IDENTIFICATION OF DPB1-TCE GROUP IN UNRELATED DONORS AND PATIENTS IS LIKELY

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INTRODUCTION

HLA-DPB1 permissive matching based on T cell epitope (TCE) groups should be considered when selecting among equally matched HLA-A, -B, -C, -DRB1, -DQB1 unrelated hematopoietic stem cell donors to improve patient survival. Previous studies have defined 3 TCE groups based on functional assays of alloreactivity. Combinations of donor and recipient DPB1 alleles with low immunogenic potential identify permissive donors, who provide no increased risk of mortality compared with DPB1–matched donors. Although there are biological differences between transplantation with DPB1 allele matches and permissive mismatches, selection of either is preferentially recommended above a nonpermissive DPB1–mismatched URD.

OBJECTIVE

The aim of our study was to determine the likelihood of identifying a DPB1 permissive–matched URD for patients with 10/10 high-resolution–matched URDs in the Brazilian Bone Marrow Donor Registry.

MATERIAL AND METHODS

Patient and Donor DPB1 alleles were classified into 3 TCE groups based on functional distance scores of DPB1 alleles: group 1 (high), 2 (intermediate), or 3 (low) immunogenic potential from the newest classification method [7, 15]. The patient TCE group was assigned based on the most immunogenic TCE group of the 2 alleles (ie, group 1 > 2 > 3).

RESULTS

We identified 50 DPB1 alleles among the 2.623 donors typed for this locus and 42 alleles among the 1.062 patients in a total of 717 DPB1 alleles described to date. DPB1*04:01 is the most frequent allele in both donor and patient databases with 1.562 copies (29.78%) and 579 copies (27.26%), respectively. Table 1 shows how TCE groups are represented in each database.

	Donors database (REDOME)				Patients database (REREME)			
	Nº of alleles	%	Nº of copies	%	Nº of alleles	%	Nº of copies	%
Group 1	5	10,42%	361	6,88%	5	13,16%	151	7,12%
Group 2	11	22,92%	686	13,08%	9	23,68%	292	13,76%
Group 3	32	66,67%	4.197	80,03%	24	63,16%	1679	79,12%

CONCLUSION

The high amount of recombination in this “hot spot” results in weak linkage disequilibrium between the DP genes and the remainder of the class II loci; therefore, it is difficult to predict unrelated donor (URD) DPB1 through association with specific DR and DQ alleles or with MHC haplotypes. TCE groups based on functional assays of alloreactivity play an importante role on selecting donors and once we could identify mainly the TCE groups involved, we can develop a predective tool for those donors/patients pairs that are not DPB1 typed thus enabling to save time and resources.

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