Identifying the Degree of Major Histocompatibility Complex Matching in Genetically Unrelated Dogs With the Use of Microsatellite Markers


Abstract:

Background. The dog has served as an important experimental model for biomedical research such as transplantation and developing immunosuppressive agents. Although major histocompatibility complex (MHC) in dogs is a dominant factor of graft rejection, it has not been well investigated in dogs compared with human. For that reason, imprecise cross-matching or time-consuming sequence-based typing methods have generally been used to choose specific donor and recipient pairs. Investigation of matching distribution of MHC in dogs with the use of simple and accurate methods would be beneficial for biomedical researchers. The aim of this study was to identify the diversity of dog leukocyte antigen (DLA) types in genetically unrelated dogs by means of microsatellite markers. Methods. Thirty-three Beagle and Shih-Tzu dogs, which were negative in cross-matching, were chosen. The genomic DNA was isolated from peripheral blood leukocytes, and highly polymorphic short tandem repeats located in MHC class I and II were amplified with the use of specific primers. Results. Among all of the dogs, MHC matching groups, including class I full matched class II full matched (M-M), class I full matched class II haplo matched (M-H), class I haplo matched class II full matched (H-M), class I haplo matched class II haplo matched (H-H) groups, were 1.55%, 0.39%, 1.94%, and 6.59%, respectively. MHC class I nonmatched class II nonmatched (U-U) groups were 58.14% of the total dogs. Conclusions. Because differences of histocompatibility between donor and recipient leads to various allograft rejections, knowledge of the distribution of MHC matching in unrelated dogs would be helpful in designing studies and to get more accurate results from experiments using dog transplantation models.

Keywords:

Major Histocompatibility Complex Microsatellite Markers

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