CDR3 and V- genes show distinct reconstitution patterns in T-cell repertoire post allogenic bone marrow transplantation

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Abstract

Restoration of T-cell repertoire diversity after allogenic bone marrow transplantation (allo-BMT) is crucial for immune recovery. T-cell diversity is produced by rearrangements of germline gene segments (V (D) and J) of the T-cell receptor (TCR) α and β chains. During segment joining, nucleotide inserted and deleted at the junctions between pairs of rearranging genes form the complementarity determining region 3 (CDR3).

We used a new means of comparing multiple T-cell repertoires to follow T cell repertoire changes post allo-BMT in HLA-matched related donor and recipient pairs. Our analyses of the differences between donor and recipient CDR3 beta composition and V-gene profile show that a duality exists between the reconstitution of these two following transplantation; while CDR3 sequences were consistently influenced by recipients' parameters, V genes followed a time-dependent pattern, as they got the donor profile following transplant and then shifted back to the recipients' profile. The final

long term repertoire was more similar to that of the recipient's original one than the donor's; some recipients converged within months while others took multiple years.

Based on the results of our analyses, we propose that donor- recipient V-gene distribution differences may serve as clinical biomarkers for monitoring immune recovery.

1 Introduction

Over the last decades, bone marrow transplantation is being used to treat numerous malignant and non-malignant diseases in which a renovation of hematopoietic stem cells is needed (1–3). Immune reconstitution and regain of function after allogeneic bone marrow transplantation (allo-BMT) relies primarily on homeostatic proliferation of mature T lymphocytes (T-cells) and is slow and complex (1,4–6).

T-cell reconstitution can be influenced by several factors such as patients age, human leukocyte antigen (HLA) mismatches, source of stem cells and the occurrence of graft versus recipient disease (GVHD)(5,7–9).

Complete reconstitution of the T cell compartment after allo-BMT occurs through two distinct pathways: an initial peripheral expansion and a later T cell production by the thymus (10). In the early post-transplant period (soon after transplant ,day +30 or later), adoptively transferred donor T cells or recipient T cells that survive conditioning expand in the periphery (8). In the later post-transplant period naive T cells are produced *de novo* in the recipient's thymus (11). which is seeded by lymphoid progenitors derived directly from the graft or arising from donor hematopoietic stem cells (10).

T-cell receptor (TCR) repertoire formation results from two major procedures: Rearrangements of the TCR α and β chains gene segments (V (D) and J) and formation of the junctions between them (12). A large part of repertoire diversity and its binding to target MHC-peptide are determined by the beta chain (TCRβ) (13). During segment joining, nucleotide are inserted and deleted at the junctions between pairs of rearranging genes (12), forming the highly variable complementarity determining region 3 (CDR3) that is directly implicated in antigen recognition, and further augmenting diversity (12,14).

Repertoire next-generation immune-sequencing (often denoted rep-seq) (15) supplies relatively detailed information on T cell repertoires (16–20) and has been applied to tracking T-cell

reconstitution after allo-BMT (2,3,7,21–23). Current analytical approaches for the comparative analysis of TCR repertoires are mainly based on statistical inference and include repertoire diversity, repertoire overlap, V-gene and J-gene segments usage similarity, and amino acid composition of the CDR3 (24,25). A recent quantitative work on the organization of post allo-BMT repertoire compared donor-recipient TCRβ V-J repertoires by self-similarity mathematical measures and found differences between recipients who had GVHD and those who did not (26).

We here propose a new means of comparing multiple T-cell repertoires. We first characterize each repertoire by either its CDR3 beta or V-gene distribution and then compared these characteristics in all other repertoires.

We used this method to study the changes in post allo-BMT TCRβ repertoire and show how V gene usage and CDR3 sequences composition, although anatomically tied together, when tracked separately, provide information on the co-existence between the donor and recipient immune systems. Our findings suggest that the regenerating repertoire is influenced at different time points by both donor and recipient of the transplant and that this dual contribution promotes the convergence towards the original homeostatic distributions.

Materials and Methods

Subjects and samples

The data used for this study was derived from a prospective clinical study (NCT00809276) by Kanakry et al (1). The dataset is freely available at the Adaptive Biotechnologies database (Seattle, WA; https://clients.adaptivebiotech.com).

TCR repertoires from four pairs of individuals were analyzed; each pair is composed of a donor and a recipient of bone marrow from the same family. In addition, seven patients did not have pre-transplant sequencing data for all time points (TP) post-transplant, so only repertoires from one month and one year post transplant were compared. Donor- recipient pair details are available in Table 1.

All recipients were treated with myeloablative treatment of 40 mg/m^2/day IV Fludarabine plus Busulfan based on real time PKs to achieve a target concentration of 900 ng/mg. IV daily for 4 days prior to transplantation and high-dose post-transplantation cyclophosphamide (PTCy), which effectively reduces graft-versus-host disease, on days 3 and 4 post transplantation as single-agent for

GVHD prophylaxis (27). Donors provided peripheral blood samples on the day of bone marrow harvesting(1).

The analyses focused on TCR β chain sequencing data of peripheral blood mononuclear cells (PBMC) samples taken from the donors and from recipients at time points 0 (transplantation),1, 12 and 36-48 months post transplantation.

CDR3 amino acids sequences and V-gene segments were extracted from the sequencing files after removing out-of-frame sequences. In the V-gene frequency analysis, we ignored all sequences with 'unresolved' V-gene. We did not analyze J genes as they are rather uniform and thus supply very limited information.

We used the processed data by the authors in the original manuscript(1). Similar clones were merged in the original analysis. In the processed data there are practically no clones with equal CDR3 sequences, as can be clearly see by the distance distribution between clones in samples from the different time points (Figure S1).

We randomly picked a sample of 1000 clones per file. One file (037, 1 month post-transplant) does not contain enough data (it contains 767 sequences) so we used it as is.

We here propose a relatively simple means of comparing multiple T-cell repertoires. We utilize a 1.000 randomly picked sequences from each repertoire. While T-cell repertoires are theoretically huge, in practice they have an order of 1.e6-1.e7 clones. Moreover, our sampled repertoires represent mainly the larger clones, which are typically between 1,000 and 10,000 clones in the vast majority of samples. Indeed, we used 1,000 clones that constitute a big fraction of the total number of clones (See **figure 2S** for the total number of clones in each sample).

Method of analysis

We analyzed two aspects of the TCR repertoire: CDR3 beta sequences and V-gene distribution. Analyses flow chart is illustrated in Figure 2.

To find the level of similarity (referred to here as 'distance') in CDR3 composition between samples , we calculated for each CDR3 sequence in every sample its distance from all sampled CDR3 sequences in another sample and found its nearest neighbor (i.e. the sequence in the other sample

with the lowest edit distance). We then computed the average edit distance of these closest neighbors. We then created an optimal distance matrix of CDR3 sequence distances between samples with Edit Distance (Levenshtein distance) (28).

Levenshtein distance is a means to compare one sequence of letters to another (CDR3 being represented as letters sequences). Levenshtein distance represents the number of insertions, deletions, and substitutions required to change one word to another (29). We here used Levenshtein distance to compare CDR3 sequences and determine their level of similarity.

The edit distance (Levenshtein distance) between two samples S_1 and S_2 (S is CDR3 sequence) was determined as the average of all minimum values per row in M, where M is a 1000x1000 distance matrix of the edit distances of all CDR3 sequences in both samples.

When computing the self-distance, which is the distance between S and S, the diagonal values (edit distances between the same sequences, all zeros) were ignored.

When analyzing V, the V-gene distributions of each sample were first found by a previously used methodology (30,31). Generally, some V genes are highly used, such as V02-01,V05-01 and V19-01, while others are very rarely used (32). These very frequent V genes are often not distinctive as they bias the computation of the absolute distance between V gene usages and often mask the signal distinguishing between individuals and time points along T cell reconstruction. To avoid this bias, we employed a symmetrized version of the Kullback- Leibler (KL) divergence (D(p,q)+D(q,p))(33) (equation 1); KL measures the difference between two V genes probability distributions, where KL of 0 indicates that the two distributions are identical. To avoid zero occurrences of V-segments, we have used a pseudo-count of 1.e-4. Although the pseudo count affects the KL, it has a very limited effect on the difference between distances (See figure S3 in supplementary for multiple random comparisons between pairs of samples using different constants).

$$1.\quad \boldsymbol{D(p||q) = \sum_{x \in X} p(x) log \frac{p(x)}{q(x)}}$$

Where p and q are the two probability distributions and x is one value out of a set of possibilities X. In addition, we measured the distance between two V distributions with Euclidian distance (Equation 2).

2. $$\boldsymbol{D(p||q)} = \sqrt{\sum_{\boldsymbol{x}} (\boldsymbol{p(x)} - \boldsymbol{q(x)})^{\boldsymbol{2}}}$$

The second step was to visualize the similarity between samples and find clusters of similar samples. A multidimensional scaling (MDS) algorithm was used; MDS is a form of non-linear dimensionality reduction used to display the information contained in a distance matrix.

In our case, the matrix contains the distances between each pair of CDR3 sequences (derived from the calculation of the ED), or the distances between each two V genes probability distributions (derived from the calculation of the KL given in equation number 1).

The MDS algorithm places the distances into a multi-dimensional space such that the between-object distances are preserved as well as possible (34). We chose to use three dimensions, so the algorithm produced three-dimensional scatter plots of the resulting points, with each point representing a sample.

All analyses were performed in Python language, version 3.6. The edit distance between two sequences was calculated using 'jellyfish.levenshtein_distance' package, Euclidean distance between two V distributions was calculated with package 'numpy.linalg.norm' and MDS was calculated with 'sklearn.manifold.MDS' package.

Statistical analyses were performed in Python language, version 3.6. The difference between the four groups in our analysis (detailed below) was tested using ANOVA ('scipy.stats.f_oneway' package). If the ANOVA was significant, we performed the paired student's t-tests to compare the two groups d ('scipy.stats.ttest_ind' package). A Benjamini Hochberg False Discovery Rate correction(35) was performed for multiple comparisons with three comparisons in figure 2C and six comparisons in 3A.

We compared four groups of samples pairs:

- The baseline group composed of all recipients (R) immediately post-transplant. All samples are at the same time point (TP). Intra-sample distance is 0 here per definition but is required as baseline for the following analyses. The group is referred to as (TP+R+).

- A group composed of pairs of different recipients whose repertoires are compared at the same time point (TP+R-).
- A group composed of the repertoires from the same recipient at different time points (TP-R+).
- A group composed of pairs of different recipients whose repertoires are compared at different time points (TP-R-).

An ANOVA test was performed with all groups and also after excluding the first group of 'same time point, same recipient' due to the low mean. Then, student's t-tests were performed between all group pairs in order to find significantly different groups.

Clustering of samples was performed with Hierarchical cluster analysis (HCA) (https://link.springer.com/article/10.1007/BF02289588) on the KL and ED distances matrixes ('scipy.cluster.hierarchy.linkage' and 'scipy.cluster.hierarchy.dendogram' packages). HCA is a method which builds a hierarchy of clusters in a greedy manner.

Regression model

The relationship between the edit distance and its components can be described by an equation:

Distance (recipient1 at TP1, recipient2 at TP2) = Distance (recipient1, recipient2) + Distance (TP1, TP2) + noise

To understand how the edit distance between the samples (left side of the equation) is influenced by the distance between individuals and by the time point (right side of the equation), we performed regression analysis with Python package 'scipy.optimize.nnls' which computes non negative least squares. The analyses determined how the edit distance changes when one of the independent variables, i.e., distance between each pair of individuals or time points is varied, while the other independent variable is held fixed.

Results

V usages among samples:

V usage analysis is the main element that is conserved and evolving in the post-transplant dynamics. To properly compare the V usage, the same number of clones in each sample should be used. We have here estimated the distribution with a 1,000 clone sample (Figure S5 shows a validation that this sample is large enough).

To account for the bias in V-gene usage over the entire repertoire (explained in the methods section), the Kullback Leibler (KL) (33) distance was used. We applied this measure that computes the expected value of the log of the V-gene usage to all sample pairs (Fig 2B).

The samples showed a clear division into two groups, each showing intra-group similarity but distinct from the other group, as demonstrated in the dendrogram and distance heatmap (Fig. 2A and 2B) and in the distance distribution (Figure 2C) (t-test p-value< 1.e-10). The similarity within a group of samples of the same time point was much lower than the similarity within recipients, as can be seen in Figure 2A.

The multi-dimensional scaling (MDS) analysis illustrates sample clusters in a three-dimensional space (maintaining the distances as in Fig 2B). We can see that each group contains different shapes (each shape depicts one individual) of the same color (each time point has its own color) and deduct that the groups are defined by time point and not by recipient (Figure 2D).

As shown in Figure 2F, donors and pre-transplant recipients are the most distant (i.e. non similar). One-month post-transplant the repertoire in most samples and all CMV-negative recipients but one is very similar to the donors and different from the pre-transplant (Figure 2E). In all other samples two distinct groups can be observed, which are both equally distant from the donor and the recipient, but far from the first group of one-month post-transplant. However, all groups slowly converge after either one or four years toward a new distinct repertoire which is more similar to the original recipient's than to the donor's (Fig. 2F, p-value< 0.05 for all pairwise time point comparisons and for ANOVA on all time points). The results are consistent for each patient separately (Fig S6). We did not observe any effect of GVHD on the evolution of V-gene repertoire. We performed a similar analysis using the regular Euclidean distance between repertoires, which yielded similar but less

distinctive results, suggesting that the KL distance is indeed a better measure for V-gene similarity (Figure S7 A and B).

CDR3 composition among samples: The CDR3 distance distribution follows the recipients' repertoire much more closely than the V-gene distribution Specifically, the similarity between the CDR3 of samples from the same recipient is higher than between CDR3 from different recipients at the same time point (both are more similar than CDR3 sequences from different recipients and different time points) (t-test<0.001), as can be seen in Figure 3A and 3B.

To test whether the distance in CDR3 composition was derived from difference between recipients or from the time points along reconstitution, we separated the distance between samples (See Methods) into positive components based on the differences between recipients and components determined by the time points. The distance between recipients is by one order larger than the distance between the time points (Figure 3C-3G). When comparing recipients, most have similar distances between each other, except for recipient 022 (Figure 3C, 3D), who shows a unique combination of positive CMV status, acute and chronic GVHD and a very low TCR count. In summary, repertoires at all post transplants time points are similar to each other, while both donor and recipient pre-transplants repertoires are farther away (as shown in Figure 3E and illustrated by the density of the post-transplant clusters as opposed to the dispersity of the pre-transplant cluster in Figure 3F). This is in accordance with Kanakry et al.(1)

The development of the repertoire is often defined using clone size distributions and estimates on the repertoire diversity based on such distributions. Although clone size distributions help in estimating the immune potential of the regenerating repertoire, such measures are sensitive to sampling depth. Furthermore, the clone size distribution does not measure the difference between clones. To address that, we define the "diversity" of samples as the average distance of each clone to the most similar clone in the same sample. A short distance implies clones are close to one other, while a large distance implies that clones are uniformly distributed and not in proximal groups.

One can clearly see that the main feature of the developing CDR3 repertoire is not a shift from the donor to the recipient (since there was no large difference to start with), but rather a change in the CDR3 diversity (Figure 3H), which drastically decreases following transplant, and then converges back to the pre-transplant level.

Discussion

We here propose a relatively simple means of comparing multiple T-cell repertoires. Characterizing each post allo-BMT TCRβ repertoire by either its CDR3 beta or V-gene distribution showed that V-gene and CDR3 sequences compositions, when tracked separately, can provide information on the co-existence between the donor and recipient immune systems.

We found a clear difference between the reconstitution patterns of V genes and CDR3 beta sequences in the re-forming repertoires: V genes followed a time- dependent pattern; following transplant they shifted from the recipient to the donor profile and then back to the recipient's profile. CDR3 beta sequences, on the other hand, remained in line with the recipient's profile.

We propose that these different reconstitution patterns reflect the two pathways of T-cell regeneration that act at different time points post transplantation: The initial peripheral thymic-independent pathway (5,7,8) expands mostly the CD8+ memory T cells from the mature donor graft, which have previously encountered pathogens and are less dependent upon recognition of self MHC–peptide complexes for survival (5–8**).** In our analysis CDR3 diversity decreased at this stage, in accordance with the fact that the initial wave of recovery leads to a shrinkage and skewing of the TCR repertoire (10).

Interestingly, a dominance of pre-transplant CDR3 beta sequences was apparent. This finding is confusing, since, given that recipients had myeloablative conditioning, it is unlikely that residual recipient T cells had survived. We propose that this dominance of pre-transplant CDR3 beta sequences may result from recipient-derived selection applied in the course of peripheral expansion in response to viral antigens, with cytomegalovirus (CMV) being a known driving force in V gene usage for CMV+ patients (36), whereas non-CMV positive recipients likely respond to other viral antigens which may be recognized by similar T cells in the donor that would have existed in the recipient.
Duration of this transitional pathway varies significantly among recipients.

In the second stage, which may take between less than a year and a few years, a thymic-dependent pathway is activated in the majority of patients(5,7), in which naïve T cells from progenitors of donor origin are increasingly produced *de novo* in the recipient thymus (5,7,8,37,38).

Recovery through the thymic-dependent pathway accounts for the durable and clonally diverse reconstitution of the T-cell compartment (8,10). The timing of this process probably accounts for our observation that one year post-transplant, V-gene segments in most samples and all CMV-negative recipients but one formed two distinct groups which were both equally distant from the donor and the recipient, but far from the group of one month post-transplant.

V-gene composition differed significantly between pre-transplant recipients and their donors, probably because both disease conditions and treatments had affected the recipients' repertoires. We suggest that the shift of V-genes from patient to donor profile one year post transplant reflects the thymic *de novo* production of naïve T cells from *donor origin* in the six to twelfth months post transplantation. This has also been suggested by Meier et al.(2019) (26).

Timely reconstitution and regain of function of a donor-derived immune system is of utmost importance for the recovery and long-term survival of patients after allogeneic hematopoietic stem cell transplantation. In fact, the slow T cell reconstitution(6,8) is regarded as the primary cause for deleterious infections, occurrence of graft-versus-recipient disease and relapse (9,39). It takes weeks to months to produce naive T cells from infused stem cells and a plateau level of thymic output is reached only after at 1 to 2 years post transplantation (11), rebuilding only completed after 2 to 3 years (11). We show that the transfer back to a repertoire similar to the pre-transplant one has different rates: in some patients the convergence back is fast while in others it is quite slow. Donors and pre-transplant recipients' repertoires were the most distant. This is in accordance with the findings of Buhler et al.,(2019)(40), who studied a large cohort of 116 full chimeric recipients and their respective HSC donors pre- transplant and at 1 year post-transplant. The recipients' repertoire one year post transplant was very different from the donors', with only a few overlaps. This finding led them to suggest that a new repertoire can be reconstituted at any age through thymic dependent or independent pathways(40).

As has been previously shown(26), the final long-term repertoire was more similar to that of the patient's original one than the donor's. We suggest a graphic illustration of the repertoires' reconstitution that is based on the results of our analyses, as shown in Figure 2E: One-month post transplantation, some recipients' repertoires share similarities with the donors and some are more similar to their own pre-transplant repertoires. After only one year, most repertoires from the slower-rate group become more similar to before-transplant repertoires. Then, in the 3-4-year group all recipients are closer to their pre-transplant repertoires than to their donor's repertoire.

With recent advances in hematopoietic cell transplants, immune-monitoring is of major importance to identify patients at risk and provide them with early immune interventions(9). For instance, patients with low TCR diversity are at risk for hematopoietic cell transplantation-related complications such as GVHD and could benefit from adjuvant immunotherapies, such as low-dose IL-2, administration of regulatory T cells, or leukemia/virus-specific dendritic cells and/or other specific T cells(9).

If our hypothesis is confirmed by larger-scale studies, then V-gene reconstitution, and especially the distribution of rare V genes, can serve as a biomarker for the thymic-independent regeneration pathway. As V-gene segment usage profiling is a relatively simple procedure that is widely used and can be performed with limited sampling depth (41–43), we propose that testing the evolution of the V gene usage in recipients can serve as simple functional measure of immune recovery that may guide clinicians in monitoring immune recovery post allo-BMT transplant.

Figures

Figure 1

A flow chart of the analyses performed in this study.

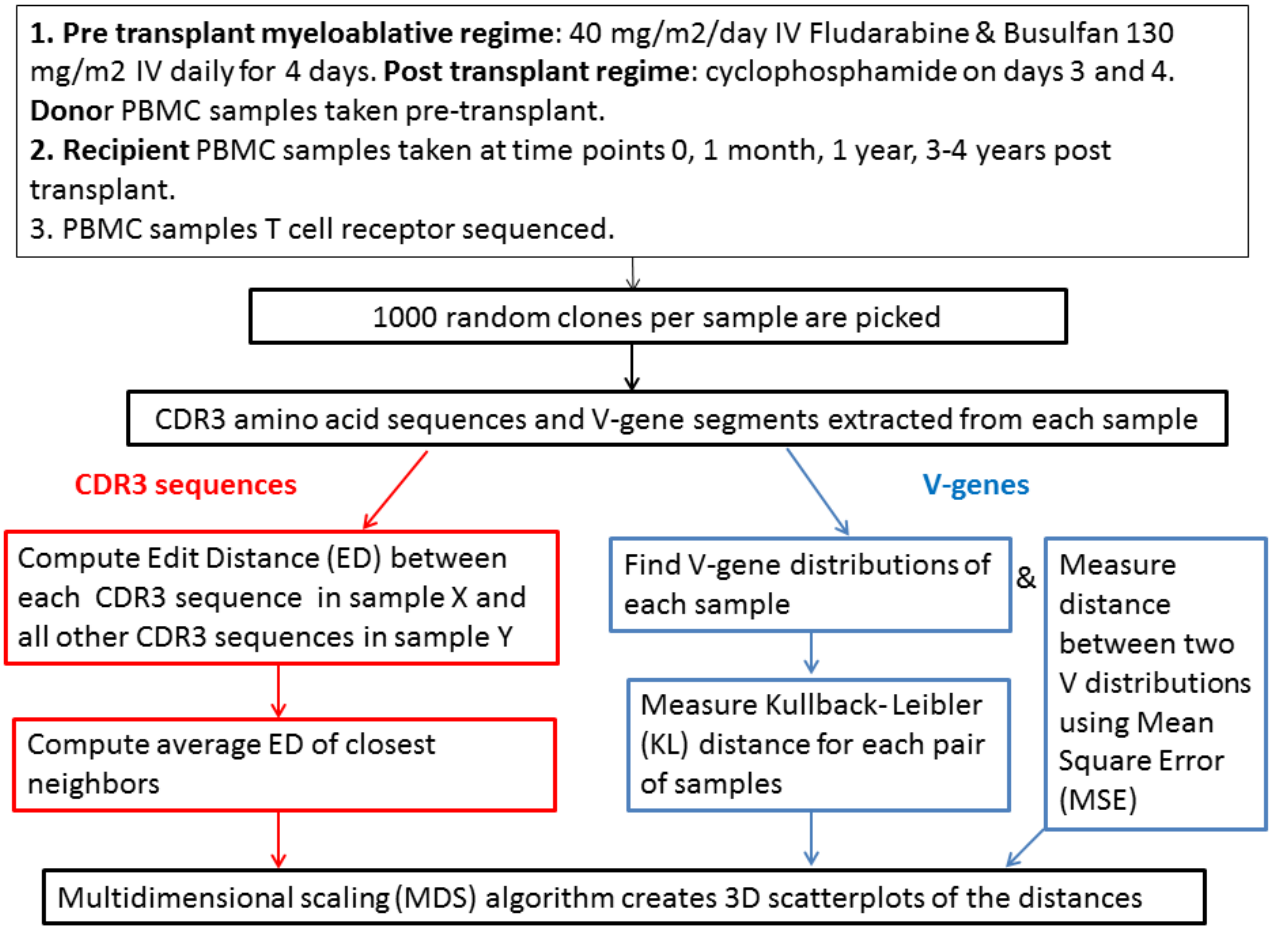


Figure 2

A. V-gene Hierarchical clustering. The KL distances between samples were clustered with 'single' method. The first half of the labels indicates one of the five states: Donors (D), Pre-transplant (P), 1-month post (1M), 1-year post (1Y) and 3-4 years post-transplant (4Y). The second half of the labels indicates the ID of the recipient. Labels are colored according to TPs.

B. KL distance calculations were tested on uniform samples of 1000. In the KL V-gene distribution heatmap each cube represents the KL result from two distributions of V-gene usage. Blue indicates smaller KL values, i.e., closer samples. Samples are positioned by the order of the dendrogram leaves from 2A.

C. A swarm plot (i.e., a categorical scatterplot) of KL distances from 2B, grouped into 4 categories: 'same TP, same recipient' (time point= TP) (Blue), 'same TP, different recipient' (Green), 'different TP, same recipient' (Red) and 'different TP, different recipient' (Purple). Each point represents a sample. The t-test's p-value is indicated by * (p-value < 0.05).

D. A multi-dimensional scaling analysis projected the samples into a three-dimensional space, (maintaining the distances as in Fig 2B), with each point representing a sample. The analysis shows that the groups are defined by time point and not by recipient (Figure 2D). Different time points are shown in different colors and different sample IDs are indicated by a variety of shapes. We can see that each group contains different individuals from the same time point.

E. A graphic illustration of the repertoires' reconstitution: One-month post transplantation, some recipients' repertoires share similarities with the donors and some are more similar to their own pre-transplant repertoires. After only one year, most repertoires from the slower-rate group become more similar to before-transplant repertoires. Then, in the 3-4-year group all recipients are closer to their pre-transplant repertoires than to their donor's repertoire.

F. KL distances of four recipients (011, 037, 016, 019) from their original pre-transplant repertoires and from their donors' repertoires as a function of time. Recipients' curves are in red, donors' are in green.

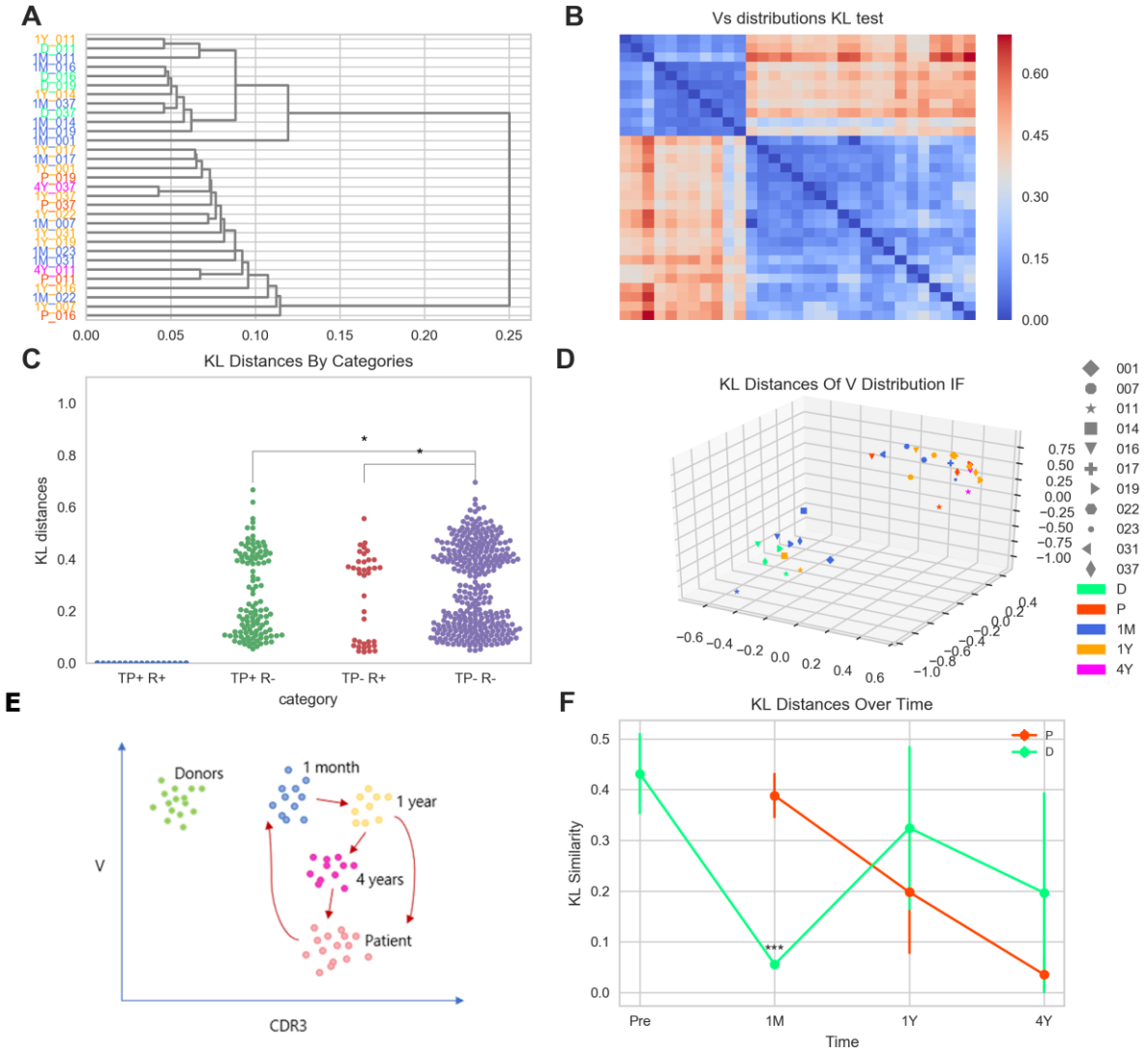

A
B
Vs distributions KL test
C
KL Distances By Categories
KL distances
TP+ R+
TP+ R-
TP- R+
TP- R-
category
D
KL Distances Of V Distribution IF
001
007
011
014
016
017
019
022
023
031
037
D
P
1M
1Y
4Y
E
Donors
1 month
1 year
4 years
Patient
V
CDR3
F
KL Distances Over Time
KL Similarity
Pre
1M
1Y
4Y
Time

Figure 3

The main feature of the developing CDR3 repertoire is not a shift from the donor to the recipient (since there was no large difference to start with), but rather a change in CDR3 diversity (i.e., distances between clones).

A. CDR3 Edit Distance by categories. Swarm plot of ED distances from 2B, grouped into 4 categories: 'same time point' (time point = TP), 'same recipient' (Blue), 'same TP, different recipient' (Green), 'different TP, same recipient' (Red) and 'different TP, different recipient' (Purple).

B. MDS of the ED distance matrix; each point represents a sample. Different IDs are shown in different colors and different timeline states are indicated with five shapes.

C. Regression values heatmap of all recipients' distances. Recipients are ordered by Figure 3D leaves.

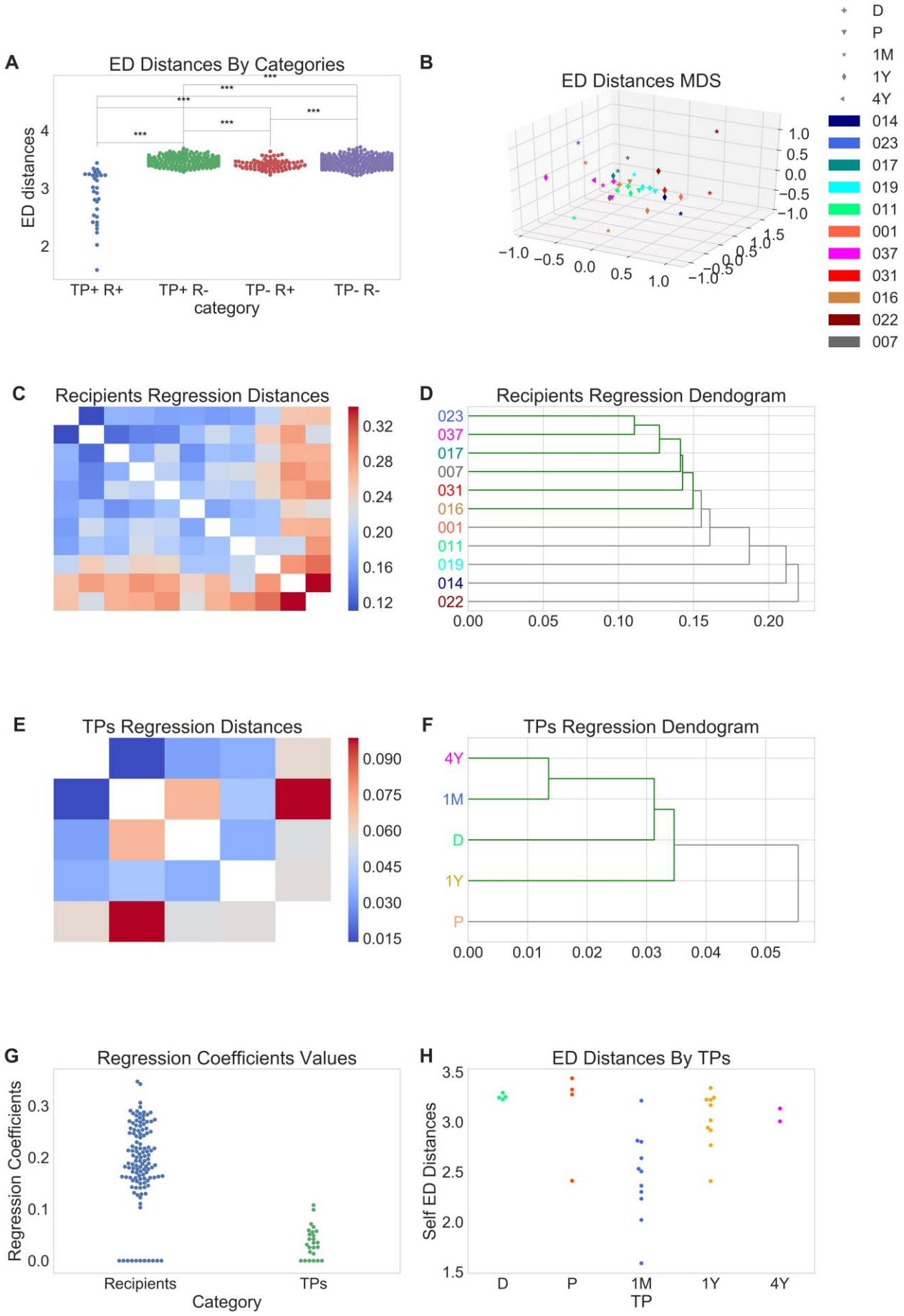
D. Dendrogram of the values from Figure 3C. Labels colors match those of the IDs from Figure 3B.

E. Regression values heatmap of all time-points distances. Time points are ordered by Figure 3F leaves.

F. Dendrogram of the values from Figure 3E. Labels colors match those of time points from Figure 2D.

G. Swarm plot shows the regression distances from C and E of the recipients and time points. Each point in the swarm plot represents a sample. When comparing the time points, repertoires at all post transplants time points are similar to each other, while both donor and recipient pre-transplants repertoires are farther away, as illustrated by the density of the post-transplant clusters as opposed to the dispersity of the pre-transplant cluster.

H. Swarm plot of self ED distances by time points, colors match those of time points from F. Each point in the swarm plot represents a sample.


A
ED Distances By Categories
ED distances
category
TP+ R+
TP+ R-
TP- R+
TP- R-
B
ED Distances MDS
D
P
1M
1Y
4Y
014
023
017
019
011
001
037
031
016
022
007
C
Recipients Regression Distances
D
Recipients Regression Dendogram
E
TPs Regression Distances
F
TPs Regression Dendogram
G
Regression Coefficients Values
Regression Coefficients
Recipients
TPs
Category
H
ED Distances By TPs
Self ED Distances
TP

Tables

Table: Donor- recipient pairs. The table lists each recipient with his/her donor. For seven recipients no donor repertoire was available. The numbers in the time point columns show the number of sequences in each file.

Donor	Recipient	Additional details	Donors	Pre-transplant	1 month post transplant	1 year post transplant	3-4 years post transplant
002-011, male, 38 years	002-011, female, 46 years	CMV+, no GVHD	57072	54627	2785	15633	16530
002-037, female, 35 years	002-037, male, 38 years	CMV+, acute GVHD only	50271	4614	767	3255	11120
002-016, female, 67 years	002-016, female, 62 years	CMV+, no GVHD	46170	40681	2919	7117	
002-019, female, 44 years	002-019, female, 33 years	CMV+, no GVHD	19556	85156	1343	19940	
002-001, male, 41 years	002-001, female, 29 years	CMV+, Acute and chronic GVHD			4226	27835	
002-007, male, 59 years	002-007, female, 60 years	GVHD Status: Acute GVHD			4914	7788	
002-014, female, 54 years	002-014, female, 59 years	No GVHD			4087	12064	
No details on donor	002-017, male, 58 years	Acute GVHD only			6895	11913	
No details on donor	002-022, female, 45 years	Acute and chronic GVHD			1942	14185	
002-023, male, 54 years	002-023, female, 58 years	No GVHD			4391		
002-031, male, 52 years	002-031, female, 57 years	Acute GVHD only			3592	15709	

Conflict of Interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

2 Author Contributions

3 SD designed the formalism and implemented it.

4 NTM collected the data and wrote the manuscript.

5 AR and AAK collected the data and prepared it.

6 YL supervised the work and wrote the manuscript.

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8 Supplementary Material

Supplementary Material is uploaded separately.

Data Availability Statement

The dataset analyzed in this study can be found in the Adaptive Biotechnologies database (Seattle, WA; https://clients.adaptivebiotech.com).