Sexually dimorphic impact of the iron-regulating gene, HFE, on survival in glioblastoma

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Abstract

Background. The median survival for patients with glioblastoma (GBM), the most common primary malignant brain tumor in adults, has remained approximately 1 year for more than 2 decades. Recent advances in the field have identified GBM as a sexually dimorphic disease. It is less prevalent in females and they have better survival compared to males. The molecular mechanism of this difference has not yet been established. Iron is essential for many biological processes supporting tumor growth and its regulation is impacted by sex. Therefore, we interrogated the expression of a key component of cellular iron regulation, the HFE (homeostatic iron regulatory) gene, on sexually dimorphic survival in GBM.

Methods. We analyzed TCGA microarray gene expression and clinical data of all primary GBM patients (IDH-wild type) to compare tumor mRNA expression of HFE with overall survival, stratified by sex.

Results. In low HFE expressing tumors (below median expression, n = 220), survival is modulated by both sex and MGMT status, with the combination of female sex and MGMT methylation resulting in over a 10-month survival advantage (P < .0001) over the other groups. Alternatively, expression of HFE above the median (high HFE, n = 240) is associated with significantly worse overall survival in GBM, regardless of MGMT methylation status or patient sex. Gene expression analysis uncovered a correlation between high HFE expression and expression of genes associated with immune function.

Conclusions. The level of HFE expression in GBM has a sexually dimorphic impact on survival. Whereas HFE expression below the median imparts a survival benefit to females, high HFE expression is associated with significantly worse overall survival regardless of established prognostic factors such as sex or MGMT methylation.

Key Points

• There is a sex-specific effect of HFE mRNA expression in GBMs on survival.
• High HFE results in poor survival in GBM regardless of patient sex or MGMT status.
• Survival differences may be due to HFE related immunosuppression in the tumor microenvironment.
Glioblastoma (GBM) is the most common type of primary malignant brain tumor in adults. Despite aggressive therapy, the median survival for GBM patients has remained at about 1 year, necessitating the need for a new paradigm to GBM treatment.\textsuperscript{1,2} Recent evidence suggests that GBM is a sexually dimorphic disease.\textsuperscript{3,4} GBMs are less common in females, yet females have better survival.\textsuperscript{5,6} Prognostic indicators like O[6]-methylguanine-DNA methyltransferase (MGMT) and Isocitrate Dehydrogenase (IDH) status also modify survival based on sex. Females with MGMT methylated GBMs have better survival rates than males and males have improved survival with IDH-mutant GBMs.\textsuperscript{7,8} The molecular mechanism that underlies this sex-based difference has yet to be established.

Iron homeostasis is essential for cellular energy production and DNA synthesis, particularly in rapidly dividing cells, and thus plays a critical role in cancer development and maintenance.\textsuperscript{9-11} Elevated expression of iron-regulating genes is correlated with worse survival in multiple cancers including breast, prostate, and colon.\textsuperscript{10-14} In breast cancer, a molecular signature representing decreased iron acquisition is associated with better outcome whereas a signature indicating decreased iron export is associated with worse outcome.\textsuperscript{15} In GBMs, both glioma and cancer stem cells can upregulate the iron transporter transferrin, conferring improved iron extraction from the tumor microenvironment to promote proliferation.\textsuperscript{16,17}

A key regulator of cellular iron uptake is the homeostatic iron-regulator protein (HFE), which binds to transferrin receptors (TFRs) decreasing TFR affinity to transferrin, consequently reducing iron uptake. Mutations of the HFE gene result in cellular iron overload, and one of the mutations C282Y was first discovered as the genetic cause of an iron overload disorder found predominantly in men; hemochromatosis.\textsuperscript{18} To date, the role of HFE in tumor biology has focused primarily on the impact of HFE mutations.\textsuperscript{19-23} For example, we have previously shown female GBM patients who carry C282Y HFE polymorphism have shorter survival than both wild-type (WT) patients and male metastatic brain tumor patients with C282Y.\textsuperscript{23}

Despite the interest in the incidence and effect of common HFE gene mutations on the disease, including cancer, very little data have been published on the impact of expression of WT HFE gene levels in cancer. Reuben et al.\textsuperscript{24} previously described higher levels of HFE expression in tumor cell lines from melanoma, lung, and kidney cancers, yet few studies have looked at HFE expression in patient tumor samples. We previously identified several iron metabolism genes associated with changes in survival for patients with low-grade glioma (LGG) and found high HFE gene expression resulted in a 5-year decrease in patient survival compared to low HFE expression.\textsuperscript{25}

Here we present data revealing that there are significant sex differences in overall survival associated with HFE gene expression and that a synergistic interplay exists between MGMT methylation status, sex, and HFE expression that impact patient survival in GBM.

**Methods**

**HFE mRNA Expression and Survival Data**

Gene expression, tumor phenotype, and de-identified patient data were acquired from The Cancer Genome Atlas (TCGA) GBM \((n = 525)\). This dataset was downloaded from a publicly available data visualization software program, GlioVis.\textsuperscript{26} Microarray data were chosen for its large sample size \((n = 525)\) and availability of data including sex, survival status, and tumor MGMT methylation status. Updated survival data for TCGA GBM were contributed by Dr Joshua B. Rubin’s group. To identify and remove outliers, Cook’s distance was calculated based on a linear regression of survival times with respect to HFE mRNA expression. Any observation with Cook’s distance greater than 98th percentile was noted as an outlier and removed from data analysis \((n = 10)\). We excluded nonprimary tumors \((n = 21)\) and IDH-mutant GBMs \((n = 34)\) from the analysis group resulting in 460 total samples for analysis.

We first determined the median HFE mRNA expression of all GBM samples to establish the high and low HFE groups. We then focused our analysis on primary, IDH-WT tumors \((n = 460, \text{low } n = 220, \text{high } n = 240)\). To determine whether the impact of HFE on survival may be therapy dependent, we compared individuals who had received temozolomide (TMZ) \((n = 274)\) versus those who did not \((n = 170)\). Positive TMZ therapy was defined by any patient who had TMZ therapy, in combination with any other therapy, for example, concomitant radiation therapy. See Table 1 for demographics summary.

We attempted to replicate our main results in other datasets but to appropriately assess our model, we needed to identify datasets that contained all of the variables used in the original model, which includes survival time, sex, MGMT methylation status, and recurrence status, in addition to the gene expression profiles of the tumors. At least one of these main variables was missing from each of the available datasets except for the Murat dataset (although this did not include IDH status).
Statistical Analysis

Sample test for equality of proportions was used to detect baseline differences for sex, MGMT, resection, and TMZ and Welch two-sample t-test was used for age and KPS. Median HFE mRNA expression was based on all GBM patients provided by TCGA GBM, including IDH-mutant, nonprimary, and outlier samples (determined by Cook’s distance). Removal of those samples results in an n = 20 difference in HFE groups, as opposed to n = 220 equal split as would otherwise be expected. Not all phenotype data are available for each sample, thus the number of available samples are included next to category name.

Table 1. Demographics of GBM Patients Included in the Study

| Category          | Overall (n = 460) | High HFE (n = 240) | Low HFE (n = 220) | P  |
|-------------------|-------------------|--------------------|-------------------|----|
| Sex               |                   |                    |                   |    |
| Female, % (n)     | 61.52 (283)       | 58.75 (141)        | 64.55 (142)       | .24|
| Male, % (n)       | 38.48 (177)       | 41.25 (99)         | 35.45 (78)        |    |
| MGMT (n = 301)    |                   |                    |                   |    |
| Methylated, % (n) | 42.52 (128)       | 41.33 (62)         | 43.71 (66)        | .76|
| Unmethylated, % (n) | 57.48 (173)   | 58.67 (88)         | 56.29 (85)        |    |
| Age               |                   |                    |                   |    |
| Median (range)    | 61 (10–89)        | 60 (14–86)         | 61 (10–89)        | .62|
| KPS               |                   |                    |                   |    |
| Median (range)    | 80 (20–100)       | 80 (20–100)        | 80 (20–100)       | .83|
| Rejection (n = 457) | Biopsy, % (n)  | 12.25 (56)         | 11.76 (28)        | .85|
|                   | Tumor resection, % (n) | 87.75 (401)       | 88.24 (210)       |    |
| TMZ (n = 444)     | No, % (n)         | 38.29 (170)        | 39.47 (90)        | .67|
|                   | Yes, % (n)        | 61.71 (274)        | 60.53 (138)       |    |

Two-sample test for equality of proportions was used for sex, MGMT, resection, and TMZ and Welch two-sample t-test was used for age and KPS. Median HFE mRNA expression was based on all GBM patients provided by TCGA GBM, including IDH-mutant, nonprimary, and outlier samples (determined by Cook's distance). Removal of those samples results in an n = 20 difference in HFE groups, as opposed to n = 220 equal split as would otherwise be expected. Not all phenotype data are available for each sample, thus the number of available samples are included next to category name.

Gene Expression Analysis

The aim of our gene expression analysis was to identify gene sets which were significantly different between low and high HFE groups and subsequently, the expression of which also correlated with HFE mRNA expression. Herein, we only focused on 2 subsets of gene expressions that were shown to have the greatest survival differences between low and high HFE while also presenting comparative information on sex differences: males with MGMT methylated tumors and females with MGMT methylated tumors. Genes found to be most different between the 2 groups were then analyzed through PANTHER GO Enrichment Analysis of Biological mechanisms.29

Microarray Data Processing by GlioVis

HFE mRNA expression was reported by microarray data collected from the Affymetrix expression array HG-U133 platform. GlioVis downloaded available raw.CEL files from TCGA and processed in R using the Bioconductor suite. The “affy” package was used for robust multi-array average normalization followed by quantile normalization. The median of all probes was used for genes with several probe sets.

GlioVis provided mRNA data on approximately 12,000 genes analyzed in each GBM tumor sample. These data were downloaded and analyzed as described in Gene Expression Analysis section. To elucidate the meaning of differential gene expression, gene sets were analyzed by GO Enrichment Analysis.
associated with HFE in the presence of several other genes. We conducted penalized elastic net regression (R package glmnet) with HFE expression as response and the gene expressions from step (1) as covariates. The elastic net model had a considerable higher weight for ridge regression than LASSO so that the number of resulting genes were not over-regularized. This regression controls the problem of multicollinearity by shrinking the coefficients of highly correlated gene expressions. We chose only those genes whose coefficients are non-zero, implying an association with HFE.

The final set of genes are both common to genes obtained from step (2) and step (3). Note that this multilevel strategy was stricter and controlled for spuriously correlated gene expressions. Please see Figure 3 for schematic and results of this analysis strategy.

**Results**

**High HFE Expression Is Associated With Significantly Worse Patient Survival in Brain Tumors**

In the TCGA GBM LGG microarray dataset, tumors expressing HFE above the median are associated with shortened survival for all brain tumor populations (114 months vs 21.3 months, log-rank $P < .0001$, Figure 1A). Restricting the analysis to the TCGA GBM data also revealed a similar and significant difference (Figure 1B; $P = .0088$) between the high and low HFE GBM expressing groups. HFE expression increases with increasing grade of the tumor (all adjusted $P < .05$, Figure 1C) and is the highest in GBM ($P < .0001$, Figure 1D). Furthermore, within GBM subtypes, HFE expression is highest in the mesenchymal subtype, associated with worse patient prognosis, and lowest in the proneural subtype ($P < .0001$, Figure 1E).

A CoxPH regression model was then run with HFE as a continuous variable. After controlling for known prognostic factors (sex, MGMT status, KPS, resection, and age), the impact of HFE on survival was not significant, yet neither was KPS, resection, sex, nor MGMT methylation status (Table 2 and Supplementary Table S1). Because MGMT and sex have been established as significant prognostic indicators, this was an unexpected finding. Thus, we considered whether HFE, MGMT status, and sex may interact, suggesting that HFE expression might be negatively influencing survival based on the patient’s sex and MGMT methylation status. To nullify the possibility of confounding of HFE expression by sex and MGMT methylation status, a simple linear regression was performed, verifying HFE expression did

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**Figure 1.** (A–E) Survival and expression differences of HFE in low-grade gliomas and glioblastoma. Survival in low HFE (blue) versus high HFE (red) in all brain tumors (A) and in glioblastoma (B). HFE mRNA expression based on tumor grade (C), tumor histology (D), and glioblastoma subtype (E). These figures were directly rendered by and downloaded from GlioVis.
| Table 2. Survival Differences Based on HFE Group, MGMT Status, Sex, and Temozolomide Therapy |
|-----------------------------------------------|
| **All Data** | **Low HFE mRNA (<Median)** | **High HFE mRNA (≥Median)** |
| **N** | **Deaths** | **Median (CI)** | **P** | **N** | **Deaths** | **Median (CI)** | **P** | **N** | **Deaths** | **Median (CI)** | **P** |
| Male | 283 | 242 | 12.7 (11.9–14.0) | .8 | 142 | 120 | 12.6 (10.9–13.9) | .07 | 141 | 122 | 12.9 (11.9–14.9) | .1 |
| Female | 177 | 142 | 12.5 (10.5–15.3) | .049* | 78 | 62 | 14.7 (11.5–20.1) | .003** | 99 | 80 | 10.7 (8.6–14.9) | .7 |
| Log rank | | | | | | | | | | | | |
| MGMT | Male: Methylated | 66 | 55 | 13.3 (10.7–17.6) | .002** | 40 | 35 | 13.3 (10.2–19.5) | <.0001**** | 26 | 20 | 12.9 (7.6–20.4) | .7 |
| Female: Methylated | 62 | 45 | 17.8 (13.8–21.3) | .12 | 26 | 19 | 24.9 (17.8–33.2) | .014* | 36 | 26 | 13.6 (7.0–20.7) | .6 |
| Male: Unmethylated | 112 | 87 | 12.6 (10.6–14.0) | .002** | 57 | 45 | 10.9 (9.5–14.0) | <.0001**** | 55 | 42 | 12.9 (11.9–15.0) | .4 |
| Female: Unmethylated | 61 | 45 | 11.7 (9.9–175) | .001*** | 28 | 21 | 11.7 (9.9–22.2) | <.0001**** | 33 | 24 | 12.2 (8.8–179) | .3 |
| MGMT (All therapy) | Male: Methylated | 47 | 38 | 16.5 (13.3–20.8) | .002** | 31 | 26 | 16.1 (12.7–21.1) | <.0001**** | 16 | 12 | 18.1 (12.9-NA) | .7 |
| Female: Methylated | 43 | 28 | 20.7 (15.6–26.9) | .0008*** | 19 | 14 | 25.7 (19.9-NA) | <.0001**** | 24 | 14 | 15.6 (12.4-NA) | .2 |
| Male: Unmethylated | 81 | 60 | 12.9 (12.2–14.9) | .0002*** | 40 | 31 | 12.7 (11.3–15.4) | <.0001**** | 41 | 29 | 13.9 (12.6–16.6) | .6 |
| Female: Unmethylated | 38 | 27 | 14.5 (10.2–21.9) | .0008*** | 18 | 13 | 11.7 (9.9-NA) | <.0001**** | 19 | 14 | 14.9 (12.2-NA) | .3 |
| Temozolomide Therapy | Male: Methylated | 18 | 17 | 3.1 (2.0–76) | .06 | 9 | 9 | 2.0 (1.1-NA) | .05 | 9 | 8 | 5.9 (2.8-NA) | .7 |
| Female: Methylated | 15 | 14 | 6.6 (3.6–25.4) | .06 | 5 | 4 | 15.1 (3.6-NA) | .03* | 10 | 10 | 5.5 (2.3-NA) | .8 |
| Male: Unmethylated | 27 | 23 | 5.8 (1.6–10.6) | .05 | 16 | 13 | 76 (1.1-NA) | .01 | 11 | 10 | 5.3 (1.6-NA) | .7 |
| Female: Unmethylated | 20 | 16 | 6.6 (4.6–175) | .05 | 8 | 7 | 6.1 (4.1-NA) | .002*** | 12 | 9 | 9.1 (2.9-NA) | .6 |
| No Temozolomide Therapy | Male: Methylated | 18 | 17 | 3.1 (2.0–76) | .06 | 9 | 9 | 2.0 (1.1-NA) | .05 | 9 | 8 | 5.9 (2.8-NA) | .7 |
| Female: Methylated | 15 | 14 | 6.6 (3.6–25.4) | .06 | 5 | 4 | 15.1 (3.6-NA) | .03* | 10 | 10 | 5.5 (2.3-NA) | .8 |
| Male: Unmethylated | 27 | 23 | 5.8 (1.6–10.6) | .05 | 16 | 13 | 76 (1.1-NA) | .01 | 11 | 10 | 5.3 (1.6-NA) | .7 |
| Female: Unmethylated | 20 | 16 | 6.6 (4.6–175) | .05 | 8 | 7 | 6.1 (4.1-NA) | .002*** | 12 | 9 | 9.1 (2.9-NA) | .6 |

NA, upper confidence interval could not be calculated/infinity.
* CoxPH P-value based on hazard coefficients.
** Robustified CoxPH P-value for the overall model fit.
*P-value < .05, **P-value < .01, ***P-value < .001, ****P-value < .0001.
not differ significantly based on sex or MGMT status (Table 1).

High HFE Expression Abrogates Survival Benefit of Both Female Sex and MGMT Methylation

The dataset was then divided into 2 separate groups, low HFE and high HFE based on median HFE expression. CoxPH analysis of these groups, controlling for the same factors as mentioned above, revealed 2 distinct and sexually dimorphic survival patterns. A low HFE tumor expression level is associated with better survival for females (Figure 2A) compared to males but there is no sex difference in survival in the high HFE tumor expressing group (Figure 2D). The established MGMT tumor methylation survival benefit was seen in the low HFE group, but not in the high expressing HFE group (Figure 2B and E). There was a clear effect of sex and HFE status on the MGMT effect; females with low HFE and MGMT methylated tumors survive significantly longer than males regardless of their MGMT status. High HFE expression negated the MGMT and sex benefits to survival (Figure 2C and F).

We determined to use the median HFE expression to help maintain equal sample sizes for the analysis groups (low HFE vs high HFE) to prevent imbalance in the groups. To confirm that impact of HFE on survival does not depend on the chosen median cutoff, we reproduced our main result using 40th and 60th percentile cutoffs (Supplementary Table S2). Furthermore, interrogation of the Murat data using the median HFE expression generated similar results (Supplementary Table 3).

High HFE Negates the Impact of MGMT Methylation in TMZ Treatment

We confirmed that irrespective of HFE status, sex, and methylation status, receiving TMZ therapy versus treatments without TMZ (but did receive radiation) was beneficial for survival. Supporting our previous results, for patients taking TMZ, the survival advantage of being female is amplified by positive methylation status in the low HFE group (25.7 months vs 16.1 months in methylated males, Table 2). Regardless of MGMT status or sex, high HFE continued to abrogate survival advantages seen at low HFE (Table 2).

In patients who did not receive TMZ, we observed the same pattern of sex-based survival differences, with females having a survival advantage over males at low HFE and similar survival to males at high HFE (Table 2). At low HFE, the median survival of females in the methylated group was 15 months versus 2 months for males in the same group. Similarly, to the group treated with TMZ, high HFE expression negated the survival benefit of the combination of female sex and methylation status in the group that was not treated with TMZ (Table 2).

**Figure 2.** (A–F) Impact of HFE expression, sex, and MGMT status on survival in glioblastoma. The top row represents all samples with low HFE expression (below median) and is separated into 3 columns based on differences in survival in males versus females (A), MGMT status (B), or both sex and MGMT status (C). Similarly, the row below is also separated by the same comparisons as above yet representing individuals with high HFE expression (D–F).
Gene Expression Profiles

To begin to interrogate the relationship between HFE expression and the tumor microenvironment, over 3000 genes were found to be significantly different in the low and high HFE expressing groups (Figure 3) including sex-based differences. When comparing upregulated genes, males and females shared 884 genes in the low HFE group and 694 genes in the high HFE group (data not shown). Gene enrichment analysis in low HFE groups shows upregulation of genes responsible for DNA topological change, synaptic vesicle assembly, and microtubule development (Figure 4A and B) in both sexes. A unique pathway upregulated in males with low HFE includes negative regulation of histone H3-K9 methylation (Figure 4A). Females in the low HFE group show unique upregulation in nucleosome disassembly and response to hydroxyurea (Figure 4B).

High HFE expression, regardless of sex, is associated with upregulation of pathways involving T-cell activation, chemokine production, and cell apoptosis, among others (Figure 4C and D). Specifically, the most highly upregulated genes in both males and females with high HFE were those associated with the regulation of CD4-positive, T-cell proliferation (Figure 4C and D). Males with high HFE showed enrichment for genes associated with positive regulation of antigen presentation and processing (Figure 4C), while females uniquely showed upregulation of pathways associated with ganglioside catabolic processes and AMP biosynthesis (Figure 4D).

Discussion

We present data showing that the level of gene expression of a key iron-regulating protein, HFE, is a prognostic indicator of survival in patients with brain tumors. Furthermore, in GBMs, the prognostic value of HFE is impacted by sex and MGMT methylation status. Not only
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advantage only when those studies. For example, we show that female sex is an positive MGMT methylation. positive prognostic indicators, specifically female sex and expression completely abrogates previously published reports that females have a more significant survival benefit from MGMT methylation. Moreover, this finding extends to MGMT methylated tumors where only females with low HFE expression and methylated tumors experience a significant survival advantage. When HFE tumor expression is high, methylation no longer conferred a survival advantage to females. In contrast, we did not find significant differences in male survival based on HFE expression status. Had we not separated these HFE analyses by sex, the significant differences for the expression data would have been washed out by the male survival data. There was no additional benefit of HFE expression level to the MGMT methylation status and survival for males. These data are consistent with reports that females have a more significant survival benefit from MGMT methylation.7

Sex may also influence treatment response, with females responding better to the standard of care therapy, including TMZ, and our analysis found similar trends.6 We confirmed that in patients treated with TMZ, methylation is advantageous to females, yet only when HFE levels are low. In the high HFE group, MGMT methylation no longer conferred a survival advantage to females who were...
treated with TMZ. Because HFE status was determined by the median mRNA expression of all GBM patient tumor samples, our data predict that half of all females with GBM would not have the anticipated better survival due to MGMT methylation. In the TMZ group, survival differences widened slightly. Females at low HFE and MGMT methylated tumors have a median survival of 25.7 months, which is close to twice the median survival of patients with GBM overall. These data support results by Yang et al., yet, with the caveat that females had improved response to TMZ only if their HFE expression was lower than the median, otherwise, it was similar to males. From these data, it can be postulated that HFE is either actively modulating response to TMZ or is a marker of response to TMZ therapy. However, even those females who do not receive TMZ therapy still experience the greatest survival advantage when their tumors have the combination of MGMT methylation and low HFE expression. The effects of HFE in the tumor microenvironment do not simply reflect sex-based levels of HFE expression in the tumors (Table 2). Thus, the HFE survival effect appears to be intrinsic to the tumor microenvironment. The underlying mechanism is currently being explored but could be related to epigenetic influences. For example, iron is a required co-factor for demethylases, thus its availability directly impacts on histone and DNA methylation, and consequently on gene expression. Iron overload dysregulates global methylation and mice with HFE mutations have lower rates of global methylation than WT mice. Likewise, iron chelation also results in epigenetic alterations in breast cancer cells making them more susceptible to doxorubicin and cisplatin. These data link HFE expression, which regulates cellular iron status, to methylation state. This information could have clinical value. For example, the gene expression data showing the upregulation of topoisomerase genes in both male and female low HFE groups suggests that these tumors could be more susceptible to topoisomerase inhibitors.

HFE and Immunity

Gene expression data acquired from tumor samples provide information not only on the neoplastic cells but also on the infiltrating immune cells which are critical to tumor proliferation. Macrophages make up the bulk of infiltrating immune cells in GBMs and play a critical role in regulating the tumor microenvironment. HFE is highly expressed in macrophages and these cells are key regulators of iron. Thus, HFE mRNA expression may be reflective of the volume of these cells in the tumor. HFE expression may also be directly influencing the immune cell function in the tumor microenvironment. Expression of HFE interferes with MHC class I antigen presentation and impairs activation and differentiation of CD8+ T lymphocytes. HFE’s role as a negative regulator of CD8+ T cells may allow for the predominance of other lymphocytes consistent with the significant upregulation of CD4+ T-cell genes identified in the high HFE groups.

Finally, an obvious goal of identifying the sex-based differences in GBMs prevalence and outcomes is to help develop models to guide therapeutic strategies. Although our studies and others in this field are in their infancy, insights can begin to be discussed. For example, a developing therapeutic area for GBM has been immunotherapy, specifically with regard to the use of PD-L1 inhibitors. Binding of PD-1 to PD-L1 delivers a signal to encourage the suppression of T-cell proliferation. Uptregulation of PD-L1 in circulating monocytes and tumor-associated macrophages is associated with cytotoxicity to T cells, while also inducing and maintaining T regulatory cells (CD4 T cells) in glioma with increased expansion, perhaps to maintain immunosuppressive environment through T regulatory cells in the tumor, which is ultimately associated with worse GBM prognosis. Interestingly, this finding is consistent with observations in the high HFE groups, both in males and females; an upregulation of genes involved in T-cell proliferation and activation. PD-L1 expression is higher in IDH-WT glioma and higher in higher grade tumors, which seems to follow the same pattern as HFE expression (higher in IDH-WT and GBM). Both mechanisms may be related, and if so, may help explain the discrepancies seen between studies in PD-L1 inhibitor efficacy, as only half of all GBM patients would potentially benefit from PD-L1 inhibitors. This is an example of how the use of HFE status of GBMs in clinical settings may prove to be useful in identifying patients who are likely to benefit from PD-L1 inhibitors.

Lastly, in contrast to our findings in GBMs, high HFE expression in breast cancer tumors was associated with better survival in an all-female study. Despite the differences in our findings, these studies underscore the key role of HFE gene expression in predicting survival but indicate that the results are sex- and cancer specific.

Conclusions

Expression of the iron-regulatory gene, HFE, is associated with sexually dimorphic survival in GBM patients. Furthermore, at low expression, the survival effect is impacted by sex and MGMT methylation status. Conversely, high HFE expression completely abrogates previously published positive prognostic indicators, specifically female sex and positive MGMT methylation. The data support further investigation of characterizing the sex-dependent iron signature of GBMs and suggest a relationship between the immune system (including tumor-associated macrophages) and iron biology in the tumor microenvironment.

Supplementary Data

Supplementary data are available at Neuro-Oncology online.

Keywords

glioblastoma | HFE | iron | sex | tumor
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