Eplet: A unique comrade with the finest expression in transplantation immunology

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Abstract

Over the past two decades, organ transplantation procedures have become a potential milestone in the field of modern medicine. Even though physiological barriers and technical limitations exist in the process of organ transplantation, the therapeutic breakthroughs happened during the recent years has made this process a historic achievement. Human Leucocyte Antigen (HLA) has been known for its complexity as well as its identity in becoming a protein fingerprint. The lack of a healthy matching donor is one of the major problems faced during renal transplantation. Till this time, the question of what causes graft rejection still possesses a multifaceted answer which leaves the clinicians confused. In general, allo-graft transplantation causes strong immune reaction between a donor and the recipient as both the individuals possess sequentially different HLA.

Identification of a single molecular target between such protein complexes like HLA and T Cell Receptor (TCR) could be a breakthrough in transplantation immunology. Use of high-throughput molecular simulation techniques or a highly established protein docking binary systems might be of great use for clinicians as this can lead to reduction in the use of administration of immunosuppressants. The traditional procedures incorporates direct complement depended cell cytotoxicity crossmatching (CDC-cxm) and HLA Typing which still possess its significance in transplantation medicine. Our aim relies on another perspective which targets Eplets. Eplets are those amino acid triplet confirmations which are spatially adjacent but linearly discontinuous.

Epitope and Eplet matching has been a great part globally. The analysis of eplet matching after pinpointing the HLA ID of both donor and recipient are performed molecularly as well as computationally. Therefore targeting the identification and matching of each eplets between unrelated individuals may open new avenues in modern medicinal research. Analysis and calculation of antibody–verified eplets can be used to predict the outcome of less matched allo-graft transplants. The method of protein-protein docking can be also implemented to identify the hotspots in HLA which might cause such strong immune reactions.