



**Methodology Employed for Annual Report on
Hematopoietic Cell Transplant Center-Specific Survival Rates**
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Introduction

The purpose of the annual report on transplant center-specific survival rates is to provide potential hematopoietic cell transplant (HCT) recipients, their families, and the general public with a comparison of survival rates among the centers in the C.W. Bill Young Cell Transplantation Program (CWBYCTP) network. Transplant centers may use these reports for quality improvement initiatives. Reporting center-specific survival rates is a requirement of the TRANSPLANT Act of 2021, previously the Stem Cell Therapeutic and Research Act of 2005 (re-authorized in 2010 and 2015), and prior to that, the 1990 Transplant Amendments Act. Because centers vary considerably in the risk level of cases treated, a statistical model was developed to adjust for several risk factors known or suspected to influence outcome. The outcome reported is one-year overall survival, for recipients of allogeneic HCT in the United States only. No attempts are made to incorporate other outcomes, such as relapse or disease-free survival.

The first center-specific risk-adjusted comparisons were published in 1994¹ and yearly since then. The current iteration of the report prepared by the Center for International Blood and Marrow Transplant Research (CIBMTR) includes recipients of both unrelated and related donor transplants facilitated by the CWBYCTP for a three-year time window. The methodology for this analysis has undergone various transformations over the years. The methodology in current use has been employed since 2005, thus allowing direct comparisons over the most recent time periods. This method adjusts for risk using a censored data logistic regression model²⁻⁴ that allows inclusion of recipients with incomplete one-year follow-up. Note that although the method has remained the same, the types of patients studied changed with the inclusion of related-donor transplants in the 2010 report, which may affect comparisons over time. A risk-adjusted one-year survival rate is calculated for each center, based on results of the censored data logistic regression.

Results are available via the CWBYCTP website (http://bloodcell.transplant.hrsa.gov/research/transplant_data/us_tx_data/index.html), and a version of this report, as approved by the Health Resources and Services Administration (HRSA), is distributed to HCT centers. This information is available online at www.bethematch.org/tcdirectory/search. Raw numbers of transplants and surviving recipients are published for each center, stratified by diagnosis and age. Each center included in the report performed at least one unrelated or related donor transplant over the three-year window of time for analysis.

Methods

Recipients and data

The current analysis includes first unrelated or related donor transplants performed in a three-year time interval, with follow-up through one year after the last recipient was transplanted. The rolling three-year window of transplants for inclusion was adopted with the 2011 report, replacing a rolling five-year window used previously. This change was based on the recommendation of the 2010 Center-Specific Outcomes Analysis Forum⁵. A minimum of one-

year follow-up is required for all eligible cases. All U.S. transplant centers that performed at least one HCT in the time interval are considered for inclusion in the report, provided they had sufficient data with at least one year of follow-up available. Typically, about 180 U.S. transplant centers are included in the analysis, with more than 25,000 first allogeneic transplants performed by domestic transplant centers in the CWBYCTP network during this time. Occasionally, centers with quality problems involving data fields that affect survival modeling recognized during CIBMTR data quality audits are excluded from the analysis.

Demographics of the included cases are provided in tables for recipients of unrelated donor transplants and recipients of related donor transplants, broken down by donor type according to unrelated vs. baseline and follow-up data used for the analysis are provided to the CIBMTR by the transplant centers at the time of transplant (baseline), and at 100 days, six months and annually post-transplant. Race was self-reported by recipients or by the staff at the center.

Risk factors considered

Based on recommendations developed at the Center-Specific Outcomes Analysis Forum⁶, variables recognized as clinically important were forced into the model regardless of whether they were statistically significant. After careful discussion with clinical and statistical transplant experts, the following essential risk factors were included in the model:

- Recipient age
- Recipient race (self-reported)
- Recipient Karnofsky / Lansky Performance Status score at transplant
- Coexisting disease (HCT Comorbidity Index (HCT-CI), Sorrow⁷)
- Low body mass index (BMI) of adults age 18 or older, or low BMI or weight-for-age percentile for age < 18
- Recipient cytomegalovirus (CMV) serology
- History of mechanical ventilation
- History of invasive fungal infection
- Prior autologous transplant
- Diagnosis and disease status / stage
- Acute myeloid leukemia (AML) European LeukemiaNet (ELN) risk group (Döhner et al.⁸)
- AML transformed from myelodysplastic (MDS) / myeloproliferative (MPN) diseases
- Number of induction cycles to achieve latest complete remission (CR) before HCT for AML and acute lymphoblastic leukemia (ALL) patients in CR
- Time from diagnosis to transplant for AML and ALL not in first complete remission (CR1) or primary induction failure (PIF) (used as surrogate for length of CR)
- ALL cytogenetic risk group (Moorman et al.⁹)
- MDS Revised International Prognostic Score (IPSS-R) at HCT (Greenberg et al.¹⁰)
- MDS with predisposing conditions
- Resistant disease in non-Hodgkin lymphoma (NHL) and Hodgkin lymphoma (HL) only
- Plasma cell disorder disease status at HCT
- Year of transplant
- Donor type: matched sibling donor vs. other related vs. unrelated donor

- Human leukocyte antigen (HLA) matching* (Weisdorf et al. ¹¹)
- Recipient and donor sex
- Donor age (for unrelated bone marrow (BM) or peripheral blood stem cells (PBSC) donors only)
- Socioeconomic status (median household income) based on zip code of residence of recipient

In addition, the following variables were believed to be of uncertain clinical relevance, and so they were included in the model only if statistically significant ($p < 0.05$).

- Recipient ethnicity
- Therapy related AML or MDS
- ALL molecular marker - BCR/ABL at any time between diagnosis and HCT
- T-cell lineage in ALL, Philadelphia chromosome in ALL
- Del 17p in chronic lymphoblastic leukemia (CLL)
- NHL subtype
- Multiple myeloma cytogenetics risk group (Palumbo et al. ¹²)
- Multiple myeloma International Staging System (ISS) stage at diagnosis
- Unrelated BM or PBSC donor ethnicity
- Unrelated BM or PBSC donor race
- BM or PBSC donor CMV serology
- BM or PBSC donor parity

Statistical Analysis

Rationale for a fixed effects censored data logistic regression model

One of the CIBMTR's goals for the transplant Center-Specific Survival Analysis is to calculate a fair and accurate predicted survival rate given a center's recipient case mix. To do this, a fixed effects censored data logistic regression model is used. The fixed-effects logistic regression model provides information about how the recipients actually treated in a particular center would have fared had they undergone transplant at a "generic" transplant center within the CWBYCTP. This model assumes *no center effect*. In other words, it assumes that recipients are dying at the same uniform rate across all CWBYCTP transplant centers, after adjusting for covariates. The model also adequately accounts for recipients with incomplete follow-up at one year.

* For PBSC and BM transplants, high-resolution typing at HLA-A, -B, -C, and -DRB1 was used for the cases where it was available. For the remaining patients with PBSC and BM graft sources, the best available matching information at HLA-A, -B, -C, and -DRB1 was used (Weisdorf et al. (Weisdorf D, 2008)). For single UCB transplants, high-resolution typing at HLA-A, -B, -C, and -DRB1 was used for the cases where it was available. For the remaining patients with single UCB graft source, low/intermediate-resolution typing at HLA-A and -B, and high-resolution typing at -DRB1 only were considered. For multiple UCB transplants, low/intermediate-resolution typing at HLA-A and -B, and high-resolution typing at -DRB1 only were considered. The match grade of the worst-matched unit was analyzed.

Every effort is made to update follow-up information on each recipient. Some recipients are indeed lost to follow-up, and their final survival status at one year is unknown. To address this problem, the analysis only includes centers that demonstrated 90% completeness of follow-up, meaning that the one-year status was known for at least 90% of their recipients. However, there are still some recipients for whom survival status at one year is incomplete, although many recipients had follow-up done just prior to one year. If these recipients are excluded from the Center-Specific Survival Analysis, it may bias the survival estimates. A censored data version of logistic regression based on pseudo-values proposed by Andersen et al.², Klein and Andersen³ and Klein et al.⁴ addresses this issue. This method is a generalization of logistic regression that simplifies to logistic regression (on the one-year survival probabilities) when there is no censoring present. This regression technique is used to estimate the fixed effects and predict the recipients' survival probabilities based on their patient characteristics alone. These predicted survival probabilities are then used to construct confidence limits for the probability of survival for all patients at a center, according to the characteristics of the patients who underwent transplant at that center. The actual survival observed at that center can be compared to these intervals to assess the performance of the center. This method is described in more detail below.

Details of fixed effects censored data logistic regression and confidence limits

Modeling for the center-specific survival analysis can be broken down into four steps, as outlined below.

Definition of pseudo-values

To compute the pseudo-value for recipient i , first compute the pooled sample Kaplan-Meier estimate of survival at one year based on the entire sample, $\hat{S}_p(1)$. Next compute the Kaplan-Meier estimate of survival at one year based on the entire dataset with observation i removed $\hat{S}_p^{(i)}(1)$. The i th pseudo-value is defined by $\hat{\theta}_i = n\hat{S}_p(1) - (n-1)\hat{S}_p^{(i)}(1)$.

If there is no censoring, then the i th pseudo-value is simply the indicator that the i th recipient was alive at one year. These pseudo-values will then be used in a regression model using a logit link, similar to a standard logistic regression model, as described in the next section. The parameters of the regression model can be estimated using generalized estimating equations (GEE), which are implemented in PROC GENMOD in SAS.

Predicted and observed survival

From the fitted logistic regression model, each recipient has an estimated survival rate

$$\hat{p}_i = \frac{\exp(\hat{\phi}_i)}{1 + \exp(\hat{\phi}_i)}$$

based on his or her risk characteristics. The predicted survival rate at center j based on recipient characteristics $E(S_j)$ is the average of the estimated survival rates for all recipients at center j ,

$$E(S_j) = \left(\sum_{i \in C_j} \hat{p}_i \right) * \frac{1}{n_j}.$$

The observed one-year survival rate at center j can be computed using the Kaplan-Meier estimate of survival using the recipients at center j . This simplifies to the sample proportion of recipients alive when there is no censoring prior to one year present.

Model building

Let (Z_{i1}, \dots, Z_{ip}) denote the set of covariates in the final model for recipient i . First fit a fixed effects censored data logistic regression model with no center effect,

$$\varphi_i = \ln \frac{\theta_i}{1 - \theta_i} = \beta_0 + \sum_{l=1}^p \beta_l Z_{il} .$$

Confidence Limits

Confidence limits are generated using a bootstrapping methodology. However, the bootstrap technique was modified slightly from previous years’ reports to improve the coverage probabilities of the intervals, as described in Logan et al.¹³ Previously, binary outcomes were generated for each individual to simulate the confidence limits; however, a more accurate prediction interval that controls the type I error rate can be obtained by re-sampling the residuals from the general linear model instead. Define the scaled Pearson residual for patient i by

$$r_i = \frac{\hat{\theta}_i - \hat{p}_i}{\sqrt{\hat{p}_i(1 - \hat{p}_i)}} ,$$

then the bootstrap re-sampling algorithm to generate a prediction interval for center j is as follows. For $b=1$ to 10,000:

1. Generate r_i^{*b} for patient i by sampling with replacement from the set of residuals

$$\{r_i, i = 1, \dots, n\}$$

2. Compute the bootstrap predicted value for patient i as

$$Y_i^{*b} = \hat{p}_i + r_i^{*b} \sqrt{\hat{p}_i(1 - \hat{p}_i)}$$

3. Compute the predicted center outcome for center j as

$$S_j^{*b} = \frac{1}{n_j} \sum_{i \in C_j} Y_i^{*b} .$$

Then the 95% predicted confidence bounds for survival at center j are obtained by taking the 2.5th and 97.5th percentile of S_j^{*b} across the 10,000 bootstrap samples.

This confidence interval refers to the survival rate that might be observed at that center if there were no center effect and those recipients had undergone transplant at any center in the network. The observed survival rate can be compared to this confidence interval to see if there is evidence of the center over-performing or under-performing the overall network.

Handling missing data for risk factors

Occasionally, data are not available for significant characteristics for patients as reported by the centers. If there were sufficient numbers of such patients, they were included in the multivariate modeling as a distinct category of the covariate. However, when the number of

patients with data not available for a variable is too small (generally less than 20 patients) to fit the model as its own category, those patients were imputed to the relevant highest frequency category within the variable for categorical variables, and to the median value for ordinal or numeric variables (e.g., HCT-CI).

Handling the potential impact of the COVID-19 pandemic

The Center-Specific Survival Analysis in 2021 included patients who underwent transplant in 2019 whose post-transplant care may have been affected by COVID. These impacts were tested in the model as described in the 2021 report [Methodology for Report on Center-Specific Survival Rates](#)¹⁴, and after censoring for COVID infections reported to the CIBMTR, did not significantly affect the risk adjustment. However, patients who received HCT in 2020 are included in the 2022 Center-Specific Survival Analysis, and their pre-HCT, transplant and post-HCT experience may have been affected by changes in care related to the pandemic¹⁵⁻¹⁷. Therefore, the CIBMTR performed several updated analyses to explore and potentially address the impacts of the COVID pandemic for HCT recipients in 2019 and 2020. These exploratory analyses were recommended during the [Center Outcomes Forum](#)¹⁸ held on November 12, 2021.

Summary of recommendations for the 2022 Center-Specific Survival Analysis from the Center Outcomes Forum

- Includes first allogeneic HCT recipients Jan. 1, 2018 – Dec. 31, 2020
- The CIBMTR should perform exploratory analyses of potential impact of the COVID pandemic on practice changes and HCT outcomes in the first-year post-HCT
 - Exploratory analyses will focus on patients as the unit of analysis, as opposed to focusing on centers as is done for the final Center-Specific Survival Analysis. The analyses will focus on:
 - Broad impacts during the pandemic, including calendar timing of COVID infection “waves”
 - Differential effects across centers based on local variation reflected in COVID incidence/impact
 - If observed, the CIBMTR should assess whether any differential effects can be adjusted through multivariate analysis.
 - Censoring for COVID infection in the analysis, as performed for the 2021 Center-Specific Survival Analysis, assumes that COVID infection is an independent censoring mechanism. The CIBMTR should further assess this assumption by modeling the likelihood of a COVID infection as a function of baseline and post-HCT patient characteristics, and test the multivariate model results with and without censoring for COVID at the time of infection as reported by centers.
- Results of the exploratory analyses should be used to guide formal approach for the 2022 Center-Specific Survival Analysis

Overview of results from exploratory analyses:

The CIBMTR began collecting additional information from centers related to HCT practice changes implemented during COVID beginning in August 2020 and was collected retrospectively back to March 2020. This information, “COVID-approach variables,” was available and complete for approximately 80% of US HCT centers. Among centers completing the information, it appears at most 30% of patients may have had a different approach to their transplant during 2020. Most of these changes involved changes in the transplant date (30%) and use of a cryopreserved product. The use of a cryopreserved product was required by policy by National Marrow Donor Program (NMDP) for nearly all unrelated donors between mid-March and August of 2020, and thereafter was a choice of transplant centers. This variable was not included in the Center-Specific Survival Analysis because it would not differentially affect HCT outcomes across centers between March and August 2020. Thereafter, use of a cryopreserved product reflects centers’ choices on approach to HCT, much like selection of preparative regimen or GVHD prophylaxis (which are also not included in the model) and will not be included in the risk-adjustment model.

Changes in COVID approach were not reported by centers for approximately 20% of patients, completeness of reporting was not random by center size or region and there was substantial variability in reporting by center. There also appears to be a correlation between geographic COVID incidence and reported impacts of COVID on the HCT approach during the first quarter of the pandemic for those patients for whom data were reported. Because of non-random completeness issues, the COVID-approach variables are not suited for inclusion in the risk adjustment model.

Cox regression modeling using patient, disease, and transplant characteristics from the 2021 analysis to test for factors associated with COVID infection suggest year of HCT, patient age, and incidence of aGVHD are associated with likelihood of developing COVID infection. It is possible that censoring for COVID infection after HCT could introduce bias in the multivariate analysis since centers’ rates of acute GVHD may influence development of COVID infection. Censoring at COVID infection, therefore, could artificially affect overall survival at centers with high GVHD incidence.

Exploratory analyses to assess whether pandemic-related factors (pandemic time period, geographic COVID incidence rate, geographic mortality rate) influence outcomes were tested for HCT recipients in 2019 and 2020. The methodology was similar to that used in the 2021 preliminary analyses, however for patients who underwent transplant in 2020, these factors were tested as time-fixed covariates pre-HCT and time-variable covariates post-HCT in the Cox model. A summary of results follows:

- Time-fixed pandemic-related factors, including history of pre-HCT COVID infection for 2020 recipients were not significantly associated with mortality.
- Time-varying pandemic factors, including calendar time using several different time period cutpoints, were not significantly associated with mortality after HCT for recipients of HCT in 2019 or 2020 **with censoring for post-HCT COVID infection.**

Pandemic-related factors were also tested for interactions with patient time period after HCT (first 100 days, 100 days – 6 months, 6 -12 months), and incidence of acute and chronic GVHD. There were no significant interactions at the level of statistical significance $p < 0.01$.

- To test the impact of censoring, time-fixed pandemic factors and time-varying pandemic factors and interactions were also tested in the same multivariate model **without censoring for post-HCT COVID infection**. None of the time-fixed factors were associated with survival. None of the time-varying pandemic-related factors were associated with survival, and there were no statistically significant interactions at the $P < 0.01$ level in these analyses. There were minor, but not statistically significant differences in the hazard ratios derived from the model with and without censoring for COVID infection after HCT.
- Interactions between COVID incidence rates and calendar time periods for 2020 with 1-year survival were tested to determine whether the impact of variation in COVID incidence on overall survival is limited to certain time periods that may be handled by excluding a time period from the analysis. There was no significant impact of infection rates during any quarter of the pandemic in 2020 **with and without censoring** for COVID infection post-HCT.
- COVID-approach variables available for about 80% of centers were examined to determine whether they significantly affected survival for HCT recipients in 2020 using a time-fixed Cox regression model. Patients for whom the data were not reported were considered unknown. None of the COVID-approach variables was associated with survival.

Application to final Statistical Model

After evaluating the results of these exploratory analyses, a decision was made to use the traditional logistic regression model for the Center-Specific Survival Analysis in 2022 without further COVID-related adjustments and **without censoring** for post-HCT COVID infection for recipients of HCT in 2019 and 2020. While censoring for COVID infection was undertaken in 2021, based on the exploratory analyses performed by the CIBMTR, it is not essential for the 2022 analysis and serves to complicate the analysis without adding value. It could also introduce bias to the results based on incidence of GVHD as a risk factor for COVID infection.

Results

Patient demographics

Demographics of patients are provided in the report, by unrelated vs. related donor.

Risk factors included in final multivariate model

The results of the multivariate model are presented in a set of tables where each variable and its associated odds ratio are described, along with 95% confidence limits. Factors included in the final model are:

- Recipient age
- Recipient race**

- Karnofsky / Lansky score at transplant
- Sorrow HCT-CI
- Adult BMI group
- Pediatric BMI group**
- Recipient CMV status
- History of mechanical ventilation
- History of invasive fungal infection
- Prior autologous transplant**
- Disease and disease status/stage
- AML ELN risk group
- AML transformed from MDS/MPN
- AML therapy related
- Number of induction cycles for AML and in CR1**
- Time from diagnosis to transplant for AML and ALL in CR2 and CR3+/relapse (used as surrogate for length of CR)
- ALL cytogenetic risk group**
- Philadelphia chromosome in ALL patients
- Number of induction cycles for ALL and in CR1**
- MDS IPSS-R risk score at HCT
- MDS with predisposing condition**
- NHL subtype
- Sensitivity to chemotherapy in NHL
- Sensitivity to chemotherapy in HL
- MM ISS stage at diagnosis
- Plasma cell disorder disease status
- Year of transplant
- HLA matching by donor and graft type
- Donor/recipient sex match (bone marrow or PBSC only)
- Donor age (unrelated bone marrow or PBSC donors only)
- Recipient median household income based on zip code

The model is similar to last year, except for the following:

- Censoring for COVID-19 infection was not performed for this year's analysis
- Therapy-related MDS was included in the model this year
- MM ISS stage at diagnosis was not statistically significant and was not included

The Beta_0 intercept term for the model is made available in the formal report.

** Maintained in the model due to clinical relevance but not statistically significant

Center-specific results

Final center-specific results are presented, along with centers' historical performance in tables, and on the public website. Numbers of transplant recipients at each center, actual (observed) survival at one year, predicted survival at one year, 95% confidence intervals for predicted survival, and performance status are displayed for each center. Centers whose actual survival is outside the 95% confidence limits for predicted survival have a “-1” in the performance status column if performing below the confidence limit, and a “1” in the performance status column if performing above the confidence limit. Centers with a “0” in the performance status column are performing as predicted. Most centers performed as predicted with respect to overall performance in previous years. Since the censored data logistic regression model assumes no center effect, centers with smaller numbers of transplants (e.g. N = 1 or 2) will *not* have their predicted survival proportion regress toward the network average. Rather, the confidence limits around the predicted survival at that center will simply be much wider than those of larger centers. Confidence limits for the prediction estimates are generally unreliable for centers whose HCT volume is ≤ 10 patients over the time period. Therefore, interpretation of performance in these centers should be considered with appropriate caution.

Results are also displayed for centers via a visual box-plot graphic. Centers are arranged by center number, while reading from left to right across these figures. The actual survival at each center is superimposed with each box plot (using the symbol ‘•’) to give the reader an instantaneous picture of how close to under- or over-performing the center was.

Patients can find information about all U.S. transplant centers performing allogeneic transplants in the online U.S. Transplant Center Directory on <http://bethematch.org>. Listings are organized by state and can be found at bethematch.org/tcdirectory/search. Along with center outcomes, each listing includes a description of that center's program, contact information, the number of transplants performed over a specified time period and survival statistics by patient's age, disease type and stage for both related and unrelated donor transplants. A link to the Transplant Center Directory can also be found on the Health Resources and Services Administration (HRSA) website <https://bloodstemcell.hrsa.gov/data/donation-and-transplantation-statistics>.

Because the outcome of interest is one-year survival, at least one year of follow-up time is required to be included in the analysis. Data are refreshed once a year. After the report on transplant center-specific survival rates is approved by HRSA, the Transplant Center Directory is repopulated with the new data.

Summary

A fixed effects censored data logistic regression model is fitted to survival data for first unrelated and related donor hematopoietic cell transplants at U.S. centers. The model is adjusted for recipient age, recipient race, Karnofsky/Lansky score, Sorror HCT-CI, adult BMI group, pediatric BMI group, recipient CMV status, history of mechanical ventilation, history of invasive fungal infection, prior autologous transplant, disease/stage, AML ELN risk group, AML

transformed from MDS or MPN, AML therapy related, number of induction cycles for AML in CR1, interval from diagnosis to transplant in ALL and AML in CR2 and CR3+/relapse, ALL cytogenetic risk group, Philadelphia positive-status in ALL, number of induction cycles for ALL in CR1, MDS IPSS-R risk score at HCT, MDS predisposing condition, CLL and other chronic leukemia disease status, NHL subtype, sensitivity to chemotherapy in NHL and HL, MM ISS stage at diagnosis, plasma cell disorder disease status, year of transplant, donor type/graft type/HLA matching, BM or PBSC donor/recipient sex match, unrelated BM or PBSC donor age at transplant, and recipient median household income. The report on transplant center-specific survival rates helps to identify centers that may have under-performed or over-performed compared to the overall network of transplant centers during this specified time period.

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