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INTRODUCTION

Transplantation of allogeneic hematopoietic stem cells (HSC) is increasingly performed in patients with high-risk leukemia or inherited disorders. For patients lacking a genotypically HLA-matched sibling, an unrelated HSC transplantation can be proposed. Estimates of HLA-A, -B, -DRB1 haplotype frequencies have provided valuable information in calculating the chances of finding unrelated donor

OBJECTIVE

The aim of the present study was to investigate HLA haplotypes among Brazilian patients in an unrelated HSCT program (REREME).

MATERIAL AND METHODS

13.572 individuals were analyzed at 2-digit level only by sequence-specific oligonucleotide and sequence-based typing methods. Haplotype frequencies values were calculated by the maximum likelihood method utilizing Arlequin 3.5v software.

RESULTS

The most frequent haplotypes in REREME are A*01-B*08-DRB1*03 with 1.8%, A*29-B*44-DRB1*07 with 1.3% and A*03-B*07-DRB1*15 with 1.1%. Figure 1 shows the top-10 haplotypes in REREME. These 10 haplotypes comprise only 2.595 patients or 19% of the total analyzed. The HLA-A, -B and -DRB1 loci had high observed heterozygosity values: 87.4%, 92.6% and 88.2%, respectively.

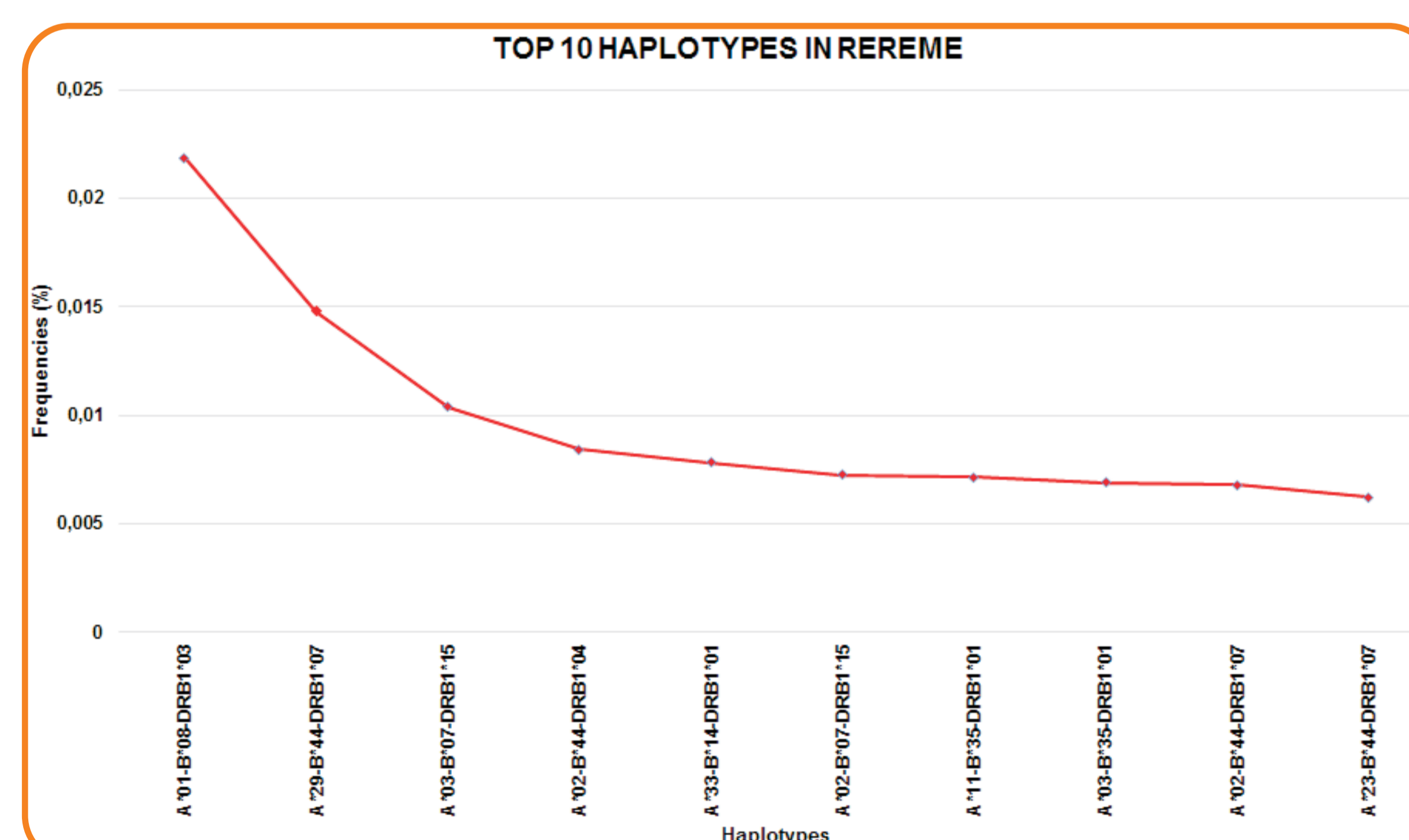


Fig1. Haplotype distribution in REREME. The curve tends to amalgamate beyond that point.

CONCLUSION

These data are important for phylogenetic, comparative and medico-legal studies and are of particular value in estimating the likelihood of obtaining appropriately matched donors for Brazilian patients awaiting bone marrow transplantation.

Keywords: rereme, transplantation, hla, haplotype, recipients