The Role of Gender-Related Immune Genes in Childhood Acute Myeloid Leukemia

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The study of immune genes and immune cells is highly focused in recent years. To find immunological genes with prognostic value, the current study examines childhood acute myeloid leukemia according to gender. The TARGET database was used to gather the “mRNA expression profile data” and relevant clinical data of children with AML. To normalize processing and find differentially expressed genes (DEG) between male and female subgroups, the limma software package is utilized. We identified prognostic-related genes and built models using LASSO, multivariate Cox, and univariate Cox analysis. The prognostic significance of prognostic genes was then examined through the processing of survival analysis and risk score (RS) calculation. We investigated the connections between immune cells and prognostic genes as well as the connections between prognostic genes and medications. Finally, five immune genes from the TARGET database have been identified. These immune genes are considerably correlated to the prognosis of male patients.

1. Introduction

One of the most frequent blood malignancies, acute myeloid leukemia (AML), makes up about 1% of all cancers [1–4]. Because of the clonal growth of “undifferentiated myeloid progenitor cells,” reduced haematological function and failed bone marrow (BM) are characteristics of AML, both of which can have fatal consequences [5–7]. The main treatment strategy of AML was intensive induction chemotherapy and postremission treatment. Although many AML patients can obtain significant remission through chemotherapy at first, the complete elimination of the disease is still rare and it is very easy to relapse. Pediatric AML accounts for about 25% of pediatric leukemia. Although the incidence is relatively low, the prognosis is poor, so it has a very huge clinical challenge [8–11]. Pediatric AML is a complex disease. The response to treatment varies greatly, even in tumors with comparable histological features. Therefore, we are interested in learning how men and women differ in children AML.

The “tumor microenvironment” (TME) has collected a lot of interest recently [12–15] due to its potential significance in the growth of cancer. TME indicates the cellular setting in which tumor lesions are present. The two most important nontumor components among them, stromal cells and immune cells, were of key significance to the diagnosis and prognosis of cancer [16–20]. Our knowledge of the immunological microenvironment’s function is still lacking, nevertheless, because of its complexity and dynamic nature. Immune cells that have infiltrated tumors were a part of a complex microenvironment [21–23]. Strengthening research on tumor immune cell infiltration in children with AML was particularly important. They are crucial in preventing or promoting the growth and development of tumors. We can develop and use these effects to study the effective targeting of drugs and improve the prognostic survival of patients.

For this work, we used clinical data from the TARGET database to match the “mRNA expression profile data” of children having AML. In order to study the difference in gender in children AML, we performed differential genetic
Volcano

Male (n) = 186  
Female (n) = 172  
Up-diff = 118  
Down-diff = 286

(a)

(b)

Type
F
M

(c)

Figure 1: Continued.
Response to lipopolysaccharide
Response to molecule to bacterial origin
Cellular response to lipopolysaccharide
Cellular response to molecule of bacterial origin
Cellular response to biotic stimulus
Antimicrobial humoral response
Leukocyte chemotaxis
Cell chemotaxis
Antimicrobial humoral immune response mediated by antimicrobial peptide
Granulocyte chemotaxis
Collagen–containing extracellular matrix
Secretory granule matrix
Cytoplasmic vesicle lumen
Vesicle lumen
Golgi lumen
Tertiary granule lumen
Specific granule lumen
External side of plasma membrane
Endoplasmic reticulum lumen
Receptor ligand activity
Signaling receptor activator activity
Cytokine activity
Cytokine receptor activity
Growth factor activity
Growth factor receptor binding
Chemokine receptor binding
Chemokine activity
G protein–coupled receptor binding
Transforming growth factor beta receptor binding
Antimicrobial humoral immune response mediated by antimicrobial peptide

Figure 1: Identification of differentially expressed gender-related prognostic immune genes and functional enrichment analysis in children AML. (a, b) Identification of DEGs in male and female subgroups. (c) Identification of immune-related DEGs. (d, e) GO and KEGG analyses.
identification between the male subgroup and the female subgroup. To discover the function and role of immune genes, we screened immune-related genes from DEGs. GO and KEGG analysis results show that it is related to some important functional pathways in tumors. The prognosis-related genes are screened to evaluate the prognostic significance of important genes. The association and relationship between important genes and immune cells was examined using the "CIBERSORT algorithm" to assess the immune cell situation of the male subgroup.

We further explored the association of key genes and drugs.

2. Materials and Methods

2.1. Database. Children with AML have their mRNA expression reports and accompanying clinical data gathered from TARGET [24]. Clinically insufficient data was removed and classified by gender. In the male group, there were 186 patients, and in the female group, there were 172 patients.

2.2. Detection of Gender-Related Immune Genes. Using the "limma package," various stated genes (DEGs) were discovered between the male and female groups [25, 26]. Adjusted p value < 0.05 and genes with |log FC| > 1 were defined as

| Description | p value | KEGG | Description | p value |
|-------------|---------|------|-------------|---------|
| BP Response to lipopolysaccharide | 2.35E-14 | KEGG | Cytokine-cytokine receptor interaction | 4.87E-20 |
| BP Response to molecule of bacterial origin | 4.14E-14 | KEGG | IL-17 signaling pathway | 6.58E-09 |
| BP Cellular response to lipopolysaccharide | 6.45E-13 | KEGG | JAK-STAT signaling pathway | 6.22E-08 |
| BP Cellular response to molecule of bacterial origin | 9.61E-13 | KEGG | Rheumatoid arthritis | 1.15E-07 |
| BP Cellular response to biotic stimulus | 3.42E-12 | KEGG | Viral protein interaction with cytokine and cytokine receptor | 2.03E-07 |
| BP Leukocyte chemotaxis | 9.23E-10 | KEGG | TNF signaling pathway | 4.87E-07 |
| BP Cell chemotaxis | 1.13E-09 | KEGG | Legionellosis | 2.98E-05 |
| BP Antimicrobial humoral response | 7.96E-11 | KEGG | Amoebiasis | 4.50E-05 |
| BP Granulocyte chemotaxis | 2.65E-09 | KEGG | Chemokine signaling pathway | 0.00021 |
| BP Antimicrobial humoral immune response mediated by antimicrobial peptide | 1.82E-09 | KEGG | Malaria | 0.000285 |
| CC Collagen-containing extracellular matrix | 1.58E-05 | KEGG | Inflammatory bowel disease | 0.000779 |
| CC Secretory granule lumen | 2.95E-05 | KEGG | Transcriptional misregulation in cancer | 0.001381 |
| CC Cytoplasmic vesicle lumen | 3.19E-05 | KEGG | Pertussis | 0.001402 |
| CC Vesicle lumen | 3.32E-05 | KEGG | EGFR tyrosine kinase inhibitor resistance | 0.001618 |
| CC Golgi lumen | 0.000188 | KEGG | African trypanosomiasis | 0.001685 |
| CC Tertiary granule lumen | 0.0000186 | KEGG | Measles | 0.000192 |
| CC Specific granule lumen | 0.000691 | KEGG | Phospholipase D signaling pathway | 0.00253 |
| CC External side of plasma membrane | 0.000767 | KEGG | MAPK signaling pathway | 0.002611 |
| CC Endoplasmic reticulum lumen | 0.001677 | KEGG | TGF-beta signaling pathway | 0.00306 |
| MF Receptor ligand activity | 1.38E-28 | KEGG | Hematopoietic cell lineage | 0.003689 |
| MF Signaling receptor activator activity | 1.83E-28 | KEGG | AGE-RAGE signaling pathway in diabetic complications | 0.003824 |
| MF Cytokine activity | 2.34E-23 | KEGG | Chagas disease | 0.004106 |
| MF Cytokine receptor binding | 3.65E-21 | KEGG | Toll-like receptor signaling pathway | 0.004401 |
| MF Growth factor activity | 6.99E-19 | KEGG | Tuberculosis | 0.005383 |
| MF Growth factor receptor binding | 2.09E-10 | KEGG | Axon guidance | 0.005975 |
| MF Chemokine receptor binding | 9.74E-10 | KEGG | NOD-like receptor signaling pathway | 0.005975 |
| MF Chemokine activity | 6.83E-09 | KEGG | PI3K-Akt signaling pathway | 0.007218 |
| MF G protein-coupled receptor binding | 1.32E-07 | KEGG | Kaposi sarcoma-associated herpesvirus infection | 0.0078 |
| MF Transforming growth factor beta receptor binding | 1.61E-05 | KEGG | Cortisol synthesis and secretion | 0.008345 |
| KEGG | Osteoclast differentiation | 0.009117 |
2.3. Analysis of DEGs. The database Kyoto Encyclopedia of Genes and Genomes (KEGG) is utilized in deducing advanced roles of biological systems from molecular-level information. Gene Ontology (GO) can be utilized to carry out enrichment analysis. We used “org.Hs.eff.db,” “clusterProfiler,” “richplot,” and “ggplot2” software packages to carry out KEGG and GO function enrichment analyses on DEGs. A p < 0.05 was set as a “cut-off criterion.”

2.4. Survival Analysis and Cox Regression and ROC Curve. A univariate Cox analysis was performed on the identified key DEGs, and a p of <0.05 was considered meaningful. To identify the most important prognostic genes, the LASSO analysis and multivariate Cox were carried out in both gender groups, respectively. A model was then built. The “LASSO coefficients” (β) observes the following: Risk Score = ∑nβiExp βi[29–31].

In the above formula, the βi stands for the regression coefficient, while Exp shows the gene expression value. By comparing specificity and sensitivity of risk-based survival prediction, using OS time (1, 3, and 5 years) of the patient, "ROC" curves are used to assess prognostic performance accuracy. In order to evaluate the prognostic value, the part under the curve (AUC) was also determined.

2.5. Evaluation of Immune Cell Type Fractions. A potent analytic technique called CIBERSORT uses gene expression profiles made up of 547 genes [32–34]. It precisely quantifies the components of various immune cells. It employs a deconvolution technique to distinguish each type of immune cell. We subsequently examined the immune cell infiltration in male subsection using the results of the prior investigation. The maximum limit established was at p value (0.05).

2.6. The Correlation Analysis between Key Genes and Drugs. In the current research, the R software is applied to examine the main gene-drug interactions in our work after acquiring data on gene-drug interactions from the CellMiner database [35].

2.7. Analysis. The "glmnet" software programme was used to conduct the LASSO analysis. To plot the survival ROC, we used the "survivalROC" software tool. The "rmda" software package was used to do the decision curve analysis. The "nomogram" and "calibration" diagrams have been created by using the "rms" software package. The "survival" software package is utilized to calculate the c-index and conduct a survival analysis. R version 3.5.1 was employed to conduct the aforementioned investigation, and "p 0.05" was thought as an important value.

3. Result

3.1. The Identification of Differentially Expressed Gender-Related Prognostic Immune Genes and Functional Enrichment Analysis in Children AML. We separated the mRNA expression data for children’s AML into subgroups of males and females using the TARGET database, and then, we looked for differences in the genes between the two. According to the findings, there were 118 DEGs that were notably upregulated, while 286 DEGs were downregulated (Figure 1(a)). First 50 genes were visualized (Figure 1(b)). Then, we compared DEGs with the immune gene set to obtain immune-related DEGs (Figure 1(c)). Using CellMiner data on gene-drug interactions from the CellMiner database, and then, we separated DEGs [32]. It precisely quantifies the components of various immune cells. It employs a deconvolution technique to distinguish each type of immune cell. We subsequently examined the immune cell infiltration in male subsection using the results of the prior investigation. The maximum limit established was at p value (0.05).

3.2. Model Construction and Verification. Male and female subgroups were imperiled to “univariate Cox analysis,” where results revealed that 10 genes in the male subgroup and 4 genes in the female subgroup were significantly related to prognosis (Table 2). Then, to screen genes, we used LASSO analysis. The female subgroup’s outcome was 0, which has no analytical significance (Figures 2(c) and 2(d)). The male subgroup’s outcome was significant (Figures 2(a) and 2(b)). Then, a multifactor Cox analysis on the male subgroup was further performed, and 5 genes (MET, MMP9, MUC4, SEMA3D, and TSLP) used to construct the model were identified (Table 3). For the prognostic ability evaluation of a given standard, we divided male subgroups. The median risk score was the base for this subgroup. Patients were categorized into high-risk and low-risk groups. Patients’ survival was then analyzed. The findings demonstrated that the OS rate of the group having more risk decreased as compared to one having low risk (Figure 2(e)). The assessment can be performed in better way by the prognosis of this model by completing the time-related ROC analysis (Figure 2(f)). Additionally, the "survival status distribution," "risk score distribution," and "heat map" were examined (Figures 2(g)–2(i)). WT1 mutation and risk score can be employed as independent prognostic indicators for
Figure 2: Continued.
Figure 2: Continued.
Figure 2: Continued.
the model as per the findings of univariate and multivariate Cox analysis (Figure 3). In addition, we used 5 genes including MET, MMP9, MUC4, SEMA3D, and TSLP to construct nomograms to foresee one-, three-, and five-year OS (Figure 4(a)). We also constructed a calibration graph. Good accord was observed between the expected and observed findings as shown by graph below (Figures 4(b)–4(d)).

3.3. The Relationship between Genes of the Model and Immune Infiltrating Cells. CIBERSORT was employed for evaluation of 22 immune cells in man patients (Figure 5(a)). A heat map is created (Figure 5(b)), as well as analyzed the association of various “immune infiltrating cells.” The objective was to discover relationship between “immune infiltrating cells” in the male subgroup and genes.
of the model (Figure 5(c)). A high immune cell score is linked to a poor prognosis, according to the results of a survival analysis, later on we conducted (p = 0.034; Figure 6(a)). Furthermore, we looked at the association and relationship between prognosis and the expression levels of various immune cells. The results revealed that high expression of T cells CD4 naive (p = 0.002), macrophage M1 (p = 0.032), and T cell gamma delta (p = 0.001) was associated with a reduced and poor prognosis, whereas high expression of B cells naive (p = 0.025) was associated with a better prognosis (Figures 6(b)–6(e)). Finally, the connection between genes and immune cells was examined, and p < 0.05 was considered meaningful (Figures 6(f)–6(i)). The results showed that MET has a positive relationship with macrophage M1 (R = 0.36, p = 2.2e–05), MUC4 consumes an encouraging association with T cell follicular helper (R = 0.74, p < 2.2e–16), MMP9 and macrophage M0 interact favorably (R = 0.82, p < 2.2e–16), and SEMA3D has a positive relationship with mast cells activated (R = 0.4, p = 1.9e–06).

3.4. The Correlation between Drugs and Genes. We examined the association between the model’s genes and medications in order to further examine their potential relevance in clinical treatment, and we then displayed the top 16 with the highest correlation (Figure 7). The results show that MUC4 has a negative relationship with pertolrex (Cor = −0.613, p < 0.001), epothilone B (Cor = −0.610, p < 0.001), and floxuridine (Cor = −0.438, p < 0.001). MMP9 has a helpful relationship with rebimastat (Cor = 0.559, p < 0.001). MET has a negative association with lomustine (Cor = −0.532, p < 0.001), fenretinide (Cor = −0.472, p < 0.001), lmxenon (Cor = −0.466, p < 0.001), carmustine (Cor = −0.464, p < 0.001), and XK-469 (Cor = −0.456, p < 0.001) and a positive correlation with staurosponine (Cor = 0.491, p < 0.001) and kahalide f (Cor = 0.437, p < 0.001). SEMA3D has a positive correlation with E-7820 (Cor = 0.527, p < 0.001) and a positive association with mitramycin (Cor = −0.518, p < 0.001) and depsipeptide (Cor = −0.470, p < 0.001).

4. Discussion

Due to the rapid advancement of immune checkpoint treatment in recent years such as CTLA-4 and PD-1 in AML, scientists have paid more and more attention to the research of immune genes and immune cells [36–40]. About 25% of paediatric leukemia is paediatric AML. Although the incidence is relatively low, the prognosis is poor, so it has a very huge clinical challenge. In addition, childhood leukemia also has great heterogeneity between tumors, so we want to explore the difference between male and female leukemia. This research used TARGET database to get the “mRNA expression profile data” of children with AML and the related clinical data. Gender based male and female groups were made and differential genes were found in male and female groups which were n = 186 and n = 172, respectively. The outcome was that 118 DEGs were considerably upregulated and 286 DEGs were significantly downregulated (Figure 1(a)). Then, we screened out 57 immune-related genes (Figure 1(c)).

GO analysis results show that “cytokine receptor binding,” “cytokine activity,” “growth factor activity,” “growth factor receptor binding,” “chemokine receptor binding,” “chemokine activity,” “G protein-coupled receptor binding,” “transforming growth factor-beta receptor binding,” etc. have performed significant roles. KEGG analysis results show that many “cancer-related pathways” play a role in it. This may include “cytokine-cytokine receptor interaction,” “IL-17 signaling pathway,” “JAK-STAT signaling pathway,” “TNF signaling pathway,” “chemokine signaling pathway,” “transcriptional misregulation in cancer,” “MAPK signaling pathway,” and “PI3K-Akt signaling pathway.”

“Univariate Cox analysis” was conducted on these immune-related DEGs in order to further examine them. The findings revealed that 10 genes in the group of males and 4 genes in the group of females were associated with prognosis (Table 1). "LASSO analysis" and “multivariate Cox analysis” revealed 5 independent prognostic genes in the male group, but no genes were screened in the female group (Figures 2(a)–2(d)). Patients in male subgroup were divided into high- and low-risk groups on the basis of median risk score. Then, their survival rate was examined to assess the prognostic capability of this model. According to the findings, the high-risk subgroup patients had a considerable low OS rate than that of the low-risk subgroup (p = 0.014; as shown in Figure 2(e)). Risk score can be utilized as an independent “prognostic indicator” for the model, according to the findings of “univariate and multivariate Cox analyses” (Figure 3). We also created a nomogram to forecast one-year, three-year, and five-year OS.

To analyze the formation and composition of 22 immune cells in male patients, we employed CIBERSORT in order to investigate the association between “immune infiltrating cells” in the male subgroup and model genes (Figure 5(a)). The results of survival analysis exhibited that high scores were associated to poor prognosis (p = 0.034; Figure 6(a)). The association and correlation results show that high expression of “T cell CD4 naive (p = 0.002),” “macrophage M1 (p = 0.032),” and “T cell gamma delta (p < 0.001)” was associated with a poor prognosis, and high expression of B cells naive (p = 0.025) was related to better prognosis (Figures 6(b)–6(e)). Additionally, the link between genes and immune cells showed that MET has a positive connection with “macrophage M1 (R = 0.36, p = 2.2e–05),” MUC4 has a positive relationship with “T cell follicular helper (R = 0.74, p < 2.2e–16),” MMP9 has a positive association with “macrophage M0 (R = 0.82, p < 2.2e–16),” and SEMA3D has a positive relationship with “mast cells activated (R = 0.4, p = 1.9e–06).”

| ID | HR  | HR.95L | HR.95H | p value |
|----|-----|--------|--------|---------|
| MET | 1.000132 | 1.000007 | 1.000257 | 0.037817 |
| MMP9 | 1.000022 | 1.000001 | 1.000044 | 0.039233 |
| MUC4 | 1.000785 | 1.000291 | 1.001279 | 0.00185 |
| SEMA3D | 1.000555 | 1.000007 | 1.001104 | 0.047121 |
| TSLP | 1.003106 | 1.00091 | 1.005307 | 0.005552 |
The association between genes and drugs was also assessed. The results show that MUC4 has a negative relationship with "pelitrexol (Cor = −0.613, p < 0.001)," "epothilone B (Cor = −0.610, p < 0.001)," and "flouxuridine (Cor = −0.438, p < 0.001)." MMP9 has a positive association with "rebimastat (Cor = 0.559, p < 0.001)." MET has a negative connection with "lomustine (Cor = −0.532, p < 0.001)," "fenretinide (Cor = −0.472, p < 0.001)," "ilmexon (Cor = −0.466, p < 0.001)," "carmustine (Cor = −0.464, p < 0.001)," and "XK-469 (Cor = −0.456, p < 0.001)" and a positive relationship with "staurosporine (Cor = 0.491, p < 0.001)" and "kahalide f (Cor = 0.437, p < 0.001)." SEMA3D has a positive connection with "E-7820 (Cor = 0.527, p < 0.001)," "mithramycin (Cor = −0.518, p < 0.001)," and "depsipeptide (Cor = −0.470, p < 0.001)."

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One of the widely studied matrices is "metalloproteinases (MMPs)." MMP-9 is a key protease that is essential for numerous biological processes and can be utilized as a range of cancer biomarkers, according to previous research findings [41, 42]. A possible therapeutic target for several cancers (non-small-cell lung cancer) is the hepatocyte growth factor receptor (MET) (NSCLC). Numerous mechanisms that impact the survival, proliferation, and invasiveness of cancer cells are thought to be involved in the activation of the MET pathway in NSCLC [43]. Being a membrane-bound mucin, MUC4 accelerates the growth of different carcinomas. It is frequently suggested as a "promising biomarker" [44–46]. In pancreatic cancer immunotherapy, MUC4 has become a new tumor antigen. A secreted protein called SEMA3D has been associated with the
Figure 4: Continued.
happening and development of thyroid, pancreatic, and colorectal cancers [47, 48]. Thymus stromal lymphopoietin (TSLP) is a key cytokine for Th2 immunity. It has been proven that TSLP is believed as an important element to keep up immune homeostasis and adjust mucosal barrier inflammation. It plays a key role in inflammatory diseases and cancer [49, 50].

5. Conclusion

The results show the 404 differential genes from the male and female subgroups. In the Venn diagram, 57 intersect genes related to immunity were screened. “Functional enrichment cluster analysis” revealed the potential role of intersecting genes. Through “univariate Cox analysis,”
Figure 5: Continued.
Figure 5: The CIBERSORT to evaluate the composition of 22 immune cells in male patients.
Figure 6: Continued.
multivariate Cox analysis,” and “LASSO analysis,” five prognostic-related genes were identified in the male subgroup. RS was calculated. The findings of “survival analysis” exhibited that high RS was linked to a reduced and poor overall survival \( (p = 0.014) \). The results show that these 5 genes have good predictive power. We evaluated the immune cell scores in the male subgroup through the CIBERSORT algorithm showing that high scores were related to a reduced and poor prognosis \( (p = 0.034) \). We also found that prognostic genes were related to some “immune infiltrating cells.” We have identified 5 immune genes from the TARGET database that has an important relationship with the prognosis of male patients.

Through this research, we provide new approach to assess the function of gender-related immune genes in AML, especially in the male subgroup. In addition, the results may provide us with new prognostic indicators and help in future treatment.

In future work, in this study, we revisited the role of 5 genes in childhood AML, especially in the male subgroup. These results may help the study of AML in children. However, there are some limitations and drawbacks of this...
research. At first, research data mainly comes from the TARGET database. Most patients are Asian or from white race. Therefore, we should be extra cautious when extending the results of the study to patients who do not belong to the above mention races. Second, the consistency of the results of the study to patients who do not belong to the GET database. Most patients are Asian or from white race.

Overall, the role of gender-related immune genes in the prognosis of childhood leukemia is thoroughly investigated.

Data Availability

The datasets analyzed in the current study are available in the TARGET database (https://ocg.cancer.gov/programs/target/data-matrix).

Conflicts of Interest

The author has no conflict of interests.

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References

[1] N. J. Short, M. E. Rytting, and J. E. Cortes, “Acute myeloid leukemia,” Lancet, vol. 392, no. 10147, pp. 593–606, 2018.
[2] R. M. Shallis, R. Wang, A. Davidoff, X. Ma, and A. M. Zeidan, “Epidemiology of acute myeloid leukemia: recent progress and enduring challenges,” Blood Reviews, vol. 36, pp. 70–87, 2019.
[3] E. H. Estey, “Acute myeloid leukemia: 2019 update on risk-stratification and management,” American Journal of Hematology, vol. 93, no. 10, pp. 1267–1291, 2018.
[4] A. J. Martí-Carvajal, V. Anand, I. Sola, and Cochrane Haematological Malignancies Group, “Treatment for disseminated intravascular coagulation in patients with acute and chronic leukemia,” Cochrane Database of Systematic Reviews, vol. 2015, no. 6, article CD008562, 2015.
[5] Z. Fan, K. Xiao, J. Lin, Y. Liao, and X. Huang, "Functionalized DNA enables programming exosomes/vesicles for tumor imaging and therapy," Small, vol. 15, no. 47, article e1903761, 2019.
[6] Y. Liu, J. P. Bewersdorf, M. Stahl, and A. M. Zeidan, “Immunotherapy in acute myeloid leukemia and myelodysplastic syndromes: the dawn of a new era?,” Blood Reviews, vol. 34, pp. 67–83, 2019.
[7] C. DiNardo and C. Lachowiez, “Acute myeloid leukemia: from mutation profiling to treatment decisions,” Current Hematologic Malignancy Reports, vol. 14, no. 5, pp. 386–394, 2019.
[8] L. E. Winestone and R. Aplenc, “Disparities in survival and health outcomes in childhood leukemia,” Current Hematologic Malignancy Reports, vol. 14, no. 3, pp. 179–186, 2019.
apy, memory T cells: new players in immune surveillance and therapy for Immunotherapy of Cancer. Jour-
tory T cells, critical components in tumor immunology, role of CD4+ T cells in CD8+ T cell memory, and therapy through the modulation of the tumor microenvi-
ronment.

[24] https://ocg.cancer.gov/programs/target/data-matrix.

[25] M. E. Ritchie, B. Phipson, D. Wu et al., "limma powers differential expression analyses for RNA-sequencing and microarray studies," Nucleic Acids Research, vol. 43, no. 7, article e47, 2015.

[26] J. Liu, S. Zhou, S. Li et al., "Eleven genes associated with progression and prognosis of endometrial cancer (EC) identified by comprehensive bioinformatics analysis," Cancer Cell International, vol. 19, no. 1, p. 136, 2019.

[27] https://www.immport.org/shared/home.

[28] http://bioinformatics.psb.ugent.be/webtools/Venn/

[29] M. Cao, J. Cai, Y. Yuan et al., "A four-gene signature-derived risk score for glioblastoma: prospects for prognostic and response predictive analyses," Cancer Biology & Medicine, vol. 16, no. 3, pp. 595–605, 2019.

[30] J. Chu, N. Li, and F. Li, "A risk score staging system based on the expression of seven genes predicts the outcome of bladder cancer," Oncology Letters, vol. 16, no. 2, pp. 2091–2096, 2018.

[31] T. Kawaguchi, L. Yan, Q. Qi et al., "Novel microRNA-based risk score identified by integrated analyses to predict metastasis and poor prognosis in breast cancer," Annals of Surgical Oncology, vol. 25, no. 13, pp. 4037–4046, 2018.

[32] A. M. Newman, C. B. Steen, C. L. Liu et al., "Determining cell type abundance and expression from bulk tissues with digital cytometry," Nature Biotechnology, vol. 37, no. 7, pp. 773–782, 2019.

[33] A. M. Newman, C. L. Liu, M. R. Green et al., "Robust enumeration of cell subsets from tissue expression profiles," Nature Methods, vol. 12, no. 5, pp. 453–457, 2015.

[34] S. Narayanan, T. Kawaguchi, L. Yan, X. Peng, Q. Qi, and K. Takabe, "Cytolytic activity score to assess anticancer immunity in colorectal cancer," Annals of Surgical Oncology, vol. 25, no. 8, pp. 2323–2331, 2018.

[35] https://discover.nci.nih.gov/cellminer/loadDownload.do.

[36] A. Ghosh, P. Barba, and M. A. Perales, "Checkpoint inhibitors in AML: are we there yet?," British Journal of Haematology, vol. 188, no. 1, pp. 159–167, 2020.

[37] P. Valenti, I. Sadovnik, G. Eisenwort et al., "Immunotherapy-based targeting and elimination of leukemic stem cells in AML and CML," International Journal of Molecular Sciences, vol. 20, no. 17, p. 4233, 2019.

[38] H. J. Liu, P. H. Lizotte, H. Du et al., "TSC2-deficient tumors have evidence of T cell exhaustion and respond to anti-PD-1/anti-CTLA-4 immunotherapy," JCI Insight, vol. 3, no. 8, article e98674, 2018.

[39] P. Boddu, H. Kantarjian, G. Garcia-Manero, J. Allison, P. Sharma, and N. Daver, "The emerging role of immune checkpoint based approaches in AML and MDS," Leukemia & Lymphoma, vol. 59, no. 4, pp. 790–802, 2018.

[40] M. Noviello, F. Manfredi, E. Ruggiero et al., "Bone marrow central memory and memory stem T-cell exhaustion in AML patients relapsing after HSCT," Nature Communications, vol. 10, no. 1, p. 1065, 2019.

[41] H. Huang, "Matrix metalloproteinase-9 (MMP-9) as a cancer biomarker and MMP-9 biosensors: recent advances," Sensors (Basel), vol. 18, no. 10, p. 3249, 2018.

[42] H. Dong, H. Diao, Y. Zhao et al., "Overexpression of matrix metalloproteinase-9 in breast cancer cell lines remarkably increases the cell malignancy largely via activation of transforming growth factor beta/SMAD signalling," Cell Proliferation, vol. 52, no. 5, article e12633, 2019.

[43] A. Drilon, F. Cappuzzo, S. I. Ou, and D. R. Camidge, "Targeting MET in lung cancer: will expectations be met?," Journal of Thoracic Oncology, vol. 12, no. 1, pp. 15–26, 2017.

[44] N. Jonckheere and I. Van Seuningen, "Integrative analysis of the cancer genome atlas and cancer cell lines encyclopedia large-scale genomic databases: MUC4/MUC16/MUC20 signature is associated with poor survival in human carcinomas," Journal of Translational Medicine, vol. 16, no. 1, p. 259, 2018.

[45] S. K. Gautam, S. Kumar, V. Dam, D. Ghersi, M. Jain, and S. K. Batra, "MUCIN-4 (MUC4) is a novel tumor antigen in pancreatic cancer immunotherapy," Seminars in Immunology, vol. 47, article 101391, 2020.
[46] S. K. Gautam, S. Kumar, A. Cannon et al., “MUC4 mucin- a therapeutic target for pancreatic ductal adenocarcinoma,” Expert Opinion on Therapeutic Targets, vol. 21, no. 7, pp. 657–669, 2017.

[47] N. R. Jurcak, A. A. Rucki, S. Muth et al., “Axon guidance molecules promote perineural invasion and metastasis of orthotopic pancreatic tumors in mice,” Gastroenterology, vol. 157, no. 3, pp. 838–850.e6, 2019.

[48] Z. Wang, M. Ding, N. Qian et al., “Decreased expression of semaphorin 3D is associated with genesis and development in colorectal cancer,” World Journal of Surgical Oncology, vol. 15, no. 1, p. 67, 2017.

[49] J. Corren and S. F. Ziegler, “TSLP: from allergy to cancer,” Nature Immunology, vol. 20, no. 12, pp. 1603–1609, 2019.

[50] S. Li, Z. Yi, M. Deng et al., “TSLP protects against liver I/R injury via activation of the PI3K/Akt pathway,” JCI Insight, vol. 4, no. 22, article e129013, 2019.