 0.002, Log-rank test; Supplementary Table 4). Multivariable Cox analysis further showed that high HOTAIR expression is a poor prognostic factor (p = 0.022) independently of other known prognostic factors such as age at diagnosis, surgery (partial or complete resection), KPS, treatment, and IDH and 1p19q status. The median survival is 1.4 years [0.7–2.5] in the group of 28 grades III. Survival medians are respectively of 2 years in the group of patients with HOTAIR-lower expression (n = 16, median HOTAIR expression = 0.0002 [2.96e-6 – 0.0053]) and of 0.7 years in the group of patients with HOTAIR-higher expression (n = 12, median HOTAIR expression = 0.0387 [6.4e-6 – 0.0332]).

Finally, we found that high HOTAIR expression is also associated with shorter overall survival in grade II

Figure 3: Expression levels of HOTAIR and HOXA9 are significantly correlated in GBM clinical specimens. (A–C) Correlation graphs of HOTAIR and HOXA9 expression levels in GBMs from the Portuguese dataset (A), and IDH-wt GBMs from the French dataset (B), and IDH-wt GBMs the TCGA dataset (microarray data) (C), showing statistically significant correlations between their expressions in all datasets. (A) Pearson’s r = 0.655, p < 0.0001; (B) Pearson’s r = 0.649; p = 0.002; (C) Pearson’s r = 0.494; p < 0.0001.
and grade III (n = 240) glioma patients in the RNA-seq data from the larger TCGA dataset (Supplementary Tables 5 and 6; p = 0.020 and p < 0.0001, respectively; Log-rank test), and independently of patient age, gender, and molecular subtype (IDH and 1p/19q status) in the case of grade II gliomas (p = 0.032; Cox regression model), but not for grade III gliomas (p = 0.395; Cox regression model), in which high HOTAIR levels were highly correlated with wild-type IDH.

Taken together, our findings establish HOTAIR as a clinically-relevant biomarker of prognosis in malignant glioma patients.

**DISCUSSION**

An increasing focus has been given to lncRNAs as key regulators of a range of biological functions and as crucial players in the etiology of disease, especially in
Figure 4: High levels of HOTAIR expression are significantly associated with shorter survival in GBM patients. Kaplan–Meier overall survival curves of HOTAIR prognostic value in (A) 554 GBM patients from TCGA, (B) 367 IDH-wt GBM patients from TCGA and (C) 67 GBM patients from REMBRANDT dataset, showing patients whose tumors present high HOTAIR expression have a statistically significant shorter overall survival compared to those with HOTAIR-low tumors, in both independent datasets (A, \( p = 0.026 \); B, \( p = 0.032 \); C, \( p = 0.005 \); Log-rank tests).
cancer [8, 9]. The relevance of HOTAIR in cancer was first reported by an association between HOTAIR expression and increased metastatic potential and diminished survival of breast cancer patients [30]. Later studies evaluated the roles of HOTAIR in several tumor types (reviewed in [13–15]), globally highlighting oncogenic roles of HOTAIR. Likewise, HOTAIR expression was associated with more aggressive disease in glioma patients [16–19]. While some oncogenic functions of HOTAIR have been reported in glioma [17, 31, 32], the underlying mechanisms responsible for HOTAIR activation in such a devastating disease have remained unknown thus far. Here, we explore the multi-layered complexity of HOTAIR activation by integrating molecular (genetic and epigenetic) analyses, in silico approaches, and data from glioma patients and cell lines. Additionally, we further investigated the relevance of HOTAIR as a prognostic biomarker in GBM, and in malignant WHO grade II and III glioma.

We show that HOTAIR is overexpressed in a subset of high-grade gliomas, particularly in GBMs. Of note, our study includes data from independent patient datasets, and obtained with different complementary techniques, including qPCR, expression microarrays, microfluidic-based qPCR analysis (Fluidigm) and RNA-Seq data. To understand the molecular mechanisms regulating the expression of HOTAIR, we evaluated copy number aberrations and DNA methylation levels, and searched for putative transcription factors with binding sites in HOTAIR’s promoter region. Copy number alterations in HOTAIR locus were rare and did not associate with its expression levels, suggesting this is not a prominent underlying mechanism in GBM. Contrarily, modulation of DNA methylation levels in GBM cell lines by the demethylating agent 5-Aza indicated that intragenic CpGs in HOTAIR locus affected its transcriptional levels in a cell line-dependent manner (globally, most cell lines increased HOTAIR levels upon demethylation, while U87MG did not, possibly attributable to different kinetics of 5-Aza response and/or lack of expression of all necessary HOTAIR transcriptional regulators). Moreover, methylation probes covering CpG islands in HOTAIR locus showed significant inverse correlations between HOTAIR’s intragenic DNA methylation and expression levels in GBM specimens. In fact, it was previously shown that intragenic DNA methylation is associated with decreased gene expression by altering the chromatin structure and reducing the efficiency of RNA Pol II elongation [33, 34]. Although these results indicate that DNA methylation may regulate HOTAIR expression in GBM, this association was not universal, so other transcriptional regulation mechanisms are involved in glioma. Previous observations from our group suggested HOXA9 as a possible regulator of HOTAIR in glioma [26]. HOXA9 is an oncogenic transcription factor whose expression was described in a subset of highly aggressive GBMs, and associated with patients’ decreased OS [26, 28]. Interestingly, we found HOTAIR and HOXA9 are frequently co-expressed in gliomas, but this was not observed in patients with lung, leukemia, colorectal, and breast cancers, suggesting that this co-expression may be an exclusive event of gliomas. Indeed, our ChIP data indicates a direct regulation of HOTAIR by HOXA9, which binds to HOTAIR promoter region to activate its transcription. While HOXA9 and other HOX genes have been shown to be transcriptionally regulated by HOTAIR [10, 35] in fibroblasts and breast cancer cell lines, it is currently unknown whether a similar regulation of HOXA9 may also occur in glioma. Indeed, the expression of HOXA9 in GBM is known to be epigenetically regulated by the PI3K pathway via inhibition of EZH2-mediated H3K27 trimethylation at the HOTAIR locus [36], and HOTAIR is known to interact with PRC2 complex (containing EZH2 and other subunits) to guide it to target loci [10, 13, 37]. Therefore, it is conceptually feasible that HOTAIR might regulate HOXA9 expression, which together with other transcription factors can regulate the expression of HOTAIR, in a putative loop mechanism. Of note, the roles of HOXA9 in glioma and in breast cancer are very distinct: while in the first it displays a variety of oncogenic functions, associated with tumor aggressiveness, higher grades of malignancy, tumor implantation in in vivo models, therapy resistance and shorter survival of patients [26, 38–40], in breast cancer HOXA9 is a tumor suppressor gene whose expression is frequently lost, leading to cell growth, survival, invasiveness and changes in morphogenesis [41]. These studies highlight the importance of cell context for the biological effects mediated by HOXA9, which do not thus preclude the possibility that the transcriptional regulatory mechanisms between HOTAIR and HOXA9 may also be distinct in glioma and breast cancer. Although conceptually possible, this hypothesis has not been tested in GBM, and warrants further elucidation in new studies. We report here for the first time the ability of HOXA9, a homeoprotein, to directly regulate the expression of HOTAIR. While we provide strong indications that HOTAIR-positive GBMs may result from altered intragenic DNA methylation levels and/or HOXA9 binding, other mechanisms cannot be excluded. For example, the CT variant of the functional single nucleotide polymorphism rs12826786 in HOTAIR locus was associated with its higher intratumoral expression in glioma [42], and would require further addressing. Thus, our work provides novel insights on HOTAIR’s transcriptional regulators, widening our understanding of the HOTAIR-associated mechanisms of aggressiveness and malignancy in gliomas. Interpreting our findings at the light of other studies further supports the classic tissue-specific roles and regulatory mechanisms of IncRNAs [43].

The prognostic value of HOTAIR that we observed in 3 independent datasets further supports the reported
clinical value of \textit{HOTAIR} in glioma \cite{16}. Critically, this is the first study establishing a prognostic value for \textit{HOTAIR} in lower grade glioma (grades II and III). Importantly, we also found that \textit{HOTAIR} expression was able to identify a subset of GBM patients with poor prognosis even in the universe of \textit{HOXA9}-negative GBM patients, indicating that the combinatorial evaluation of \textit{HOTAIR} and \textit{HOXA9} expression levels may prove advantageous towards a molecularly-based stratification of GBM patients. Testing how the concomitant inhibition of \textit{HOTAIR} and \textit{HOXA9} may affect the behavior of GBM \textit{in vitro} and \textit{in vivo} will be interesting and warrants further investigation in future studies. Furthermore, the clinical importance of \textit{HOTAIR} suggests it as a putative therapeutic target. While drugs directly interfering with \textit{HOTAIR} function are currently being studied \cite{44–47} but still not clinically used in glioma, it may be interesting to test pharmacological approaches that act upstream of \textit{HOTAIR} activation, namely PI3K inhibitors (e.g., PI-103 \cite{48} and LY294002 \cite{49}) that have been shown to silence \textit{HOXA9} transcription, and might thus result in \textit{HOTAIR} downregulation. In addition, part of \textit{HOTAIR} effects in glioma may also be limited by using drugs directed to PRC2 components, as the EZH2 inhibitor DZNep \cite{50}, or drugs that specifically target LSD1 activity and have been tested in cancer \cite{51, 52}.

In summary, our study shows that (i) \textit{HOTAIR} is highly expressed in a subset of malignant gliomas, independently of gene copy number alterations; (ii) epigenetic marks at the level of DNA methylation in particular CpG sites associate with \textit{HOTAIR} levels in GBM; (iii) co-expression of \textit{HOTAIR} and \textit{HOXA9} occurs frequently in high-grade glioma, but not in other cancer types; (iv) \textit{HOTAIR} is prognostically valuable in malignant glioma patients; and (v) \textit{HOTAIR} and \textit{HOXA9} may be useful biomarkers to integrate a molecularly-based stratification of GBM patients. We anticipate that \textit{HOTAIR} may mediate some of the effector mechanisms by which \textit{HOXA9} creates a more aggressive and therapy-resistant form of GBM. Further studies are warranted to better identify \textit{HOTAIR} downstream target genes at the genome-wide level in GBM, in an attempt to better understand the mechanisms by which \textit{HOTAIR} affects survival of patients, and ultimately investigate new therapeutic opportunities.

\textbf{MATERIALS AND METHODS}

\textbf{Glioma primary samples and cell lines}

Glioma tumor specimens were obtained from “Hospital Braga” (\(n = 34\)) and “Hospitais da Universidade de Coimbra” (\(n = 39\)), Portugal, and from the Clermont-Ferrand University Hospital Center (\(n = 51\)), France (Supplementary Table 1), upon approval by each Hospital’s ethical committee and patients signed a written individual informed consent according to institutional guidelines. Tumor tissues were snap-frozen in dry ice or isopentane cooled in liquid nitrogen directly from the operating room, and stored at \(-80^{\circ}\) C. In the French dataset, 57% of the samples were IDH1 genotyped by EpigenDx (Worcester, MA) using pyrosequencing (assays ADS1703 and ADS1704), while the other 43% by analyzing the most frequent IDH1 mutations in exon 4 (codon 132) using RFLP \cite{53}. Regarding 1p19q samples characterization, the analysis was performed using the Vysis 1p36/1q25 and 19q13/1p13 FISH probe kit (4N6020, Abbott), according to manufacturer’s instructions. For some cases lacking 1p19q characterization, internexin A (INA) immunohistochemical analyses were carried out on paraffin sections using antibodies directed against internexin neuronal intermediate filament protein alpha (INA). Since INA expression was reported to be a surrogate marker of 1p19q codeletion \cite{54, 55}, its expression was assessed to indirectly inquire about the 1p19q deletion status. Pediatric glioma cell lines KNS42, Res259, Res186, SF188, and UW479 were cultured in DMEM/F12 ( Gibco, Grand Island, NY, USA) supplemented with 10% Fetal Bovine Serum (FBS; Biochrom, Berlin, DE), and 1% Penicillin-Streptomycin (Pen-Strep; Invitrogen, Grand Island, NY, USA) as previously described \cite{56}. Commercially-available adult glioma cell lines A172, GAMG, SNB19, SW1783, U251, and U87MG were originally purchased from ATCC (Rockville, MD, USA), and the primary GBM-derived culture GBM-L18 (established in our lab) were cultured in DMEM (Gibco, Grand Island, NY, USA) supplemented with 10% FBS, and 1% Pen-Strep. U87MG (which do not express \textit{HOXA9} endogenously) were previously \cite{28} genetically-engineered with murine stem cell virus (MSCV) retroviral vectors containing the \textit{HOXA9} coding region to obtain \textit{HOXA9} overexpressing cells (U87MG-HOXA9) or with control empty vector (U87MG-MSCV). Selection of retrovirally-infected cells was maintained with 500 \(\mu\)g/mL G418 (Sigma-Aldrich, St. Louis, MO, USA). Incubations were performed at \(37^{\circ}\) C, in a humidified atmosphere containing 5% \(CO_2\).

\textbf{TCGA data meta-analysis in glioma patients}

\textit{HOTAIR} gene expression, copy number, DNA methylation and clinical data were downloaded from TCGA; available from: \url{http://cancergenome.nih.gov/}, accessed 2017 \cite{57}.

TCGA Agilent’s G4502A 244K gene expression profiles from 572 GBMs, 27 grades II and III gliomas (Supplementary Table 1), and 10 unmatched normal samples were analyzed, and “level 3” values of \textit{HOTAIR} (probe \textit{A}\_\textit{32}\_\textit{P168442}) and \textit{HOXA9} (probe \textit{A}\_\textit{23}\_\textit{P500998}) were used. \textit{HOTAIR}-high was considered when “level 3” value \(\geq 0\), and \textit{HOXA9}-high when \(\geq 2\). RNA-
seq data from additional 161 GBMs, 511 grades II and III glioma patients and 5 unmatched normal samples were also collected (Supplementary Table 1). These data were evaluated using Illumina HiSeq 2000 sequencing system. Genes with a “level 3” value = 0 were considered to have undetectable levels of mRNA expression. Cases were classified based on WHO malignancy grade and considering genetic information according to latest WHO recommendations [1]. To: IDH-wt; IDH-mut (without 1p/19q codeletion), and IDH-mut and 1p/19q codeleted.

Gene copy number data were assessed by Affymetrix Genome-Wide Human SNP Array 6.0 in 372 GBM samples. Gene amplifications or deletions were considered for Log2 copy number tumor/normal ≥0.5 (gene copy number ≥3) or ≤–0.5 (gene copy number ≤1), respectively.

Tumor DNA methylation profiles were detected by Illumina Infinium Human DNA Methylation 450 array and include the methylation status of 74 GBM samples. We evaluated 56 probes that span from the HOXC12 (upstream of HOTAIR) to HOXC11 (downstream of HOTAIR). High methylation was considered for β-values > 0.5.

Analysis of HOTAIR expression in Oncomine and REMBRANDT

The human cancer microarray database Oncomine (www.oncomine.com; Oncomine™, Compendia Bioscience, Ann Arbor, MI) was used for analysis and visualization [58] of HOTAIR expression (probe 239153_at) in 45 WHO grade II, 98 WHO grade III, and 296 primary WHO grade IV gliomas (Supplementary Table 1). Categorization of HOTAIR-positive and HOTAIR-negative glioma patients was based on the Log2 median-centered intensity values of HOTAIR probe. Log2 median-centered intensity values >0 correspond to high HOTAIR expression, and Log2 values ≤0 correspond to low/negative HOTAIR expression. The Oncomine database was also used to identify genes frequently co-expressed with HOTAIR in gliomas and other cancer datasets [lung (n = 167), breast (n = 593), leukemia (n = 197), and colorectal cancer (n = 237)]. Details on the normalization techniques and statistical calculations can be found on the website (www.oncomine.com) [58].

The REMBRANDT platform (National Cancer Institute REMBRANDT, accessed 2013 June; available now at https://gdoc.georgetown.edu/gdoc/) was queried to evaluate 67 GBM patients (Supplementary Table 1); the cut-off for HOTAIR high expression was established as ≥4-fold than HOTAIR expression in non-tumor samples.

RNA extraction, cDNA synthesis, and gene expression analyses in primary glioma samples and cell lines

Total RNA was extracted from glioma patient samples and cell lines using the TRIzol method (Invitrogen, Carlsbad, CA, USA) for the Portuguese dataset or the RNeasy Mini Kit (Qiagen, Hamburg, GmbH) for the French dataset, and cDNA was synthesized using High Capacity cDNA Reverse Transcription kit (Applied Biosystems, Foster City, CA, USA) according to the manufacturer’s protocol.

For the Portuguese dataset, gene expression levels were assessed by RT-PCR (Amplitaq Gold 360, Applied Biosystems, Foster City, CA, USA) and quantitative reverse transcriptase real-time PCR (qPCR; KAPA Biosystems, Foster City, CA, USA) according to manufacturer’s instructions (primer sequences in Supplementary Table 7). Housekeeping genes used to normalize gene expression levels were hGUS, TBP, HPRT1, or ACTIN, as stated on each analysis. For all tested genes, the standard PCR parameters were as follows: 4 minutes at 94°C, 35 cycles of denaturation for 30 seconds for the RT-PCR or 3 seconds for the qPCR at 94°C, annealing for 30 seconds (Supplementary Table 7), extension at 72°C for 30 seconds, and final extension at 72°C for 8 minutes for conventional PCR, or increments of 1°C each 5 seconds from 65 to 95°C for the qPCR. The cut-off for high expression of both HOTAIR and HOXA9 was established as >5% of relative expression (upon normalization to housekeeping gene).

In the French dataset, microfluidic-based quantitative analysis (Fluidigm) was used to assess HOTAIR and HOXA9 genes expression levels. cDNA was preamplified for 14 cycles with the pool of primers available in Supplementary Table 7 by using the TaqMan PreAmplication Master Mix (Applied Biosystems). qRT-PCRs were next conducted and validated on Fluidigm 96.96 Dynamic Arrays using the Biomark HD system (Fluidigm Corp.) according to the manufacturer’s instructions. The relative quantification in gene expression was determined after normalization to a geometrical mean of housekeeping genes expression, namely PPIA, HPRT1 and TBP. For each condition, data presented in this study are obtained from two independent experiments, each analyzed in duplicate.

5-Aza-2′-deoxycytidine treatment, DNA isolation, bisulfite conversion and HOTAIR methylation-specific PCR

Glioma cell lines were treated with 5 µM 5-Aza (Sigma-Aldrich®, St. Louis, MO, USA) or dimethyl sulfoxide (DMSO; Sigma-Aldrich®, St. Louis, MO, USA) for 72 hours with daily renewal. Cells were collected by trypsinization, and DNA and RNA were extracted by the TRIzol method. RNA was used to assess HOTAIR expression levels as previously described, and DNA was subjected to sodium bisulfite conversion using the EZ DNA Methylation-Gold™ Kit (Zymo Research, Foster City, CA, USA), according to the manufacturer’s protocol. Touchdown MSPs for HOTAIR promoter were performed (AmpliTaq Gold 360; 3 cycles at 62°C with decrement of 1°C; 6 cycles at 59.5°C with decrement of 0.5°C; and
29 cycles at 57° C; primers in Supplementary Table 7). Blood DNA of a control subject (NB569) was bisulfite treated and used as an unmethylated control for MSP reactions. The same DNA was in vitro methylated ( CpG Methyltransferase M.SssI; New England Biolabs Inc.) according to manufacturer’s protocol, followed by sodium bisulfite treatment, and used as a methylated control.

In the French dataset, HOTAIR DNA methylation profile was obtained by Illumina Infinium Human DNA Methylation 450 array performed on the 43 glioma samples. We evaluated 26 probes that cover the HOTAIR locus between HOXC11 and HOXC12 (chr12:54,355,686–54,369,516). High methylation was considered for β-values > 0.5.

In silico analysis of transcription factor binding sites in HOTAIR promoter by Genomatix

MatInspector from Genomatix software [59] (www.genomatix.de) was used to investigate putative transcription factors binding sites in HOTAIR gene. This in silico tool identifies transcription factor binding sites in nucleotide sequences based in a large library of weight matrices [59, 60]. A perfect match gets a matrix similarity of 1 when the tested sequence corresponds to the most conserved nucleotide at each position of the matrix. A good match to the matrix was considered when matrix similarity >0.80.

Chromatin-immunoprecipitation analysis

ChIP experiments were done as previously described [61]. In brief, U251, U87MG-MSCV and U87MG-HOXA9 cells were cross-linked with 1.42% formaldehyde for 15 minutes, followed by quenching with 125 mM glycine for 5 minutes. Cells were then lysed with immunoprecipitation buffer (150 mM NaCl, 50 mM Tris-HCl, 5 mM EDTA, 0.5% NP-40, 1% Triton X-100) and chromatin was sheared by sonication (Sonics Vibra Cell VC70T, 21 cycles for 15 seconds) to obtain DNA fragments of approximately 0.5–1kb. The volume of sheared chromatin equivalent to 2 million cells was incubated with the required antibody in an ultrasonic bath for 15 minutes, followed by incubation with protein A-sepharose beads (Amersham, Uppsala, SE) and Chelex 100 (BioRad, Hercules, CA, USA). The following antibodies were used per immunoprecipitation: 4 μg anti-HOXA9 (Santa Cruz Biotechnologies, Santa Cruz, CA), and 3 μg anti-Immunoglobulin G (IgG; Sigma-Aldrich, St. Louis, MO, USA) as ChIP negative control. The input represents a control for the amount of DNA used in precipitations. DNA amplification was done by qPCR (KAPA SYBR FAST, KAPA Biosystems) according to manufacturer’s instructions with primers designed to amplify a portion of the HOTAIR promoter region that spans from bp -991 to -826 from the HOTAIR transcriptional start site (Supplementary Table 7). The qPCR parameters were as follows: 4 minutes at 94° C, 35 cycles of denaturation for 3 seconds, annealing for 30 seconds at 60° C, extension at 72° C for 30 seconds, and final extension consisting in increments of 1° C each 5 seconds from 65 to 95° C. The U251 fold enrichment of HOTAIR promoter over IgG, and the fold change occupancy of HOTAIR promoter in HOXA9-overexpressing over their negative counterparts for U87MG, were calculated for each experiment using the ΔΔCt method as described previously [62]. Three biological replicates were tested, and each qPCR experiment was performed in triplicates.

Statistical analyses

Statistical analyses were performed using the SPSS 22.0 software (SPSS, Inc., Chicago, IL, USA) for the TCGA and Portuguese datasets, and the Stata software, version 13 (StataCorp, College Station, TX, US) for the French dataset. Tests were two-sided, with a type I error set at α = 0.05. Due to more limited sample size in the French dataset, HOTAIR threshold has been determined according to ROC curve analysis, and estimation of several indexes recommended in literature [63–65] and biological relevance. Univariable survival analyses to assess the prognostic value of HOTAIR and of other clinicopathological features (patient age, gender, KPS, use of chemoradiation therapy, and institution where the patients were treated) were performed by the Log-rank test whenever these data were available. Additionally, the independent prognostic value of HOTAIR was further analyzed by a multivariable Cox proportional hazard model adjusted for those potential confounding variables. The Chi-square test was used to assess differences between the distributions of tumors with high and low HOTAIR expression, stratified for methylation levels (β-value, TCGA). Correlation between the expression levels of HOTAIR and HOXA9 were calculated by Pearson’s or Spearman’s correlation as indicated throughout the text, and according to data normality. HOTAIR expression level differences between histological groups was assessed by one-way ANOVA (Kruskal-Wallis test) for the TCGA dataset. The qPCR differences in ChIP experiments and between histological groups in the French dataset, and genes expression were calculated by Mann-Whitney test and unpaired Student’s t-test, respectively, using Prism GraphPad software (version 6.0a, San Diego, CA, USA). In Oncomine [58], each gene was evaluated for differential expression using Student’s t-test in the case of two-class analyses (e.g. tumor tissue versus respective normal tissue); for multiclass analyses (e.g. grade II, III, and IV gliomas) Pearson’s correlation was used. The association between methylation indexes of HOTAIR and its expression levels in the TCGA dataset was measured by the Pearson’s correlation (r) using SPSS 22.0 software.
Abbreviations


Author contributions

A.X-M. and C.S.G. designed, conducted and analyzed experiments, and wrote the manuscript. A.F. and B.P. conducted experiments and analyzed data from the French dataset. A.F., T.L. and P.A. assisted in manuscript writing. T.L. and M.P. assisted in obtaining the glioma specimens and generation of DNA and RNA, and provided intellectual input. M.C.L., I.C., O.R. and H.T. provided the samples from the Hospital Coimbra dataset. J.L., R.M. and A.A.P. provided the samples from the Hospital Braga dataset. M.R., C.J., R.M.R, J.F.C., P.A., and N.S. assisted during data analysis and provided intellectual input and valuable discussion. B.M.C. designed and supervised experiments, analyzed data, and wrote the manuscript.

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CONFLICTS OF INTEREST

The authors disclose no potential conflicts of interest.

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