세미나 초록

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발표 주제	Deciphering Human B cell Receptor Repertoires: What Have We Learned?
발표 내용	B cells recognize antigens via membrane-expressed B-cell receptors (BCR). BCR is the hetero-tetrameric complex of heavy and light chain polypeptides and the heavy chain plays major role in antigen binding. With the combination of IGHV, IGHD and IGHJ genes, the heavy chain can achieve the theoretical complexity of 1 X 10E12. A high-throughput genomic analysis of BCR heavy chain likewise estimated a complexity of 3.5 X 10E11. Meanwhile, the number of B cells in humans does not exceed 1 X 10E11 and the number of B cell clone defined by unique BCR sequence is even smaller. Therefore, individual human-beings are destined to harbor only a fraction of theoretically achievable BCR repertoire. The mechanism shaping the BCR repertoire in each person is yet to be clarified but would be influenced by environmental factors like microbiome and infectious agents. In accordance with this assumption, humans share common BCR clonotypes with much higher frequency than mathematically calculated. Furthermore, stereotypic BCR clonotypes are commonly found in COVID-19, Sjogren's syndrome, rheumatoid arthritis and Alzheimer's disease patients. We believe that BCR repertoire analysis and finding stereotypical BCR clonotype signature related to human pathology have diagnostic potential. And disease-modifying BCR clonotypes have a potential to be developed as therapeutic measures.