The IgE repertoire in PBMCs of atopic patients is characterized by individual rearrangements without variable region of the heavy immunoglobulin chain bias.

BACKGROUND: Patients with atopic diseases are characterized by high levels of specific IgE production. However, little is known about the composition of their B-cell repertoires. OBJECTIVES: We sought to analyze the complete PBMC-derived IgE repertoire and to compare clonal expansions between different patients. METHODS: We have analyzed the IgE-bearing B-cell receptor repertoire in highly atopic patients (>1000 IU/mL) using quantitative RT-PCR, complementarity determining region 3 spectratyping, and sequence analysis. Three representative patients were additionally followed during anti-IgE therapy. RESULTS: Atopic patients exhibited 100 to 1000 times more IgE-specific transcripts than control individuals. These patients used a variable region of the heavy immunoglobulin chain (VH) epsilon repertoire highly similar to their IgM and IgG repertoires, with preference of VH3b, VH4, VH3a, and VH1 segments. Each patient harbored individual clonal expansions, most probably as correlation of allergen-specific IgE production. Common expansions within the complementary determining region 3 shared by several individuals with similar sensitization patterns were found in spectratyping analysis. However, these antigen-driven expansions showed differences on the sequence level. In
omalizumab-treated patients the clinical improvement was paralleled by a clear increase in the ratio of IgG/IgE transcripts. CONCLUSION: The IgE repertoire in atopic patients follows the VH use patterns seen for other immunoglobulins and seems to preferentially recruit individual rearrangements rather than public expansions. CLINICAL IMPLICATIONS: The detailed analysis of the IgE B-cell repertoire is highly suitable to follow changes in IgE uses during different therapy modalities.