Clonal expansion is a characteristic feature of the B-cell repertoire of patients with rheumatoid arthritis

ABSTRACT

The aim of this study was to determine the extent of B-cell clonal diversity in patients with rheumatoid arthritis, using HCDR3 as a marker. They also used PCR techniques to identify and differentiate between numerically expanded and un-expanded B cells using genomic DNA or complementary (c)DNA from peripheral blood and synovial fluid, which allowed for the identification of various autoimmune reaction vectors. These results support the idea that cellular genetic information may be relevant in understanding the causes of immune responses in inflammatory markers like reder

INTRODUCTION

Introduction Clonal expansion is a common feature of the B-cell repertoire, whose repertoire of 854 distinct T-cell subtypes is divided into 3 main sub-categories:

i) B-cell subtypes with a specific repertoire of T-cell subtypes, which are the most abundant sub-categories of B-cells in the patient, and

ii) B-cell subtypes without a specific repertoire of T-cell subtypes, which are the most abundant sub-categories of B-cells in the patient.

Clonal expansion is also referred to as "clonal amplification" or "clonal acquisition" in the literature. However, in a recent study, it was shown that the term "clonal expansion" is misleading Support for T-cell involvement in rheumatoid arthritis includes the description of limited subsets of T cells in the blood and synovial tissue that either express or exclude certain surface membrane proteins or a limited repertoire of antigen receptors: For example, clonal recombination alterations of CD8+ CD57+ T cell repertoire are frequently observed in patients with RA; expanded cytoplasmic copies of tick (CD4+) CD28- T Cells in their rat host tissues and these cells show that these mice showed markedly low but high density receptor Unlike the detailed investigations into the clonal distribution of T cells in rheumatoid arthritis, there is limited information about the extent to which B-cell diversity is present in this disease. However, previous studies indicate that the repertoire of B cells is also restricted. Examples include flow cytometry analysis of circulating B cell types, cell culture experiments, and evidence suggesting that immunoglobulins of restricted heterogeneity are secreted spontaneously by synovial tissue explants. Contemporary molecular analyses of immunopeptidin genes expressed by B This is important because, at B- and T-cell levels, an ongoing immune response occurs that is directed at restricted sets of (auto)antigens. To this end, we reformulated the immunoglobulin VH gene fingerprinting method using the length of the third complementarity determining region (CDR3) to study the level of clonal diversity in human RA cells; thus, our data points are more likely to indicate that B–cell expansion is a common feature of advanced rheumatoid arthritis, both the patient host host

CONCLUSION

The data suggest that clonal expansion is a frequent occurrence in the B-cell repertoire of patients with rheumatoid arthritis. This process involves both resting memory B cells and activated B cell types, some of which are

derived from the memory (and thus may not be directly affected) as well as developing locally due to alterations in their local tissue composition. Recent research has revealed that the synovial tissue of rheumatoid arthritis patients can develop lymphoidic aggregates that contain the cellular components of an ectopic germinal center and can support B-cell clonal expansion and diversification. It is likely that these B cells, which mature in these 'pseudogerminal centers' and those that we have identified in our current studies, are responding to specific (auto)antigens. Therefore, the identification of antigenic reactivations of these active B cell